





# PhreePlot

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## Creating graphical output with PHREEQC

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<http://www.phreeplot.org>

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# Table of contents

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<b>1</b>	<b>INTRODUCTION .....</b>	<b>1</b>
1.1	What does PhreePlot do?.....	1
1.2	What PhreePlot does not do.....	2
1.3	What you need to know before using PhreePlot .....	3
1.4	Navigating this document .....	3
<b>2</b>	<b>INSTALLATION.....</b>	<b>5</b>
2.1	Installing PhreePlot.....	5
2.1.1	Windows .....	5
2.1.2	Linux and Mac OS X .....	7
2.2	Checking for updates .....	7
2.3	Changing the console appearance.....	7
2.4	Installing Ghostscript and GSview .....	8
2.4.1	Launching PhreePlot from Windows Explorer or similar .....	8
2.4.2	Specifying the input file name on the command line .....	8
2.4.3	Specifying input and output filenames in PhreePlot input files .....	8
2.4.4	Setting the PhreePlot environment variable .....	9
2.4.5	Adding the path to PhreePlot to the Windows PATH setting .....	9
2.4.6	Search path for files .....	9
2.4.7	Ensuring that the correct databases are found .....	9
2.5	Other useful software .....	10
2.6	Trouble-shooting .....	11
	File conversions .....	11
	Problem and bug reporting.....	11
<b>3</b>	<b>GETTING STARTED.....</b>	<b>13</b>
3.1	The command line interface and batch processing .....	13
3.2	Running the demo examples .....	13
3.3	The 'pp.log' file.....	14
3.4	Examining the results of the run.....	15
3.5	Making a working directory .....	15
3.6	Getting familiar with the options .....	16
3.7	Using batch files to run a set of runs.....	16
3.8	Stopping a run .....	16
<b>4</b>	<b>PHREEQC BASICS .....</b>	<b>17</b>
4.1	Online PHREEQC documentation .....	17
4.2	How PHREEQC interacts with PhreePlot.....	17
4.3	Thermodynamic databases .....	18
4.4	Types of output produced by PHREEQC.....	19
4.5	The <code>SELECTED_OUTPUT</code> and the <code>USER_PUNCH</code> data blocks.....	19
4.5.1	The <code>SELECTED_OUTPUT</code> filename and forcing the file to be written .....	20

4.5.2	Scope of PHREEQC keywords .....	21
4.5.3	What is sent to the <code>SELECTED_OUTPUT</code> file? .....	22
4.6	Setting up the <code>SELECTED_OUTPUT</code> file for input to PhreePlot .....	22
4.6.1	Possibilities for looping of PHREEQC input files .....	22
	Predominance plots .....	23
	Data-led calculations.....	24
	Custom plots .....	25
	Knowing which minerals might form using the given database .....	27
4.6.2	Setting up the loop iterator .....	28
4.7	Running PHREEQC without any plotting.....	29
4.8	Include files .....	29
4.8.1	Use of 'include' files .....	29
4.8.2	Supplied include files .....	30
4.9	Using PHREEQC's <code>_RAW</code> and <code>_MODIFY</code> keywords.....	30
<b>5</b>	<b>PHREEPLOT INPUT AND OUTPUT FILES .....</b>	<b>33</b>
5.1	Input/output files .....	33
5.1.1	Use .....	33
5.1.2	Difference in execution of input files between PhreePlot and PHREEQC	
33		
5.2	Input files .....	34
5.2.1	Different types of input file .....	34
5.2.2	Structure of the main input files .....	35
5.2.3	The input file pre-processor .....	36
5.2.4	The colour dictionaries and other files .....	36
5.2.5	Format of all input files .....	36
	Physical and logical lines.....	36
	Specifying keyword-value pairs and keyword-lists .....	37
	Format of keywords and their associated values.....	38
5.2.6	Data separators and parsing input files .....	38
5.2.7	Case sensitivity of input .....	39
5.2.8	Reporting of errors in input files .....	39
5.3	Tags.....	39
5.3.1	What are tags used for? .....	39
5.3.2	Rules for choosing tag names .....	40
5.3.3	Tag expressions .....	40
5.3.4	Numeric tag expressions and available functions .....	40
5.3.5	Tags for character variables .....	41
5.3.6	System tags .....	41
5.3.7	User-defined tags .....	42
5.3.8	The scope of tags, their initial values and their order of evaluation .....	43
5.3.9	Examples of the use of tags .....	45
5.4	Output files .....	46
5.4.1	Output files produced .....	46
5.4.2	The logical switches .....	48
5.4.3	'log' file ( <code>log</code> ) .....	48
5.4.4	'out' file ( <code>out</code> ) .....	48
5.4.5	'track' file ( <code>trk</code> ) .....	50
5.4.6	'points' file ( <code>pts</code> ) .....	50
	Predominance plot calculations (ht1 only).....	50
	Other calculations.....	50

5.4.7	'vectors' file ( <code>vec</code> ) .....	50
5.4.8	'polygon' file ( <code>pol</code> ) .....	51
5.4.9	'labels' file ( <code>labelFile</code> ) .....	52
5.4.10	Other output files .....	52
5.4.11	Redirecting the output files .....	53
5.5	Inserting plot files into Microsoft Word, Powerpoint and other software .	53
5.6	Speed of computations and plotting.....	54
<b>6</b>	<b>RUNNING PHREEPLOT .....</b>	<b>57</b>
6.1	Conventions for data input .....	57
6.1.1	Types of variables .....	57
6.1.2	PHREEQC notation for chemical formulae .....	57
6.2	PhreePlot Looping .....	58
6.2.1	Loop variables and their use .....	58
6.2.2	Looping over a list of character variables .....	59
6.2.3	An example of the use of various looping mechanisms .....	59
	Using the <code>&lt;x_axis&gt;</code> tag.....	59
	Using the <code>&lt;loop&gt;</code> tag .....	60
	Using a loop file .....	61
	Using the 'simulate' calculationMethod.....	61
	Looping over two variables .....	62
6.2.4	Looping in multi-simulation input files - pre-loop simulations and the main loop	63
	Introduction.....	63
	Basic structure of a multi-simulation PHREEQC input file .....	64
6.2.5	Dynamic switching between PHREEQC models (code) .....	65
6.2.6	Defining the expected output in the selected output file .....	66
6.2.7	Timing execution .....	66
6.2.8	Speeding-up calculations .....	67
6.3	Possible types of calculations and plots.....	67
6.4	Preparing the SELECTED OUTPUT file.....	68
6.4.1	Normal behaviour .....	68
6.4.2	The use of the 'headings' identifier .....	68
	Controlling the plotting of individual columns.....	70
	Use of labels in a custom plot and the minimum text size.....	70
6.5	Debugging .....	71
6.5.1	Types of problem .....	71
6.5.2	Checking the return status of a <b>PHREEQC</b> run .....	72
6.5.3	General approach to debugging .....	72
6.5.4	Using the <code>debug</code> keyword .....	73
6.5.5	The most common reason for a failure to converge .....	74
6.5.6	Changing PHREEQC's convergence parameters .....	76
6.6	Interrupting execution and changing keyword values .....	77
6.7	Running the standard PHREEQC examples .....	77
6.7.1	Going round for just one iteration .....	78
6.8	Return status and exit codes .....	78
<b>7</b>	<b>PLOTTING BASICS.....</b>	<b>79</b>
7.1	Introduction.....	79
7.2	Types of plot.....	79
7.3	Summary of basic plotting.....	80

7.3.1	Introduction .....	80
7.3.2	Setting up the plotting area .....	80
7.3.3	The colour palette .....	80
7.3.4	Automatic or explicit colours .....	81
7.3.5	Setting up the axes scales, tick marks and grid lines .....	81
7.3.6	Axis numbering and annotation .....	82
7.3.7	Adding fills, lines and points .....	82
7.4	Controlling the style of lines and points (symbols) in Custom plots.....	83
7.4.1	The default style and colour for lines and points (symbols) .....	83
7.4.2	Lines .....	84
	Line styles .....	84
	Automatic colouring of lines and points.....	84
7.4.3	Points (symbols) .....	85
7.4.4	Order of plotting of lines and points (symbols) .....	86
7.5	Labelling plots .....	86
7.5.1	Label names and label position .....	86
7.5.2	Overriding calculated label positions and angles .....	87
7.5.3	Legend .....	88
7.6	Inputting text strings .....	88
7.6.1	Available fonts and character sizes .....	88
7.6.2	Available characters and inserting 'special' characters .....	89
7.6.3	Text enhancements (bold, italic, subscript, superscript) and Greek characters	90
7.6.4	Accented and other 'foreign' characters - the Latin-1 encoding .....	91
7.6.5	Non-printing characters .....	92
7.6.6	Justification .....	93
7.6.7	Angle .....	93
7.6.8	Tags in text strings .....	93
7.7	Special PhreePlot variables or tags.....	93
7.7.1	Available tags .....	93
7.7.2	System pH, system pe and system temperature .....	93
7.8	Axis scaling.....	93
7.8.1	Auto or user-defined axis scaling .....	93
7.8.2	Secondary y axis (the 2y axis) .....	94
7.9	Controlling the properties of text, symbols, polygon fills and lines .....	94
7.9.1	Principles .....	94
7.9.2	The colour dictionaries .....	96
	Fill colours.....	96
	Line colours and auto line colouring.....	96
	Point colours.....	98
	Filled symbols with a different rim colour.....	98
7.9.3	Directories for the colour dictionaries .....	98
7.10	Labelling.....	98
7.10.1	Predominance plots .....	99
7.10.2	Contour plots .....	100
7.10.3	Custom plots .....	100
7.11	Replotting without recalculating.....	101
7.11.1	The 'replot' option .....	101
7.11.2	The 'reprocess and replot' option for predominance plots .....	102
7.12	Adding extra lines, symbols and text.....	102
7.12.1	Lines and symbols .....	102

7.12.2	Text .....	103
	<input> .....	104
	<loop> or <loop...> .....	105
	<legend> .....	105
	<mainspecies> .....	106
7.12.3	Formatting numbers in plots – varying the number of significant figures displayed	106
7.12.4	Making fancy plots .....	106
<b>8</b>	<b>PREDOMINANCE PLOTS .....</b>	<b>109</b>
8.1	setting up a file to calculate a predominance diagram .....	109
8.1.1	The ‘water limits’ .....	109
8.1.2	The ‘grid’ and ‘ht1’ approaches .....	110
	Grid approach .....	110
	‘Hunt and track’ approach.....	111
8.1.3	Using the <code>ht1.inc</code> code to return the dominant species .....	112
8.1.4	Problems with the ‘hunt and track’ approach – failure and ‘unclosed polygons’	113
8.1.5	Polygon label is outside of the polygon .....	114
8.1.6	Optimising the calculation efficiency .....	114
8.1.7	Predominance vs mineral stability diagrams .....	114
8.1.8	Using <code>ht1minerals.inc</code> to determine the minerals present .....	114
8.2	The ‘grid’ approach.....	115
8.3	The ‘Hunt and track’ approach .....	116
8.3.1	Strategy .....	116
8.3.2	Details of the ‘hunt and track’ algorithm .....	116
	Applying the concepts of hunting and tracking at the practical level	116
	Definitions of ‘predominance’ and mineral stability .....	118
8.3.3	Failure of the ‘hunt and track’ approach .....	119
8.4	Feasible domains and the preparation of Eh (pe) -pH diagrams.....	119
8.4.1	General principles .....	119
8.4.2	Domain tags - avoiding speciation calculations .....	121
8.4.3	Speciation failure when there is not enough reactant present .....	121
8.5	Choice of the resolution of the plot.....	122
8.6	Monitoring the progress of a ‘hunt and track’ run.....	122
8.7	Plotting and Replotting.....	123
8.8	Modifying the appearance of predominance plots .....	123
8.9	Adding lines and points to a predominance plot.....	124
8.10	Controlling the labelling of plots and the plotting of fields.....	125
8.11	Why do I not see methane gas when using <code>11n1.dat</code> ?.....	127
8.12	Failure to complete a predominance diagram .....	127
<b>9</b>	<b>CONTOUR PLOTS.....</b>	<b>129</b>
9.1	What are contour plots? .....	129
9.2	Implementation .....	129
9.2.1	Generating the contour data .....	129
9.2.2	Choosing the contour levels .....	130
9.2.3	Types of contour plot .....	130
9.2.4	Changing the appearance of the contour lines. ....	131
9.2.5	Colouring the plot .....	131
9.2.6	Labels and Legend .....	132

9.2.7	Flow of data .....	132
9.2.8	What if PHREEQC fails? .....	132
9.3	A simple example.....	133
9.4	Some details of the data processing .....	135
9.4.1	Algorithm .....	135
9.4.2	Problematic cases .....	136
9.5	Modifying the appearance of the plot .....	137
9.6	Refining a plot – replotting without recalculating.....	139
9.6.1	Where to start? .....	139
9.6.2	Smoothing the z-data .....	140
9.7	Overlapping or misplaced label.....	140
9.8	What happens if <b>PHREEQC</b> fails during contouring calculations? .....	140
<b>10</b>	<b>CUSTOM PLOTS .....</b>	<b>141</b>
10.1	Overview .....	141
10.2	Preparation of the input file.....	141
10.2.1	Introduction .....	141
10.2.2	Controlling the scope of custom plots .....	142
10.3	Simple looping .....	142
10.4	Calculating speciation on a 2-D grid .....	143
10.5	Modifying the appearance of custom plots.....	143
10.5.1	Overview .....	143
10.5.2	Customising the plot .....	144
<b>11</b>	<b>SPECIES PLOTS .....</b>	<b>147</b>
11.1	What is special about a ‘species’ plot?.....	147
11.2	Modifying the appearance of species plots.....	149
11.3	Adding other variables to a species plot.....	149
<b>12</b>	<b>FITTING AND SIMULATIONS.....</b>	<b>151</b>
12.1	Introduction and Choice of Algorithms.....	151
12.2	Fitting is special .....	152
12.3	Approach to fitting .....	152
12.4	Practical Setup .....	153
12.4.1	Approach .....	153
12.4.2	Flow of data and information during fitting .....	155
12.4.3	The parameters .....	156
12.4.4	Variables .....	158
12.4.5	Passing the fitted values from PHREEQC to PhreePlot: preparing the input file	158
One pass to generate a single data value .....	158	
One pass to generate all data values.....	159	
Skipping unwanted PHREEQC selected output.....	159	
Global optimization - switching models.....	159	
12.4.6	Data file .....	161
12.5	The optimization routines .....	162
12.5.1	The objective function .....	162
12.5.2	Choice of fit algorithm .....	162
12.5.3	Scaling of parameters .....	163
12.5.4	Constrained optimization .....	163
12.5.5	Control parameters .....	163

Finite difference step size ('nlls' only) .....	165
Convergence criterion .....	165
Step size.....	165
Maximum iterations .....	165
Weighting method .....	165
12.6 Preparing an input file.....	166
12.6.1 Simple example .....	166
12.6.2 Automatic updating of parameter values in an input file .....	167
12.7 Interrupting or stopping the fitting .....	167
12.8 Forcing relations between parameter values .....	167
12.9 Standard errors of fitted parameter values and the correlation matrix .....	167
12.10 Multi-objective fitting .....	168
12.11 Output files.....	168
12.12 Response in the event of a failure of PHREEQC to converge.....	168
12.13 Plotting the results of the fitting.....	169
12.13.1 Plots of observed and calculated results .....	169
12.13.2 Contour plot of the residual sum of squares .....	170
12.14 Simulations .....	171
12.15 Root finding – solving equations, adding constraints.....	171
<b>13 THE INPUT FILE PRE-PROCESSOR.....</b>	<b>175</b>
13.1 Use of the pre-processor .....	175
<b>14 KEYWORDS .....</b>	<b>177</b>
14.1 Summary of available keywords.....	177
14.2 Conventions.....	180
14.3 Keyword description .....	181
all.....	181
axisLineColor.....	181
axisLineWidth .....	182
axisNumberColor .....	182
axisNumberFormat .....	182
axisNumberSize .....	183
axisTitleColor .....	183
axisTitleSize .....	183
backgroundColor.....	183
beep .....	184
blockRangeColumn .....	184
calculationMethod .....	185
calculationType .....	186
changeColor .....	186
characterTags .....	187
checkForUpdate.....	188
colorModel .....	189
contourDashesPerInch.....	189
contourFillColor.....	190
contourLabelColor.....	190
contourLabelFigs .....	191
contourLabelFont .....	191
contourLabelSize.....	191
contourLineColor .....	192

contourLineType.....	192
contourLineWidth .....	192
contourOptions.....	193
contours .....	194
contourShiftLabel.....	195
contourZvariable .....	197
convertLabels .....	198
customLoopManyPlots.....	198
customXcolumn .....	199
dashesPerInch, dashesPerInch2y.....	199
database.....	200
databaseVersion.....	200
dataFile .....	200
dataSeparators .....	201
dateDatabase .....	204
debug .....	204
dependentVariableColumnObs .....	205
dependentVariableColumnCalc.....	206
domain .....	206
dominant .....	207
eps.....	207
extradat .....	208
extraSymbolsLines.....	209
extraText .....	211
fillColorDictionary.....	211
FIT.....	212
fitAdjustableParameters .....	212
fitConvergenceCriterion.....	212
fitFiniteDiffStepSize.....	213
fitLogParameters .....	213
fitLowerParameterValues.....	214
fitMaxIterations.....	214
fitMethod.....	215
fitnpt.....	215
fitParameterNames .....	216
fitParameterValues .....	216
fitStepSize .....	216
fitUpperParameterValues .....	217
fitWeightingMethod .....	217
font .....	218
gridColor.....	220
gridDashesPerInch .....	221
gridLines .....	221
gridLineType.....	221
info .....	222
initialValue.....	223
jobTitle .....	223
jpg.....	223
labelColor.....	224
labelEffort .....	224
labelFile.....	225

labels.....	226
labelSize .....	227
legendBox .....	227
legendTextColor .....	228
legendTextSize .....	228
legendTitle.....	228
lineColor, lineColor2y .....	229
lineColorDictionary .....	229
lines, lines2y .....	230
lineType, lineType2y .....	230
lineWidth, lineWidth2y.....	231
log.....	231
logDepVariable .....	232
logVariableIn .....	232
loopFile.....	233
loopIndexStartNumber .....	235
loopInt.....	235
loopLogVar.....	236
loopMax .....	236
loopMin.....	236
loopVal .....	237
mainLoop .....	237
mainLoopColumn .....	238
mainspecies .....	239
minimumAreaForLabeling.....	240
minimumYValueForPlotting .....	240
missingValue.....	241
multipageFile .....	241
nameSpeciationProgram .....	242
nudge.....	242
nudgeFile .....	244
numberOfFitParameters .....	244
numericTags .....	245
objectiveFunction .....	246
omitAccumulate.....	246
onePass .....	246
out .....	247
overlay .....	248
pageOrientation .....	250
paperSize.....	250
pdf.....	251
pdfMaker.....	252
PHREEQC.out .....	253
PLOT .....	253
plotFactor .....	253
plotFrequency .....	254
plotOrder.....	254
plotTitle.....	254
plotTitleColor.....	255
plotTitleSize .....	255
png .....	255

pointColor, pointColor2y .....	256
points, points2y.....	257
pointsSameColor.....	257
pointSize, pointSize2y .....	257
pointType, pointType2y .....	258
pol.....	258
post .....	259
postSize .....	260
pplog.....	260
prefix.....	261
printScreenFrequency.....	261
ps .....	262
pts .....	262
pxdec.....	262
pxmajor.....	263
pxmax .....	263
pxmin.....	263
pxminor .....	263
pydec, p2ydec.....	264
pymajor, p2ymajor .....	264
pymax, p2ymax .....	264
pymin, p2ymin.....	265
pyminor, p2yminor .....	265
resolution .....	265
restartColorSequence.....	267
rimColor .....	267
rimFactor .....	268
screen .....	268
selectedOutputFile .....	269
selectedOutputLines.....	269
simplify .....	270
skip .....	271
SPECIATION .....	271
speciationProgram .....	272
speciationProgramVersion .....	272
startTemperature.....	272
stopOnFail .....	272
svg.....	273
symbolsLines .....	274
text.....	275
tickColor.....	277
tickSize.....	278
trackSymbolColor .....	279
trackSymbolSize .....	280
trk .....	280
units .....	281
unrecognisedKeywordIsFatal .....	281
updateFitParameters.....	282
useLabelsFile .....	282
useLineColorDictionary .....	282
vec.....	283

weightColumn .....	283
writeAllInputFiles .....	283
writePlaceholder .....	284
xaxisLength .....	284
xmax .....	284
xmin .....	285
xoffset .....	285
xtitle .....	285
yaxisLength .....	286
ymax .....	286
ymin .....	286
yoffset .....	287
yscale .....	287
ytitle, 2ytitle.....	288
<b>15 EXAMPLES.....</b>	<b>289</b>
Predominance plots (grid approach).....	290
1 Fe-H <sub>2</sub> O (grid approach) .....	292
2 Cu-S-C ('island' found with 'grid') .....	296
Predominance plots (ht1 approach) .....	299
3 Fe-H <sub>2</sub> O ('Hunt and track' approach) .....	300
4 Fe-H <sub>2</sub> O: close-up (predominance criterion) .....	302
5 Fe-H <sub>2</sub> O: close-up (stability criterion) .....	304
6 Fe-H <sub>2</sub> O (pe scale).....	306
7 Fe-H <sub>2</sub> O (Eh scale) .....	308
8 As-O <sub>2</sub> (g)-H <sub>2</sub> O.....	310
9 As-O <sub>2</sub> (g)-H <sub>2</sub> O (sub-dominant) .....	312
10 Fe-As-C-S.....	314
11 Fe-As .....	318
12 Fe-As-Hfo (ht1.inc) .....	320
13 Fe-As-Hfo (ht1c.inc) .....	322
14 Fe-S-As (without sorption) .....	324
15 Fe-S-As (low Fe, without surface speciation).....	328
16 Fe-S-As (goethite, CD-MUSIC) .....	332
17 Fe-As-S (high Fe).....	336
18 Fe-CO <sub>2</sub> -SO <sub>4</sub> -H <sub>2</sub> O with sample points .....	340
19 Fe-Ni-S .....	344
20 Fe-Zn-C-H <sub>2</sub> O (HFO).....	348
21 Fe-Zn-C-H <sub>2</sub> O (HFO).....	352
22 Ca-Fe-Na-X-HFO (adsorption and ion exchange).....	356
23 Acid mine drainage.....	360
24 AMD (carbon) .....	364
25 Ca-Mg-Zn-CO <sub>3</sub> .....	368
26 U-CO <sub>3</sub> .....	372
27 Ca-Mg-CO <sub>3</sub> at high T.....	374
28 P-Ca-Mg-CO <sub>3</sub> (aq).....	376
29 P-Ca-Mg-CO <sub>3</sub> (with solids) .....	378
30 Mn-CO <sub>2</sub> -H <sub>2</sub> O (no minerals).....	382
31 Mn-H <sub>2</sub> O (with minerals) .....	384
32 Mn-CO <sub>2</sub> -H <sub>2</sub> O .....	386
33 Pu-F-H <sub>2</sub> O .....	388
34 U-C-H <sub>2</sub> O (wateq4f.dat) .....	390
35 U-C-H <sub>2</sub> O (NAPSI) .....	392

36	U-C-H <sub>2</sub> O (llnl.dat).....	394
37	U-Fe-C-H <sub>2</sub> O .....	398
38	U-Fe-C (risk colours).....	402
39	U-H <sub>2</sub> O (redox state) .....	406
40	U-F-P (U).....	408
41	U-F-P (F).....	412
42	U-F-P (P).....	414
43	Cu-S-C ('island' not found with 'ht1') .....	416
44	Cu-S-C (simplification factor = 1) .....	418
45	Cu-S-C (simplification factor = 3) .....	422
46	Cu-EDTA-H <sub>2</sub> O .....	426
47	Ca-F-P-C-H <sub>2</sub> O.....	430
48	Ni-S-C-H <sub>2</sub> O.....	432
49	Zn-S-C-H <sub>2</sub> O .....	436
50	Cd-S-C-H <sub>2</sub> O .....	440
51	Pb-S-C-P-H <sub>2</sub> O .....	444
52	Sb-S.....	448
53	Se-S .....	452
54	Clay mineral stability diagram.....	454
Custom plots.....		457
55	Gibbsite solubility vs pH.....	458
56	Acid titration of groundwater (using 'REACTION') .....	462
57	Acid titration of groundwater (using PhreePlot looping).....	464
58	Redox sequence.....	468
59	K <sub>d</sub> 's for trace metals as a function of pH.....	472
60	Cd speciation vs pH.....	476
61	Zn-HFO: %sorption vs pH curves.....	480
62	Zn-HFO: Surface speciation .....	484
63	As-HFO: reduction in surface area.....	488
64	CD-MUSIC: As(III) adsorption on goethite .....	492
65	CD-MUSIC: As(V) adsorption on goethite .....	494
66	Kinetics of pyrite oxidation .....	498
67	Kinetics of quartz dissolution.....	502
68	Symbols and lines .....	506
69	Varying symbols and lines in plots .....	508
70	Text .....	512
71	Simple PHREEQC looping .....	514
72	PHREEQC mineral species .....	518
Species plots.....		520
73	Cd speciation vs pH (species plot).....	522
74	Cd speciation vs pH (log species plot).....	526
75	U species plot (oxidizing).....	528
76	U species plot (reducing).....	530
77	Carbon speciation vs pH.....	532
78	CD-MUSIC: As(V) surface speciation on goethite.....	534
79	Test plot output formats .....	538
Fitting models to data .....		540
80	Langmuir isotherm (1).....	542
81	Langmuir isotherm (n).....	546
82	Langmuir isotherm (pre-processor) .....	552
83	Ni sorption by goethite.....	556
84	As(V) sorption on hydrous ferric oxide .....	560
Contour plots.....		563
85	Contour two metals at three resolutions.....	564
86	Contour Fe solubility as a function of Eh-pH.....	568

<b>16 THE WATEQ4F.DAT DATABASE .....</b>	<b>571</b>
References.....	605
Acknowledgements .....	607
Appendix 1. Glossary of terms .....	609
Appendix 2. Thermodynamic databases .....	611
Appendix 3. Symbol numbers and names .....	624
Appendix 4. The Standard and Latin-1 character sets .....	628



# 1 Introduction

---

## 1.1 WHAT DOES PHREEPLOT DO?

**PhreePlot** makes it possible to produce certain types of high quality geochemical plots using **PHREEQC** ([Parkhurst and Appelo, 2013](#)). **PHREEQC** is a popular and freely-available program for calculating geochemical speciation and mass transport. It has a very flexible input structure that makes it easy to customise the type of calculations performed. This includes the ability to modify the thermodynamic database used. It also has a very flexible mechanism for outputting the results of these calculations which makes it straightforward for programs such as **PhreePlot** to interface with it. In short, it is an excellent geochemical calculator.

**PHREEQC** originally did not include any charting options or any mechanism for repeating blocks of calculations with a `DO ... ENDDO`-type structure. It was these two missing features that led to the development of **PhreePlot**.

An early fork of **PHREEQC**, **PHREEQC for Windows** ([Post, 2011](#)) incorporated some simple charting and this has been extended and is now fully incorporated in the latest Windows version of **PHREEQC** (Version 3). So **PHREEQC** can now produce many of the plots that **PhreePlot** does but it does not include some of the plots that require more extensive calculations like Eh-pH plots and fitting.

The functionality of **PHREEQC** is also now available as a module in **iPhreeqc** ([Charlton and Parkhurst, 2011](#)). This includes most of the functionality of the batch version and means that **PHREEQC** can be incorporated into programs written in C++, Fortran as well as in interpreted languages such as Python and R (there is an R 'PHREEQC' package). It is also available as a Windows COM server and so can be linked to spreadsheets and databases. These options allow fine-grained programming giving the developer a large degree of control over the calculations made. These programming languages also usually have access to libraries of other useful functions to facilitate programming.

So what does **PhreePlot** do? **PhreePlot** sits on top of **PHREEQC** and makes it relatively straightforward to do certain kinds of repetitive **PHREEQC** calculations, the type of calculations that are often needed to make a plot. It does this while maintaining the basic structure of **PHREEQC** input files. **PhreePlot** uses tags placed within the **PHREEQC** input files to identify places where substitutions are to be made and has several mechanisms to control the values substituted and the looping done. It also contains software for generating Postscript plot files. If **Ghostscript** is installed then automatic conversion to pdf, png, jpg and eps formats is possible. The aim is to achieve publication quality. If **Inkscape**, **ImageMagick** or some other suitable software is installed, conversion to svg format is also possible. With this basic functionality, **PhreePlot** can be used to generate predominance diagrams, contour plots, and to fit observations to **PHREEQC** models.

One of the motivations for developing **PhreePlot** was to develop the ability to calculate predominance and mineral stability diagrams, often known as Eh-pH or pe-pH diagrams, based on a full chemical speciation. This numerical approach is different from the 'equation-based' approach typically found in textbooks and originally employed in software such as the **Geochemist's Workbench (GWB)** ([Bethke, 2005](#)). One of the advantages of the numerical approach is that reactions that do not obey the classical speciation model can also be included in the diagrams. This includes adsorption, ion exchange and co-precipitation reactions. Since a full speciation is undertaken, the impact of all interactions, no matter how complex, are automatically taken into account. **PHREEQC** keeps an accurate track of all mass and charge

balances, including that of water. The results are then fully consistent with those of other speciation and reaction path calculations undertaken using the same software and database.

The intellectual ‘penalty’ with this approach is that realistic and solvable reaction paths have to be devised to map the whole of the domain of interest. The practical penalty is that the large number of computations required means that the numerical approach is significantly slower than the analytical approach.

A consequence of this approach is also that the activity of a species is the result of the defined reactions and cannot in general be fixed *a priori*. There are ways around this by defining real or fictitious phases (‘pure phases’ define activities, as with solids and gases, and the `Fix_H+` approach) but this can have consequences which constrain the feasible calculations. As a result of this, making activity-activity diagrams in **PHREEQC** to emulate those produced by **GWB** is often difficult or impossible. Activities are derived quantities in **PHREEQC** and so cannot be used as independent master variables.

A more recent version of the **GWB** ([Release 15](#)) includes the `Phase2` and `P2plot` programs which have the ability to produce 2D plots including ‘true’ Eh-pH diagrams, much like **PhreePlot**. Other software has been also developed to produce Eh-pH diagrams in a broadly similar way.

We have developed two ways of constructing predominance diagrams: the ‘grid’ approach simply calculates the speciation at all points on a grid and while the ‘hunt and track’ attempts to track the boundaries between predominant fields. This approach usually requires considerably fewer speciation calculations than the ‘grid’ approach to produce a diagram of equivalent quality but it makes the assumption that all fields are interconnected and can be reached in some way by tracking along their boundaries. This is not necessarily the case and so fields can be missed<sup>1</sup>. This appears to be relatively uncommon in practice but is nevertheless an important limitation of the ‘hunt and track’ approach. The ‘grid’ approach makes no such assumption and so should always be the final arbiter.

A somewhat different way of looking at predominance diagrams is to ‘contour’ the data for some diagnostic variable such as the total dissolved amount or concentration of some element. **PHREEQC** is very flexible in the way that it can define its output and this is translated into a great flexibility in the variables that can be contoured.

**PhreePlot** also makes use of its looping capability to fit chemical models to data. This can be used, for example, to derive log K values from experimental data.

**PhreePlot** makes use of the **PSPLOT** Postscript library ([Kohler, 2005](#)) to produce high quality Postscript plot files. These can be edited, printed or converted to other graphical formats using various software packages, e.g. [GPL Ghostscript/GSview](#), **LibreOffice Draw**, **Adobe Illustrator**, **Inkscape**, **Affinity Designer 2**, **GIMP**, etc. We have found that **Inkscape**, **Affinity Designer 2** and **ABBYY FineReader** are amongst the easiest ways of moving labels in a pdf file.

As of February 2018, **Ghostscript** is optionally included in the **PhreePlot** distribution and if selected to be installed, does not need to be separately installed. **Inkscape** is currently probably the best free vector graphics editor capable of editing native Postscript text while **LibreOffice Draw** provides a relatively simple approach to editing pdf files, e.g. for adjusting labelling and other text, and adding or removing lines.

## 1.2 WHAT PHREEPLOT DOES NOT DO

The iteration scheme available in **PhreePlot** is quite limited and follows a fixed format: once through zero or more ‘initialization’ or pre-loop simulations and then a four-loop iteration scheme (x, y, z and character). If something else is wanted, then this will have to be programmed specifically using the **iPhreeqc** module as mentioned above ([Müller et al., 2011](#)).

---

1. Thanks to Hans Meeussen for pointing this out.

**PhreePlot** leaves getting the geochemistry right and the necessary output produced up to the user. You will have to be reasonably proficient with **PHREEQC** before attempting to use **PhreePlot**. We provide many demos to help get you started and it is often easiest to use one of these as a template for other diagrams.

The plotting is hopefully of a high quality but the types of plots produced are rather limited. If more sophisticated plots are wanted, then some other plotting program must be used. There are many. Some of these such as **R**, **Python**, **Matlab** and **Mathematica** allow external programs to be run and so could still use **PhreePlot** to generate the data with all the communications being done via files.

The interface to **PhreePlot** is via a console or command prompt. There is no GUI. You will need to use a text editor to edit the input files.

### 1.3 HOW TO READ THIS DOCUMENT

This document is very long and is best read with a pdf viewer that has a bookmark bar for navigation, e.g. Adobe Acrobat Reader. Navigating to '14 Keywords' should produce a list of all the keywords from where it is possible to scroll down to read details about the implementation of the various keywords. Follow the hyperlinks if necessary. Other section headings are self-explanatory.

### 1.4 WHAT YOU NEED TO KNOW BEFORE USING PHREEPLOT

**PhreePlot** currently runs on the Windows operating system. It contains **iPhreeqc**, an embedded version of **PHREEQC**, and so does not need another copy of **PHREEQC**. However, it will be necessary to have an up-to-date version of **PHREEQC** available for the documentation, release notes, licence conditions and other information.

The plotting part of **PhreePlot** uses as input the output from **PHREEQC**, as communicated through the 'selected output'. **PHREEQC** provides very versatile facilities for writing this information. Therefore it is necessary to be fairly competent at running **PHREEQC** in the normal way and of manipulating the selected output. If you are not, follow the documentation provided with **PHREEQC** and study the examples included in that manual carefully, initially choosing the one closest to your needs as a template. The demos included with **PhreePlot** also provide examples and templates for many types of plot.

Since **PHREEQC** includes a BASIC interpreter for customising output to the selected output, some knowledge of BASIC programming is useful. A careful study of the demo examples provided here should give an introduction to this.

### 1.5 NAVIGATING THIS DOCUMENT

This Guide is primarily intended for online browsing not for printing. There are several aids to help navigate around the document using Adobe Reader. Some tips for navigating the document are given below though these may vary slightly depending on the version of Adobe Reader used.

A roadmap to the documentation can be seen by enabling the bookmarks for this document in Adobe Reader. If these bookmarks cannot be seen, toggle them on by clicking the bookmark icon  or  on the left-hand side of the Reader window or go through the menu system and tick the View|Navigation Panels|bookmarks item.

Various hyperlinks are available within the Guide including links to all of the keywords used in the text. These link to the corresponding description in the Keywords section ([Section 14](#)). Links appear in blue text and are underlined. Hyperlinks are indicated by the cursor changing to a pointed finger when hovering over the link.

You can navigate over your navigation history in one of three ways: (i) use the  or

  toolbar icons; (ii) use the `Alt+Left` arrow. to go backwards; `Alt+Right` arrow navigates forward again, or to go backwards (iii) use the `Previous View` item from the right click (context) menu. If the toolbar icons are not already visible in Adobe Reader, activate them with the `Tools|Customize Toolbars|Page Navigation Toolbar` dialog or similar.

## 2 Installation

---

### 2.1 INSTALLING PHREEPLOT

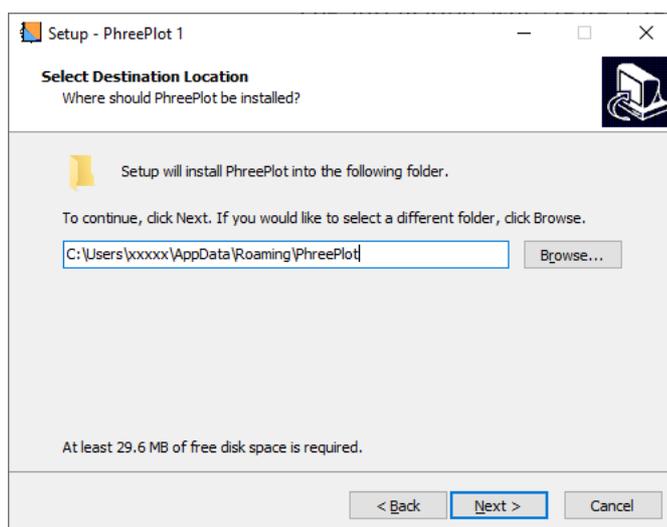
The latest version of **PhreePlot** can be downloaded from <https://www.phreeplot.org>. The file-name for the Windows installer should have the format, `setup-pp-xxxxx-yyymmdd-zzzz.exe` where `xxxxx` is the target system (`win32` or `x64`), `yyymmdd` is the date of the **PhreePlot** build and `zzzz` is the **PHREEQC** build number.

Some of the detailed descriptions given below may vary with the version of Windows being used.

#### 2.1.1 Windows

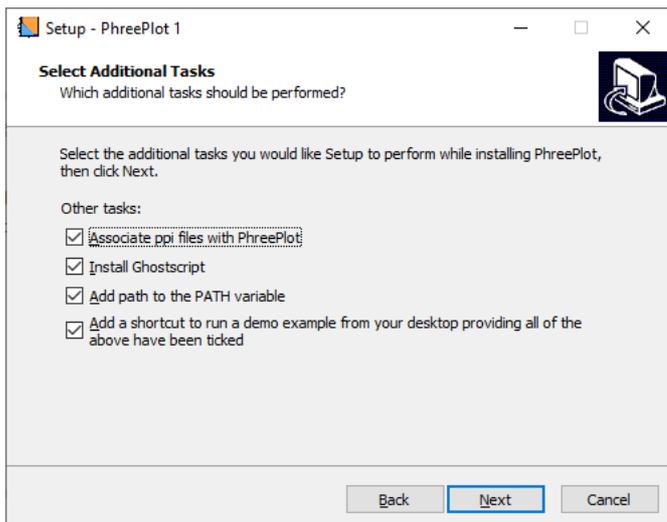
**PhreePlot** is available in both 32-bit (`win32`) and 64-bit Windows (`x64`) versions. The `win32` version will run in both 32- and 64-bit versions of Windows whereas the 64-bit version will only run in native 64-bit versions of Windows. The 32-bit and 64-bit executables both have the same file name, `pp.exe`, so that the batch files will work for both versions in a straightforward manner. The banner sent to the screen and log file will indicate the version of **PhreePlot** actually being used.

The installer should be executed and **PhreePlot** installed to your preferred directory (called a 'folder' in Windows parlance). The default directory is a **PhreePlot** sub-directory in your application data directory. This can be changed during the initial installation (but not when **PhreePlot** is updated on top of an existing installation).



There are also options during installation to (i) Associate `ppi` files with PhreePlot; (ii) Install Ghostscript, (iii) Add the executable path to the `PATH` variable, and (iv) Run a simple demo example following installation. All four options are recommended but can be skipped here and manually selected later.

The installation will create a series of sub-directories in which the **PhreePlot** files will be installed. However, the program executable (`pp.exe`) will normally be installed in the Program



Files directory, e.g. `C:\Program Files\PhreePlot\` (or in `C:\Program Files (x86)\PhreePlot\` when installing the 32-bit version of **PhreePlot** on a 64-bit system). This requires administrator rights. You normally have no control over this. This is the recommended location for executable files in Windows. However, if you do not have administrator rights, choose the 'noadmin' x64 version which can be installed anywhere.

The following files and directories will be created:

`\system`

`\demo`

`\doc`

where

`\system` the PhreePlot 'system' directory

`pp.set` user-defined initial settings

`override.set` any override settings

`ht1.inc` PHREEQC USER\_PUNCH code to calculate predominance diagrams.

`ht1c.inc` as above but combines all adsorbed species into a single species for any given sorbent-element combination.

`\system` contains many more .inc and other 'system' and database files

`\demo` a directory containing examples (ppi and associated files), one or more ppi files per subdirectory (see the Examples Section)

`\doc`

`PhreePlot.pdf` this user guide

`changes.pdf` list of changes made plus other documentation files.

Override settings are read after a normal input (\*.ppi) file has been read and will be applied every time **PhreePlot** is run. Each of the `demo` sub-directories contains a specific example, or collection of related examples. These include a **PhreePlot** input file and any other input files required. Input filenames generally have the extension `.ppi` though this is not necessary.

However, if `ppi` is associated with the **PhreePlot** executable during installation, as recommended, then double clicking a `ppi` file in Windows Explorer or similar will automatically execute it with **PhreePlot**. This is the easiest way to run **PhreePlot** as there is no GUI.

Spaces in input filenames should work but if in doubt, enclose the filename in quotes (or preferably, avoid!). The search path for the input file follows the normal operating system conven-

tions although as with most **PhreePlot** searches, **PhreePlot** will also search the system directory if necessary. In batch files, the current working directory is the directory from which the batch file originated. Use the ‘change directory’ (`cd . . .`) command in a batch file to change to a new working directory if required.

If **PhreePlot** is having trouble finding the input file, use the full path name including the drive.

Output files are automatically put in the same directory as the input file using the input file name minus the extension as the root.

**PhreePlot** also needs to know where to find certain files such as **Ghostscript** files. It does not use the Windows registry for this and so some file paths need to be set explicitly. The steps outlined below should be taken to ensure that **PhreePlot** knows where to find the necessary files.

The installer should be executed and **PhreePlot** installed to your preferred directory.

The **PhreePlot** executable, `pp.exe`, does not require Administrator privileges to run. If set, these should be turned off by opening the Properties dialog for the `pp.exe` file (right-click the file), opening the Compatibility tab and unticking the ‘Run this program as an administrator’ tick box. The same should be done for all users by clicking the ‘Show settings for all users’ button. This should prevent UAC prompts when running **PhreePlot**.

Batch files such as `demo.bat` also do not need Administrator privileges to run but will need permission to ‘Read & execute’ (set under the Security tab of the file’s properties).

Reboot, or sign out and re-login, immediately after installation to ensure that the `PHREEPLOT` and `PHREEPLOT_PATH` environment variables have been set.

### 2.1.2 Linux and Mac OS X

The Windows version of **PhreePlot** has been reported to work on Apple Mac’s with Windows emulators such as **Wine** and **Parallels**. It can also be run under Linux using various hypervisors such as **VirtualBox**.

Native ports for these operating systems may become available – check the **PhreePlot** website. If so, this guide will also apply to these versions with the exception that operating system specific details will vary. This notably applies to installation, the use of batch files and file naming in general which will follow the rules of the operating system in operation. Separate release notes will provide more information.

## 2.2 CHECKING FOR UPDATES

The latest version will always be available for download from the **PhreePlot** website, [www.phreeplot.org](http://www.phreeplot.org). If the keyword, `checkForUpdate` is set to `TRUE`, then **PhreePlot** will automatically check the server to see if a more recent version is available. This uses the `wget` program. The second parameter for the `checkForUpdate` keyword sets the minimum time gap (in days) between checking. Setting this to 1 means that the server will be checked once every day whereas setting it to 0 will mean that the server will be checked every time **PhreePlot** is executed.

## 2.3 CHANGING THE CONSOLE APPEARANCE

The default appearance of the console is white text on a black background. If you want to change this, right click on an existing console and select Defaults. This gives the option of changing the default window size and position, the text font and the foreground and background colours, e.g. to black text on a white background.

These settings should become the default for all new console windows. If only a temporary change is required, use the console Properties dialogs instead.

## 2.4 INSTALLING GHOSTSCRIPT AND GSVIEW

As of 2018, **PhreePlot** optionally comes with **Ghostscript** installed but it is possible to install it yourself in the normal way. If you want to use your installed version, you must point the [pdfMaker](#) setting to the appropriate path (see [pdfMaker](#)). It is also useful to install a native ps viewer such as [GSview](#).

**GSview** 5.0 is available from Ghostgum Software Pty Ltd at <http://www.ghostgum.com.au/software/gsview.htm>. If the internal version of **Ghostscript** has been selected, after downloading, run **GSview** and under Options|Advanced Configure|Ghostscript DLL enter `<%PHREEPLOT_PATH%>\gsdll<nn>c.dll` where `<%PHREEPLOT_PATH%>` is the long-hand description of the folder containing `pp.exe` (**GSview** does not accept environment variables here), `<nn>` is either 32 or 64 depending on which version of **PhreePlot** you have installed. This should point to the folder that contains your `pp.exe` executable. If this does not work, install **Ghostscript** in the usual way and use these settings for **GSview**.

**GSview** is no longer being actively supported although it is still available for download. However, changes to the version numbering of **Ghostscript** means that it will only work with **Ghostscript** 9.04 - 9.52.

If the complications of installing a separate **Postscript** viewer are too much, then it is always possible to automatically convert the ps output files to a more manageable format, e.g. pdf, png or jpg, or to use **Ghostscript** itself as a ps viewer, e.g.

```
gswin64c -r150 %PHREEPLOT%\demo\test\plot.ps
```

for Windows.

If **PhreePlot** has been installed correctly, typing

```
pp -v
```

from a console should show some information about the current version of **PhreePlot** including its release date, whether the 32- or 64-bit versions is running and whether **Ghostscript** is installed, and if so, its source and version.

Running the `demo\test\test.ppi` file or `\demo\demo1.bat` will indicate whether your **Ghostscript** setup has been successful. If successful, this should produce ps, pdf, png, eps and jpg plot files.

### 2.4.1 Launching PhreePlot from Windows Explorer or similar

If the `ppi` extension has been associated with the **PhreePlot** executable, then double clicking a `ppi` input file in Windows Explorer or similar should launch **PhreePlot**. This is probably the easiest way to run **PhreePlot**.

### 2.4.2 Specifying the input file name on the command line

**PhreePlot** expects an input file to be given on the command line following `'pp'`. The usual file naming conventions apply in terms of the use of quotes, `..` (parent directory). Windows filenames are not case sensitive and respect both forward and backward slashes as separators. It can get complicated when batch files and changes of directory are used and **PhreePlot** may not be able to find the required input file. In such cases, launch from a console window and use the full pathname. In Windows, the environment variable `%PHREEPLOT_PATH%` should point to the folder containing the executables so `"%PHREEPLOT_PATH%\pp.exe"` should always find the executable and provides a safe way of specifying it in a console and in batch files. Note that the quotes are necessary here because of the space in the Program Files directory and the possibility of command line arguments.

### 2.4.3 Specifying input and output filenames in PhreePlot input files

Various file paths can be specified in **PhreePlot** input files but somewhat stricter requirements than above apply when specifying these file paths.

File paths should not contain a '+' sign even though this is legal in Windows. **PhreePlot** uses a system shell command to copy various files and your system may interpret an unquoted + sign as the beginning of another file to copy.

File names can in principle contain any characters that are compatible with normal operating system rules (Windows disallows / ? < > \ : \* | "). In order to avoid having to escape characters, it is wise to also ignore parentheses, brackets and the ampersand. Other characters including the + sign, comma, semi-colon, percent sign and space are also best avoided. In other words, keep it simple for an easy life!

File paths are not case sensitive in Windows so any mixture of cases will do. However, whatever is entered is preserved in **PhreePlot**. **PhreePlot** itself tends to use lowercase filenames with the exception that chemical elements follow their normal notation.

#### 2.4.4 Setting the PhreePlot environment variable

The environment variable, `PHREEPLOT`, must be set before **PhreePlot** will work. The installer should set this to the **PhreePlot** directory that you specify during installation, i.e. the root directory containing the `system`, `demo` and `doc` directories. In Windows, this could be your AppData directory (default) or a location that you chose during installation such as `C:\PhreePlot`. Note that there is no trailing backslash.

The environment variable, `PHREEPLOT_PATH`, is also set to the location of the **PhreePlot** executable, `pp.exe`, e.g. `C:\Program Files\PhreePlot`.

You can check that this has been done correctly by typing 'set PhreePlot' in a console window. This will return the two directories currently set.

Once set, the 'demo directory' for example could be referred to as "%PHREEPLOT%\demo in batch files.

#### 2.4.5 Adding the path to PhreePlot to the Windows PATH setting

The installer should automatically add the path to the **PhreePlot** executable (`pp.exe`) to your `PATH` during installation if requested. Otherwise it can be done through the Settings menu or Control Panel. These can be accessed in different ways with different versions of Windows but typing 'Environment variables' in the run box works for Windows 10.

#### 2.4.6 Search path for files

The search path for all input and data files is, in order of checking: (i) the specified filepath; (ii) the current directory; (iii) the **PhreePlot** 'system' directory, and (iv) the path, if any, defined by a <file> tag.

If in doubt, include the full path to be sure. Put in quotes if there is a space in the file name.

#### 2.4.7 Ensuring that the correct databases are found

The `database` keyword points to the location of the thermodynamic database file to use. This should be a standard **PHREEQC**-format database file. Several of these are included in the normal **PHREEQC** distribution and have been copied to the **PhreePlot** system directory for convenience. Check the **PHREEQC** website (<https://www.usgs.gov/software/PHREEQC-version-3>) for the latest files. Several other public-domain databases are also provided here (see [Appendix 2](#)). Providing that the database files are kept in the system directory, they should be able to be located by **PhreePlot** from their filenames alone, e.g. `wateq4f.dat`, since the system directory is automatically included in the search path. Some demo examples specify other freely-available databases that are not included in the **PhreePlot** distribution. This is usually because obtaining them requires some form of registration.

The correctness of the results of geochemical calculations is directly related to the quality of the associated thermodynamic databases. It is entirely your responsibility to make sure that the

databases used are adequate for the purposes for which you are using them - *caveat emptor*. Keeping a critical eye on the quality of the databases used is an important part of geochemical modelling, and **PhreePlot** is a useful tool for comparing the impact of different databases. Other caveats, notably that thermodynamic equilibrium is not always, even rarely, achieved should also be borne in mind. This is particularly true for many dissolution and precipitation reactions.

## 2.5 OTHER USEFUL SOFTWARE

Each to their own, but we have found the following software to be useful when working with **PhreePlot**:

- [Notepad++](http://notepad-plus-plus.org/) a free and highly capable text editor that includes syntax highlighting for a large number of file types. The normal **PHREEQC** installations now come with a file to colour **PHREEQC** keywords in pqi and ppi files (<http://notepad-plus-plus.org/>).
- [7-zip](http://www.7zip.org/) free file compression utility that is efficient and easy to use (<http://www.7zip.org/>).
- [xplorer2](http://zabkat.com/index.htm) dual pane Windows Explorer that makes a great way for launching **PhreePlot** files and for viewing the graphical and text files produced (plus many of the other things you have to do for file management) (<http://zabkat.com/index.htm>).
- [CoPlot](http://www.cohort.com/coplot.html) Flexible and powerful scientific plotting package (<http://www.cohort.com/coplot.html>).
- [R](http://www.r-project.org/) Powerful and well-supported open-source working environment for data processing including flexible, high quality graphics (<http://www.r-project.org/>).
- [LibreOffice](http://www.libreoffice.org/) The Writer component makes an excellent and free word processor which natively supports import of a wide range of image types including eps and pdf. The Draw component can edit pdf files and this provides a relatively easy way of graphically editing the pdf files produced by **PhreePlot**. The Impress component provides a powerful presentation option for making slide shows.
- [Inkscape](http://www.inkscape.org/) Open-source vector graphics editor capable of manipulating Postscript files and exporting svg-format files (<http://www.inkscape.org/>). Can be used to produce svg-format files in **PhreePlot**.
- [ImageMagick](https://www.imagemagick.org/) Open-source bitmap graphics editor capable of manipulating Postscript files and exporting svg-format files (<https://www.imagemagick.org/>). Can be used to produce svg-format files in **PhreePlot**.

It is useful to have access to [software](#) that can edit native ps files so that other features can be added and label positions etc changed. You will need a vector graphics editor such as **Inkscape** for this. An alternative, and possibly easier, approach is to use **PhreePlot** and **Ghostsript** to produce a pdf file and then to edit this with **LibreOffice Draw**.

Although **PhreePlot** does contain some plotting functionality, it is quite limited in what it can do and is not intended to replace a proper scientific plotting package. The ASCII-format output files are designed to be read by more powerful plotting and data analysis packages including those mentioned above.

## 2.6 TROUBLE-SHOOTING

### *File conversions*

File conversions from `ps` to other formats can be automatically carried out by **Ghostscript** under the control of **PhreePlot**. The `demo/test/test.ppi` file should indicate whether these conversions are working. If all else fails, read in the `ps` file into **GSview** and make the required conversions in the normal **GSview** way.

Once installed correctly, all the demo examples should run (see [Section 3.2](#)).

### *Problem and bug reporting*

Contact David Kinniburgh ([david@phreeplot.org](mailto:david@phreeplot.org)).



# 3 Getting started

---

## 3.1 THE COMMAND LINE INTERFACE AND BATCH PROCESSING

Like the batch version of **PHREEQC**, **PhreePlot** can be run from a console or executed via a shortcut providing the following format is given:

```
pp input_filename [otherpp.set]
```

where `input_filename` is the name of a valid input file (see [Section 5.2](#)). If only a partially qualified filename is given, care must be taken to ensure that it is sufficient for the file to be found ([Section 2.4.2](#)). We have adopted the convention of using the `ppi` extension for input filenames. The optional `otherpp.set` is the name of a settings file to use instead of the default `pp.set` from the system directory. Normally this second parameter is left blank and the default used.

Output will normally be sent to the screen and to various output files. If `input_filename` contains blanks, embed it in quotes.

If the `ppi` extension is associated with **PhreePlot**, as recommended, then the easiest way of running a **PhreePlot** input file is to double click it in an Explorer window.

Collections of the above-type statements may be collected together in a batch file and run as one job. The `demo.bat` file included in the distribution is one such example. This is the mechanism for plotting multiple curves from different runs in a single custom plot – the output files are created in the initial runs and then the last run does all the plotting using the [extradat](#) keyword to load the output from the earlier runs.

Using the `override.set` file with [calculationMethod 2](#) can make global changes to the output from a set of already-calculated files without changing the individual `ppi` files.

Input files should be prepared with a standard text editor. Notepad will do but many better editors exist. It is useful to have an [editor](#) that automatically checks for and loads more recently-updated files. **PhreePlot** is not interactive (no GUI) but with a little effort in setup, it can be made to work quite efficiently.

Most ordinary **PHREEQC** input files can be run by just adding the line `CHEMISTRY` to the beginning of the input file (otherwise **PhreePlot** will interpret this input as **PhreePlot** keywords). Adding [all T](#) or [debug 2](#) just before this will cause the `*.all` file to be created which will contain a copy of all the normal **PHREEQC** output.

## 3.2 RUNNING THE DEMO EXAMPLES

Providing the paths have been set correctly as described above, launching the `demo1.bat` file from the `\demo` directory should begin the calculations. This can be done either by double clicking on the `demo1.bat` file in a Windows Explorer-type window, or by opening a console and executing it from there (as below).

This demo is an example of using the ‘hunt and track’ algorithm for producing a predominance diagram for an Fe-Cl system. It also creates `pdf`, `eps` and `jpg` files if **Ghostscript** is installed and so can be used to test that installation.

The output looks something like:

```
*** PhreePlot 1 (x64) 11:41:57 31 Mar 2020
    Incorporating the iPhreeqc library (3.6.2-15100-x64)
```

by DL Parkhurst, SR Charlton (USGS), & CAJ Appelo (Amsterdam)  
 Hunt & Track by DG Kinniburgh, and DM Cooper (CEH, NERC)  
 Fitting by MJD Powell and others  
 Postscript plotting by KE Kohler

Input filename: D:\PhreePlot\demo\test\test.ppi.

Main species = "Fe"

Calculating... 1

1	2.0000	-85.0000	-11 H2(g) > 1 a	Fe+2	0.9044	-2.0195
2	2.0000	-81.6000	11 Fe+2	FeCl+	-2.0196	-3.3583
3	2.0000	-83.3000	-11 H2(g) > 1 a	Fe+2	0.0544	-2.0196
4	2.0000	-81.6000	11 Fe+2	FeCl+	-2.0196	-3.3583
5	2.0000	-82.4500	11 Fe+2	FeCl+	-2.0196	-3.3583
6	2.0000	-82.8750	11 Fe+2	FeCl+	-2.0196	-3.3583
7	2.0000	-83.0875	11 Fe+2	FeCl+	-2.0196	-3.3583
8	2.0000	-83.1937	-11 H2(g) > 1 a	Fe+2	0.0013	-2.0196
9	2.0000	-83.0875	11 Fe+2	FeCl+	-2.0196	-3.3583
10	2.0000	-83.1406	11 Fe+2	FeCl+	-2.0196	-3.3583
11	2.0000	-83.1672	11 Fe+2	FeCl+	-2.0196	-3.3583
12	2.0000	-83.1805	11 Fe+2	FeCl+	-2.0196	-3.3583
13	2.0000	-83.1871	11 Fe+2	FeCl+	-2.0196	-3.3583
14	2.0000	-83.2828	-21 H2(g) > 1 a	Fe+2	0.0458	-2.0196
15	2.0000	-82.4242	22 Fe+2	FeCl+	-2.0196	-3.3583
16	2.1010	-82.4242	23 Fe+2	FeCl+	-2.0196	-3.3583
17	2.1010	-83.2828	-24 H2(g) > 1 a	Fe+2	0.0458	-2.0196

The screen output provides feedback on progress. The columns are: (i) iteration number; (ii) x-axis variable (automatically generated); (iii) y-axis variable (automatically generated); (iv) the type of step being taken; (v) truncated name of the predominant species (most abundant); (vi) truncated name of the sub-dominant (second most abundant) species; log concentrations of the dominant and sub-dominant species (mol/kgw) when solution species or log partial pressures when gases. Where one or more constraints are operating, these are elevated to the top-most position(s) and the values given are determined by the type of species as outlined above.

The above example makes use of the `ht1.inc` [include file](#). This determines exactly what values are returned to **PhreePlot**.

The code returned for the type of step taken is determined as follows:

the first digit is 1 while hunting for boundaries along an edge or 2 while tracking an internal boundary;

the second digit is either the side number or the cell corner (1-4, counted clockwise from bottom left. 1 is the left-hand y axis, 2 is the top x axis...);

a negative sign indicates that a constraint is operating;

00 is a special code for a non-tracking move (as used by a 'grid' plot).

The above example indicates that **PhreePlot** starts by hunting for boundaries along the left-hand y axis. It then starts tracking along an internal boundary at iteration 14. It will finish by tracking along the remaining boundaries to check that there are no more intersections to start tracking from. This example takes 1226 iterations to complete.

The `demo.bat` file included contains many more examples including many 'custom' plots which use the selected output from **PHREEQC** to generate a plot. This includes the standard set of examples distributed with **PHREEQC**. Each example will take from a few seconds up to several minutes or more to calculate.

Note that the demo examples are based on the `pp.set` file provided. If changes to this file are made, it may be necessary to change the input files.

### 3.3 THE 'PP.LOG' FILE

Providing, `pplog` is set to `TRUE`, a summary log of every **PhreePlot** run is written to a file called `pp.log` which is created in the **PhreePlot** system directory. This can be checked at the end of the run to make sure that all has run as expected and is especially useful for checking the results of multiple runs from a batch file.

Each run normally gives rise to two lines on the `pp.log` file. The first line indicates the time started and the second line gives the completion status. The absence of a second line indicates a crash. Normally, an 'OK' status should be returned for each input file if all has run well.

```
Time      Date      Input_file                                     Type      Method      n      Time(min) Status
9:24:38  15_June_2010 C:\PhreePlot\demo\test\test.ppi             ht1       calculate    0      0.000 Started
9:24:44  15_June_2010 C:\PhreePlot\demo\test\test.ppi             ht1       calculate    1539   0.092 OK
9:24:44  15_June_2010 C:\PhreePlot\demo\PHREEQCexamples\ex1\ex1.ppi custom    calculate    0      0.000 Started
9:24:44  15_June_2010 C:\PhreePlot\demo\PHREEQCexamples\ex1\ex1.ppi custom    calculate    1      0.004 OK
9:24:44  15_June_2010 C:\PhreePlot\demo\PHREEQCexamples\ex2\ex2.ppi custom    calculate    0      0.000 Started
9:24:45  15_June_2010 C:\PhreePlot\demo\PHREEQCexamples\ex2\ex2.ppi custom    calculate    1      0.018 OK
...
```

This log file will accumulate output from every run and so should be periodically emptied or erased. It will be automatically recreated or appended to as necessary.

If there has been a failure of **PHREEQC** such that no selected output was produced, then a '?' is appended to the right of the number of speciation calculations, *n*. Details of the offending output will be written to the log file if that was active.

If `debug` is set to 1 or `stopOnFail` is set to 1, then **PhreePlot** will stop at the first failure. If **PhreePlot** has had to adjust the resolution of a 'hunt and track'-generated predominance plot for various reasons then a '\*' is printed next to the number of speciation calculations.

If there has been an error reading one of the data input files, e.g. while reading an `extraSymbolsLines` file, then an exclamation mark (!) is appended to the status. Check the log file for details. The error may stop **PhreePlot** from running or may continue by skipping the erroneous data.

Other possible variations of the logged status on termination are:

Error	an error occurred somewhere in the calculations
Input_error	an error occurred reading input
Plotting_error	an error occurred during plotting
GS_error	an error occurred while Ghostscript was converting the ps file
No_plot	no plot was specified
Interrupted	the <Esc> interrupt was used to halt execution
Started	still running (or crashed while running)

Setting `pplog` to `FALSE` will prevent anything being written to the `pp.log` file.

### 3.4 EXAMINING THE RESULTS OF THE RUN

Various output files will be written to the input file directory. The formats of these files are described more fully elsewhere ([Section 5](#)). The file `plot.ps` is always a copy of the last Postscript plot file produced. The log file if written should give a more detailed summary of the calculations undertaken.

### 3.5 MAKING A WORKING DIRECTORY

It is best to keep all your working files in a directory that is quite separate from the setup directories. Since each run can produce a large number of files, it is best to make a new directory for each 'problem'. It is usually best to copy an existing similar working input file to this directory and edit that as needed.

Running the file should be straightforward providing the **PhreePlot** environment variable has been set properly (see [Section 2.4.1](#)), e.g.

```
C:\projects\PhreePlot>mkdir FeS2
C:\projects\PhreePlot>cd FeS2
C:\projects\PhreePlot\FeS2>pp FeS2
```

### 3.6 GETTING FAMILIAR WITH THE OPTIONS

The calculations and plotting are controlled by the various keyword-value pairs and lists which are read from various input files. There is also usually some **PHREEQC**-format appended to the end of the main input file. There are many options, some of which are more important than others, and it is difficult in the beginning to know where to start.

The best way to learn is to run the demo examples. Pick an example that is closest to what you are interested in and run it. If one of the keywords in the input file looks interesting, [look it up](#) to see what it does and experiment by changing it.

### 3.7 USING BATCH FILES TO RUN A SET OF RUNS

**PhreePlot** is designed to produce a series of plots by varying one of the looping variables (main species, loop parameter or the x- and y parameters). However, it is not designed to do more than one independent type of plot in one run. To do this, it is necessary to run **PhreePlot** multiple times and then combine the results. The [overlay](#) feature enables plots from earlier runs to be combined with the current plot to produce complex page layouts containing multiple plots.

Multiple independent plots can be executed in batch mode by preparing a batch file. This is surprisingly powerful. The results from **PhreePlot** can even be intercepted, modified by another program and returned to **PhreePlot** for plotting. Many programs exist to convert images to other image formats, for example. Even a rudimentary understanding of Windows batch scripting can be useful when processing large numbers of files.

The `demo.bat` file illustrates how a set of runs can be run in batch mode. This has obvious advantages for repeatedly running a set of examples. On multi-processor machines, it may be advantageous in terms of speed to split the batch files into two or more to take full advantage of the separate processors.

It is possible to intersperse other batch commands in a batch file of **PhreePlot** runs in order to rename, copy or delete files etc between runs.

It may be necessary to change the current working directory to that of the input file if a shortened file name is given.

The `start` command can be used to launch individual batch files simultaneously from within this file. Alternatively, use `call` to run a batch file from within a batch file. This will run the batch files sequentially.

The `override.set` file can be a useful place to add settings that will apply to all files run from a batch file. For example, to generate png files for all the plots add

```
calculationMethod 2
png t
```

to the `override.set` file and re-run.

### 3.8 STOPPING A RUN

You can usually stop a run using the `Esc` key followed by 's' for stop.

Stopping a batch file or script completely is a bit different. In Windows, `Ctrl-C` will always abort the current run and when it is a Windows batch file, you will be given the opportunity to exit the entire batch file.

# 4 PHREEQC basics

---

## 4.1 ONLINE PHREEQC DOCUMENTATION

Since the `CHEMISTRY` section of **PhreePlot** input files is itself essentially **PHREEQC** code, it is necessary to be familiar with the way that **PHREEQC** input files are set up. This is described in detail in the [PHREEQC manual \(pdf\)](#). This manual is also available online in [browser format](#). Changes and corrections added since the initial release are given in the '[Release notes](#)' on the USGS website.

## 4.2 HOW PHREEQC INTERACTS WITH PHREEPLOT

**PhreePlot** uses **PHREEQC** for all geochemical calculations and runs only slightly modified **PHREEQC** input files. **PHREEQC** calculations are controlled by an input file, a database file and the program itself. The input can include one or more simulations. These need not be related but they usually are. In many cases, only a single simulation is all that is needed to generate the output required but sometimes more than one simulation is necessary, or it may be desirable to split a simulation into two or more for the sake of efficiency (see [Example 61](#)).

A **PHREEQC** input file consists of a series of keyword data blocks separated into 'simulations' by the `END` keyword. This file is read sequentially. When an `END` is found or the end of file is reached, the statements accumulated since the last `END` are executed. We call this a 'run'.

This execution triggers the specified calculations and the writing of results to the normal and selected output (if active). A number of data structures including the composition of various `SOLUTIONS`, `EQUILIBRIUM_PHASES` etc are also created or updated.

Many of these data structures persist across simulations but some of them can be explicitly saved and re-used with the `SAVE` and `USE` keywords. The `PUT` and `GET Basic` statements also enable user-defined numeric variables to be stored in, and retrieved, from global storage, and so persist between simulations.

**PHREEQC** does not provide any explicit means of looping around specific lines of the input file although some of the keywords such as `REACTION` and `TRANSPORT` implicitly involve a user-defined set of iterations. This lack of general looping capability means that the input files required for some calculations, including those often required for plotting, can become large and repetitive.

**PhreePlot** attempts to overcome this by providing a framework for iterating across sections of the **PHREEQC** input file while requiring minimal changes to the **PHREEQC** input file itself. It does this by defining a set of four nested '`DO/FOR`' loops which iterate over certain sections of the **PHREEQC** code.

These loops, from the outside (least rapidly changing) in, are known as: (i) the 'main species' or character loop; (ii) the 'z'- or 'main' loop; (iii) the y-axis loop, and (iv) the x-axis loop. The main species loop iterates over a list of character variables while the remaining loops all iterate on numeric variables. Not all loops need to be used. Indeed, you do not need to use any of the loops.

Setting the iteration parameters for these various loops and providing instructions describing which parts of the input file to loop over, plus many other **PhreePlot** settings, are either inherited from the default settings (a file, `pp.set`) or specified at the top of the **PhreePlot** input file. **PHREEQC** input is at the bottom. A line containing the word `CHEMISTRY` separates these two

sections.

Special tags – character strings between angled brackets – are used within the **PHREEQC** input to act as placeholders which are substituted at run time by values generated by the various **PhreePlot** looping mechanisms, and by other means. **PHREEQC** never sees these tags, just the substituted values. Tags can also be used in the upper (**PhreePlot**) section of the input file. These tags serve as global variables that enable transfer between different **PHREEQC** simulations (somewhat like the Basic `PUT/GET` mechanism) but they also enable communication between **PHREEQC** and the plot, and can be used to dynamically control such things as labelling, scaling or sizing the plot.

Tags can be defined in a **PhreePlot** input file but can also be automatically generated from the output of earlier simulations, or from reading an external data file. **PhreePlot** maintains a dictionary with the current values of all these tag variables ready for substitution at the appropriate time. However, note that dynamic tags generated during execution will not be available during replots ([calculationMethod](#) 2 or 3) since no **PHREEQC** code is executed when replotting.

The sections of **PHREEQC** code iterated over are always based on contiguous blocks of one or more simulations. The default is that the main species and z- loops iterate over all the simulations while the x- and y-axis loops only iterate over the last *n* simulations where *n* is one by default.

Communication of results between **PHREEQC** and **PhreePlot** is via the selected output. **PHREEQC**'s in-built Basic interpreter gives you a great deal of flexibility in controlling what is sent to the selected output. See the [PHREEQC guide](#) for details.

Each simulation normally produces one or more lines of selected output although this can be turned on or off at will. Where no output has been requested, a blank line is produced. This output typically consists of the results of one or more initial solution etc calculations followed by one or more lines giving the results of a reaction.

It is often the results on this last line that are wanted. **PhreePlot** only reads the last *k* lines of the selected output where *k* by default is again normally one (in the cases where **PHREEQC** itself does iterations, a whole block of results may need to be read and so *k* can be set to be greater than one). This output is accumulated in a special file, called the 'out' file, which has a tabular format ready for plotting.

**PhreePlot** has limited plotting capabilities though the output that is available is normally of high quality (the native format is Postscript). The aim is to be able to get a reasonably quick visual feel of the output, and once satisfied, to be able to generate plot files later, if necessary in an automated (batch) fashion. All of the data files used to generate plots are well-structured text files (although possibly with comment lines) so can be readily imported into other plotting programs.

The ability to use tag variables in **PHREEQC** input files means that it is straightforward to keep re-running a set of simulations with a different set of values. This is the basis of the model fitting that is built into **PhreePlot**.

### 4.3 THERMODYNAMIC DATABASES

The standard databases distributed with **PHREEQC** and **PhreePlot** include a varied range of elements and ligands. The scope of these databases in terms of the elements defined are given in [Appendix 2](#). Check the appropriate web sites for updates.

It is straightforward in **PhreePlot** to change the database used using the [database](#) keyword. Bear in mind that the same minerals and gases may have different names in the different databases. This must be reflected in the use of such names in the Chemistry section of a **PhreePlot** input file.

#### 4.4 TYPES OF OUTPUT PRODUCED BY PHREEQC

**PHREEQC** can create two types of output files:

(i) normal output file: the `PRINT` and `USER_PRINT` data blocks control the output to the main output file. This consists of a well-structured but potentially verbose log of the speciation calculations split into various blocks corresponding to each stage of the calculations. It also includes any user-defined output defined by `PRINT` statements in the `USER_PRINT` or `USER_PUNCH` data blocks. In **PhreePlot**, this output is directed to the `PHREEQC.[id].out` and `*.all` files. The `PHREEQC.out` file is only written if the `PHREEQC.out` keyword is 'TRUE', or 'auto' and `debug` >0. The `*.all` file is only written if the `all` keyword is 'TRUE', or 'auto' and `debug` >1. The name of the `*.all` file can be changed by adding the new filename as the second parameter on the `all` keyword line.

The amount of text output to the normal output file can be controlled rather precisely, section by section, by a large number of switches specified in the active `PRINT` data block.

(ii) selected output file: the `SELECTED_OUTPUT n` and `USER_PUNCH n` data blocks control tabular output to the selected output file(s). The main selected output file ( $n = 1$ ) is the file normally used by **PhreePlot** for generating plots and it is normally this file that has to be manipulated to give the required output. Certain rows of data from the selected output are accumulated in the 'out' file which is often used to generate plots. Therefore familiarity with the ways of controlling output to the `SELECTED_OUTPUT` is a prerequisite for running **PhreePlot**. The [PHREEQC guide](#) gives details.

The built-in BASIC interpreter in **PHREEQC** provides a very flexible approach for defining the selected output. The interpreter provides access to most of the fundamental system variables such as species concentrations and activities. It also includes various summary functions such as `TOT()`, `SURF()` and `SYS()`. The data sent to the selected output from various stages of **PHREEQC** calculations can be controlled in the `USER_PUNCH n` data block(s) by checking the `STEP_NO` and jumping over any `PUNCH` statement(s) for which the output is not wanted.

Care has to be taken to avoid strings in the Basic code being mistaken for tags. This hinges around use of the < and > symbols surrounding logical operators like 'and' and 'or'. Always use spaces around these operators to avoid confusion; tag names cannot contain spaces.

In general, a single line of selected output is produced for each **PHREEQC** calculation – “after each initial solution, initial exchange-composition, initial surface-composition, or initial gas-phase-composition calculation and after each step in batch-reaction or each shift in transport calculations”. If no `USER_PUNCH` variables have been defined, a blank line is output or if the selected output has been turned off with the `PRINT` statement or `-active FALSE` setting, a header line but no output is produced.

The **PHREEQC** library used by **PhreePlot** has switches to control whether the selected output is written to a physical file or to memory. In **PhreePlot**, this is controlled by the value of the `debug` setting with `debug = 0` normally writing only to memory and greater values writing increasing amounts to 'disc' (this could be a solid-state drive). It is possible to force the data to be written to a file with [selectedOutputFile](#) TRUE.

#### 4.5 THE `SELECTED_OUTPUT` AND THE `USER_PUNCH` DATA BLOCKS

All output communications between **PHREEQC** and **PhreePlot** are sent via the selected output. Therefore it is necessary to ensure that the correct output is sent to this 'file' (it may be just a piece of memory or a 'virtual' file) and to tell **PhreePlot** what the format of the selected output file is in relation to what **PhreePlot** has to do. This is done with a combination of the `SELECTED_OUTPUT/USER_PUNCH` Basic statements in **PHREEQC** and [selectedOutputLines](#) keywords in **PhreePlot**.

**PHREEQC** now supports multiple `SELECTED_OUTPUT/USER_PUNCH` blocks but only block 1 can be used for creating tags and communicating with other simulations. These blocks are

numbered with a user number,  $n$ , e.g. `SELECTED_OUTPUT n/USER_PUNCH n` where  $n$  is an integer which if not specified is given the value 1. This is the default user number for some of the in-built scripts, e.g. `ht1.inc`, and is required for tag creation and so it is important to always use 2 and upwards for additional unit numbers (see [Section 4.7](#)). User number 1 is also the only user number for which the data are accumulated in the ‘out’ and ‘trk’ files. Any extra files punched from user numbers other than 1 will contain the data specified by the corresponding `USER_PUNCH` block and the iteration schedule. This additional output can be sent to a file using the corresponding `SELECTED_OUTPUT` block.

Set `all TRUE` or `debug 2` to get a print out of all the output files to the log file for each iteration, and if necessary add `PRINT;-reset TRUE` immediately after e.g. `ht1.inc` to turn on the printing.

There is one more important factor: the `SELECTED_OUTPUT` block must be executed in a simulation before the simulation triggering the sending of selected output to a file, i.e. the selected output switch must be set ‘on’ before the simulation generating the output is executed. In **PhreePlot**’s *modus operandi*, this means that the selected output block(s) should either be placed in a pre-loop simulation or for main loop simulations, the ‘one simulation at a time’ approach should be adopted (see [mainLoop](#)) with the selected output block placed in a simulation preceding the simulation that triggers the wanted selected output.

**PhreePlot** only transfers data from one selected output block to the ‘out’ file, the structured-output file that is used for plotting. The `SELECTED_OUTPUT/USER_PUNCH` block chosen always is the current user number which in **PhreePlot** is always 1. This setting does not affect the data that will be sent to other files specified with the `SELECTED_OUTPUT; -file` identifier.

Selected output will only be generated if both the `SELECTED_OUTPUT` and `USER_PUNCH` data blocks are both present somewhere in the **PHREEQC** part of the input file. By default they are active from the point of definition downwards. Selected output will be triggered from all simulations with a defined `SELECTED_OUTPUT n/USER_PUNCH n` pair each time an initialization, reaction or timestep occurs. These can be selectively turned off/on with the `-selected_output` identifier in the `PRINT` block and the `-active` and `-user_punch` identifiers in the `SELECTED_OUTPUT` block. A `PUNCH` statement can also be skipped over in a `USER_PUNCH` block (e.g. `IF (STEP_NO < 1) THEN GOTO ...`) but this will emit a blank line in the output since the block has been entered. There has to be a reason to emit some output so usually at least one `SOLUTION/REACTION` block is needed (it can be empty).

It may also be useful to include the `-reset FALSE` and `-high_precision TRUE` identifiers to suppress unnecessary headers and to retain maximum precision in the output numbers. The system variables like `SIM_NO` are only produced without being explicitly defined when  $n = 1$  in `SELECTED_OUTPUT n/USER_PUNCH n`.

While the ‘out’ file is the principal data file used for plotting, other files can be used to supply data for plotting by specifying them with the [extradat](#) keyword.

#### 4.5.1 The `SELECTED_OUTPUT` filename and forcing the file to be written

The default name of the `SELECTED_OUTPUT` file in **PhreePlot** is ‘selected\_1.0.out’ but this can be changed using the `SELECTED_OUTPUT -file` identifier, as normal in **PHREEQC**. As mentioned above, the selected output in **PhreePlot** is normally written to a ‘virtual’ file (a block of memory) and is not necessarily written to a ‘physical’ or disc file. The writing of the physical file is controlled by a switch set by the [selectedOutputFile](#) keyword. This setting applies to all selected output files created during the run.

For `debug > 1` a physical file will always be produced with the given file name so that the output can be inspected. There will be small performance penalty because of the file writing.

It can be useful to force a physical file to be written with multi-simulation input files. Data from each simulation could be sent to a different file and plotted accordingly using the [extradat](#) keyword to define the data files to be searched for plot data.

If the `-selected_out` identifier of the `USER_PUNCH` data block is set to `FALSE`, no lines are written to the selected output file. However, a selected output file will still be produced but it will be blank. This will be translated to a set of variable values all given zero values, i.e. all output variables will be reported as `0.000000000000E+00` in the log file.

If a change in the structure of the selected output is wanted, make sure the simulations involved are executed as separate blocks (see [mainLoop](#)).

#### 4.5.2 Scope of PHREEQC keywords

Each **PHREEQC** simulation consists of a series of keyword data blocks which define the calculations for that simulation. The order of these keywords within a simulation is normally not important other than if a keyword is replicated, the last instance overrides earlier ones. An exception is that the position of the `-reset` in `USER_PUNCH` keyword blocks can be important. Also the position of the [units](#) and [numberOfFitParameters](#) keywords can be important in relation to the related settings that follow.

The simulations are separated from one another by an `END` keyword. Each `END` can therefore be interpreted as ‘Calculate!’.

Other keywords such as `SELECTED_OUTPUT` and `USER_PUNCH` have a broader scope and operate from their point of insertion forward.

For example, the following input defines four Cd solutions and does an ‘initial solution’ calculation (speciation) for each one. The four simulations are essentially unrelated.

```
SOLUTION 1 # Simulation 1
  Cd 1.0
END
SELECTED_OUTPUT #Simulation 2
  high_precision true
  reset false
USER_PUNCH
  headings Cd+2
  10 punch mol("Cd+2")
SOLUTION 2
  Cd 0.1
END
SOLUTION 3 #Simulation 3
  Cd 0.35
END
SOLUTION 4 #Simulation 4
  Cd 0.6
END
```

This produces the following output in the `selected_1.0.out` file when the `wateq4f.dat` database is used:

```

                Cd+2
9.992072733798e-005
3.497329579806e-004
5.995528842616e-004
```

Note that no output has been produced for the first initial solution calculation since it is in a simulation that precedes the definition of the `SELECTED_OUTPUT` data block. The `SELECTED_OUTPUT` file is ‘turned on’ in simulation 2 and the output appears from this point forward, hence the three lines of output representing output from simulations 2 to 4. Additional `PUNCH` statements within a simulation result in more output columns. The ‘headings’ line in the `USER_PUNCH` data block controls the header used for the column in the selected output file.

Therefore, for as long as the selected output file is turned on, at least one line of output is produced by each simulation providing that a `USER_PUNCH` block has been defined. The output for the whole job accumulates in the selected output file. **PhreePlot** accumulates ‘selected data from the main selected output file’ into a single output file called the ‘out’ file or outfile. The default is to accumulate only the last line from the last simulation here the `5.995528842616e-004`.

The scope of many other **PHREEQC** ‘structures’ is global in the sense that once created in a simulation they persist for the remainder of the run unless overwritten. For example, solutions defined by the `SOLUTION` keyword are automatically preserved across simulations. These solutions can be used in subsequent simulations providing that the solution number is not reused or redefined by a reaction. The same is true of `PHASES`, `SOLUTION_SPECIES` etc.

#### 4.5.3 What is sent to the `SELECTED_OUTPUT` file?

Both numeric variables and text strings can be sent to the `SELECTED_OUTPUT` file by defining them in a `USER_PUNCH` data block. The column headings should reflect each entry on a one to one basis. If the list of headings is shorter than the list of variables output, the missing headings are given the value ‘no\_heading’.

The names of the column headings take on especial importance in **PhreePlot** since they are used to automatically generate the names of new tags (see [Section 6.4.2](#)) which, among other things, can be used to label plots.

The number of significant figures sent to the `SELECTED_OUTPUT` file is controlled by the `-high_precision` identifier in **PHREEQC**. It is normally safest to set this to `TRUE`, i.e. output at high precision (12 decimal places, 13 significant figures). Normal precision is 4 decimal places (5 significant figures) by default. However, the default is `TRUE` in **iPhreeqc** so the `high_precision` identifier does not need to be set explicitly as above. The high precision option is definitely preferable when fitting data to models and when calculating predominance diagrams.

The sequence of columns sent to the `SELECTED_OUTPUT` file is set by the following rules:

(i) one column for each of the `SELECTED_OUTPUT` data item switches (simulation, state, solution...) that is set to `TRUE`. The column headers for these switches, and their order, is given by: `sim`, `state`, `soln`, `dist_x`, `time`, `step`, `pH`, `pe`, `reaction`, `temp`, `Alk`, `mu`, `mass_H2O`, `charge` and `pct_err`. The default value for the first eight of these is `TRUE` and for the remainder is `FALSE`. It is normally advisable to use the `-reset false` option at the top of the `SELECTED_OUTPUT` data block to turn all of these off. Then the ones that are wanted can be turned on by explicitly defining them as `TRUE`.

(ii) one column for each variable defined in the list data items such as `-totals`, `-activities` etc. output in the sequence specified.

(iii) one column for each item `PUNCHED` within the `USER_PUNCH` data block in the cumulative order in which they are specified by the `BASIC` statements. There can be one or more items per `PUNCH` statement.

Character output should be enclosed in double quotes. These may have to be added by concatenation, e.g. `''' + name$(1) + '''`.

An example is:

```
SELECTED_OUTPUT
  high_precision true
  reset false
USER_PUNCH
  headings  pH Ca Mg element
  10 punch -la("H+"), tot("Ca"), tot("Mg"), "<mainspecies>"
```

## 4.6 SETTING UP THE `SELECTED_OUTPUT` FILE FOR INPUT TO **PHREEPLOT**

### 4.6.1 Possibilities for looping of **PHREEQC** input files

It is assumed that the primary output to be transmitted to **PhreePlot** is derived from `SELECTED_OUTPUT 1/USER_PUNCH 1` data blocks. The ‘1’ is optional and is the default if no number is given. Other data can also be sent to secondary output files (see [Section 4.7](#)).

The structure of **PHREEQC** input files is very flexible in terms of the number of simulations within a file and the relation between the various simulations. These are executed sequentially

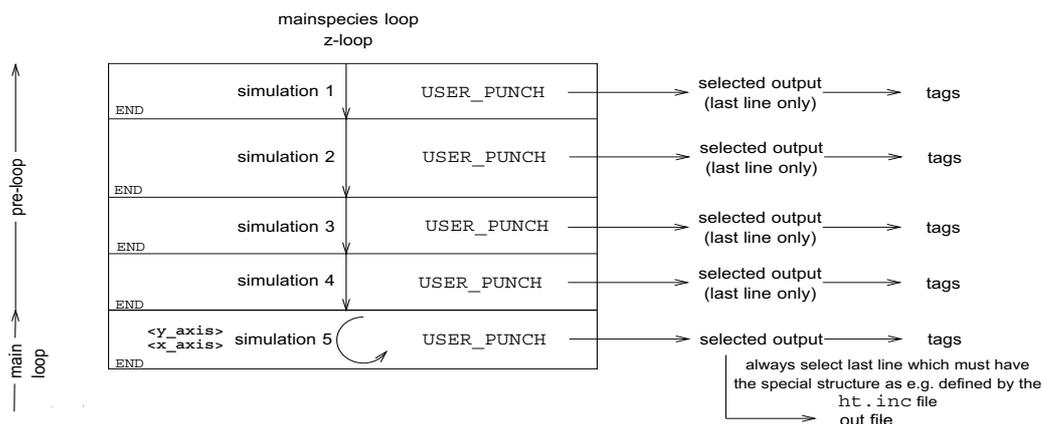
until the end of file is found. **PHREEQC** originally did not contain any mechanism to enable looping of the various simulations and this is what **PhreePlot** attempts to do without impinging unduly on the overall structure of the **PHREEQC** input. In return, **PhreePlot** expects a certain **PHREEQC** structure in order to control this looping. This structure depends on the [calculationType](#) and certain other keyword settings.

The general philosophy in preparing **PhreePlot/PHREEQC** input files should be to (i) keep the input file as simple as possible; (ii) put any preliminary calculations that only need to be executed once in one or more ‘pre-loop’ simulations at the beginning of the file; (iii) finish with the simulation, or range of simulations, that need to be repeated many times with minor changes (the ‘main loop’).

**PhreePlot** also recognises two types of looping: (i) a ‘continuous’ type of looping which focuses on the ‘resolution’ of the calculations, (ii) a ‘discontinuous’ type of looping which generates a list of discrete values to be used. The x- and y-axis loops belong to (i) and reflect the fact that **PhreePlot** is especially designed to produce 2D plots. The main species and z-loop belong to (ii) which in effect provides a looping mechanism for producing a series of 2D plots. These differences are reflected in the way that the iterations are specified: (i) are specified in terms of a minimum value, a maximum value and a ‘resolution’ while for (ii), the main species loop uses a list of character variables and the z-loop uses a minimum value, a maximum value and an increment value. An irregular list of z-loop values can also be supplied.

Typically, the x- and y-axis loops are used to control the smoothness of generated curves for plotting while the main species loop can be used to repeat the calculations over a range of chemical elements while the z-loop controls the spacing between curves based on a range of discrete values of some important variable such as the total concentration of an element in the system.

It is only the ‘main loop’ simulations that are repeated under the x- and y-axis looping mechanisms. The pre-loop simulations should be used for ‘one-off’ calculations such as initial solution calculations or database definitions that do not need to be varied during the main loop but which might need to be used recalculated for each of the main species and z- loops. More details about **PhreePlot** looping and the structure of multi-simulation input files is given in [Section 6.2](#).

*Predominance plots*

**Figure 4.1.** Flow during the execution of a multi-simulation file generating a predominance plot (calculationType 'ht1' or 'grid'). Simulations 1–4 are 'pre-loop' simulations used for initial solution etc calculations. The <x\_axis> and <y\_axis> tags are only present in the 5th or 'main loop' simulation. It is this one which is repeatedly called while tracking or traversing the specified domain. It is always the last line of the selected output generated by this main loop simulation that returns the predominant species for **PhreePlot** to process. The selected output file has a special structure and is normally generated by including the `ht1.inc` file or some variant of it in the input file. Note that this flow diagram refers to a single value of the main species and z-loop variables.

The structure of the input file to generate a predominance diagram typically consists of two simulations (Figure 4.1). It could all be done with one simulation but it executes more rapidly if the initialization parts (the 'pre-loop' calculations which only need to be executed once) are separated from those calculations that vary and that need to be calculated repeatedly (the 'main loop' calculations). The number of the first main loop simulation is identified with [mainLoop](#).

The first simulation usually pulls in the `ht1.inc` file which defines the `Fix_H+` phase and sets up the selected output 'file' and the required `USER_PUNCH` definitions that send the predominant species to **PhreePlot**. It also includes a `SOLUTION` data block which defines the total quantities of all elements in the system of interest.

The second simulation uses the chemical system defined above and subjects it to control by the x axis and y-axis variables.

A simple example for generating an Fe predominance diagram is:

```
# the first simulation defines the total quantities involved
include 'ht1.inc'
SOLUTION 1
  pH      1.8
  units   mol/kgw
  Fe(3)   1e-2
  Na      1e-1
  Cl      1e-1
END

# the second simulation carries out the reaction to the desired endpoint
USE SOLUTION 1
EQUILIBRIUM_PHASES 1
  Fix_H+ <x_axis> NaOH 10
    -force_equality true
  O2(g) <y_axis> 1
    -force_equality true
  Fe(OH)3(a) 0 0
END
```

Defining an equilibrium phase to consist of a single species and then using the `EQUILIBRIUM_PHASES` keyword to define its saturation index (SI), as here to fix the pH, is the

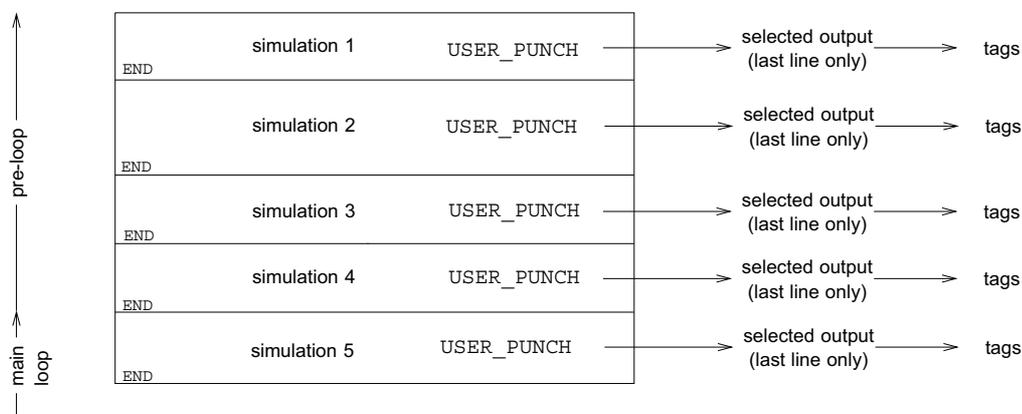
**PHREEQC** way of fixing a species activity. This simply forces the log activity to be numerically equal to the SI since  $SI = \log(IAP/SP) = \log(aH^+/\log_k) = \log(aH^+)$  where IAP is the ion activity product and SP is the solubility product.

Note that solution 1 is titrated with NaOH and  $O_2(g)$  to achieve the required endpoints. The initial pH of solution 1 should normally be less than the minimum pH of interest so that adding NaOH can be guaranteed to achieve the full range of pH's required. This is actually a simplification since side reactions, e.g. oxidation/reduction of S, can also contribute to the proton mass balance, and negative quantities of NaOH are permitted to be added (reducing the pH) providing there is enough  $Na^+$  to make this possible. But it remains a useful rule-of-thumb, and it is always the user's responsibility to ensure that 'fixing' the x- and y-axis tag values over the whole domain is defined in a chemically feasible way.

If the <mainSpecies> tag has more than one variable associated with it or if the <loop> variable has been set up to perform more than one z-loop, then the entire input file is run each time one of these loop variables changes value. This can be used to prepare a set of predominance plots for several elements each with the its total concentration, for example, varying by some amount. The `...\demo\loop_ht1` examples produce Fe predominance diagrams for a range of total Fe concentrations. If an irregular sequence of z-loop values is required use the [loopVal](#) keyword, or for more complex situations in which more than one variable is changed on each iteration of the z-loop, use the [loopFile](#) keyword to read the values from a file.

If the main loop contains more than one simulation, then by default all of these simulations are executed in a single run of **PHREEQC**. This means that tags will not be updated between simulations. If this is needed, it is necessary to run the main loop simulations one at a time. This is done by setting the optional [oneSimulationAtATime](#) switch to `TRUE`.

#### Data-led calculations



The simulation(s) used for each data point depend on the value or range of values specified in the column defined by the `blockRangeColumn` of the data file. The pre-loop/main loop division is determined by the value in the `mainLoopColumn`.

Figure 4.2. Flow during the execution of data-led calculations ('simulate' or 'fit' calculation types) in which the

The 'fit' and 'simulate' calculation types both read in certain parameters from a fit data file. In order that the global optimization can include data calculated by different chemical models, each data point can point to a different chemical model (Figure 4.2). Each chemical model is defined by one or more simulations in the **PHREEQC** input code. These are specified by a data column in the fit data file - the column used for this is defined by the [blockRangeColumn](#). The default value for the simulation is 1 which is the value assumed if no [blockRangeColumn](#) is present in the fit data file. In this case, all values are calculated by the same chemical model. If more than one simulation is needed, then a contiguous range can be

entered, e.g. "1-2" (or equivalently "1\_2") to indicate that simulations 1 and 2 will be used. There should be no spaces in the string.

### Custom plots

The 'custom' calculation type can be used to generate data for a variety of **PHREEQC**-type calculations especially where repetition is required that is not covered under the normal **PHREEQC** options (Figure 4.3).

A custom calculation generally consists of zero or more pre-loop simulations which calculate various initializations and then one (or more) simulations which are iterated using **PhreePlot**'s x- and y-looping mechanisms. Normally it is the last line from the selected output generated from the last simulation that is accumulated in the 'out' file and used in any subsequent plotting.

If a z-loop variable is included, the whole input file is re-run for each z-value including any pre-loop simulations.

The following input first defines a 1 mmol/kgw solution of  $\text{CdCl}_2$  and then equilibrates this

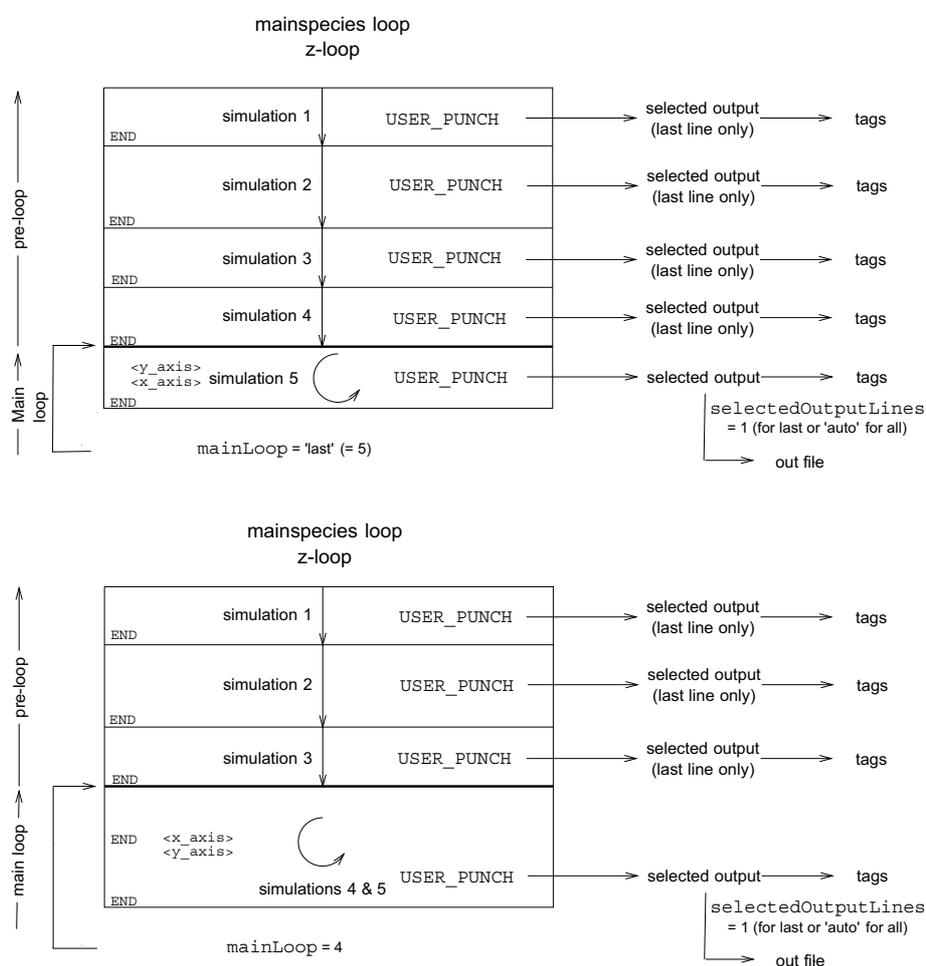


Figure 4.3. Normal flow during the execution of a multi-simulation input file for custom calculations. The output depends on various settings including whether each simulation is executed in turn with just the final simulation contributing to the 'out' file (upper figure) or whether the has been set to point to an earlier simulation (lower figure). Only simulations from that number forward are repeated during any 'looping' and are by default used to populate the 'out' file.

with carbon dioxide at a  $PCO_2$  partial pressure of  $10^{-3.5}$  atm. Solution 1 is saved and carried

forward to the second simulation. This simulation fixes the pH at 8.0 by titrating with NaOH and allows amorphous cadmium hydroxide to precipitate if its solubility product is exceeded (which it is). Note that a maximum of 1 mol NaOH is allowed to be used to prevent very high ionic strengths from being created (the Pitzer option would have to be used for very high ionic strength solutions).

```

SELECTED_OUTPUT #Simulation 1
  high_precision true
  reset false
USER_PUNCH
  headings Cd+2 SI_Otavite
  10 punch mol("Cd+2"), SI("Otavite")
SOLUTION 1
  Cd 1.0
  Cl 2.0 charge
SAVE solution 1
END

USE SOLUTION 1 #Simulation 2
PHASES
Fix_H+
  H+ = H+
  log_k 0.0
EQUILIBRIUM_PHASES
  Otavite 0 0 #Otavite is CdCO3
  CO2(g) -3.5 10
  Fix_H+ -8 NaOH 1
END

```

The selected output for this looks like this:

```

                Cd+2                SI_Otavite
4.409910346467e-007    0.000000000000e+000

```

This output is from the second (final) simulation. It gives the Cd<sup>2+</sup> concentration after otavite has precipitated most of the Cd. These data are also transferred to the 'out' file.

In this example, the first simulation sets up the initial Cd solution and the second simulation performs the reaction. The same effect could have been achieved by reducing the whole file to a single simulation by removing the END and USE keywords. The selected output then looks like:

```

                Cd+2                SI_Otavite
8.738892163591e-004    -9.999000000000e+001
4.409910346467e-007    0.000000000000e+000

```

with the first line of output being derived from the initial solution calculation and the second line having been derived from the second (reaction) simulation.

Another way of running both simulations together would be to set [mainLoop](#) to 1 so that both simulations are run together as 'main loop' simulations. By default, the 'out' file only picks up the last line of the selected output but if all three lines are wanted, [selectedOutputLines](#) for the simulation should be set to 3 or 'auto'. 'auto' will always transfer all the data lines to the 'out' file.

If only the final concentration is wanted and the two simulations are run separately, then it is also possible to omit the output from the first simulation by turning the selected output off then on again in the second simulation using the `-selected_output` identifier of the PRINT data block, e.g.

```

SELECTED_OUTPUT #Simulation 1
  -high_precision true
  -reset false
PRINT
  -selected_output false
SOLUTION 1
  Cd 1.0
  Cl 2.0 charge
EQUILIBRIUM_PHASES

```

```

    Otavite 0 0 #Otavite is CdCO3
    CO2(g) -3.5 10
    Fix_H+ -8 NaOH 10
SAVE solution 2
END

USE SOLUTION 2 #Simulation 2
PRINT
  -selected_output true
EQUILIBRIUM_PHASES
  Otavite 0 0 #Otavite is CdCO3
  CO2(g) -1.5 10
  Fix_H+ -8 NaOH 10
END

```

gives the selected output as:

```

          Cd+2          SI_Otavite
4.409910346467e-007    0.000000000000e+000

```

### *Knowing which minerals might form using the given database*

**PHREEQC** has no simple way of automatically inserting a valid set of minerals into an `EQUILIBRIUM_PHASES` keyword block such that any mineral that is predicted to form does form. This normally has to be done manually. The mineral names will depend on the database used and the solution composition. The `printphases.inc` [include file](#) extracts a list of all possible minerals by using the `SYS()` function. This include file can be added to an input file to get the mineral names printed to the file `PHREEQC.out`. These can then be pasted back into the input file as needed.

An alternative and slightly simpler approach for ht and grid plots is to just set the [resolution](#) to 1. This automatically inserts the `printphases.inc` code directly into the **PHREEQC** input stream just ahead of the first (and hopefully only) `SOLUTION` keyword block. It also ensures that the `PHREEQC.out` file is written and that all the `PRINT` settings are reset to `TRUE`. This will only work properly for single simulation input files and providing that there are no `USER_PRINT` blocks following the `SOLUTION` keyword block (these would override the inserted code).

With these provisos, a single iteration is performed with all loop variables set at their initial values and the names of all possible mineral species are written to `PHREEQC.[id].out` in a ‘User print’ output block, commented out and ready to paste into an input file.

It is possible to use **Phreeplot** to automatically generate a list of all possible mineral species in one simulation, write them to a tag, and then to retrieve this tag in the `EQUILIBRIUM_PHASES` data block of a subsequent simulation. This approach is used in `demo\minstab\allminerals.ppi` to generate a predominance diagram that automatically adds all of the minerals in the database to the list of potentially precipitating minerals. This must be used with caution since many minerals, while thermodynamically stable, do not form in a reasonable time scale.

It is possible to exclude certain minerals from these calculations by permanently removing them from the database (by commenting out), or by redefining the `log_k` for the reaction to make such a value as to make precipitation impossible, e.g.

```

PHASES
Hematite
    Fe2O3 + 6H+ = 2Fe+3 + 3H2O
    log_k          99

```

will push the reaction to the right and keep prevent precipitation of hematite. A collection of such exclusions can be collected together in a file and then ‘included’ at the appropriate place with `include` or `include$`.

## 4.6.2 Setting up the loop iterator

The z-loop or loop variable is used for discontinuous variables and will result in a separate calculation and associated curve (or plot) for each value of the loop variable. This contrasts with

the x- and y-variables which are designed for ‘continuous’ variables in which the resolution defines the number of calculations per curve.

There are several ways of defining a list of loop values: (i) use `loopVal` to define any list of numeric values; (ii) use `loopMin`, `loopMax`, `loopInt` to define a regular sequence of values, or (iii) if more than one variable has to be carried in parallel for each iteration, then a loop file must be created. The precedence over definitions is given by the sequence above.

In each case, each iteration of the loop increments the loop value to the next one in the list. This value is associated with the `<loop>` tag which can then be used in an input file. If `loopLogVar` is set to 1, the loop value is anti-logged,  $10^{\text{loop}}$ . So if the loop values are initially input as -3 -2 and -1, `<loop>` will take on the values  $10^{-3}$ ,  $10^{-2}$  and  $10^{-1}$ .

The loop file is an ASCII file which is read in free format. This file is primarily intended to contain numeric data but it can also include character data. It can optionally contain a header row with column names and an initial column with loop names. The format is deduced from the first two columns and first two rows of the file. Columns are either numeric or character. The first two columns of the first row determine if it is a header row (if both are character variables). The first column of the first two rows determine if loop names are present (if both are character variables). The remaining columns can be either numeric or character – this is determined by the type of data in the first non-header row. It may be necessary to introduce a dummy numeric column as column 1 or 2 to force the correct interpretation of the file.

The four possible formats are shown in Figure 4.4.

(a)	(b)	(c)	(d)
no header no loop names	no header loop names	header no loop names	header loop names
<i>num num</i> <i>num num</i>	<i>char num</i> <i>char num</i>	<i>char char</i> <i>num num</i>	<i>char char</i> <i>char num</i>
	<i>num</i> = numeric value <i>char</i> = character value		

Figure 4.4. The format of fit data files is determined by the type of data in the first two rows and first two columns of data.

The column headers if present are used to make the tag names, e.g. Na will make the tag `<Na>`. Make sure that the column headers, if present, give rise to unique tag names including in any extradat files.

If the header line is absent, then the tag names will be automatically set to `<loop1>`, `<loop2>` for numeric column 1, 2 etc. These tags can be used in the input file. `<loop1>` is also known simply as `<loop>`.

The loop names, if present, are used in exactly the same way as the loop names read in with the `labels` keyword. Names in the loop file takes precedence.

A blank line in the loop file forces a blank line to be written to the ‘out’ file in the corresponding position. This is useful for creating line breaks in plots.

#### 4.7 WRITING DATA TO ADDITIONAL SELECTED\_OUTPUT FILES

Apart from the data output to the primary `SELECTED_OUTPUT 1` file, it is also possible to monitor other data by writing to separate `SELECTED_OUT` files. For example using the `SELECTED_OUTPUT 2;-file extra.out;USER_PUNCH 2` combination will write any PUNCH’ed data to the file `extra.out`. In order for the data to be output to an actual file, the first [selectedOutput-File](#) option must be set to `TRUE` and the second optional setting can be set to ‘append’ or ‘asis’

depending on whether data for all iterations is to be accumulated or not.

## 4.8 RUNNING PHREEQC WITHOUT ANY PLOTTING

The looping facilities in **PhreePlot** make it useful for some types of repetitive **PHREEQC** calculations which do not require a plot. Setting [calculationMethod](#) <0 will suppress any plotting, as will setting [plotFactor](#) = 0. If data are to be read from a data file, as in fitting, then the [calculationType](#) = “simulate” setting should be used to avoid calling the fitting routine. The “simulate” setting can also be used to make a set of simulations after fitting, e.g. to plot a simulated curve.

The input data file, which is probably most conveniently prepared in a spreadsheet or database and exported in csv or tab format, contains the data to be used. Tags are created from the headers.

The `SIS/SIS.ppi` demo file gives an example of the use of ‘simulate’ for calculating saturation indices. It contains a translation table that assists in converting non-standard headings in the text data file to standard **PHREEQC** format. **PhreePlot** is used to loop one-by-one through a data file containing analyses of groundwater chemistry. It runs a small **PHREEQC** [include file](#) which contains the `USER_PUNCH` code necessary to calculate various saturation indices and other parameters. This can be readily modified. The results are accumulated in the ‘out’ file.

The use of a fit data file for passing on information is similar to the use of a standard loop file ([Section 6.2.1](#)).

## 4.9 INCLUDE FILES

### 4.9.1 Use of ‘include’ files

The input files can contain `INCLUDE` statements to pull in other files, e.g.

```
INCLUDE ht1.inc
```

The text following the `INCLUDE` statement, here `ht1.inc`, is the name of a file. The filename can be optionally embedded in quotes. The normal rules apply for the search path when looking for include files ([Section 2.4.6](#)).

All of the statements in this file will be inserted line by line at the insertion point. This substitution occurs when the input file is initially read, before any code execution. This makes it possible to have a library of commonly-used pieces of code. The include statement is recursive – an include file can itself contain references to other include files.

The **BASIC** program runs strictly in the order of the **BASIC** line numbers not necessarily the sequence of lines in the file. If a line number is repeated, the last one read is used. This means that it is possible to add edits to an include file by including an ‘edit file’ after the main file (see e.g. `ht1s.inc`).

Using include files can reduce repetition of commonly-used code and make it easier to manage such code. It also can increase the readability of input files.

**PHREEQC3** contains its own version of ‘include’ in the form of the `INCLUDE$` keyword. This is a more powerful form of include than **PhreePlot**’s since it is ‘dynamic’ (dollar for dynamic!): the include file is read anew each time the directive is encountered. Therefore an earlier piece of **PHREEQC** code within the same run may write or modify the contents of the include file using `PUNCH` statements for example. However, the main file only contains a reference to the include file, not the code itself, and so it cannot contain tags for substitution. In contrast, **PhreePlot** only reads the include file once – at the beginning, before the **PHREEQC** code has been executed, and it includes the text *as is* at this stage and so it can contain tags for later substitution. Conclusion – use `INCLUDE$` if you want to read a file

that is generated dynamically during a **PHREEQC** run but do not use it if the include file contains tags that need to be substituted. Remember that if the file is not found in the current directory, **PhreePlot's INCLUDE** automatically looks in the system directory whereas **INCLUDE\$** does not.

#### 4.9.2 Supplied include files

A large number of include files are provided for commonly-used functions. These will be found in the `system` sub-directory. The uses of some of them are summarised in Table 4.1.

Table 4.1. Some of the supplied include files and their functions

file	function
<code>ht1.inc</code>	for calculating predominance plots
<code>ht1combined.inc</code>	as above but combines all adsorbed fields for a common surface into a single field; also gives an option of using the mineral stability criterion for identifying boundaries
<code>ht1cCO3.inc</code>	as above but includes an additional total CO <sub>3</sub> constraint
<code>ht1cStability.inc</code>	as above but includes the stability criterion
<code>ht1s.inc</code>	as <code>ht1.inc</code> but also adds '(s)' to the labels for mineral names
<code>ht1minerals.inc</code>	as <code>ht1.inc</code> but also writes a list of all precipitating and potentially precipitating minerals to the log file (needs <code>out = TRUE</code> )
<code>ht1_phase_formula.inc</code>	as <code>ht1.inc</code> but also adds the mineral formula below the mineral name when labelling the plot
<code>minstabl.inc</code>	used for calculating traditional mineral (only) stability diagrams
<code>ht1allminerals.inc</code>	as <code>ht1.inc</code> but automatically adds all possible minerals as potentially precipitating mineral phases
<code>printphases.inc</code>	used to print the possible mineral phases to the <code>PHREEQC.out</code> file
<code>speciesvspH.inc</code>	used for making species-pH plots
<code>logspeciesvspH.inc</code>	used for making species plots with log y-scale

`ht1.inc` can be used to calculate a predominance diagram. There are many variations of this which vary in how they promote a species to be top of the list (predominant) and it relatively straightforward to use these examples to devise your own custom method. If adsorbed species are present, then their concentration is considered on a species by species basis just like solution species. `ht1combined.inc` is similar except that all adsorbed species of one element and one surface are combined into a single species (a 'superspecies') for the purposes of the predominance calculations (ranking) and for plotting. Other include files are variations on these. See the examples in the `\demo` directory for their use.

#### 4.10 USING PHREEQC'S `_RAW` AND `_MODIFY` KEYWORDS

**PHREEQC** (Version 3) introduced new keywords to retrieve and modify various existing data structures. These are based on existing keywords with the suffixes `_RAW` and `_MODIFY`. They are intended to provide more flexibility in the ways that the chemical system can be defined and modified, and provide ways of reading in data structures sent to a file by `DUMP`. These new keywords are not expected to be widely used.

They enable the updating of concentrations to be simplified and maybe speeded up. For example, the `SOLUTION` keyword always does an initial solution calculation whereas `SOLUTION_MODIFY` does not. It may also be possible to avoid initial exchange and initial surface calculations in an analogous way.



## 5 PhreePlot input and output files

---

### 5.1 INPUT/OUTPUT FILES

#### 5.1.1 Use

**PhreePlot** uses a number of files for input and output. The default ‘settings’ file, `pp.set`, is used to read in default values for all keywords. These are modified, and the **PHREEQC** chemistry part is added in the ‘normal’ input file (usually with a `ppi` extension), and finally keyword values can be overridden with the `override.set` file.

All of these input files are in ASCII text format and so can be read and written with a normal text editor. The input files determine the calculations that will be carried out. The extension is stripped from the input filename and this is used as the ‘root’ for automatically naming the output files. Many of the output files are optional and their production is controlled by a series of logical switches which can be set to `TRUE` or `FALSE`.

In ‘Safe’ mode (the way **PhreePlot** has currently been set), all the necessary files needed to produce the specified plots, and to be able to replot them, will be created even if their logical switches have been set to `FALSE`. Where file switches are specified to be `FALSE`, the corresponding files will be deleted at the end of the run if present, even if they were created from an earlier run.

Any existing files with the same name as the files to be created/deleted will be overwritten or deleted without warning.

#### 5.1.2 Difference in execution of input files between PhreePlot and PHREEQC

Aside from the substitution of tags with values in **PhreePlot** input files, the `CHEMISTRY` part of a **PhreePlot** input files looks very like a **PHREEQC** input file, and in fact, it is often easiest to test small pieces of code using **PHREEQC** or **PHREEQC Interactive**. When there is only one simulation in a file, there is essentially no difference in terms of execution.

However, where there is more than one simulation, **PhreePlot** has greater flexibility in the way that individual simulations are run. There are two key features here: (i) a separation between ‘pre-loop’ simulations and ‘main loop’ simulations, and (ii) the way that the main loop simulations are executed.

The *modus operandi* of **PhreePlot** is that some simulations may be required to set up the database, define other fixed things, prepare initial solutions etc and these need only be done once. These are called ‘pre-loop’ simulations. Following this in terms of layout and execution, there may be one or more ‘main loop’ simulations which are iterated or ‘looped’. Normally there will be one or more x- and y-axis tags in the ‘main loop’ part which will be altered during each iteration, thus varying the output, and ultimately preparing a set of data for fitting or plotting.

**PHREEQC** necessarily runs all simulations consecutively and without user intervention. Data structures are carried from simulation to simulation and some between-simulation user data can be transmitted via the Basic `PUT()`/`GET()` functions, but there are few other opportunities for dynamically altering values given in the input file.

**PhreePlot** has greater opportunities since it has the option to control the way that a multi-simulation input file is executed. As indicated above, there is the basic division between pre-loop and main loop simulations. There is another important option. **PhreePlot** feeds the input file that it has read into **PHREEQC** line by line. Calculations are only begun when a

whole simulation has been read in (as defined by an `END` statement) but **PhreePlot** decides when to look at the results of each simulation by exiting **PHREEQC** and looking at the output, updating the tag dictionary, making new substitutions etc.

Two options are available in **PhreePlot**: (i) ‘one simulation at a time’ mode or (ii) ‘all at once’ mode. (i) cedes control to **PhreePlot** after every simulation has been executed which gives some opportunity to alter values for subsequent simulations. (ii) is faster in execution but **PHREEQC** only returns to **PhreePlot** after all simulations have been executed. This means that there is no opportunity to intervene midway.

**PhreePlot** normally operates as follows:

(i) all pre-loop simulations will be run ‘one at a time’ (being executed just once, speed is not such an issue while the added flexibility can be useful).

(ii) there is the option of running main loop either ‘one at a time’ or ‘all at once’.

These two features are controlled by the [mainLoop](#) keyword. e.g.

```
mainLoop 3 false
```

means that the main loop simulations start at simulation 3 (simulations 1 and 2 are therefore ‘pre-loop’) and that ‘one simulation at a time’ is false, i.e. all main loop simulations will be run together in one block.

The default in `pp.set` is

```
mainLoop auto false
```

where `auto` normally refers to the last simulation, i.e. the looping will only occur over the last simulation. For [calculationType](#)’s `fit` and `simulate`, `auto` is set to 1.

Using [debug](#) equal to 2 or greater will log the details of how the simulations are executed to the log file.

## 5.2 INPUT FILES

### 5.2.1 Different types of input file

There are three main types of input files: (i) those that define certain keyword values or settings plus the chemical definition of the problem and dictionary files (‘main input files’); (ii) those auxiliary files that provide additional data such as data for fitting and additional data or text for plotting (‘data input files’), and (iii) those that contain chunks of **PHREEQC** code to be included in one of the main input files (‘**PHREEQC** input files’).

This section describes the first of these while the separators used for parsing input files is described in [Section 5.2.6](#).

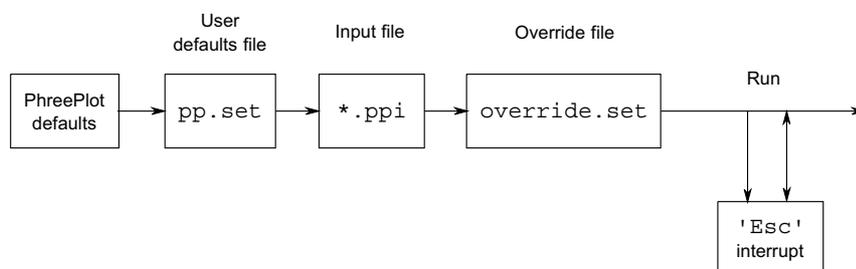


Figure 5.1. Diagram showing the sequence of setting of the keywords.

**PhreePlot** runs in response to the settings of various keyword-value pairs and lists. The values associated with these keywords can be defined in various ways (Figure 5.1). In running order, these are:

1. **PhreePlot** program defaults: set by **PhreePlot** internally; usually provide minimal functionality;
2. the `pp.set` file: user-defined default values read from a file; contains general preferences;
3. the main input file, the one given on the command line. It defines values for the particular problem of interest and normally contains the line 'CHEMISTRY' somewhere in it. This must be on a line by itself. It divides the input files into two with **PhreePlot** keywords in the upper section and **PHREEQC**-format chemistry, if any, in the lower section. It is best if this main input file is given the `ppi` file extension so that it can be associated with the **PhreePlot** program;
4. the `override.set` file: useful for overriding one or more settings without having to edit the main input file(s);
5. input made during interrupts during execution of **PhreePlot**: emergency redefinitions, e.g. changing the debug level (see [Section 6.6](#)).

Normally when a keyword and its settings are read, these settings will override all previous ones for this keyword. The exceptions are for [numericTags](#), [characterTags](#) and [overlay](#) where multiple instances will add to the list of tags or overlay files to be processed.

The full list of keywords is normally given in the default `pp.set` file. The `pp.set` and `override.set` files should always be in the `system` sub-directory if present. The `pp.set` file should be modified to set commonly-used attributes that remain constant between runs, including system-specific features such as the filepath for **Ghostscript** as well as a wide range of plotting parameters including the preferred units of length.

The override file (`override.set`), if present, is read after the input file and can be used to override any previously-defined values. It is especially useful for temporarily changing attributes for a whole series of files called via a batch file, e.g. changing the plot method, a font, a colour or turning the beep off.

### 5.2.2 Structure of the main input files

These files are the problem file (`*.ppi`), the `pp.set` file and the `override.set` file.

Although **PhreePlot** input files are rather unstructured, they logically divide into the following four sections:

SPECIATION	Details of the speciation calculations
FIT	Details of any fitting
PLOT	Controls the plotting parameters
CHEMISTRY	Contains the <b>PHREEQC</b> code.

The first three of these four sections headings may be included anywhere in the input files. These section headings are only included for improving the legibility of the files and are not used by **PhreePlot**. If present, the `CHEMISTRY` keyword signals the beginning of **PHREEQC**-type input and, must appear as the last entry in the upper **PhreePlot** section, i.e. the main input file must always end with the `CHEMISTRY` section if it is expected to do any chemical calculations.

The structure of a typical input file is therefore:

...

```
<PhreePlot section heads and keywords that define various keyword settings and tag values.
This section also defines the looping parameters and what type of plot, if any, will be produced>
```

...

CHEMISTRY

...

<**PHREEQC**-format chemical input which is normal **PHREEQC** code but can include optional **PhreePlot** tags for substitution during execution>

...

There is essentially no limit to the number of lines in the **PhreePlot** or **PHREEQC** parts. The **CHEMISTRY** line, which should be on a line of its own, defines the divide between the two sections.

The **CHEMISTRY** section includes the **PHREEQC** code. This can only be included in the main input file and any 'include' files called by the main input file. This determines what is calculated and has almost the same format as a normal **PHREEQC** input file. The principal difference is that it can contain special tags ('<...>') that are substituted with appropriate values before running **PHREEQC**.

Results from **PHREEQC** calculations are communicated to **PhreePlot** via the selected output which itself is generated in response to the **PHREEQC** `USER_PUNCH` and `SELECTED_OUTPUT` blocks.

Therefore the **CHEMISTRY** section is essentially a **PHREEQC** input file with tags. The tags provide placeholders for substituting variable values generated by **PhreePlot** and give **PhreePlot** the ability to loop, fit data to models etc. The **PhreePlot** section defines how the tag values are generated. The keyword values can be floating point (stored as double precision), integer, character or logical.

### 5.2.3 The input file pre-processor

Where a simulation is repeated many times with the only change being an increment in one or more numbers, the simulations can be replaced with a single 'template' simulation which has tags indicating the start and end of the sequence to be repeated, the increment and where to substitute the generated number. This part of the code is executed before the input file is processed. The input file pre-processor is described in detail in [Section 13](#).

### 5.2.4 The colour dictionaries and other files

There are two colour dictionaries which store the colours used for the lines, points and fills: (i) line colour dictionary for plots based on a custom plot, and (ii) the fill colour dictionary for predominance diagrams. Contour plots do not of themselves use the dictionaries.

These files can be edited to change any colours. For fill colours, this is all that need be done. For line and point colours, it is necessary to set [useLineColorDictionary](#) to 1 or 2 to force the use of the dictionary.

There are also optional data files for loop variables, for data to be used in simulations or fits, and for 'nudging' the position of labels in plots.

### 5.2.5 Format of all input files

#### *Physical and logical lines*

All input files including data files have a similar structure. The input format conventions are similar to those used for standard **PHREEQC** input files. The maximum length of input lines is only limited by memory but most strings and character expressions are limited to 10000 characters.

A physical line is a text string ending with a normal line ending which for the Windows operating system is <CR><LF>. Each physical line appears as a distinct line of text in a text editor. It can consist of less than one, one or more than one logical lines.

A logical line is a string which is interpreted as a single block of data by **PhreePlot**. The keyword-value(s) combination of **PhreePlot** input files must always be present on a single logical line.

Strings containing spaces (or more specifically, separators) should be enclosed in quotes, paired single or double. One or more separators must precede and follow these quotes for it to be recognised.

Any input following a comment character (#) is ignored for the rest of that logical line. This includes ; and \ (see below). Blank lines and lines which are entirely made up of a comment are not counted as logical lines and are ignored. So

```
pdf TRUE \
<BLANK LINE HERE>
png TRUE
```

will fail because the continuation will ignore the blank line and join the other two lines to give

```
pdf TRUE png TRUE
```

Logical lines are terminated by a normal line ending, or by a semi-colon (;). A comment character takes precedence over ‘;’. For example, the comment in

```
# PHASES; Fixed_H+; H+ = H+; log_k 0.0
```

will comment out all four logical lines.

The above rules for # and ; even apply when embedded in quotes. Their special behaviour takes precedence over quotes. **Therefore it is not possible to use these characters even in quoted text strings, i.e. “Sample #76” and “Bloomington; Rochester” would produce errors.** This is not true in **PHREEQC** where the quotes take precedence.

A logical line may be split across two or more physical lines by using a continuation character. A continuation character is a backslash (\) providing it is present as the last non-whitespace character on a physical line after comments have been removed. So unlike **PHREEQC**, this is true even when the \ is followed by spaces and a comment character, i.e.

```
numericTags <logH> = -<x_axis> \ # comment
              <pH> = -<logH> # -pH
```

is valid as is

```
#pdf \
T
```

is not.

Tabs are treated as whitespace by **PHREEQC** but can be significant in data files. Consecutive tabs may signify a blank or missing field. However, a line consisting only of tabs is always treated as a blank line. Data files prepared by pasting from a spreadsheet into a text editor can contain tabs, including trailing tabs. Such files should be read using the tab as a separator. This is done by adding “\t” after the filename. An alternative to this way of reading null values is to explicitly use the ‘missing data’ code, namely -99999.

A colon (:) is sometimes used to specify the ‘end of list’ as in [nudge](#).

### *Specifying keyword-value pairs and keyword-lists*

Keywords and their values are separated by any number of separators on a logical line.

Quotation marks should always be used when there is a space or tab embedded within a character variable. Numbers can be quoted too. A null character variable is entered as a pair of quotation marks with or without one or more blanks, e.g. “”, ‘ ’, “ ” or “ ”. It is necessary to use this format when entering a blank value for a character variable.

The following are some examples of valid input lines:

```

jobTitle      Iron
jobTitle      "Iron hydrolysis"
jobTitle      `Iron hydrolysis`
calculationType  htl;
calculationType  htl
calculationType  htl #This is a comment
pxmin 0;  pxmax 10;  pymin -10;  pymax 20
pxmin 0pxmax 10 pymin 10  pymax 20

```

### *Format of keywords and their associated values*

Many keywords are followed by just a single value of a specified type, either an integer, a floating point number, a character string or a logical. Case is not significant except within character strings and tags. Other keywords are followed by a list of variable length, e.g. [mainSpecies](#).

An integer is any set of digits with or without a sign. A number is any set of digits with or without a valid exponent (in E format), decimal point or sign and includes all integers. A character string is any set of valid characters (see below), and is optionally placed within a pair of delimiters (a pair of single or double quotes). A logical value can be entered as TRUE or FALSE or T or F, irrespective of case. Examples are given below, each value being separated by a comma:

```

Integers: 0, 12345
Numbers: 1, 2., 3.1, 4e0, 5E0, 6d0, 7D0
Character expressions: PhreePlot, "PhreePlot", "PhreePlot program", "", " ", 'This is
                    "PhreePlot"', "This is `PhreePlot`"
Logical: t, T, true, TRUE, True, f, F, false, FALSE

```

## 5.2.6 Data separators and parsing input files

All of the input files consist of a set of logical lines with a collection of zero or more ‘words’ on a line. The difference between physical and logical lines is described above. In many cases, the first logical line of a file is used as a ‘header’ to describe the data that follows. In some cases, these header names are converted to variable (tag) names for the columns. All of the input files are read in ‘free format’, i.e. the column position of the entry on the line is not important.

The words on a line are separated by ‘data separators’, sometimes called delimiters. The parsing of input files (separating the words) depends on the structure of the input file and the data separator(s) specified. You have to ensure that the two match so that the file can be parsed correctly.

Commonly-used separators are spaces, (horizontal) tabs and commas.

The main input files are read in ‘very free format’ in which case all of the three main separators – a blank, tab or comma – are treated as valid separators and consecutive separators of any sort are treated as a single separator.

Quotes should be used to specify character strings containing these separators ([Section 5.2.5](#)). A quoted string should always be followed by a separator or an end-of-line marker. If not, the text after the closing quote is added to the quoted part of the string and an additional quote added to the end of the string.

Spaces and other special characters (other than ; and #) enclosed within quotes (single or double) are treated as part of a character string and will not be split.

Since data files such as those used for fitting ([datafile](#)) or plotting (e.g. [extradat](#)) can come from many sources and can include blank fields, a somewhat more rigid type of ‘free format’ is required for this type of file. The default data separator is always taken from the first entry in [dataSeparators](#) but this can be overridden by appending a format string after the filename.

Valid entries for this format string are:

- “\w” signifies whitespace (one or more blanks or tabs)
- “\b” signifies one or more blanks

"\t" signifies a single tab (often found in files derived from spreadsheets)

",," signifies a single comma (for csv files)

"\" or "" (null string) signifies whitespace or one or more commas (if at the end of a line, make sure that \ is embedded in quotes otherwise it will be interpreted as the line continuation character). This is the 'very free format' option that is used to read the input files and will read many of the most-common types of formatted files.

"char" where "char" signifies any valid single character.

Note that when a single tab, comma or character are used as separators, consecutive separators will define a blank field. This means that blank fields can be preserved when reading files based on single character separators such as those produced by Microsoft Excel and OpenOffice Calc.

### 5.2.7 Case sensitivity of input

Most of the text in the main input files is case insensitive. This includes all keywords. The only exceptions are the names of tags (anything between angle brackets) including text within tags (e.g. <input...>) and the names of column headings used to define columns in a data file – these are case sensitive. File names under Windows are not case sensitive.

In general terms, things that have been defined by **PhreePlot** are not case-sensitive whereas things that you have defined are case sensitive.

### 5.2.8 Reporting of errors in input files

**PhreePlot** stops if it detects any errors in one of the keyword input files. These errors include syntax errors as well as any errors based on 'compile time' inconsistencies in the settings. These are signalled with an error message to the screen and to the log file if open, e.g.

```
File: test.ppi:6
Keyword: xmax
Input: xmax 1x2
Error: Expecting a number.
```

The message indicates the file involved and the position in the file where the error was detected in terms of the physical line (here line 6). The keyword involved (if known), the line of text where the error was detected, and an error message are also given. These may not identify the location or prime source of error exactly but should be sufficient to help to identify it.

Where an error occurs within a section where continuations (\) are being used, then the physical line indicated will be the end of the position of the offending section and the word will be a negative number indicating the number of words to count back to the offending input (roughly).

The whole input file is checked before reporting the error and exiting. Where several errors occur on the same logical line, only the first error will be reported.

Errors in other input files are signalled in a similar way.

## 5.3 TAGS

### 5.3.1 What are tags used for?

Tags are special symbols which have values associated with them (i.e. variables). Each tag has a name which is a text string embedded within angle brackets, e.g. <x\_axis> is the tag that holds the current value of the x-axis variable.

When tags are used within a file, they are essentially place markers which indicate where vari-

ous substitutions are to be made at a later time. Tags can be used to define ‘global’ variables that retain their values between simulations. Some tags are automatically created by **PhreePlot** in order to make their values available for subsequent use.

Tags come in two flavours. Tags can be either numeric or character depending on the type of value that they represent.

Each tag has a tag expression associated with it. These are evaluated before running **PHREEQC** and the derived tag values substituted in the appropriate places within the script. The tag expressions for numeric tags can include simple arithmetic expressions as well as more complex expressions using other previously-defined tags.

If the substitutions are not made correctly within the **PHREEQC** code section, e.g. because a tag is not recognised or not defined, **PHREEQC** will normally fail because of the illegal characters found at run time.

Tags can be placed anywhere in an input file and in the optional [extraText](#) and [extraSymbolLines](#) files. There is no limit to the number of tags used.

Tags, combined with the looping facilities within **PhreePlot**, are used to vary the calculations made by **PHREEQC** in a dynamic way. Some tags are defined by **PhreePlot**, others are defined by the user. They provide a simple way of defining variables and of giving **PHREEQC** some basic looping capabilities without changing the format of the **PHREEQC** input file greatly.

Each tag has three parts: (i) tag name; (ii) ‘=’, and (iii) a single expression enclosed in quotes if necessary, e.g. <mytag> = “my expression”. The spaces either side of the equal sign are optional.

### 5.3.2 Rules for choosing tag names

Tag names should always start and finish with open and closed angle brackets, e.g. <tagname>. Tag names should preferably be restricted to upper and lower case letters, numbers, the dollar sign, and the underscore. Other characters can be included although they will be temporarily replaced by a full stop (‘.’) and so tag names with multiple characters such as +, - etc. can become degenerate. This also applies to tag names automatically created from the selected output and fit data files and from the fit parameter names so the parent names (column headings) should also follow this advice.

The first character of a tag name must be alphabetic, i.e. in the sets a-z or A-Z. Tag names should not contain any spaces

System tag names are ‘reserved’ names and should not be redefined. These are: <x\_axis>, <y\_axis>, <loop>, <logloop>, <mainspecies>, <timedate>, <nexecute>, <systemtime>, <PHREEQC\_status\_0>, <pxmin>, <pxmax>, <pymin>, <pymax>, <p2ymin> and <p2ymax>.

Case is significant in tag names. There is no length limitation to tag names.

If the last character of a tag name is a dollar sign (\$) then that will force the tag to be a character tag. This overrides any attempts by **PhreePlot** to determine the tag type itself.

### 5.3.3 Tag expressions

Tag expressions are the text on the right-hand side of a tag equation. These are stored as character strings and can contain any valid combination of numbers, character strings and other tag names (see below). The tag expression can be any length. Long expressions can be subdivided and saved as separate sub-expressions.

Numeric tags store numeric values or numerical expressions; character tags store character strings or character expressions.

### 5.3.4 Numeric tag expressions and available functions

[Numeric tag expressions](#) can be simple numbers such as 1, 1.2, 1.2e2, 1.2d-4 or arithmetic

expressions such as  $2^4$ ,  $\log_{10}(3.5)$ ,  $2+(3^4)$  etc. The arithmetic operators available are: +, -, \*, / and ^ (exponentiation).

The following functions are also allowed: `abs`, `exp`, `log10`, `log`, `sqrt`, `sinh`, `cosh`, `tanh`, `sin`, `cos`, `tan`, `asin`, `acos`, `atan`, `rand` and `nrnd`.

The random number generators, `rand` and `nrnd`, return a single pseudo random value generated from the uniform (range = (0,1)) or normal (mean = 0, standard deviation = 1) distributions, respectively. Both functions take a single integer argument which acts as a seed. If the seed is positive this value is used to start the distribution. Using the same seed on different runs means that the same pseudo random sequence will be generated. Using 0 or a negative integer value for the seed means that the system date and time are used to generate the start of the random sequence. This will ensure that a different sequence is started for each run.

Parentheses are used for specifying precedence in the normal way. All numeric tags are stored and evaluated with high precision (double precision).

Tag expressions can also include other tag variables providing that they have already been defined. The sequence in which the tags are evaluated is controlled by the order in which they are defined.

Undefined numeric tags have the value `UNDEFINED` which is stored internally as `-99999`.

Valid tag expressions are:

```
log10(<loop>)
2*<x_axis>
```

When tag values are substituted, they are rounded and then trimmed of leading and trailing spaces. Therefore

```
-<x_axis>
```

should work providing that the value of `<x_axis>` is not negative.

### 5.3.5 Tags for character variables

These tags are substituted at the indicated positions. If the tag expression contains spaces, enclose in quotes. Quotes are always removed before substitution and so they may need to be added to the tag expression, e.g. "`<mainspecies>`" in order that the substituted expression is correctly parsed.

### 5.3.6 System tags

Certain tags are automatically created and updated by **PhreePlot**. These are:

<code>&lt;x_axis&gt;</code>	the value of the x-axis variable (numeric)
<code>&lt;y_axis&gt;</code>	the value of the y-axis variable (numeric)
<code>&lt;loop&gt;</code>	the value of the z-loop variable after being exponentiated ( $10^x$ ) if necessary (numeric)
<code>&lt;logloop&gt;</code>	$\log_{10}$ of the value of the z-loop variable (numeric)
<code>&lt;mainspecies&gt;</code>	the name of the main species (character)
<code>&lt;nexecute&gt;</code>	the number of times that <b>PHREEQC</b> has been called
<code>&lt;timedate&gt;</code>	a time (hr:min:sec.millisecond)/date string with the format 23:30:45.123 23 September 2004 (character)
<code>&lt;systemtime&gt;</code>	uses the system clock to get the elapsed time (in sec) since the beginning of <b>PhreePlot</b> execution (this reflects 'wall time' not cpu time). Resolution about 1 msec.

<PHREEQC_status_0>	returns the exit status from the last PHREEQC run: 0 = OK, >0 = error
<pxmin>	the value of <a href="#">pxmin</a> (numeric)
<pxmax>	the value of <a href="#">pxmax</a> (numeric)
<pymin>	the value of <a href="#">pymin</a> (numeric)
<pymax>	the value of <a href="#">pymax</a> (numeric)
<p2ymin>	the value of <a href="#">p2ymin</a> (numeric)
<p2ymax>	the value of <a href="#">p2ymax</a> (numeric).

These tags are known as ‘system’ tags and are updated throughout a run. They have reserved names, effectively making them ‘read-only’. They should not appear on the left-hand side of a tag expression.

There are also some additional tags which are created on start-up or after fitting:

<command_line>	the values of the $n$ command line arguments ( $n=0$ gives the name of the <code>pp.exe</code> file, $n=1$ gives the name of the <code>ppi</code> file, $n=2, 3, 4, \dots$ give any additional arguments) (character)
<R2>	the value of $R^2$ after a successful fit, see <a href="#">Section 5.3.7</a> (numeric)
<RMSE>	the RMSE after a successful fit (numeric)
<nFit>	the number of ‘observations’ in a fit (numeric)
<fitMethod>	the fitMethod (char)
<objectiveFunction>	the objective function, “L1”, “L2” etc (char).

If a [loop file](#) is read, then a separate tag value is automatically created for each column. These are by default named <loop1>, <loop2>, ... for column 1, 2, ... but they will be named after their column header names, if present.

Other tag names are reserved for formatting text ([Section 7.6.3](#)). These are:

```
<sub> and </sub>
<sup> and </sup>
<i> and </i>
<b> and </b>
<g> and </g>
<subsup> and </subsup>
<br>
```

Some other tags are automatically defined by the user or automatically created during the course of calculations ([Section 12.13](#)) and can be used in an [extraText](#) file.

### 5.3.7 User-defined tags

User-defined tags are defined in one of the input or data files using the [numericTags](#) or [characterTags](#) keywords. The order of definition is important since once defined, these tags can themselves be used to define new tag values in subsequent tag expressions. Ultimately every numeric tag will need to be evaluated to provide a numeric value ready for substitution in an input file.

The order of evaluation of numeric tags is given in [Section 5.3.8](#).

Examples of numeric tag expressions are:

```

<log_H> = 7.5
<log_H> = -<x_axis>
<pH> = -<log_H>
<H> = 10^(-<pH>)
<Cu2x> = "TOT("Cu") * 2"

```

Substitution takes place on each iteration just before the **PHREEQC** calculations are performed.

Numeric tag expressions can include other numeric tags but character tags must not be used in numeric tag expressions. For example

```

<x> = "4 + <x_axis>"
<y> = "6 + <y_axis>"
<z> = <x>+<y>

```

are all valid numeric tags. Note the use of quotes where the tag expressions contain spaces. The tag expression must appear as a single text string.

Character tag expressions (the right-hand side) must also be single strings and so enclosed in quotes if they contain spaces. They can contain one or more tags, numeric and character, and other text. Numeric tags are evaluated at the time of printing. Tabs are expanded to three spaces. Valid trailing whitespace is preserved, i.e. if it is part of a quoted string. Valid expressions are therefore

```

<c1>="Example " # trailing space ignored - the outer quotes are discarded
<c2>=' "Example "' # trailing space is included
<c3>="<c2>6"

```

Illegal character tag expressions are

```

<c5> = "Title"+<c2>
<c6> = "<mainSpecies>+Cu"

```

where <c1>, <c2> and <c3> are character tags, are invalid tag definitions because the addition mixes character and numeric tags.

Numeric and character tags can be defined in [extradat](#) files in much the same way that they are defined by selected output.

### 5.3.8 The scope of tags, their initial values and their order of evaluation

Each tag is defined by a tag expression. Since these expressions can themselves contain tags, it is important to understand the order in which they are evaluated in order to avoid a tag referring to an as-yet undefined tag or getting an out-of-date value for a tag.

Tags can be defined in a number of ways: by **PhreePlot** itself (system tags), from user-defined tags in an input file, from reading a loop file or fit data file, from the selected output file, or as a result of fitting.

The tags, their expressions and their current values are stored in a tag dictionary. This is used to substitute the values of any tags found in the input files before carrying out the next simulation. The whole tag dictionary is available for all simulations.

Tags can also be used in any text strings that are used in plotting: [plotTitle](#), [xtitle](#), [points](#) and [lines](#) and their 2y equivalents, [customXcolumn](#) and in [text](#) lines and [extraText](#) files. Tags used in the 'lines' and 'points' lists can themselves be lists.

The initial value of all numeric tags is set to UNDEFINED (-99999) but can be set to another value with the [initialValue](#) keyword. This same value is applied to all undefined numeric tags. The initial value of character tags is set to the null or empty string.

It is also possible to set the initial value of an individual tag by using a pre-loop simulation, e.g.

```

SOLUTION
SELECTED_OUTPUT
  -reset FALSE

```

```

USER_PUNCH
  -heading z
10 PUNCH 1.0
END

```

will set the initial value of the <z> tag to 1.0. SOLUTION ensures that the selected output is actually written. A pre-loop simulation is only executed once.

After a block of one or more simulations has been computed by **PHREEQC**, new tags are formed if appropriate and all tag values are updated. This updating only occurs after all the simulations within the block have been completed. **PHREEQC** has complete control during this execution phase. Therefore tag values cannot be passed from one simulation to another when they are part of the same execution block since execution does not leave the **PHREEQC** module and so the tags cannot get updated by **PhreePlot**. This has implications on how the input file is set up.

With some discretion, tags can be used in the ‘upper’ part (the part before CHEMISTRY) of an input file as well as the in **PHREEQC** section (the part that follows CHEMISTRY). Do not use tags in the upper part to alter the way that **PhreePlot** actually executes. Tags can also be in [extraText](#) and [extraSymbolsLines](#) files which, if present, are updated during the plotting.

Once set, tag values retain their values until reset. Tags provide a simple mechanism for passing a numeric value from one **PHREEQC** simulation to another as well as for providing the values of certain system variables which can be used for looping and other tasks. Tags can also be used during the plotting phase to control text input and its positioning.

The order of evaluation of numeric tags (first to last) is:

system tags	defined internally by <b>PhreePlot</b> (<x_axis>, <y_axis>, <loop>, ...);
independent variables	from the column headers in a loop or data file;
extradat file tags	tags defined by a two-line (header and data) extradat file;
USER_PUNCH tags	the names of the tags defined in the header line of the SELECTED_OUTPUT file created in a <b>PHREEQC</b> USER_PUNCH data block within the Chemistry Section. The values are those that were ‘PUNCHED’;
fit parameters	from <a href="#">fitParameterNames</a> and <a href="#">fitParameterValues</a> as defined in one of the input files, or after fitting (<R2> etc);
user-defined tags	from <a href="#">numericTags</a> in one of the input files defined in the order the files and tags are read.

The input files are read in the order:

- (i) the user-defaults file (*pp.set*)
- (ii) the main input file (*\*.ppi*)
- (iii) the override file (*override.set*).

The tags should not be used until after they have been defined, e.g. if a tag is defined in the second simulation, it should not be used until the third or later simulations). Substitution of all tags takes place before execution of a simulation and so the values of tags created during an execution cannot be used to update other tags that depend on the values created during that execution. For example, USER\_PUNCH tag definitions cannot refer to other USER\_PUNCH tags defined in the same simulation.

The input files can contain tag expressions which may themselves refer to other tags whereas the system, user punch, and fit tags are generated automatically by **PhreePlot** and simply have numeric values associated with them, i.e. they are read-only.

Tags can be used to pass numeric values from one simulation to a later one (this is also possible using PHREEQC's PUT/GET mechanism). For example, it may be wanted to subtract the initial value of a calculated variable such as the pH from all subsequently generated pH values to find the change in pH. This can be done by first generating the initial pH in a simulation. Send this pH to the selected output using a USER\_PUNCH data block and a column name such as 'pHorig'. This will automatically generate a tag <pHorig> with the desired value which will be stored for the duration of the run. In subsequent simulations, either write the new pH to the selected output using a new column name such as 'pH' or generate the change in pH directly in the USER\_PUNCH data block (e.g. `la("H+") - <pHorig>`) and output this difference directly to the selected output. In the first case, this will create a <pH> tag with a new value each time the simulation is run. Use [numericTags](#) to subtract the two.

In order to see which tags have been defined and their values, set `debug=1, 2 or 3` and enable the log file (`log TRUE`). A list of the tags defined at each iteration and the values of all tags used will then be written to the log file. These tables can be used to identify undefined tags.

### 5.3.9 Examples of the use of tags

The following example shows how user-defined tags can be used to manipulate the PHREEQC input file when there are multiple simulations (ENDS) and when the early simulations prepare for looping on the final simulation.

Adsorption is defined with the SURFACE data block and in one of its forms requires values for the number of adsorption sites (in moles), the specific surface area (in m<sup>2</sup> per gram) and the mass of adsorbent (in grams).

```
SURFACE
surface binding-site name, sites, specific_area_per_gram, mass
```

In order to see how the amount of metal adsorption might vary in a system as the specific surface area changes, it is reasonable in the first instance to assume a constant surface site density (i.e. a constant number of sites per m<sup>2</sup>). For the weak sites of HFO, we have

```
isite = sdm/gfa
```

and

```
sdm = isite/isa
```

where

```
isite = initial number of sites (mol)
sdm = density of sites per mol HFO (mol/mol),
gfw = gram formula weight of HFO,
isa = initial specific surface area (m2/g),
sd = site density of sites (mol/m2)
```

and

```
m = mass (g).
```

So for any other specific surface area, sa, the number of sites (mol) is

```
site = sa*sdm*m.
```

This can be implemented by defining a series of numeric tags as follows:

```
<initial_site_density_w_per_mol> = 0.2 mol/mol Fe \
<gfw> = 89 g/mol \
```

```
<initial_site_density_w_per_g> = <initial_site_density_w_per_mol>/<molecular_wt> \
<initial_specific_area_per_g> = 600 m2/g
```

Note the structure is

```
<tag> = <tag_expression>
```

where the tag has a unique name (case significant), followed by an equal sign (spaces optional), followed by an expression. The expression can contain other tag values provided they have already been assigned a value.

Therefore

```
<site_density_w_per_m2> = <initial_site_density_w_per_g>/(<initial_speci-
fic_area_per_g>) \
```

and for any surface area and mass, we have

```
<surface_area> = 300 m2/g \
<mass> = 1 \
<sites> = <surface_area>*<site_density_w_per_m2>*<mass>
```

The final tag defines the number of sites as required by **PHREEQC**. The density of strong sites can be defined similarly.

The **PHREEQC** input is therefore given as:

```
SURFACE 1
-equilibrate with solution 1
Hfo_w <sites> <surface_area> <mass>
```

In order to create a plot of the amount adsorbed vs surface area, `<surface_area>` must be replaced by `<x_axis>` or redefined as such, and the amount adsorbed must be written to the selected output file. An example that implements this procedure is given in [Example 63](#).

## 5.4 OUTPUT FILES

The various output files are used internally for storing intermediate data as well as the data actually used for plotting (and later replotting). The output files can be used to examine in detail the **PHREEQC** output, the intermediate results generated by **PhreePlot**, or to export data to other packages for further analysis or plotting. If the structure of the **PHREEQC** input file is relatively straightforward, **PhreePlot** provides a quick way of looping through **PHREEQC** calculations that would otherwise be rather tedious to set up (see [Section 6.2](#) and [Example 71](#)). **PHREEQC**-type calculations can be made without generating any plot files by setting `plotFactor` to 0.

### 5.4.1 Output files produced

The output is sent to a variety of files, most of which derive their names from the root of the input filename with an added extension. For example, if the main input file for a ht1 or grid calculation is `C:\PhreePlot\demos\amd\amd.ppi`, then the root or prefix is `C:\phreeplot\demos\amd\` which will then produce a series of files with the general format

```
root_[mainspecies][loopIndex].ext
```

where `root` is the root, `mainspecies` is the name of the main species, `loopIndex` is the index value (1...nz) of the loop variable and is only included when number of loop values is greater than one. `ext` is the output file extension.

Possible extensions are:

```
log          log file (filename is simply <root>.log)
```

pts	points file (boundary points, species distribution)
trk	tracking file with output from each <b>PHREEQC</b> iteration
vec	vector file for predominance and contour plots including the boundaries
pol	polygon file for predominance and contour plots defining each field
ps	Postscript graphics file, potentially multi-page (not eps)
eps	encapsulated Postscript (eps) graphics file with bounding box suitable for embedding in documents (single page only)
pdf	pdf (portable document format) file
png	png (portable network graphics) graphics file
log	log file containing details of run
lab	editable labels file giving the position and orientation of labels in a predominance diagram. Edit and replot with <a href="#">calculationMethod</a> 2 or 3.
out	tabular output file with accumulated results from the <code>SELECTED_OUTPUT</code> file used as input by some of the plotting routines.
all	cumulative output from <b>PHREEQC</b>

All files are output as space or tab-delimited ASCII files. The first five of these files are mainly for **PhreePlot**'s internal use and for debugging while the latter ones provide graphical and text output for further analysis. The output from each file can be turned on or off using one of the logical keywords assigned to the file type ([Section 5.4.2](#)).

Looping of the main species variable always produces a separate 'out' file for each value of the main species variable.

With custom and fit calculations, looping of the z-loop variable produces a single 'out' file with, by default, a blank line separating each value of the loop variable. This blank line can be suppressed by setting the fourth entry in [dataSeparators](#) to the null string, "".

Whether the corresponding plots are in separate files or not, and the naming of the file(s), depends on the [multipageFile](#) setting.

For example, assuming the [multipageFile](#) setting is set to `FALSE` and `ps` is set to `TRUE`, if there are two main species, Fe and Zn, and two iterations of the z-loop variable, then the following four files will be produced:

```
C:\phreeplot\demos\amd_Fe1.ps
C:\phreeplot\demos\amd_Fe2.ps
C:\phreeplot\demos\amd_Zn1.ps
C:\phreeplot\demos\amd_Zn2.ps
```

Other extensions are generated as appropriate. The log file in the example above will be called `C:\phreeplot\demos\amd.log`.

If [multipageFile](#) is set to `TRUE`, a single file will be produced:

```
C:\phreeplot\demos\amd.ps
```

and it will contain all four plots in the order given above.

With custom and fit plots, only one plot file is normally produced even when the `<loop>` variable is used. The results from the various loops are all plotted on the same plot with the labelling (from the selected output file column headings or the [labels](#) keyword) appended with an underscore and the loop number. This file has the same name as the multipage file above. If separate plots are wanted, set [customLoopManyPlots](#) to true.

The file `plot.ps` is a copy of the last Postscript file generated and is always produced if a plot is generated. It is also the name of the file generated as the temporary tracking plot file when the 'p' key is pressed during predominance calculations ([Section 6.6](#)), or when the calcula-

tions are interrupted (`ESC`) and then terminated (`s`). Derivatives of the `ps` file under such circumstances will be given the corresponding names such as `plot.pdf`, `plot.eps` etc.

### 5.4.2 The logical switches

Each output file has a logical switch associated with it (`TRUE` or `FALSE`). These are designed to give the user some control over the number of files produced. In general, the output data (text) files that are needed for plotting will be created whatever the value of their logical switch and they will not be deleted by **PhreePlot** at the end of a run. This ensures that plots can be edited and replotted without recalculating the underlying data. The most important switches for the user to control are for the log and track files which can both be large and are informative rather than being essential for the plotting (except that the track file is used to replot a grid plot).

Providing `plotFactor` is greater than zero, the following files will definitely be produced and retained during the following types of plots: `ht1` – points, vectors, polygons and labels; `grid` – track; `custom` and `species` – output; `fit` and `speciate` – points and output. If any of these files are deleted manually, then it will not be possible to carry out a ‘replot’; it will be necessary to recreate them. Sometimes the files are created but nothing is written to them. This will result in zero byte files.

The primary output data file produced by the `ht1` method is the points file. The vector, polygon and labels files are generated from this. These four files are all used to create the `ps` plot file during plotting and replotting. If the ‘reprocess and replot’ method ([calculationMethod 3](#)) is requested, then the calculations start with a pre-existing points file and recreate the other files anew. This will regenerate all the label positions and if appropriate, rewrite the labels file. This setting should be used when, for example, the `yscale` is changed. Replotting alone ([calculationMethod 2](#)) starts with all the existing data files including the labels file and then regenerates the plot files. With this setting, editing the labels file can be used to move the labels.

The grid plot uses the track file as the primary data file. The custom plots use the output file. The fit plot uses the points file.

Unlike the ‘data’ files, the plot files are all optional and the logical switch determines whether they are created or not, or more specifically, whether they are retained at the end of a run. There are some interactions amongst the various plot file types because the `ps` file is the primary plot file and is required in order to produce all the other graphic files using **Ghostscript**, e.g if the settings are `ps FALSE` and `pdf TRUE` then the `ps` file will be created because it is necessary in order to produce the `pdf` file but it will be deleted at the end of the run because the `ps` switch was set to `FALSE`.

### 5.4.3 ‘log’ file (`log`)

The log file provides a log of the calculations performed and for monitoring progress. It is most useful for debugging. The amount of information sent to the log file can be very large. It increases as the `debug` parameter increases from 0 (small) to 3 (large). A copy of the main input file (i.e. the file specified on the command line) is written to the log file. This includes any comments.

### 5.4.4 ‘out’ file (`out`)

The ‘out’ file accumulates the selected lines of output from the main selected output file (always user number 1) and is used by custom-type plots for plotting. The format of the ‘out’ file depends on the task being undertaken. In general, the output file contains the accumulated information sent by **PHREEQC** to **PhreePlot** via the `SELECTED_OUTPUT [1]` file. This does not include all the lines in the selected output but only those chosen. By default, this is just the last line of the last simulation (assuming that this contains the chosen selected output block). It is assumed that earlier lines are from unwanted intermediate calculations such as initial solution calculations etc. There are three ways to avoid unnecessary output (see

PHREEQC documentation):

- (i) use `PRINT;-selected_output` to control output, potentially for each simulation;
- (ii) use `SELECTED_OUTPUT;-user_punch/active` similarly. When set to `FALSE`, the former still outputs the headings whereas the latter does not.
- (iii) use an `IF` statement in the `USER_PUNCH` block to skip over the `PUNCH` statement when output is not wanted. However, this will still produce a blank line in the output, not nothing.

Although **PhreePlot** ignores any output above the specified bottom [selectedOutputLines](#) of selected output, it is simpler to follow if you ensure that the `USER_PUNCH` produces a clean output ‘file’, omitting any unnecessary output from initial solution calculations etc.

No output file is created during a replot (or resimplify).

In fit mode, the output file is an accumulation of the selected output from each call to **PHREEQC**, one line per data point. The order of the headings is dictated by the way in which the `SELECTED_OUTPUT` data block was written but should definitely contain the dependent variable (fitted value) and probably the independent variables (see the `-headings` line in the `USER_PUNCH` block).

In ‘grid’ and ‘ht1’ calculations, the ‘out’ file contains a cumulative version of the data sent to the selected output using a `PUNCH` statement often from an include file such as `ht1.inc`. After a header line, the ‘out’ file has the following format:

an ordered list of `species name, species value` pairs for each of the five species types given below finishing with five counters giving the number of entries of the various types.

The lists run consecutively one after the other. If there are no entries for a species type, then nothing is written. The five counters tell **PhreePlot** how many name-value pairs of each type have been `PUNCH`’ed. They are used by **PhreePlot** to read the data and construct a predominance diagram. The name-value pairs can be seen being set in the `ht1.inc` and `ht1c.inc` [include files](#).

In summary, the five counters are:

- |                    |  |
|--------------------|--|
| <code>nout1</code> | the number of candidate predominant solution/adsorbed/exchanged/mineral species and their ‘concentrations’ <code>PUNCH</code> ’ed. This can be any number but, after <b>PhreePlot</b> sorts them by concentration, only the largest three at most are passed on for further consideration. At present, only the largest two – the dominant and sub-dominant species – are actually used by <b>PhreePlot</b> .  |
| <code>nout2</code> | the number of mineral species and their concentrations <code>PUNCH</code> ’ed – if one or more minerals is actually stable and present, then when the stability criterion is used. these will be sorted in terms of ‘concentration’ and the one with the largest concentration will take precedence over all solution species. This can be any number but, after <b>PhreePlot</b> sorts them by concentration, only the largest three at most are passed on for further consideration. |
| <code>nout3</code> | the number of constraints <code>PUNCH</code> ’ed as name-value pairs – these may override the <code>nout1</code> species (e.g. they can be used to impose the ‘ <a href="#">water limits</a> ’). This can be any number.   |
| <code>nout4</code> | the number of ‘carry’ variables <code>PUNCH</code> ’ed as name-value pairs – these are numeric values that are not used in predominance calculations but which you might want to examine for some other reason. These ‘species’-value pairs are sent to the ‘out’ and ‘trk’ output files for viewing and are summarised in the log file. The values are also added to the tag dictionary. This can be any number.  |

`nout5` the number of 'system' variables returned. This must be 5! Always in the order: pH, pe, PO2(g), PH2(g), temperature (°C).

More details about the expected format of the selected output are given in [Section 4.5](#).

With predominance and contour plots, a blank line is written to the 'out' file when no selected output is produced when it should have been – e.g. when the speciation has failed or when a calculation has been skipped because it is not in the calculation domain.

#### 5.4.5 'track' file (`trk`)

This records the results of each speciation calculation. It is generated from the selected output after species coding. The header line for a predominance plot and the first data line look like this:

```
n x y pe TC step species1 isp1 species2 isp2 c1 c2
1 -12.0000 -85.0000 -12.4518 25.0000 -11 "H2(g) > 1 atm" -4 "Fe(OH)3-" 1 0.90370 -2.0100
```

`n` is the sequential number of the speciation calculation including preloop calculations; `x` and `y` are the x- and y-values, `pe` is the calculated pe, `TC` is the temperature, `step` is the type of step being taken (see [Section 3.2](#)), then the dominant and sub-dominant species (after any overrides have been applied) with their names (`species.`), species code number and concentration (mol/kgw). These data are normally echoed to the screen during execution.

The track file can also be turned on during other calculations including fitting. It will contain a copy of the convergence monitoring with the number of the function evaluation, value of the objective function (RSS) and its logarithm, and a list of the current parameter values. If multiple fitting methods are chosen, then the headers to the track file are subscripted with the names of the method, e.g. `RSS_n11s`, `log10(RSS)_bobyqa`, `logK_n11s` etc. This differentiates the results from different algorithms for the purpose of plotting.

#### 5.4.6 'points' file (`pts`)

The format of the points file depends on what task created it.

##### *Predominance plot calculations (ht1 only)*

This records the results of calculating boundary positions (see [Section 8.3.2](#)). These points are the raw data for calculating predominance diagrams. The number of points can be very large (even while tracking a straight line) and so these data are subjected to simplification to reduce the size of the file and to improve the appearance of the diagram. It is these simplified lines that are written to the vectors file and then to the polygon file.

##### *Other calculations*

This is an ASCII file in space-delimited format. It is created by a 'species' plot and contains a table of species suitable for plotting. This variables in this file are automatically added to the search list of variables and so can be used explicitly for plotting.

It is also the default file for collecting together data from a fit or simulation and is used for plotting rather than the 'out' file since it combines both observed and fitted data.

#### 5.4.7 'vectors' file (`vec`)

This file is generated from the points file and it stores the boundaries of the fields in a 'ht1' predominance diagram as a series of vectors. The order of the vectors is determined by the order of tracking. The individual polygons are assembled from this file, and coloured accordingly. These vectors divide two fields. They are not drawn for the domain boundary. The file looks like this:

```
250 1190 3562 16 25.000000000000 -0.9995420904108 0.2499810326136 20.79331349261
-12.000000000000 -83.300000000000 4 1 1 -12.04377661614
```

```

-12.00000000000    -83.12734375000  4  1  1  -12.00061311406
-10.74000000000    -83.13000000000  4  1  1  -10.74144424834
-10.74000000000    -83.13000000000  3  1  2  -10.74144424834
-10.74000000000    -81.77000000000  3  1  2  -10.40145620289

```

The first line contains the values of various system parameters that were in force when the file was created: the [resolution](#), the number of points in the points file, the number of times that the speciation program was executed, the number of species recorded as dominant or sub-dominant, the temperature of the last speciation and three numbers defining the relationship between pe and the x- and y-axis variables.

The subsequent lines have the following columns:

```
x-value    y-value    species1    species2    vector_sequence_number    pe
```

where x- and y-value are the x and y values, species1 and species2 are the integer codes for the two species at the boundary, vector\_sequence\_number is the sequential number assigned to the vector and pe is the calculated pe returned by **PHREEQC**. In a contour plot, the pe is replaced by a distance parameter – this is a scaled distance reflecting the relative distance of the point from the drawn line. It is a measure of the influence or importance of the point – large distance means large influence.

A species code of 99 indicates a domain boundary.

This file is used in ‘ht1’ plots to draw the outlines of the predominance fields. Commenting out or deleting lines from this file combined with [calculationMethod](#) = 2 can be used to omit specific lines from the plot. This can be useful for removing domain boundaries (those that include a 99 code) in a pe-pH plot.

A ‘vec’ file is also produced by a contour plot. It has a different header line but again the file contains all the vectors needed to draw the contours and to assemble the polygons used for colouring. It contains information about the type of boundary, normally the fields (class 1 and class 2) differ by one but if they are the same, then this indicates a non-intersecting contour (with the domain boundary) or ‘island’.

With contour plots, the order of the vertices is always written with ‘the high side to the right’ when reading down the file.

Although data in a polygon file are sufficient to draw the polygon boundaries, if they were used in this way, many boundaries would have double lines form adjacent polygons. Further, line simplification must be carried out on the vectors not the polygons.

#### 5.4.8 ‘polygon’ file (pol)

This file is generated from the vectors (‘ht1’ and ‘contour’) or track (‘grid’) files and is used to colour-fill the polygons. It is also used to determine a default labelling position near the polygon centre in predominance plots. It is assembled from the vectors file (‘ht1’ and ‘contour’) by selecting the appropriate set of vectors for each field based on the ‘species’ involved and matching the ends until polygon closure has been achieved. In grid plots, ‘pixel aggregation’ is used to determine the polygon boundaries. This is sometimes called ‘dissolving’ the polygons.

The header line includes the x- and y- resolution, the species code to which the polygon corresponds (see the labels file for the full species name in predominance plots), the number of points represented by each polygon segment, and the pe at each point. A species code of 99 stands for the domain boundary.

The [pol](#) keyword can be used to omit specified fields from a predominance plot.

Commenting out all the lines for a polygon can also be used to omit a particular polygon from the plot providing [calculationMethod](#) = 2 is used. In ‘ht1’ and ‘contour’ plots, the lines outlining each field are drawn using the vectors file but in a ‘grid’ plot these outlines are drawn using the polygon file.

If the value of *sp* (the species number) for all the points making up a particular polygon in the

'pol' file are less than or equal to zero, the field will not be drawn. It is necessary to edit the 'pol' file and replot ([calculationMethod](#) = 2) for this to work.

The polygon file must be in 1:1 synchrony with the labels file (see below) in terms of the number and order of polygons specified.

#### 5.4.9 'labels' file (labelFile)

This file is generated by predominance plots. It provides the dictionary to connect the species number in the vector and polygon files with a species name. It also includes the angle of the text. Editing this file provides a means of moving and rotating a label although using a [nudge](#) may be easier.

This file is used to tell the plot where to centre the labels as well as providing a list of the species names. It also includes other attributes of the label such as rotation (theta in degrees from the horizontal measured clockwise). The pe is carried so that the labels can be placed properly if the y axis is changed to pe or a derivative of that. A labels file looks something like this:

```

sp      x      y      pe      angle      %area      Species
#! -.9999962564643800 .249990833525500 20.7964049901900 .999997920415700
5      -8.300  -32.338  4.406  0      61.62      Fe(OH)3(a)
1      -11.541 -81.218  -11.054 0      0.41      Fe(OH)3-
6      -4.789  -61.095  0.735  0      32.10      Fe+2
10     -2.371  -12.279  15.333 0      2.10      Fe+3
11     -2.854  -11.174  15.15  0      0.49      Fe2(OH)2+4
3      -10.189 -81.442  -9.75  0      0.25      FeOH+
9      -2.783  -22.242  12.454 0      0.00      FeOH+2
4      -6.990  -83.939  -7.177 0      2.49      H2(g) > 1 atm
13     -7.000  -0.212  13.745 0      0.50      O2(g) > 0.21 atm

```

The #! line gives the results of the estimated fit used to estimate pe when it is not available. The fourth parameter is the goodness-of-fit ( $R^2$ ). Label size and [colour](#) are determined by the [labelSize](#) and [labelColor](#) keywords. Individual labels and the colouring of their associated polygons can be removed by commenting out the appropriate lines in the labels file. Alternatively, making the species number (sp) negative means the label will not be plotted. Setting the species number to zero will plot the label and field but will not colour it. In order to not plot the field or its label at all, use [pol](#) to exclude the polygon or edit the polygon file to give negative species numbers. The [minimumAreaForLabelling](#) setting and editing of the area field in the labels file can be used to omit a label, e.g. make the area negative and set [minimumAreaForLabelling](#) to 0.1, say.

If [labelColor](#) is set to 'nd' or [labelSize](#) is set to 0.0, no labels will be plotted.

A species can have more than one label if it occupies more than one distinct field. The order of the labels is important and corresponds with the order that the polygons are read from the polygon file. This should not be changed.

Species names may be changed by editing this file and replotting with [calculationMethod](#) 2. Species names are assumed to be in PHREEQC formula format and numbers will be sub- and super-scripted accordingly. The species names can be appended with an identifier which will not be sub- or super-scripted. This should follow the species name and be preceded by an underscore. In order to allow surface species to still be interpreted correctly, the following rules apply: the identifier will not be subscripted if it is 3 or less characters long, or if at least one other underscore precedes it, e.g. the numbers in the identifiers for Cd+2\_1 or Cd+2\_\_A2014 (two underscores) will not be subscripted whereas the charge in Hfo\_Cd+2 will be super-scripted.

Possibly the easiest way of moving labels is to use [nudge](#), or for many, a '[nudge file](#)'. This can be used for all plots.

#### 5.4.10 Other output files

Various other files are produced, some of which are temporary files and normally deleted, others are left in the file system for perusal.

plot.ps	this is always a copy of the last ps file produced (and the name of the tracking file optionally produced during calculations)
selected_1.0.out	this is the default name of the file containing the output from user number 1 ( <code>SELECTED_OUTPUT [1]/USER_PUNCH [1]</code> ) returned by <b>PHREEQC</b> (it is continually being overwritten with new data on each iteration). Other file names can be set using the <code>SELECTED_OUTPUT -file</code> identifier in the <code>CHEMISTRY</code> section.
PHREEQC.out	this is the normal <code>PRINT</code> output from <b>PHREEQC</b> for the last iteration when <code>ABS(debug)&gt;0</code>
*.all	this is an accumulation of the normal <code>PRINT</code> output from <b>PHREEQC</b> for all iterations and is only produced when <code>ABS(debug)&gt;1</code> or when the <code>all</code> keyword is set to <code>TRUE</code> . It contains end-of-file (Control-z) characters at the end of each iteration's output. This file can be very large which may prove problematic when opening with some text editors.

Whether the latter two files are produced or not is controlled by the [debug](#) keyword and possibly the value of [resolution](#).

If the two colour dictionary files are undefined and needed, then the files `lineColor.dat` and `fillColor.dat` will be automatically created in the working directory, i.e. the same directory as the main input file. Note that since the label positions are recorded in the line colour dictionary, it may be important that each problem run from the same directory is given a different dictionary name.

Some other temporary files may be produced during a run. These are normally deleted at the end of the run.

#### 5.4.11 Redirecting the output files

Normally the data and image output files that are created are stored in the same directory as the input file. These can all be redirected to another directory using the [prefix](#) setting.

Alternatively, individual image files can be redirected to another location by appending a filename to the corresponding switch, e.g. `pdf t t F:\new.pdf`. Check the specific switch setting for the format.

## 5.5 INSERTING PLOT FILES INTO MICROSOFT WORD, POWERPOINT AND OTHER SOFTWARE

The information given below is likely to vary with the version of the software being used, and will in any case age quickly, so treat this as a starter and experiment yourself. Unfortunately, the eps format seems a moving feast and no longer transfers well. Graphic files in various formats can in principle be imported into office software such as Microsoft **Word** and **Open Office/LibreOffice**. The filters available depend on the versions used. They must be single page ps files of course. The latest versions of **Word** no longer support eps or ps files. **LibreOffice Draw** is currently one of the easiest ways of editing pdf files and obviously integrates well with the rest of the **LibreOffice** suite. As of 2020, probably the simplest approach to import a diagram into a document without resorting to other editing software is to export from **PhreePlot** in the png format, and then to import this file. Most software that imports images can import png files. jpg files can also be imported directly in the same way but they will not normally be of such good quality as the png files since they are bit maps rather than vector-based and so will not scale so well.

These page-sized images can either be separately cropped with image editing software, or the

cropping done after being imported into a document.

Rather than importing the files into **Word** on a one-off basis, the ‘pictures’ can be linked to a particular file using the ‘Link to file’ option available on the Insert drop-down menu. This inserts an `INCLUDEPICTURE` field code into the document and reduces the document size since the actual code for the image is no longer included in the file. The file is automatically updated in the **Word** document when the file is reopened or when the fields are updated (Cntrl-F9). The link file name can be viewed by viewing the field codes (Alt-F9).

Using the ‘Insert and Link’ option when importing will insert the code for the picture and link it to the file for updating. This results in a larger document size than linking alone.

**Powerpoint** is not able to render Postscript files. Probably the best format for inserting into **Powerpoint** is `png`. If all else fails use high resolution `jpg`. If the default resolution of the `png` file produced by **PhreePlot** (300 dpi) is not what is wanted, change the resolution using the second `png` parameter. Slideshows can also be prepared using **LibreOffice Impress** which means that `eps` and `pdf` files can be used directly for a presentation.

If the graphic files need to be edited, **LibreOffice Draw**, **Inkscape** or other suitable vector-based software can be used. **LibreOffice Draw** obviously integrates well with the other **LibreOffice** modules. **Inkscape** is vector-based (based on the `svg` format) and is versatile, modern and free; **ImageMagick** is bitmap-based but good for file conversions. **GIMP** is free and powerful but is raster-based and has quite a steep learning curve. There are also many ways of merging `pdf` files including use of Adobe **Acrobat** and Cloud-based methods (e.g. <http://www.mergepdf.net/>).

The vector-based quality of Postscript files should be retained for as long as possible and text should preferably be kept as text rather than bit-mapped.

## 5.6 SPEED OF COMPUTATIONS AND PLOTTING

The speed with which calculations and plotting take place clearly depends on the processing power available and the number of computations undertaken. It also depends on certain settings that are under user control. Normally most of the time is taken up within **PHREEQC** so particular attention should be taken to the **PHREEQC** setup.

The following tips might help speed up computations:

reduce the number of species considered: the speed of **PHREEQC** computations depends strongly on the number of pure phases present. These are defined in the `EQUILIBRIUM_PHASES` keyword block. Reducing the number of phases being considered will reduce the computation time required. For example, phases that are obviously not going to feature in the calculations can be removed from consideration. The same is probably true to a lesser extent for the number of solution species. Reducing these will involve either changing the database used, or not including them as species in the `EQUILIBRIUM_PHASES` keyword block. With predominance diagrams, the `htmlminerals.inc` file ([Section 8.1.8](#)) can be used to monitor the saturation indices (`SI's`) of all the possible minerals using the ‘carry variables’ approach. The summary statistics for these `SI's` are written to the log file. If the maximum value is zero or very close to it, then this indicates that the mineral has precipitated somewhere in the calculations.

reduce the resolution of the plot: this will reduce the number of calculations undertaken at the expense of the smoothness and maybe the accuracy of the plot. Once the plot is what is wanted, the resolution can be increased for a final, production plot.

alter the **KNOBS** settings: these do not normally need to be adjusted but they can affect the speed with which **PHREEQC** converges (and even if it does converge) and so may be important in certain cases (see [Section 6.5.5](#) and [Section 8.12](#)). Their impact may vary with the different versions of **PHREEQC** due to changes in the solution finding strategy.

The structure of the **PHREEQC** library used by **PhreePlot** has not been optimised for carrying out the types of calculations often done with **PhreePlot**. For example, successive calculations are often similar to each other with just a minor difference. However, **PHREEQC** normally starts from essentially the same starting point each time. Sometimes 'setup'-type calculations can be taken 'outside the main loop' by making use of the `END` keyword to place setup code in the pre-loop section.

It may be possible to speed up certain slow calculations using the `EQUILIBRIUM_PHASES_MODIFY` approach (see the `demo\FeAsS-cd-music\FeAsS-cd-music-faster.ppi` example). Often it is just a matter of experimenting.



## 6 Running PhreePlot

### 6.1 CONVENTIONS FOR DATA INPUT

#### 6.1.1 Types of variables

Each keyword has an associated value or list of values associated with it. These can be of four types as given in Table 6.1

Table 6.1. Examples of how a **PHREEQC** column heading will be interpreted during plotting

Input	Graphical output	Examples
Integer (I)	Integer	-1, 0 1, 123
Floating point number (F)	Non-integer numbers. Range allowed depends on storage type: usually stored as IEEE 'doubles' (=xxx to +***) but plotting parameters are stored as 'singles', *** to +**	-1.0, 1.23, 1e-5
Logical (L)	Logical value	TRUE, FALSE, true, false, t, f, T, F
Alphanumeric (A)	Strings consisting of the following characters: (0-9, a-z, A-Z, (space), !, %, ^, & *, ( ) _ + [ ] ; < > ? / Enclose strings in single or double quotes if they include a space. If the string is enclosed in square brackets, these are removed and the rest of the string is taken literally, i.e. not interpreted. The following are <b>not allowed</b> : £ - ! \ @	1, A, abc, "two words", 'three small words', "C:\Program Files\PhreePlot\System\color.dat", "" (null string)

#### 6.1.2 PHREEQC notation for chemical formulae

**PHREEQC** has a super/subscript-free way of specifying chemical formulae (Table 6.2) and this is used by **PhreePlot** to interpret formulae strings when labelling plots.

Table 6.2. Examples of various chemical formulae in **PHREEQC** format

Conventional formula or name	PHREEQC format	PhreePlot
B	B	B
Br <sup>-</sup>	Br-	Br <sup>-</sup>
SO <sub>4</sub> <sup>2-</sup>	SO4-2	SO <sub>4</sub> <sup>2-</sup>
Ca <sup>2+</sup>	Ca+2	Ca <sup>2+</sup>
CaSO <sub>4</sub> ·2H <sub>2</sub> O	CaSO4:2H2O	CaSO <sub>4</sub> ·2H <sub>2</sub> O
FeS <sub>1.7</sub>	FeS1.7	FeS <sub>1.7</sub>
(CH <sub>3</sub> ) <sub>2</sub> COOH	(CH3)2COOH	(CH <sub>3</sub> ) <sub>2</sub> COOH
Hg <sup>0</sup>	Hg0	Hg <sup>0</sup>
Phenanthroline	Phenanthroline	Phenanthroline
HFO <sub>s</sub>	Hfo_s	Hfo_s
Fe(3)	Fe(3)	Fe(3)
<sup>18</sup> O	[18O]	18O
As(V)	[As5]	As5

**PhreePlot** assumes that some of the character strings (e.g. species and labels) used in **PhreePlot** may represent formulae in **PHREEQC** format and attempts to translate them accordingly. The places where this occurs are listed elsewhere ([Section 10.1](#)).

This interpretation of strings as formulae can be turned off by setting [convertLabels](#) to `FALSE`. This setting applies to all strings. A second, optional logical switch to [convertLabels](#) controls the conversion of colons when the **PHREEQC** conversion is true (default is false). This controls whether `ZnCO3:H2O` is converted to `ZnCO3.H2O` (`TRUE`) or to `ZnCO3:H2O` (`FALSE`).

## 6.2 PHREEPLOT LOOPING

### 6.2.1 Loop variables and their use

Looping, or iteration, is at the centre of **PhreePlot**. The other important feature is the separation of **PHREEQC** simulations into pre-loop and main loop simulations (see [Section 4.6.1](#)).

There are four loop variables available in **PhreePlot** and these operate in a nested fashion with the outer loop going round most slowly. These loops and their tag names are as follows:

```
Outer loop:      main species loop (<mainspecies>)
                  z-loop (<loop>)
                  y-axis loop (<y_axis>)
Inner loop:      x-axis loop (<x_axis>) (most rapidly changing)
```

The ‘main species loop’ loops on a list of character strings (each up to 30 characters), typically element names, but it can be any character string that requires substitution.

The y-axis loop and x-axis loops are set internally to loop over the specified y- and x-axis ranges, [ymin](#) to [ymax](#) and [xmin](#) to [xmax](#), respectively, with the intervals of both controlled by the same [resolution](#) keyword. The [resolution](#) gives the number of **PHREEQC** iterations used. So if calculations are wanted over an x-range from 0 to 10 inclusive in steps of 0.1 then [xmin](#) = 0, [xmax](#) = 10 and [resolution](#) = 101. If [xmax](#) = [xmin](#) then no looping is undertaken. [resolution](#) = 1 may signal some special behaviour. The y-variables are defined in exactly the same way. The pre-loop simulations are executed once and only the main loop simulations are looped.

The z-loop is controlled in several ways, most simply by the keywords [loopVal](#) or [loopMin](#), [loopMax](#), [loopInt](#), and [loopLogVar](#). Alternatively the `<loop>` variable can be set to any discrete set of values, including an irregular series using a [loop file](#). The loop file approach provides a mechanism for carrying varying values of other variables in parallel for each z-loop iteration including character variables. The z-loop iterates on both the pre-loop and main loop simulations.

Note that the x- and y-axis tag names use underscores not hyphens. The x- and y-axis loops are used in predominance plots where movement along both axes is required. The resolution in both dimensions is always the same. This arrangement also applies to custom plots but is rarely so useful. Here it is more common to use the x-axis loop to drive the principal independent variable, like pH, and the z-loop to alter some other factor or ‘level’ in a systematic way.

The main species loop produces a new plot for each iteration. These may or may not be in the same file depending on the [multipageFile](#) setting.

The z-loop either produces a new plot for each value or introduces a blank line in the ‘out’ file every time its value changes. This gives a break in the plotted line at each of these changes. Whether or not a new file is produced or a blank line is introduced depends on the type of plot and the [customLoopManyPlots](#) setting. A new plot file will always be produced for species plots.

In summary, by default, a blank line is inserted in the output files for each iteration of the

`<loop>` variable. This results in a break in the plotted curve. This does not happen with the `<x_axis>` or `<y_axis>` variables. The `<x_axis>` and `<y_axis>` variables are primarily designed for continuous variables whereas the `<loop>` variable is primarily designed to loop over discrete values of a variable. This difference is not rigid but there are some differences in the output that reflect this motivation.

For example, in predominance plots, the z-loop can be used to loop over a discrete range of concentrations of the main species.

z-looping can also be used to repeat **PHREEQC** calculations in which just one or two parameters are changed between runs, such as the pH. The custom plot option is used for this.

**PHREEQC** also has its own internal looping mechanisms, for example with the `CELL/RUN`, `REACTION` and `KINETICS` blocks, and also to some extent with `SOLUTION_SPREAD`, and of course with `TRANSPORT`. The late binding of include files with `include$` also means that input files can be dynamically written by earlier simulations.

An example of the `simulate` approach is given below and in the calculation of saturation indices for a batch of water samples (see the `SIS` example in the `\demo\SIS` directory).

## 6.2.2 Looping over a list of character variables

The 3-parameter z-looping mechanism discussed above is designed to loop over a range of numeric values. If you want to loop over a list of character variables, either use a [loopFile](#) with character columns or in simple one-variable cases, use the [mainspecies](#) loop (even if the variables involved are not actually elements or ‘species’).

## 6.2.3 An example of the use of various looping mechanisms

A series of examples described below shows how the various looping mechanisms can be used to calculate the solubility of iron oxide as a function of pH in a fluoride-rich medium. These examples highlight the different setups that can be used to implement looping in **PhreePlot** and are found in the `demo\FeSolubility` directory.

### Using the `<x_axis>` tag

The first example uses the `<x_axis>` variable. The input file (`FeSolubilityXaxis.ppi`) is:

```
SPECIATION
  calculationType      "custom"
  calculationMethod    1
  xmin                 2
  xmax                 12
  resolution            101
  numericTags          <log_H> = -<x_axis>
PLOT
  plotTitle            "Fe(OH)3(a) solubility vs pH"
  xtitle               "pH"
  ytitle               "log<sub>10</sub> Fe<sub>T</sub> (mol/kgw)"
  pymax                0
  customXcolumn        1
  lineColor            blue
  useLineColorDictionary 0
  legendTextSize       0
  label                0
CHEMISTRY
PHASES
Fix_H+; H+ = H+; log_k 0
SELECTED_OUTPUT
  reset false
USER_PUNCH
  headings pH FeT_
10 PUNCH -la("H+"), log10(TOT("Fe"))
SOLUTION 1
  pH      1.8
  units   mol/kgw
```

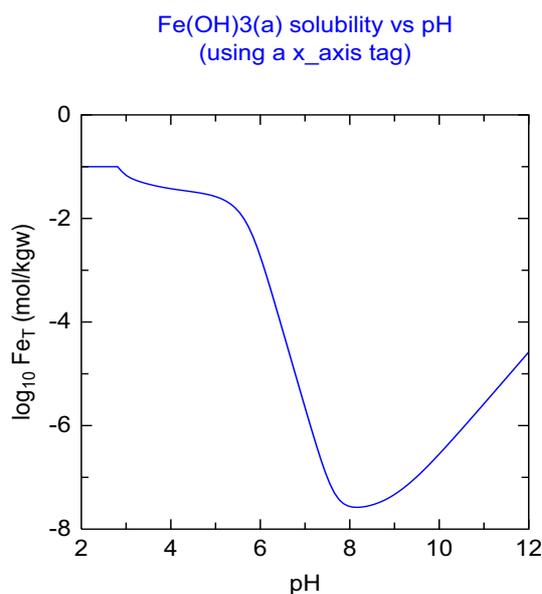


Figure 6.1. Amorphous iron oxide solubility as a function of pH calculated using the `<x_axis>` loop variable.

```

Fe(3)      1e-1
Na         1e-1
F          1e-1
EQUILIBRIUM_PHASES 1
  Fix_H+ <log_H> NaOH 10
    -force_equality true
  O2(g) -0.677
  Fe(OH)3(a) 0 0
END

```

The range of the `<x_axis>` variable is given by `xmin` and `xmax`. The span in pH is 10 units and the `resolution` is 101 so calculations will be made at `<x_axis>` values of 2.0, 2.1, 2.2...12.0. The `<y_axis>` variable has been left undefined (here and in the other input files) and so is unused.

The `<log_H>` tag is defined as the negative of the `<x_axis>` variable so that it can be substituted on the `Fix_H+` line. This is the only tag used within the `CHEMISTRY` section.

The plot produced from this file is shown in Figure 6.1. Exactly the same plot can be produced by using the `<y_axis>` variable in place of `<x_axis>`.

The `useLineColorDictionary` setting of 0 means that the line colour dictionary is ignored as a source of line and point colours or label coordinates, even if they are present in the dictionary. Rather auto colouring is used starting with the colours given in the `lineColor` setting (here set as `blue`). The colour dictionary is always created if absent or updated if present with the latest colours and coordinates.

### *Using the <loop> tag*

Exactly the same plot can be produced using the `<loop>` variable. This requires several changes to the `SPECIATION` section but none to the sections following that. The modified input is shown below:

```

SPECIATION
  calculationType          "custom"

```

```

calculationMethod      1
loopMin                 2
loopMax                 12
loopInt                 0.1
numericTags             <log_H> = -<loop>
dataSeparators          "\" "\t" "\p" "" "\r" ""

```

The two main differences are that [loopMin](#), [loopMax](#) and [loopInt](#) replace [xmin](#), [xmax](#) and [resolution](#). The fourth data separator must also be redefined to remove the blank line that would normally be placed after each iteration of the [<loop>](#) variable. It is set to the null separator which means that no new line (paragraph) is put between each iteration. Since blank lines in the 'out' file are interpreted as line breaks when custom plotting, without this change to the data separator, 101 separate lines would be plotted rather than a single curve.

This is why it is normally preferable to use the [<x\\_axis>](#) approach for continuous variables and to leave the [<loop>](#) variable for defining discrete intervals or levels of a variable.

### Using a loop file

It is also possible to read the 101 values from a loop file. The name of a loop file needs to be given and the [dataSeparators](#) may need to be redefined. The input is:

```

SPECIATION
calculationType          "custom"
calculationMethod        1
loopFile                 FeLoop.txt
numericTags              <log_H> = -<loop>
dataSeparators           "\" "\t" "\p" "" "\r" ""

```

The `FeLoop.txt` file looks like this:

```

#pH
2.0
2.1
2.2
2.3
...
12.0

```

It has 101 rows of data with a comment at the top which is ignored. This gives the same plot as in Figure 6.1.

### Using the 'simulate' calculationMethod

This method also reads the data from a file, this time the file specified by the [dataFile](#) keyword. The relevant part of the input file looks like this:

```

SPECIATION
calculationType          "simulate"
calculationMethod        1
dataFile                 FeSimulate.txt
logVariableIn            0
dependentVariableColumnCalc 2
numericTags              <log_H> = -<pHin>
...
customXColumn            3

```

The `FeSimulate.txt` file looks like this:

```

pHin
2.0
2.1
2.2
2.3
...
12.0

```

Note that as for the loop file, this file has a header row which define a series of tags, one per

column. While the header row is optional for the loop file, it is compulsory for this data file. Here the `<pHin>` tag is defined which is used in the definition of `<log_H>`. The [logVariableIn](#) keyword (a list of 0, 1 or -1's) must also be included to indicate the number of columns in the data file and whether any data transformations are required. Here, a single 0 indicates one column without any transformation on input.

It is also necessary to define where the dependent variable (the calculated value) is to be found in the main selected output file - this is done with the [dependentVariableColumnCalc](#) keyword. The [customXcolumn](#) also has to be set. This is the only plot type that uses the 'pts' file rather than the 'out' file, for plotting and this file has a slightly different format from the 'out' file consisting of the line number from the input file, calculated values and all of the variables read in from the data file - whether they were used or not.

### *Looping over two variables*

It is also possible to plot several curves on the same plot by using two looping variables. a line break is normally The following file (`FeSolubilityXaxisLoop.ppi`) does this:

```
SPECIATION
  calculationType          "custom"
  calculationMethod        1
  xmin                     2
  xmax                     12
  loopmin                  -4
  loopmax                  -1
  loopint                   1
  looplogvar                1
  resolution                101
  debug                     0
  numericTags              <log_H> = -<x_axis>
PLOT
  plotTitle                "Fe(OH)3(a) solubility vs pH"
  xtitle                   "pH"
  ytitle                   "log<sub>10</sub> Fe<sub>T</sub> \
(mol/kgw) "
  labels                   "10<sup>-4</sup>M F" \
"10<sup>-3</sup>M F" \
"10<sup>-2</sup>M F" \
"10<sup>-1</sup>M F"
  pymax                    0
  customXColumn            1
  linecolor                 blue
  useLineColorDictionary   0
  legendTextSize           2
  label                    1.5
CHEMISTRY
PHASES
Fix_H+; H+ = H+; log_k 0
SELECTED_OUTPUT
  reset false
USER_PUNCH
  headings pH FeT_
10 PUNCH -la("H+"), log10(TOT("Fe"))
SOLUTION 1
  pH          1.8
  units       mol/kgw
  Fe(3)       1e-1
  Na          <loop>
  F           <loop>
EQUILIBRIUM_PHASES 1
  Fix_H+ <log_H> NaOH 10
  -force_equality true
  O2(g) -0.677
  Fe(OH)3(a) 0 0
END
```

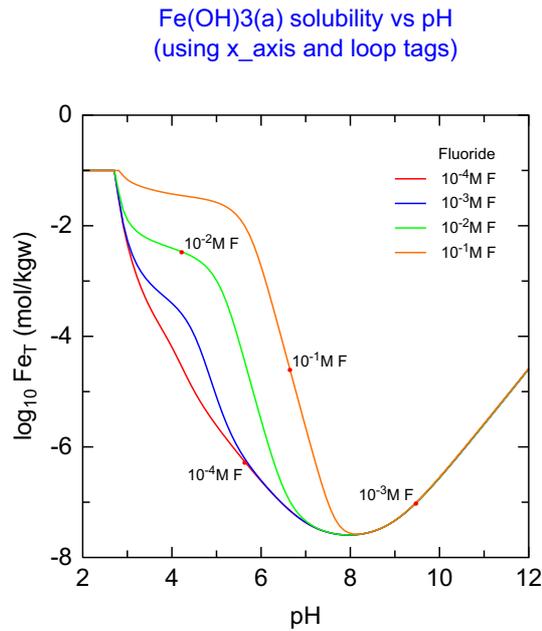


Figure 6.2. Amorphous iron oxide solubility as a function of pH and NaF concentration calculated using the `<x_axis>` and `<loop>` variables.

This is similar to the other files but has the `<x_axis>` tag to drive the x axis (pH) and the `<loop>` tag to drive the variable Na and F concentrations. The `<loop>` or z loop adds a blank line at the end of each iteration. These are interpreted as line breaks by the custom plotting routines which then plots them separately with different line colours (Figure 6.2). The `labels` keyword provides a list of names to use for labelling the curves and producing the legend.

If a separate plot is wanted for each value of the z-loop variable in a multiple-z value custom plot, set `customLoopManyPlots` to `TRUE`. There are also additional parameters to choose whether to append the loop index to label names in order to enable curves to be distinguished in multi-loop plots.

#### 6.2.4 Looping in multi-simulation input files - pre-loop simulations and the main loop

##### *Introduction*

Decisions had to be made about how **PhreePlot** would deal with multi-simulation input files, i.e. those with more than one `END` keyword (assuming the file finishes with an `END`). In principle these files can be of any degree of complexity and can include completely unrelated simulations.

Two aspects had to be considered.

Firstly, which simulations are repeated and which are not. There is obviously a time and clutter penalty in repeating invariant operations that do not have to be repeated such as reading in a database. This led to the concept of pre-loop (once only) simulations and main loop (repeated) simulations.

Further, when several simulations need to be run, should they be fed to **PHREEQC** one at a time or all together. **PhreePlot** can only update tags and make substitutions to the input file when control is returned to itself between runs.

Secondly, which results of the various simulations are picked up and sent to the various **PhreePlot** files ready for fitting, plotting etc. Some simulations produce no useful output

while others produce one or more lines of useful output.

The format of the output produced by a given block of code can depend on whether the simulations are executed one-at-a-time or in a single run.

Controlling these aspects of the input and output is the key to running **PhreePlot** successfully.

### *Basic structure of a multi-simulation PHREEQC input file*

Each **PHREEQC** simulation in an input file is numbered consecutively from the top down, 1, 2, 3, ... A multi-simulation input file can be viewed as a series of one or more contiguous simulations or 'blocks' of simulations. A block of simulations is therefore defined by a range of simulations.

In many cases, **PhreePlot** considers the input file to be a single block but it can also be treated as a series of unrelated blocks. This is possible with the 'fit' and 'simulate' types of calculations where each line of data (each 'observation') in the associated data file can point to a different block of **PHREEQC** code.

Each block is itself treated as having two parts: (i) the top part consists of zero or more 'pre-loop' simulations, and (ii) the lower part consists of one or more 'main loop' simulations.

The innermost two **PhreePlot** loops (the y- and x-axis loops) act only on the main loop simulations. This division between the two is designated by the [mainLoop](#) setting which is the number of the simulation in the block starting counting from the top of the block, i.e. the starting point of the looping.

The default is 'last' which automatically sets [mainLoop](#) to the number of the last simulation in the block. Setting [mainLoop](#) to 1 would mean that all the simulations in that block are treated as main loop simulations.

Much of this behaviour is hidden when running **PhreePlot** in normal mode but setting [debug](#) to 1, 2 or 3 will cause more or less of the calculation trail to be written explicitly to the log file.

The following decisions were made based on the [calculationType](#):

For custom, species and predominance-type calculations, it is assumed that the **PHREEQC** input file is written to perform a single set of calculations and consists of zero or more initial simulations to set up the database, do initial solution calculations, and to define other static settings. This is then followed by one or more simulations which will be subject to the y- and x axis **PhreePlot** looping mechanisms. Any simulation which contains a tag which is expected to change on each iteration must be in this latter block. This division into 'pre-loop' and 'main loop' simulations is specified with the [mainLoop](#) keyword which specifies the number of the **PHREEQC** simulation at which the main loop starts.

In a multi-simulation input file, **PhreePlot** x-, y-looping only applies to the simulations numbered from [mainLoop](#) onwards. The simulations before this are assumed to be 'pre-loop' simulations. Each of these pre-loop simulations is run individually and the tag dictionary updated between runs (Figure 6.3). This means that tag variables can be passed from one simulation to the next in these pre-loop simulations.

The 'main loop' iterates as rapidly as possible over the y-axis and x-axis loops. This loop runs with minimum overheads and is intended for the most repetitive calculations. All simulations in this main loop are run as a single **PHREEQC** run so there is no possibility of using tags created in one simulation in the next. The tags are updated just once then the whole block of simulations is executed.

The earlier ('pre-loop') simulations are re-run for each value of the main species and z-loop, i.e. the z-loop iterates over the entire input file.

The default value for [mainLoop](#) is 'auto' which sets [mainLoop](#) to the number of simulations found in the input file, i.e. it means that looping will only take place over the last simulation.

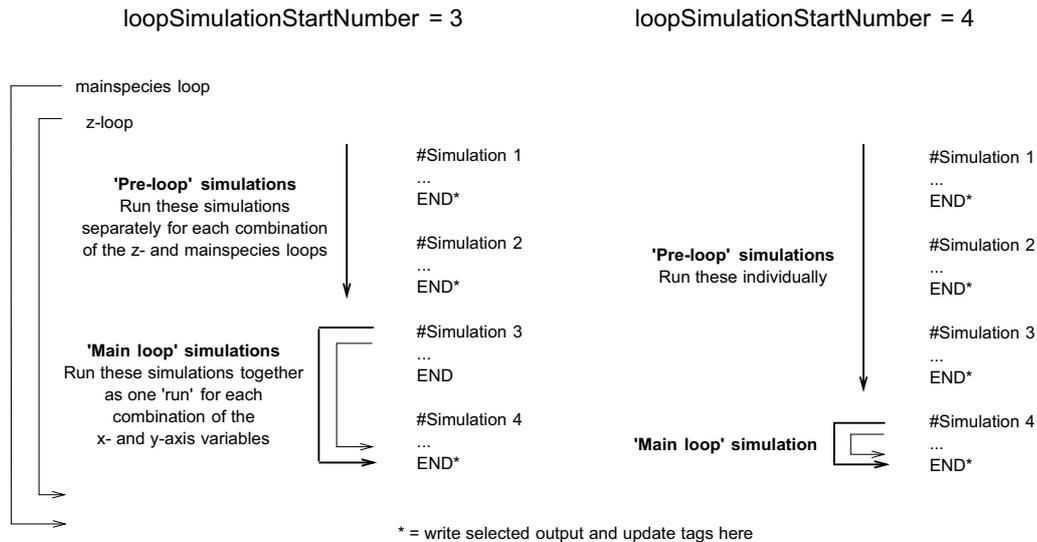


Figure 6.3. Two examples to illustrate how the [mainLoop](#) defines the division between 'pre-loop' simulations and the 'main loop' simulations in which the x- and y-axis variables operate. In this example, the difference controls the number of times simulation 3 is run and consequently when selected output is normally written to the 'out' file and the tags updated. The default ('last') is for the [mainLoop](#) to only loop over the last simulation, as illustrated on the right. The 'pre-loop' simulations are each run separately and sequentially. In contrast, the 'main loop' simulations are run as a single block with no updating of tags between simulations.

Care needs to be taken with the selected output when looping over more than one simulation. A `USER_PUNCH` data block entered in simulation 1 say will remain active in subsequent simulations unless specifically turned off with the `-selected_output` identifier in a `PRINT` data block. If the `USER_PUNCH` data block is redefined in later simulations then the output may become confusing since a new header line is not written to the 'out' file.

With multi-simulation input files, [selectedOutputLines](#) controls the amount of selected output actually sent to the 'out' file. The number specified refers to the number of lines sent from the `SELECTED_OUTPUT` in the chosen simulation (`SELECTED_OUTPUT 1` block).

The 'out' file is often used directly for plotting and the challenge is to end up with a well-formed file suitable for plotting. Normally this should be a rectangular table with a header row and columns of data possibly with blank rows to signify breaks in the data.

The exception to the above behaviour is during fitting and simulations. The 'fit' and 'simulate' [calculationTypes](#) do not allow looping since they use multi-simulation files to allow for the possibility of doing different calculations for each data point (observation) or set of data points. Each data point can in principle choose its own range of simulations and its own [mainLoop](#) parameter. This makes it possible to optimise over a number of different types of calculations within the same fit ('global optimization'). The simulation or range of simulations to be used for each point is specified in a special column in the fit data file, the [mainLoopColumn](#). Weighting of the residuals becomes a particularly important consideration when mixing 'apples and oranges' in this way. More details are given in the Chapter ["Fitting and simulations"](#), p. 151.

### 6.2.5 Dynamic switching between PHREEQC models (code)

It is sometimes necessary during looping to switch between different pieces of **PHREEQC** code to obtain the required output. This switch may reflect the results of an earlier simulation or the value of some tag variable.

The most flexible approach is to engineer for a tag to be the 'switch' tag and to then use this in the `USER_PUNCH` code to calculate what is required and to send the required output to the

selected output. This can often be made possible using the 'one simulation at a time' mode (see [mainLoop](#)) based on the fact that in this mode `USER_PUNCH`'ed output from intermediate simulations is automatically turned into tags which can then be used in subsequent simulations. Furthermore, this intermediate output does not get copied to the 'out' file and so will not interfere with the output used for plotting or fitting. So a simulation can calculate something, punch a switch value to the selected output and then the next simulation can make the switch accordingly, perhaps even repeating the previous simulation with slightly different input or output.

### 6.2.6 Defining the expected output in the selected output file

Use [selectedOutputLines](#) to define the number of lines (rows) to be read from the output defined by the targeted `SELECTED_OUTPUT (n) / USER_PUNCH (n)` block, counting lines from the bottom upwards and excluding the header line. Set to 1 to pick just the last line, 2 to pick the last two lines etc., or 'auto' to pick all lines. During fitting, the number of lines picked will automatically be set to 1 when [onePass](#) is `FALSE` and to that given by the number of observations in the fit data file when [onePass](#) is `TRUE`.

If the [selectedOutputLines](#) value is 0, no data transfer will take place. This option can be used when **PhreePlot** is used to produce some other output file such as a print file.

In order to accumulate output from all the simulations in one input file into a single selected output file (the 'out' file), set [mainLoop](#) to 1 and put the `SELECTED_OUTPUT (n) / USER_PUNCH (n)` block in the first simulation. This ensures that all the simulations will be run in a single run and so forces the accumulation of all output data into a single output file. Don't use any other looping mechanism, i.e. just loop through the whole set of simulations once. However, note that tags will only get updated and substituted once at the beginning of the run.

It may be necessary to define a 'break variable' to force the plotted curves to break between simulations. This can be done with the sixth parameter of the [dataSeparators](#) keyword or by using `dataSeparators break="<break_variable>".` Whenever the break variable is encountered, a blank line is sent to the outfile.

### 6.2.7 Timing execution

It can be useful to see the difference between execution times for different iterations. This can be done by making use of the `<systemtime>` system tag. This is initialised to zero at the beginning of a **PhreePlot** run and returns the cumulative time in seconds for each iteration thereafter. It can be accessed using this tag in the `USER_PUNCH` section. The time taken for each iteration can be calculated by using the `PUT/GET` mechanism to save the time of the previous iteration and subtracting it.

For example, in a custom plot add code something like

```
-headings nexecute time dt
100 IF (EXISTS(1)=0) THEN PUT(0,1)
200 dt = <systemtime> - GET(1)
300 PUNCH <nexecute>, <systemtime>, dt
400 PUT(<systemtime>,1)
```

and monitor the 'out' file. For a predominance plot, add something like the following as 'carry' variables in the `ht1.inc` (or similar) file.

```
295 IF (EXISTS(1)=0) THEN PUT(0,1)
296 dt = <systemtime> - GET(1)
297 PUNCH "nexecute", <nexecute>, "time", <systemtime>, "dt", dt
298 PUT(<systemtime>,1)
299 nout4 = 3
```

and monitor in the 'track' file (`trk TRUE`). If a plot of this timing is wanted, set up another `ppi` file something like

```

PLOT
  extradat          hfo.trk
  customxColumn    nexecute
  lines            dt
  labelsize        0
  legendtextsize   0
  xaxislength      150

```

and execute the two together with a batch file.

### 6.2.8 Speeding-up calculations

Sometimes calculations are noticeably slow because the initial solution calculation is a poor estimate of the final solution. In these cases, it may be possible to speed-up calculations significantly by saving the result of the last calculation and using it as a starting point for the next calculation. This makes use of one or more of the ‘\_MODIFY’ PHREEQC keywords.

A typical scenario for preparing a predominance diagram would be:

```

# simulation 1 - pre-loop, once only
SOLUTION 1
....
EQUILIBRIUM_PHASES 1
Fix_H+      -7 NaOH
  -force_equality true
O2(g)      -45
  -force_equality true
...
SAVE SOLUTION 2
SAVE EQUILIBRIUM_PHASES 2
END

# simulation 2 - main loop, iterate here
USE solution 2
USE equilibrium_phases 2
USE surface 2
EQUILIBRIUM_PHASES_MODIFY 2
  -component Fix_H+
  -si <x_axis>
  -component O2(g)
  -si <y_axis>
SAVE solution 2
SAVE equilibrium_phases 2
SAVE surface 2
END

```

If other reactions such as surface reactions are involved, then these must also be SAVE'd and USE'd in the same way. This approach makes most sense for grid-type calculations but can also be used to speed-up ‘hunt-and-track’ style calculations. It makes little or no difference when the chemistry is ‘simple’ and calculations are relatively fast, e.g. `demo\Fe\hfo.ppi`.

An example to demonstrate this approach, `FeAsS-cd-music-faster.ppi`, is given in the `C:\PhreePlot\demo\FeAsS-cd-music\` folder.

A similar approach using `RUN_CELLS` is also possible.

## 6.3 POSSIBLE TYPES OF CALCULATIONS AND PLOTS

The types of calculations undertaken and the type of plot produced is controlled by the [calculationType](#) keyword (Table 6.3).

The other critical keyword that should be included in each input file is that of [calculation-Method](#) which has the following values:

- 0 = do calculations but do not plot anything
- 1 = do calculations and plot everything from scratch
- 2 = don't re-speciate or reprocess data but replot using existing plot data files

Table 6.3. Types of calculations undertaken by **PhreePlot**

calculationType	Use
ht1	makes one or more predominance diagrams using the ‘hunt and track’ algorithm. The scope of calculations is given by <a href="#">xmin</a> , <a href="#">xmax</a> on the x axis and <a href="#">ymin</a> , <a href="#">ymax</a> on the y axis. The step size during hunting and tracking is controlled by <a href="#">resolution</a> .
grid	makes one or more predominance diagrams using the ‘brute force’ or grid algorithm. The number of cells along each axis (nx = ny) is controlled by <a href="#">resolution</a> .
custom	any calculations requiring a series of straightforward iterations (default)
fit	fitting model parameters to observations and plotting the resultant fit.
simulate	like <code>fit</code> but only calculates the fitted values rather than adjusting parameter values to get a good overall fit
species	calculates the percentage or log concentration of all species present for a given element in a well-defined system

3 = as for 2 but goes back one stage further and reprocesses the output from speciation.

## 6.4 PREPARING THE SELECTED OUTPUT FILE

### 6.4.1 Normal behaviour

**PhreePlot** receives output from **PHREEQC** via its selected output mechanism. Originally **PHREEQC** had just one combination of `SELECTED_OUPTUT` and `USER_PUNCH` keyword blocks but this has now been extended to any number of `SELECTED_OUPTUT n` and `USER_PUNCH n` blocks where the integer `n` defines a specific combination. The main (default) selected output is `n = 1`, and it is this file that provides the data that are extracted to the ‘out’ file.

Although the selected output was originally sent to a disk file that could be accessed via the operating system in the usual ways, one of the options with the **PHREEQC** library used in **PhreePlot** is to make this transfer entirely in memory. Storing the results in memory reduces I/O and speeds up execution. However, it does not leave a file to be inspected after execution has finished. **PhreePlot** uses this memory approach when `debug=0` but uses the permanent file approach when `ABS(debug)>0` or with `selectedOutputFile TRUE`.

It is also often neater to turn off the default selected output using the `-reset false` option in the `SELECTED_OUTPUT` keyword block. This minimises the transfer of unwanted data. If this option is not used, default selected output variables, like ‘state’, ‘simulation’ etc. will be included in the output files.

The selected output is constantly being overwritten with the results of the last iteration. The ‘out’ file (see [Section 5.4.4](#)) accumulates the relevant lines (see [selectedOutputLines](#)) that are produced each time the selected output is ‘punched’, once per iteration of the `USER_PUNCH` block providing that it is not blank and that the output has not been turned off with `PRINT; -selected_output FALSE` OR `SELECTED_OUTPUT 1; -active FALSE`.

### 6.4.2 The use of the ‘headings’ identifier

The `-headings` line in the `USER_PUNCH` block defines the column labels that are output to the first line of the selected output file. These column labels in turn are used to define the tag names for the variables that are automatically produced from the selected output.

Because of the way that headers are used to define variable names in **PhreePlot** and because of the limitations of the **PhreePlot** function parser, the choice of header names is somewhat more restrictive in **PhreePlot** than in **PHREEQC**. In particular, the following special characters `+/*()<>^\\` can cause problems. Quotes are not treated specially. Therefore quoted strings should not be used for headings and spaces are not allowed within an individual heading name – spaces are used as separators. In general, if a column heading ends with a \$ sign, the data in this column will be assumed to be character data rather than numeric data.

If one or more of the special characters is found, **PhreePlot** will replace each of them with a

period (.). This means that “ $a+b$ ” and “ $a-b$ ” will both be translated to “ $a.b$ ”, leading to an error if both are present. Providing that such degeneracy is avoided, the use of special characters in headers should cause no problem. The reporting of tag values in the log file and the use of column headers in defining plot variables is based on the original names.

The list of column headings are associated in turn with each of the punched variables:

```
SELECTED_OUTPUT
  -high_precision      true
  -reset               false
USER_PUNCH
-headings  pH Zn Cd ZnOam
-start
10 sorbedZn=SURF("Zn", "Hfo")
20 totZn=SYS("Zn")
30 sorbed1=100*sorbedZn/totZn
40 mineral=100*equi("ZnO(a)"/totZn
50 punch -la("H+"), sorbed1
60 sorbedCd=SURF("Cd", "Hfo")
70 totCd=tot("Zn")*tot("water")+sorbedCd
80 sorbed2=100*sorbedCd/totCd
99 punch sorbed2, mineral
```

pH will head the column containing values of `-la("H+")`.

Zn will head the column containing values of `sorbed1`.

Cd will head the column containing values of `sorbed2`.

ZnOam will head the column containing the percentage of Zn in the mineral ZnO(a).

The column headings are used by **PhreePlot** in four ways:

- (i) to generate tag names like `<pH>`, `<Zn>` etc
- (ii) to label the curves plotted in the main plot area (suppress with `labelSize<=0`)
- (iii) to label the legend to the plot (suppress with `legendTextSize=0`)
- (iv) to control whether the data column is to be plotted as points, lines, both or not at all.

If `convertLabels` is `TRUE`, then column headings are checked by **PhreePlot** to see if they are consistent with **PHREEQC** chemical formulae format and if so are interpreted accordingly when used as in-plot labels for curves and polygons, and in any legend. This means that numbers within the text string will normally be interpreted as a stoichiometry and subscripted. A check is made to see if the numbers could be interpreted as valences rather than stoichiometries. This checking is not particularly thorough and some strings may be interpreted as formula when in fact they are not.

If certain characters are found in the heading which indicate that the string is not a formula then this prevents the translation to **PHREEQC** formula format. These characters are: `~@?!%^^&*'_`. Some of these (`~%`) are non-plotting characters with ASCII encoding and so they can be used to force interpretation as a non-**PHREEQC** formula on a one-off basis without affecting the appearance in the plot, e.g. `~Zn8` will plot as Zn8 rather than as Zn<sub>8</sub>. However, these non-plotting characters should be used with caution as their behaviour is non-standard and may be unpredictable. In any case, they are plotted as normal characters when the Latin-1 character encoding is in force.

Starting a heading with a lowercase character will force it to *not* be interpreted as a formula since formulae start with an upper case character, opening parenthesis or bracket.

The backslash has special behaviour in a heading since on printing **PHREEQC** strips out the `\` and the following character from the name. It is therefore necessary to use `\\` if a backslash is wanted. In **PhreePlot**, a backslash is also used to indicate that the next character is to be interpreted as a Greek character so `\b` or `\\b` in a heading would print the Greek character beta and a backslash immediately followed by three digits indicates that the character corresponding to that octal code for the character set in force. If Windows file paths are to be printed, use for-

ward slashes rather than backslashes to avoid this conversion. Some examples which demonstrate these rules are given in Table 6.4.

Table 6.4. Examples of how a **PHREEQC** column heading (label name) will be interpreted during plotting

Input	Graphical output	Interpretation
CH4	CH <sub>4</sub>	normal PHREEQC formula (first character is uppercase)
cH4	cH4	not a formula (first character is <b>not</b> uppercase)
C(-4)H4	C(-4)H <sub>4</sub>	PHREEQC formula but (-4) is a valence not a charge
C(-4)	C(-4)	PHREEQC formula as above
C-4	C <sup>4-</sup>	PHREEQC formula but -4 is treated as a charge
-CH4	CH4	Non-printing character at beginning prevents interpretation as a PHREEQC formula (ASCII encoding)
\C(-4)	(-4)	PHREEQC removes backslash and first character after it and the remaining is interpreted literally (it is not a formula)
\\C(-4)	C(-4)	the first \ removes the second \ and the remainder is interpreted as in the first example above
\\\C(-4)	X(-4)	the first two \s are removed leaving a single \ which indicates that the next character should be treated as a Greek character (here chi). This indicates that it is not a formula.
T(\260C)	T(°C)	260 is the octal code for the degree symbol in the Latin-1 character set

Remember that # and ; have special meanings in **PHREEQC** input files and should be avoided in headings. Single and double quotes may also be interpreted in a special way in strings including headings. Tags such as `<sub>...</sub>` will always be interpreted as indicated and so can be used to force certain behaviour, e.g. `%Zn<sup>2+</sup>` will appear as %Zn<sup>2+</sup>.

Unpaired quotes should not be used in column names. Strings enclosed in square brackets will be stripped of the brackets and then interpreted literally.

### *Controlling the plotting of individual columns*

Data from the selected output are accumulated in one or more output files. These files may then be used for plotting the data.

The [points](#) and [lines](#) keywords (and their 2y counterparts) control whether points and/or lines are selected for plotting. Properties of these points and lines such as colour, size or width are controlled by a series of keyword lists such as [lineWidth](#), [pointSize](#) (and [lineWidth2y](#) and [pointSize2y](#)). Each dataset selected to be plotted with points and lines has a corresponding entry in a property list, or if the list is short, is either generated automatically ([pointColor](#) or [lineColor](#)), or recycled from the existing list.

For example, if [pointSize](#) is set to 0.0 or the [pointColor](#) is set to 'nd' then no symbol will be drawn for any of the selected point datasets. If [pointSize](#) is set to 5.0 3.0 and [pointColor](#) is set to red blue then the symbols for the selected datasets will alternate red-blue-red-blue ... as needed with sizes alternating 5, 3, 5, 3 ....

The six standard filled symbols (1-6) can have a coloured rim with their colours and widths set by the corresponding [rimColor](#) and [rimFactor](#) keyword lists.

### *Use of labels in a custom plot and the minimum text size*

The labels are used for labelling the lines/points in a custom plot and its legend. The size of the label text is given by [labelSize](#). The minimum height of text is 0.01 inch and is reset to this value if it is entered as a smaller positive value than this. 0.0 suppresses plotting of text altogether.

The headings can contain super- or subscript tags, e.g. H<sub>2</sub>O or Fe<sup>2+</sup>, and Greek characters as per the normal rule (only to the first level – no superscripted Greek

characters are allowed).

Label headings must be unique.

## 6.5 DEBUGGING

### 6.5.1 Types of problem

If a file has not run as expected or has crashed then some debugging is required. Providing that the run has not returned an immediate error report giving the file:line location of a syntax error, the input file must be syntactically correct and the problem must lie deeper. An audible low beep signifies a recognised calculation problem of some sort.

First check the screen and log files if present to see if there are any messages which might give a clue to the problem. Then it is necessary to work out whether it is **PHREEQC**/chemistry problem or a **Phreeplot** problem.

If the problem has failed on its first iteration of **PHREEQC**, there is probably something wrong with the input file, either the **PhreePlot** part or the **PHREEQC** part.

It may be helpful to get the **PHREEQC** code working first by pasting the chemistry code into a standalone version of **PHREEQCI**, **PHREEQC** or **PHREEQC for Windows**. It will be necessary to temporarily substitute values for all the tags before running the code.

**PhreePlot** problems should be reported to the address given on [www.phreeplot.com](http://www.phreeplot.com).

The flags for ancillary output files such as the track file in the case of a predominance diagram should be set to `TRUE`. Also make sure that all **PHREEQC** output is sent to the various log files by ensuring that

```
PRINT; -reset TRUE
```

has been set in the **PHREEQC** input (`CHEMISTRY`) section. If there are several `PRINT` data blocks in the `CHEMISTRY` section, it is the value of the last one set that is used. This is useful since several of the include files (e.g. `ht*.inc`) use `-reset false` which means none of the normal **PHREEQC** output will be printed. Therefore during debugging, providing the line above is included **after** the include file, `reset` will be set to `TRUE` and the **PHREEQC** output will be sent to the **PHREEQC** output files without needing to edit the include file.

Once this has been set, you can use `debug = 2` or `debug = 3` (adds more screen output) to get a listing of all the **PHREEQC** output copied to the file `*.all` (see below). Examine this carefully making sure that all the expected substitutions have been made properly. The values of all the tags just before executing **PHREEQC** can be found in the log file so it should be able to tell if it is a **PhreePlot** problem or **PHREEQC** problem.

As usual, first simplify the input file as much as possible.

You may just need a few iterations run. You can interrupt a run by pressing `ESC` and entering 's' for Stop.

When the run is crashing later on and the early runs look good, it is more likely to be a failure to converge in **PHREEQC**. This is most likely to be due to an user error in setting up the **PHREEQC** input file leading to extreme chemistry of some kind. Failure of **PHREEQC** on well-defined and well setup problems is rare enough to be dismissed as the most likely explanation. However, failure of **PHREEQC** to converge can be quite a common problem and is usually due to the calculations straying into some region of 'unrealistic' territory. Occasionally the chemistry may be too complex and **PHREEQC** struggles to find a solution – this can be tested by simplifying the problem including reducing the number of `PHASES`. The most common source of error is trying to fix a value with `EQUILIBRIUM_PHASES` and not providing a plausible chemical to do that with, e.g if a solution has an initial pH of 7, `EQUILIBRIUM_PHASES Fix_H+ -3.5 NaOH` will not work (unless there is an excess of  $\text{Na}^+$  present). Either change the initial pH or change the chemical to an acid, or provide more  $\text{Na}^+$ . This is dis-

cussed in more detail below ([“The most common reason for a failure to converge”, p. 74](#)).

**PHREEQC** rarely fails from programming errors or bugs but calculating predominance plots can explore a large range of chemistries in terms of redox, acid-base, mineral stability, adsorption etc. and only the best speciation programs are robust enough to always complete such a challenging set of calculations reliably. Unlike some other speciation programs, **PHREEQC** keeps a mass balance on water and sometimes reactions can use up all the water leaving extremely concentrated solutions which can eventually fail – remember reducing lots of  $Zn^{2+}$  to Zn metal in the presence of acid can decompose water!!

### 6.5.2 Checking the return status of a **PHREEQC** run

It is possible to check the status of a **PHREEQC** run by outputting the status return using the `<PHREEQC_status_0>` tag in a `USER_PRINT` or `USER_PUNCH` block. This system tag is automatically created and updated after each run. The 0 reflects the thread number of the run. A status return of zero indicates successful completion while a positive value gives the number of errors detected.

In principle, it is possible to check the status of a run, take avoiding action if it has failed and then rerun the simulation, all in one script. For example, it is possible to automatically switch the chemical used to achieve the target value in an `EQUILIBRIUM_PHASES` block, see the `\demo\switch` examples.

### 6.5.3 General approach to debugging

Debugging is an acquired skill and some general principles apply whatever the language. [David Agans](#) has nine general rules for debugging. In a review of Agans' book, David A. Wheeler listed them as:

*Understand the system:* Read the manual, read everything in depth, know the fundamentals, know the road map, understand your tools, and look up the details.

*Make it fail:* Do it again, start at the beginning, stimulate the failure, don't simulate the failure, find the uncontrolled condition that makes it intermittent, record everything and find the signature of intermittent bugs, don't trust statistics too much, know that "that" can happen, and never throw away a debugging tool.

*Quit thinking and look* (get data first, don't just do complicated repairs based on guessing): See the failure, see the details, build instrumentation in, add instrumentation on, don't be afraid to dive in, watch out for Heisenberg, and guess only to focus the search.

*Divide and conquer:* Narrow the search with successive approximation, get the range, determine which side of the bug you're on, use easy-to-spot test patterns, start with the bad, fix the bugs you know about, and fix the noise first.

*Change one thing at a time:* Isolate the key factor, grab the brass bar with both hands (understand what's wrong before fixing), change one test at a time, compare it with a good one, and determine what you changed since the last time it worked.

*Keep an audit trail:* Write down what you did in what order and what happened as a result, understand that any detail could be the important one, correlate events, understand that audit trails for design are also good for testing, and write it down!

*Check the plug:* Question your assumptions, start at the beginning, and test the tool.

*Get a fresh view:* Ask for fresh insights (just explaining the problem to a mannequin may help!), tap expertise, listen to the voice of experience, know that help is all around you, don't be proud, report symptoms (not theories), and realize that you don't have to be sure.

*If you didn't fix it, it ain't fixed:* Check that it's really fixed, check that it's really your fix that fixed it, know that it never just goes away by itself, fix the cause, and fix the process.

The ‘divide and conquer’ rule applies well for solving **PhreePlot**-type problems. Simplify the failing example until it works and then work forward, adding more complexity in increments until the source of the error is found.

Sometimes it is the data that is giving the problem and the ‘divide and conquer’ approach can work well for that too. Split the data into two and see if both halves cause a failure. If only one half does, keep dividing the failing half into two until the data giving the problem can be identified. Then work out what is special about those data.

#### 6.5.4 Using the `debug` keyword

You often need to know exactly what is being computed especially when there appears to be a problem. The higher the `debug` setting (0-3), the more information is returned to the screen and log file. If there has been a failure in **PHREEQC**, the relevant **PHREEQC** output is normally sent to the log file and echoed to the screen and so examining this output should be the first thing to do. The exception to this is during the calculation of predominance plots with `debug=0` when **PhreePlot** will record a NA species and attempt to battle on. In this case, setting `debug=1` will induce **PhreePlot** to stop immediately it has detected an error.

In general, with the default (‘auto’) settings for the `PHREEQC.out` and `all` keywords, `debug` works in the following way:

<code>debug=0</code>	minimal diagnostic output
<code>debug=1</code>	<code>selected_1.0.out</code> and <code>PHREEQC.out</code> produced
<code>debug=2</code>	<code>selected_1.0.out</code> , <code>PHREEQC.out</code> and <code>*.all</code> produced
<code>debug=3</code>	as for <code>debug=2</code> except that the input is echoed to the screen on each iteration and the <b>PHREEQC</b> output is also inserted into the log file.

`selected_1.0.out` is the `SELECTED_OUTPUT` file from user number 1 from the last iteration and if produced, will be found in the working directory. `PHREEQC.[id].out` contains the normal **PHREEQC** output from the last iteration and is controlled by the **PHREEQC PRINT** keyword. A copy of this is also sent to the log file and the screen.

`Debug` also controls the degree to which the input files are echoed to the log file. With `debug = 0`, only the main input file is written. With higher debug levels, all include files and the `override.set` file are also copied.

The file `*.all` file is generated with `debug=2` or greater, or when the `all` keyword switch is set to `TRUE`. This accumulates `PHREEQC.out` from all of the iterations. This can produce a very large file but it is the definitive record of all that **PHREEQC** has done. It may be necessary to change the `-reset` option in the `PRINT` keyword block to `-reset TRUE` to ensure that all of the **PHREEQC** output is written to the output file.

The log file will also give the value of many of the **PhreePlot** settings, including all the tag values and loop variables that have been generated. It will also have a copy of input to **PHREEQC** after substitution. In the case of a failure, this should be checked for errors to make sure that **PHREEQC** is receiving valid code. This input can also be seen on the screen by setting `debug=3`.

If **PHREEQC** fails (usually because of syntax or setup errors), then the **PHREEQC** output is usually written to the log file and echoed to the screen, and calculations stop. The exception to this is that with `debug=0` and when calculating a predominance or contour plot, or when `stopOnFail` is set to 0, computations continue unless stopped manually with the `ESC` key.

The `selected_1.0.out` file will indicate whether the expected output is being sent from **PHREEQC** to **PhreePlot**. If **PHREEQC** has failed to converge, this file may not be formed properly.

### 6.5.5 The most common reason for a failure to converge

As mentioned above, **PHREEQC** is a very reliable and well-tested program and rarely fails to converge given ‘reasonable’ chemistry. We have run it through millions of iterations without problems. However, it can be easily be made to fail if it is forced to make calculations under conditions for which it and its chosen database were not designed, namely very high ionic strengths (e.g. above 5 mol/kgw). Such conditions can arise from rather benign starting conditions if the system is subjected to extreme constraints. For example, at the extremes of *pe*, water decomposes leading to small volumes of water remaining. This concentrates the initial solutes and **PHREEQC** may, not unreasonably, then fail to converge. This is exacerbated at high temperatures. Therefore in non-obvious cases of failure always check for high ionic strengths or diminishing volumes of water. Always check that the ionic strength and mass of water are roughly what you would expect.

As mentioned above, a common failure is when a phase is designated to adjust the activity of some species but in reality cannot. In the present context, this most often arises when trying to fix the pH by adding an acid or base but choosing the wrong one. For example, trying to change the pH of a solution initially at pH 3 to pH 9 by adding HCl is impossible. **PHREEQC** attempts to do this by adding negative concentrations of HCl (removing HCl) but if there is not enough Cl in the system to do this, **PHREEQC** will fail. For example,

```
PHASES
Fix_H
  H+=H+
  log_k 0
SOLUTION 1
  units mol/kgw
  pH 3
  Na 1e-3
  Cl 1e-3
EQUILIBRIUM_PHASES
  Fix_H -9 HCl
END
```

will fail. If the initial pH was 4, there is sufficient Cl available to be removed and **PHREEQC** converges without difficulty. Of course, if NaOH is specified as the reactant, **PHREEQC** does not fail even starting at pH 3.

The problem is that it is neither always obvious what reactant should be used nor is it necessarily possible to specify a single reactant to cover the entire range of conditions desired (this can be very wide when constructing *pe*-pH diagrams). For example, redox reactions can produce or consume large amounts of acidity. So changing a sulphate-rich oxidising solution to a reducing one at a higher pH may actually require acid not base to be added because of the large amount of OH<sup>-</sup> released as a result of sulphate reduction.

One way around this problem is to try and arrange for it not to happen by starting at an extreme pH such that addition of the specified acid/base will always succeed.

Alternatively, add a ‘large’ amount of the co-solute (here Cl<sup>-</sup>) such that the above balancing reaction can always be used to withdraw negative quantities of HCl. More generally when ‘large’ is not known, add a relatively benign equilibrium phase such as NaCl such that it always maintains a finite (but probably small) concentration of the co-solute to allow the required removal to be achieved, e.g.

```
SOLUTION_MASTER_SPECIES
  [Na] [Na]+ 0 23 23
  [Cl] [Cl]- 0 35 35

SOLUTION_SPECIES
  [Na]+ = [Na]+
  log_k 0

  [Cl]- = [Cl]-
  log_k 0

PHASES
```

```

Salt
[Na][Cl] = [Na]+ + [Cl]-
log_k    0

Fix_H+
H+=H+
log_k 0

SOLUTION 1
units mol/kgw
pH    3
Na    1e-3
Cl    1e-3

EQUILIBRIUM_PHASES
Fix_H+          -9 H[Cl]
Salt            -12 [Na][Cl] dissolve
END...

```

By defining [Na] and [Cl] as new ‘elements’, there will be no additional side-effects arising from reactions in which Na and Cl are involved. These new notional ions will be included in the calculation of the ionic strength though this can be avoided by making their atomic masses 0.0. Adding ‘dissolve’ means that this action is only taken when needed, i.e. when Na needs to be added – this becomes more important when simple Na and Cl are used as it prevents the disappearance or ‘precipitation’ of Cl. Of course this approach does not actually reflect a plausible reaction path.

An alternative approach is to run a simulation, then in the following simulation check whether **PHREEQC** has run properly by testing the <PHREEQC\_status\_0> tag, then using this information either re-run the original simulation or change it in some way and then rerun, e.g. change the chemical used in EQUILIBRIUM\_PHASES.

Using the `-force_equality TRUE` option in the EQUILIBRIUM\_PHASES keyword block is recommended to ensure that the target value for one of the axis variables, such as `Fix_H+`, is reached exactly. This setting should only be used for phases that are definitely present, not for conditional phases. It may be helpful to use it for  $\text{CO}_2(\text{g})$  at high pH but this can cause problems at low pH.

There can be occasional lack of convergence to a reasonable solution brought about by excessive mass transfers from one of the PHASES, e.g. of  $\text{O}_2(\text{g})$  or  $\text{CO}_2(\text{g})$ . For example, the mass transfers of  $\text{O}_2(\text{g})$  required to fix the pe in most systems is rather small, usually much less than 0.1 mol/kgw and so unless there are compelling reasons otherwise, include a limited reservoir size as the second parameter in the definition of a the activity of a phase (the default is large, 10 mol), e.g. use

```

EQUILIBRIUM_PHASES
O2(g)    <y_axis>    0.1

```

rather than

```

EQUILIBRIUM_PHASES
O2(g)    <y_axis>

```

or

```

EQUILIBRIUM_PHASES
O2(g)    <y_axis>    10.

```

Similar comments apply to  $\text{CO}_2(\text{g})$ . High concentrations of carbonate (> 0.1 mol/kgw) can be created when solutions above pH 10 are equilibrated with  $\text{CO}_2(\text{g})$  at atmospheric partial pressures or above. Even at lower pH’s, it may be necessary to limit the size of the  $\text{CO}_2(\text{g})$  reservoir to a value less than the default value of 10 moles. This can prevent rare problems in **PHREEQC** convergence.

Limiting the reservoir in this way is part of the normal **PHREEQC** setup. No error is triggered by **PHREEQC** when the target phase activity is not achieved because of insufficient res-

ervoir size. Therefore care is necessary with the setup to ensure that what is being calculated is what is required.

Occasionally, **PHREEQC** may fail simply because the system is just too complex. Finding the set of equilibrium mineral phases has always been one of the challenges in chemical speciation calculations, and this is still the case especially at high ionic strengths where the non-linearities can make it harder. The best advice is to simplify as much as possible: especially limit the number of mineral phases in the `EQUILIBRIUM_PHASES` block as much as possible, and if a mineral phase has a surface reaction associated with it, split the reaction into two, e.g. replace

```
# simulation 1
SOLUTION
...
EQUILIBRIUM_PHASES
...
SURFACE
...
END
```

with

```
# simulation 1
SOLUTION
...
EQUILIBRIUM_PHASES
...
SAVE solution 2
SAVE equilibrium_phases 2
END

#simulation 2
USE solution 2
USE equilibrium_phases 2
SURFACE
...
END
```

This way, the mineral assemblage in the first simulation is likely to be closer to the final mineral assemblage and solution composition, and therefore easier to find convergence when the surface is added in the second simulation.

### 6.5.6 Changing PHREEQC's convergence parameters

It is occasionally necessary to alter the default `KNOBS` settings in **PHREEQC** to get convergence. We have found the four most critical options to adjust are `-iterations`, `-convergence_tolerance`, `step` and `-pe_step_size`. The 'nuclear' option for testing would be to set `KNOBS` as:

```
KNOBS
-iterations 1000
-convergence_tolerance 1e-10
-step 3
-pe-step_size 1.5
```

The `-high_precision` setting should be changed from `TRUE` to `FALSE` either in the `ht1.inc` file or by redefining it later in the input file.

The [FeAsS.ppi example](#) is an example in which **PHREEQC** fails to converge in one place with the default convergence tolerance. Relaxing the criterion from 1e-12 to 1e-10 solves the problem. Such intricacies may change with time as **PHREEQC** develops and algorithms are tweaked.

Another `KNOBS` setting that can help convergence is:

```
KNOBS
-diag T
```

Note that `KNOBS` only applies to the simulation in which it is placed so if two simulations are used, as is common in calculating predominance diagrams, `KNOBS` should be placed in the simulation which does the mass transfer calculations.

Another approach to solve the lack of non-convergence is to add the following fictitious species:

```
SOLUTION_SPECIES
H2O + 0.01e- = H2O-0.01; log_k -9.0
```

This can help convergence (see the [PHREEQC 3 manual](#), `KNOBS` p 117) as demonstrated in the `demo\Cuedta` example.

## 6.6 INTERRUPTING EXECUTION AND CHANGING KEYWORD VALUES

**PhreePlot** can often be stopped or interrupted using the `Esc` key. This returns the following prompt:

```
Press "s" to stop, "i" for input or <CR> to continue
```

`<CR>` (the Enter key) resumes execution, “s” stops the execution and “i” gives the following prompt:

```
Enter keyword-value pairs/lists, "s" to stop or <CR> to continue:
```

at which keyword-value pairs or lists can be entered in the same way that they are entered for input files. These new settings will take effect immediately on resumption of the calculations. No checking on the reasonableness of the new settings is made and since it is clearly possible to cause great confusion, this option should be used with care. A blank `<CR>` ends the input.

If the letter ‘s’ is entered, execution will be stopped as soon as possible. If a fit is being processed, then execution will not stop until the calculations have been completed for a whole set of data points. If a fit plot has been requested, a plot will be produced that reflects the best fit up to that point. For other calculations, the stopping will be almost immediate.

If a run is stopped during the execution of a batch file, the next line in the batch file will be executed. `Control-break` will enable execution of the whole batch job to be halted.

Pressing the ‘p’ key (case insensitive) during the execution of a `ht1` or `grid` plot will write a plot file, `plot.ps`, showing the progress of the calculations (this does not work for ‘`grids`’ plots). This plotting can be automatically done on a regular basis by setting the [plotFrequency](#) keyword to the frequency of the speciation calculations for which the automatic plotting is to be done. The plot file will then be renewed every `n`’th iteration. A message, ‘File “`plot.ps`” written’, is sent to the screen whenever this file is written. This option can only be used when the [multipageFile](#) option is set to `FALSE`, i.e. a separate file is being created for each plot within a run. This is because only one instance of the plotting routine can be in operation at any time (a single thread) and multipage plots leave the plot file open between plots.

## 6.7 RUNNING THE STANDARD PHREEQC EXAMPLES

It is possible to run most of the **PHREEQC** example input files distributed with **PHREEQC** from within **PhreePlot**.

These examples can usually be run using a minimal template such as:

```
calculationMethod    -1          # calculate but don't attempt to plot
all                  TRUE         # accumulate output in *.all file

CHEMISTRY
```

```
include ".\examples\ex1"
```

The output will be sent to the directory from which the example is run and will include the normal **PHREEQC** output in the \*.all file.

The main challenge with these examples is to isolate the data that need plotting or tabulating from that which does not. In most cases, the aim is to get a well-formed 'out' file. This can usually be achieved with judicious use of `PUNCH` and the `-selected_output` switches in the **PHREEQC** code, and the [mainLoop](#), [selectedOutputLines](#) and [dataSeparators](#) in the **PhreePlot** section.

### 6.7.1 Going round for just one iteration

In predominance plot calculations, it is useful to know the set of minerals that could theoretically form given the input chemistry and database used. Setting the [resolution](#) to 1, [all](#) to `TRUE` and ensuring that `PRINT` is `TRUE` in the `Chemistry` section automatically includes a commented block of `USER_PRINT` statements in the cumulative **PHREEQC** output (\*.all) that give a commented list of all possible mineral species in the system being considered. This text can then be pasted back into an `EQUILIBRIUM_PHASES` data block and those which can realistically be expected to form activated by un-commenting them.

This can be semi-automated using the `<allmin>` tag (see `\demo\minstab\allminerals.ppi`).

## 6.8 RETURN STATUS AND EXIT CODES

**PhreePlot** will normally give a return status of 0 if it has run without errors. If it returns with one or more errors, the return status is normally 1. This can be useful when constructing sequences of runs in a batch file or script.

For example, the following Windows batch file script will only run the second input file if the first one exited successfully:

```
pp file1.ppi
IF %ERRORLEVEL% EQU 0 (
  pp file2.ppi
)
```

# 7 Plotting basics

---

## 7.1 INTRODUCTION

**PhreePlot** will normally attempt to produce a plot after a run. The type of plot produced is determined by the plot type, currently `grid`, `htl`, `custom`, `species`, `fit` or `simulate`. See the appropriate Sections below for details.

The Chemistry section of the input file largely governs the type of data generated. What is plotted and its appearance is governed by a series of keyword settings. A full list of these can be found in the `pp.set` file and are described in more detail in Section 14.

The data plotted is always read from a file, by default, this is usually the 'out' file but the file type does depend on the type of calculation and any other files that are specified using [extra-dat](#). The default file for fit plots is the 'pts' file not the 'out' file. The 'out' file is prepared from the selected output file(s) from **PHREEQC** which in turn derives its output from `USER_PUNCH` blocks specified in one or more input files.

These files used for plotting should all have a header row with column names. These column names are used as variable names for specifying a column for plotting but columns can also be specified by column number. Normally a blank row in a column of data signifies a break in the data when plotting. If there is no break but one is needed, then if this may be specified using a 'break' column (see [dataSeparators](#)) which will detect a change in the direction of a monotonic sequence and insert a break when there is a change.

## 7.2 TYPES OF PLOT

There are six options for generating potentially plottable output. These are controlled by the [calculationType](#) setting:

<code>grid</code>	'brute force' method for making predominance or pe-pH diagrams
<code>htl</code>	hunt and track method for making predominance or pe-pH diagrams
<code>contour</code>	2D contour plots
<code>custom</code>	direct plotting of output from the <code>SELECTED_OUTPUT</code> file (the default)
<code>species</code>	plotting species distribution plots, e.g. % species vs pH
<code>fit</code>	calculating and plotting the fit of observations to a <b>PHREEQC</b> chemical model. The observations and associated independent variables are read from an external file.
<code>simulate</code>	similar to <code>fit</code> but without the observations and so no fitting.

There are only two basic types of plots: (i) an x-y filled-area plot used for displaying predominance diagrams and contour plots, and (ii) an x-y plot with lines and points for displaying other data.

It is possible to add lines and points on predominance plots but not *vice versa*. It is also possible to overlay multiple `ps` files to give a single plot.

In order to suppress the generation of any plot file(s), set [plotFactor](#) to 0.0 or use a negative [calculationMethod](#).

## 7.3 SUMMARY OF BASIC PLOTTING

### 7.3.1 Introduction

A plot can be produced directly after the generation of the data or by replotting an existing plot without generating the chemical data a second time. This is governed by the [calculation-Method](#) keyword.

### 7.3.2 Setting up the plotting area

A plot is positioned on a notional piece of paper. The size of the paper is set with the [paperSize](#) keyword. It can be either one of the ISO sizes (A0-A5, B4-B5), US sizes (Ledger, Letter or Legal) or Note.

The [pageOrientation](#) can be set to 0 (portrait) or 1 (landscape).

It is simplest if all dimensions use the same units as defined by the [units](#) keyword. The units can be 'mm', 'inch' or 'pt' for points. The units used during plotting are determined by the last set value of the [units](#) keyword as read from the various input files. This applies to any features defined in the [extraText](#) or [extraSymbolsLines](#) files. This is best set in the `pp.set` file so that it is read in first and does not need to be reset. All of the other default settings that use these units should also be changed in the `pp.set` file.

The [font](#) can be set for the document as a whole but the font used cannot be changed for individual text strings except through the extra [text](#) mechanism. It is best to set your default font in the `pp.set` file.

The plot area is set on this piece of paper. The bottom left-hand corner ('origin') of the plot area is offset by [xoffset](#) from the left and [yoffset](#) from the bottom of the paper. The length of the x axis is given by [xaxisLength](#) and the y axis by [yaxisLength](#).

The [colorModel](#) used is either 'rgb' for red-green-blue, 'gray' for grayscale, or 'b&w' for black and white. Colours for text, lines, symbols and fills are specified on the rgb scale by [colour codes](#) such as `red4` or raw rgb numbers and, if necessary, transformed to the other colour models.

The background colour of the plot area (within the axes) is given by [backgroundColor\(1\)](#). This setting is less useful with predominance plots as they are normally completely filled with colour (including 'white'). The background colour of the whole page is given by [backgroundColor\(2\)](#). The background colour of text labels is given by [backgroundColor\(3\)](#).

[plotFactor](#) can be used to rescale everything plotted by a given factor.

### 7.3.3 The colour palette

Colours are most easily defined using the Cohort colour palette ([Cohort Software, 2004](#)). This has 14 base colours, each one with 10 shades of increasing colour density or darkness (Figure 7.1) plus 'black', 'white' and 'nd' (for 'not drawn'). The base colours are centered on number 4, e.g. 'red4' is pure red. Numbers from 3 to 0 have increasing amounts of white in them while numbers from 5-9 have increasing amounts of black in them. Therefore 'red0' is the palest red (more like a pink) and 'red9' the darkest red. Colour names are not case sensitive.

A null colour string, '', is interpreted as 'take the next auto colour' and so is different from 'nd'.

Colours can also be defined using rgb (red:green:blue) colour numbers. These are defined by an 11-character string with the format `xxx:xxx:xxx` where `xxx` = 000 to 255. Note that each colour level is defined by a 3-digit number (even when it is 0). Therefore `red4` is `255:000:000`.

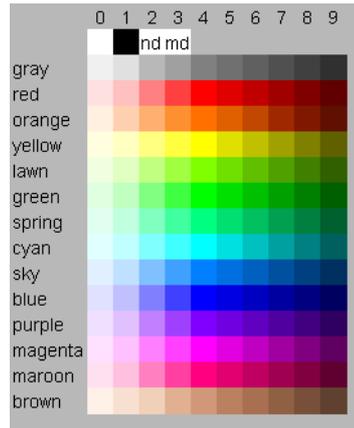


Figure 7.1. The Cohort colour palette used by **PhreePlot** ([Cohort Software, 2004](#)).

If a colour name is not recognised, then it is either recorded as an input error or substituted by black or white with a warning. This depends on its origin and context.

The actual colour of the plotted lines, fills and symbols will depend on the [colorModel](#) setting: `rgb` for colour, `gray` for grayscale and `b&w` for black and white.

#### 7.3.4 Automatic or explicit colours

The colour of text, symbols and lines can be specified explicitly in the input files. If this is not done, **PhreePlot** will choose its own colours according to a set of rules. These are described below. The colours used in the plots can be changed without recalculating the original plot. This is done either by specifying or changing the relevant attribute in the input file or editing one of the colour dictionaries and then re-running the problem with [calculationMethod](#) set to 2 (just replot) or 3 (reprocess and replot).

#### 7.3.5 Setting up the axes scales, tick marks and grid lines

The axis scales are set up by minimum and maximum values of the axes on user coordinate x- ([pxmin](#), [pxmax](#)) and y-scales ([pymin](#), [pymax](#)) with the 'p' standing for 'plot'. The first tick mark, a major tick, for both axes is placed at the plot origin (bottom left-hand corner) by default but this can be modified by the optional second parameter to [pxmin](#) or [pymin](#) which indicates the location of the first major tick mark (and label). Major tick marks are then added at intervals of [pxmajor](#) and [pymajor](#) and minor ticks at [pxminor](#) and [pyminor](#). By default, minor axis ticks are plotted at the centre of each major tick interval. The minor ticks can be turned off by setting [pxminor](#) or [pyminor](#) to 0. No ticks or labels are drawn if [pxmajor](#) or [pymajor](#) are set to 0. Axis scaling is discussed in more detail in [Section 7.8](#).

If any 2y lines or points have been specified, a second y axis ('2y axis') will be used on the right-hand side of the plot with settings [p2ymin](#), [p2ymax](#), [p2ymajor](#), and [p2yminor](#). It shares a common x-axis scale with the main y axis. It is used by specifying the [lines2y](#) or [points2y](#) variables.

All or any of these settings can be set to 'auto' for automatic scaling based on the range of data being plotted.

The colour of the axes is set with [axisLineColor](#) and the width with [axisLineWidth](#). Four axes will always be drawn, each with major and minor tick marks. Tick lengths are set with [tickSize](#) and colour with [tickColor](#). Separate tick sizes can be chosen for each of the major and minor x axes, major and minor y axes, and major and minor 2y axes and individual tick colours can be similarly specified. The line width of the major tick marks is the same as the axis line width while the width of the minor tick marks is half the axis line width. By default, the minor ticks

are half the length of the major ticks.

[tickSize](#) can also be used to specify the position of the ticks in relation to the axis – ‘inside’ or ‘outside’. Just add the ‘inside’ or ‘outside’ qualifier to the end of the list of ticksizes.

Grid lines can be plotted by setting the appropriate [gridLines](#) setting to `TRUE` or choosing a very large tick size (more than half the length of the ‘other’ axis). These can be dashed if the corresponding [gridLineStyle](#) style is greater than 1. Alternatively, a negative tick size can be used to indicate a dashed line. The appearance of the dashed line is also controlled by the [gridDashesPerInch](#) setting.

### 7.3.6 Axis numbering and annotation

Axis numbers will be drawn at the major tick marks. The numbers of digits after the decimal point are determined by [pxdec](#), [pydec](#) and [p2ydec](#), -1 means integer. These can be ‘auto’.

Very large and very small numbers automatically invoke scaling of the numbers using the ‘divide/multiply by a power of ten’ approach.

The size of the axis numbers is given by [axisNumberSize](#) and their colour by [axisNumberColor](#).

Axis titles are given by [xtitle](#) and [ytitle](#) along with [axisTitleSize](#) and [axisTitleColor](#). An optional second string for the axis title is put after any ‘divide by a power of ten’ scaling so that the units can be correctly placed to give dimensionless scales.

An overall plot title is controlled by [plotTitle](#), [plotTitleSize](#) and [plotTitleColor](#). This is centered above the plot.

### 7.3.7 Adding fills, lines and points

Fills can only be added in predominance and contour plots. Lines and points (or symbols) can be added to these plots or more commonly used to generate their own ‘custom’ plots. All this plotting is controlled by reading data from files, either from files generated during the run or from existing files. These files are all ASCII files and so can be viewed and edited with a text editor. These files should normally be in a spreadsheet-type format in rows and columns. They should have a header row which is used to name each column. The separators can be specified as spaces, tabs or commas.

The lines and points to be plotted are read from the [lines\(2y\)](#) and [points\(2y\)](#) keywords and are specified by the column header name(s) from the data file(s) being read.

Predominance plots maintain a [fillColorDictionary](#) which holds the colour to use for each species. If the dictionary is not initially present or a species not found, a sequence of pale fill colours will be automatically generated and used. The fill colour dictionary will always be updated with the colours used at the end. A labels file is also generated with the positions of the labels used. This can be edited to move the labels.

Contour plots normally derive their properties from a series of lists, one value for each contour or for each fill, specified by settings such as [contourFillColor](#). These lists are recycled if they are shorter than required.

[points](#), [points2y](#), [lines](#) and [lines2y](#) are used to specify the lists of custom data series to plot. The names used are the column names normally from the outfile though data series from extra files can be added with [extradat](#) providing that they share a common x-axis name given by [customXcolumn](#) name. A special name for points is ‘auto’ in which case points will be automatically be added to all lines plotted. Column numbers can also be used for specifying a column starting with the outfile and then the [extradat](#) files in the order specified.

Points are plotted with symbols, some of which (symbol type 1-6) are ‘filled’ symbols which have separate fill and rim colours. The filled colour can be white and so when combined with a coloured [rim](#), can give the appearance of open symbols. Point size(s) are determined by [pointSize](#) and colour(s) by [pointColor](#). The colour(s) for points from data series for which the

colour has not been defined by [pointColor](#) are either automatically selected based on a rotating 15-colour palette or are taken from the line colour dictionary depending on the [useLineColorDictionary](#) setting.

'auto' can also be specified as a colour in which case **PhreePlot** chooses a colour. If [changeColor](#) is also `TRUE`, then different colours will normally be chosen for different lines. Otherwise the colours will be the same or different shades of the same colour for subsets.

All lines are drawn with a thickness given by [lineWidth](#). Negative values will give dashed lines. The dash density is given by [dashesPerInch](#). As with the points, the starting line colour(s) are either determined by the [lineColor](#) setting and then automatically follow the default sequence, or are taken from the line colour dictionary.

The line colour dictionary also contains information about the in-plot position of labels for the lines and can be edited and replotted accordingly. [labelSize](#) and [labelColor](#) can be used to adjust the appearance of the labels or turn them off completely. Label names for lines are automatically generated from the column names but can be overridden with the [labels](#) keyword.

It is possible to synchronise the point and line color for the same data series with [points-SameColor](#).

A simple legend with an optional [legendTitle](#) and [legendBox](#) is automatically drawn to the right of the plot. It can be turned off by setting [legendTextSize](#) to 0. The position of the legend can be moved with a line of [text](#) or [extraText](#) file and the `<legend>` tag.

Additional lines, points, symbols and text can be added to a plot with [extraLinesSymbols](#), [text](#) and [extraText](#) as described in more detail below. Points or lines from additional files can be added with [extradat](#).

## 7.4 CONTROLLING THE STYLE OF LINES AND POINTS (SYMBOLS) IN CUSTOM PLOTS

### 7.4.1 The default style and colour for lines and points (symbols)

Each [lines](#) variable has a [lineType](#) associated with it. This defines the line style and is specified by a number from 1 to 20:

- 1 solid line
- 2-10 dashed line with an increasing proportion of space
- 11 dotted line
- 12-20 dot-dashed line with an increasing proportion of dash

The appearance of a line can also be changed with [lineColor](#) and [lineWidth](#) as described below. There are 2y equivalents of these keywords.

Similarly, the symbol styles of [points](#) are defined by their respective [pointType](#). See [below](#) for a description of the symbols.

Each dataset (lines, points, lines2y, points2y) has its own list of 15 colours. These are picked off one by one as needed. Specifying specific colours in an input file promotes that colour or colours to the top of the list.

Each list starts with the same default list of colours. This is:

```
red
blue
green
orange
cyan
magenta
brown
sky
purple
gray
yellow
maroon
```

```
lawn
spring
black
```

So by default, the first colour to be used will be `red`, the second `blue`, etc. The default colour density is 4, i.e. `red4`, `blue4`, ...

The various colour keywords such as [lineColor](#) provide a mechanism for promoting a colour to the top of the list.

```
lineColor purple green
```

means that the line colour list becomes:

```
purple
green
red
blue
orange
cyan
magenta
brown
sky
gray
yellow
maroon
lawn
spring
black
```

Once the list is exhausted, it is recycled but the colour density may also be cycled 4, 6, 8, 2, 4... depending on the [changeColor](#) setting. Points are plotted after lines and may inherit the same colour as the corresponding line by using the [pointSameColor](#) setting.

## 7.4.2 Lines

### *Line styles*

The line style pattern is defined by a number in the range 1-20. These are shown in Figure 7.2 using a dash density of 5 dashes per inch. The demo file, `\demo\linestyle\linestyle.ppi`, can be used to generate a similar figure for a range of dash densities.

### *Automatic colouring of lines and points*

The [colour](#) of lines and points are selected based on the amended colour sequence in effect (see above). The colour picked is determined by the position of the variable being plotted in the input list ([lines](#), [lines2y](#), [points](#), [points2y](#)) and the position of any colours specified explicitly in the corresponding colour setting ([colorLines](#), [colorLines2y](#), [colorPoints](#), [colorPoints2y](#)) if necessary taking into account the recycling rules, e.g.

```
lines pH Ca Mg Na K
lineColor purple green
```

will give the following colours: `pH = purple4`, `Ca = green4`, `Mg = purple4`, `Na = green4`, `K = purple4` when [changeColor](#) is false and `pH = purple4`, `Ca = green4`, `Mg = red4`, `Na = blue4`, `K = orange4` when [changeColor](#) is true.

Colours can be set multiple times in a list to force a particular colour. Rims for filled symbols also have their own colours that follow the same colouring rules.

Sometimes there are subsets of data with the same heading. This occurs where a line break (blank line) in the data file has been found. The colour for all lines from this column will follow the colour selected above but the colour density will change if the colour was specified without a colour density (no number at the end, e.g. `red`) and if [changeColor](#) is `TRUE`. If the colour is specified explicitly as `red4` then this will always be used with no change in density.

'`auto`' can also be used as a colour. This will cause different colours to be used following the

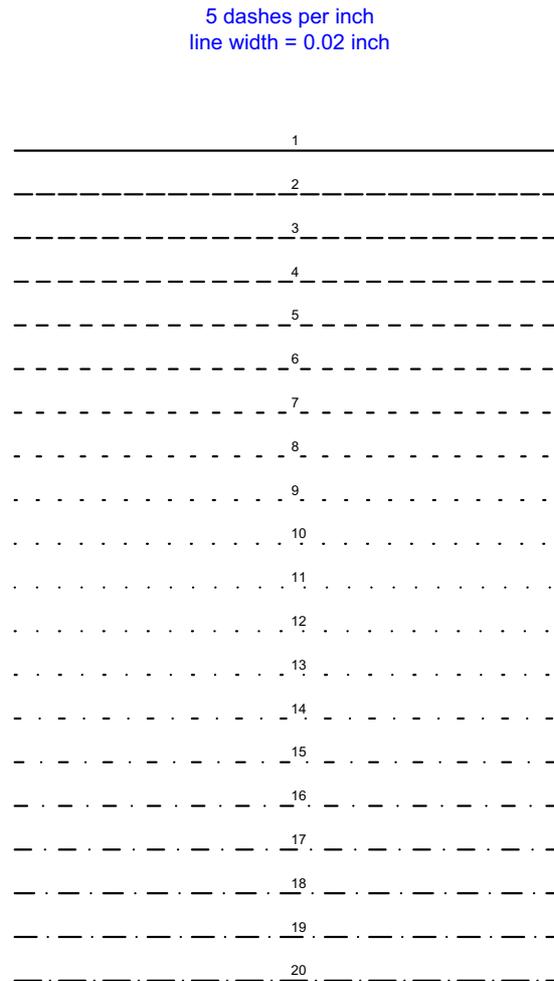


Figure 7.2. Examples of the 20 line style patterns available. These are specified with the [lineType](#), [lineType2y](#), [contourLineType](#) or [gridLineType](#) settings. The

colour sequence in effect. ‘nd’ (‘not drawn’) is also a colour that is distinct from the background colour, and ‘white’ is also a valid colour.

When there are multiple plots/datasets per run, [restartColorSequence](#) controls whether the line color sequence for auto-generated colours is restarted from the beginning of the sequence for each plot/dataset, or not.

Colours can also be controlled explicitly with the line colour dictionary ([Section 7.9.2](#)). All points and line segments within a given sequence will have the same colour. If different attributes are wanted for each point or line segment, use an [extraSymbolsLines](#) file.

The selection strategy outlined above is followed for the colour of all lines and points,  $y$  and  $2y$ .

### 7.4.3 Points (symbols)

Symbols can be plotted to represent the data points in a curve. The symbol used is specified with the [pointType](#) keyword and can be specified by a number or a name. The available symbols and their symbol codes are shown in [Appendix 3](#) and [Figure 7.5](#).

The six standard filled symbols and their code numbers are:

- 1 filled circle
- 2 filled square
- 3 filled triangle
- 4 filled upside down triangle
- 5 filled diamond
- 6 filled octagon

The list of symbols is recycled as needs be. The default symbol type is 1.

If [pointsSameColor](#) is `FALSE`, [pointColor](#) controls the colour of the symbols using the point colour list as for the lines described above.

If [pointsSameColor](#) is `TRUE` and lines are plotted, the symbols will always have the same colour as their corresponding lines irrespective of the [pointColor](#) setting.

There is no guarantee that all symbols will be centered exactly though the first six should be.

The size of symbols is specified by the [pointSize](#) keyword list.

Filled symbols can have a separate rim colour ([rimColor](#)) and rim width specified as a fraction of the corresponding symbol size ([rimFactor](#)). This enables open circle symbols to be specified. If these lists are short, the values are recycled.

The minimum size of positively-sized symbols is set to 0.01 inch. A size of 0.0 suppresses plotting of symbols.

#### 7.4.4 Order of plotting of lines and points (symbols)

The general order of plotting of lines and points (symbols) is controlled by the [plotOrder](#) keyword. The default is lines then points. Within a given class, e.g. 'lines', the order of plotting of individual lines is controlled by their order of definition in the keyword in the input file(s).

The order of plotting affects any overprinting - the last plotted will appear on top.

Although [plotOrder](#) does control the order of plotting of separate sets of lines and points, when the same variable is plotted as both a line and a set of points, the line is always plotted first. This means that the points will always overprint the line.

## 7.5 LABELLING PLOTS

Fields and lines in plots will normally be labelled, although the precise way this is done depends on the type of plot and the various settings available.

Labelling of plots is important but it can be difficult to automate optimal placement. It is therefore always possible to edit a 'labels' file to rename labels or to move their positions. Some details on the choice of label names and their positioning is given below.

### 7.5.1 Label names and label position

Label names (up to 30 characters long) are automatically assigned a value depending on the type of plot.

In 'ht1' and 'grid' plots, label names are derived directly from the species names and x- and y-coordinates of the label positions are approximately centered in the field. The species name is in turn derived from the database and any changes subsequently made by the `ht1.inc` or similar file. The labels file can be edited to change the label positions and/or the label attributes and the plot replotted ([calculationMethod](#) = 2). The plot should not be recalculated ([calculationMethod](#) = 3) as this will recalculate the label positions and return them to their original positions.

The label position for predominance plots is, by default, placed near the centre of each field. In custom and fit plots the positioning is more complex and an attempt is made to place the labels in a legible place (Section 7.10.3). This can take a lot of effort to avoid overlapping – a brute force (simulated annealing) approach is taken. The time taken is broadly controlled by the `labelEffort` setting (0-3). The second parameter, if present, provides an upper limit to the time taken (in sec).

In custom plots, the centre of the label position is stored in the line colour dictionary which can be edited and the plot remade. The label name can be edited in the same way.

Label names for each of the ‘curves’ (including a set of points) can be overridden with a list of names given by the `labels` keyword. ‘label’ names are simply picked from this list (as seen in the legend) one by one as required. Multiple curves generated in the same iteration because of the presence of line breaks will be picked first, then multiple values of the loop or z-variable, then any more ‘outer’ iterations. The list is recycled if necessary. Label names for custom plots can also be read from the first column of the `loopFile` if present though the `labels` setting takes priority if not null.

When labels are derived from column headings, these may be set in the input file or in the case of a simulate or fit plot, from the column headings of the fit data file.

Label names are automatically tested to see if they are plausible **PHREEQC** chemical formulae and if so, subscripted and superscripted appropriately. Whether a label name is interpreted as a formula or not depends on its format (Section 6.4.2). This conversion can be bypassed by setting `convertLabels` to `FALSE`, or individually by including a non-printing character in the label name or surrounding the chosen label name with square brackets (Section 6.4.2). These brackets will not be plotted but should still be used to identify the line.

Label names stored in the line colour dictionary and used as labels in plots and legends are automatically appended with a special character when referring to the secondary (2y) axis. By default this is a ‘\*’ but this can be changed (see [ytitle](#)). This character should not be used as the last character in undecorated label names.

### 7.5.2 Overriding calculated label positions and angles

Sometimes it is necessary to omit a particular label from a plot or move its position or change its angle.

For predominance plots, removing a label can be done by changing the relevant species number in the labels file to a negative number, e.g. change 4 to -4.

This can also be achieved in other plots by editing the line colour dictionary as described above.

The label positions and angles can also be changed by ‘nudging’ them with the `nudge` or `nudgeFile` keywords. Nudges can be applied to all plot types and are applied just before plotting.

A nudge file is simply a collection of nudges. These specify either an incremental shift (‘diff’) or an absolute position (‘abs’) for x, y and angle for a label. The justification of the label string can also be set for the absolute definition.

A nudge file should have a single header line (e.g. to remind yourself of the column headings) followed by 6 or 7 columns of data in free format as follows, e.g.:

```
plot  labelno  species_name      type  xmm  ymm  angle  pos
auto  1        "H2(g) > 1 atm"    diff  1.2  -6   0      0 # left-justified
auto  2        "O2(g) > 0.21 atm" diff  1.2  5.5  0      1 # centered
1     0        "Fe+3"            diff  4     6   0      2 # right-justified
```

The water limits and methane labels are automatically rotated on pe/Eh/mV predominance plots if the label angle is originally exactly 0.0 degrees.

`plot` refers to the sequential plot number (as given by the `info` block) of the file for which this

override applies. 'auto' or 0 means that it applies to all of the plots. `labelno` refers to the sequential label position (see the log file) and is necessary because the same label can be used several times in a plot. 'auto' or 0 means that it applies to all of the labels with the given label name.

If the type keyword parameter is 'abs', this sets a new value for x,y coordinates and angle. The position set by the coordinates is for the centre of the label in the units used for plotting (mm, inch, etc). This contrasts with the labels file where the x,y coordinates are specified in terms of graph units. x and y are for the anchor position of the label; y is located at the vertical centre of the label (when horizontal), and the angle is in degrees from the horizontal, rotated down clockwise. The seventh column, `pos`, is only used for 'abs' shifts and specifies whether the anchor position given is for the left end of the label (0), middle (1) or right end (2).

If the type parameter is 'diff', then this does the same as above but specifies the *shift* in the position and angle of the label from its initial calculated position. The `pos` column is not used for diff nudges.

These nudges only apply if the plot number and species name match that in a plot.

It is possible to delete a label from plotting by nudging it completely off plot. Nudging can be useful for adjusting the rotation of the labels for the water limits in predominance plots. The preferred angle for this is given in the log file.

### 7.5.3 Legend

A legend is automatically drawn for [custom plots](#).

Normally a simple legend will be drawn to the right of the plot. This shows the colour of the plotted lines and symbols against their label names. The size of the legend text is controlled by [legendTextSize](#) but this setting will be overruled by an explicit `<legend>` size setting in a text string. The line thickness is the same as in the plot. The [colour](#) of the legend text is controlled by [legendTextColor](#).

The order of items in the legend is controlled by the [plotOrder](#) setting and the orders specified in the [lines](#) and [points](#) settings in the input file(s).

The legend will normally not be drawn if [legendTextSize](#) is 0.0 or if all of the lines or symbols have the same colour.

The legend and all labelling can therefore be suppressed by setting both [legendTextSize](#) and [labelSize](#) to zero. Individual labels can be suppressed by setting their colour to 'nd' in the line colour dictionary and forcing the dictionary to be used by setting [useLineColorDictionary](#) > 0.

A legend box can be drawn around the legend using [legendBox](#).

The placement of the legend can be changed by specifying its position in a [text](#) line or [extra-Text](#) file using the special `<legend>` option. `<legend>` is not like a typical tag but rather acts as a placeholder for the legend contents.

This approach can also be used to suppress the legend by specifying its coordinates to be outside of the page area.

A legend title can be also be added by preceding the `<legend>` tag with text, e.g.

```
auto 9 -20 "<b>Concentration</b><br> mg/L<legend>" 1.5 blue
```

`auto` in the line above means that the text will be applied to every plot. Any text after `<legend>` but within the double quotes is ignored. The position of the legend can be automatically controlled using the `<pxmin>` etc tags (see [Section 7.12](#)).

## 7.6 INPUTTING TEXT STRINGS

### 7.6.1 Available fonts and character sizes

Fonts from the Helvetica, Helvetica-Narrow, Bookman, Avantgarde, Times, Palatino, NewCenturySchoolbook and Courier font families are available (see [font](#)). These are the eight font families included in the 35 standard Postscript fonts. The regular, italic and bold faces of these fonts can be specified with **PhreePlot** and should be able to be displayed and printed by Postscript-conforming devices. The italicized ZapfChancery font is also available.

The `symbol` and `dingbats` fonts are also used for plotting Greek characters, symbols and various icons.

All of these fonts are available with the standard **Ghostscript** distribution.

However, the fonts cannot be mixed. Only one of the font families can be specified for the main text (in titles etc) although text enhancements such as bold and italic can be used. Text in other fonts can only be written using the [text](#) or [extraText](#) mechanism.

The set of characters available within a font depends on the character encoding used. The default is '[Latin-1](#)' which includes many of the accented characters of Western European languages plus a few other symbols. The popular Windows-1252 character set adds a few extra accented characters to this (plus the euro sign) but is not available here. The alternative, '[Standard](#)' encoding, includes all 7-bit ASCII characters plus a smaller range of extended characters which depend on the setup of your computer. This standard set was the default character set in **PhreePlot** until January 2014 and includes the 7-bit ASCII codes (decimal 0-127) which has all the numbers, lower and upper case Latin alphabet, some punctuation as well as some special characters (as found on most keyboards).

The size of characters can usually be specified by a character size parameter given as a number. The length units used depends on the [units](#) keyword in force. These are nominal character sizes and do not usually match the actual size of the characters as plotted. For example, an uppercase 'O' in Helvetica font with a specified size (height) of 10 mm will actually be about 12.8 mm high. Other fonts will differ somewhat from this.

### 7.6.2 Available characters and inserting 'special' characters

Text is required as input for various options such as the plot title, axes titles and extra text. General features of text input are:

With the standard encoding, all ASCII characters (32-126) are available including numbers, alphabetic characters and some special characters. These include: `\|! "$%&*'()_ - += { } [ ] : ; @ ~ # < , > . ? /`. A space can be included but when this is done, the entire text string must be included in single or double quotes, e.g.

"Zinc concentration" or 'Zinc concentration'

The two types of quote should not be mixed. If a single quote character itself needs to be included as well as a space, embed the text string in double quotes; *vice versa* for including a double quote character. A warning will be given if an unpaired quote is found without being embedded in quotes. In this case, the string will not be plotted. Note that the quotes should be of the simple vertical type, not the angled open/closing quote marks beloved of word processors and their fancy fonts (as here, so be careful not to copy/paste these!)

"It's easy"

and

'A double quote (") can also be used.'

are acceptable.

It's easy

and

(")

are not. If in doubt, include the text string in paired quote delimiters.

Ultimately the fonts available to the printer and display device will determine which characters are available. In principle, most devices are able to print the standard ASCII set of characters without a problem, and the Latin-1 set also. [Example 68](#) provides a view of many of the available characters. The full range of characters is determined by the encoding and can include [accented characters](#).

Text strings can contain system and user-defined tags. These should be assigned values using the [numericTags](#) or [characterTags](#) keywords or have their values assigned by **PhreePlot**.

If the character is not readily available on your keyboard or input device, then any valid character can be added to a text string by using a backslash followed by the [3-digit octal code](#) for the character from the character set in force (\000-\377). For example, using the Latin-1 encoding, 20¢ (twenty cents) can be entered as 20\242 since 242 is the octal code for cent (decimal 162). \260 is the degree symbol. [See "Accented and other 'foreign' characters - the Latin-1 encoding" on page 92](#) for more details.

### 7.6.3 Text enhancements (bold, italic, subscript, superscript) and Greek characters

A certain degree of text enhancement is possible although the possible combinations are rather limited. The following tags are available for modifying the appearance of text. Case is significant. All text enhancement tags should be in lowercase.

Most of the tags are paired and should be turned 'on' and 'off' in their nested order otherwise unpredictable output may result.

Bold: `<b>This is bold text</b>`

Italic: `<i>This is italic text</i>`

Italic: `<b><i>This is text</i></b>` # N.B. tags must be properly nested

Superscript: `e = m c<sup>2</sup>`

Subscript: `Ca(NO<sub>3</sub>)<sub>2</sub>`

Sub and superscript: `Sum <subsup>under over</subsup>`

Subscript first then the superscript separated by a space. This gives Sum  $\overset{\text{over}}{\underset{\text{under}}{\cdot}}$ .

Greek strings: `<g>abcdef</g>` gives  $\alpha\beta\gamma\delta\epsilon\phi$ .

The mapping of lower and uppercase Greek characters is:

$\alpha\beta\gamma\delta\epsilon\ \phi\eta\theta\iota\phi\ \kappa\lambda\mu\nu\ \pi\theta\rho\sigma\tau\ \upsilon\omega\xi\psi\zeta$   
 abcde fghij klmno pqrst uwxxyz

ΑΒΧΔΕ ΦΓΗΙΘ ΚΛΜΝΟ ΠΘΡΣΤ ΥΩΞΨΖ  
 ABCDE FGHIJ KLMNO PQRST UWXYZ

An alternative way of getting a single Greek character is to precede the corresponding letter with a backslash:

`\a` gives  $\alpha$

`\mg/L` gives  $\mu\text{g/L}$

If a backslash itself is wanted, escape the backslash by using two consecutive backslashes or insert a blank ‘do nothing’ string immediately after the backslash, e.g. `\<i></i>p` will print `\p`.

If a Windows filename with backslashes in it is to be printed, and it is defined in a tag, either change the tag definition such that backslashes are replaced with double backslashes, or if this is not possible, either use forward slashes when entering file paths, or if the tag has been derived from a loop file, enter a new column, say `file$`, with the entries as filenames with double backslashes, and then use `<file$>` tag.

Characters embedded in a Greek string for which there is no translation to a Greek character will be replaced by a space.

Break: `<br>` produces a line break. Each line is treated as a separate text string. Therefore any other tags such as `<b> </b>` must be properly paired tags before and after any `<br>` and may need to be repeated, e.g. `<b>bold1</b><br><b>bold2</b>`.

All but `<br>` are paired tags. If one of the pair is missing or has been mistyped or the tag has not been recognised, that part of the string will be printed as is.

In most cases, text enhancement tags (i.e. Greek, bold, italics, subscript, superscript, supersubscript) cannot be embedded within one another, e.g.

```
<sup><i>this gives superscript but not italics</i></sup>
```

and

```
<b>this will not be bold<br>this will not be bold</b>
```

will not work and may produce incorrect output but

```
<b>bold</b><i>italics</i>
```

and

```
<b>bold</b><br><b>bold again</b>
```

will work. The exceptions are that bold can be used with other tags: `<b><i>...</i></b>` and `<i><b>...</b></i>` will both produce the bold-italic font and `<b>Cu<sub>T</sub></b>` will work as hoped. Note that the order of the ‘off’ tags is important to maintain the correct nesting otherwise unpredictable results may occur. Illegally nested tags will be ignored or incorrectly translated.

It is **not** possible to define subscripted superscripts such as  $a_{\text{Fe}}^{3+}b$

```
a<sub>Fe<sup>3+</sup></sub> (illegal)
```

or superscripted superscripts

```
a<sup>Fe<sup>3+</sup></sup> (illegal)
```

or superscripted Greek characters.

It is also not possible to enhance any Greek characters, e.g. Greek italics or Greek bold are not supported.

It is possible to embed many **PhreePlot** tags such as `<loop>` and `<mainspecies>` (but not `<input>`) between text enhancement tags since the text substitution has already taken place before being interpreted for plotting:

```
"As = 10<sup><loop></sup>M".
```

Ensure embedded spaces are enclosed using single or double quotes.

### 7.6.4 Accented and other ‘foreign’ characters - the Latin-1 encoding

The default or ‘Standard’ encoding is based on the ASCII 7-bit characters plus a variable number of characters from an ‘extended’ character set found on many keyboards. Many Western European languages have accented characters which are not in this set. These are found in the ISO-8859-1 character encoding (Latin-1) which is similar to the Windows 1252 (Western European) character set minus a few characters.

The Latin-1 character encoding is supported in Postscript and in the Postscript fonts supplied by **Ghostscript** and many other Postscript interpreters. The full character sets are shown in [Appendix 4](#).

There are two ways of entering accented and foreign characters not available directly from your keyboard:

(i) most Windows text editors such as **Notepad** and **Notepad++** support the Latin-1 encoding (and others) and accented characters can be entered by using Alt-num key codes. This is done by holding the Alt key and then typing the decimal code for the character with the numeric keypad including the leading zero, e.g. Alt-0200 for È. The editor must be configured to view and export the text with the correct encoding (i.e. ISO-8859-1 or ANSI) which may not be the default.

(ii) Postscript interprets 3-digit numeric strings preceded by a backslash as octal codes and associates these with the appropriate characters according to the encoding in force, e.g. \310 for È and \350 for è with Latin-1. So these octal codes can be included directly in text strings, e.g. `caract\350res europ\351ens` for `caractères européens`. Note that with octal codes, no digit can be greater than 7 (unlike the decimal codes above).

The first method is probably better if the Latin-1 encoding is being used since this follows closely the Windows encoding and so the text can be read and checked visually in the monitor. The second method is less easily interpreted on-screen but avoids any problems with encoding of the text from editor/monitor to Postscript. Internally, the extended characters are always replaced by their octal codes in the Postscript output.

The usual limit on the length of plotted text strings is 400 characters. This includes the tags such as `<sub>` and any necessary replacement of the extended characters using their octal representation, i.e. each extended character takes four ASCII characters. Longer lines will either be truncated or any translation aborted.

The default is to interpret text strings with the Latin-1 encoding. In order to enable the Standard encoding, use the [font](#) keyword

```
font Helvetica Standard
```

or to retain the current font

```
font Standard
```

The encodings for both ‘[Standard](#)’ and ‘[Latin-1](#)’ encodings are given in [Appendix 4](#). Alternatively visit a website such as [http://en.wikipedia.org/wiki/ISO/IEC\\_8859-1](http://en.wikipedia.org/wiki/ISO/IEC_8859-1) for Latin-1.

As well as the accented characters, umlauts and inverted marks, Latin-1 includes some other useful characters such as the degree (°), plus-minus (±) and some common fractions. On the other hand, the standard encoding has some characters that Latin-1 does not, such as the per-mil symbol and the oe ligature.

### 7.6.5 Non-printing characters

It is sometimes useful to add a non-printing character to the plotted output. Postscript interpreters usually just ignore these characters.

Whether a character (decimal code) will print or not depends on the font and its encoding. With the ASCII encoding, the `¬` (‘Not sign’) character does not print and is found on many keyboards. This does print with Latin-1 and Standard encodings so other characters are

required. Characters not available on keyboards can be entered with either of the two methods discussed above, namely Alt-num key codes and octal codes. Characters with decimal codes from 129 to 159 (octal codes 201 to 237) may not be defined and are not normally printable but avoid those before decimal 138 (octal 212) as these are used internally by **PhreePlot**.

### 7.6.6 Justification

This can usually be specified as either left, centre or right justified horizontally. The text is also aligned on the text baseline (bottom of the letter a) though the exact position can depend on the particular characters and font. Where a `<br>` is included, the x and y coordinates refer to the bottom of the first (top) line.

For accurately centered symbols, use the [extraSymbolsLines](#) symbols rather than the [extraText](#) symbol font.

### 7.6.7 Angle

The text can be rotated. The angle of rotation is given in degrees from the horizontal, rotating down clockwise.

### 7.6.8 Tags in text strings

Tags can be added to text strings and their values, if known, substituted at plot time. Tags generated during a run are not stored and so will be `UNDEFINED` on replotting.

## 7.7 SPECIAL PHREEPLOT VARIABLES OR TAGS

### 7.7.1 Available tags

A number of special variables, or tags, can be included in a **PhreePlot** input file or extra text file. These are substituted by values or specific operations at run time. These are:

<a href="#">&lt;x_axis&gt;</a>	The current value of the x-axis variable
<a href="#">&lt;y_axis&gt;</a>	The current value of the y-axis variable
<a href="#">&lt;loop&gt;</a>	The current value of the loop (z) variable
<a href="#">&lt;logloop&gt;</a>	The current log10 value of the loop (z) variable
<a href="#">&lt;mainspecies&gt;</a>	The name of the main species
<a href="#">&lt;legend&gt;</a>	The entire legend key as used in the current plot
<a href="#">&lt;input...&gt;</a>	Part of the input file (only in <a href="#">text</a> lines or <a href="#">extraText</a> files)
<a href="#">&lt;pxmin&gt;</a> etc	The value of pxmin etc at plot time
<a href="#">&lt;command_line0&gt;</a> etc	The values of the command line arguments

In addition, several special tags are automatically produced during a fit which contain information about the fit.

### 7.7.2 System pH, system pe and system temperature

Internally, **PhreePlot** needs to know certain system variables to convert from one yscale to another. Sometimes this information is passed through standard `PUNCH` output formats, e.g. for predominance plots (`ht1.inc` etc), but sometimes it is not done automatically, e.g. for contour plots. However, this information can be passed by `PUNCH`'ing the appropriate columns and naming the columns in a particular way. These three variables, pH, pe and temperature (Celsius) are recognised by the column headings, "pH", "pe" and "TC" (case sensitive), respectively.

## 7.8 AXIS SCALING

### 7.8.1 Auto or user-defined axis scaling

Axis scaling is set with keywords such as [pxmin](#), [pxmax](#) etc. Axis scaling can either be automatic or manual. A keyword value of 'auto' means that **PhreePlot** attempts to choose the axis scaling so that all valid data in the data file are included in the plot and the tick intervals are at 'pretty' intervals.

Manual scaling by setting [pxmin](#) etc gives more control over the minimum and maximum range, the numbering of the axes and the positioning of tick marks. It also enables 'zooming in' on particular parts of the plot without recalculation though this is often better done by recalculating with the new domain settings. Automatic label placement for lines is only carried out after a new calculation.

The first major tick mark for both axes is placed at the plot origin (bottom left-hand corner) by default but this can be modified by the optional second parameter to [pxmin](#) or [pymin](#) which indicates the location of the first major tick mark (and label). The x and y axes are then labelled every [pxmajor](#) (or [pymajor](#)) graph units until [xmax](#) (or [ymax](#)) is reached. There is a label at each major tick mark. There is not necessarily an axis label at the maximum value. Additional minor tick marks are calculated according to the value of the [pxminor](#) and [pymenor](#).

When a plot has a max-min range of 0–100, say and a lot of data are at or close to 0., then this can create a lot of untidy plotting and labelling close to the lower x axis. This can be avoided either by removing the offending columns completely from the plot or by shifting the y-axis scale by a small amount, e.g. to 0.001 and 100.001, respectively. This will remove the columns where all the data are below 0.001 from both the plot and from the key. Of course, some information is lost in the process. It is also possible to eliminate lines by setting the [minimumYValueForPlotting](#) keyword at an appropriate value, e.g. for eliminating very minor or fictive species from species plots.

If the scope of a predominance plot calculation (set by [xmin](#), [xmax](#) etc) is changed and the plot is replotted rather than recalculated then the scale and positioning of the polygon labelling and axis scaling will reflect the selected data from the original files and may appear somewhat odd - not much of the original data may be selected if the plot area is a small part of the original area or if not many points are selected from the polygon file. The corresponding polygon and label files should therefore be regenerated using 'Reprocess and replot' ([calculationMethod](#) = 3) or 'Calculate and plot' ([calculationMethod](#) = 1) to ensure the correct positioning of labels.

### 7.8.2 Secondary y axis (the 2y axis)

The left-hand vertical axis is the main y axis. The ticks on this axis are normally mirrored on the right-hand y axis. It is also possible to define different scaling for the right-hand y axis (the secondary or '2y' axis) using keywords such as [p2ymin](#), [p2ymax](#), [2ytitle](#) etc. Variables for this axis are specified for this scale using [points2y](#) and [lines2y](#) keywords as for the main y-axis variables. An example in which the 2y axis is used as an expanded y-scale is shown in Figure 7.3.

The 2y title is plotted if any variables have been defined with [points2y](#) or [lines2y](#). If [2ytitle](#) is set to 'auto', the first variable name from [points2y](#) or [lines2y](#) is used. If labels or a legend are drawn, the names of any labels referring to the 2y axis have, by default, an asterisk (\*) appended to their label name. This modified name is also stored in the line colour dictionary. The asterisk can be replaced with any single character using the third parameter of the [2ytitle](#) setting.

There is no corresponding [minimumYValueForPlotting](#) for the 2y axis.

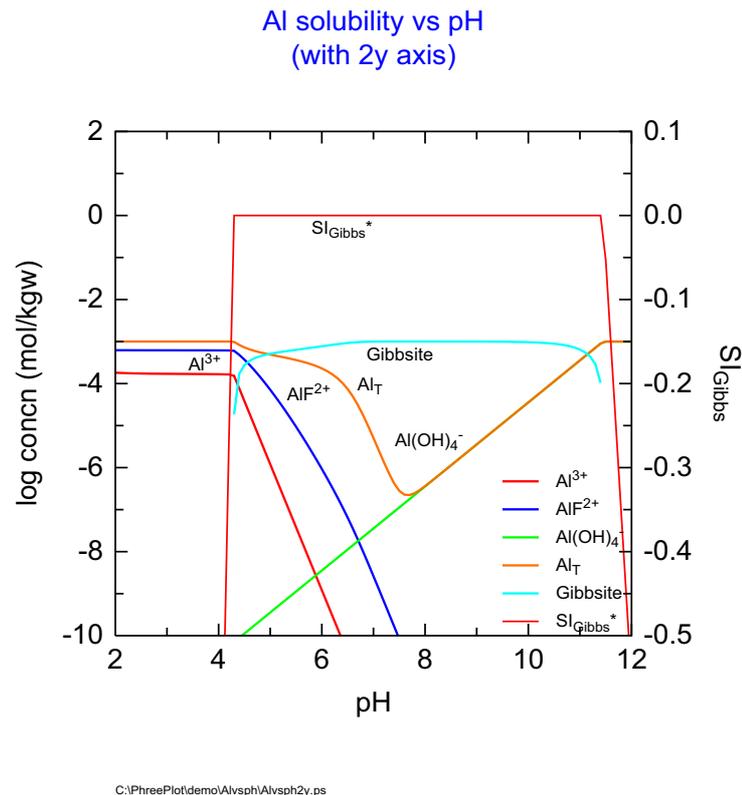


Figure 7.3. Use of the secondary (2y) axis to provide an expanded y-scale for displaying the saturation index.

## 7.9 CONTROLLING THE PROPERTIES OF TEXT, SYMBOLS, POLYGON FILLS AND LINES

### 7.9.1 Principles

Text, symbols, polygon fills and lines have various properties associated with them such as type, size and colour.

Some of these are fixed by **PhreePlot** but many can be set in **PhreePlot**. However, the way that this is done can depend on the type of plot involved – predominance plot, custom plot or contour plot. These properties often take on default values specified in the `pp.set` file but many of the colours, such as those for lines and symbols, can either be auto-generated or set more explicitly.

Some properties such as the colour of the plot title only have a single value and these are usually set by a separate keyword, here `plotTitleColor`. Other properties, e.g. those of lines and points (symbols) in custom and contour plots, have an array of values, one for each separate line or set of symbols.

In custom plots, these array properties are set in two ways: line and point colours are automatically picked from a sequence of 15 colours including black while other properties such as line width, point size and where appropriate, rim colour and size, are recycled from the list associated with the various keywords such as `lineWidth`, `pointSize`, `rimColor` and `rimFactor`. The principle here is that some properties such as `lineWidth` are often constant within a given plot and so it would be tedious to specify them for each line. Hence properties such as these only need to be specified once and are then recycled.

However, it is often desirable to colour each line separately (within reason) and so here a

longer list is recycled. There is always a default and ordered list of colours associated with the plotted lines but specific colours can be promoted to the top of the list to ensure that they are used first. Four of these colour lists or sequences are stored, one for points (symbols), one for lines, and one each for their 2y counterparts.

Lines of a particular dataset are always plotted before the points. This ensures that the points will overwrite the lines.

The ways that these colour sequences are used and their interactions are controlled by three keywords: [pointsSameColor](#) (ensures points have the same colours as any associated lines), [changeColor](#) (individual datasets are plotted with different colours as far as possible), and [restartColorSequence](#) – if true, restarts the auto-generated color sequence for each new plot and for each new plot type (lines, points).

Colours from custom plots are stored in the line colour dictionary. This can be edited to change the line and symbol properties (see [useLineColorDictionary](#)).

With contour plots, the properties of each contour are derived from a corresponding list, e.g. [contourLineColor](#).

Fill colours used in predominance diagrams are also automatically selected from a colour sequence but unlike line and point colours cannot be preset. They can however be changed by editing the fill colour dictionary and replotting.

While the colours used are always stored with their colour names, the rendered colours may be changed if the grayscale or black & white colour models are used.

Details about how to add additional text to a plot and how to format numbers is given in [Section 7.12](#).

### 7.9.2 The colour dictionaries

There are two colour dictionaries which control the placement of labels and the colour of fills and lines. The location of these is specified by the [fillColorDictionary](#) and [lineColorDictionary](#) settings in the input files. Both files are automatically created and maintained by **PhreePlot** but can be edited to change their settings, e.g. the colours, or in the case of the line colour dictionary, the placement of the labels in a custom plot (repositioning/removing labels in a predominance plot is achieved by [nudging](#) or editing the labels file).

The dictionaries are read in free format in the same way as the input files. The species name can contain blank characters if embedded in single or double quotes. If the labels appear to be chemical formula in **PHREEQC** format, sub- and superscripts are substituted as appropriate.

If the dictionaries are not present, then they will be automatically created with the name specified. Default names are 'fillColor.dat' and 'lineColor.dat'.

#### *Fill colours*

The fill colours are used for the area fills of predominance plots and the line colours are used for the lines in custom plots including fit plots. By default and in the absence of a fill colour dictionary, or when the species is absent from the dictionary, the fill colour is chosen from a sequence of pale colours (starting at `sky1...`). These default colours are overruled by settings in the fill colour dictionary. The fill colour dictionary contains a list of the 'species' names (as returned by **PHREEQC**) and their corresponding colours. Contour plots have their own way of specifying the appearance of lines, fills and labels.

#### *Line colours and auto line colouring*

The line colour dictionary is used for custom and fit plots and contains a list of the label name, x and y location (in graph coordinates) and [colour](#) of the various plotted lines. The colours are only used if the line or symbol is plotted, and by themselves do not dictate whether this is the case. For example, if a line has zero width or a symbol has zero size, it will not be

plotted.

The line colour dictionary is used or created whenever a custom plot is made. If the file already exists, then it may be used to determine the line colour associated with a particular 'species' if it is present.

The line colour dictionary consists of seven columns of data containing: the label name, x- and y- plotting positions in graph coordinates and three colours, the first applies to the line colour, the second to the points colour and the third to the rim colour of filled symbols, for each label. The last column is the code number for the type of symbol used ([pointType](#)), 0 for no symbol. If a points colour has not been defined, it will be written as a blank field (""). The x-position refers to the horizontal centre of the label and the y-position refers to the baseline.

UNDEFINED refers to an undefined ('not set') coordinate, e.g. when labels are not plotted. An empty string ("") for a colour will force automatic selection of the colour, if necessary. This is the default when the colour dictionary is rewritten and the when the point or line colour has not been set.

An example of a line colour dictionary is:

# label	x	y	lines	points	rims	symbol
"Cd+2"	9.7065	48.624	green4	red4	""	0
"Cd2OH+3"	9.3670	-3.5947	orange4	blue4	""	1
"CdCl+"	8.1980	2.2705	cyan4	black	""	1
"CdCl2"	8.5480	-3.5722	magenta4	nd	""	0

Whether the settings in these dictionaries are used or overridden in a custom plot is determined by the [useLineColorDictionary](#) and [changeColor](#) settings. If [useLineColorDictionary](#) is 0, then the labels and line colours are either taken from the [lineColor](#) setting in one of the input files or are automatically generated. The line colour dictionary is ignored. If [useLineColorDictionary](#) is 1 or 2 then the line colour dictionary will be searched for the species being plotted and if found will use the colour (= 1 or 2) and label position (= 2) from the line colour dictionary. [changeColor](#) determines whether all the curves have the same base colour (= FALSE) or not (= TRUE). If [changeColor](#) is set to FALSE and [useLineColorDictionary](#) is 1, then the line colour dictionary will take precedence.

If the species colour is not found or if [useLineColorDictionary](#) is 0, then a line colour will be automatically selected according to the line colour sequence starting at the top of the list of colours in effect at the time. The default sequence is:

```
red
blue
green
orange
cyan
magenta
brown
sky
purple
gray
yellow
maroon
lawn
spring
black
```

Yellow is not plotted by default as a line or point colour as it is often difficult to see (it will be included if explicitly given a colour density, e.g. `yellow4`). The sequence specified by this list is modified by the [lineColor](#) settings which promotes the given colour(s) to the top of the 15-long list. If the number of [lineColor](#)'s is greater than 15, the list is extended to accommodate all of these. The default [lineColor](#) setting in `pp.set` is 'auto' which means the colour sequence will be red, blue, green, ... as above. If [lineColor](#) setting is set to blue, then the sequence would be: blue, red, green, ... . If the number of colours required is greater than the length of the list, the list is recycled. If this is not wanted, use the colour dictionary to specify colours.

Autocolours only consider the basic colors (colors without a number). If the `lineColor` setting is `red2`, `red6`, `black`, the autocolour selected for the next (fourth) color would be `blue4`, the next unused colour in the sequence.

If a dataset is not plotted because there is no valid data in the plotting domain, then the corresponding auto-generated colour for that dataset is skipped.

If `changeColor` is set to `FALSE` and `useLineColorDictionary` is 0 then the colour(s) in the `lineColor` list will be used first (unless this colour is 'auto'). If there are several subsets of data for the same variable the actual colour will rotate the colour density, 4, 6, 8, 2, 4..., e.g. `red4`, `red6`, `red8`, `red2`, `red4`,... providing the colour was defined without a density, i.e. as 'red' rather than 'red4'. If a density is given, this colour will always be used.

With `calculationMethod` 2 or 3 (replot), **PhreePlot** uses the dictionary coordinates if present otherwise it omits the label. Use this to change the colour or position of labels (or use `nudge`), lines and markers. Use `calculationMethod` 1 to regenerate a fully populated dictionary.

When there are several plots produced per run, for example due to use of the loop variable, there is an option of whether to restart the auto-generated colour sequence at the beginning for each plot, or whether to continue where the colour sequence ended on the previous plot. This is controlled by the `restartColorSequence` keyword. `TRUE` will restart it, `FALSE` will not.

If the `trackSymbolSize` is greater than zero and `trackSymbolColor` is not 'nd' then a coloured track symbol or anchor point is drawn at the point on the line to which any automatically positioned labels have been associated. This symbol is not drawn on replots.

The x,y position of the label placement is calculated by **PhreePlot** when `calculationMethod` 1 (calculate) although whether this position is actually used is determined by the various settings described above. The position is always read from the file when `calculationMethod` 2 or 3 (replot) is used.

The line colour dictionary is always updated with the latest species and colours at the end of each plot and the results written to the dictionary file at the end of each run.

If a record from a colour dictionary cannot be read properly, it is ignored.

Line widths are set by the `lineWidth` setting for each particular line (recycled as necessary). Negative line widths indicate dashed lines. The appearance of dashed lines is controlled by their respective `dashesPerInch` and `lineType` settings.

### *Point colours*

Points are coloured in the same way as lines except that the initial colour is defined with `pointColor`. If `pointsSameColor` is `TRUE`, then the points will always have the same colour as the lines if defined. If the line colour dictionary is present, the second colour setting can be used to override the automatic selections. Delete or rename the dictionary or set `useLineColorDictionary` to 0 if this is not wanted.

The interactions between the `changeColor` and `pointsSameColor` settings for the automatic selection of colours (`useLineColorDictionary` set to 0) are illustrated in Figure 7.4. These examples can be found in the `autocolorn.ppi` files found in the `demo\PHREEQCllooping` directory.

### *Filled symbols with a different rim colour*

Normally points are plotted as simple symbols. However, there are six filled symbols which can have a separate rim colour. The filled colour is controlled by the `points`, `pointSize`, `pointColor` and `changeColor` settings.

Points will be plotted providing their size is greater than zero and their `colour` is not 'nd'. Rims will be added if the rim colour defined by `rimColor` is not 'nd' and the line width of the rim defined by `rimFactor` is greater than zero. If `changeColor` is `FALSE` so that all the lines are the same colour (as set by `lineColor(1)`), then `pointColor` is used for all the lines.

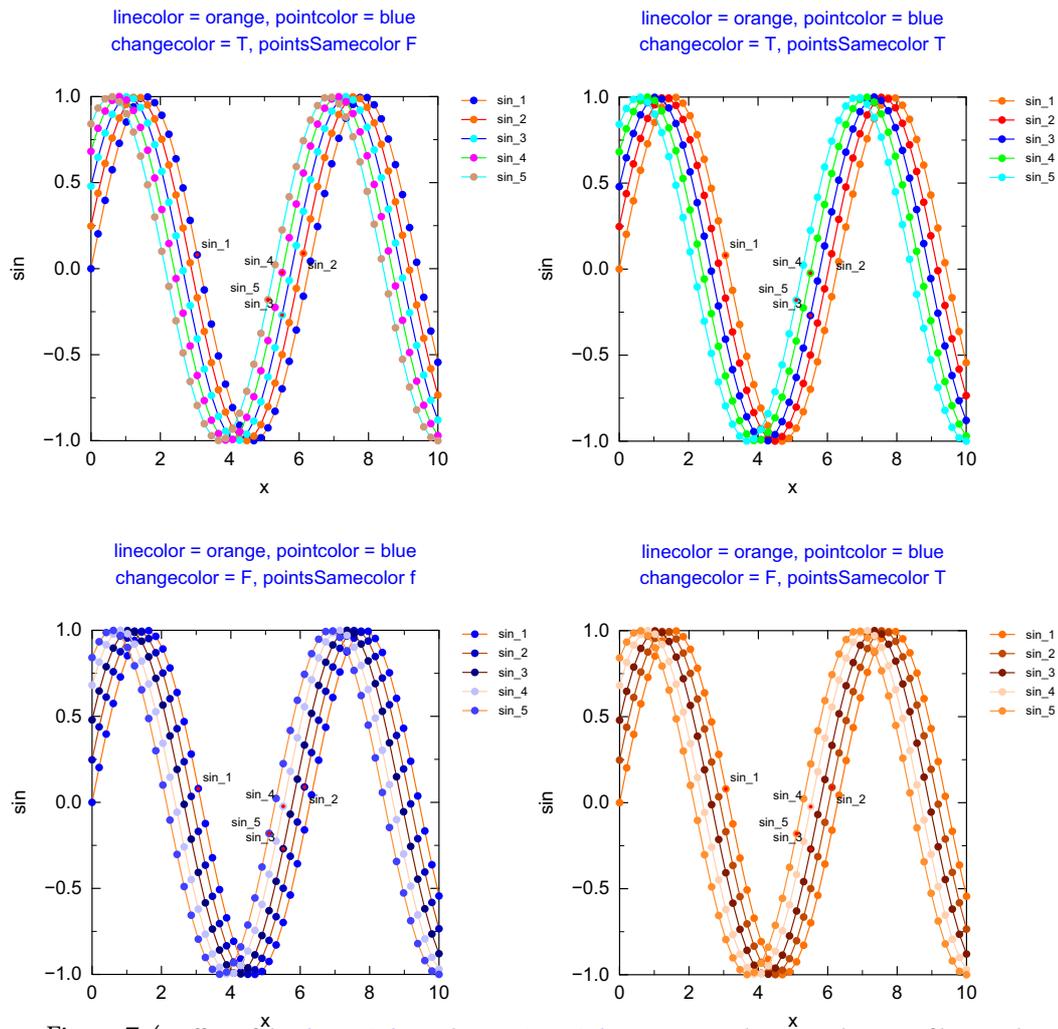


Figure 7.4. Effect of the `changeColor` and `pointsSameColor` settings on the auto colouring of lines and points for a data file (the ‘out’ file) containing several data sets created using PhreePlot’s in-built looping mechanism. The `lineColor` was set as orange4 and the `pointColor` was set to blue4. These provide the starting values of the auto-selected colour sequence. Top left: `changeColor = TRUE` and `pointsSameColor = FALSE`; top right, `changeColor = TRUE` and `pointsSameColor = TRUE`; bottom left, `changeColor = FALSE` and `pointsSameColor = FALSE`; bottom right, `changeColor = FALSE` and `pointsSameColor = TRUE`.

### 7.9.3 Directories for the colour dictionaries

If only the filename is given, then the specified file is sought following the usual search path rules (Section 2.4.6). If in doubt, give a full path name.

## 7.10 LABELLING

By default, all filled contour plots are automatically labelled and a legend produced to the right of the plot. An attempt is made to do this ‘nicely’ but this can be time-consuming especially when there are a large number of labels and when there is the potential for overlap. It is difficult to find a universal set of criteria that define good placement and it may be necessary to manually move labels using individual `nudge`s or by editing the appropriate label file. In the case of contour plots, the labels can also be moved along the contour using the `contourShift-Label` setting.

The algorithms employed at present are ‘experimental’ and rather inefficient. The time taken for labelling goes up roughly as the square of the number of labels and so can quickly become

excessive. The effort taken and the number of possible label positions can be controlled using the [labelEffort](#) keyword (see below).

With lines-only contour plots, the labelling is only done via the legend which takes the attributes of the contour lines.

### 7.10.1 Predominance plots

Labels are automatically placed approximately at the centre of each field. There is some effort to try and resolve overlapping labels should any be identified and to ensure that labels are placed within their respective polygons (not necessarily the case with concave polygons). The present approach cannot deal with polygons with holes or islands in them. [calculationMethod](#) 2 uses the label coordinates from the labels file if present whereas [calculationMethod](#) 3 re-calculates the label coordinates. The latter is necessary to re-centre labels if the plotting domain has been changed. [labelEffort](#) = 2 or greater may help with concave polygons when the label is on or near a polygon boundary.

Normally with [calculationMethod](#) 1 and 3, the label positions are automatically recalculated but it is possible to force **PhreePlot** to take the properties from the labels file (if present) by setting [useLabelsFile](#) TRUE. This enables the position or angle of a label to be preset although using [nudge](#) is probably an easier way of doing this.

### 7.10.2 Contour plots

Labels are automatically placed at the centre of the 'longest, straightest' part of a contour segment. If this is not satisfactory, the alternative option is to place all the labels at the centre of their contour – this is done by setting the [contourOptions](#) `labelPosition=centre`.

It is also possible to shift contour labels individually by 'nudging'. Also see the [contourShift-Label](#) setting for an alternative approach.

### 7.10.3 Custom plots

Simulated annealing is used to determine the position of label placement in custom plots. This is why 'temperature' appears in the output as the notional 'temperature' is gradually reduced allowing less freedom to roam randomly in search of a better set of label positions. This approach is experimental and can be very slow. The [labelEffort](#) keyword controls the amount of effort put into searching for good label placement. It only applies with [calculationMethod](#) 1 or 3.

The main objectives are to make the labels legible and their attribution unambiguous. The size of the labels is an important parameter ([labelSize](#)) since small labels obviously tend to overlap less than large labels. Set against this is the overall readability of the labels.

The [labelEffort](#) parameter is used as follows:

<a href="#">labelEffort</a> = 0	Labels are plotted roughly half-way along x axis; avoids the issue of label overlap etc altogether but rarely satisfactory
<a href="#">labelEffort</a> = 1	Minimal effort; this should take no more than a few seconds
<a href="#">labelEffort</a> = 2	Medium effort; slower
<a href="#">labelEffort</a> = 3	Much effort; much slower, can take many minutes – designed for batch processing where time is not such an important factor.

The following objectives are sought when deciding where to place labels:

- avoid labels overlapping with other labels
- avoid labels overlapping lines

- avoid labels being placed outside the plotting area
- place labels as close to the centre of the plot as possible

For custom plots, a second parameter, if present, provides an upper limit to the time taken (in sec) for optimizing label placement.

These objectives will conflict to some extent and **PhreePlot** tries to find a reasonable compromise. This is computationally demanding and the optimum solution may not be found in the time available.

Interrupting this process using the `ESC` key will exit gracefully while retaining the best label positions found up to that point.

In custom plots, each label is anchored to one of the calculated points. This anchor is shown by a small filled circle (by default red) which is controlled by the track symbol ([trackSymbol-Color](#) and [trackSymbolSize](#)). This symbol is not drawn if the label has been ‘nudged’.

## 7.11 REPLOTTING WITHOUT RECALCULATING

### 7.11.1 The ‘replot’ option

It is often necessary to ‘fine tune’ the appearance of existing plots. The [calculationMethod](#) parameter controls the extent of recalculating: 1 = calculate from scratch and plot; 2 = just replot; 3 = reprocess data, relabel and replot but do not re-speciate. This enables the appearance of a plot to be changed without repeating the underlying calculations.

1 does speciation calculations; 2 and 3 do not. The replot options make use of the output files produced during an earlier calculation. These files must be present.

It is possible to make the following changes during a replot:

- change the base font
- change the size and [colour](#) of all text, symbols and lines
- add, remove or change any extra text, symbols and lines that are specified by a [text](#) line or the ‘[extraText](#)’ and ‘[extraSymbolsLines](#)’ files
- implement any changes made to the label file or colour dictionaries including deletion or repositioning of labels
- change from a native y-axis scale to some other scale in predominance plots
- change the sign on the x- or y axis
- change which graphic output files are produced (`pdf`, `png` etc).
- change from a series of single page graphic files to a multipage file and vice versa.

Unpredictable results will occur if you:

- change anything to do with the scope of the calculations involved, e.g. `xmin`, `xmax`, `ymin`, `ymax`, looping, number and type of main species, fitting parameters, extent of simplification
- change the resolution
- change the thermodynamic database used.

All the required files must be present and in the correct format for replotting to work. If they are not, regenerate them from scratch ([calculationMethod](#) = 1). The following output files are required for replotting:

- |                  |   |
|------------------|---|
| <code>ht1</code> | <code>vec, pol, lab</code> ( <a href="#">calculationMethod</a> = 2) |
|                  | <code>pts, vec, lab</code> ( <a href="#">calculationMethod</a> = 3) |

grid	pol, lab ( <a href="#">calculationMethod</a> = 2) trk ( <a href="#">calculationMethod</a> = 3)
contour	vec, pol ( <a href="#">calculationMethod</a> = 2) out, vec, pol ( <a href="#">calculationMethod</a> = 3)
fit or simulate	out
custom	out
species	out

Adobe Acrobat Reader locks open files so a new pdf file cannot be recreated while a file with the same name is already open. Close it first. This limitation does not apply to files opened by **GSview**.

It is possible to use the `replot` option to enable **PhreePlot** to make a plot of any data in a user-derived text file providing the file format and name are correct, i.e. data in regular columns with the first line containing the labels. The filename should be the base filename with the extension 'out'. The [calculationType](#) should be 'custom' and [mainSpecies=](#)', say. Alternatively it can be imported with the [extradat](#) option. This approach can be used for adding data to both custom and predominance plots.

### 7.11.2 The 'reprocess and replot' option for predominance plots

The `reprocess` and `replot` option ([calculationMethod](#) = 3) goes back one stage further than simple replotting and starts with the stored output from the speciation calculations. For the `ht1` calculation type this is the `pts` file rather than the `vec` file. With 'grid' plots, this is the 'trk' file and with 'grids' plot this is the 'out' file. In all cases, the polygons are re-assembled and the label positions recalculated before replotting. In the case of the `ht1` calculation type, this enables the degree of simplification to be changed without recalculating the chemistry.

In the case of the 'grid' and 'grids' plots, if the speciation calculations have been terminated early for some reason, the track and out files, respectively, will not be fully populated and it may not be possible to complete the plot. This can happen when `ESC` has been used to terminate calculations early or if **PhreePlot** has crashed part way through the speciation calculations, for example if the operating system has run out of virtual memory.

Restarting 'grids' plots with [calculationMethod](#) = 3 will attempt to fill incomplete 'out' files thus preserving the effort of earlier calculations.

## 7.12 ADDING EXTRA LINES, SYMBOLS AND TEXT

Lines and symbols can be added to predominance plots using the 'lines' and 'points' method used by 'custom' plots (these read the data from data files) but if this is not appropriate, or if individual extra text, symbols or lines need to be added to any plot, these can be specified in using [text](#) and [symbolsLines](#) keywords or their file equivalents, [extraSymbolsLines](#) or [extraText](#). Tags can also be used in these text strings.

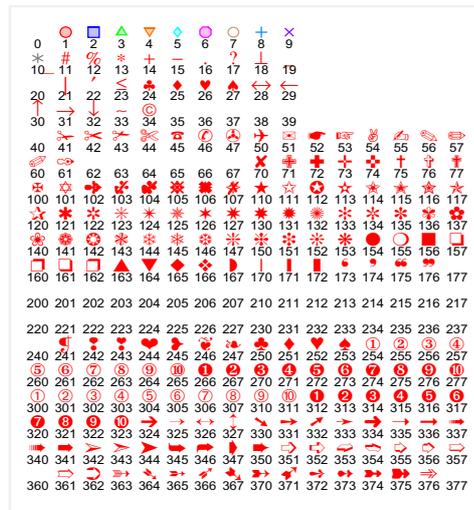
### 7.12.1 Lines and symbols

Points on plots are plotted with symbols. Extra symbols can be added to a custom plot or predominance plot with [symbolsLines](#) or an [extraSymbolsLines](#) file. Each entry has the format:

```
plotnumber,x,y[,lw,[linecol,[isymb,[sizesymb,[symbcol,[rimcol,[rimfactor,[line-
type,[dashesperinch]]]]]]]]].
```

See [symbolsLines](#) for more details. A full list of the symbol numbers and their names is given in [Appendix A3](#) and [Figure 7.5](#). The default is to draw a black line but most combinations of line and symbol size, colour and type are possible by explicitly specifying them. Once set,

### Symbols, dingbats and lines



All symbols have a nominal height of 2 mm (without rims).

C:\PhreePlot\demo\symbols\symbols.ps

Figure 7.5. The symbols available in the native, Symbols and ZapfDingbats fonts and their corresponding `isymb` codes. This diagram can be generated from the `...demo\symbols\symbols.ppi` file.

these properties stay in force until changed.

The first ten symbols are centered symbols:

- 1 = filled circle
- 2 = filled square
- 3 = filled triangle
- 4 = filled upside down triangle
- 5 = filled diamond
- 6 = filled octagon
- 7 = open circle
- 8 = plus
- 9 = multiply
- 10 = star

The six ‘filled’ symbols above can each have a separate rim colour and associated rim thickness. It is therefore possible to plot an open circle using the filled circle code but specifying that the point or symbol colour is ‘nd’. Specifying the symbol colour as ‘white’ will have a similar effect on white ‘paper’ except that it will remove any underlying features.

#### 7.12.2 Text

Additional text can be placed inside or outside the plot area (as defined by the axes) using a text line or a file containing one or more text lines. The format for these is defined in detail under the `text` and `extraText` keywords. Each entry has the format:

```
plotnumber,x,y,text[,height,[colour,[angle,[justify,[digits,[font]]]]]]
```

`plotnumber` is the plot number (auto for ‘all’), `x` and `y` are the x- and y-coordinates of the anchor position, and `text` is the single text string (usually embedded in quotes). This text string can contain tags from the tag dictionary or special [plotting tags](#) such as subscript/superscript. There are also other [special tags](#) which can be used.

The remaining parameters are optional. Although these are optional it is necessary to keep the parameters in order, i.e. you can omit `font` and include the rest but cannot omit `colour` and keep `angle`, `justify`, `digits` and `font`. If necessary specify all the parameters explicitly.

Defaults for the optional parameters if left blank are:

```

height      = legendTextSize
colour      = 'black'
angle       = 0 (degrees)
justify     = 0
digits      = -3 (if numbers are being printed, this provides some control over the
              format: default is three figures/decimal places depending on the type of
              number involved; the negative sign indicates that trailing zeros will be
              removed)
font        = the font (name or number, 1-44), or the current font if undefined.

```

`plotnumber` is the plot number (starts at 1) for which the text applies. 'auto' means all plots. The plot number is the sequential number of the plot and is always printed on the first line of the [info](#) block if that whole block is printed. For more detail on the numbering see the [text](#) summary. Text is truncated to 400 characters. This includes any text used to specify tags (see below). Enclose the text within paired single or double quotes if the text contains a delimiter (space, comma or tab). This will keep the text as a single string entity.

`x` and `y` can be made dynamic by making use of the `<pxmin>` etc tags which are set after the plotting limits have been determined., e.g. first set

```
numericTags      <px> = "<pxmin>+0.3*(<pxmax>-<pxmin>)"
```

then use `<px>` in place of say `x` in the text line.

The `y`-position always refers to the main `y` axis. If a point needs to refer to the 2`y` axis, then the corresponding `y` value must be calculated separately. This can be done using a numeric tag expression like:

```
<p2y> = "(<2y>-<p2ymin>)/(<p2ymax>-<p2ymin>)*(<pymax>-<pymin>) + <pymin>"
```

where `<2y>` is the wanted position on the 2`y` axis and should be defined using [numericTags](#). The `<p2y>` tag can then be used in an [text/extraText](#) or [symbolsLines/extraSymbolsLines](#) entry.

When printing, leading tabs are replaced with three spaces and subsequent tags replaced by single spaces. Multiple spaces are also reduced to a single space. Spaces might appear with variable length with proportional fonts.

`justify`: refers to the justification of the string (0= left, 1= centre, 2= right) irrespective of the angle, i.e. as if rotated about the appropriate character, so `justify=2` with `angle=180` will rotate around the last character whereas `justify=0` will rotate about the first character. The `x` and `y` coordinates therefore by default specify the left-hand baseline (bottom left-hand corner) of the text. `x` defines the left-hand edge; `y` defines the baseline of the text string ('g' extends below the baseline). Where there is more than one line because of the use of embedded line breaks, `<br>`, `y` refers to the first line. If the text goes off the bottom of the screen, increase [yoffset](#) to reposition the plot higher, or increase the page size. Remember the page size of the printing or viewing device controls what part of the plot will actually be seen.

`digits`: specifies the number of digits to print when a numeric tag is substituted by a value. It is specified by an integer, `n`. `n` gives the number of digits printed after the decimal point (valid range  $0 > n >= 16$ ). 0 prints the nearest integer. If a negative integer is given, trailing zeros are removed. If the absolute value of the number is less than  $1e-3$ , it is printed in scientific (`x.xEee`) format. This format applies to all numeric tags in the text string (default `n = -3`).

font: The font is either specified by a defined font name (see `fonts.dat`, if present) or by a font number, numbered consecutively across and down the `fonts.dat` table, if present, e.g. `Times-Roman` or `17`. If the font or font number is unrecognised, the current font is used if defined else it reverts to the number 1 (Helvetica) font.

Any tags can be included as appropriate in extra text. Some special and some commonly-used tags are discussed in detail below.

### *<input>*

A special piece of text for copying all or part of the text from the input file(s) next to a plot is:

<code>&lt;input&gt;</code>	prints all lines from the input file(s).
<code>"&lt;input:str1&gt;"</code>	prints all lines from the input file(s) starting at the first line containing <code>str1</code> to the last line of the <code>CHEMISTRY</code> section.
<code>"&lt;input:str1,str2&gt;"</code>	prints all lines from the input file(s) starting at the first line containing <code>str1</code> to the first line containing <code>str2</code> inclusive.

`str1` and `str2` are ASCII character strings. Case is significant for both `str1` and `str2`. Use the quotes for the second form otherwise the comma will be parsed and `str2` will be set to `col` and then the text ignored completely. Justification, if present, is ignored. The input searched is the final concatenated input from all input files with comments and blank lines removed, include files expanded but tags not substituted.

The printed text will be left justified, vertically aligned with the top of the text at `ypos` and starting at `x`. `x`, `y` may be outside the plot axes. `mjust` is ignored – the text is always left justified. Multiple spaces and tabs are replaced by single spaces except any leading spaces (indentation) are preserved. A leading tab is replaced by three spaces. Blank lines are omitted.

The first example will print the entire input file. This is based on the input file as `input` - not the expanded input file that is created after expanding any [include files](#).

The second example will print the input file starting from the first line containing `str1` and finishing at the first line containing `str2`. If `str1=""`, then printing starts at the first line; if `str1` is non-blank and `str2=""`, printing continues to the last line. If `str1` is found but not `str2`, then the text is printed from `str1` to the end of file but if `str2` is found and `str1` is not, then nothing will be printed.

`<br>` is not recognised within this tag. If `str1=str2`, only that line is printed.

Angle is the angle in degrees from the horizontal, rotating clockwise.

The size and [colour](#) of the text is either given on the `<input>` line or by default takes on the values of [legendTextSize](#) and `'black'`, respectively. The legend can be turned off by setting [labelColor](#) to `'nd'`.

If [info\(1\)](#) is set to `'nd'` then this input text will not be printed. This allows clean plots to be produced without editing the individual `extraText` files, possibly by using the `override.set` file.

### *<loop> or <loop...>*

Substitutes the current numeric value of the appropriate `loop` variable. The primary loop variable is `<loop>` which if a regular sequence, can either be defined in an input file using the [loopMin](#), [loopMax](#), [loopInt](#) and [loopLogVar](#) settings.

If the sequence of loop values is irregular or if more than one variable value needs to be set on each iteration, use the loop file approach instead ([Section 4.6.2](#)). `<loop>` is equivalent to `<loop1>`, the first column of numbers in the loop file. Successive numeric columns are set to the `<loop2>`, `<loop3>` etc tags if there is no header with column names present. If a header row is present, this is used to generate the tag names.

The loop variable is printed as an integer if it is an integer otherwise it is printed in floating point format. No extra spaces are added to the number. The value of the loop variable used is the value at the time of plotting.

### *<legend>*

Inserts the legend for custom plots at  $x, y$  rather than in its normal position to the right of the plot. If found, all other text in the string is ignored. Height and [colour](#) can be included but if absent, the defaults are:

text height = the [legendTextSize](#) setting  
colour = black.

e.g.

```
auto 4 -12 "<b>Key</b><legend>" 2 blue
```

will insert the top left-hand corner of the surrounding legend box (if drawn) at  $x, y$  (here 4, -12) based on the plot scale. If explicitly set, the text height, takes precedence over the [legend-TextSize](#) keyword setting. If no legend box is drawn, legend lines/symbols will be left-justified at approximately  $x$  and the top line/symbol placed at  $y$ . The contents of the legend are always left justified; if entered, the justification setting for this entry will be ignored.

Any text before `<legend>` is treated as the legend title and will override the [legendTitle](#) setting. The legend title will therefore be 'Key' in the above example. If no title is defined in the `<legend-end>` line, [legendTitle](#) will be used.

Text after `<legend>` is ignored. Text tags such as `<b>` will be ignored if split by a `<br>`.

This option allows the legend to be moved inside the plot area, or by using out-of-range  $x$  and/or  $y$  coordinates, removed completely from the plot. An alternative approach with a little more flexibility is to use the [legendBox](#) keyword.

### *<mainspecies>*

Inserts the name of the current main species into the text string, e.g. "`<mainspecies>`" would substitute "Fe" if that was the main species.

## 7.12.3 Formatting numbers in plots – varying the number of significant figures displayed

Numbers in text strings can be formatted using an underscore or dollar suffix to indicate the number of significant figures required and whether to use an exponential (E) format or not. This is useful when numeric tags are placed within a text string that is to be plotted. This also applies to tags in the upper (**PhreePlot**) section of an input file.

The default representation for floating point numbers in plotted output is to round them to 3 significant figures and to remove trailing zeros. A floating point format (e.g. 7.98) is used when 3 significant can be maintained but the exponent (E) format is used for larger and smaller numbers.

It can be useful to be able to control the number of significant figures displayed explicitly, e.g. 6.58928137 could be displayed as 6.59 (3 significant figures) or 6.589281 (7 significant figures). This can be controlled by appending an underscore to the number or tag followed by the number of significant figures required, e.g. 6.58928137\_3. The number of significant figures (`sigfigs`) can vary from 1 to 16 (although normally only 14 are significant). A negative value for the number of significant figures will format to `ABS(sigfigs)` and then remove trailing zeros. If the underscore or dollar sign is actually wanted, precede with a backslash.

Very large (`ABS(x) > 1e15`) numbers will always default to the exponent format. Very small numbers, numbers less than an absolute value of `1e-15`, are plotted as 0.

If an exponent format is wanted, use \$ instead of \_, e.g. 1.3463\$3 will plot as 1.35E+00 and

Table 7.1. Use of the appended underscore/dollar sign to specify the number of significant digits used in plotting numeric strings

Text string	Appearance in plot
"6.58928137"	6.59
"6.58928137_4"	6.589
"6.58928137\$6"	6.58928E+00
"125734.123_4"	125700
"125734.123_0"	
"617.000_2"	620
"617.000_-4"	617
"617_-2"	620
"612_-2"	610
"6.1_3"	6.10
"6.1_-3"	6.1
a6.1\$3	a6.10E+00
"a6.1\_3"	a6.1_3
1.23456789e-20	1.23456789e-20
"<a>" where <a>=1.23456789e-20	0
"<a>_5"	1.2346E-20
"<bb>" where <bb>=-1.23456789e20	-1.23E+20
<bb>_6	-1.23457E+20
<bb>\$6	-1.23457E+20

1.34600\$-5 as 1.346E+00.

This approach is especially useful for formatting numeric strings derived from a tag in a text line or extraText file, or in a plot or axis title. Some examples are shown in Table 7.1 It is used to format fit output in the extraText file of the `demo\kineticsSi\kineticsSifit1.ppi` demo file.

#### 7.12.4 Making fancy plots

There is a limited capability in **PhreePlot** to add additional features to a plot (see [Section 8.9](#)).

Firstly it is possible to add text, lines or symbols using the [text](#), [extraText](#) and [extraSymbolLines](#) keywords.

Secondly it is possible to add lines or points to a predominance or contour plot by including the [lines](#) or [points](#) keywords (but not the 2y equivalents) and making sure that the data are read in correctly. This could include the following additions to your input file:

```
extradat filename.dat # load this file with a header line giving column names
customxcolumn xcol # make this column the x-variable
lines ycol # make this column a y-variable (there can be several)
points col # ibid
linecolor red
pointcolor blue
```

The file containing the additional data could have been generated during the main plotting stage or read in from an external file. Several ppi files can be run and then the combined data plotted in some way. Batch files can orchestrate this.

Thirdly, it is possible to overlay one or more plots on top of each other using the [overlay](#) keyword.

Finally it is possible to change the plot in ways that **PhreePlot** cannot do by editing one of the plot files using an interactive image editor such as **Inkscape**. It is also possible to run **PhreePlot** from within another program such as **Python** or **R** and manipulate the output with these programs.



## 8 Predominance plots

---

### 8.1 SETTING UP A FILE TO CALCULATE A PREDOMINANCE DIAGRAM

**PhreePlot** offers a flexible approach to drawing predominance plot. The criteria for selection as a predominant species are user-defined in `USER_PUNCH` blocks (often in `inc` files) that are easily edited. These must simply return a series of name-value pairs and its the pair with the greatest value that is considered predominant. The values returned could be simply species concentrations whether dissolved, solid, surface or gas. They could be based just on aqueous species, they could sum all adsorbed species and treat the total as a ‘super’ species, or they might take some other factor, such as redox state, into account.

In order to draw a predominance diagram, **PhreePlot** expects that the last simulation executed will return the predominant species in the format expected. There can be other pre-loop and main loop simulations but these must precede this final simulation.

From that point onwards, **PhreePlot** treats all data in the same way and attempts to draw a 2D diagram showing the predominance fields. In fact, **PhreePlot** contains two distinct methods for drawing predominance plots – the ‘grid’ and ‘hunt and track’ approaches – and these differ in the way that they sample the 2D data space to identify the field boundaries.

Another approach is to contour some variable such as the total dissolved concentration of an element or species - also possible in **PhreePlot** - but the predominance diagram remains a beguilingly simple way of describing the chemical behaviour of complex systems.

The results should be quite close to those obtained using traditional analytical approaches such as used by the classical equation-based Geochemist’s Workbench (GWB) approach ([p. 605](#)). However, they will not be exactly the same since the simplifying conditions required in the analytical approach are often unrealistic and can be difficult to achieve in practice. The full speciation approach requires that all parts of the domain under study be accessible via a plausible and specifiable reaction path. Activities should reflect all the interactions in the system rather than simply being imposed on the system. Achieving constant activities along a boundary usually requires variable quantities of an element to be present whereas more realistic systems have constant total concentrations of elements and variable activities.

The results from **PhreePlot** should be similar to other programs that produce predominance diagrams using a rigorous approach to speciation. This includes **GWB**’s recently updated approach with their Phase2/P2plot programs which follows **PhreePlot**’s ‘grid’ approach. [Spana \(formerly HYDRA/Medusa\)](#) also adopts this approach and is free to use. It produces a number of different types of geochemical diagrams including predominance plots using the **HALTAFALL** speciation program and has a simple but effective user interface. The domain of interest is also sampled on a regular grid.

#### 8.1.1 The ‘water limits’

The ‘water limits’ in an Eh-pH diagram are often indicated to show the area where water is unstable. Under strongly reducing conditions water decomposes to hydrogen gas and under strongly oxidizing conditions it decomposes to oxygen gas. When the total pressure exceeds that of the surroundings, these gases will ‘bubble out’. This is normally at 1 atm.

These limits are applied as user-supplied constraints (type 3), normally hidden in the `.inc` file used to output the predominant species. Note that the limits specified in `ht1.inc` are for a pressure of >1 atm H<sub>2</sub>(g) on the reducing side and >1 atm O<sub>2</sub>(g) on the oxidising side. These

limits can be easily changed by editing `ht1.inc` or the equivalent file. An upper limit of 0.21 atm for  $O_2(\text{gas})$  is also useful since this indicates the region where atmospheric oxygen would react with the system with maximum effect. In practice, there is only a small difference in the Eh-pH diagrams between these two options.

A check is also made on the methane partial pressure since this can be high in strongly reducing, carbon-containing systems.

If some or all of these constraints are not wanted, remove them completely from the appropriate inc file.

### 8.1.2 The 'grid' and 'ht1' approaches

#### *Grid approach*

**PhreePlot** is able to calculate predominance diagrams based on a full speciation of the system using the grid and ht1 algorithms. The grid approach is a direct search approach that calculates speciation on a grid while the ht1 approach finds and tracks the field boundaries. If the total quantity is kept constant, then the concentrations of dominant species at boundaries will be close to half the total concentration while at triple points will be close to one third of the total concentration.

The grid method is a 'brute force' method in that **PhreePlot** simply calculates the speciation at each point on a rectangular grid and reports the dominant species. The range and spacing of the grid points is determined by the [xmin](#), [xmax](#), [ymin](#), [ymax](#) and [resolution](#) parameters. This method requires `nres2` speciation calculations plus any pre-loop calculations, e.g. initial solution calculations.

The matrix of predominant species can be rendered directly by colouring each species differently but this does not identify field boundaries and results in rather large image files. **PhreePlot** uses a 'pixel aggregation' technique to identify the boundaries. This enables the fields to be polygon-filled with colour and so avoids pixelation of the generated image. This results in better rendering of the plots and much smaller file sizes.

One or more main species can be specified. With the 'grid' approach, a new set of speciation calculations is repeated for each main species even though the grid is the same. With the 'grids' approach, the speciation calculations are made for all main species in one pass and the results written to individual 'out' files in the normal way. Progress during the speciation calculations is shown by a series of dots on the screen. Each dot represents 10 speciation calculations and a full line of dots 500 calculations. The individual 'out' files are then processed in a second pass to give the plots.

This approach needs different `USER_PUNCH` statements to export the data since the 'grids' option requires that the full speciation for *all* elements be returned and written to the appropriate 'out' files in one call to `USER_PUNCH`. 'grid' uses the 'ht1.inc' file or similar, while 'grids' uses the 'grids.inc' file or similar.

It is possible to add a z-loop to 'grid' and 'grids' plots. Normally the z-loop is inside the main species loop but in 'grids' plots, the results of all main species calculations are returned in one speciation calculation and so in this case the z-loop must be outside the main species loop. This special case is intercepted when the first z-loop is executed. This is reflected in the output in the log file, and affects the calculation of the printed timings of individual plots. These timings are estimated by dividing the total speciation time by the number of main species to give an approximate time taken per main species.

This construct also means that it is not possible to change the resolution of 'grids' plots with the z-loop iterator.

The 'grids' approach carries considerably more overheads but can be faster for two or more main species especially when the speciation calculations are themselves relatively slow. See the `demo\grids` directory for an example.

*'Hunt and track' approach*

The ht1 method uses a 'hunt and track' approach to find and track the field boundaries. It is based on the assumption that all such boundaries can be reached from the domain ('axis') boundaries, i.e. that there are no 'islands'. In fact, islands can occur (see [Example 43](#)) and so while this method is usually quicker than the grid approach, it is not so reliable and so the results of the ht1 approach should always be compared against the grid approach.

The ht1 approach first works along the domain boundaries looking for a change in the dominant species. This is the 'hunting' mode. Once it has found a change-over on the boundary, it tracks internally along it. During this tracking, it only makes evaluations (speciation calculations) on a fixed grid defined by the same parameters that the grid method uses. It bounces along the boundary keeping track of where changes in the dominant species occur and noting where triple points - the intersection of three equally dominant species - occur. Where possible, more precise boundary positions are estimated by interpolation along a cell edge using the logarithm of the dominant and subdominant concentrations.

It is possible to define constraints that override the normal predominance criteria. The traditional 'water limits' are commonly applied in presenting predominance diagrams. The ht1.inc code provides a check to see if these have been exceeded and **PhreePlot** elevates them to the top of the list if they have.

The overall strategy is best appreciated by examining the ht1.inc and ht1c.inc files which provide generic pieces of **PHREEQC** code for returning the predominant species. These are used by both the hunt and track and grid methods. ht1.inc is the simpler of the two scripts in that it treats all adsorbed species as distinct species whereas ht1c.inc combines all adsorbed species into a single 'super' species for the purposes of counting and display.

**PhreePlot** expects the SELECTED\_OUTPUT to have a specific format in order to be able to draw a predominance diagram. The list of data required consists of five different blocks of data, each of which can contain a variable number of species name-number (often a concentration) pairs. The counts for each of these blocks is given by five numbers at the end of the list. These can be zero if no pairs are returned. This ensures that **PhreePlot** knows how to read the data list returned. All the data are written by USER\_PUNCH statements in ht1.inc. Do not write any output using the SELECTED\_OUTPUT keyword data block as this will contravene the expected structure and will lead to a mismatch in the expected and found number of columns received.

The structure of the ht1.inc file is summarised in Figure 8.1.

nout1	nout2	nout3	nout4	nout5	
Dominant species	Dominant minerals	Constraints	Carry variables	5 system variables	5 counts

Figure 8.1. Data structure expected to be returned to **PhreePlot** in the selected output in order to calculate a predominance diagram using the ht1 and grid plot types.

ht1c.inc also gives the option of calculating either a predominance or stability diagram ([Section 8.1.7](#)). In a stability diagram, mineral species assume predominance over solution species no matter what their relative concentrations. This is done by commenting out either line 20 or 30 (using a # or REM statement).

The script defines the five blocks of species which must be returned by PUNCHING them. These blocks are:

1. the three dominant species (solution, mineral, gas or adsorbed), (normally nout1<=3 although any number can be returned and **PhreePlot** will sort them to find the largest)
2. the three dominant mineral species, i.e. those which account for the largest concentrations of the main species (nout2<=3)

3. any constraints: these will override all other considerations and if the constraint is true will force the species to be treated as the dominant one. Limits on the partial pressures of  $\text{H}_2(\text{g})$ ,  $\text{O}_2(\text{g})$  and  $\text{CH}_4(\text{g})$  are usually included ( $n_{\text{out}3}=3$  usually) and can be used to plot the usual ‘[water limits](#)’. Other constraints are possible. See the carbonate example with constraints on the total carbonate in the system ([Example 25](#))

4. any ‘carry’ variables ( $n_{\text{out}4}$ )

5. the ‘system’ variables - pH, pe, the log partial pressures of  $\text{O}_2(\text{g})$  and  $\text{H}_2(\text{g})$  and temperature ( $^{\circ}\text{C}$ ) (always these five pairs of values in that order).

The final items PUNCHED are the five counts,  $n_{\text{out}1}$ - $n_{\text{out}5}$ . **PhreePlot** receives the five groups of species, their values and their counts as one long list. The counts tell **PhreePlot** how to read the list.

The minimum output required to prepare a predominance diagram is one dominant species ( $n_{\text{out}1} = 1$ ) and five system variables ( $n_{\text{out}5} = 5$ ).

‘Carry’ variables are user-defined numeric variables that are wanted to be output but which play no part in the calculation of the predominance diagram. They are sent as name-value pairs. For example, the script `ht1minerals.inc` script can be used to list all the minerals that precipitate somewhere in a predominance diagram. This can be used to reduce the mineral phases considered during the speciation calculations. In this example, a list of the summary statistics (count, minimum, mean and maximum value) for each species output as a variable is listed in the log file provided the out file has been turned on (`OUT T`). The ‘carry’ variables are written to the out and track files and automatically added to the tag dictionary. The track file uses the species names found on the first iteration as the column heading and so you must ensure that the same ordered list is produced on all subsequent iterations.

The `ht1.inc` and `ht1c.inc` scripts use the `SYS()` function to return a list of the concentration of all the species of the element of interest, the so-called ‘main species’. This list is returned from **PHREEQC** pre-sorted in decreasing amount of the main species element. This is not necessarily in terms of decreasing species concentrations where polynuclear species are involved.

The top three of these are sent back to **PhreePlot** as block 1 via the `SELECTED_OUTPUT` ‘file’ by PUNCHing them in the sequence:

```
name1 concn1 name2 concn2 name3 concn3
```

where `name1` has the highest concentration and `name3` the lowest. If less than three species exist, then either one or two is returned depending on the number available (the predominance diagram is trivial if there is only one species).

The remaining output is written to the selected output ‘file’ in a similar manner, i.e. always as a species name followed by a numeric value, usually a concentration.

An example where a large number of carry variables are written at each calculated point of a predominance plot is given in `demo\grid\gridhfo_with_carry.ppi`. Here the carry variables are contained within a separate file, `carry.inc`, and give a detailed breakdown of the system in terms of species concentrations for the ‘main species’ and the minerals and gases present at each point. It is fairly straightforward to tailor this file to your particular needs.

### 8.1.3 Using the `ht1.inc` code to return the dominant species

A predominance diagram is most easily calculated using the `ht1.inc` code described above. A simple example is given below for preparing a pe-pH diagram for Fe (see [Example 3](#)).

The `CHEMISTRY` section starts with the include file (its position within a given simulation is unimportant) and then has a `SOLUTION` keyword block to define the initial conditions - the total amount of each element present in the system. This is constant and so can be setup in a separate simulation.

This is followed by a second simulation which includes an `EQUILIBRIUM_PHASES` keyword block. This provides the mechanism for traversing the x- and y-axes, and for defining mineral phases that may precipitate (or dissolve). This means that the two tags, `<x_axis>` and `<y_axis>` have to be present, either explicitly or implicitly. Note that the x axis is controlled by `Fix_H+` (defined in `ht1.inc`) and is therefore the pH. The initial conditions include the total concentration of  $\text{Fe}^{3+}$ .

The pH is adjusted by adding (or subtracting) NaOH. Note that the initial pH is low (and is preferably set to less than the minimum pH required on the x axis) The y axis is linked to a fixed partial pressure of  $\text{O}_2(\text{g})$  supplied by an external reservoir of  $\text{O}_2$  (10 mol). The plot created is therefore one of  $\log f\text{O}_2(\text{g})$  vs pH. This runs faster than using a 'Fix\_pe' approach. Since the pe is always carried in the calculations and in the output files, a switch of y scales can be done either when the plot is being generated or afterwards by replotting using the [yscale](#) setting (pe, Eh or mV).

```
CHEMISTRY
include 'ht1.inc'
SOLUTION 1
  pH      1.8
  units   mol/kgw
  Fe(3)   1e-2
  Na      1e-1
  Cl      1e-1
END

USE SOLUTION 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 1
  Fe(OH)3(a) 0 0
END
```

Note the negative sign directly in front of the `<x_axis>` tag. This enables the x axis to be specified in directly terms of pH. This works because the substitution of the tag is done without introducing extra spaces around the tag. This approach works providing the value of `<x_axis>` does not become negative. The alternative is to use a [numericTags](#) relation to define a new tag as `-<x_axis>`.

In summary, you have to supply the initial solution conditions (total concentrations), the means of traversing the x- and y-axes by including the `<x_axis>` and `<y_axis>` tags, and you must include any phases that might precipitate in an `EQUILIBRIUM_PHASES` keyword block.

It is possible to modify the `ht1.inc` file to alter the logic by which a species is promoted to the top. For example, the `minstab1.inc` and `minstab2.inc` files are designed to highlight the most abundant or most likely minerals present. It is also possible to alter the way that species names are presented, for example, for minerals, by adding the mineral formula underneath the mineral name (e.g. see for an example of this) or instead of the mineral name.

#### 8.1.4 Problems with the 'hunt and track' approach – failure and 'unclosed polygons'

Although numerical problems in speciation were initially thought to be the largest likely problem with the 'hunt and track' approach, the greatest difficulty in practice has been marrying up the 'hunt' and 'track' parts of the procedure at the boundaries of the plot, or having two or more internal 'triple junctions' too close to each other. In this case, **PhreePlot** may abort the calculations.

If a field boundary coincides with, or is very close to, a boundary of the calculation domain then this can result in lots of 'bubbles' and ultimately will fail because of 'unclosed polygons'. All polygons must be perfectly closed to enable the colouring and labelling. If any of the speciation calculations have failed, then this adds to the probability of unclosed polygons.

If you are using the 'ht1' calculation type and there is a failure, the first thing to do is to try the 'ht2' type which uses a slightly different algorithm. Using the 'grid' calculation type

should always produce a diagram and will make it easier to see where there are problems.

Although **PhreePlot** may restart automatically with a different resolution, thereby potentially shifting the field boundary away from the domain boundary, this is no guarantee of success. Increasing the size of the calculation domain (`xmin`, `ymin`, ...) is a better solution – the plotting domain (`pxmin`, `pymin`, ...) does not have to coincide with the calculation domain.

It is best to avoid field boundaries being very close to the domain boundaries where possible. A common problem is when the upper water limit set at exactly 1 atm O<sub>2</sub>(g) in `ht1.inc` and then `ymax` for (log O<sub>2</sub>(g)) is set to 0. This places the boundary for calculations exactly on a field boundary – in this case, the artificial boundary created by the upper water limit. If there are problems, it is better to either set the upper limit (`ymax`) of the calculation domain to be somewhat greater, say 1 or more, or to alter the water limit slightly. The alternative is to set the water limit at exactly 1 atm but to set `ymax` somewhat higher.

### 8.1.5 Polygon label is outside of the polygon

This can happen with concave or very narrow polygons. With concave polygons, `labelEffort = 2` or greater may help. With `nudge`, you can specify a shift in relative or absolute label position.

### 8.1.6 Optimising the calculation efficiency

Minimizing the size of the tag dictionary can significantly increase the speed of computations and therefore unused tags should be removed wherever possible. Minimizing the number of mineral phases considered will also improve the calculation speed.

### 8.1.7 Predominance vs mineral stability diagrams

A predominance diagram always shows the predominant species (unless overridden by a constraint). The predominant species is the species accounting for the largest number of moles of the main species. A stability diagram is similar except that if a mineral species is present, it overrides all solution species in precedence no matter what their concentration. The diagrams are not too different since minerals are often quite insoluble and often dominate the overall speciation not far from solution-mineral boundaries. If more than one mineral species is present, the most abundant mineral (in terms of moles of the main species) takes precedence.

The choice of calculating predominance and mineral stability diagrams can be readily implemented by including the `ht1c.inc` code in the **PHREEQC** code.

If a mineral stability diagram containing only mineral species is wanted then the main species should be set to the special value 'minerals' and most importantly, the `minstabl.inc` include file used instead of `ht1.inc` ([Example 54](#)). Precedence is then calculated in terms of the most abundant mineral species (in terms of moles of mineral), if present. Precedence in this case can therefore depend on the mineral formula used.

### 8.1.8 Using `ht1minerals.inc` to determine the minerals present

Many of the minerals in a database will never actually become stable anywhere in a predominance plot even where all the necessary components are present in the system. They may never be anywhere near saturation or may be protected from precipitating by a closely-related but more stable mineral.

These non-precipitating minerals can be excluded from the speciation calculations without any loss of accuracy. This is significant since excluding these unnecessary minerals from the `EQUILIBRIUM_PHASES` data block can speed up calculations considerably.

The include file, `ht1minerals.inc`, is similar to `ht1.inc` except that it also writes as 'carry' variables all minerals that have a saturation index of zero or above for each speciation calculation, i.e. these are the species that are either saturated or supersaturated.

**PhreePlot** automatically analyses all the ‘carry’ variables in the out file, if present, and sends summary statistics to the log file. In this case, there will be a table of all the minerals species for which  $S_{I>=0}$  at some point. Looking at the ‘max’ column in this table gives the required information. All species which have a max value of 0 (or very close to it) have precipitated and must have already been included in `EQUILIBRIUM_PHASES`. Those with a max value significantly greater than 0 might precipitate if included and are therefore potentially relevant.

The supersaturated minerals will be those that exist in the database and which might have precipitated but have not done so since they have not been included in the `EQUILIBRIUM_PHASES` data block. Re-running with all of these minerals included will enable a minimum set of minerals to be identified, i.e. those that then have a max value close to zero.

Using `ht1minerals.inc` therefore identifies all minerals in a database that may be relevant to the present system – as well as those that are definitely not. This includes all minerals, not just those containing the main species.

This option requires that the out file is actually produced – it is not by default. This is achieved by setting ‘out T’ in the input file. Other than that just replace ‘ht1.inc’ by ‘ht1minerals.inc’ in the input file.

Since this approach only analyses the speciation calculations actually carried out, it is necessary to cover the whole domain of interest fairly systematically. This is best done with the ‘grid’ method.

An alternative approach is to automatically include all possible minerals in the `EQUILIBRIUM_PHASES` data block. This is the approach taken by the `ht1allminerals.inc` include file and the `demo\minstab\allminerals.ppi` example.

## 8.2 THE ‘GRID’ APPROACH

The grid approach ([Example 1](#)) is simple and reliable but relatively slow especially at high resolutions. One advantage is that it does not rely on being able to access all internal boundaries from the domain boundaries nor does it require relatively noise-free boundaries. The ht1 approach requires both of these conditions. The disadvantage is that it can spend a lot of time analyzing parts of the domain where there is no change in dominant species.

The `resolution` specified for a grid plot divides the x- and y-axis ranges into a square grid with the specified number of nodes in each direction. There are therefore `resolution-1` grid cells in each direction, each with a node at its centre. Since the cells are centered on the nodes and the plot is clipped on the domain boundaries, the peripheral set of cells around the plot are actually plotted as half cells.

Speciation calculations are carried out at each node and the dominant species identified for each node-centered cell. The results of these calculations are stored in the track file. This is the file that is used for replotting.

Each cell or pixel is ‘coloured’ according to the dominant species and the boundaries between species located to give polygons. This approach does not go down to the vector (individual line segment) level which means that it is not possible to simplify the boundaries using the same algorithm as used in the ht1 approach. The characteristic steps in the original pixel boundaries are therefore retained.

By default all of the polygons are coloured and labelled. This includes polygons such as  $H_2(g)$  and the ‘not available’ or an `NA` field that is produced when the **PHREEQC** speciation fails. Any field can be omitted from a replot by setting the species (sp) number in the labels file (`*.lab`) to a negative value.

The polygons are rendered in order of decreasing size, largest first.

The results of the speciation are stored in the track (‘`trk`’) file. Since these are calculated in a well-defined manner, the calculations can be restarted from a partially complete set of calculations produced by a crash or by using an interrupt and stop. To do this, set [calculationMethod](#)

to 3 and restart. This should resume calculations from where they left off and applies to both the track file and the out file if selected. This works with both the 'grid' and 'grids' calculation methods.

### 8.3 THE 'HUNT AND TRACK' APPROACH

#### 8.3.1 Strategy

The 'hunt and track' approach finds and follows internal boundaries on predominance and mineral stability diagrams. It starts by hunting along the left-hand y axis until it finds a cross-over of predominant species then uses this to track internally. Once this has been exhausted, it hunts along the remaining axes. Critically, this approach relies on the assumption that all such boundaries can be reached from a domain (axis) boundary, i.e. that there are no 'islands'. This is often the case ([Example 1](#) and [Example 3](#)), but not always ([Example 2](#) and [Example 43](#)).

The 'ht1' algorithm tracks the internal boundaries using single steps of fixed length along an imaginary grid. At each point, the algorithm requests a speciation calculation to be made and expects the speciation program to return the concentration and name of the top three species, i.e. the three most abundant species. These are transmitted via the `SELECTED_OUTPUT` file. The precise way that these are calculated is controlled by the user using statements within the `USER_PUNCH` block of a **PHREEQC** input file. It is also possible to provide user-defined constraints that override the normal predominance sequence. This enables infeasible areas of the diagram to be clearly defined.

The input file also controls all other aspects of the chemistry including the initial chemical setup, e.g. total element concentrations and a list of all the gas, mineral and adsorbed phases potentially present, and the way in which the x- and y-axes of the diagram are to be traversed in response to requests from the ht1 algorithm.

The ht2 algorithm is similar to ht1 but can cope better with multiple junctions (including boundary junctions) within a given cell.

The step size and resolution of the grid is controlled by the [resolution](#) parameter. The step size is simply the span of each axis (maximum value – minimum value) divided by the resolution-1. The resolution is always the same for both x- and y-axes. Each cell is centered on a calculated grid point.

#### 8.3.2 Details of the 'hunt and track' algorithm

##### *Applying the concepts of hunting and tracking at the practical level*

We assume that presented with values for the two 'master' variables (representing the x and y axes on the predominance diagram), the speciation program can return either a complete speciation or at least, the predominant species. This is what the `ht1.inc` script does.

As mentioned above, the ht1 strategy for locating the field boundaries makes the assumption that all domain and axis boundaries are interconnected, i.e. there are no 'islands' (Kinniburgh and Cooper, 2004).

The grid approach on the other hand is rather inefficient since many of the points evaluated will be far from a boundary and will therefore contribute little useful information. It is also difficult to guarantee locating all of the fields without a fairly large computational effort. The ht1 approach concentrates on locating and tracking the various boundaries and puts no effort into computations far from the boundaries. It requires no initial grid of points. The algorithm is similar to that sometimes used to locate 'zero phase fraction lines' in phase diagrams and starts by systematically hunting along each axis boundary in turn until a change in predominance field is found. Once a change has been located, the algorithm tracks along the boundary until it reaches another axis, remembering any junctions with other predominant species as it goes. It then returns to these junctions to follow these paths until all of the internal boundaries have been followed. It then hunts along any remaining axes, again tracking internal bounda-

ries until all four axes have been searched.

Our hunt and track algorithm is based on a fixed regular grid over the domain of interest defined by the x and y axes. The domain is usually rectangular, with its boundaries (axes) also being on the grid. The algorithm assumes that at least one predominance boundary actually crosses an axis (if none does, there must be just a single predominant species).

The first task is to identify such a crossing point by searching along boundaries. Starting at a selected corner of the domain, the predominant species is identified. The next point for computation is the nearest grid point on the axis defining the domain boundary, moving in a selected direction. If this has the same predominant species, the algorithm moves on to successive grid points on the axis until a change is found. This is the 'hunting' part of the algorithm. Once a point of change has been identified, the algorithm moves into "tracking" mode, following the predominance boundary within the domain.

Figure 8.2 shows an example with a predominance boundary (shown as a dashed line), whose precise location is unknown, crossing the y axis of a rectangular domain. Grid points where speciation calculations are undertaken are identified in Figure 8.2 by numbered open and filled circles. The numbering indicates the order in which the grid points of interest are visited.

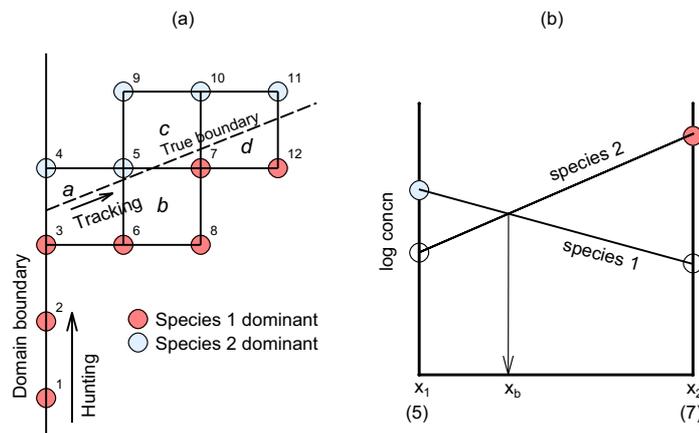


Figure 8.2. Strategy for tracking the boundary between two fields. (a) after locating a change in dominance on a domain boundary, cells are explored in the order a, b, c.... The numbers indicate the order and location where speciation calculations are undertaken and the filled and open symbols at the grid intersections indicate the dominant species returned by these calculations; (b) method of linear interpolation used to establish boundary location in cell d).

In this example, the first grid point in the sequence is on the y axis where the algorithm is in hunting mode. It continues through points 2 and 3, where there is no change in predominant species, reaching point 4 where a change is identified. There must therefore be an intersection of the y axis with the predominance boundary between points 3 and 4. The tracking mode now begins with predominance values calculated at points 5 and 6, which complete rectangle a on the grid. The predominance boundary must exit through one of the remaining three sides of this rectangle. This is immediately identified as the side linking points 5 and 6. This exit side for rectangle a becomes the entry side for rectangle b, the second to be constructed. Calculation of predominant species at points 7 and 8 shows that the exit side for rectangle b is the side linking points 5 and 7. Rectangle c is built on this side, with exit side linked by points 7 and 10, on which rectangle d is constructed.

This technique tracks a sequence of grid squares through which the predominance boundary runs. It does not provide coordinates through which the line passes. These can be approximated by linear interpolation along each exit or entry side. Four values are required to carry out this interpolation (Section 8.2). These are the concentrations of the dominant and subdominant species at the end points of the side. Denote the end points  $(x_1, y_1)$  and  $(x_2, y_2)$ , and the dominant and subdominant  $\log_{10}$  concentrations are  $d_1, s_1, d_2$  and  $s_2$ . Then the linearly

interpolated approximate location (xb,yb) of the predominance boundary as it crosses the line joining (x1,y1) and (x2,y2) is:

On a rectangular grid, either  $x1=x2$  or  $y1=y2$ , so one or other of the equations will always be degenerate, with either  $xb=x1$  or  $yb=y1$ . It is straightforward to extend this concept to three components. This improves the all-important location of triple points.

The successive construction of exit/entry lines, and rectangles on the fixed grid continues until it either exits from the domain, or a junction on the predominance boundary is identified. A junction is indicated when more than two species are identified as dominant amongst the four corners of a rectangle. If, for example, there are three dominant species then these define two exit sides from a single rectangle. The two boundary lines from this rectangle are then tracked in turn, with appropriate flagging of the necessary sequence of operations. For more complex examples, a predominance boundary may return to a previously identified junction. The algorithm keeps track of when this occurs. Finally, the line segments are assembled into polygons.

The domain boundary should be exhaustively searched in hunting mode to ensure no predominance boundaries are missed. Once a crossover point has been established, its location is progressively refined with sub-grid accuracy. It is sometimes necessary to increase the grid resolution to ensure that the hunting and tracking sequences join up properly. This is done automatically but requires a complete restart.

The present approach of stepping sequentially through every domain boundary grid point is recognised as inefficient, though guaranteed to detect all crossings within the resolution (grid spacing) chosen. If the grid is too coarse, the location of junctions may be poorly estimated. For a fixed grid algorithm of this sort there will be a trade-off between computational efficiency and accuracy. A grid spacing equivalent to a resolution of 1/500 of the domain boundary normally gives smooth and reliable curves. The advantage of using a fixed grid is that quite complex curves may be tracked. However, the scheme does not take full account of the known characteristics of some predominance boundaries inherent in the underlying chemical model. This can lead to some inefficiency. We make no assumptions about the curvature of the field boundaries which are often straight but which can be curved and can even show very sharp changes of direction.

A similar tracking procedure can be followed when the stability criterion is used or when an artificial boundary is added as a result of a user-defined constraint, e.g.  $H_2(g) = 1$  atm. In these cases, linear interpolation can no longer be used to refine the point of intersection and so the mid-point is always chosen.

### *Definitions of 'predominance' and mineral stability*

In classical mineral stability diagrams, the position of the mineral-solution boundary depends on the assumed activity of the solution components at the boundary. Garrels and Christ, following Pourbaix, defined the boundary as the point where the 'sum of the activities of the ions in equilibrium with the solid exceeds some chosen value'. They chose  $10^{-6}$  as a default value on the basis that if it is less than this value, the solid will tend to behave as an immobile constituent in the environment. In the full speciation approach, the activity at the boundary is determined by the system specification and the speciation calculation and will normally be specified by either a fixed total amount of the various components or by a fixed activity/fugacity, e.g. for gases. There is no need for excessive simplification of the system and so such diagrams can be customised for systems of particular interest. The only decision is whether to draw the boundary for the predominance domain or the stability domain.

When adsorption reactions are included, it is possible to compare the total number of moles of the main species in each of the phases (gas, solid, solution, adsorbed) to determine the predominant phase (out of the four possibilities). Alternatively, more detail can be revealed if each species is considered independently as is normally done in solution-only predominance diagrams. The predominant species is then defined as the species accounting for the greatest number of moles in the whole system. The `ht1.inc` code treats each adsorbed species as a sep-

arate entity, just like a solution species. The definition of 'species' becomes more ambiguous when an 'adsorbed' phase is considered since the normal definition of an adsorbed species is in terms of the type of binding site and so would make the diagrams very sensitive to adsorption model adopted. Probably a more useful approach is to lump all adsorbed species together into one 'super species' for the purposes of ranking. This is the approach adopted in the `ht1c.inc` code. If the detailed adsorbed speciation is of particular interest, then `ht1.inc` should be used.

### 8.3.3 Failure of the 'hunt and track' approach

One advantage of the 'hunt and track' approach is that it can create a vectorised diagram directly. This leads to a small plot file size and after smoothing of the field boundaries can produce smooth-looking boundaries as opposed to the jagged boundaries of the grid approach.

In principle the 'hunt and track' approach can produce better quality diagrams with less computational effort - the effort depends on the length of the boundaries that must be tracked rather than on the square of the resolution as with the grid approach. But the important caveat is that it can miss potentially important fields if they do not cross any of the domain boundaries. This can occur when 'wedges' intersect the domain boundary

Such islands appear to be quite rare and the phase rule indicates that they are likely to be confined to solution species. One example is given in [Example 43](#). We have checked all the other diagrams in this report and have found no other 'islands'.

Nevertheless, it is always important to check that there are no islands by switching the [calculationType](#) from 'ht1' to 'grid' and reducing the [resolution](#) setting to a more reasonable value.

A second problem is that in order to generate the required field boundaries and associated polygons, it is necessary that all the various line segments produced during tracking fit together exactly. Because of numerical errors implicit in the numerical approach used by **PHREEQC**, this is not always the case and it is possible to get lack of closure of some polygons.

It is also sometimes problematic connecting the 'hunt' part which is moving along the domain boundaries and the 'track' part which is moving along the internal boundaries. This is especially true when a field boundary happens to intersect, or runs very close, to a domain boundary. This can lead to a failure to close all the polygons, i.e. to create the clean polygons necessary for colour filling. This can sometimes be avoided by changing the resolution of the plot - and **PhreePlot** will attempt to do this to some extent automatically - but if this fails then manually changing the domain boundaries so that there is no intersection very close should help. Alternatively try the 'grid' approach.

The 'ht1' algorithm assumes that each grid cell has just one triple junction inside it. Occasionally this is not the case, especially close to a domain boundary, and so it will fail. In such cases, it is worth trying the 'ht2' algorithm which is a bit more robust in this regard. You may receive an error message suggesting this change in [calculationType](#). If all else fails, try the 'grid' approach.

## 8.4 FEASIBLE DOMAINS AND THE PREPARATION OF EH (PE) -PH DIAGRAMS

### 8.4.1 General principles

The classical Pourbaix diagrams extend from pH 0 or less to pH 14 and over a wide range of redox conditions effectively ranging in oxygen partial pressures, say from more than 1e0 to less than 1e-100 atm. Extreme conditions such as these may not be physically realistic and are only considered in classic Pourbaix diagrams because the constraints of a full speciation are not imposed. This is also not entirely within the domain within which **PHREEQC** is able to operate (at least using its ion association activity model) especially under the extremes of redox conditions where water is itself not stable - making the concept of 'dissolved' species a nonsense. **PHREEQC** keeps track of the mass of water and when most of it has evaporated, the concentration of the remaining solutes can become extremely high in the small amount of water remaining. This domain of failure can be mapped and is shown using the ht1 approach

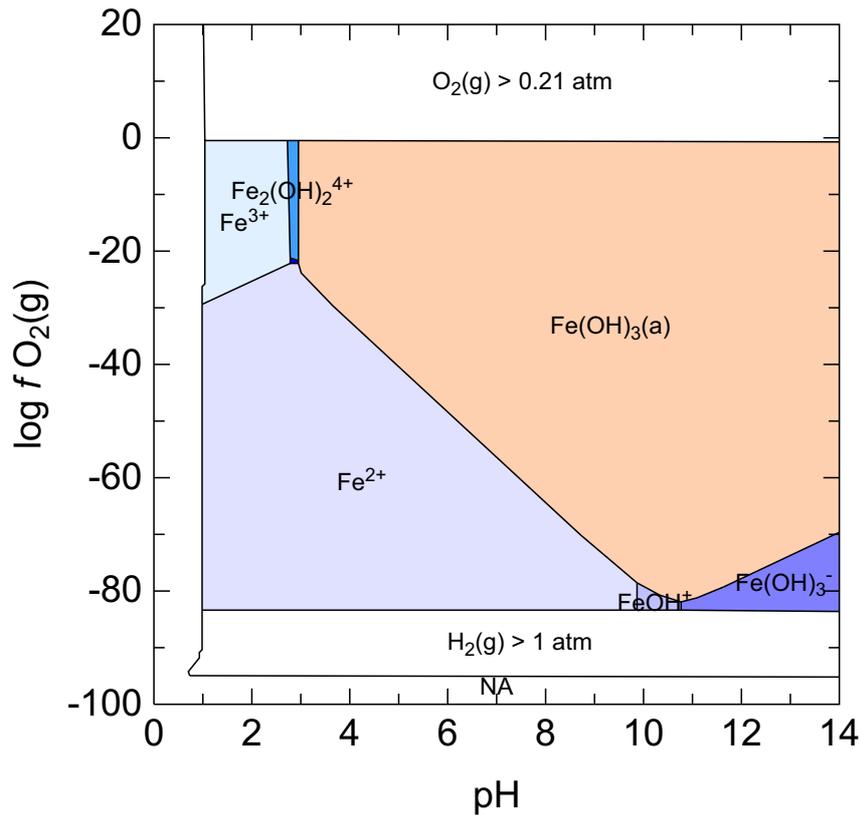


Figure 8.3.  $\log f_{\text{O}_2(\text{g})}$  vs pH diagram for the Fe-H<sub>2</sub>O system at 25°C calculated using the hunt and track approach for a domain range of  $-100 > \log f_{\text{O}_2(\text{g})} > +20$  and  $0 < \text{pH} < 14$ . It shows the regions with  $\log f_{\text{O}_2(\text{g})} < -95$  and  $\text{pH} < 1$  where **PHREEQC** fails to converge (label = NA).

(Figure 8.3). The grid approach gives a similar result.

At 25°C, the failure occurs at below  $\log f_{\text{O}_2(\text{g})}$  of -96 atm and arises because of the strong decomposition of water under these conditions – it decomposes releasing H<sub>2</sub>(g). (see the [‘water limits’](#)) This failure occurs at a higher  $\log f_{\text{O}_2(\text{g})}$  at higher temperatures, e.g. at  $\log f_{\text{O}_2(\text{g})}$  of -86 at 60°C. There is also a limit to the maximum O<sub>2</sub>(g) partial pressure that can be sustained in aqueous systems since it combines with H<sup>+</sup> to produce water. **PHREEQC** will eventually fail under these extreme conditions, though not without trying hard (and taking quite a lot of time attempting to find a solution).

As a consequence of these reactions and of limits to the practical limits of O<sub>2</sub>(g) that are reasonable, a typical Eh(pe)-pH has upper and lower diagonal lines that demarcate regions where the diagram is not evaluated.

On an orthogonal  $\log f_{\text{O}_2(\text{g})}$ -pH diagram, these ‘no evaluation’ regions can be simply excluded from being calculated by specifying appropriate upper and lower limits to the O<sub>2</sub>(g) fugacity.

Therefore a pe-pH diagram can be most easily prepared by specifying the y-axis variable to be  $\log f_{\text{O}_2(\text{g})}$  and then converting the redox scale with the [yscale](#) setting. It is possible to drive the y axis with the pe by defining the pe in an analogous way to that used for pH:

```
Fixed_e-
  e- = e-
  log_k 0.0
```

and then

...

```
EQUILIBRIUM_PHASES
...
Fixed_e- <loge- > O2(g)
```

where the sign of the y-axis variable is reversed using

```
numericTags      <loge- > = -<y_axis >
```

#### 8.4.2 Domain tags - avoiding speciation calculations

The calculation domain for a predominance diagram or a contour plot is always a rectangular area defined by ([xmin](#), [xmax](#), [ymin](#), [ymax](#)). It can be useful to omit certain parts of this domain from the speciation calculations, e.g. because the speciation is known to be unsuccessful or unnecessary in some region(s).

A special set of tags called *domain tags* can be used to clip the speciation domain, e.g.

```
<domain1_value > = "<x_axis >+<y_axis >" \
<domain1_min > = -2 \
<domain1_max > = 22
```

There can be up to 9 sets of domain tags, namely `<domain1_value >` up to `<domain9_value >` and their corresponding min and max tags.

These tags are defined in the usual [numericTags](#) block. `<domainn_value >` is evaluated before each speciation calculation and compared with the corresponding minimum and maximum values set with the `<domainn_min >` and `<domainn_max >` tags. If any of the values are outside this range, then the speciation calculation is skipped.

Note that the domain value needs to be determined *before* the speciation calculations and so the definition of the `<domain1_value >` tag should only use those tags that are known *before* speciation. The most obvious ones are the `<x_axis >` and `<y_axis >` tags.

The above test is only applied to main loop simulations. Pre-loop simulations will always be calculated in full.

These tags can be useful when generating a pe-pH diagram in order to eliminate speciation calculations from areas outside of the lower and upper bounds for the stability of water.

The 'ht1' method of calculating a predominance diagram requires that access to the boundaries is available from one of the domain boundaries. So it is not possible to reduce the domain size on all four sides since there will then be no access to the inner region. However, the 'grid' approach would work with these conditions.

The skipped calculation is by default assigned the 'species' name "skip" and speciation values are set to UNDEFINED. The results are included in the track file as usual. A '-' sign precedes the iteration number of the rolling summary shown on the screen for skipped iterations.

The species name and therefore the label used can be renamed by editing the labels file and replotting, or by adding a special character tag with the name, `<domain1_name >`. The name can be the empty string, "". The name of the field used is taken from the first out-of-domain criterion searching from 1 to 9.

#### 8.4.3 Speciation failure when there is not enough reactant present

This most frequently happens when trying to fix the pH using the 'Fix\_pH' ploy. PHREEQC will fail to converge at low pH if the reaction being used to achieve the desired pH is not feasible. For example, if NaOH is being used to change a solution from pH 2 to pH 1, it will likely eventually fail. In the presence of a background electrolyte containing Na such as NaCl, this failure will not occur at exactly pH 2 but at a somewhat lower pH depending on the amount of Na present. PHREEQC will attempt to achieve the low pH by withdrawing NaOH (negative NaOH additions) until all the Na has disappeared at which point it will fail. This problem can be solved by linking the Na to a large reservoir of a Na-containing mineral ([Section 6.5.5](#)) such as NaCl (halite) but this itself can have undesirable side effects. The problem can be more complicated when other side reactions such as redox reactions are themselves producing/consuming protons. Then when both pe and pH are changed, it is not necessarily obvious

whether acid or base needs to be added to change the pH.

## 8.5 CHOICE OF THE RESOLUTION OF THE PLOT

The speed of calculation depends on many factors including the complexity of the chemistry, especially the number of mineral phases, the length of the `USER_PUNCH` code and the resolution of the plot. A reasonable approach is to start at a low resolution, say 50-100 for a ht1 plot or 20-50 for a grid plot, and increase it when a production quality plot is required. The resolution must be 10 or greater and should normally be less than 2000. The ht1 algorithm can fail to resolve junctions at low resolutions which can lead to a failure to close all the polygons properly.

If more detail is required for a particular area, zoom in by reducing the domain size with the [xmin](#), [xmax](#), [ymin](#), or [ymax](#) parameters and recalculate rather than just replotting at the new scale.

**PhreePlot** sometimes overrides the resolution originally set in the input files and either increases or decreases it. It does this when it either needs more resolution to resolve apparent 4-way junctions or when a junction is too close to a domain boundary: Changing the relevant domain boundaries ([xmin](#), [xmax](#), [ymin](#), or [ymax](#)) would avoid the latter problem. A reduction in resolution is sometimes necessary if the output from **PHREEQC** is for any reason unstable.

## 8.6 MONITORING THE PROGRESS OF A 'HUNT AND TRACK' RUN

Providing that the screen output has not been disabled, progress of the tracking will be displayed on the screen. An example is given below:

```
*** PhreePlot *** Pre-release 0.01 (3 Jan 2008)
    Incorporating the PHREEQC library by DL Parkhurst, SR Charlton (USGS),
      & CAJ Appelo (Amsterdam)
    Hunt & Track by DG Kinniburgh, BGS and DM Cooper, CEH (NERC)
    Fitting by MJD Powell (University of Cambridge)
    Postscript plotting by KE Kohler

<mainspecies> = Se
  1  2.0000 -80.0000 11 Se      H2Se      -3.0010    -5.6388
  2  2.0000 -76.8000 11 Se      H2Se      -3.0000    -7.2388
  3  2.0000 -73.6000 11 Se      H2Se      -3.0000    -8.8388
  4  2.0000 -70.4000 11 Se      H2Se      -3.0000   -10.439
  5  2.0000 -67.2000 11 Se      H2Se      -3.0000   -11.847
  6  2.0000 -64.0000 11 Se      H2Se      -3.0000   -13.447
  7  2.0000 -60.8000 11 Se      H2Se      -3.0000   -15.047
  8  2.0000 -57.6000 11 Se      H2Se      -3.0000   -16.647
  9  2.0000 -54.4000 11 Se      H2Se      -3.0000   -18.247
 10  2.0000 -51.2000 11 Se      H2SeO3    -3.0000   -18.105
 11  2.0000 -48.0000 11 Se      H2SeO3    -3.0000   -14.905
 12  2.0000 -44.8000 11 Se      H2SeO3    -3.0000   -11.705
 13  2.0000 -41.6000 11 Se      H2SeO3    -3.0000    -8.5055
 14  2.0000 -38.4000 11 Se      H2SeO3    -3.0029    -5.3055
 15  2.0000 -35.2000 11 H2SeO3   HSeO3-    -3.1277    -3.5938
 16  2.0000 -36.8000 11 Se      H2SeO3    -3.1333    -3.7055
 17  2.0000 -35.2000 11 H2SeO3   HSeO3-    -3.1277    -3.5938
 18  2.0000 -36.0000 11 H2SeO3   HSeO3-    -3.1277    -3.5938
 19  2.0000 -36.4000 11 H2SeO3   Se        -3.3055    -3.4738
 20  2.0000 -36.6000 11 Se      H2SeO3    -3.2358    -3.5055
 21  2.0000 -36.4000 11 H2SeO3   Se        -3.3055    -3.4738
 22  2.0000 -36.5000 11 Se      H2SeO3    -3.3256    -3.4055
 23  2.0000 -36.4000 11 H2SeO3   Se        -3.3055    -3.4738
 24  2.0000 -36.4500 11 H2SeO3   Se        -3.3555    -3.3892
 25  2.0000 -36.4750 11 Se      H2SeO3    -3.3553    -3.3805
 26  2.0000 -36.4500 11 H2SeO3   Se        -3.3555    -3.3892
 27  2.0000 -36.4625 11 H2SeO3   Se        -3.3680    -3.3717
 28  2.0000 -36.4687 11 Se      H2SeO3    -3.3634    -3.3743
 29  2.0000 -36.4625 11 H2SeO3   Se        -3.3680    -3.3717
 30  2.0000 -36.8000 21 Se      H2SeO3    -3.1333    -3.7055
 31  2.0000 -36.0000 22 H2SeO3   HSeO3-    -3.1277    -3.5938
 32  2.0800 -36.0000 23 H2SeO3   HSeO3-    -3.1496    -3.5356
 33  2.0800 -36.8000 24 Se      H2SeO3    -3.1415    -3.7055
 34  2.0000 -36.8000 11 Se      H2SeO3    -3.1333    -3.7055
 35  2.0000 -36.4687 11 Se      H2SeO3    -3.3634    -3.3743
 36  2.0000 -36.8000 21 Se      H2SeO3    -3.1333    -3.7055
 37  2.0000 -36.0000 22 H2SeO3   HSeO3-    -3.1277    -3.5938
 38  2.0800 -36.0000 23 H2SeO3   HSeO3-    -3.1496    -3.5356
```

39	2.0800	-36.8000	24	Se	H <sub>2</sub> SeO <sub>3</sub>	-3.1415	-3.7055
40	2.0800	-36.0000	22	H <sub>2</sub> SeO <sub>3</sub>	HSeO <sub>3</sub> -	-3.1496	-3.5356
41	2.1600	-36.0000	23	H <sub>2</sub> SeO <sub>3</sub>	HSeO <sub>3</sub> -	-3.1744	-3.4804
42	2.1600	-36.8000	24	Se	H <sub>2</sub> SeO <sub>3</sub>	-3.1514	-3.7055
43	2.2400	-36.0000	23	H <sub>2</sub> SeO <sub>3</sub>	HSeO <sub>3</sub> -	-3.2026	-3.4285
44	2.2400	-36.8000	24	Se	H <sub>2</sub> SeO <sub>3</sub>	-3.1638	-3.7055

The columns are from left to right:

iteration number (number of speciation calculations)

x-axis value

y-axis value

type of move

sign: a -ve sign means a 'constraint' (a forced value) is in operation

first digit: 1 = hunting along an edge 2 = tracking an internal boundary

second digit: 1-4, side being traversed (starting with the left-hand y axis as 1 and counting clockwise).

'00' is used for 'grid' plotting. '20' for a 'multi-point' point

dominant species name

subdominant species name

log concentration (mol/kgw) of dominant species

log concentration (mol/kgw) of subdominant species.

Where a constraint is operating, the indicated 'dominant species' is the constraint species, such as a gas or in the case of a mineral stability diagram, a mineral. The indicated 'subdominant' species is the species that would be dominant in the absence of the constraint. The numeric values of constraints are the log's of the constraint value. In the case of pure phases (gases and minerals), this is the saturation index.

In the above example, the algorithm starts hunting along the y axis, finds a boundary crossing the axis between -36.4625 and -36.8 and then starts tracking inwards along that boundary. The boundary being tracked is between H<sub>2</sub>SeO<sub>3</sub> and Se.

A full record of the tracking is recorded in the track file.

A graphical display of the grid or ht1 tracking can be obtained by using the 'ESC p' combination. A plot file 'plot.ps' will then be written to the input file directory showing progress. In a ht1 plot, the blue filled circle shows the current calculating position. This plot only records the tracking phase, not the hunting phase.

## 8.7 PLOTTING AND REPLOTTING

[calculationMethod 1](#) does a full set of speciation calculations and will generate all the files necessary for plotting (most calculations)

[calculationMethod 2](#) does not recalculate the speciation or redo the calculation of the polygon boundaries but reads in these results from the polygon file and the label names and positions from the labels file (least calculations).

[calculationMethod 3](#) does not recalculate the speciation but does recalculate the polygons and label placement (intermediate calculations).

## 8.8 MODIFYING THE APPEARANCE OF PREDOMINANCE PLOTS

The appearance of the plot can be modified through many of the keywords. These can be changed in the input file and the file rerun with one of the two replot options - there is no need to redo the calculations unless a different resolution is required.

The colours of the fields can be modified by editing the appropriate fill colour dictionary - that is a file with the default name of `fillcolor.dat`.

Fields are known primarily by the number assigned to them. The labels file translates this number into a field name. The colouring of individual polygons can be turned off by setting the species number in the labels file to zero.

The appearance of internal boundary lines is controlled by the settings: [linecolor](#), [lineWidth](#), [lineType](#) and [dashesPerInch](#). The 'ht1' method uses the vector file to plot the boundary and only plots each boundary once. The 'grid' method uses the polygon file to plot the boundaries and common boundaries will be plotted twice. This is likely to affect the appearance of dashed lines in 'grid' plots since the overwriting may have different starting points.

Individual polygons, and their boundaries, can be removed from the plot by setting the species number for all points ('lines') for the polygons of interest in the polygon file to zero or a negative number (reversing the sign in a text editor is the most convenient way of doing this).

The label position and orientation can be changed by [nudging](#) or editing the labels file. Editing the labels file can include changing the species name even to a blank field name, "". The label is known internally by its species number. Normally the label attributes are recalculated each time new field boundaries are generated ([calculationMethod](#) 1) but this can be changed by setting [useLabelsFile](#) to `TRUE`. This ensures that the readings from the labels file will be used if possible. If the file does not exist, it will be created. [calculationMethod](#) 2 has the same effect for a replot.

It is possible to change the y scale (native, pe, mV or V) without recalculation using [yscale](#).

Plot limits can be changed using [pxmin](#) etc but beware that if a larger range is specified there will be a blank area around the plot and if a smaller domain is chosen the field boundaries will appear correspondingly coarse - would be better to recalculate at the new resolution which will also calculate the label positions better.

The 'steppiness' of the boundaries in 'ht1' plots can be controlled with the [simplify](#) keyword. The default value is 1 so choose a larger value (up to 10 say) to smooth the line more. Recalculate the boundaries and replot using [calculationMethod](#) 3 rather than 2 since the smoothing has to be redone. A [simplify](#) value of 0 will show all the boundary points. 'grid' plots are by definition 'steppy' and [simplify](#) has no effect on this.

Additional text, including labels, can be added with [text](#) or [extraText](#). There is full control over the plot on which to apply the text plus the font, size, colour, justification and orientation of the added text.

Additional data from other files can be added to the plot using the [points](#) and [lines](#) keywords combined with the [extradat](#) keyword to add the additional data files to the search path. These data must be in regular tabular output format. The x-column of each file should be labelled with 'x' in the header since this is the label that is always used in predominance plot files. There is no automatic labelling or generation of a legend for lines or points added in this way. [text](#) or [extraText](#) can be used to add labelling manually. [symbolsLines](#) or [extraSymbolsLines](#) can be used where more control is wanted over the symbols used or the line widths.

The entire plot can be rescaled with [plotFactor](#).

Some of the main settings are shown in Figure 8.4. For more complete control over the appearance of the plot transfer the data to a more powerful plotting package. This can be done at either the image (ps file) or data (pol and vec files) level.

## 8.9 ADDING LINES AND POINTS TO A PREDOMINANCE PLOT

The usual way of adding lines and points to a plot is through [symbolsLines](#) or an [extraSymbolsLines](#) file.

However, it is also possible to add lines and points to a predominance plot using the [lines](#) and [points](#) keywords and data read from a file. However, these data are not included in the auto



ber and species name so editing this file can change the appearance of labels and their position during a replot. The exclude list of the [pol](#) keyword can be used to omit specific fields com-

Table 8.1. Influence of the [calculationMethod](#) setting on when and where labels are plotted,

Setting	Action
<a href="#">calculationMethod</a> = 1	Does a full speciation calculation. Generates new labels and polygon files which are used for positioning labels and identifying fields. If a labels file of the correct format* exists before calculations, then a negative sign in front of a species number will suppress the plotting of that label. The labels file will normally be rewritten but this can be prevented by setting <a href="#">useLabelsFile</a> to TRUE in which case edits to the file will be preserved even with <a href="#">calculationMethod</a> = 1.
<a href="#">calculationMethod</a> = 2	Does not carry out any new speciation calculations and does not regenerate the labels and polygon files. If a labels file of the correct format* exists before calculations, then a negative sign in front of a species number will suppress the plotting of that label. You can also rename the species name including to blank ("").
<a href="#">calculationMethod</a> = 3	Does not carry out any new speciation calculations but does regenerate the labels and polygon files. Reassembles and resimplifies the field polygons starting with the results of the initial speciation which are read in from the points ('ht1') or track ('grid') files. The labels file names (not species numbers) can be edited as for 2 above.

\* Each row of a correctly formatted labels (\*.lab) file corresponds one to one in order and species number with the species (sp) specified in the polygon (\*.pol) file.

pletely including their boundary lines, coloured infill and labels.

Label names are regenerated whenever [calculationMethod](#) 1 is used. If you want to override a label name at this stage, then you can edit the `ht1.inc` file to make the appropriate substitution. For example, in the `demo\Fe\hfo.ppi` file, say you wanted to rename `Fe(OH)3(a)` to `Hfo` then add the following line

```
131 IF (n$(i) = "Fe(OH)3(a)") THEN n$(i) = "Hfo"
```

and it will intercept the name and change it. Save the file with a different name and use this in the ppi file. Alternatively, for a one-off, you can add the above line directly to your ppi file

...

```
include 'ht1.inc'
```

```
131 IF (n$(i) = "Fe(OH)3(a)") THEN n$(i) = "Hfo"
```

...

since the Basic interpreter executes the lines in line number order.

The [domain](#) keyword controls whether the domain boundaries will be plotted or not. The default is `TRUE` which will plot the boundaries. If the native scale and automatic axis scaling are chosen, the domain boundaries will coincide with the axes boundaries. It can be useful to switch the domain boundaries off when a plot is rescaled and a constraint such as a gas partial pressure exists, e.g. to remove the outer lines specifying the ['water limits'](#) in pe-pH plots.

The default x- and y-limits to a predominance plot are set to the calculation domain as specified by [xmin](#), [xmax](#) etc and any fields with out-of-plot boundaries are clipped. The plot limits can be reset with [pxmin](#), [pxmax](#) etc.

Since predominance plots calculated with the `'grid'` approach have cell-centered speciation values, the first and last rows and columns of the grid are half clipped when the default (auto) x- and y-limits are specified.

The labels are allowed to extend beyond the plot domain by 15% of the axis length. Anything beyond that is clipped.

### 8.11 WHY DO I NOT SEE METHANE GAS WHEN USING `11n1.dat`?

Unlike when using the `wateq4f.dat` database, you are unlikely to see methane gas ( $\text{CH}_4(\text{g})$ ) as a predominant species when using the `11n1.dat` database even under strongly reducing conditions and in the presence of carbon. Why is this since it appears to be in the database?

The answer is that the `11n1.dat` has many more ‘exotic’ species in its database compared with `wateq4f.dat`. This includes the dissolved species  $\text{CO}$ ,  $\text{C}_2\text{H}_4$  and  $\text{C}_3\text{H}_6$  as well as  $\text{CO}(\text{g})$ . Perhaps surprisingly, given the relative abundance of methane in the natural environment, these species are calculated to be thermodynamically dominant over methane in many reducing environments. The fact that they are not so abundant in most natural environments suggests that kinetic factors may be preventing their dominance in the ‘real’ world.

Therefore in order to see methane in predominance diagrams using **PhreePlot**, remove these ‘exotic’ species from consideration either by adding the species to an input file and changing the `log_` value to make it insignificant or, for a more permanent solution, delete them from the database file by commenting them out.

Of course this all becomes clearer if you plot a predominance diagram with C as the main species!

### 8.12 FAILURE TO COMPLETE A PREDOMINANCE DIAGRAM

The grid approach should always produce a valid diagram although its quality will be determined by the resolution chosen. There is no requirement for any spatial continuity between adjacent cells.

There is no guarantee that the ‘hunt and track’ approach will always work. Either **PHREEQC** may fail or the tracking may fail. Possible reasons for the failure of **PHREEQC** have been discussed elsewhere ([Section 6.5.5](#)).

The simple ‘hunt and track’ algorithm used in **PhreePlot** assumes that the speciation is returned without error and tracks accordingly. Clearly since all speciation programs, including **PHREEQC**, use numerical methods to derive their solution, the boundaries between fields must contain some ‘noise’. This may mean that the fields reported near field boundaries may themselves be in error, e.g. varying 1212 rather than 1122. This may in turn mean that the fields (polygons) cannot be closed properly and so cannot be plotted as coloured polygons. This is par for the course and is not an error in **PHREEQC** *per se* but in the way it is being used.

In **PHREEQC**, the `convergence_tolerance` parameter in the **KNOBS** keyword block specifies a relative error for an element’s mass balance and this controls when a valid solution is deemed to have been achieved. Typically this parameter is set at  $1\text{e-}12$  when `SELECTED_OUTPUT; -high_precision` is set to true. Either use **KNOBS** to increase it (e.g. to  $1\text{e-}8$ ) or set `-high_precision` to false. It may be helpful to change this setting where there is a problem in convergence typically seen when the residuals are very small but exceed  $1\text{e-}12$ . Other possibilities have been discussed [earlier](#).

If the tracking grid falls on or very close to a true predominance boundary, **PhreePlot** could end up tracking noise, or more likely, some of the results of the speciation calculation could be erroneous resulting in confusion for the tracking algorithm as indicated above. This can also occur when a field boundary–domain boundary intersection is very close to one of the four domain corners. If detected, **PhreePlot** attempts to get round this automatically by reducing the resolution of the plot by about 10% and recalculating but this does not always work. A ‘\*’ in the `n` column of the `pp.log` file indicates that an automatic restart has been made. The [Mn.ppi](#), [fluoritepredominance.ppi](#) and [fluoritestability.ppi](#) demos are examples of this.

It also sometimes occurs that the ‘ht1’ method requires a greater resolution than given to resolve a junction or to close all polygons. In these cases, **PhreePlot** will automatically restart with a doubling of the resolution. This increase will be repeated if necessary up to a maximum

resolution of 2000.

Other actions that can be used to resolve failures of the method involve moving the grid in other ways: changing the domain of the calculations ([xmin](#), [xmax](#), [ymin](#), [ymax](#)) or by reducing the resolution more radically.

In rare cases, **PHREEQC** does not converge at all. This is usually, but not necessarily, clearly signalled by **PhreePlot** and can often be seen by the failure to write the `SELECTED_OUTPUT` file. Convergence can sometimes be helped by (i) changing the `-high_precision` setting in the `SELECTED_OUTPUT` section of the `ht1.inc` file (if used) to `FALSE`; (ii) reducing the convergence tolerance, (iii) reducing the `pe_step_size` (under [KNOBS](#)), or (iv) increasing the allowed maximum number of iterations (also under [KNOBS](#)). However, by far the most common reason for failure to converge is because of a poorly-constructed **PHREEQC** input file, i.e. inconsistent chemistry somewhere.

With [debug](#)  $\geq 1$ , failure, if detected, will result in an immediate halt to execution and a dump of the offending `PHREEQC.out` file, and in the case of [debug](#) = 2 and 3, of all the **PHREEQC** output to that point. With [debug](#) = 0, the failed region will be mapped as its own species ('NA') and a question mark will be added to the `pp.log` file to indicate a failure.

# 9 Contour plots

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## 9.1 WHAT ARE CONTOUR PLOTS?

Contour plots are the sort of plots you see when looking at a topographic map, i.e. a diagram showing lines of equal height. Each height is called a ‘contour’. Contours do not normally cross each other and always change in a regular sequence, one contour followed by one of its nearest neighbours. There should be no missing, intervening contours.

This concept of ‘height’ can of course be generalised to any continuous variable and that is what is done here. Note however that not all geochemical variables are continuous variables. Phase changes for example can introduce step changes and this can cause problems in contouring.

Contour plots provide another way of viewing  $x$ ,  $y$ ,  $z$  data where  $z$  is the variable being contoured. In some senses, they complement predominance diagrams.

Contour plots only work well for relatively smooth, continuously varying variables of which the latter characteristic is the most important. Sometimes, gradients in geochemical variables can either be so large that they do not appear continuous or the reporting of the variable has been truncated to such an extent that the variable is no longer continuous. Then contouring does not work well.

Contours are produced by generating a uniform grid of data over the given  $x$ - and  $y$ -domain. It is assumed there are no missing or undefined points in this data set.

Also, it is assumed that all the contoured data is valid data, i.e. that all **PHREEQC** calculations have converged properly. If the  $x$  and/or  $y$  variable are being ‘fixed’ by adding an equilibrium phase, e.g. as in `Fix_H+`, then it is wise to check that the target value has actually been achieved. Sometimes, **PHREEQC** does not trigger an error when there has been a failure to converge; it just gives a warning. It will also not issue an error if the reservoir has run out. If in any doubt, add the `-force_equality TRUE` identifier to all phases.

This check can often be done by adding the value(s) achieved and the target value(s) to the selected output, e.g. if the  $x$ -axis is supposed to be the pH, then comparing the actual pH achieved, `-la("H+")`, with the `<x_axis>` tag will indicate if convergence has occurred. The track file will also give blank output values where there has been a failure to converge and where an error return has been indicated.

Contours can in principle be viewed from various angles. Here we deal only with a view directly from above rather like in a topographic map.

## 9.2 IMPLEMENTATION

### 9.2.1 Generating the contour data

The contouring algorithm requires smooth, regularly-gridded data. This is generated by **PhreePlot** in the same way that is done for ‘grid’ plots using `xmin`, `xmax`, `ymin`, `ymax` and `resolution`. The resolution must be greater than 1 and normally should be in the range 10–100. The gridded data is picked up from the ‘out’ file.

A contour plot is usually made by specifying the `calculationType` to be ‘contour’ and by specifying a `contourZvariable`. This is the name of one of the variables in the ‘out’ file. For all contour plots, you must provide the **PHREEQC** code to calculate a  $z$ -value at each  $x$ ,  $y$  point.

This is normally done using the `SELECTED_OUTPUT` and `USER_PUNCH` data blocks. The name of this variable is given by the [contourZvariable](#) keyword defined in an input file and should correspond with one of the `USER_PUNCH` 'out' file headings.

If the plot is to use a transformed yscale, such as Eh, then  $\text{pe} (-1a("e-"))$  and temperature (TC) must also be exported to enable the transformation to be made – these columns must have the headings 'pe' and 'TC', respectively, so that they are recognised as such. They can be located in any position. See the file `\demo\contour\contour_hfo_pretty.ppi` and the [Example](#) for some discussion.

If the [contourZvariable](#) is not defined or not found, then a fatal error is issued.

It is not necessary to output the corresponding x- and y-variable values since these are defined implicitly by their respective ranges, the grid resolution and the iteration number. However, if the output data are to be used by some other software package, it may be helpful to output their values. Simply add the `<x_axis>` and `<y_axis>` tags to the list of variables to be 'punched'.

Note that because the x- and y-values are implicit, you have to be careful to make sure that you regenerate the whole set of data when changing any of the parameters that define the domain of the grid or the speciation calculations. The contouring package has no knowledge of these x- and y-values explicitly – it calculates their values from their position in the 'out' file. If the speciation fails and there is no output, an UNDEFINED value placeholder is normally written to the `out` and `trk` files. This can be prevented by setting [writePlaceholder](#) to `FALSE`. A `FALSE` setting is useful when a failed speciation is repeated as in the `\demo\switch` examples.

The z-data can be smoothed using a five point nearest-neighbour moving average algorithm. This is specified with the [contourOptions](#) `smooth=1` statement. Somewhat greater smoothing can be gained using `smooth=2`. This is a 9-point nearest neighbour algorithm. The smoothed data are not stored externally but are generated from the raw data as needed. A setting of `smooth=0` turns off all smoothing.

### 9.2.2 Choosing the contour levels

The contour levels are specified with the [contours](#) keyword. This can either be a list of user-defined values in ascending order, or can be one of several automatic selected sets of values. See [contours](#) for details. The default is for a list of 17 values to be automatically generated by sub-dividing the range of the z-data values into 16 equal intervals (empirical values). It is also possible to choose the contour values based on percentiles.

The main requirement for the selection of a set of contour values is that the values are well separated – they should not be so close to each other that they enter the area of 'noise' created by the numerical procedures used in generating the data being contoured. It is also unwise to set a contour exactly on a value which for some reason (chemical buffering, numerics) is very common. This strategy will avoid the problem of the contour running along a boundary leading to a sensitivity to numerical errors.

The number of contours used will be automatically reduced if neighbouring contour values are deemed to be too close to each other. Successive contours should always differ by at least  $1e-8 \times$  average value of successive pairs of values. This is to try and minimise the effect of small numerical errors on the drawing of the contours. The 'simplified percentiles' `auto` option requires a greater separation between contour values and prunes the set of contour values even more aggressively (see [contours](#)).

### 9.2.3 Types of contour plot

Two types of contour plots are available:

- (i) a plot consisting of contour lines with colour-fill in between the contours (sometimes called a 'level' plot)
- (ii) a 'lines only' plot.

The [contourOptions](#) keyword determines which of these two types of plot is used.

A plot with colour fills is usually the most pleasing and can be customised in terms of the number and position of the contour levels, the fill and line colours, and the line, label and legend styles.

The lines only plot ([contourOptions](#) `fill FALSE joinSegments FALSE`) uses the most straightforward way of producing a contour plot since it does not require the various segments produced by the contouring algorithm to be combined together and with border segments to produce the polygons required for colour filling. The ‘lines only’ plot comes in two flavours: the simplest one is merely a plot of the short segments produced by the contouring algorithm scanning across the domain at each contour level. In this case, there is no requirement for the segments to be plotted in any particular order. This is an advantage in noisy, high resolution plots where defining the numerous polygons can be rather slow and the numerous line segments can sometimes be difficult to assemble in the proper order – the `joinSegments FALSE` option avoids this possibility and is therefore the ‘fall back’ option.

If you change the `joinSegments` option, you will have to regenerate the plot from scratch (not just replot it) since the structure of the vector file varies between the two approaches.

The lack of joined-up line segments can lead to visibly poor curves since the better-looking line joins cannot be used. It is also not possible to take account of the full length of the line when calculating the best position for dashes in dashed lines resulting in poor dashed lines especially when the resolution is high. In particular with dashed lines each line segment will have at least one ‘dash’ and so the dash density may be greater than specified by the [contourDashesPerInch](#) setting (unlike in the legend). It is best to avoid dashed lines with this option.

Finally no line simplification is undertaken giving more intricate contours and larger plot files.

A better strategy is to at least sort the segments into continuous contour lines which can then be simplified and plotted as a single curved line with proper line joins ([contourOptions](#) `fill FALSE joinSegments TRUE`).

Adding the various boundary segments to the sorted contour lines then enables the polygons to be closed and so filled with colour ([contourOptions](#) `fill TRUE`). It also enables a place for an in-line contour label to be put. This is the default plot type.

Of course the fill colours can be set to ‘nd’ or ‘white’ to produce what looks like a contours only plot. However there are still subtle differences in the way that the contours are labelled and the type of legend produced.

If a colour fill plot is selected but **PhreePlot** fails to close all the polygons properly for some reason, then the polygons that could not be closed are not drawn. Sometimes changing the smoothing option from 0 to 1 or 2, or vice versa, is sufficient to allow the plot to complete properly. A lines only plot should always work.

#### 9.2.4 Changing the appearance of the contour lines.

The [contourLineType](#) keyword allows the line types for the contour lines to be specified using the usual recycling rules. [contourDashesPerInch](#) defines the dash density, [contourLineColor](#) defines the color and [contourLineWidth](#) defines the line width. For normal ([contourOptions](#) `fill TRUE`) plots, [contourLabelSize](#) controls whether a label is printed in the contour line and how large it is. If the `fill` option is `FALSE`, the contour values will only be given in the legend so normally `fill` should be `TRUE`.

#### 9.2.5 Colouring the plot

The contour lines, contour fill and contour label can all be independently coloured using [contourLineColor](#), [contourFillColor](#) and [contourLabelColor](#) as lists of colours that are recycled as necessary. Each of these has an ‘auto’ setting by default meaning that **PhreePlot** will choose the colours.

All colours in a given list, or individual ones, can be ‘turned off’ by setting the colour to ‘not drawn’ (‘nd’). For colour fills, it is safer to set an unwanted colour to the background colour, e.g. ‘white’ rather than using ‘nd’ since in the case of closed contour levels, the colours levels are filled from the outside in and the colouring relies on successively overwriting an outer colour by the next inner colour.

### 9.2.6 Labels and Legend

If a lines only plot is produced, the legend or key simply consists of lines with the colour and width of the corresponding contour lines and labelled with the contour value. The size of this text is controlled by the [contourLabelSize](#) setting.

The labels are placed within the longest line segment on the simplified contour but the position of all contour labels can be quickly changed by changing the `labelPosition` option in [contourOptions](#). If this setting is set to ‘centre’ rather than ‘longest’, the labels will be placed at the centre of each plotted line.

A contour may consist of several non-connected segments. At most, one label is present per segment. The position of the label on each segment can be moved using the [nudge](#) or [contour-ShiftLabel](#) keywords. `nudge` is free to move the label anywhere whereas `contourShiftLabel` moves it along the contour line, forward or backwards, point by point. The label font, size and colour can be changed with [contourLabelFont](#), [contourLabelSize](#) and [contourLabelColor](#), respectively. The number of significant digits in the labels is controlled by [contourLabelFigs](#).

If a colour-filled plot is produced then the legend consists of a colour key with the range of values for each of the fields.

A legend or key title can be specified with [legendTitle](#). [LabelColor](#) determines the colour of the legend title. The [legendTextSize](#) keyword controls the size of the text used for the legend title (if any) and the legend text (the numbers). It also determines whether a legend is produced or not – a positive value automatically places a legend at the top right of the plot. A zero size means no legend is produced.

A legend box can be added or moved with [legendBox](#).

The legend key can be moved, resized or re-coloured by using the `<legend>` tag in a text line or an `extraText` file. This can also provide the legend title. If present, this overrides any title given by [legendTitle](#).

### 9.2.7 Flow of data

The plotting of contours is carried out in three steps: (i) calculation of the regular grid of specification data with **PHREEQC**; (ii) contouring of these data to produce a list of unsorted segments denoting the contours, and (iii) sorting of these segments into their contours, adding boundary segments to produce polygons for colour filling. This sequence is shown in Fig. 9.1.

### 9.2.8 What if PHREEQC fails?

Contour plots are best if the data are smooth and continuous and if there are no ‘missing data’ in the set of grid data to be contoured.

If there are ‘missing data’ but a value such as `-99999` or `-99` has been substituted as happens when **PHREEQC** fails to converge, then the plot will still be attempted but will pay no special heed to the missing value. It will be treated as a valid value and will attempt to contour around it, probably by plotting it as a very low area or ‘hole’. This may still produce an informative plot though it is unlikely to be worthy of publication.

If **PHREEQC** fails to converge and fails to produce any output, then the z-value is assumed to be undefined (this is stored in memory for plotting) and a single `UNDEFINED` value (`-99999.000`) written to the ‘out’ file for replotting.

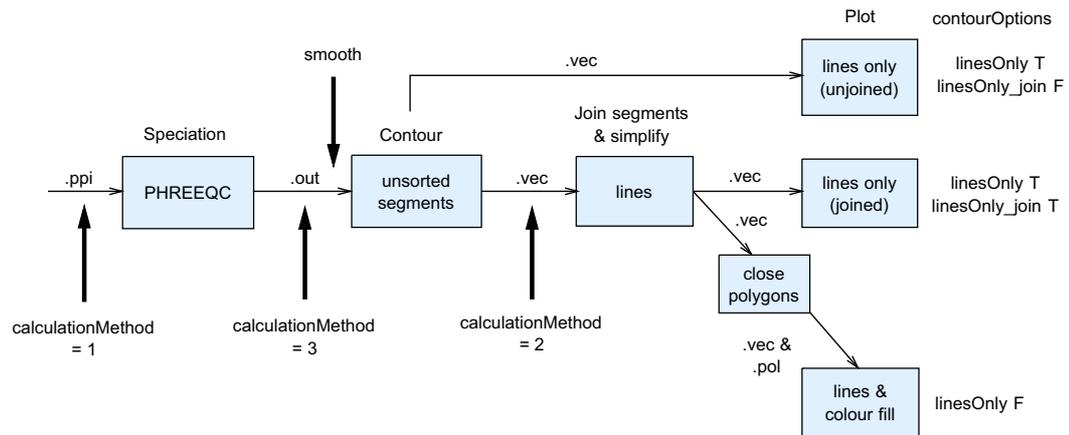


Figure 9.1. Flow of data used in generating a contour plot.

### 9.3 A SIMPLE EXAMPLE

A simple example is to gain another view of the solubility of Fe (total Fe = 1e-2 mol/kgw) in a system where the mineral  $\text{Fe}(\text{OH})_3(\text{a})$  may precipitate. This complements the predominance diagram produced by the input file `demo/Fe/hfo.ppi`. The input file would look something like:

```

SPECIATION
  calculationType          "contour"
  calculationMethod        1
  contourZvariable         FeT
  xmin                     2.0
  xmax                     12.0
  ymin                     -90.0
  ymax                     0.0
  resolution               50

PLOT
  plotTitle                "Fe solubility<br>(a) percentile contours"
  xtitle                   pH
  ytitle                   "log <i>f</i> O<sub>2</sub>(g) (atm)"
  extraText                 extratextcontour_hfo.dat

CHEMISTRY

# first simulation - fixed bits
PHASES
Fix_H+; H+ = H+; log_k 0.

SELECTED_OUTPUT
-reset FALSE
-high_precision TRUE

USER_PUNCH
-headings FeT
10 PUNCH log10(TOT("Fe"))

SOLUTION 1
  pH          1.8
  units       mol/kgw
  Fe(3)       1e-2
  Na          1e-1
  Cl          1e-1
END

# second simulation - loop on this
USE solution 1
EQUILIBRIUM_PHASES 1

```

```

Fix_H+ -<x_axis> NaOH 10
-force_equality true
O2(g) <y_axis> 0.1
Fe(OH)3(a) 0 0
END

```

The keywords controlling the appearance of the contour plot are all implicitly set at their default values as read from the `pp.set` file. The following are these default settings:

```

contours                auto 17 p
contourFillColor        auto
contourLineWidth        auto
contourLineColor        auto
contourShiftLabel       c
contourLabelSize        2
contourLabelFont        "Helvetica"
contourLabelColor       auto
contourLabelFigs        auto

```

The plotting domain is from pH 2 to pH 12 (x axis) and from -90 to 0 atm  $\log f_{\text{O}_2}(\text{g})$  (y axis) and the z-variable is defined by `FeT`. The principal task for the user is to set up the calculation of the z-data. This requires defining (a) a z-variable, here the total dissolved Fe, `FeT`, in the `USER_PUNCH` data block, and (b) a resolution, here a 50 x 50 grid.

`FeT` is calculated with:

```

USER_PUNCH
-headings FeT
10 PUNCH log10(TOT("Fe"))

```

The name of this column (`FeT`) matches that in the [contourZvariable](#) setting and this provides the necessary link. The value of the x- and y-variables are implicit and not required but these and others variables could also be exported, for example, with

```

USER_PUNCH
-headings x y FeT Fe(OH)3(a) water
10 PUNCH <x_axis>, <y_axis>, log10(TOT("Fe")), MOL("Fe(OH)3(a)"), TOT("water")

```

If this is done, then the `USER_PUNCH` data block must be moved from the first to the second simulation otherwise `<x_axis>` and `<y_axis>` will not get updated on each iteration.

The plot produced from this input file is shown in [Figure 9.2\(a\)](#). The legend has been omitted. This plot has been made with auto-generated contour values and the default colouring which ranges from dark blue (low) to dark red (high). It is possible to specify any set of contour values and any set of colours.

The main task in generating a contour plot is to decide on a set of suitable contour values. With the defaults operating, this is done by dividing the z-data into 17 approximately equally-occupied intervals. This is called the 'percentile' or 'p' option as in [Figure 9.2\(a\)](#).

The major variation in the concentration of dissolved Fe shown by the plot occurs where  $\text{Fe}(\text{OH})_3(\text{a})$  has precipitated. Under more acidic and more reducing conditions where  $\text{Fe}(\text{OH})_3(\text{a})$  does not precipitate, the concentration of dissolved Fe is necessarily very close to that added, namely  $1\text{e-}2$  mol/kgw. This results in several contours with the same truncated label (-2) since the actual contour values used (from the log file) are -2.000191900824, -2.000191868200, and so on. The small but systematic variation in Fe concentration in the absence of  $\text{Fe}(\text{OH})_3(\text{a})$  precipitation is due to small changes in the mass of water which in turn reflects various hydrolysis reactions.

A second option when auto-generating a set of contour values is to start with the percentile values and then to eliminate any values which are fairly close in value to each other (within a relative difference of less than  $1\text{e-}4$  of the z-data range). This is called the 'simplified percentile' or 's' option ([Figure 9.2\(b\)](#)).

A third auto option is to define the contours by dividing the range of z-values (maximum z - minimum z) by the number of contours, by default, 17, to give arithmetically-spaced inter-

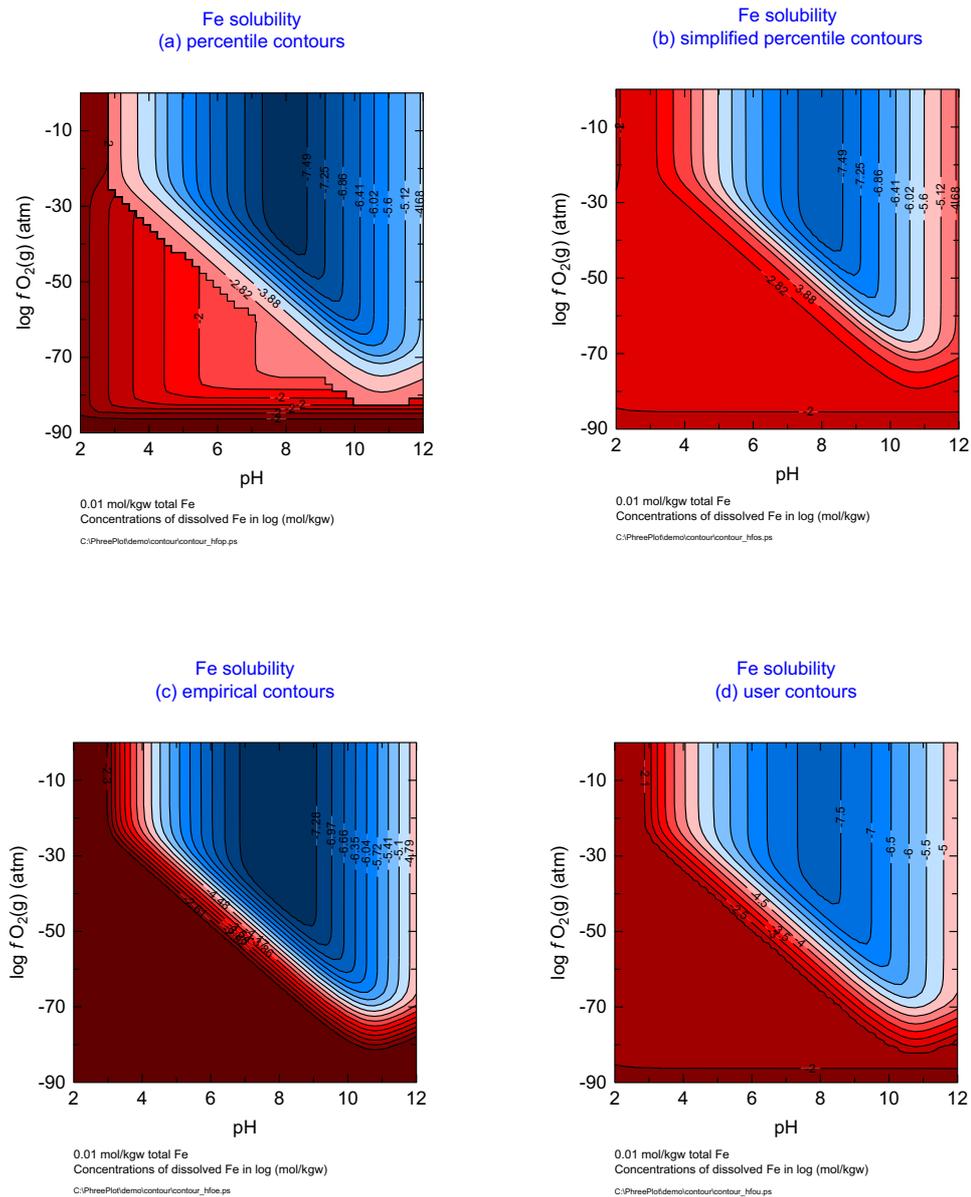


Figure 9.2. Four options for defining contour intervals for the same z-data: (a) contours ‘auto’ option with percentile contours (‘p’); (b) same with simplified percentile options (‘s’); (c) same with empirical (‘e’) option; (d) a user-supplied set of contour values.

vals. This is called the ‘empirical’ (or ‘e’) choice (Figure 9.2(c)).

Of course, a list of any number of contour values can also be entered explicitly (Figure 9.2(d)).

However derived, the set of contour values defines a set of lower class values, namely, <contour(1), contour(1)-contour(2), contour(2)-<contour(3), ... >contour(n). There will always be one more class for colour filling than the number of contours specified. Internally, an additional very large contour value is automatically added to the set of contours so that all data values will fit into one of the contour intervals defined. If a value sits exactly on a contour boundary, it is allocated to the higher class.

## 9.4 SOME DETAILS OF THE DATA PROCESSING

### 9.4.1 Algorithm

The speciation data generated by **PHREEQC** are stored in the 'out' file as normal.

These data are scanned line by line to produce the contours. The quality of the plot obviously depends on the resolution of the grid. Normally this should be 10 or greater for draft, and 50 or greater for production.

The contouring procedure, `CONREC` ([Bourke, 1987](#)), used to calculate the contour location is a 'local' one and only makes use of the enclosing four grid points. This may not be as efficient as some more sophisticated interpolation procedures but has proven to be robust given some of the extreme changes in slope and discontinuities encountered in geochemical-based contour plots.

After the z-data have been generated on the requisite grid, the domain is scanned horizontally, cell by cell, top down, and the various contour crossings established. In each cell where there is a crossing, the contour level forms a horizontal plane that intersects an inclined plane formed by the z-surface. This intersection is output as a short segment and eventually all such segments for a given contour level are joined together to form the contour. The raw contour data are treated in much the same way as in a 'ht1' plot in that the data first undergo a line simplification to reduce the number of points. The intention is to reduce the file size without substantially changing the accuracy of the plot. This can usually be achieved with a `simplify` value of 1. Smaller values will include more points, larger values, fewer points. A value of 0 will include all of the original points, i.e. no simplification.

The simplified vectors are written to the vector ('vec') file along with the boundary vectors. The individual vectors or line segments are assembled into polygons ('pol' file) for colouring. The vector and polygon files include 'direction' information – walking forward along the contour in the sequence given in the file, the high side is always on the right. This is sometimes necessary to differentiate between 'peaks' and 'holes'. The polygons are also listed (and plotted) in order of decreasing polygon area.

A given contour may give rise to more than one polygon if it leaves and enters the plotting domain more than once.

Finally, the domain boundary segments are added for each contour level to enable closed polygons to be formed and therefore for the polygons to be filled with colour.

Once these 'vec' and 'pol' files have been written, they are used to produce a plot.

### 9.4.2 Problematic cases

The contouring is normally successful but the very steep boundaries and step changes that can be produced by geochemical data, e.g. at mineral-solution boundaries, can give rise to practically convergent contours. The reverse situation can also occur: the surface can be extremely flat (and inevitably somewhat 'noisy') leading to a relatively large error in locating the contours. This can lead to 'wiggly' contours. This often happens when contour values are auto-generated with the 'percentiles' option. Judicious choice of contour values can usually reduce the impact of both of these problems.

These problems can lead to attempts to contour along a boundary that is particularly 'noisy'. This in turn can lead to an excessive amount of jumping across a contour boundary and will eventually lead to a termination of the plotting with the message:

```
"Error: too many separate contour segments. 'Noisy' contour? Try changing contour values, e.g. auto 10 e."
```

This problem can usually be avoided by changing the contour values so that the positions of the boundaries do not correspond with the noisy region, for example, as suggested by choosing a set of equally-spaced 'empirical' contour values.

A good example of this is when contouring the variation of a saturation index of a potentially precipitating mineral in a given pH-log  $f\text{O}_2(\text{g})$  domain. The saturation index will be negative over the areas where the mineral is unstable but will be zero or ‘very close to it’ where the mineral is stable. Depending on the convergence settings in **PHREEQC**, the value of ‘very close to it’ will vary but can be  $-3\text{e-}14$  to  $3\text{e-}14$  or smaller. It is entirely reasonable that the SI value can be anywhere in this range. Therefore if a contour value of 0.0 (exactly) is chosen either manually or automatically, there are likely to be an excessive number of contour crossings as the contour attempts to track the boundary.

This is made worse in this case because of the discontinuity in the slope at the mineral precipitation boundary and the fact that the change is from a fairly steep slope while undersaturated to a slope of exactly zero when the mineral is present.

In this and similar cases, setting a contour value of exactly 0.0 should be avoided. A small negative value, e.g.  $-1\text{e-}6$ , would probably avoid these problems and still identify the precipitation boundary accurately enough.

A zero (or very small) contour value is likely to be selected in this case when the auto percentile option is chosen since many of the SI values are likely to be 0.0 or very close to it. Either set the contour values manually as described above to avoid the ‘noisy’ region around 0.0 or choose the ‘empirical’ option for the auto selection of contour values which will probably avoid this region anyway.

In order to fill the contour levels with colour, it is necessary to close the polygons for filling. If **PhreePlot** fails to close a polygon, including the domain boundaries, a message to that effect is issued and only the closed polygons plotted. The problem may disappear if a different set of contours is chosen or if the resolution is increased.

## 9.5 MODIFYING THE APPEARANCE OF THE PLOT

The number of contours, their values and the overall appearance of the plot can be changed explicitly with a number of contour-related keywords. These are listed in Table 9.1 and discussed in more detail under their individual headings in [Section 14](#).

Table 9.1. Contour-related keywords

Keyword	Action	Default values
<a href="#">contours</a>	list of increasing values at which to draw contours <i>or</i> 'auto [n [p e]]' for auto-selection of contour values	'auto 15 p' = choose 15 contours with spacing based on approximately equally-spaced percentiles. Round values to three figures and remove any replicates. Could also choose the e option which spaces the n contours equally across the z-data range.
<a href="#">contourFillColor</a>	list of colours to fill contour intervals	'auto' = picks a color from a range of colours initially from dark blue to light blue to light red to dark red with other colours added as the number of classes increases up to a maximum of 100
<a href="#">contourLineWidth</a>	list of line widths of contours. Negative widths define dashed lines.	'auto' = same as main line width
<a href="#">contourLineColor</a>	list of the colours of contour lines	'auto'='black', 'red', 'blue', 'green', 'orange', 'cyan', 'magenta', 'brown', 'sky', 'purple', 'gray', 'yellow', 'maroon', 'lawn', 'spring'
<a href="#">contourShiftLabel</a>	list of labels to move and by how much	c = plot as contour values and do not move any labels from their default positions, c 1 5 +2 would shift label number 5 in plot 1 forward 2 positions. n = plot label number instead – useful for subsequently defining the shift to apply
<a href="#">contourLabelSize</a>	list of label sizes	'auto' = same as main label size
<a href="#">contourLabelFigs</a>	list of number of significant figures in labels	'auto' = depends on value but usually 3 or less
<a href="#">contourLabelFont</a>	list of fonts for labels	'auto' = same as main font
<a href="#">contourLabelColor</a>	list of colours for labels	'auto' = main label colour
<a href="#">contourOptions</a>	controls smoothing, colour fill, line drawing and the interpolation of missing data (undefined values)	smooth=0 fill=TRUE joinSegments=TRUE

In principle, apart from [contourShiftLabel](#), the lists above have a length that is equal to the number of contours + 1. A list of these contours is given in the log file. If the specified list is shorter than required, it is recycled. If it is longer, the excess is ignored.

The property associated with each contour is then simply picked off the appropriate list based on the corresponding position of the contour of interest within the list of contours.

In this way it is easy to repeat sequences of properties, e.g. if [contourLineWidth](#) 0.3 -0.3, then this would alternate a full line and a dashed line.

It is also possible to add extra text, lines and symbols with [text](#), [extraText](#) and [extraSymbolLines](#) in the normal way.

Figure 9.3(a) shows the above example plotted with user-defined contour values and default values for most of the other settings. [contourFillColor](#) has been set to 'nd' in order to give a black and white plot. This could also be achieved using the [contourOptions](#) fill=FALSE setting but in this case there would be no inline contour labels.

Figure 9.3(b) shows the same example but with some tweaking – the grid resolution has been increased from 50 to 200 to remove the 'wiggle' in the -2.10 contour, the label size has been reduced, the number of digits in the label reduced to 2 and the labels moved to increase legibility, the contour line width has been reduced and now alternates full line-dashed line with corresponding colours black-gray4. The settings were:

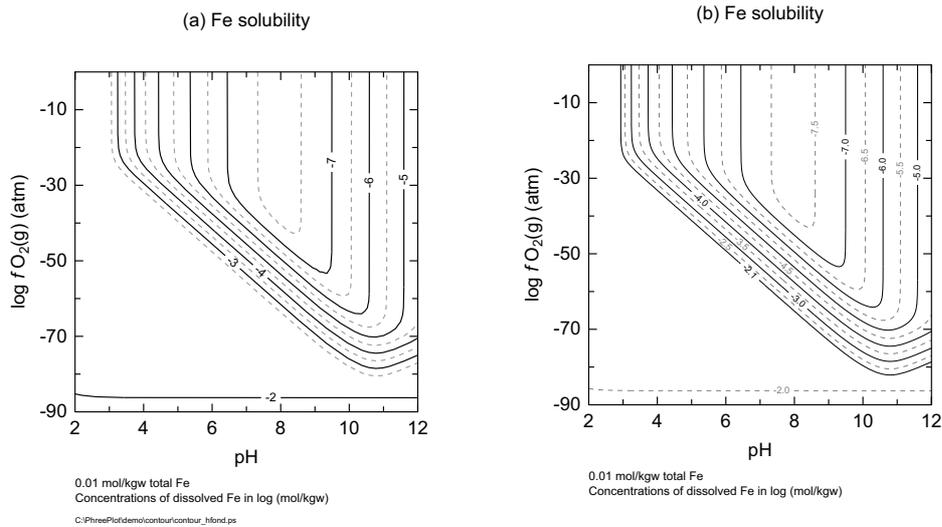


Figure 9.3. Black and white versions of the contour plot. (a) version made with a grid resolution of 50 and mainly default settings; (b) the same but with a grid resolution of 200 and minor tweaking to the plot settings.

```

resolution                200
contours                  -8 -7.5 -7 -6.5 -6 -5.5 -5 -4.5 -4 -3.5 -3 -2.5 -2.1 -2.0
contourfillcolor          nd
contourLineWidth          0.2 -0.15
contourLineColor          black gray4
contourShiftLabel         c 1 10 1 1 7 1 1 8 -1 1 12 60
contourLabelSize          1.5
contourLabelFont          "Helvetica"
contourLabelColor         black gray4
contourlabelFigs          2

```

## 9.6 REFINING A PLOT – REPLOTTING WITHOUT RECALCULATING

### 9.6.1 Where to start?

As with the predominance plots, it is possible to change various plotting parameters and to replot without going through the potentially slow process of regenerating the geochemical data. The various points of entry are shown in Figure 9.1.

[calculationMethod](#) = 1 uses **PHREEQC** to produce the ‘out’ file containing the z-grid of values based on the specified speciation calculations. It then produces the intermediate ‘vec’ and ‘pol’ data files and the plot. Since the calculations start at the beginning, any of the contouring parameters can be changed (maximum computing effort)

[calculationMethod](#) = 2 starts with the existing ‘vec’ and ‘pol’ files and uses these to generate a new plot. There is no recalculation of contours or line simplification. You can change plotting parameters including shifting the labels but not ‘calculation’ parameters such as the grid resolution or the number or values of the contour levels.

[calculationMethod](#) = 3 starts with the existing ‘out’ data file, recontours the data and regenerates the ‘vec’ and ‘pol’ files with renewed line simplification before replotting (intermediate computing effort).

Therefore, if the number or values of the contour intervals is changed or the line simplification factor altered or a different smoothing option used, it is necessary to use [calculationMethod](#) = 3 otherwise the somewhat quicker [calculationMethod](#) = 2 can be used.

If the geochemical model has changed in any way or the resolution changed, it will be necessary to regenerate the geochemical data with [calculationMethod](#) = 1.

### 9.6.2 Smoothing the z-data

A ‘low pass’ moving-average filter is available to smooth the z-data before contouring. This is invoked with one of the ‘[contourOptions](#) smooth=0’ options: `smooth=0` applies no smoothing; 1 applies N-S-E-W nearest neighbour (4) plus central cell averaging, and 2 averages all the 8 nearest neighbours plus the central cell. The smoothed data are not saved but generated internally from the raw (unsmoothed) data each time the data are plotted.

It is also possible to simplify contour boundaries with the [simplify](#) setting.

## 9.7 OVERLAPPING OR MISPLACED LABEL

One label is normally plotted for each distinct contour segment. The position of the label is normally chosen to be at the centre of the longest, ‘straightest’ part of the contour. This is derived from the output of the line simplification procedure if it has been used. Such a strategy often produces a satisfactory placement, but certainly does not always. For example, no account is taken of the spatial relationship between the various labels – they may overlap.

If this is unsatisfactory, the quickest change to make is to place the contour labels near the centre of their contour using the ‘[contourOptions](#) labelPosition=centre’.

For a given plot, the size of the contour label and its likelihood of overlapping other labels, is governed in part by the label text height ([contourLabelSize](#)) and in part by the number of digits actually printed in the label ([contourLabelFigs](#)). If **PhreePlot** thinks that there is not enough space to print a contour in the desired position, it will not be printed at all.

It is common, especially where there are rapidly changing conditions near mineral-solution boundaries, that two or more labels will overlap rendering them illegible. One strategy for dealing with this (other than changing the contour intervals or reducing the label size) is to move one or more of the offending labels with [contourShiftLabel](#), even moving them so far that they are not plotted at all. With a little effort, it should be able to derive satisfactory label positions.

A second approach is to move or nudge one or more of the labels using the [nudge](#) keyword and possibly a [nudgeFile](#).

The [contourLabelSize](#) can also be set to 0.0 or the [contourLabelColor](#) set to ‘nd’. This will suppress all labelling of this contour. However, the ‘shift’ approach is more versatile where there is more than one label per contour since it addresses individual contour labels rather than all the labels for a given contour level.

Alternatively, all labels can be suppressed with the scale relying on the legend boxes.

## 9.8 WHAT HAPPENS IF PHREEQC FAILS DURING CONTOURING CALCULATIONS?

The contouring package expects a full set of regularly-spaced data and currently cannot deal with ‘missing data’. The calculations stop and no plot is produced.

# 10 Custom plots

---

## 10.1 OVERVIEW

'Custom' plots do not have any of the intricacies of predominance diagrams or of fitting. They simply take the selected output that has accumulated from one or more **PHREEQC** simulations and make a plot using the columns of data found. The challenge is to get the results to produce a well-formed 'out' file ready for plotting.

One column has to be defined as an 'x axis' and all the other chosen columns are plotted using a common 'y axis'. A secondary y axis can be chosen if wanted. The headings given in the `SELECTED_OUTPUT` file become column labels in the normal **PHREEQC** fashion and these are used to select the column ('variable') to plot and to label it. Additional text, lines and symbols can be added to the plot through 'extra' text and data files.

The simplest approach is to use the `USER_PUNCH` keyword data block to only send the results that need plotting, or at least, to ensure that these results are the last thing written following any output from any initial solution etc calculations. If the problem is similar to one of the examples given here, use the example as a template to get started.

Keep it simple to begin with, and use the log file with `debug = 2` to take a close look at what is being done. Decide which calculations can be put into pre-loop simulations and which belong best to the main loop.

A loop file provides a flexible way of defining variables if more than one is wanted since the variables do not have to increment in any particular way, and any number of variables can be made to change 'in parallel'. Each row in the loop file results in a separate iteration. The results are accumulated in the 'out' file which can be used to produce a custom plot. Data from pre-existing 'out' files (or other files with a similar tabular format) can be imported and added to the plot.

If no `SELECTED_OUTPUT` file is created or the `plotFactor` is set to zero or `calculationMethod` is negative, then no plot will be created. Therefore custom-type plots can be used to do **PHREEQC** type calculations in the normal way without any plotting. **PhreePlot** has the advantage that it is possible to do some simple looping and so generate a stream of output suitable for viewing or for input to other software. For example, it is possible to accumulate all of the normal **PHREEQC** output from a series of runs in the `*.all` file (see [Example 71](#)).

## 10.2 PREPARATION OF THE INPUT FILE

### 10.2.1 Introduction

Custom plots are used for all x-y plots other than predominance plots. This includes species plots and fit plots.

A custom plot calculation normally expects **PHREEQC** to produce selected output data with an x-variable in the column defined by `customXcolumn`, and `y1...yn-1` in the other columns where `n=no. of columns`. Data for plotting are selected from these columns using the `lines` and `points` keywords.

The 'out' file is the primary file used for plotting but additional files can be included by using the `extradat` keyword. The specified `customXcolumn` must be present in each file.

Selected data are copied from the main selected output to the 'out' file. Normally this will be

just the last line that is copied but more lines can be transferred using the [selectedOutputLines](#) keyword. **PhreePlot** gets the label names from the selected output header line. Only the first 198 characters will be used to define tag names.

The **PHREEQC** headings identifier which should be included as part of the `SELECTED_OUTPUT` data block has the format

```
-headings xxxx xxxx ...
```

where `xxxx` should not contain whitespace (spaces or tabs) or `\` or `/`. Commas are not required as separators and so should not be included.

Values transferred with the value [missingValue](#) are treated as missing data.

If no data are found within the plot area, the label is printed in the legend but no entry is sent to the `lineColor.dat` file and no label is plotted on the graph.

The size of the legend labels is controlled by [labelSize](#) – the same setting as used for the labels. If a species appears in the legend but is not shown on the plot, this is because it is not found within the plot area.

Labels are taken from the names of column headers as sent from **PHREEQC** to the selected output using the header identifier: The labels are by default interpreted as **PHREEQC** species and formatted accordingly (see [Section 6.4.2](#)). This behaviour can be overridden with the [convertLabels](#) keyword. In order to avoid generating situations such as `<sub>.<sub>...</sub>.</sub>`, no attempt will be made to translate column headers if they contain `<sub>` or `<sup>` before translation.

The position of labels can be adjusted using ‘[nudge](#)’ or a ‘[nudge file](#)’.

The `<x_axis>` increment is controlled by [xmin](#), [xmax](#) and [resolution](#).

### 10.2.2 Controlling the scope of custom plots

Execution of custom plots is controlled by:

[xmin](#), [xmax](#) etc controls the x-axis scope.

[ymin](#), [ymax](#) does not matter as y is calculated

[loopMin](#), [loopMax](#) and [loopInt](#) are used as an additional loop variable (the z-dimension) by the `<loop> t1.inc`.

If [loopInt](#)=0., then only one circuit round the loop is made. This uses `<loop>=loopMin`. This is useful for checking the input file for a specific setting. Alternatively the `<loop>` variable can be omitted from the `CHEMISTRY` section which will then only run through the loop once assuming the normal default settings.

## 10.3 SIMPLE LOOPING

One use of a custom plot procedure is to simply loop on a calculation many times changing one or more variables on each iteration. It is not necessary to actually produce a plot. This is something that can be awkward to do in **PHREEQC** at present. The `PHREEQC_looping\Fespecies` demo example ([Example 71](#)) shows how this can be done. The input file looks like this:

```
SPECIATION
  calculationType          "custom"
  calculationMethod        -1
  xmin                     -10.0
  xmax                     -4.0
  resolution               3
  all                      T

CHEMISTRY
PRINT
  -reset false # don't output initial solution calculation
```

```

PHASES
Fix_H+
  H+ = H+
  log_k 0
SOLUTION 1
  pH      2
  units   mol/kgw
  Fe      1e-2
  Na      1e-1
  Cl      1e-1
# no reaction so no need to SAVE solution 1
END

USE solution 1
PRINT
  -equilibrium_phases true
  -species TRUE
EQUILIBRIUM_PHASES
  Fe(OH)3(a) 0 0
  Fix_H+ <x_axis> NaOH
  -force_equality true
END

```

where the pH is controlled by the `<x_axis>` tag which is generated from [xmin](#), [xmax](#) and [resolution](#). **PHREEQC** will be run [resolution](#) times with the values -10, -6 and -4 being substituted in turn for the `<x_axis>` tag.

The **PHREEQC** code is split into two simulations, an initialization (pre-loop) simulation and a second iteration which is the one that is iterated.

[all](#) is set to `T` so as to create the `*.all` file which contains the accumulated `PHREEQC.[id].out` output from all iterations. All of the normal **PHREEQC** output is first turned off with `-reset false` and then the species output is turned on to minimize the file size.

The [calculationMethod](#) is set to -1 so as not to produce a plot. No selected output is produced.

It is also possible to use a loop file to provide the successive values of the loop variable(s) (see [loopFile](#)). Another approach is to use the 'simulate' plot type which takes loop values from a fit data file.

One of the challenges of running custom calculations for more complex examples is to ensure that a 'well-formed' outfile is produced so that any plotting that is needed produces the desired results. This can usually be achieved by splitting the **PHREEQC** input part into the 'correct' number of simulations (using `END`'s), using [mainLoop](#) to define the divide between pre-loop and main loop simulations thereby controlling the looping and selected output from these simulations, and finally using [selectedOutputLines](#) to control the number of lines (rows) of data sent to the 'out' file ([Section 4.6](#)).

## 10.4 CALCULATING SPECIATION ON A 2-D GRID

Although the 'grid' approach to calculating predominance diagrams and the 'contour' method both calculate speciation on a grid, they go on to do other things. The most straightforward way to simply calculate speciation on a 2-D grid is to use the 'custom' method with the x-axis and y-axis parameters both defined. Use `SELECTED_OUTPUT` and `USER_PUNCH` to define what you want output. These will then be written to the 'out' file.

## 10.5 MODIFYING THE APPEARANCE OF CUSTOM PLOTS

### 10.5.1 Overview

Many of the keywords can be used to control the appearance of the final plot (Figure 10.1).

Axis scaling can either be 'auto' or can be forced using keywords such as [pxmin](#), [pxmax](#) etc.

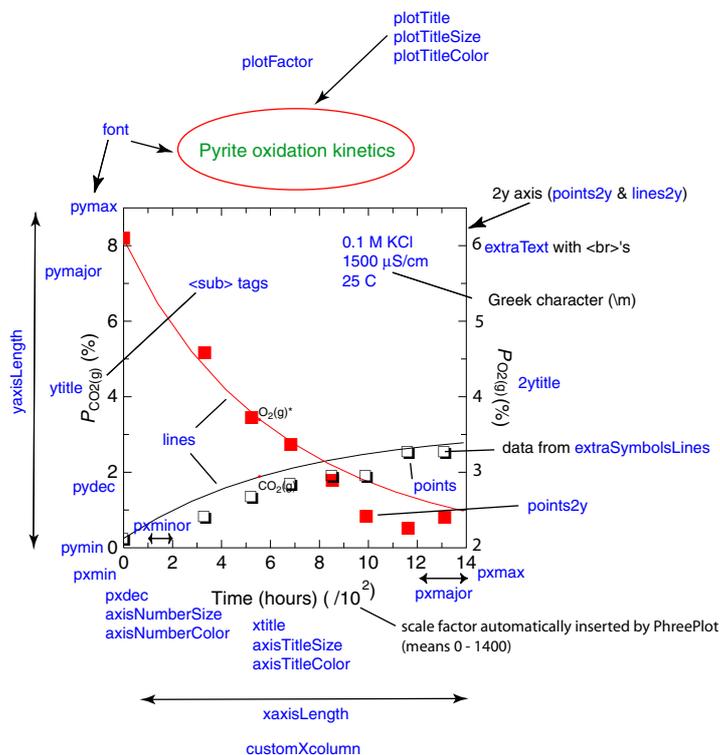
Note the use of the x-axis scale factor, a dividing factor, which is automatically used by

**PhreePlot** for very small or large numbers. Since this approach always produces some confusion, it is usually better to avoid the problem altogether by rescaling (changing units) in the selected output to bring the scale somewhere in the range  $1e-3$  to  $1e3$ .

A second, independent y-axis scale can be used for the right-hand y axis. Point and lines that use this scale are specified with [points2y](#) and [lines2y](#) in the same way as for [points](#) and [lines](#).

[Tags](#) can be used to give super and subscripted text, italics, bold or line breaks. Single Greek characters can be entered with the `\letter` notation or more generally Greek text can be added with `<g> ... </g>` ([Section 7.6.3](#)).

Additional data from other files can be added to the plot using the [points](#) and [lines](#) keywords combined with the [extradat](#) keyword to add the additional files to the search path. These data must be in regular tabular output format. [extraSymbolsLines](#) can be used where more control is wanted over the symbols used or the line widths.



Figure

### 10.5.2 Customising the plot

Providing [legendTextSize](#) is greater than zero, the default is to print a simple legend just outside of the plot area close to the top right corner of the plot. This legend provides a key for the plotted lines and symbols. The position of the legend can be moved inside or outside the plot area using the `<legend>` tag in a `text` line or `extraText` file. `auto` for `x` or `y` coordinate position chooses the default value.

The labels associated with each item in the legend are derived in various ways. Most simply they are generated from the column names in the plot data file from which the plotted data were derived. Often these are derived from the 'out' file which is automatically generated from the **PHREEQC** selected output. The labels appear in column output order which itself is determined by the `PUNCH` order. The data and labels used can also be derived from another file provided it is in the tabular out file format and that it is defined in the search path given by

[extradat](#).

Where there are completely blank lines in the plot data file, these generate line breaks and each line is labelled separately in the legend. Consecutive blank lines count as a single break. Comment lines do not produce breaks. By default, the column name is appended with “\_n” where n starts at 1 and increments by 1 for successive datasets.

These names can be replaced with your own names by using the [labels](#) keyword. This provides a list, one name for each successive value of the loop variable. This list is recycled as needed, or names can be read from a loop file or from the plot data file used in simulations and fitting. If only one loop name is given, then the plot data file providing the data plotted is searched to see if this name appears as a column label. If it does, then this column is used to provide the legend label for that dataset. Since only one name is needed per dataset, this is taken from the first row of each dataset. Variable values can also be ‘posted’ next to plotted points using the [post](#) keyword.

A legend is automatically placed to the right of a plot if the [legendTextSize](#) is greater than zero. It is also often useful to include a heading for the legend. This can be done using the [legendTitle](#) keyword or the [<legend>](#) approach in the [text](#) keyword which can also be used to move the legend to somewhere else or resize the text. Any text in the text string that precedes [<legend>](#) is used as the legend title. This can include text enhancement tags and line breaks. If a dataset has the ‘nd’ colour then that dataset will not be drawn and no entry in the legend will be made.

Line and point colouring can either be left to **PhreePlot** or defined in the line colour dictionary. Line curves are automatically labelled if [labelSize](#) is greater than zero and the [labelColor](#) is not ‘nd’. When there are many overlapping lines finding the ‘optimal’ label placement can be slow. The optimization can be turned off by reducing [labelEffort](#) to zero. Label positions can be micro-adjusted using ‘[nudge](#)’ or a ‘[nudge file](#)’. A red ‘tracking’ symbol is used to show the label anchors. These can be turned off by setting [trackSymbolSize](#) to zero.



# 11 Species plots

## 11.1 WHAT IS SPECIAL ABOUT A 'SPECIES' PLOT?

A 'species' plot is a special type of custom plot which shows the distribution of species for a particular element in terms of their concentration or percentage distribution versus some master variable, such as pH. The element is specified with the `mainspecies` keyword. The percentage is calculated in terms of the moles of an element in a given species as a percentage of the total number of moles of that element present in all species.

Often the `mainspecies` is a chemical element such as 'Fe' but there are a number of special 'mainspecies': (i) "elements", 'phases', 'aq', 'equi', 'ex', 'kin', 'surf', 's\_s' and 'gas' which return subsets of the system (see the `SYS()` function in 'The Basic interpreter' section of the **PHREEQC** guide for details of each of these subsets); (ii) 'all' which will plot the percentages or concentrations of all species for all elements. These options provide considerable flexibility in the subsets of species included.

Two common types of species plots are shown in Figure 11.1 and discussed in more detail in the Examples section ([Example 73](#) and [Example 74](#))

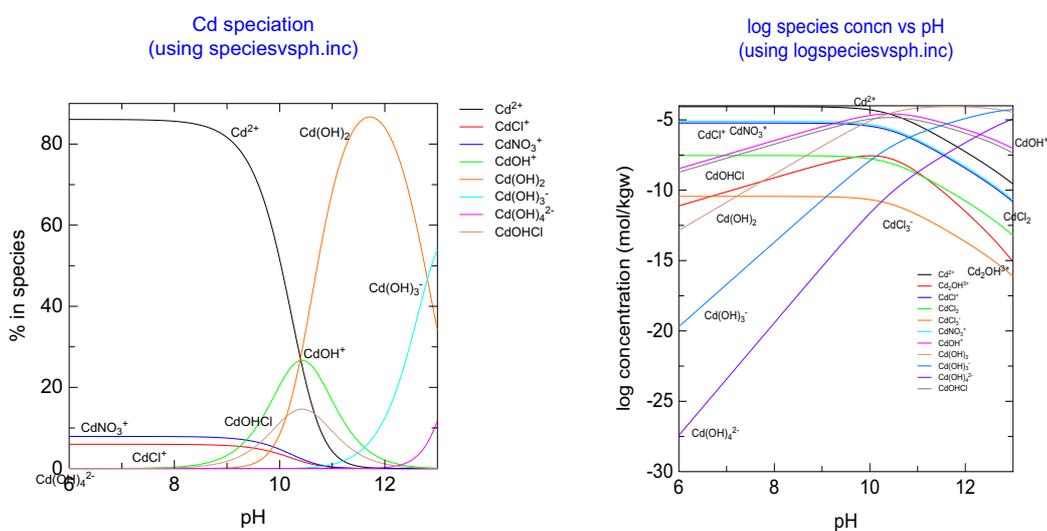


Figure 11.1. Two common types of species plots produced using the 'species' method showing the distribution of Cd species with pH. The two plots use different 'include' files to generate the selected output.

A species vs pH plot is obtained by setting `calculationType` to 'species' and by including one of the special 'include' files in the `CHEMISTRY` section. An example of using the 'speciesvsph.inc' include file is given in Figure 11.1 (left). The 'logspeciesvsph.inc' file is used to generate a plot of log species concentrations vs pH (Figure 11.1, right). These files can be edited to filter out unwanted species – H and O species which normally dominate aqueous systems are filtered out by default.

It was necessary to make the species plot a special type of custom plot since **PHREEQC** cannot automatically generate a set of heading names (column titles) at run time to correspond with the species found. Therefore it is necessary to write the species name to the selected out-

put file along with each value. Furthermore, the `SYS()` function that is used to extract the set of species present and their concentrations is written to the selected output file in order sorted by concentration rather than sorted alphabetically. This means that the sort order is likely to vary and must be reordered to enable species distribution curves to be plotted.

The ‘species’ method expects a specific type of input to be returned in the selected output. This consists of a series of species name-value pairs. The species names are used for the labels while the values are plotted. The [customXcolumn](#) should be set to the column where the x-axis variable is located. The other pairs of columns are assumed to contain y-values (species percentages or concentrations) to be plotted. For example, if the x-axis variable is PUNCH’ed first, then the [customXcolumn](#) would be set to 2 and the default name of the x axis is taken from the name given in column 1. The remaining columns are the names-species pairs to plot.

Six [include files](#) for making species plots are included in the system directory. These are for analysing solution species or adsorbed species and report in either relative concentrations (%) or in absolute concentrations (mol/kgw), see Table 11.1. The files can easily be edited to customise their behaviour. For example, instead of pH as the independent variable, other variables can be chosen, or the files can be edited to exclude various species from the plot.

Table 11.1. The two standard include files used for generating species plots

Name of file	Purpose
speciesvsph.inc	<mainspecies> specifies the ‘element’, or ‘elements’, to analyse, e.g. “Cd” or “aq”, “phases”, “elements”, “surf”, “s_s”, “gas”, “all” for all species for a specific element or aqueous, solid, etc species. Output is in terms of the relative concentration (in %) of all species, including minerals and adsorbed phases, containing the main element vs pH. If the <mainspecies> is “elements” then the analysis is done at the element level for all elements.
logspeciesvsph.inc	As for speciesvsph.inc but the output is in terms of the $\log_{10}$ (mol/kgw) concentration of each species.

These files pick up the main species from the [mainspecies](#) setting and use the `SYS()` function to obtain a list of the species present for this ‘element’ and their amounts (in moles). These are then either converted to percentages of the total amount present or converted to log concentrations and punched in name-value pairs to the `SELECTED_OUTPUT` file which, in turn, is copied to the [out](#) file, one row per pH.

There can be more than one main species. A separate plot is produced for each.

The column headings in the ‘out’ file are those given by **PHREEQC** for unnamed columns, namely, `no_heading_1` for column 1 and so on. The species are written to the ‘out’ file starting with the most abundant species followed by all the other species in order of decreasing abundance. The order of the species written will tend to vary with chemistry of the system.

A sorted table of the speciation results is written to the [pts](#) file if the ‘pts’ setting has been set to `TRUE` (the default) in one of the main input files. This can be used for plotting the results with other software or with the [lines](#) or [points](#) keywords. The appearance of these lines (dashes and dots) and points (type of symbol, size) can be set with the associated settings such as [lineType](#), [dashesPerInch](#), [pointType](#), [pointSize](#), [rimColor](#), and colors with the line color dictionary and the [useLineColorDictionary](#) setting. [colorModel](#) can be used to vary between a coloured and black and white plot.

**PhreePlot** automatically displays the distribution of all species as lines. No [lines](#) keyword is required in the input file. The colour of the lines drawn is determined by the normal line colouring algorithm, i.e. using auto colour selection or the line colour dictionary depending on the [useLineColorDictionary](#) setting. The line width is controlled by the [lineWidth](#) setting. The [minimumYValueForPlotting](#) setting is useful to remove minor species from the plot.

If [mainspecies](#) is set to “elements”, the distribution is over the total concentrations of all dis-

solved elements and valence states (solution master species) in the system rather than for the concentrations of all species of a particular element.

The ‘adsorbed’ option considers the distribution of adsorbed species vs pH either for just one element or of all elements, as determined by the [mainspecies](#) setting.

A list of main species can also be specified to give multiple plots. The [multipageFile](#) setting controls whether all the ps and pdf plots produced will be combined into one file or not.

If the main species is set to ‘all’, then the percentages or log concentrations of all species of all elements is plotted (with the exception of certain species including water - see the Basic code in `speciesvsph.inc` and `logspeciesvsph.inc`). Percentages are calculated as the percentage of the total amount of the main ‘element’ being considered (calculated with the `SYS()` function). It is possible to filter out other unwanted species by modifying the Basic code in the `*.inc` files.

Much the same effect can be achieved using an ordinary custom plot but here the sorting has to be done with BASIC code in the `USER_PUNCH` block ([Example 60](#)).

The ‘species’ calculation method discussed above can be modified to plot a variety of things providing the selected output is set up to produce a fixed set of name-value pairs.

Note that in Figure 11.1 (left) the curves for several minor species have been omitted for clarity. This was achieved by setting [minimumYValueForPlotting](#) to a value of 5. Only curves with a maximum value exceeding 5% are plotted.

If the x-axis variable wanted is not pH but some other variable then it is straightforward to edit the include files to ensure that the required variable is the first one to be punched to the selected output, and to associate [customXcolumn](#) with it.

It is possible to make multiple plots by using the loop variable.

## 11.2 MODIFYING THE APPEARANCE OF SPECIES PLOTS

If the default x-axis title for a species plot is set to ‘auto’ then the x-axis title is set to the name of the `customXcolumn`, e.g. “pH” and that for the y-axis title is either “% in species” for a linear scale plot or “log concentration (mol/kgw)” when a log scale has been inferred, i.e. when [minimumYValueForPlotting](#) is less than or equal to zero and there are no 2y axis variables to plot. The plot title is automatically set to “Distribution of <mainspecies> with pH”. All of these defaults can be overridden from the input files.

Species plots are produced with the custom plot procedure and so all the same keyword settings discussed for custom plots apply. Many of these are illustrated in Figure 11.2.

Points can be automatically added to all the plotted lines by setting [points](#) to ‘auto’. Point attributes are determined in the normal way.

There can be a bewildering array of lines in species plots and it may help if the labelling is coloured as well as the lines. This can be achieved by setting [labelColor](#) to ‘auto’. Lines and labels will then have the same colour in both plot and legend.

## 11.3 ADDING OTHER VARIABLES TO A SPECIES PLOT

It is possible to plot other variables on a species plot.

Add any additional variables to the list of `PUNCH`’ed items in the `speciesvsph.inc` file. They can be added anywhere providing the x-column remains the first to be `PUNCH`’ed. Normally, they would be added before or after the actual species have been `PUNCH`’ed. This makes sure that they will be included in the outfile. Thereafter they are treated as if they are ordinary species, i.e. they will be plotted on the main y axis.

The column names in the outfile from a species plot will be in pairs beginning `no_heading_1`, `no_heading_2` . . . . for the most abundant species followed by the other species in order of decreasing abundance.

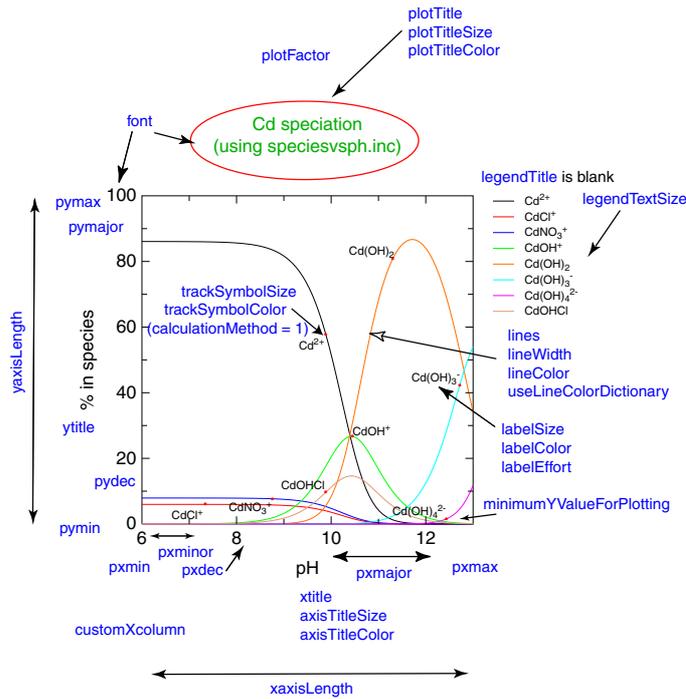


Figure 11.2. Some of the keywords used to control the appearance of custom plots.

For species type plots, a table with fixed column positions is required. This is given in the 'pts' file. This file is automatically added to the search path and so the indicated species can be plotted with the [lines](#) or [points](#) settings.

# 12 Fitting and simulations

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## 12.1 INTRODUCTION AND CHOICE OF ALGORITHMS

Calibrating models is a key part of modelling but can be rather daunting in the beginning. Fitting with **PhreePlot** definitely belongs to the ‘advanced’ category of tasks. You have to get quite a few things working correctly together to be successful and while it would be nice to have a ‘fire-and-forget’ approach for this, it is rarely that straightforward.

The setup for fitting is very flexible. Each observation can be simulated using either the same block of **PHREEQC** simulations (containing variable tags) or a different block of simulations as specified in the fit data file. This enables different models to be applied to different observations – a form of ‘global’ optimization. For example, several ‘metals’ could be fitted to a similar model, or each ‘metal’ could be fitted to a different model, at the same time. It is also possible to globally fit parameters by combining data from potentiometric titrations for proton binding with sorption data for metal binding, for example.

The overriding principle is that each line in a fit data file corresponds with an observation and that these must be paired one-to-one with corresponding calculated values in the ‘out’ file. Then there must therefore be ways of defining how to calculate the expected values for each observation and of weighting the various observations, or more specifically, the residuals.

**PhreePlot** includes a number of easy-to-use optimization algorithms that can be used to fit models to data, i.e. they automatically adjust a set of parameter values defined in a **PHREEQC** input file to their optimal values based on a set of observations (data) and an objective function to provide a measure of the overall goodness of fit. The objective function used here for this is the weighted sum of squares of the residuals.

The algorithm to be used is chosen with [fitMethod](#). The five optimizers currently available are:

(i) ‘`nlls`’: this modified Levenberg-Marquadt procedure is described in [Powell \(1965\)](#). The version used here is based on the **VA05** routine from the Harwell Subroutine Library ([HSL](#)) Archive;

(ii) ‘`lm`’: the Levenberg-Marquadt procedure as implemented in the **MINPACK-1** package by [More, Garbow and Hillstrome](#). It uses a forward difference method for approximating the Jacobian.

(iii) ‘`newuoa`’ (NEW Unconstrained Optimization Algorithm): this is not specifically a least squares optimizer although it is used here as such. **NEWUOA** is a general-purpose optimizer that uses a quadratic model to approximate the objective function in a ‘trust region’ ([Powell, 2007](#)). The ‘trust region’ is a restricted part of the objective function in which the quadratic approximation is ‘trusted’ to be correct. This region is progressively enlarged as the approximation improves. **NEWUOA** is robust and has proven to be capable of dealing with a large number, i.e. hundreds, of adjustable parameters. It has been largely superseded by **BOBYQA**.

(iv) ‘`bobyqa`’ (Bound Optimization BY Quadratic Approximation): **BOBYQA** is similar to **NEWUOA** except that it allows lower and upper bounds to be specified for each adjustable parameter ([Powell, 2009](#)).

(v) ‘`subplx`’ (Simplex algorithm which searches in subspaces) by [Rowan \(1990\)](#) is a generalization of the Nelder-Mead simplex method. It is said to be well-suited for situations in which the functions are noisy and discontinuous at the solution.

A list of these methods can be given to [fitMethod](#) and then the methods will be run sequentially on the same data set with all settings the same (although some parameters may take on somewhat different meanings since the convergence criteria used by the various algorithms may differ).

All of these methods are derivative-free meaning that you do not need to provide functions to calculate the derivatives. This makes the fitting of new models much easier – and even possible – but there is a penalty in terms of speed of execution and more importantly, stability. When numerical derivatives are themselves calculated from a numerical model which itself carries estimation errors, as all **PHREEQC** calculations do, care has to be taken to ensure that the derivatives are obtained with sufficient accuracy to be useful. In most of the above implementations, this is largely outside of the control of the user but can be controlled to some extent by the convergence criterion chosen and with the ‘nlls’ optimizer by the [fitFiniteDiffStepSize](#) parameter.

The parameters to be optimised, and the independent variables used, are identified using tags defined by the user and placed in the **PHREEQC** input code of the Chemistry section of the main input file. The adjustable parameters are each systematically varied in such a way as to find the minimum value of the objective function. This should correspond with an optimal fit between calculated and observed values of the dependent variable(s) taking into account the weight assigned to each observation.

Weighting options are: unit weighting (all weights are automatically assigned a value of 1), relative weighting (weights are 1/observed value), or the weights for each observation can be read from the data file.

The calculations can be run either in simulation (‘simulate’) or fitting (‘fit’) mode. ‘Simulations’ ([calculationType](#) ‘simulate’) in the present context mean using the same setup as a fit input file but only calculating the ‘dependent’ variable once for each observation rather than using these values to refine the values of the adjustable parameters. This is useful to get some idea of what results the initial set of parameter values will give.

The simulation mode is also useful where a particular **PHREEQC** input file is wanted to be run with various sets of parameter values or variables (sometimes called ‘independent variables’). These values can be entered in the ‘data file’ and picked up from there with each row in the data file corresponding to a separate simulation. The headings of the data file are used to generate tag names. The corresponding tags are used to mark the position of a substitution in the input file.

If the number of degrees of freedom in a fit file is 0, i.e. there are the same number of adjustable parameters as data points, then least squares optimization is not appropriate as there is an exact solution. **PhreePlot** assumes that the problem is then one of ‘root finding’ and will attempt to find the solution by iteration. This also applies when no data file is given, i.e. the fit data file name is blank. In this case, the ‘target’ value(s) is/are automatically set to zero.

## 12.2 FITTING IS SPECIAL

Fitting includes its own form of looping and is outside the normal looping built into **PhreePlot**. So the x-, y-, z (loop) and mainspecies loops do not operate. And as described below, the way that it treats multi-simulation input files is also different from normal. The division between pre-loop simulations and main loop simulations is based on a subset of simulations, potentially unique to each data point, rather than the whole set of simulations. This provides maximum flexibility in the way that different types of data can be globally optimized.

## 12.3 APPROACH TO FITTING

There are two distinct components to fitting:

- (i) defining the objective function, i.e. defining what is to be minimized subject to any constraints

on the values that the function variables ('adjustable parameters') may take. Here we use a sum of squares of the weighted residuals. Other functions are possible;

- (ii) adjusting the given set of variables in such a way as to locate an acceptable minimum value of the objective function;

Given (i), the challenge of (ii) is simply defined but finding fast and reliable approaches has exercised numerical analysts for a long time. All optimizers should in principle converge to the same minimum given the same (i).

In our case, the objective function itself consists of three components:

- (i) the chemical model used to calculate the value of the dependent variable(s);
- (ii) the corresponding observations of the dependent variable(s);
- (iii) the weighting applied to each observation or more particularly to the residuals (the difference between (i) and (ii)) for each observation.

Again, given a well-defined chemical model (including the thermodynamic database) and the same weighting scheme, all fitting programs should in principle converge to the same final solution – the 'best' fit. This can be tested by comparing the values of the fitted parameters and the individual residuals. The relative degree of success of fitting by various procedures can be judged by a measure of the overall 'goodness of fit' such as the root mean square error (RMSE) or coefficient of determination ( $R^2$ ). The aim is that the fit should at least be better than assuming the mean value of the dependent variable throughout – it can of course be worse giving an at first seemingly improbable negative  $R^2$ .

Ultimately, the details of exactly how the model calculated the individual contributions to the objective function should make no difference. It is assumed that this has been done reliably, though of course this is a critical assumption, and is itself a measure of model quality.

Pitfalls in the fitting involve converging to a local not a global minimum, and not finding a unique minimum perhaps because of two or more highly correlated variables. The latter situation leads to the optimiser 'wandering along a long flat valley bottom' and is a sign of an over-parameterised model. This does not mean that the model is wrong, just that there are insufficient data to uniquely define all variables. The usual solution to this is to reduce the number of variables by fixing one or more of the variables at an acceptable value, or by adding one or more constraints on the values that the variables can take ('constrained optimization').

## 12.4 PRACTICAL SETUP

### 12.4.1 Approach

It is helpful to break down the overall task into several more manageable sub-tasks:

#### 1. Organise your data

A file needs to be made containing the data ('observations') that are to be fitted. This should be an ASCII-coded flat file. It can be easily prepared in a spreadsheet and exported in tab or csv format. It should have one line per observation with columns which include all the independent variables. The first line should be a header containing the column labels – keep these simple by avoiding spaces and other special characters, e.g. use only upper and lowercase characters, numbers, the dollar sign ('\$') and the underscore ('\_'). The data should start on the second valid line (not counting comments and blank lines). Columns can contain either numeric or character data (not mixed within a column). By default, all columns are assumed to be numeric. If the last character of a column label is a dollar sign, then that column is assumed to be a character column. If a variable in this second line was assumed to be numeric but a character (non-numeric) value is found in the first data line, then the whole column will be assumed to be character. If necessary, rearrange the order of rows or insert a dummy 'format' line to make sure that this is so. Also decide which data separator(s) is (are) to

be used and tell **PhreePlot** either with the [dataSeparators](#) keyword or with the optional second parameter of the [dataFile](#) keyword. Beware of tabs and other ‘invisible’ characters in your data file. If you want multiple consecutive tabs to signify missing data set the data separator explicitly to “\t” although a complete line of tabs with no other characters is always treated as a blank line. If you want tabs and spaces to be treated equally, and multiple tabs and spaces to be treated as a single separator, use “\ ”. This is often an appropriate option.

If additional lines need to be included but not used in the calculations, turn them into comments by making the first non-blank character a hash (#).

When reading entries, quotes are stripped from the entry and the entry is then read as numeric or character according to the format established above. Non-numeric values are assumed to be character. Quotes alone do not define a character value, e.g. “1.23”, “4.56”, ... will be interpreted as valid numeric values.

Empty fields are given the [missingValue](#) if the column is designated numeric or as the empty string (“”) if designated character. An ‘NA’ in a numeric field is also given the missing value. The missing value is treated as a valid value in calculations unless it is assigned the value of UNDEFINED (-99999) in an input file. The default missing value is set as UNDEFINED.

If fitting, you will need to decide how you want to weight the observations and if necessary include a ‘weights’ column.

## 2. *Get the chemical model working*

Each observation is associated with a block of simulations, i.e. a contiguous set of **PHREEQC** simulations. Each observation can refer to the same block of simulations (with some tag(s) within the block varying the actual code for each observation) or each observation can have its own distinct block of simulations, or anywhere between these two extremes. This enables global optimization – fitting essentially unrelated datasets/models all at the same time.

Each block is split into two parts:

- (i) zero or more pre-loop simulations
- (ii) one or more main loop simulations.

All the pre-loop simulations for all the specified blocks are run sequentially just once per run before the fitting proper begins. This enables static code such as loading databases or preparing solutions to be executed just once. Where the model is similar for all observations, it is often convenient to associate pre-loop simulations with just the first observation. The blocks of code for each observation and the pre-loop/main loop division are specified along with the observations using the [blockRangeColumn](#) and [main-LoopColumn](#) in the fit data file as described below.

Each observation and its block of **PHREEQC** code will include tags specifying the independent variables and will ultimately output the value of the dependent variable in a `USER_PUNCH` keyword block. Each block of code will therefore usually contain at least the `SOLUTION` and `USER_PUNCH` keyword blocks. Check that the code is working properly by checking the calculation for a single point. It might be convenient to develop this using **PHREEQCi** after manually substituting the tags with reasonable values. The column headings defined in the `USER_PUNCH` data block are used to name the columns in the output files (and so can be used for identifying which columns to use for plotting) as well as for telling **PhreePlot** where to expect the calculated value of the dependent variable. Columns can be referred to by column name or column number.

If debug is set to 2, then a table showing the **PHREEQC** simulations that are executed as pre-loop and main loop simulations is sent to the log file. This contains an entry for each observation.

## 3. *Make up the PhreePlot input file*

If possible, choose an existing input file of a similar fitting problem as a template and edit accordingly. This will remind you of the parameters that need to be considered. You will need to define the name of the data file ([dataFile](#)), the column in that file containing the observations ([dependentVariableColumnObs](#)) and the column in the selected output file containing the value of the dependent variable ([dependentVariableColumnCalc](#)). Each column in the data file is converted into a tag which can be used in the **PHREEQC** model code to indicate where a substitution needs to be made.

Decide which fitting algorithm to use ([fitMethod](#)) and which variables need to be defined as model parameters – usually this is all the parameters that may need to be adjusted at some stage – and define the model names and other parameter switches accordingly ([numberOfFitParameters](#), [fitParameterNames](#), [fitAdjustableParameters](#)). The [numberOfFitParameters](#) should be set to the number of distinct parameters specified by tags in the input file – it should include both fixed and adjustable parameters. Set the initial parameter values for all parameters ([fitParameterValues](#)) and the bounds on these parameters if appropriate. It is important that this combination of parameter values works so if necessary check with **PHREEQC** or by other means. You may have to fine tune some of the fitting algorithm's operational settings controlling such things as the step size, the maximum number of iterations etc. Finally decide what the most diagnostic plot will be and define [customXcolumn](#) and [points](#) accordingly. Any columns defined in the 'pts' file can be used for plotting including the automatically-generated 'observed', 'calculated' and 'residuals' columns. Refinements include adding extra text ([text](#) or [extraText](#)) and labelling individual points using [post](#).

Each data point will have to be associated with a block of one or simulations which will be used to calculate the fitted value for that observation. It is best to (a) identify all 'constant' **PHREEQC** blocks, i.e. those blocks that are always the same and do not change – these can be put in a pre-loop simulation; (b) identify all **PHREEQC** blocks that are constant for all observations (data points) but which may vary during fitting – these can be included in the simulation for observation 1; (c) identify the simulation or range of simulations that will be used for each observation – these should mainly contain non-constant data blocks, i.e. those containing a tag that will vary. This can include extra simulations too.

For maximum speed, in step (c) above, associate all of the observations with the same range of simulations, e.g. 2-11 and use the `onePass TRUE` option. This means that all the simulations will be calculated in a single call to **PHREEQC**.

#### 4. Run the file

Run the file using `debug = 2` or `3` if necessary. You may need to adjust some of the fitting parameters particularly [fitFiniteDiffStepSize](#). The R2 value is a guide to how well the model is actually fitting the data. If the model seems to be running properly but **PhreePlot** refuses to adjust the adjustable values, check the model and data carefully, e.g. by looking at the table of observed and calculated values near the end of the log file. This type of failure is usually because the model cannot work out how to improve the fit and is often a sign that there is something wrong with the model. When you think you have a good fit, confirm its uniqueness by starting from a different set of initial parameter values, or even by using one of the other algorithms.

### 12.4.2 Flow of data and information during fitting

A summary of the overall flow of data and information during fitting is shown in Figure 12.1. Data are read in from the data file ([dataFile](#)). If necessary, the data are transformed before being stored in memory ([logVariableIn](#)). These data contain values for the dependent variable (for a fit), the weight to be applied to each observation if applicable and any independent variables needed in the calculations. It can contain additional columns of data but these are ignored. The column headings are used to define special 'fit data' tags. These are used in the **CHEMISTRY** part of the input file to identify the variables to be substituted when calculating the

value of the dependent variable. It is also necessary to identify which column contains the dependent variable. This is done by the column position or name ([dependentVariableColumnObs](#)). The **PHREEQC** simulation(s) used for each data point are indicated by the integer value or integer range found in the column of the data file given by the [blockRangeColumn](#). These simulations can be shared by different observations or can be different for each observation.

There can also be a column in the fit data file to indicate which simulations within each block range are pre-loop simulations and which are the main loop simulations. Like the [blockRangeColumn](#), this can be specified separately for each observation. The name of the column is given by the [mainLoopColumn](#) keyword. If this is not specified and the [mainLoop](#) keyword has a valid setting, then this setting is used for all observations. This setting is relative to the start of the block of simulations used for each observation.

The default setting of [mainLoop](#) is `auto` which for fitting and simulations is set to '1', i.e. all simulations will be run on each iteration. Remember that '1' refers to the first simulation in the specified block not the first simulation in the whole set of simulations.

All pre-loop simulations are executed only once per run – at the very beginning of the run. Pre-loop simulations should include static data such as database blocks. If there are data blocks that vary but apply to all data points in a given set of function evaluations and so only need to be run once per iteration, include them in the block of simulations specified for the first data point. The simulations specified for the second and subsequent data points should only refer to the simulations specifically required for those data points.

The input files define the number and names of parameters used by the chemistry model to calculate the value of the dependent variable ([numberOfFitParameters](#) and [fitParameterNames](#)) for a given set of conditions. Parameters can be fixed or adjustable ([fitAdjustableParameters](#)) and may be fitted as log parameter values ([fitLogParameters](#)). The parameter values set ([fitParameterValues](#)) are either used as initial estimates if adjustable or as fixed values.

The `CHEMISTRY` section contains the code that is used to calculate the dependent variable and this is normally output via the main selected output 'file'. The column for this is given by [dependentVariableColumnCalc](#) and whether it should be transformed or not by [logDepVariable](#). The observations from the data file are compared with calculated value of the dependent variable and the difference (the 'residual') multiplied by the given or calculated weight ([fitWeightingMethod](#) and [weightColumn](#)). This weighted residual is passed to the optimizer.

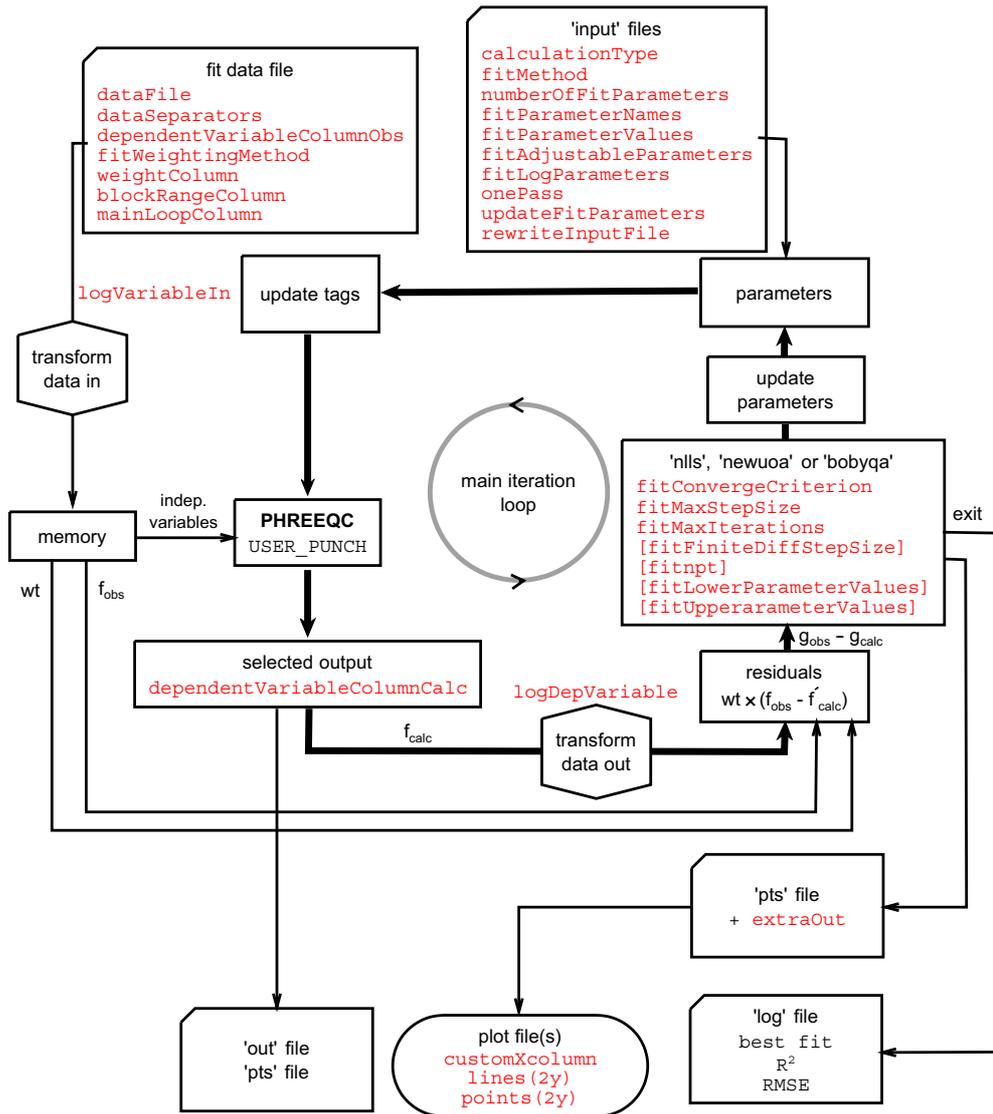
The optimizer adjusts the adjustable parameters, identified by [fitAdjustableParameters](#) until the convergence criterion of some other factor signals an exit. After convergence, summary statistics are calculated, some tabular output produced and a plot made. The plot is made from the 'pts' file with the columns used specified by the [lines](#) and [points](#) keywords. Data from other files, including the 'out' file, can be used by adding the relevant files to the search path with [extradat](#). The value of [customXcolumn](#) controls the x-axis variable. If no satisfactory convergence is achieved, a message is issued accordingly.

### 12.4.3 The parameters

Parameters are variables that remain constant during a simulation, i.e. they have the same value for all observations with a given data set. Parameters can either be fixed or adjustable depending on whether they are to be adjusted by **PhreePlot** to provide the best fit or not.

The number of parameters should be defined first using the [numberOfFitParameters](#) keyword. Each parameter has various attributes associated with it such as its name, its value and whether it is fixed or adjustable, whether the log of the parameter should be optimized, and any constraints (lower and upper bounds). These are specified by a series of lists, one entry per parameter.

Unlike most other settings, the order of the [numberOfFitParameters](#) keyword in the input file is important. Specifically this setting should always come before any of the other parameter list settings in the input file since it automatically re-initialises all these other parameter settings to



arrays of the specified length and with the system default values. This is to ensure that all the parameter lists have the correct length. The parameter list settings (all have length of `numberOfFitParameters`) are: `fitParameterNames`, `fitLogParameters`, `fitAdjustableParameters`, `fitParameterValues`, `fitLowerParameterValues`, and `fitUpperParameterValues`.

The parameter tag names are defined by the `fitParameterNames` keyword in an input file, one name for each parameter. Once defined, these names can be used as tags in the **PHREEQC** input file (the tag is generated by enclosing the name in angle brackets). These names must not be used for other tag definitions. The values assigned to these parameters is determined by the fitting procedure in **PhreePlot**.

The initial values of each of the parameters are defined by the `fitParameterValues` keyword. `fitStepSize` controls the largest permissible change in a parameter value during an iteration for the 'nlls' algorithm. It defines RHOBEQ, the initial radius of the 'trust region' in the 'newuoa' and 'bobyqa' algorithms. In the 'lm' and 'subplx' methods it defines the initial step bound. The parameter values are either fixed or automatically adjusted by **PhreePlot** to provide the best possible fit. This option is controlled by the `fitAdjustableParameters` keyword.

#### 12.4.4 Variables

Variables can vary for each observation within a given dataset. The dependent variable is the variable that is calculated from the model(s) and a combination of the given parameters and the independent variables. It is the variable which is fitted when optimisation is being undertaken. Fitting minimises the weighted sum of squares of the differences between the observed and calculated values of the dependent variable. It is assumed that the independent variable contains all the errors, both errors of observation and model errors.

There can only be one dependent variable per line of input in the data file plus any number of independent variables on the same line giving the fit input file a tabular or spreadsheet layout.

The independent variables are the variables that are fixed by the user and control the value of the dependent variable. It is assumed that the independent variables are known without error. It is possible to have no independent variables as in a ‘root finding’ problem or where the model itself varies from observation to observation.

#### 12.4.5 Passing the fitted values from PHREEQC to PhreePlot: preparing the input file

There are limitations to the structure of the **PHREEQC** input file that can be used during fitting. This particularly relates to the use of multi-simulation input code and the way in which the value of the dependent variable is calculated.

There are two principal calculation options: either one pass through the **PHREEQC** code is made to calculate a single value of the dependent variable, or all dependent variable values are calculated in a single, multi-simulation pass. There is no half-way house. The latter is computationally faster but the input file is more complex and less flexible since it must either include a separate simulation to generate each data value or must include a **PHREEQC** keyword that generates a sequence of data via its own iterations, e.g. `REACTION` and `TRANSPORT`.

Typically many iterations (or function evaluations) are made through the whole data set during fitting and so the former approach will make  $n_{data} \times n_{iterations}$  calls to **PHREEQC** while the latter approach will make just  $n_{iterations}$  calls.

The difference between these two approaches can be seen in the *iso* ([Example 80](#)) and *ison* ([Example 81](#)) examples.

##### *One pass to generate a single data value*

When `onePass` is `FALSE` during ‘simulate’ or ‘fit’ calculations, only one data value should be written to the selected output at a time. This may be because the whole input file must be repeated each time in order to calculate one value or because a different block of simulations is used to calculate each value. If there is more than one line of selected output data, the last line in the selected output is always used.

The `SELECTED_OUTPUT` keyword block (optionally plus a `USER_PUNCH` block) should generate at least one line of data in the selected output file for each calculation (i.e. after “any initial solution, initial exchange-composition, initial surface-composition, or initial gas-phase-composition calculation and after each step in batch-reaction or each shift in transport calculations”).

The **PhreePlot** keyword `selectedOutputLines` is not used since only one line will ever be picked up. The `PRINT -selected_output` statement (or similar in `SELECTED_OUTPUT`) can be used to control which **PHREEQC** simulations send data to the selected output file and so which simulation actually sends the last line of data.

The `dependentVariableColumnCalc` keyword controls the column where the dependent variable will be found.

The **PHREEQC** code can include several simulations, for example, different types of simulations can be combined into a single global optimization, but only one can be used to generate the value for each data point. The block of simulations to be used are set by the value or range set in the column defined by the `blockRangeColumn` keyword providing `onePass` is set to

FALSE. This means that completely different models can be used to generate the various values of the dependent variable for each data point.

### *One pass to generate all data values*

When `onePass` is TRUE, all of the data values is expected to be written to the selected output file in a single pass through the designated block of **PHREEQC** code. If there are more lines of data than required to pair off with the number of observations in the fit data file ( $n$ ), then the last  $n$  lines of selected output will be selected.

It is up to you to ensure that the `USER_PUNCH` code does actually produce the required output. The ‘one pass’ option is most often used for `REACTION`, `KINETICS`, `ADVECTION` and `TRANSPORT` calculations where **PHREEQC** has its own built-in iterators. Here a single call to `USER_PUNCH` transfers all of the required output values. Alternatively, a whole set of different simulations can be run in one call to **PHREEQC** which will also result in a multi-line block of selected output containing all of the required dependent variable values. This approach uses the `mainLoop` setting to select more than the last simulation to iterate on.

Since the `onePass` TRUE option along with the default `oneSimulationAtATime` switch of the `mainLoop` keyword set to FALSE means that all the main loop simulations are expected to be produced in a single call to **PHREEQC**, there is normally no updating of tag values between simulations. If variables need to be passed from one simulation to another, use **PHREEQC**’s own `PUT/GET` mechanism or set both the `onePass` and `oneSimulationAtATime` switches to TRUE. The `PRINT -selected_output` statement can be used to control which **PHREEQC** simulations send data to the selected output file and so which simulation actually sends the last line(s) of data.

In the case of a fit, the ‘auto’ option controlling the number of selected output lines is set to one when `onePass` is FALSE and to the number of data points when `onePass` is TRUE.

The selected output produced by a given input file can be easily viewed by setting `debug` to 2 – the output is written to the screen and also written to the file `selected_1.0.out` (default name) which will be found in the working directory.

### *Skipping unwanted PHREEQC selected output*

A `USER_PUNCH` block may lead to unwanted lines of data being sent to the selected output file and so prevent the 1:1 match between the sequence of observations in the fit data file and the computed values in the selected output file.

Excess lines of selected output are automatically deleted counting from the bottom upwards and so some initialization output may not matter. However, sometimes unwanted data are produced in the middle of an output file and so would matter.

It is often possible to suppress unwanted output by either turning off all selected output for a simulation with the `PRINT; -selected_output FALSE` statements or for individual simulations by including a test at the beginning of a `USER_PUNCH` block followed if necessary by a jump over the `PUNCH` statement. For example, testing for valid values of `STEP_NO` or `SIM_NO` can avoid inclusion of the output from initial solution calculations.

Where this is not possible, e.g. in `TRANSPORT` calculations with `onePass` set to TRUE, it may be possible to amend the input data file containing the observations so that it includes dummy (placeholder) values to match the unwanted lines of output and then to include weights of zero for these unwanted ‘observations’. They will then not affect the fitting. The 1:1 matching of lines of input and output is a prerequisite for fitting with **PhreePlot**.

### *Global optimization - switching models*

Where global optimization over various data sets and models is to be undertaken, then there needs to be a way to switch the code (model) used to give the calculated values in the `USER_PUNCH` block.

This can be achieved in various ways depending on the degree to which the models vary.

*(i) Using an independent variable set in the fit data file*

```
USER_PUNCH
  -heading logc solute
    10 IF (STEP_NO > 0) THEN PUNCH log(TOT("<solute>")), "<solute>"
```

where the fit data file looks like this

```
observed    weight    solute
# Ca
-5.00E+000    1        Ca
-5.10E+000    1        Ca
-5.00E+000    1        Ca
...

# SO4 - the blank line in the data file above breaks the line in a plot
-5.20E+000    1        Mg
-5.10E+000    1        Mg
-4.98E+000    1        Mg
...
```

As each of the observed values is read from this data file, a tag is made of the other variables (columns) in the file, namely `<weight>` and `<solute>`, and the values of these changed in parallel to correspond with each observation. The value of `<solute>` is then substituted in the `USER_PUNCH` block above. This file could also define one or more numeric values to use, potentially different for each observation.

The corresponding weight is not transmitted through its tag value but by naming the weight column with the [weightColumn](#) keyword.

The `'IF (STEP_NO > 0)'` above is a means of avoiding sending any output for the initial solution calculations.

*(ii) Explicitly using the simulation number as a switch*

For example, using the same model setup but optimizing different parts of it, e.g. different elements. Simulation 1 does the calculation for Ca and simulation 2 does it for Mg.

```
USER_PUNCH
  -heading depvar solute simulation
    10 IF (SIM_NO = 1) THEN PUNCH log(TOT("Ca")), "Ca", SIM_NO ELSE PUNCH
log(TOT("Mg")), "Mg" , SIM_NO
```

The simulations may contain keyword blocks such as `REACTION` or `KINETICS` which themselves generate multiple observations.

*(iii) Giving a range of simulations to use in the fit data file*

If each data point requires a different model (= set of simulations) to calculate the dependent variable, then these can be specified in a separate column in the fit data file.

```
observed    weight    sim
# Ca
-5.00E+000    1        1-2
-5.10E+000    1        3-4
-5.00E+000    1        5-8
...
#SO4 - blank line above breaks line in plot
-5.20E+000    1        13-14
-5.10E+000    1        25-26
-4.98E+000    1        16-17
```

The [blockRangeColumn](#) keyword is here defined as `sim` and the `sim` column defines the simulations to use for each observation. These do not have to be in order or to contain the same

number of simulations. They are to some extent independent but will inherit **PHREEQC** data structures from simulation to simulation in the normal way. Each of these mini-blocks of simulations can have its own pre-loop and main loop simulations as defined by a separate column specified with the [mainLoopColumn](#) keyword.

#### 12.4.6 Data file

The data file consists of the observations, one line per observation. It needs to be sorted in x-column in order to make the plot that is automatically produced sensible (the fitted values are plotted as a continuous line).

The data separator needs to be specified to match that found in the data file (see '[Organise your data](#)').

Each line in the data file contains: values for each of the independent variables (if present) and the single value of the dependent variable (if present). The first line contains a list of headers, one per column variable. The header names are automatically converted to tags so must adhere to the tag naming convention, i.e. they must not contain operators (+-\*/^) and will be case sensitive. If the dependent variable is not present, then only simulated values can be calculated.

Anything following a number sign (i.e. pound sign or hash symbol, #) is treated as a comment and is ignored. One or more blank lines indicates a break in the data set. The break is preserved in the 'out' file and produces a break in line plots.

The data file can also contain columns containing alphanumeric data (descriptive columns). These also produce tags which can be used for substituting character strings in the input files. The type of column (numeric or character) is determined by analysing the first valid row of data. If necessary rearrange the row order to ensure that the correct column type is indicated in row 1 of the data.

If the descriptive text contains spaces, embed in quotes. Only the first 20 characters are transferred, 18 if the text contains embedded spaces and quotes need to be used.

If the [blockRangeColumn](#) has been set to a positive integer or valid column name, then this column (counting from the left) is assumed to contain the **PHREEQC** simulation number (or range of simulations) to be used for calculating the dependent variable for this line of data. The default value of [blockRangeColumn](#) is 0 (undefined) in which case each observation is assumed to use all simulations. Similarly the [mainLoopColumn](#) if defined contains the position of the beginning of the main loop simulations within the block of simulations that is used for an observation. If [mainLoopColumn](#) is not defined, [mainLoop](#) defaults to the [mainLoop](#) setting in the input files. Not defining a [blockRangeColumn](#) and a [mainLoopColumn](#) may work but may repeat unnecessary calculations.

For example, say the fitting requires three simulations, the first two simulations to define static data such as the database and the third to calculate and output the dependent variable for each observation. This third simulation also contains the tags, <PT> and <CaT>, which define the values of the two independent variables.

Then the data file for the first two observations will look something like this:

```

...      PT          CaT          sim_num    main_loop
...      6.3e-4       1e-2         1-3        3
...      6.6e-4       2e-2         3         1

```

The [blockRangeColumn](#) is set to 'sim\_num' and the [mainLoopColumn](#) is set to 'main\_loop'.

The first observation is defined by three simulations (1-3) and the main loop starts at the third simulation in this block, i.e. simulation 3. So simulations 1-2 must be pre-loop simulations.

The second observation is defined by just one simulation, simulation 3, and the main loop starts at the first simulation in this block, i.e. simulation 3.

The sequence of simulations executed is therefore as follows:

- (i) pre-loop 1: execute simulation 1, update tags
- (ii) pre-loop 2: execute simulation 2, update tags
- (iii) main loop: execute simulation 3 for observation 1, update tags  
main loop: execute simulation 3 for observation 2, update tags  
[repeat (iii) above] until
- ... main loop: execute simulation 3 for last observation, update tags

On subsequent iterations, the sequence starts at (iii) above.

If some **PHREEQC** code needs to be repeated just once on each iteration of the dataset, then include it in the main loop of the first observation, not as a pre-loop simulation of this observation.

The data file can also be used in simulation mode ([calculationMethod](#) = `simulate`) which has a similar setup to that of `fit` but does not compare observed and calculated values and does no ‘fitting’. No dependent variable need be defined though it can be. A summary of the selected output is sent to the `out` file. Simply changing the [calculationMethod](#) from `fit` to `simulate` will produce an output file with results for all the observations using the initial parameter values. This can be useful for quickly checking the initial estimates.

The log file contains the mean and standard deviation of the numeric data in the input data file. It also contains the sum of the relative standard deviations of each of the columns. This figure can be used as a crude ‘checksum’ to indicate whether two data files are the same or not.

The number of observations (lines of data) in the data file (`n`) fixes the number of lines to be read from the `out` file: if [onePass](#) is `TRUE`, then the last `n` lines will be read (irrespective of the [selectedOutputLines](#) setting). If [onePass](#) is `FALSE`, then only the last line will be read from the `out` file. These two options are demonstrated in the `demo\kineticsSi\kineticsSifit.ppi` and `demo\kineticsSi\kineticsSifit1.ppi` examples, respectively. The latter option is used for fitting kinetic models when the observations are at irregular time intervals.

## 12.5 THE OPTIMIZATION ROUTINES

### 12.5.1 The objective function

The optimization routines aim to find the combination of model parameters that produce the minimum value of the objective function. The objective function can either be based on minimizing the weighted residual sum of squares (L2 norm) or the weighted sum of absolute differences (L1 norm). This is controlled by the [objectiveFunction](#) setting.

### 12.5.2 Choice of fit algorithm

The choice of algorithm is determined by the [fitMethod](#) setting (Table). None of these algorithms requires derivatives to be supplied.

Table 12.1. Local optimization algorithms available for fitting

<a href="#">fitMethod</a>	Algorithm	Constraints	Reference
<code>nlls</code>	Powell’s least squares method (L2)	No	Powell (1965)
<code>cobyqa</code>	Powell’s constrained optimization by linear approximation (L1 or L2)	No	Powell (1994)
<code>newuoa</code>	Powell’s trust region method	No	Powell (2007)
<code>bobyqa</code>	Powell’s bounded optimization by quadratic approximation approach (L1 or L2)	Yes	Powell (2009)
<code>lm</code>	Levenberg-Marquadt method (L2)	No	Moré et al. (1980)
<code>subplx</code>	Rowan’s subspace-searching simplex method	No	Rowan (1990)
<code>slsqp</code>	Kraft’s sequential quadratic programming approach	Not implemented	Kraft (1988)

Providing that reasonably good initial estimates of the adjustable parameters can be given, then the ‘`nlls`’ algorithm is likely to be fastest of the available algorithms. This algorithm was especially developed for minimizing nonlinear functions involving sums of squares and is noted for its ability to rapidly home in on a solution when close to it. However, it suffers the disadvantage that it can be confused by local minima and so should be started from different starting positions to ensure the solution given is the global solution. Its behaviour is controlled by a rather small, but not-too-obscure, number of settings.

If the ‘`nlls`’ algorithm fails to converge either because of poor initial parameter estimates or because of its tendency to stray into undesirable territory (e.g. negative concentrations), then it is worth trying the ‘`bobyqa`’ or ‘`subplx`’ algorithms. These algorithms were designed for large-scale optimization problems with hundreds of adjustable parameters (‘variables’). They also have more general application than the specialised least squares optimizers such as ‘`nlls`’ and should be more efficient than the ‘`nlls`’ algorithm when the Gauss-Newton approach performs less well. This tends to be true for large residual problems with nonlinear terms in the sum of squares.

At present, ‘`bobyqa`’ is the only one of the algorithms that can apply constraints to the adjustable parameter values, in this case, simple box constraints.

Comparing the different algorithms on the same problem can provide an insight into the quality of the parameter estimates and the fitting algorithms. Ideally, they should all converge to the same set of parameter values. However, the comparisons are rarely straightforward as the nature of the approach to the minimum obviously varies. Nevertheless simple timing tests with a fixed [objectiveFunction](#) will quickly provide insight into major differences.

It is possible to apply several approaches to the same dataset by adding the list of routines wanted to the [fitMethod](#) setting. If set to do so, each method will produce its own track file and plot.

### 12.5.3 Scaling of parameters

These optimization algorithms have to estimate successive steps in multi-dimensional space in order to reduce the value of the objective function to a minimum. This requires the calculation of distances between points. The estimation of derivatives may also involve a fixed shift in parameter values (‘`nlls`’). Therefore it may be necessary to scale the adjustable parameters to ensure that the magnitudes of their expected changes are all similar. Ideally the parameter values should all be close to one. Re-scaling could be done by a change in units, for example, or where appropriate, by taking logs (see [fitLogParameters](#)). Other than the option of taking logs, this scaling has to be done outside of **PhreePlot**.

### 12.5.4 Constrained optimization

The ‘`bobyqa`’ [fitMethod](#) allows simple upper and lower bounds to be put on the parameter values using the [fitLowerParameterValues](#) and [fitUpperParameterValues](#) keywords.

Implicit constraints can also be imposed indirectly, e.g. by fitting the log of parameter value. This will constrain a parameter to a positive value.

### 12.5.5 Control parameters

Details of the algorithms and their underlying control parameters can be found in the library and online documentation of the routines (‘`nlls`’, ‘`lm`’, ‘`newuoa`’, ‘`bobyqa`’ and ‘`subplx`’). Most of the critical control parameters have been translated into **PhreePlot** settings so that a large degree of control over each algorithm’s behaviour can be achieved from within **PhreePlot** (Table 12.2). In particular, the meaning of the convergence criterion varies (sometimes it refers to a change in the residual sum of squares, sometimes to the change in the parameter estimates). A uniform stopping criterion can be applied to all routines by specifying a value for the [objectiveFunction](#). If the objective function falls below this, then the search stops for all

Table 12.2. Translation of PhreePlot settings into the control parameters for three of the optimization algorithm's

PhreePlot keyword and action	Algorithm ('fitMethod')		
	'nlls'	'newuoa'	'bobyqa'
<b>fitFiniteDiffStepSize</b> Controls the difference used in estimating partial derivatives. Used for the initial, exploratory shift in all variables.	<b>DSTEP=fitFiniteDiffStepSize</b> Small values will mean less chance of straying too far on the first step and better estimates of derivatives but if too small there may not be a significant change in WRSS given the background noise. Choose judiciously.	not used	
<b>fitConvergenceCriterion</b> Controls the objective function used and when to stop. Smaller values mean more iterations and more accurate convergence.	<b>ACC=fitConvergenceCriterion^2</b> Converges when the predicted value of WRSS is <ACC above the true minimum or when there is little predicted change in parameters. WRSS is a sum that depends on the number of data points.	<b>RHOEND=fitConvergenceCriterion</b> Final radius of 'trust region' determines the final accuracy in the parameter estimates. Also RHOEND<=RHOBEG	
<b>fitStepSize</b> Controls the starting step size and/or the maximum step size. Smaller values mean more iterations but less chance of straying into unwanted territory.	<b>DMAX=fitStepSize</b> Maximum 'distance' of initial estimate from the solution (not scaled). Also the minimum size of the Marquadt parameter = fitConvergenceCriterion/fitStepSize.	<b>RHOBEG = fitStepSize</b> Initial radius of the 'trust region'. This controls the 'granularity' of the objective function that the algorithm will see. Diameter of the 'trust region' (2*RHOBEG) must also be smaller than each of the range of bounds (see below)	
<b>fitMaxIterations</b> Controls the maximum number of iterations allowed. Normally want a large value to avoid early termination.	<b>MAXFUN=fitMaxIterations</b>		<b>MAXFUN=fitMaxIterations</b>
<b>fitLowerParameterValues</b> <b>fitUpperParameterValues</b> Constraints on acceptable parameter values.	not used		not used $XL(:) = \text{fitLowerParameterValues}$ $XU(:) = \text{fitUpperParameterValues}$ Also $XU(:) - XL(:) = < 2 * \text{fitStepSize}$ Lower and upper bounds on parameter estimates
<b>fitAdjustableParameters</b> Provides a simple way of including/excluding model parameters from the optimization.	Counting 1's gives the number of adjustable parameters, N.	As for 'nlls' but N is also used to determine the parameter, NPT, when it has not been defined explicitly, see below.	
<b>fitnpt</b> Controls the number of interpolation conditions. Larger is better but will be slower.	not used		if fitnpt is UNDEFINED then if (N<6) then NPT=(N+2) * (N+1) / 2 else NPT=2*N+1.

routines.

Parameters that are to be fitted or made to be easily adjusted should be entered as parameters with names (up to 30 characters) ([fitParameterNames](#)) and values ([fitParameterValues](#)). These values are assumed to be either fixed values or initial estimates to be adjusted during fitting. This distinction is set by the [fitAdjustableParameters](#) keyword (0= fixed; 1 = adjustable).

The log10 of the parameter value can also be easily fitted. Set the appropriate [fitLogParameters](#) keyword value to 1 otherwise set it to 0. This can provide a useful form of scaling to bring very large or very small numbers into the same order of magnitude as other parameters. It also is a simple way of constraining a parameter to a positive value.

It is important that each of the above parameter lists should have the same length. This can be set with the [numberOfFitParameters](#) keyword but can also be allowed to be automatically set

from the length of any of the above lists as they are entered. If present, the [numberOfFitParameters](#) keyword should precede all the parameter lists in the input file.

#### *Finite difference step size ('nlls' only)*

This controls the step size of each parameter value used in the estimation of partial derivatives by finite differences numerically. The value of the step size should be large enough to achieve a significant change in the objective function while being small enough to give derivatives with sufficient accuracy. The correctness of the choice can best be seen from the first few iterations where each of the adjustable parameters is adjusted one by one by the specified step size. This should produce a significant change in the objective function for at least some of the parameters (preferably all). If it does not, increase the step size by an order of magnitude. Default 1e-6. Where approximate (numerical) methods are being used to generate the dependent variable values, as in **PHREEQC**, there will inevitably be some noise in the generated values and so a larger value may be appropriate to ensure sufficiently accurate derivatives.

#### *Convergence criterion*

The meaning of this varies with the optimization method. Read the original documentation for guidance. In all cases, this parameter determines when to stop the iterations and accept (or not) a fit. A small value will tend to increase the accuracy of the fit, albeit with more iterations, but there will be a limit when the other numerical procedures (both in the calculation of partial derivatives and in **PHREEQC**) will limit the accuracy that can be obtained. The default value is 1e-6.

The algorithm's convergence criterion can always be overridden as a stopping criterion by the [objectiveFunction](#) setting if this is satisfied first.

#### *Step size*

This usually controls the initial step size for each parameter and for 'nlls' is the maximum size of any step. A large value (say 100) will enable a large area to be searched but may lead to the focus wandering away from the best solution and even lead **PHREEQC** to fail because of unrealistic parameters.

With the **NEUWOA** and **BOBYQA** methods, the step size sets the initial size (radius) of the trust region and is an important parameter. A small value will constrain the search area to be close to the original parameter estimates which is fine provided the initial estimates were good but may lead to misleading results otherwise. A large value may lead to physically unrealistic parameter estimates during fitting and therefore to problems in **PHREEQC** convergence. The default value is 1.0.

#### *Maximum iterations*

The maximum number of function evaluations. If convergence has not been achieved by the time this limit has been reached, **PhreePlot** will exit the optimization gracefully and move on. If set to 1, this will force an immediate exit from the optimization routine but it will give an indication of the correctness of the initial estimates. The default value is 5000. Some of the methods make additional function evaluations in order to estimate the derivatives in the Jacobian.

#### *Weighting method*

[fitWeightingMethod](#) determines how the objective function is calculated from the residuals. The residuals are multiplied by weights, one for each observation. See the definition of the [fitWeightingMethod](#) for more details.

It has the following options:

- 0 absolute error: all weights = 1.
- 1 relative error: weights =  $\text{abs}(1/\text{fitted value})$  if fitted value is not equal to 0 else it is  $\text{abs}(1/\text{observed value})$ .
- 2 from the input data file: weights in the column given by [weightColumn](#).

The weights should be related to the quality of each observation in terms of the size of the observation error. For L2 optimization, weights are normally given by the inverse of the standard deviation of each observation or something proportional to that

$$w_i = 1/\sigma_i$$

where the objective function to minimize is given by

$$\text{minimize } \sum [w_i(f_{\text{obs},i} - f_{\text{calc},i})]^2$$

## 12.6 PREPARING AN INPUT FILE

### 12.6.1 Simple example

The following is a simple example based on the `iso.ppi` file found in the `\demo\fit` directory. This example fits a Langmuir isotherm to data for Zn sorption by Hfo at constant pH (pH 5.5). The `iso.dat` data file looks like this:

Znsorbed	Znconcn	pHobs	wt	sim#
0.75	0.030	5.5	1	1
1.40	0.069	5.5	2	1
1.95	0.118	5.5	2	1
2.51	0.166	5.5	2	1
3.03	0.217	5.5	5	1
3.53	0.270	5.5	5	1
4.02	0.325	5.5	5	1
4.41	0.388	5.5	5	1
4.79	0.453	5.5	2	1
5.22	0.512	5.5	1	1

where the units are mmol Zn/mol Fe for `Znsorbed`, mmol Zn/L for `Znconcn` and `pHobs` is dimensionless. `wt` is the relative weight assigned to each observation and `sim#` is the **PHREEQC** simulation number. Simulation 1 is used for all the calculations and so all simulation numbers have been set to 1.

The **PHREEQC** input file part is

```

PHASES
Fix_H+
  H+ = H+
  log_k 0.0
SURFACE_MASTER_SPECIES
  Surf Surf
SURFACE_SPECIES
  Surf = Surf
  log_k 0.0
SELECTED_OUTPUT
-high_precision true
-reset false
USER_PUNCH
# fit Langmuir isotherm
-headings sorbZn pH mmolZn& step_no
10 sorbedZn=SURF("Zn","Surf")
20 punch sorbedZn, -la("H+"), tot("Zn")*1e3, step_no
SOLUTION 1
  -units mmol/L
  -pH <pH>
  Na 1000
  N(5) 1000
  Zn <Znconcn> #tag name from iso.dat data file
EQUILIBRIUM_PHASES

```

```

    Fix_H+ -<pHobs> NaOH 10
SURFACE_SPECIES
    Surf + Zn+2 = SurfZn+2
    log_K <log_k>
SURFACE
    Surf <M1>
    -equil 1
    -no_edl
END

```

### 12.6.2 Automatic updating of parameter values in an input file

If the [updateFitParameters](#) switch has been set to `TRUE` and if the fit has been successful, then the newly fitted parameter values will replace the existing ones in the input file. A backup of the original input file (`***.bak.***`) is made if a backup file of the same name does not already exist.

### 12.7 INTERRUPTING OR STOPPING THE FITTING

The ‘`Esc`’ key will interrupt the fitting once the calculations for the current iteration have all been finished. You are then given the option to continue or to stop. If you stop and a plot is expected, then this will be produced using the best set of fitted values at the time of interruption.

### 12.8 FORCING RELATIONS BETWEEN PARAMETER VALUES

It is possible to force relations between parameter values by using the [numericTags](#) keyword to define the desired relations and then substituting the corresponding tags in the input file in the normal way.

For example, say there are four parameters and these are referred to in the input file by their corresponding tag names: `<p1>`, `<p2>`, `<p3>` and `<p4>`. If you want to force  $p_4 = p_1$  then reduce the number of parameters from 4 to 3 (`p1`, `p2`, `p3`) and add `<p4> = <p1>` in the [numericTags](#) block. `<p4>` should be left unchanged in the remainder of the input file. Its value will be updated based on the [numericTags](#) expression on each iteration.

Other more complex relations may be specified in a similar way.

Note that it is important **not** to include the redefined parameter (`<p4>` above) in the set of fit parameters since the optimizer expects to have full control over all parameter values and does not expect them to be changed by an external procedure. `<p4>` is now a tag variable rather than a fit parameter. There is no connection between the tag variables and fit parameters during optimization.

### 12.9 STANDARD ERRORS OF FITTED PARAMETER VALUES AND THE CORRELATION MATRIX

Providing an adjustable parameter has not been log-transformed ([fitLogParameters](#) = 1), an estimate of the standard error of the fitted parameter is given. If this value is large, then the fit may not be good. If two or more parameters have large standard errors but the fit looks good, then some parameters may be highly correlated. Fix the best known parameter and refit.

These standard errors are calculated numerically based on inverting the Hessian matrix. For all methods except the `nlls` method, which automatically provides the Hessian, this involves an additional  $nadj + 1$  iterations to calculate the Hessian where  $nadj$  is the number of adjustable parameters. Standard errors are not provided for any log-transformed parameters.

Where possible, the correlation matrix of fitted parameters is given. This is not calculated if any of the adjustable parameters have been log-transformed.

If some of the parameters have been log-transformed and standard errors and the correlation matrix are required, re-run the fit using the exact estimated parameters but this time without any log transformations.

## 12.10 MULTI-OBJECTIVE FITTING

It is possible to fit parameters to multiple different models at the same time. These models may share some common parameters, or may not. The principle is the same as before: each observation must take one line of data in the fit data file and produce one result with the input and output matching line-by-line. The data file must have a spreadsheet-like structure with each variable having a separate column. Where variables vary between the models, there will be rows containing columns with no data. It is easiest to set up such files in a spreadsheet and export as a tab delimited file. Then read the data into **PhreePlot** with “`fn.dat`” `\t` to indicate its tab-delimited format. Adjacent tabs will then serve as placeholders for blank columns and will not be merged.

In principle, each line of data can be derived from a different model since it is possible to specify the range or block of simulations to use for each observation in the fit data file using the [blockRangeColumn](#). More often, groups of observations use a common set of simulations. The weights should also be specified in the [weightColumn](#) with [fitWeightingMethod](#) set to 2. Alternatively, the relative error option ([fitWeightingMethod](#) 1) may be suitable. There is a problem of mixing ‘apples and oranges’ here so the weighting is critical. Be wary of over-interpreting the summary statistics such as the standard errors.

The `\demo\fit\multiobjective.ppi` file gives an example of fitting two quite distinct data sets (demonstrated individually elsewhere) at the same time and demonstrates how to set up the fit data and input files.

## 12.11 OUTPUT FILES

Other than the log and plot files, the useful files produced during fitting and simulations are the ‘out’ file and the ‘pts’ file. The ‘trk’ file will save a copy of the convergence monitoring during fitting and can be used to prepare a plot of this using the ‘extraout’ keyword to read in these \*.trk files.

The ‘out’ file contains a copy of the selected output, one record per observation. During fitting, this normally contains just one block of results containing one record per observation – the results from the last iteration (which is not necessarily the best-fitting iteration). Simulations always just contain one block of results since there is no iteration. Fits can be made to store the results of all iterations by changing the rewind data separator for the ‘out’ file to null (“”) instead of the default ‘\r’. This prevents the rewind before writing results and also introduces a blank line after each block of results. This behaviour is controlled by the fifth parameter of the [dataSeparators](#) keyword.

The ‘pts’ file contains a comprehensive list of results for each observation including both the input data, fitted, observed and weighted residuals and the results of the selected output, all from the best-fitting iteration. This is the file that is automatically chosen for plotting since it combines observed and fitted data.

## 12.12 RESPONSE IN THE EVENT OF A FAILURE OF PHREEQC TO CONVERGE

The response if **PHREEQC** should fail to converge during fitting depends on the [debug](#) setting. If [debug](#) is 0 or less, then the offending point is deleted from the input and the fitting restarted without it. When this happens, a ‘?’ is appended to the number of iterations in the `pp.log` file to indicate that this has happened.

If [debug](#) is greater than zero, then **PhreePlot** will stop if **PHREEQC** fails. A list of any offending points is sent to the log file. This gives the physical line numbers of the offending

points as found in the fit data file (counting the header line).

## 12.13 PLOTTING THE RESULTS OF THE FITTING

### 12.13.1 Plots of observed and calculated results

The 'pts' file is the primary plot data file for fitting and simulations though other files can be added using the `extradat` keyword.

The 'pts' file contains data from three sources: (i) the fitting (5 columns: row number, observed, calculated, residual, weighted residual); (ii) all the variables read in from the data file; and (iii) all the columns from the selected output with values from the 'best' fit.

A plot of the observed points (as points) and the fitted values (as a continuous line) is often useful. The lines and points which are plotted is controlled by the `lines` and `points` keywords, respectively. 'Lines' plots only make sense when the points are contiguous.

The `customXcolumn` setting is also important as this fixes the x-variable.

The accumulated output from the selected output is stored in the 'out' file if present - this is produced for `debug > 0`. If the fifth data separator is "\r", the file is rewound at the beginning of each set of function evaluations so only the last set will be found on the file (not necessarily for the 'best' fit since this may have occurred in an earlier iteration). Any other character means that there is no rewind and so all selected output results will be accumulated on the file.

The 'trk' file, if requested, contains a copy of the nlls monitoring results.

The use of the `labels` and `post/postSize` keywords can be useful for making a key and for 'posting' values beside each individual point. Such posting can be useful for identifying outliers.

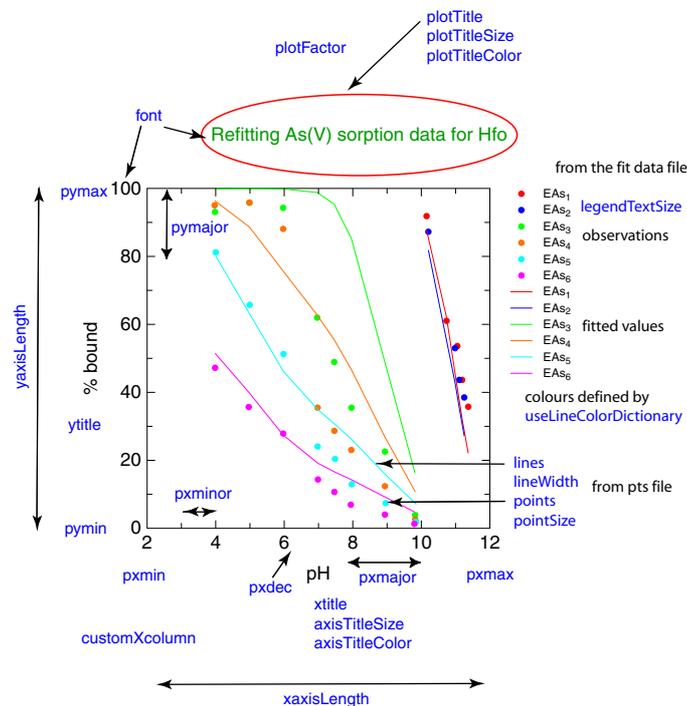


Figure 12.2. Some of the keywords used to control the appearance of fit plots.

Additional text can be added with `text` or `extraText` and additional data from other files with `extradat`. After a successful fit, three special system tags are populated. These are `<R2>`, `<RMSE>` and `<nFit>` which contain the  $R^2$ , RMSE and number of data points. These tags can be used to annotate the plot using the `extraText` approach.

An example of a fit plot with some of the more commonly used keywords is shown in Figure 12.2. Since the 'pts' file contains both observed and fitted data, it provides a useful source of data to plot. Observations are often plotted with points and calculated values with lines.

Where the dependent variable depends on more than one independent variable, it can be difficult to choose a suitable plot. In these cases, a plot of calculated or residual values vs observed values can be useful.

### 12.13.2 Contour plot of the residual sum of squares

It can be useful to view how the objective function (e.g. residual sum of squares) varies with changes in the value of the model parameters. A contour plot can show the variation of the residual sum of squares versus two model parameters and may help you to understand convergence problems. A custom plot can do the same in one dimension. These data are read from the 'trk' file.

These plots are specified using the 'fit' [calculationType](#) and setting the [fitMethod](#) set to 'contour' (2D) or 'custom' (1D). These plot the objective function (z) against two (x, y) or one (x) parameters, and provide a good means of examining the response surface, and why you might be having difficulty converging to a minimum. The normal fit file can be used as a template but change the fit method to one of the above and add <x\_axis> and, for 2D, <y\_axis> tags, to drive the generation of a sequence of [fitParameterValues](#). Then specify the usual plot parameters for 'contour' (xmin, xmax, ymin, ymax, nres, contourZvariable, contours) or 'custom' plots (xmin, xmax, nres, customXcolumn, lines/points and titles).

For a residual sum of squares plot, the data are read in as normal for fitting and compared with the model calculated values to calculate the weighted residual sum of squares (WRSS) surface.

The plot shows how the WRSS varies with the variation of two user-selected variables, most usefully two model parameters. The variation is driven by the normal x- and y-axis parameters [xmin](#), [xmax](#), [ymin](#), [ymax](#) and [resolution](#). These generate changes of the <x\_axis> and <y\_axis> tags which should then be used in the input file to vary the model output, again most usefully by changing the [fitParameterValues](#). The [contourZvariable](#) must be set to 'rss', 'log10(rss)', 'wrss', 'log10(wrss)' depending on whether the residuals have unit weights or not and whether (W)RSS is to be logged or not.

The number of times the input chemistry is run is  $nres \times nres \times \text{number of data points}$  since the `rss` is calculated at each of the grid points.

The demo example `\fit\contour_rss.ppi` shows how the residual sum of squares (RSS) plot for the `iso.ppi` isotherm fitting example varies with the two model parameters, `log_k` and `M1`. Here the RSS has been logged before plotting. The plot is invoked by setting [calculationType](#)

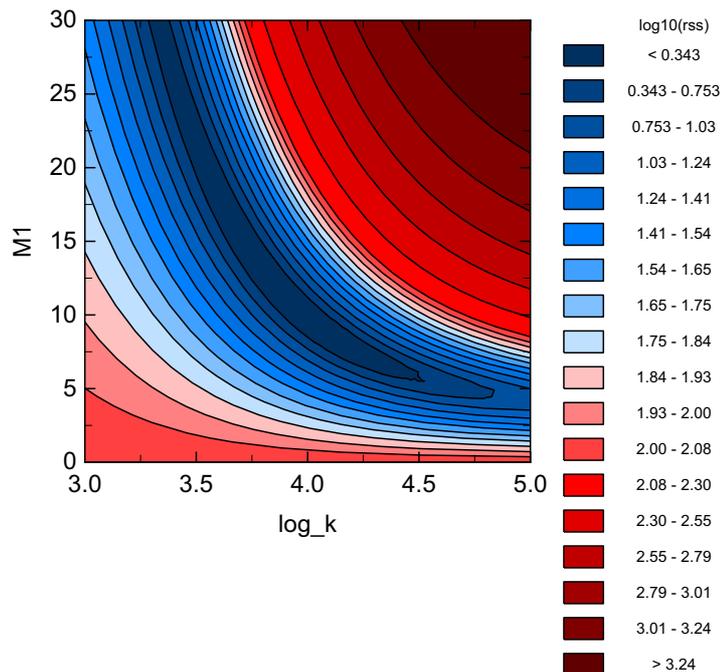


Figure 12.3. Variation of the weighted residual sum of squares versus the values of the two model parameters for the isotherm fitting example, `\demo\fit\iso.ppi`. The plot was generated with the file `\demo\fit\contour_rss.ppi`.

to `'fit'` and `fitMethod` to `'contour'`. The results are shown in Figure 12.3.

The plot shows a deep, banana-shaped valley where the optimal combination of parameters is found. The minimum is found at  $\log_k = 3.9954$  and  $M1 = 9.9011$ . The long valley reflects the relatively high correlation ( $r = 0.987$ ) between the two parameters and shows the difficulty that the fitting routine has in finding the optimal combination of parameters.

The data generated for the plot are written to the track file, `contour_rss.trk`, in the current directory in x-, y- and z-column format.

## 12.14 SIMULATIONS

Simulations use essentially the same setup as fitting except that there are no observations to compare with calculated values and so no fitting takes place. Typically simulations are used after fitting to plot a calculated curve, based on the fitted parameters. This is done by changing the `calculationType` from `'fit'` to `'simulate'`. Values of the independent variables are still read in from a data file and tags assigned, exactly as for fitting.

This mechanism provides a way of running a given piece of **PHREEQC** code for a disparate range of samples read from a file. It is somewhat similar to the use of `SOLUTION_SPREAD` in **PHREEQC** but has more flexibility in the way that the data are read in.

## 12.15 ROOT FINDING – SOLVING EQUATIONS, ADDING CONSTRAINTS

You may want to estimate the value of one or more unknown parameters in a fully-defined chemical model. Most chemical models are too complex to calculate the unknown values explicitly and so the values have to be estimated numerically. When there are more data points than adjustable parameters, the system is over-determined and `'fit'` attempts to find the optimal solution based on minimizing some kind of least squares objective function.

When the number of data points is the same as the number of unknown parameters or fewer,

there are zero degrees of freedom and the problem is then one of finding the unique set of parameter values that minimizes the objective function. This is a minimization problem with the proviso that the 'observed' values are all effectively zero. Some methods (`subplx`, `bobyqa`, `cobyqa`, `newuoa`) work happily with no extra effort but other methods (`nlls`, `lm`) need some 'observations'. Simply set up a file with observed values of zero. The objective function then becomes  $w_i(0-f(x,y))^2$  where  $f(x,y)$  and providing all function values are positive, the minimum in this squared surface will be at the minimum of the function itself.

It is also straightforward to contour the function in two dimensions using the 'contour' calculation type, see the `\demo\contour\trigp.ppi` example.

For example, assume that we want to find the volume of acid required to reach a certain pH. We set up the chemical model such that the volume of acid added is a variable and represented by some tag, say `<titre>`. The selected output is arranged to contain the pH after adding this amount of acid. The pH is the dependent variable. In this example, there is one dependent variable and no independent variables.

Then we make a fit data file with a single data point which specifies the end point pH of interest. 'fit' then adjusts the single adjustable parameter, `<titre>`, so that the match between the input and output pH is very close. The closeness is controlled by the normal convergence criteria.

```
SPECIATION
  calculationType          fit
FIT
  dataFile                  "fittitration.dat"
  dependentVariableColumnObs pHwanted
  dependentVariableColumnCalc pH
  numberOfFitParameters    1
  fitParameterNames        "titre"
  fitParameterValues       0 #initial estimate
  fitAdjustableParameters  1
PLOT
# turn off the plotting
  plotFactor                0.

CHEMISTRY

SELECTED_OUTPUT
  -reset false
  -pH true

SOLUTION 1
  pH      7.05
  units   mg/L
  water   0.050 kg # start with 50 ml water
  Na      6
  K       0.6
  Ca      124
  Mg      1.6
  Cl      11
  Alkalinity 348 as HCO3
  S(6)    3 as SO4
  Si      5.8

REACTION 1 Add 0.16M HCl to the soln
# 1 mL of 0.16M HCl
  HCl     0.16e-3
  H2O     55.5e-3
  <titre>

END
```

The fit data file, `fittitration.dat`, simply looks like this:

```
pHwanted
4.5
```

It takes 1.761 mL of acid. In this case, there is only one **PHREEQC** simulation involved and the default is to use only the first simulation in fitting. If two or more simulations were

involved, then it would be necessary to add a column to the fit data file with the range of simulations to use (e.g. "1-2") and to set [blockRangeColumn](#) to point to this column.

This example can be found in `demo\titration\fittitration.ppi`. While this particular example could be solved pretty closely using a more direct **PHREEQC** approach, the principle is general and applies to more complex examples where such direct approaches are not possible.

In principle, it is possible to extend this approach to search for a solution with many unknowns. The setup has to be slightly different since the objective function must be defined in terms of a single dependent variable. Therefore this has to be defined. A convenient measure to minimize is the RMSE (root mean square error) which can be formed from the deviations of calculated values from their target values.

The following code fragment uses  $\text{Na}_2\text{CO}_3$ ,  $\text{NaCl}$  and  $\text{CuCl}_2$  to make 1kg of a solution with a pH of 9, a Na molality of 0.01 mol/kgw and a free  $\text{Cu}^{2+}$  activity of  $10^{-10}$  ( $\text{pCu} = 10$ ), all in the presence of  $\text{CO}_2(\text{g})$ . Basic lines 10-30 calculate the three residuals and line 40 forms the objective function, the RMSE. Note that no data file is needed – it is assumed in this special case with no degrees of freedom that the ‘observed’ or target values are all zero.

You may need to apply some bounds on the solution – in the example below, only non-negative quantities are permitted – and to scale the various residuals so that they all participate in the solution. Parameter values all close to one are best. The initial values of the three parameters have each been set to one though note that the e-3 following the Cu entry effectively scales this parameter to 1000 times less than the fitted value.

Also the initial and final values of the ‘trust’ region radius, ‘*rhobeg*’ and ‘*rhoend*’, may need adjusting. ‘*rhobeg*’ controls the initial shift in parameter values and ‘*rhoend*’ controls the termination.

```
...
calculationType          fit
calculationMethod        -1
PHREEQC.out              t
fitmethod                 bobyqa
rhobeg                   1e0
rhoend                   1e-7
dependentVariableColumnCalc  rmse
numberOfFitParameters    3
fitParameterNames        mmolNa2CO3 mmolNaCl umolCu
fitAdjustableParameters  1 1 1
fitParameterValues       1 1 1
fitlowerparametervalues  0 0 0

CHEMISTRY

SOLUTION
EQUILIBRIUM_PHASES
CO2(g)    -3.5

SELECTED_OUTPUT
-reset false

USER_PUNCH
-headings rmse
10 r1 = -la("H+") - 9           # pH
20 r2 = TOT("Na") - 1e-2       # diss [Na]
30 r3 = la("Cu+2") + 10        # pCu 10
40 rmse = SQRT((r1^2 + r2^2 + r3^2)/3)
50 IF (STEP_NO=1) THEN PUNCH rmse

REACTION
Na2CO3 <mmolNa2CO3>
NaCl <mmolNaCl>
CuCl2 <umolCu>e-3
1 mmol
END
```

The above example can obviously be generalised with the full array of functions built into

**PHREEQC's** powerful Basic interpreter available for use. There is of course no guarantee of success – the problem may simply not be solvable in which case the ‘nearest’ solution should be found. When successful, the final RMSE should be very small say less than  $1e-8$ . Always check the **PHREEQC** output to make sure that the problem has been solved as intended.

# 13 The input file pre-processor

---

## 13.1 USE OF THE PRE-PROCESSOR

Although the use of tags can eliminate the need for repetitive blocks of text in an input file, this may avoid the more efficient internal looping mechanisms provided by **PHREEQC** and so might be undesirable especially when speed is an issue. This most obviously occurs during fitting where the `onePass TRUE` option is much more efficient than the `onePass FALSE` option.

For example, consider the test fitting example shown below. This is similar to the `demo\fit-preprocessor\isopp.ppi` example:

```
PRINT
  -reset false
SURFACE_MASTER_SPECIES
  Surf Surf
SURFACE_SPECIES
  Surf = Surf
  log_k 0

  Surf + Zn+2 = SurfZn+2
  log_k <log_k> # from fitParameterNames

SELECTED_OUTPUT
  -high_precision true
  -reset false

USER_PUNCH
  -headings sorbZn pH molZn step
  10 sorbedZn=SURF("Zn","Surf")
  20 if (step_no=0) THEN punch sorbedZn, -la("H+"), tot("Zn")*1e3, step_no

SOLUTION_SPREAD
  -units mmol/L
  -pH <pH>

include 'isopp.dat'

SURFACE
  Surf <M1> # from fitParameterNames
  -no_edl
  -equil 1
END

SURFACE
  Surf <M1>
  -no_edl
  -equil 2
END

SURFACE
  Surf <M1>
  -no_edl
  -equil 3
END

...
SURFACE
  Surf <M1>
  -no_edl
  -equil 10
END
```

where the ten observations are defined as a series of `SOLUTIONS 1-10` using the `SOLU-`

TION\_SPREAD keyword data block. The surface is equilibrated in turn with each of the solutions using a repetitive block of code that looks something like:

```
SURFACE
  Surf <M1>
    -no_edl
    -equil n
END
```

where *n* is the solution number.

The pre-processor provides a very simple mechanism for generating these repetitive blocks of code using a simple form of numeric substitution. This is sufficient, for example, to generate a series of simulations varying only by their SOLUTION number, moles of REACTANT, or time interval.

In the above example, the repeating blocks would be replaced by:

```
<repeatStart1> 1 10 1 # startvalue, endvalue, increment
SURFACE
  Surf <M1> # from fitParameterNames
    -no_edl
    -equil <repeatValue1>
END
<repeatEnd1>
```

The critical parts are the `<repeatStart1>` tag which defines the start of the repeat block, the `<repeatEnd1>` tag which defines its end, and `<repeatValue1>` which is a placeholder for where the generated value is to be substituted. All values must be numeric though not necessarily whole numbers.

The three parameters on the `<repeatStart1>` line define a simple looping mechanism: start value, end value, increment value. The generated values are substituted at the `<repeatValue1>` point and the whole repeat block is then added to the input with the substituted value.

All three parameters must be numeric. The sign of the increment is not important. If the second value is larger than the first, the value counts up by the given increment and if the second value is smaller than the first, the value counts down.

The '1' block identifier appended to the end of `<repeatStart` in the above example can be any unique character string of any length.

More than one repeat block can be given but these blocks either must not overlap or if they do, they must be nested 'properly'. Each named loop must have one and only one start and end tag so that each loop is unique. The blocks are expanded top down.

This expanded input is fed into the input parser in the normal way. The parser knows nothing about the pre-processing. The results of the pre-processor's expansion are written to the log file.

# 14 Keywords

## 14.1 SUMMARY OF AVAILABLE KEYWORDS

Table 14.1 gives a summary of the available keywords. The keywords are arranged in their

Table 14.1. Available keywords

Keyword	Function
<a href="#">SPECIATION</a>	section heading
<a href="#">PhreePlotVersion</a>	version of PhreePlot
<a href="#">unrecognisedKeywordIsFatal</a>	determines if unrecognised text in an input file counts as a fatal error or not
<a href="#">checkForUpdate</a>	checks PhreePlot website for a more recent version of PhreePlot
<a href="#">jobTitle</a>	title of this job for log file
<a href="#">speciationProgram</a>	speciation program used
<a href="#">speciationProgramVersion</a>	version of speciation program used
<a href="#">database</a>	thermodynamic database to use
<a href="#">dateDatabase</a>	date or version of thermodynamic database to use - no longer used
<a href="#">pdfMaker</a>	file path of ps to pdf conversion program
<a href="#">fillColorDictionary</a>	file path for fill colour dictionary used in predominance diagrams
<a href="#">lineColorDictionary</a>	file path for line colour dictionary used in custom and fit plots
<a href="#">blockRangeColumn</a>	name of column in a data file defining the range of a block of simulations
<a href="#">mainLoopColumn</a>	name of column in a data file defining the start of the main loop simulations
<a href="#">selectedOutputFile</a>	logical switch which determines if the selected output file is written to disk
<a href="#">PHREEQC.out</a>	explicit switch which determines if the PHREEQC.[id].out file is written
<a href="#">all</a>	logical switch which determines if the *.all file is written
<a href="#">log</a>	logical switch for the log file
<a href="#">trk</a>	logical switch for the track file
<a href="#">pts</a>	logical switch for the points file
<a href="#">pplog</a>	logical switch for the pp.log file
<a href="#">pol</a>	logical switch for the polygon file
<a href="#">labelFile</a>	logical switch for the labels file
<a href="#">vec</a>	logical switch for the vectors file
<a href="#">nudgeFile</a>	logical switch for the nudge file
<a href="#">nudge</a>	nudge label positions definition(s)
<a href="#">out</a>	logical switch for the output (or out) file
<a href="#">writeAllInputFiles</a>	logical switch controlling the number of input files written to the log file
<a href="#">dataSeparators</a>	controls the separator(s) used for data input files and the format of output files
<a href="#">calculationType</a>	type of calculations and plotting to do
<a href="#">calculationMethod</a>	whether to calculate and plot or just replot
<a href="#">mainSpecies</a>	main species in a predominance or mineral stability plot
<a href="#">xmin</a>	minimum x-value for calculations
<a href="#">xmax</a>	maximum x-value for calculations
<a href="#">ymin</a>	minimum y-value for calculations
<a href="#">ymax</a>	maximum y-value for calculations
<a href="#">loopFile</a>	file path for file containing values for the z-loop variable
<a href="#">loopMin</a>	minimum value for the z-loop variable
<a href="#">loopMax</a>	maximum value for the z-loop variable

Table 14.1. Available keywords (contd)

<a href="#">loopInt</a>	interval or increment for the z-loop variable
<a href="#">loopLogVar</a>	determines whether the z-loop variable value is to be anti-logged ( $10^z$ )
<a href="#">loopIndexStartNumber</a>	initial number of loop index used e.g. for naming files
<a href="#">resolution</a>	number of intervals on which x- and y-axis interval is divided
<a href="#">debug</a>	controls response to errors and extent of reporting made to log file
<a href="#">omitAccumulate</a>	filter out all lines containing the given string(s) from being sent to PHREEQC
<a href="#">printScreenFrequency</a>	frequency with which progress in ht calculations is sent to screen
<a href="#">plotFrequency</a>	frequency with which plot.ps file showing plotting progress is written
<a href="#">selectedOutputLines</a>	controls how many selected output lines are sent to the 'out' file
<a href="#">mainLoop</a>	controls the division between pre-loop and main loop PHREEQC simulations
<a href="#">dominant</a>	dominant or subdominant predominance diagram
<a href="#">numericTags</a>	number of numeric tag definitions to follow
<a href="#">characterTags</a>	number of character tag definitions to follow
<a href="#">initialValue</a>	sets the value of all undefined numeric tags
<a href="#">unrecognisedKeywordIsFatal</a>	determines whether an unrecognised keyword produces a fatal error or not
<a href="#">stopOnFail</a>	determines whether calculations stop after PHREEQC has failed or not
<a href="#">writePlaceholder</a>	add a placeholder to the out and trk files if PHREEQC fails
<a href="#">FIT</a>	section heading
<a href="#">dataFile</a>	file path for the data file containing dependent and independent variables
<a href="#">onePass</a>	determines if all dependent variable values are calculated in one pass or not
<a href="#">logDepVariable</a>	indicates whether dependent variable is entered on a linear or log scale
<a href="#">logVariableIn</a>	indicates whether independent variables are entered on a linear or log scale
<a href="#">dependentVariableColumnObs</a>	column from which to read the dependent variable from the fit data file
<a href="#">dependentVariableColumnCalc</a>	column from which to read the dependent variable from the selected output
<a href="#">skip</a>	controls the number of records read in from the fit data file
<a href="#">fitMethod</a>	choose optimization/plotting procedure(s)
<a href="#">objectiveFunction</a>	type of objective function (L1, L2 or RSS) and optional termination value
<a href="#">fitFiniteDiffStepSize</a>	finite difference step size for estimating first derivatives in fitting routine
<a href="#">fitConvergenceCriterion</a>	convergence criterion in fitting routine
<a href="#">fitStepSize</a>	starting step size and/or maximum step size in fitting routine
<a href="#">fitMaxIterations</a>	maximum iterations in fitting routine
<a href="#">fitWeightingMethod</a>	weighting method to use in fitting routine
<a href="#">weightColumn</a>	column giving the weights in the fit data file
<a href="#">numberOfFitParameters</a>	number of parameters that are defined and tagged for fitting
<a href="#">fitParameterNames</a>	names of fit parameters
<a href="#">fitLogParameters</a>	determines whether to log transform fit parameters or not
<a href="#">fitAdjustableParameters</a>	determines whether fit parameters are fixed or adjustable
<a href="#">fitParameterValues</a>	initial values of fit parameters
<a href="#">fitnpr</a>	number of interpolation points used by the NEWUOA and BOBYQA optimizers
<a href="#">fitLowerParameterValues</a>	lower constraint on fit parameters (not currently used)
<a href="#">fitUpperParameterValues</a>	upper constraint on fit parameters (not currently used)
<a href="#">updateFitParameters</a>	determines if fitted parameter values are written to the input file or not
<a href="#">PLOT</a>	section heading
<a href="#">units</a>	units to use for all dimensions
<a href="#">paperSize</a>	paper size to write to Postscript file
<a href="#">backgroundColor</a>	colour of background within the plot boundaries and for the rest of the page
<a href="#">colorModel</a>	colour model to use for all colours
<a href="#">ps</a>	logical switch for generating a ps format plot file
<a href="#">pdf</a>	logical switch for generating a pdf format plot file
<a href="#">png</a>	logical switch for generating a png format plot file
<a href="#">screen</a>	logical switch for screen output and setting for close down time on failure

Table 14.1. Available keywords (contd)

<a href="#">eps</a>	logical switch for generating an eps format plot file
<a href="#">jpg</a>	logical switch for generating a jpg format plot file
<a href="#">svg</a>	logical switch for generating an svg format plot file (needs software installed)
<a href="#">prefix</a>	changes the folder for all output files
<a href="#">overlay</a>	adds one or more graphic images (ps files) on top of the one being generated
<a href="#">plotTitle</a>	title to be placed at top of plot
<a href="#">plotTitleColor</a>	color of plot title
<a href="#">plotTitleSize</a>	height of plot title
<a href="#">xtitle</a>	x-axis title
<a href="#">ytitle, 2ytitle</a>	y(2y)-axis title
<a href="#">xoffset</a>	distance from left hand edge of page to left-hand y axis
<a href="#">yoffset</a>	distance from bottom of page to lower x axis
<a href="#">pageOrientation</a>	portrait or landscape
<a href="#">multipageFile</a>	for multiplot runs, determines whether the plots are all in one file or not
<a href="#">customLoopManyPlots</a>	make many separate plots (if T) or just one (if F) when multiple z-loops specified
<a href="#">xaxisLength</a>	length of x axis
<a href="#">yaxisLength</a>	length of y axis
<a href="#">pxmin</a>	minimum value of x axis on plot and start of major x ticks
<a href="#">pxmax</a>	maximum value of x axis on plot
<a href="#">pxmajor</a>	interval between major tick marks on x axis
<a href="#">pxdec</a>	controls number of figures after decimal point on x-axis labelling
<a href="#">pxminor</a>	x-axis interval between minor (unlabelled) tick marks
<a href="#">yscale</a>	determines the yscale of predominance plots: native, pe or Eh (V or mV)
<a href="#">pymin, p2ymin</a>	minimum value of y(2y)-axis on plot and start of major y ticks
<a href="#">pymax, p2ymax</a>	maximum value of y(2y)-axis on plot
<a href="#">pymajor, p2ymajor</a>	interval between major tick marks on y(2y)-axis
<a href="#">pydec, p2ydec</a>	controls number of figures after decimal point on y(2y)-axis labelling
<a href="#">pyminor, p2yminor</a>	y(2y)-axis interval between minor (unlabelled) tick marks
<a href="#">gridLines</a>	controls whether to plot x- and y- axis grid lines
<a href="#">gridColor</a>	colour of x- and y-axis grid lines
<a href="#">gridDashesPerInch</a>	number of dashes per inch for x- and y-axis grid lines
<a href="#">gridLineStyle</a>	line styles for major and minor x- and y-axis grid lines
<a href="#">customXcolumn</a>	column name or number of x-axis variable for plotting
<a href="#">lines</a>	list of column names or column numbers to plot as lines
<a href="#">lineWidth</a>	line width
<a href="#">dashesPerInch</a>	number of dashes per inch for dashed lines (separate version for 2y axis)
<a href="#">lineType</a>	line style for lines in custom plots (separate version for 2y axis)
<a href="#">lineColor</a>	set initial colours in the line colour sequence
<a href="#">changeColor</a>	determines if the colour changes automatically for subsets of data in custom plots
<a href="#">useLabelsFile</a>	determines if an existing labels file is used or is regenerated in predominance plots
<a href="#">useLineColorDictionary</a>	is the line colour dictionary is used for colours and label positions
<a href="#">restartColorSequence</a>	controls color sequence between plots & within subsets of the same data column
<a href="#">plotOrder</a>	controls the order of plotting of lines and points
<a href="#">points</a>	list of column names or column numbers to plot as points
<a href="#">pointType, pointType2y</a>	list of number or names of symbols used in custom plots
<a href="#">pointSize, pointSize2y</a>	size of symbols used in custom and fit plots
<a href="#">pointColor</a>	starting colour of symbols used in custom and fit plots
<a href="#">rimFactor</a>	widths of the rims of symbols (filled circles) as a fraction of symbol sizes
<a href="#">rimColor</a>	colours of the rims of filled circle symbols
<a href="#">pointsSameColor</a>	controls whether all symbols have the same colour
<a href="#">tickSize</a>	length of the tick marks and controls plotting of the grid lines
<a href="#">tickColor</a>	colour of the tick marks
<a href="#">axisNumberSize</a>	height of the axis numbers

Table 14.1. Available keywords (contd)

<a href="#">axisNumberColor</a>	colour of the axis numbers
<a href="#">axisNumberFormat</a>	enables the default 'exponential' format for large axis numbers to be overridden
<a href="#">axisTitleSize</a>	height of the axis title
<a href="#">axisTitleColor</a>	colour of the axis title
<a href="#">axisLineWidth</a>	width of the axis lines
<a href="#">axisLineColor</a>	colour of the axis lines
<a href="#">labels</a>	list of names to be used for the lines labels in custom plots
<a href="#">labelSize</a>	height of the labels used for labelling lines
<a href="#">labelColor</a>	colour of the labels used for labelling lines
<a href="#">nudge</a>	create an empty nudgeFile for editing and/or specify 'nudge' parameters here
<a href="#">nudgeFile</a>	file to 'nudge' labels to new positions
<a href="#">info</a>	colour for the text of the 'info' data accompanying each plot
<a href="#">legendBox</a>	inserts a box around a legend on a custom or contour plot
<a href="#">legendTitle</a>	text for legend (key) title in custom plots
<a href="#">legendTextColor</a>	colour of the legend text
<a href="#">legendTextSize</a>	height of text in the legend for custom, fit and grid plots
<a href="#">labelEffort</a>	controls the effort (and time) taken to improve automatic label placement
<a href="#">trackSymbolSize</a>	size of symbol used for a tracking plot and for labelling anchor positions
<a href="#">trackSymbolColor</a>	colour of symbol used for a tracking plot and for labelling anchor positions
<a href="#">domain</a>	determines if the domain boundaries are plotted in a ht1 predominance plot
<a href="#">customXcolumn</a>	number or column name pointing to the x-column in a custom or fit plot
<a href="#">font</a>	base font and character encoding to be used for all text
<a href="#">plotFactor</a>	scaling factor to be used for all plot elements
<a href="#">missingValue</a>	dummy value to signal a missing value
<a href="#">minimumAreaForLabeling</a>	minimum size of field (as a %age of total area) to plot a label in a ht plot
<a href="#">minimumYValueForPlotting</a>	minimum maximum y-value for which to plot a curve in a custom plot
<a href="#">beep</a>	turn sound on or off
<a href="#">simplify</a>	controls the degree of polyline simplification in ht plots
<a href="#">convertLabels</a>	interpret label names as PHREEQC formulae or not
<a href="#">extraSymbolsLines</a>	path name for file containing additional symbols and line data to add to plot
<a href="#">text</a>	additional text on plot
<a href="#">extraText</a>	path name for file containing additional text to add to plot
<a href="#">extradat</a>	list of path names for files to add to the search path for variables used in plotting
<a href="#">post</a>	list of names to be used for the posted text or a data file column tag name
<a href="#">postSize</a>	size of the posted text
<a href="#">contourZvariable</a>	name of the variable/column in the outfile that contains the z-data for contouring
<a href="#">contours</a>	list of values at which to draw the contour lines
<a href="#">contourFillColor</a>	list of colours to fill the contour levels
<a href="#">contourLineWidth</a>	list of the widths of the contour lines
<a href="#">contourLineColor</a>	list of the colours of the contour lines
<a href="#">contourShiftLabel</a>	list of contour labels to move and the distance to move them
<a href="#">contourLabelSize</a>	list of the size (height) of the contour labels
<a href="#">contourLabelFigs</a>	list of numbers specifying the number of digits to use in the contour labels
<a href="#">contourLabelFont</a>	list of fonts used for printing the contour labels
<a href="#">contourLabelColor</a>	list of colours used for the text of the contour labels

three major sections: SPECIATION, FIT and PLOT based on their function.

## 14.2 CONVENTIONS

The **PhreePlot** keywords are listed below in alphabetic order. Keywords are not case sensitive. Each keyword has one or more attributes associated with it. The type of these attributes is

fixed. Each one belongs to one of the following types:

logical	T (TRUE) or F (FALSE)
integer	a whole number (no decimal point)
number	an integer or floating point number
string	a character string (with or without enclosing quote marks)
filename	a valid filename which may include the path (system dependent)
filepath	a valid filepath without a filename (system dependent)
color	a valid <a href="#">colour</a> name

### 14.3 KEYWORD DESCRIPTION

The function and use of each keyword is given below. Keywords have been ordered alphabetically. Aliases are alternative names for the keywords. The default is the value set internally by **PhreePlot** and read from the `pp.set` file. These default values can be overridden from the input files (`*.ppi` or `override.set`) or during an interrupt ('Esc') while running. Values given in square brackets are optional.

---

## all

Value	'auto' or a logical (TRUE or FALSE) [filename]
Description	Switch to determine if the standard *.all file is written
Aliases	PHREEQCall.out, PHREEQC.all.out
System default	'auto'
Use	<p>Explicitly sets the switch that determines if the *.all file is definitely written (TRUE) or not (FALSE). This file accumulates all of the printed output from <b>PHREEQC</b> and will be written to on every <b>PHREEQC</b> iteration. This file can get very large and can slow down execution times. FALSE will cause the file to be deleted on termination if present.</p> <p>The 'auto' value sets the all switch depending on the debug level, FALSE if <math>ABS(debug) &lt; 2</math> else TRUE. When TRUE, the *.all file will always be created.</p> <p>'auto' is the default setting.</p> <p>The second, optional, parameter is the filename given to this file. This could be PHREEQCall.out which was the default name given to this file before December 2015. If a filename is given a blank name or the name 'auto', then the default filename will be used, namely &lt;prefix&gt;.all.</p>

---

## axisLineColor

Value	Cohort or rgb colour
Description	Determines the colour of the axes.
Aliases	
System default	<a href="#">auto</a>

Use	Enables the line <a href="#">colour</a> of the axes to be changed. Colours should be chosen from the <a href="#">colour palette</a> .  'auto' reverts to 'black'.
Example	<a href="#">38</a>

## axisLineWidth

Value	non-negative number
Description	Determines the width of the axes.
Aliases	<a href="#">axislw</a>
System default	0.3
Use	Enables the line width of the axis lines to be changed. This setting also controls the line width of the axis tick marks and grid lines (which are special long ticks). This is the same as the width of the axis line for the major ticks, and half the width for the minor ticks.
Example	<a href="#">38</a>

## axisNumberColor

Value	Cohort or rgb colour
Description	Determines the colour of the numbers on the axis scales.
Aliases	<a href="#">numberColor</a>
System default	auto
Use	Enables the line <a href="#">colour</a> of the axis numbering to be changed. Colours should be chosen from the <a href="#">colour palette</a> .  'auto' reverts to 'black'.
Example	<a href="#">38</a>

## axisNumberFormat

Value	'auto' or 'native'
Description	Determines whether the 'exponential' format can be used for numbers on the x- and y-axis scales.
Aliases	
System default	auto
Use	Large and small numbers for the axis numbering can be rendered in an 'exponential' format to make reading easier, e.g. 10000 will be replaced by 10 on the axis scale with the divisor $/10^3$ appended to the axis title.  'auto' tests the maximum/minimum axis number to see if they are sufficiently large or small to use the exponential format. 'native' overrules this

and always uses the non-exponential format.

For small numbers, it may be necessary to also set the maximum number of decimal places explicitly using [pxdec](#), [pydec](#) or [p2ydec](#) as appropriate.

## axisNumberSize

Value	non-negative number
Description	Determines the size of the axis numbers.
Aliases	<a href="#">numberSize</a>
System default	3
Use	Enables the size of the axes to be changed.
Example	<a href="#">38</a>

## axisTitleColor

Value	Cohort or rgb colour
Description	Determines the colour of the titles of the axis scales.
Aliases	
System default	auto
Use	Enables the <a href="#">colour</a> of the axis titles to be changed. Colours should be chosen from the <a href="#">colour palette</a> .  'auto' reverts to 'black'.
Example	<a href="#">38</a>

## axisTitleSize

Value	non-negative number
Description	Determines the size of the axis titles.
Aliases	<a href="#">axisTitleHt</a>
System default	3
Use	Enables the size of the axis titles to be changed.
Example	<a href="#">38</a>

## backgroundColor

Value	Cohort or rgb colour [Cohort or rgb colour, Cohort or rgb colour]
Description	Determines the background colour of the plot, the page and text labels.

Aliases	<a href="#">background</a>
System default	nd nd nd
Use	<p>Enables the background <a href="#">colours</a> to be changed. This plot background is the area bounded by the x and y axes. The plot background is overwritten by any text, lines or fills produced by the plot.</p> <p>The page background is the whole page. The page background colour, if drawn, will be overplotted by the plot background colour, if drawn.</p> <p>The text label colour is the colour of the background behind text in labels for lines, fields and added text. It applies to all such text – it is not possible to specify individual background colours.</p> <p>The second and third colours are optional.</p> <p>nd, or equivalently “”, will suppress the drawing of the colour.</p>
Example	<a href="#">70</a>

---

## beep

Value	logical
Description	Determines whether the sound is on or off.
Aliases	
System default	T
Use	<p>Switches the sound on (T) or off (F). A high-pitched beep is produced on successful completion of a plot. A low-pitched beep is produced when <b>PHREEQC</b> fails to converge or when the plot fails to complete. This option can be useful to signal progress when multiple plots are being produced in the background or to highlight when <b>PHREEQC</b> fails. It can also be irritating. Placing beep FALSE in the override file will ensure that no sound is heard from any run no matter what the setting in the pp.set and input files!</p> <p>Because of the duration of the beep, repeated low frequency beeps can significantly slow down execution. The beeping can be turned off during execution using the ‘Esc i beep F’ sequence. Alternatively, setting beep F in the override.set file will ensure that the sound is off in all subsequent runs.</p>

---

## blockRangeColumn

Value	zero or a positive integer or a column name
Description	Specifies the column number (counted from the left) or column name in the fit data file in which the range of <b>PHREEQC</b> simulations number to use to calculate each observation will be found.
Aliases	<a href="#">fitSimulationColumn</a> , <a href="#">fitSimulationNumberPosition</a> , <a href="#">fitSimulationPosition</a>
System default	0

Use	<p>Only used in ‘simulate’ and ‘fit’ calculations. When <a href="#">onePass</a> is FALSE, the dependent variable for each line of data is calculated from its own <b>PHREEQC</b> simulation, or range of simulations. This variable specifies the column name in the fit data file which contains the <b>PHREEQC</b> simulation number(s) to use for each observation. A range is entered in the form ‘m-n’ or ‘m_n’ without any spaces. Since a range such as 1-2 is non-numeric, the column must be read as a character string rather than as a number. Force this by adding \$ to the end of the column header, e.g. sim\$ rather than sim, or by ensuring that the first line of data in a fit data file is character by enclosing the value or range in quotes, e.g. “2” or “1-2”.</p> <p>In principle, every line of the data file could be specified to use a different block or set of <b>PHREEQC</b> simulations. This would make a multi-objective function fit.</p> <p>When <a href="#">onePass</a> is TRUE, <a href="#">blockRangeColumn</a> is not checked or used since the selected output from all simulations is automatically used for each observation.</p> <p>When this setting is set to 0 (the default) or a negative integer, it is assumed that the block range used for all observations is from 1-n, where n = number of simulations in the input file, i.e. the entire block of simulations is computed in a single <b>PHREEQC</b> run for each observation.</p> <p>Use <a href="#">mainLoopColumn</a> to specify a column in the data file in which the division between the pre-loop calculations and main loop calculations within each block can be set for each observation.</p>
Examples	<a href="#">80</a> , <a href="#">83</a>

---

## calculationMethod

Value	1, 2 or 3 and their negatives
Description	Determines whether to undertake the calculations and plot or just replot existing results
Aliases	<a href="#">method</a> , <a href="#">plotMethod</a>
System default	1
Use	<p>1 = calculate and plot</p> <p>2 = replot only (necessary results files must be present). For ht1 plots, the existing polygon file is used. Do not re-optimize label positions in custom plots or recalculate contours in a contour plot.</p> <p>3 = do not re-speciate but reprocess the output data and replot. With predominance plots, this generates new polygon and label files from the points file (‘ht1’) or the track file (‘grid’ and ‘grids’). With contour plots, this re-reads the raw data from the out file and recalculates the contours.</p> <p>Typically the plot files are generated first time through with a setting of 1 then set to 2 (or 3) during fine-tuning of the appearance of plots. This saves speciation time but not labeling time.</p> <p>Negative values of <a href="#">calculationMethod</a> will do the same as their positive counterparts except that no plot will be produced.</p>

Use of [calculationMethod 2](#) or [3](#) (replot) will not generate ‘run time’ values for those tags assigned values at run time, namely the user punch tags and the tags automatically created during a fit run. In these cases, user punch tags that are not defined values will not be recognised as valid tags in subsequent simulations and so will either plot as their literal text string, i.e. no substitution will be undertaken, or will produce an error message where a numeric value is required. In these cases, recalculating with [calculationMethod 1](#) is the only option.

For custom plots, [calculationMethod 2](#) does not reoptimize label positions; [calculationMethod 3](#) does.

For grid plots, [calculationMethod 3](#) can be used to resume calculations when there has been a crash or an interrupt and stop. The track file is read in and calculations resumed where they left off.

Dummy user punch tags will be defined from the second (first non-header) line of the appropriate ‘out’ file, if present, and fit tags generated from the second line of the data file, if present. This is necessary since all tags are updated just before plotting and some of these tags may be involved in tag definitions. Clearly the values will have little significance in a replot.

If the tags cannot be defined, an error will result.

In order to get dynamic tags – i.e. those generated during a run and whose effects are not stored in the various data files used for plotting – properly substituted, it is necessary to do the calculations from scratch ([calculationMethod 1](#)) each time a plot is wanted.

Example [3](#)

---

## calculationType

Value	one of ‘grid’, ‘ht1’, ‘custom’, ‘species’, ‘simulate’ or ‘fit’
Description	Determines the calculations carried out and the type of plot drawn
Aliases	<a href="#">plotType</a> , <a href="#">type</a> , <a href="#">calculation</a>
System default	“custom”
Use	Specifies one of the six calculation types available: <a href="#">‘grid’</a> , <a href="#">‘ht1’</a> , <a href="#">‘custom’</a> , <a href="#">‘species’</a> , <a href="#">‘simulate’</a> or <a href="#">‘fit’</a> . This keyword should be specified in each input file.
Examples	<a href="#">1</a> , <a href="#">3</a> , <a href="#">55</a> , <a href="#">73</a> , <a href="#">80</a>

---

## changeColor

Value	logical
Description	Determines the extent to which auto-generated colours vary for multiple sets of data especially for subsets of the same variable (column)
Aliases	<a href="#">chgCol</a>
System default	F

Use	<p>Colours for custom plots are picked from a 15-long list of colours. Colours specified by one of the colour settings, e.g. <code>lineColor</code>, are promoted to the top of the line colour list.</p> <p>If <code>changeColour</code> is set to <code>FALSE</code> and if the line colour dictionary is not being used, all line and point colours will be those specified by the <code>lineColor(m)</code> and <code>pointColor(n)</code> settings, where <math>m, n</math> are the positions of the variable in the corresponding <code>lines</code> and <code>points</code> sequences, respectively, i.e. <code>lineColor(1)</code> applies to <code>lines(1)</code>, <code>lineColor(2)</code> applies to <code>line(2)</code>, etc. If the <code>lineColor()</code> list is shorter than the <code>lines()</code> list, then the autocolor sequence is used. The <code>lineColor</code> list is recycled if necessary. All subsets of data for a given variable will have the same base colour although the colour density may vary.</p> <p>If <code>changeColour</code> is set to <code>TRUE</code> and if the line colour dictionary is not being used, the colours used for successive subsets of data and for different variables will be automatically chosen from the appropriate points or lines colour lists. In general, <code>changeColor TRUE</code> aims to ensure that a different colour is used for each dataset plotted, however generated.</p> <p>With species plots where the species are auto-generated and there is no explicit lines variable, the colours specified by the <code>lineColor</code> keyword are used, and recycled if necessary.</p> <p>The colour <code>'auto'</code> (the default) will use auto-generated colours for each distinct dataset using the colour sequence for the data type specified (<code>lines</code>, <code>points</code>, <code>lines2y</code>, <code>points2y</code>) – there is no true colour <code>'auto'</code>. This is equivalent to setting <code>changeColor</code> to <code>TRUE</code> but only applies to that specific data type.</p> <p>If <code>restartColorSequence</code> is <code>TRUE</code>, the colour sequence is reset for each new plot or each new data type (<code>lines</code>, <code>points</code> etc). This can be used to ensure that the same colour is used for the same variable within and between plots. If <code>restartColorSequence</code> is <code>FALSE</code> and the color sequence contains generic colours, i.e. colours specified without a colour density e.g. <code>red</code> rather than <code>red4</code>, then the density of the chosen colours will be cycled through 4, 6, 8, 2, 4 ... for the different subsets, e.g. <code>red4</code>, <code>red6</code>, <code>red8</code>, <code>red2</code>, ...</p> <p>These lists start with the colours specified with the <code>lineColor</code> and <code>pointColor</code> lists and then continue with the unused colours in their normal order. The list is recycled as necessary changing the colour density on each cycle if generic colours (e.g. <code>red</code>) have been specified.</p> <p>Fine tuning of colours is done by editing the line colour dictionary.</p>
Example	<a href="#">62</a>

---

## characterTags

Value	A list of character tag definitions, all on one logical line.
Description	Character tags can be used to substitute strings.
Aliases	<code>characterTag</code> , <code>numberOfCharacterTags</code>
System default	""
Use	Used to enter user-defined character tags with a similar syntax to <code>numer-</code>

[icTags](#), as list of triplets:

```
tagname = expression, e.g.
characterTags      <myTextColor> = "blue4" \
                   <mySymbolColor> = "red4"
```

If none is to be defined, use a blank string:

```
characterTags ""
```

See [Section 5.3.2](#) for a definition of valid tag names. Spaces around the '=' sign are optional. The tag expression should be a simple character string, embedded in quotes if necessary. It can also be another character tag. The initial integer, if present, and the definitions should all be on a single logical line, hence the use of \ above. A \ continuation character enables each tag definition to be placed on a separate physical line. This can aid legibility.

The tag expression must be a single 'word'. Enclose in quotes if it contains one or more spaces. A null string can be entered as "" or '. Character tag names are case sensitive.

If the last character of a tag name is a dollar, then this will always be treated as a character tag not a numeric tag – this is true for tags automatically generated from column headings.

When a character tag is substituted into an input file, no enclosing quotes are included. Therefore in situations where enclosing quotes are needed to force the string to be interpreted as a character string, enclose the tag expression itself in quotes, e.g. if <data>="Clear Lake"

```
USER_PUNCH
- headings pH dataset
10 PUNCH -log10("H+"), "<data>"
```

Character tags can also be used to replace lists of character or numeric items in an input file, e.g.

```
characterTags      <col> = "green6 purple" \
                   <contours> = "0 2 4 6 8 10"
...
lineColor          <col>
contours           <contours>
```

This keyword can be repeated and each instance will be appended to the last rather than replacing it.

## checkForUpdate

Value	logical [non-negative number]
Description	Determines whether <b>PhreePlot</b> checks the <b>PhreePlot</b> website for a more recent version of the program.
Aliases	<a href="#">checkForUpdates</a>
System default	FALSE 1
Use	If TRUE, the <b>PhreePlot</b> website is contacted and the date of the latest ver-

sion obtained. This is compared with the current version and if a more recent version is available, the option is given for opening the website for download. No download is actually made – this is left for the user to do.

The optional second parameter determines the minimum time gap between successive checks (in days) when checking is set on. Set to 0 to check whenever **PhreePlot** is run or a large number to check infrequently. The default of 1 means check once every day.

The checking is largely silent unless `debug > 0` in which case a message is given when a check is being made.

The checking requires an internet connection.

## colorModel

Value            `rgb, b&w` or `gray`

Description     Sets the colour model used

Aliases         `color`

System default   `rgb`

Use             Three colour models are available:

`rgb`            =>    the red-green-blue colour model

`b&w`           =>    black and white only

`gray`          =>    a grayscale

`rgb` colour names are based on the Cohort colour scale or raw `rgb` colour numbers. `b&w` converts all colours to black. `gray` attempts to convert colours to a grayscale based on their hue. The Postscript file produced reflects the colour model used, i.e. a black-and-white file can never be made to produce a colour plot. On the other hand, a colour plot file can often be made to produce a grayscale print on a black and white-only printer.

The ‘`b&w`’ and ‘`gray`’ colour models translate any ‘coloured’ colours to their black and white or gray equivalents at plot time. The original colours are written to the appropriate colour dictionary so that the plot can be replotted in full colour if desired.

If full control over the gray colours used is wanted, these should be entered explicitly in the colour dictionary.

An alternative way of getting a grayscale image is to prepare the image file as a `rgb` coloured image in the normal way and then to use the options available in many printer drivers to export to a file using only grayscale or black and white colours. You don’t have to actually have the printer attached, just have the printer driver installed, e.g. the Adobe pdf printer driver.

## contourDashesPerInch

Value            list of non-negative numbers

Description	Sets the dash density for contour lines
Aliases	
System default	10
Use	The list of numbers should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.

---

## contourFillColor

Value	list of colours
Description	Sets the colours used for filling in between the contour lines
Aliases	
System default	auto
Use	<p>The list of colours should be the same length as the number of contours plus one. If shorter, the list is recycled. If longer, it is truncated.</p> <p>The colours are paired off in sequence, one per contour class.</p> <p>Use 'nd' for 'not drawn' or no colour.</p> <p>'auto' generates a colour from a list of colours initially centered on <code>sky0-red0</code> with the lowest class being the darkest blue and the highest class being the darkest red. The 'blue' list is ultimately expanded to the 10-long sequence <code>sky0, sky1, ..., sky9</code> and the red list to <code>red0, red1, ..., red9</code> to give a 20-colour sequence. For shorter lists, the relative order is retained but the actual colours chosen are spaced out a bit to provide better contrast.</p> <p>As the number of colours required is increased beyond 20, additional colours are added pairwise to the low and high end: spring/magenta, cyan/purple, green/orange and blue/maroon. There are therefore a maximum of 100 distinct colors. This corresponds with 99 specified contour levels. It is an error to specify more than 100 colours. 'auto' is recycled in short lists if necessary. For example, if the number of contours is 5, the number of fill colours will be 6. So if the list of fill colours is</p> <pre>auto yellow0 auto</pre> <p>the list will be recycled twice with the second and fifth auto colours replaced with <code>yellow0</code>.</p> <p>Colours should be chosen from the <a href="#">colour palette</a>.</p>

---

## contourLabelColor

Value	list of colours
Description	Sets the colours used for the labels to the contour lines
Aliases	
System default	auto
Use	The list of colours should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.

The colors are paired off in sequence, one per contour value.

Use 'nd' for 'not drawn' or no colour. This will suppress the drawing of the label(s) for this contour level.

'auto' will copy the colour specified by [labelColor](#).

Colours should be chosen from the [colour palette](#).

---

## contourLabelFigs

Value	list of non-negative integers
Description	Determines the number of significant figures used in the numeric contour labels
Aliases	
System default	auto
Use	<p>The list of integers should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.</p> <p>The integers are paired off in sequence, one per contour value.</p> <p>The format used depends on the size of the value of the label. Exponential format is automatically used for very large or small numbers. Precede the integer with “_” to force the number to be written in floating point format and with “\$” for exponential format, e.g. \$2.</p> <p>Trailing zeros will be removed.</p> <p>Use 0 to force the value to be printed to the nearest integer.</p> <p>'auto' will use 3 or less figures depending on the value and is the default.</p>

---

## contourLabelFont

Value	list of fonts
Description	Determines the font used by the contour labels
Aliases	
System default	auto
Use	<p>The list of fonts should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.</p> <p>The fonts are paired off, one per contour value.</p> <p>The fonts are specified by font names or font family names (see <a href="#">font</a>).</p>

---

## contourLabelSize

Value	list of numbers
Description	Determines the size (height) of the contour labels

## Aliases

System default `auto`

Use The list of label sizes should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.

The sizes are paired off, one per contour value.

The units of `contourLabelSize` depend on the units in effect when `contourLabelSize` is set.

'auto' copies the size given by `labelSize`.

## contourLineColor

Value list of colours

Description Sets the colours used for the contour lines

## Aliases

System default `auto`

Use The list of colours should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.

The colors are paired off, one per contour value.

Use 'nd' for 'not drawn' or no colour. This will suppress the drawing of the contour(s) for this contour level.

'auto' will match the colour specified by `lineColor`.

Colours should be chosen from the [colour palette](#).

## contourLineType

Value list of numbers from 0 to 20

Description Sets the line type used for contour lines

## Aliases

System default `1`

Use The list of numbers should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.

The 20 line styles are shown [here](#).

Other settings such as line colour, line width and dash density will affect the appearance of the lines.

## contourLineWidth

Value list of numbers

Description Sets the width of the contour lines

Aliases	
System default	auto
Use	<p>The list of widths should be the same length as the number of contours. If shorter, the list is recycled. If longer, it is truncated.</p> <p>The widths are paired off, one per contour value.</p> <p>Use 'nd' for 'not drawn' or no colour. This will suppress the drawing of the contour(s) for this contour level.</p> <p>'auto' will copy the width specified by <a href="#">lineWidth</a>.</p>

## contourOptions

Value	string of options
Description	Sets various options for the contour plot
Aliases	contourOption
System default	smooth=0 fill=TRUE fill=TRUE joinSegments=TRUE labelPosition=straightest replaceUndefined=TRUE
Use	<p>This currently sets up to four options affecting the generation and display of a contour plot. Include only those keyword-value pairs that need changing. Separate keyword-value by either an equals sign or one or more spaces, tabs or commas. Number and order of pairs given is optional.</p> <p>The options are:</p> <p>(i) <code>smooth=0   1   2</code></p> <p>After generating the z-data, or reading it from an outfile, it is possible to smooth it using a low pass filter. This is either a five point (<code>smooth = 1</code>) or nine point (<code>smooth = 2</code>) moving average based on equal weighting of the central cell and either the four nearest neighbours (i.e. the cells N-S-E-W of the central cell) or the eight nearest neighbours (i.e. the cells N-S-E-W-NW-NE-SE-SW of the central cell). A value of 0 means no smoothing is carried out. It is not necessary to regenerate the z-data to test these various options. Once the data have been generated and plotted, use the <a href="#">calculationMethod</a> <sup>3</sup> option to smooth again and replot.</p> <p>(ii) <code>fill=TRUE   FALSE</code></p> <p>If <code>TRUE</code>, the colour fills are plotted with the simplified lines taken from the vector file and the coordinates for the polygon fills taken from the polygon file. If <code>FALSE</code>, this produces a lines only plot with no colour fill between contour levels. It comes in two flavours depending on the third option:</p> <p>(iii) <code>joinSegments=TRUE   FALSE</code></p> <p>If this is set true, then the lines are joined up and then plotted. If it is set false, then the short line segments making up a contour are plotted separately and in the order produced by the scanning algorithm used to determine the contours.</p> <p>This difference can be subtle and is best seen by looking closely at the line joins which are smoother with the <code>TRUE</code> option. Dashed lines are often much better looking with the <code>TRUE</code> option. The advantage of the <code>FALSE</code></p>

option is that its output is derived directly from the contouring routine and does not require post-assembly into a continuous line, which can be difficult. Therefore if the joining of line segments is a problem, try the option which misses this step.

If the `joinSegments FALSE` option is used to generate the original plot, then the `TRUE` option cannot be used for a simple replot ([calculationMethod 2](#)) since no polygon file will have been produced. Recalculate ([calculationMethod 1](#)) or relabel and replot with [calculationMethod 3](#) to produce the polygon file.

(iv) `labelPosition=longest | straightest | centre | center`

This controls the position of the labelling for all contour lines, either close to the longest straight section (default) or near the centre of the line. Individual labels can be shifted with [contourShiftLabels](#).

If a plot with inline labels and no fill colour is wanted, choose the `fill=TRUE` and `contourFillColor nd`.

(v) `replaceUndefined=TRUE | FALSE`

If `TRUE`, replaces all undefined values (`-99999.0`) with the average of the nearest four neighbours providing that they are all defined. Undefined values can arise from failures in speciation, attempting to log a non-positive number, or missing data.

## contours

Value	list of numbers in strictly ascending order or <code>auto [n [p s e]]</code>
Description	Sets the values of the contours to plot
Aliases	
System default	<code>auto 17 e</code>
Use	<p>This keyword defines the contour levels used. The main task is to get a set of contours that displays what you want without getting confused by numerical noise, especially around phase boundaries.</p> <p>The maximum number of contours that can be set is 99. There are several ways of defining the number and value of the contour levels.</p> <p>The first way is simply a list of user-defined contour values in a strictly ascending order (cannot be equal). The list can be of any length.</p> <p>The second way, <code>auto [n [p s e]]</code>, lets <b>PhreePlot</b> choose the number and value of the contours. <code>n</code> contours are chosen (default <code>n = 17</code>).</p> <p>These values are selected based on the z-data being contoured. This is done in one of three ways: (i) by percentiles (<code>'p'</code>) in which the various contour classes are approximately equally occupied, (ii) by simplified percentiles (<code>'s'</code>) which is the same as the <code>'p'</code> option except that any pair of adjacent contour values that are 'rather close' to each other (within less than <math>1e-2</math> of the z-data range) are replaced by a single average value, or (iii) by dividing the z-range (<math>z_{\max} - z_{\min}</math>) into <code>n</code> equally-spaced contours (<code>'e'</code>).</p> <p>The z-data statistics used in calculating contour levels using the <code>auto</code></p>

option are based on all the data read from the data file not a selection based on any redefinition of the plotting domain by changing [xmin](#) etc.

Aside from the simplified percentiles approach which explicitly ‘simplifies’ or reduces the number of contours, successive pairs of contour values must always differ from each other by at least  $1e-8$  of their average value. If specified or generated contour values are closer than this, the pair of values will be replaced by their average value.

The actual number of contours plotted may therefore be fewer than the number specified. This occurs when the contours are deemed to be ‘too close’ to each other as described above.

The empirical (‘e’) approach is the default.

The contour values actually used are always reported in the log file.

Example

[84](#)

## contourShiftLabel

Value	‘c’ or ‘n’ then zero or more triplets of integers which specify the plot number, contour number and shift amount
Description	Display label position and specify which labels to move and by how much for contour plots with inline labels (filled colour plots)
Aliases	
System default	c
Use	The first character determines what the label is: ‘c’ ‘c’ for contour. The contours are labelled with their values (default). The number of digits is controlled by <a href="#">contourLabelFigs</a> . ‘n’ ‘n’ for number. The labels show the contour line number rather than the contour value. The vertices of the contours (after line simplification) are shown with the track symbol (filled circle) of colour <a href="#">trackSymbolColor</a> and size <a href="#">trackSymbolSize</a> (1). The sequence number of each vertex is written above the vertex using <a href="#">trackSymbolColor</a> and half <a href="#">labelSize</a> and with the line number appended in parentheses.

If triplets of integers follow, these define a contour label and how much to move it from its default position. The default position is either centered within the longest straight section of each contour, or in the middle. This is controlled by one of the [contourOptions](#).

The triplets are specified as follows:

**first integer** (non-negative): the absolute value defines the plot number of interest. Each plot is numbered sequentially as plotted. The plot number is given in the log file and is printed at the top left of the [info](#) block. The sequence number increments on cycling through the main species (outer loop) and then the loop variables (inner loop).

**second integer** (non-negative): gives the contour number. The contours are plotted from the ‘vec’ file with the list of vertices of each contour being separated by a blank line. The contours are numbered sequentially as read from this file. The contour number refers to this sequential posi-

tion. Each contour can in principle be represented by more than one vector when it intersects a domain boundary, hence the reason to specify by this number rather than simply the contour class.

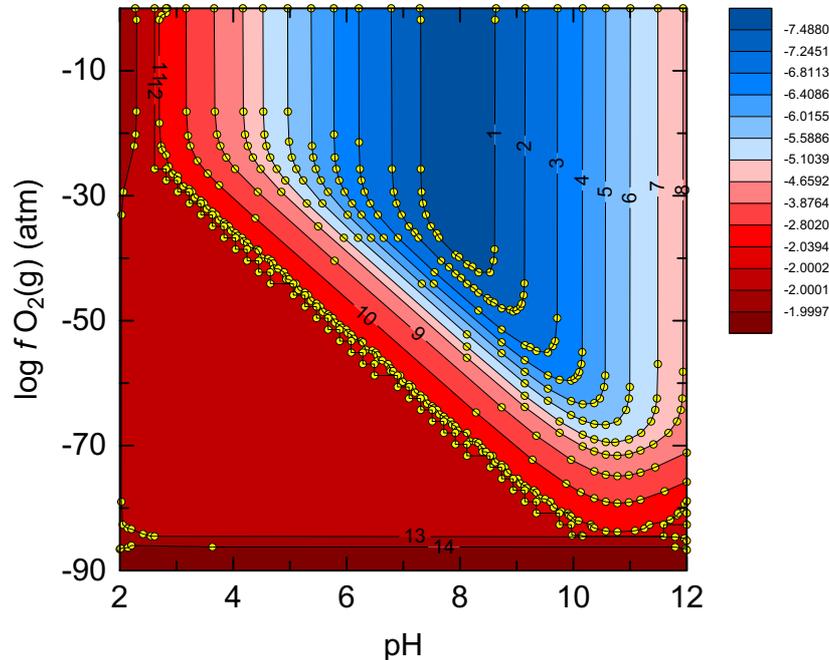
**third integer** (non-negative): gives the 'distance' to shift or move the label from its default position in terms of vertices. The default position places the label at the centre of the longest straight segment in the simplified vector. A shift of +1 moves the label to between the next pair of points, +2 to two points forward etc. -1 moves the position backwards one point etc. 'Forward' is always 'moving forward with the high side on the right'.

In order to estimate the shift settings, it is simplest to first plot with the 'n' option. This will mark all the points on the contours with coloured circles. The number of points to shift by can then be easily determined, shifting forward from the default position using positive integers and backwards using negative integers. Once the shift has been determined, the shift type can be reversed from 'n' to 'c' to plot the contour values.

Simplified straight line segments will have few vertices. The number can be increased by reducing [simplify](#).

The printing of all labels for a given contour level can be suppressed by setting the [contourLabelSize](#) to 0, or the [contourLabelColor](#) to 'nd'.

The figure below shows the contours labelled with their consecutive line numbers (1-14) using the 'n' option. The colour and size of the circle symbols have been specified with the [trackSymbolColor](#) and [trackSymbolSize\(1\)](#) settings.

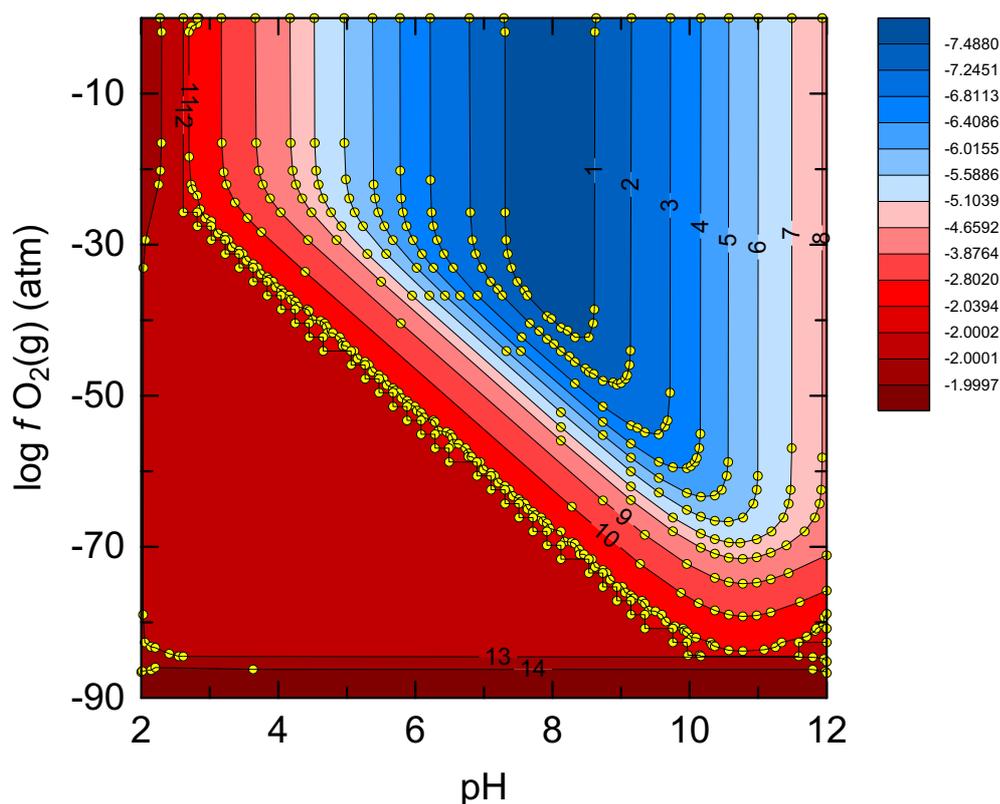


Moving the '9' and '10' labels forward one point is achieved with:

```
contourShiftLabel n 1 9 1 1 10 1
```

as seen in the figure below.

This moves the labels to the centre of the next interval. If the shift places the label outside the list of points, the label is not drawn. This is how the plotting of individual overlapping labels can be entirely suppressed.



An alternative approach is to shift the labels with the [nudge](#) or [nudgeFile](#) keywords.

## contourZvariable

Value	list of names or numbers of one or more outfile columns (case sensitive)
Description	Specifies the variables (columns) in the outfile to be used as a source of z-data for contouring
Aliases	
System default	""
Use	The length of the list defines the number of contour plots produced. The <a href="#">contourZvariable</a> must either be present in the outfile or are assumed to be the first variables PUNCH'ed to the primary (lowest numbered) selected output block. It can be specified by name or number (the column position in the outfile). Normally the name is set by the <code>-headings</code> setting in a <code>USER_PUNCH</code> data block but it may be defined dynamically in which case it may be necessary to specify the column by number or by using the default heading such as "no_heading_1".

For a residuals sum of squares contour plot, [contourZvariable](#) must be either 'obj', 'rss', 'wrss' or their log10 equivalents, e.g. 'log10(wrss)' depending on the objective function chosen. 'obj' should always be chosen for the L1 norm. The 'obj' name refers to both norms and all weightings and so should always work.

There must be  $n_{res} \times n_{res}$  rows of z-data in the outfile where  $n_{res}$  is the [resolution](#). The speciation must not fail anywhere. If it does, the calculations stop immediately and no plot is produced. Similarly, if a contour

plot is being produced, the `contourZvariable` must be found in the outfile headings.

Example [84](#)

## convertLabels

Value	logical [logical]
Description	Determines whether an attempt is made to interpret plot labels as <b>PHREEQC</b> chemical formulae with subscripts and superscripts etc
Aliases	<a href="#">convertLabelNames</a>
System default	T T
Use	If the first setting is set to T (TRUE), label names are checked to see if they are plausible <b>PHREEQC</b> chemical formulae and if so, they are converted. This does not check the thermodynamic database for formulae names but does check for basic things such as the first character must be a (, [or uppercase letter, and it must not contain any of the characters: <code>¬#~@;?!"£%^&amp;*'"</code> .

If a label does not look like a formula or if `convertLabels` is FALSE, then no attempt to interpret it as formula. For examples of the conversion see [Section 6.4.2](#).

If some labels are to be interpreted as formulae and some not, then `convertLabels` should be set to TRUE and the individual label names should be written in such a way as to prevent them being interpreted as a formula, e.g. begin names with a lower case character or include one of the ‘illegal’ characters.

The ¬ character can be read but will not be printed with the ASCII encoding and so if added to the end of a name will prevent its conversion without being seen in the final plot.

This setting applies to all label names including loop names.

The second optional setting controls the interpretation of colons in formulae. If this is set to TRUE, then colons (:) are replaced with a period (.). This is to deal with formulae such as  $ZnCO_3 \cdot H_2O$  and  $UF_4 \cdot 2.5H_2O$ . Again, it deals with all translations. If a block on a single label translation is wanted, edit the appropriate line in the labels file so that the a non-printing character such as ¬ (ASCII encoding) precedes the colon.

Example [84](#)

## customLoopManyPlots

Value	logical switch [logical switch [character]]
Description	Determines if each new value of the z-loop variable produces a new plot or not and optionally, whether the loop index is appended to the label name.
Aliases	

System default	FALSE TRUE ` _`
Use	<p>Only used for custom plots. The default (<code>FALSE</code>) means that each value of the loop variable will normally produce a separate curve on a single plot. This can be messy and so when this option is set to <code>TRUE</code>, a new plot is produced for each value of the loop variable. These can be combined into a single file using the <a href="#">multipageFile</a> option.</p> <p>The additional optional logical switch determines if the loop index is appended to the label name (<code>TRUE</code>) or not (<code>FALSE</code>) and the character determines the separator between loop name and loop index, e.g.</p> <p><code>Fe(OH)3(a)_1</code>.</p>

## customXcolumn

Value	positive integer or column name (case sensitive)
Description	Determines which column of data in the outfile is used for the x axis during custom plotting.
Aliases	<a href="#">xColumn</a> , <a href="#">customXPosition</a>
System default	1
Use	<p>Ensures that the correct column is used as the x-axis variable for plotting. The order of output is determined by the order of <code>USER_PUNCH</code> statements and the choice of other <code>SELECTED_OUTPUT</code> parameters in the <b>PHREEQC</b> code. The columns are counted from the left. Used for custom and species plots. In species plots, <a href="#">customXcolumn</a> should point to the column of either the species name or the numeric value of the pair wanted.</p> <p>If data from two or more data files are to be used in the plot, make sure that they have the same name for the x column. If this is not possible, or if two or more separate plots are wanted, plot in separate runs, possibly creating a batch file or script to execute the two runs consecutively.</p>
Examples	<a href="#">55</a> , <a href="#">73</a> , <a href="#">80</a>

## dashesPerInch, dashesPerInch2y

Value	list of non-negative numbers
Description	Determines the number of dashes (and dots) per inch for dashed lines.
Aliases	<a href="#">dashes</a>
System default	10
Use	<p>This gives the number of dashes (and dots) per inch for dashed <a href="#">lines</a> in custom plots. Dashed lines are indicated by the respective <a href="#">lineType</a> style</p> <p>In custom plots, the <a href="#">dashesPerInch</a> for a line is picked from the <a href="#">lines</a> list in order (and recycled where necessary), i.e. the first line takes the first <a href="#">dashesPerInch</a>, the second line takes the second <a href="#">dashesPerInch</a> etc.</p> <p><a href="#">dashesPerInch2y</a> is similar to <a href="#">dashesPerInch</a> but applies to the 2y axis.</p> <p>Dashed lines of varying density can also be used for the grid lines of a plot (see <a href="#">gridDashesPerInch</a>).</p>

## Examples

---

## database

Value	filename
Description	Controls which thermodynamic database file is used by <b>PHREEQC</b> .
Aliases	
System default	wateq4f.dat
Use	Set the filename of the database that is to be used by <b>PHREEQC</b> . Note that the database should be set with this keyword rather than using the <b>PHREEQC</b> 'DATABASE' keyword.  The database is not loaded until inside the z-loop and so can be changed with a loop file and tags.
Example	<a href="#">40</a>

---

## databaseVersion

Value	string
Description	Gives information about the version of the database selected.
Aliases	
System default	none
Use	If the log file is activated, this string is printed to it. It is also printed in the info block of a plot if that is selected to be printed. These provide a record of which database was used in the calculations used to make the plot. The string can be a date but does not have to be.  This setting does not affect the computations.

---

## dataFile

Value	filename [data separator]
Description	Specifies the file containing data for the simulate and fit calculations and optionally the data separator(s) used to parse it.
Aliases	<a href="#">fitDataFile</a>
System default	
Use	This text file contains the observations (dependent variable), if present, and the independent variables if present. The first line should consist of the column headers. These are converted to tags and so should conform to the tag naming conventions (e.g. arithmetic operators like + or - and other illegal characters will be automatically replaced by an underscore).  The total number of columns to be read is determined from the number of entries in the column header. This should also match the number of

entries specified by the [logVariableIn](#) setting.

Contiguous blanks are treated as a single separator but multiple other separators (e.g. , , ) will introduce null fields. Comments can be included using a # as usual. Blank lines are ignored.

Where only some non-essential data are absent, some form of missing data identifier can be used to identify such cells, essentially acting as placeholders. For example, a blank field can be entered as a null string, "", or by a missing value. A null string will be set to zero if it represents a numeric field.

The header line and the remaining part of the file will be parsed, by default, according to the separator(s) specified by the first entry in the [dataSeparators](#) keyword. If the optional data separator string is specified with the data file name, then this is used. The options for this separator are given in [Section 5.2.6](#). The columns can be either designated as 'numeric' or 'character'. Any column with a heading ending in a \$ sign is automatically designated character. For other columns, this is established from the format of the first line – whether it contains non-numeric data or not. The \$ notation is the preferred method for establishing the type of column.

The location of the column containing the dependent variable if present is specified by the [dependentVariableColumnObs](#) keyword.

The other columns that have been read in are given tags defined by their column headers with numeric or character type depending on the type of the corresponding entry in the first valid data line. These tags can then be used in the **PHREEQC** input file. Each iteration of **PHREEQC** will read in one line of the data file, generate a full set of tags and their corresponding tag values, make any tag substitutions in the **PHREEQC** input and run. A maximum of 20 characters is output by **PHREEQC** - longer strings will be truncated.

If [calculationType](#) = 'simulate', then the data file can be used to supply a list of tag values to the input file without undertaking any fitting. There need not even be a dependent variable.

If the filename is blank and the calculation type is 'fit', then it is assumed that there are no degrees of freedom and the problem is a 'root finding' one. In this case, the 'target' value is always set to 0.0, i.e.  $f(x) = 0$ . The  $f(x)$  is set in a `USER_PUNCH` block and the initial estimate(s) are adjusted to achieve the target value. This is equivalent to including a one line data file containing the target value along with [dependentVariableColumnObs](#) giving the column name.

Examples [80, Using the 'simulate' calculationMethod](#)

---

## dataSeparators

Value	up to seven separate 1- or 2-character strings
Description	Defines the separators used in data input and formatted output files.
Aliases	<a href="#">sep</a>
System default	<code>input="\ " output="\t" xyblank="\p" loop="\p" rewind="\r" break="" quote = ""</code>

Use The standard input files use a space, tab or comma for separators but this can be too flexible for formatted data files. Also it is useful to be able to specify whether blank lines (indicating a break in a plotted curve) are written to the 'out' file after a change in a loop variable. This keyword contains options that can be used to control the interpretation of various data separators.

With whitespace separators (`\b`, `\w` and `\`), contiguous separators are treated as a single separator but in the case of tab (`\t`)- or comma (`\,`)-delimited input they are treated as single separators and so can be used to read in files with blank or missing fields, e.g. `" , , "`.

If the `keyword=value` format shown above is not used then all seven separators must be included on a single line in the order given. If keywords are used, then one or more options can be specified and in any order.

Quoted fields are treated as a single field even if they contain spaces.

The seven possible entries are:

1. `input`: default separator(s) for reading data input files, e.g. by 'fit' and 'speciate' as well as loop and [extradat](#) files (the separator can also be specified separately for each file, see [Section 5.2.6](#));
2. `output`: separator to be used in formatted output files notably the 'out', 'trk' and custom 'pts' files. The same separator will also be used later for reading these files;
3. `xyblank`: controls whether a blank line is inserted into the 'out' file for each new value of `<x_axis>` or `<y_axis>`;
4. `loop`: controls whether a blank line is inserted into the 'out' file for each new value of the loop variable (z-value). `"\p"` will insert a blank line, `"` will not;
5. `rewind`: controls whether the 'out' file should be rewound at the beginning of each iteration (`"\r"`), or not (`"`).
6. `break`: a 'break variable' used to introduce one or more breaks in a column of data based on the change in slope (numeric column) or value (character column) of this variable.
7. `quote`: the delimiter for printing character strings sent to the 'out' file. Default is a double quote. Use a null string to omit the delimiter, e.g. `quote=""`.

The input separator defines the separator for reading 'user-prepared' data files (as opposed to input files with keywords, extra text files or dictionary files). The three data files that use this setting at present are the fit data file used during fitting and simulations, the loop data file and any `extradat` data files.

Use any single character or `"\t"` for a tab, `"\b"` for a blank space or `"\w"` for both (whitespace). Quoted strings are entered using paired single or double quotes and must have a separator (e.g. a space) preceding/following them, e.g. `1234 "56 78" 9` where '56 78' will be parsed as a single word. A null string, entered as a pair of quotes with nothing in between (`""`), indicates that either a tab, space(s) or comma is interpreted as a valid separator. This is equivalent to `"\`". Consecutive blanks are treated as a single separator but multiple other single character separators are not, i.e. they will be interpreted as missing data or blanks depending on their type. This allows blank fields to be read. Tabs alone are useful when an input

file has been pasted into a text file from a spreadsheet and when spaces and commas are present in text strings and the strings are not embedded in quotes. Although quoted strings will preserve whatever is inside them, the quotes can get lost on pasting to and from a spreadsheet.

“, ” should be used for the first setting in comma-separated (csv) files.

The `output` separator specifies the separator to use for formatted output files, notably the ‘out’, ‘trk’ and ‘pts’ files. Tabs (“\t”), commas(“, ”) or spaces (“\b”) are the most commonly used separators. Enclose the specified separator in quotes if necessary. Tabs are useful when the file is to be pasted into a spreadsheet. Spaces and commas are preserved in strings without the need to quote them.

When a space (“\b”) is used for the output separator, then additional spaces are inserted to justify the columns. This format is better for reading and printing. However, character strings are truncated to 18 characters to allow the strings to be quoted. Use tabs if this is a problem.

Note that “ ” is not the same as “ ”. The former is the null string; the latter is a space.

The `xyblank` and `loop` separators refer to the between-the-line separator used in the ‘out’ file. If these two strings are “\p”, then a blank line is inserted into the out file after (i) a change in the x- and y-axis loop variable (third separator); or (ii) a change in the z-loop (or <loop>) variable (fourth separator). Any other characters, including the null string, “”, means that no blank line is inserted at these points. These settings can be used to control the breaks made when plotting curves. If a loop file is used, it is also possible to insert a blank line into the ‘out’ file by inserting a blank line into the corresponding position in the loop file.

The `rewind` separator determines if the ‘out’ file should be rewound at the beginning of a fit iteration or not. A rewind is indicated by the “\r” combination otherwise there is no rewind. The net result is that if the file is rewound at the beginning of each fit iteration, the ‘out’ file will only be left with the results from the last set of calculated values returned from **PHREEQC**. Otherwise the results from each iteration, i.e. all **PHREEQC** calculations, will accumulate in this file.

The `break` separator is a break variable that can be useful for separating the plotting of a column of data in the out file into two or more separate curves (as can be done with a blank line) when there is no blank line in the out file. Sometimes it is not possible or easy to introduce a blank line in the out file where it is needed. For example, if more than one **PHREEQC** simulation is executed during a single **PhreePlot** iteration (using the [mainLoop](#)) the selected output from the two simulations is run together without a break. However, it is usually possible to arrange for some variable to indicate when a break is needed. This could be one of the loop variables or the simulation step number.

This `break` parameter is the name of the column in the outfile that is used to identify a break. This only applies to the file containing the break variable, and only one such break variable can be specified. A break is signaled when the direction of the ‘slope’ in this break variable changes for numeric columns or when its value changes for a character column. The reference direction for a numeric column is determined from the first two rows of data and is positive, negative or zero (signaled by an absolute difference of less than 1E-8). A break is made at every change of direction in

slope with each block of data being considered independently. Care should be taken to avoid choosing a variable in which the difference between adjacent data values is subject to significant numerical errors.

If a character column is defined, then label names for each of the subdivided curves are automatically set to their character values. This enables them to be plotted with different styles and the legend automatically configured accordingly.

The data separator used for reading input data for custom plots is always the separator set by the `output` separator since the file used for plotting is generated with this format. Care has to be taken to not edit the plot data files in such a way as to bring this relationship out of synchronization. If in doubt, regenerate the files, [calculationMethod](#) 1.

Examples [82, Using the 'simulate' calculationMethod](#), `\demo\SI\SI.ppi`, `\demo\Alvsphpredom\Alvsphpredom.ppi`

## dateDatabase

Value	string
Description	Gives the date of the specified database
Aliases	<a href="#">databaseVersion</a>
System default	“
Use	No longer used. The date is now obtained from the file itself and is the date that the file was last modified. It is only used for printing to the log file and the info data block.

## debug

Value	0, 1, 2, 3, 99
Description	Controls the amount of information sent to the log file and the action taken when an error is encountered.
Aliases	
System default	‘0’
Use	The higher the value, the greater is the amount of information that is sent to the log file.

There are many switches controlled by [debug](#) but the main actions are:

0 = provides the least logging and therefore gives the fastest execution times. In this case, all **PHREEQC** input/output is via memory rather than via disk files. This debug setting is the normal value for production runs. With predominance plot calculations, the species returned in the case of errors in speciation are all given the label ‘NA’.

1 = as above and also writes the values of all the tags substituted to the log file and saves a copy of the speciation output from the last simulation in the file [PHREEQC.\[idl\].out](#) providing this has not been set to false explicitly. With predominance plot calculations, any error in speciation triggers

an immediate halt to the calculations. Use this setting to check that the correct lines of **PHREEQC** code have been executed each time and that the tag values are as expected.

2 = as above and also accumulates the `PHREEQC.[id].out` data for each simulation in the `*.all` file providing the [all](#) keyword has not been set to false explicitly. Use this setting to see the detailed output from **PHREEQC**. This file can get very large.

3 = as above but also echoes the **PHREEQC** input to the screen just before it is executed. The **PHREEQC** output is also inserted into the log file. This can produce a very large log file with slow execution times. The track and log files for predominance plots are written after each speciation calculation rather than at end so that partial files will be still written if the calculations do not complete.

Debug also controls the output when the default file switches for [PHREEQC.out](#) and [all](#) are set to 'auto'. These are detailed in Table 14.2 Table 14.2.

Table 14.2. The effect that the [debug](#) setting has on the generation of **PHREEQC** output files.

PHREEQC output file	debug keyword setting			
	<=0	1	2	3
<b>Output</b> ( <code>PHREEQC.[id].out</code> )*	FALSE	TRUE	TRUE	TRUE
<b>Error</b> ( <code>PHREEQC.[id].err</code> )	FALSE	TRUE	TRUE	TRUE
<b>Log</b> ( <code>PHREEQC.[id].log</code> )	FALSE	TRUE	TRUE	TRUE
<b>Selected output</b> (e.g. <code>selected_[w].[id].out</code> )	FALSE**	TRUE**	TRUE**	TRUE**

\* with predominance plots, there is a special case when [resolution](#) = 1 in that this forces `PHREEQC.[id].out` to be written whatever. This file will contain a list of all the possible mineral phases ready for pasting into the input file. There are also the explicit [PHREEQC.out](#) and [all](#) switches.

\*\* can be overridden by the [selectedOutputFile](#) keyword.

The special value of '99' does not run the input files but rather checks the files for the use of any keyword aliases. If found these are listed along with the respective main keywords. This function operates from the point of the definition of [debug](#) onwards. Therefore to check all the files move [debug](#) to the top of the `pp.set` file and give it a value of 99.

---

## dependentVariableColumnObs

Value	zero or a positive integer or column name (case sensitive)
Description	Used in fitting to specify which column in the data file holds the dependent variable.
Aliases	<a href="#">dependentVariablePositionIn</a> , <a href="#">dependentVariableColumnIn</a> , <a href="#">yVariableColumnObs</a>
System default	""
Use	When fitting data to a <b>PHREEQC</b> model, there is always one dependent variable containing the observations and this identifies where in the data file it will be found. The columns are counted from left to right.

A value of zero should be used when a simulation is being carried out and there is no dependent variable present. If a simulation is being carried out and the data file contains a column with dependent variable data then [dependentVariableColumnObs](#) should point to this column so that it can be skipped when reading the file. This makes it possible to switch between fit and simulate without changing the data file.

If dependent variable is to be read in, then [dependentVariableColumnObs](#) should be given the value zero.

Examples [80, Using the 'simulate' calculationMethod](#)

## dependentVariableColumnCalc

Value	zero or a positive integer or column name (case sensitive)
Description	Used in fitting to specify which column in the selected output file holds the dependent variable.
Aliases	<a href="#">dependentVariablePositionOut</a> , <a href="#">dependentVariableColumnOut</a> , <a href="#">yVariableColumnCalc</a>
System default	""
Use	<p>When fitting data to a <b>PHREEQC</b> model or when calculating the results of a simulation, there is usually one dependent variable that must be calculated and sent to the selected output file. <a href="#">dependentVariableColumnCalc</a> identifies where in the selected output file this will be found. The columns are counted from the left.</p> <p>The column specified depends on the sequence of the <code>PUNCH</code> statements in the <code>USER_PUNCH</code> keyword block and whether other selected output parameters have been selected. If in doubt, set <a href="#">debug</a> 2 or 3, run and interrupt after a few iterations. Then look at the selected output file to determine its position or use the column name set in the <code>USER_PUNCH</code> block. This will also be printed in the log file.</p> <p>If no selected output is wanted, then <a href="#">dependentVariableColumnCalc</a> should be given the value zero.</p>
Example	<a href="#">80, Using the 'simulate' calculationMethod</a>

## domain

Value	logical [colour [number [number [number]]]]
Description	Determines if and how domain boundaries are plotted in a predominance diagram.
Aliases	<a href="#">plotDomain</a>
System default	F auto UNDEFINED UNDEFINED
Use	<p>The domain boundaries are the vectors going from <a href="#">xmin</a> to <a href="#">xmax</a>, <a href="#">ymin</a> to <a href="#">ymax</a> etc delineating the calculation domain. This keyword is useful for deciding whether the boundaries should be shown in <code>ht1</code> plots (this is where one of the two species codes in the vectors file is 99). With the native y-scale and default plot scales, the boundaries will normally be</p>

overdrawn by the axis lines and so this setting has little visible effect. However, this keyword setting is useful for suppressing the drawing of these boundaries in pe-pH plots calculated with a non-native pe axis (e.g. using O<sub>2</sub>(g)). If you want to see the boundary vectors, set `domain` to `TRUE`.

Alternatively it is possible to simply comment out unwanted field boundaries in the vector file with a leading # and replotting with [calculation-Method 2](#).

The second and subsequent parameters are for the colour of the line, the line type, dashes per inch and line width. If absent, “auto” or undefined, the defaults are taken from the current line parameters of the plot ([lineColor](#), [lineType](#), [dashesPerInch](#), [lineWidth](#)).

Example [46](#)

## dominant

Value	logical
Description	Determines if the dominant or sub-dominant domain boundaries are plotted in a predominance plot
Aliases	
System default	T
Use	<code>dominant</code> set to <code>TRUE</code> plots the normal predominance or stability diagram with the fields showing the dominant species.  <code>dominant</code> set to <code>FALSE</code> plots fields for the second most abundant (sub-dominant) species instead.
Example	<a href="#">2</a>

## eps

Value	logical [[ <code>epstype</code> ] filename]
Description	Determines whether the plot output (if any) is converted to a file in the Encapsulated PostScript (eps) format.
Aliases	
System default	F
Use	Encapsulated Postscript (eps) files are Postscript files that are one page long and have a bounding box included. They will only be produced for the first page in multipage files ( <a href="#">multipageFile</a> ).  eps files can be useful for embedding in other documents as they are always closely cropped but getting reliable eps files has become more difficult in recent years and it may be worthwhile resorting to high resolution png files instead.  An eps file can only be produced if <b>Ghostscript/GSview</b> is installed. If the optional <code>epstype</code> parameter is set to ‘gs’ (or ‘GS’) then the <b>Ghostscript</b> version of the eps file is produced using the <code>eps2write</code> device.



found is chosen.

The header line and the remaining part of the file will be parsed, by default, according to the separator(s) specified by the first entry in the [dataSeparators](#) keyword. If the optional data separator string is specified with the file name, then this is used. The options for this separator are given in [Section 5.2.6](#).

Each file used must contain a column of data with the same specified [columnxColumn](#) heading. Each y-column uses the x-column from the same file so that the lengths of x and y arrays will always be the same.

The [extradat](#) files can also be used as a source of the post and loop columns.

They can also be used to define tag expressions. The first header line is used to generate the tag name and the second line defines the corresponding tag values, either numeric or character. The extradat file can be generated from an earlier simulation.

Example

---

## extraSymbolsLines

Value	filename [data separator]
Description	An optional file containing details of additional symbols and lines to be added to the plot.
Aliases	<a href="#">extraSymbols</a>
System default	““
Use	<p>The file contains lines, each containing details about a symbol or line to be added to the plot.</p> <p>Each line follows the format of a <a href="#">symbolsLines</a> with one definition per line.</p> <p>The <a href="#">file</a> is useful for adding more than one or two extra symbols as well as lines to the plot with more control than can be had by using <a href="#">points</a> and <a href="#">lines</a>. For example, symbol and line properties can be varied from point to point, and tags can be used within the file.</p> <p>Normal <b>PhreePlot</b> input file conventions apply. No header line is required but can usefully be included – the first non-comment line is ignored if the first word is not an integer (i.e. plot number).</p> <p>The optional <a href="#">data separator</a> determines the parsing of the data file. By default it is treated as a standard input file in which any (commas, tabs or spaces) are treated as a valid separators and multiple white space characters are merged. If a specific separator is specified, e.g. “\t” for the tab character as from a file created in a spreadsheet, this will be used instead. In this case, adjacent separators will not be merged. This enables empty data fields to be read.</p> <p>Each row (line) represents a data point. A blank row signifies a break in the data. This will introduce a break in a line. The line is only actually drawn when all of the data for the block of data have been read.</p> <p>The last defined parameters (width, colour and type) override any previ-</p>

ously defined parameters. All line and symbol properties remain in force until redefined, i.e. they persist between data blocks.

Providing a line consists of three or more points, i.e. at least two line segments, and is a full line (`lineType = 1`), the plotted line will have rounded joins and ends. If butt (square) ends are wanted, make sure that only single line segments are drawn, i.e. insert a line break after every pair of points.

This file is often best prepared in a spreadsheet and saved as a tab-delimited file (add `/t` after the filename to indicate the format).

The lines and symbols are normally clipped exactly to the plot window. Symbols close to the plot window will be clipped. If plotting outside this window is required, break the sequence and enter a blank line at the appropriate point in the `extraSymbolsLines` file with `'noclip'` to turn off the clipping. To turn it on again, break the line and add a line with `'clip'`, e.g. for a plot window of (0,0) to (10,10):

```
plot x y lw lcol isymb sizesymb symbcol
1 1 1 1 green6 2 1.5 red
1 9 1

1 -1 2
1 11 2

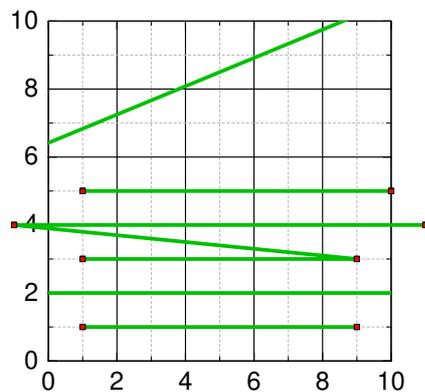
noclip

1 1 3
1 9 3
1 -1 4
1 11 4

clip

1 1 5
1 10 5
1 12 5

1 -1 6
1 11 11
```



See [Section 2.4.3](#) for how to ensure that the file will be found.

Examples [66, 69](#)

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## extraText

Value	filename [data separator]
Description	An optional file containing details of additional text to be added to the plot. Enclose filename in quotes if necessary.
Aliases	
System default	“
Use	<p>Specifies a file containing extra text to be plotted. The file is useful for adding extra text to the plot, perhaps many lines of it. Each logical line will plot a single piece of text or initiate some special text to be inserted. There is no limit to the number of lines. Normal <b>PhreePlot</b> input file conventions apply. Comments can be included in the file by using a # symbol.</p> <p>See <a href="#">‘Section 2.4.3’</a> for how to ensure that the file will be found.</p> <p>The second optional parameter is the data separator used for reading the file, e. g. “\w” for whitespace (tab or space), “\t” for tab only, “\” for whitespace or comma, the default.</p> <p>Each line in the file has the same structure as for the <a href="#">text</a> keyword. This is as follows:</p> <pre>plotnumber, x, y, text[, size[, colour[, angle[, justify[, dig- its[, font]]]]]]</pre> <p>Attributes from <code>size</code> onwards are optional and have defaults and while the list can be truncated, attributes cannot be out of order.</p> <p>See the <a href="#">text</a> keyword for details.</p>
Examples	<a href="#">3</a> , <a href="#">51</a> , <a href="#">55</a> , <a href="#">\demo\UPF\UPF.ppi</a>

---

## fillColorDictionary

Value	filename
Description	A text file that is used to store a list of chemical species and their associated fill colours. This is used during the plotting of predominance and mineral stability diagrams.
Aliases	<a href="#">fillFile</a> , <a href="#">FillDict</a> , <a href="#">FillColor</a>
System default	<a href="#">fillColor.dat</a>
Use	<p>This is a file containing a list of species names and associated colours used for the colouring of polygons.</p> <p>If the specified file exists, it will be used and any additional species automatically added. Colours can be changed by editing this file and replotting.</p> <p>If the specified file does not exist, it will be created in the input file directory with the filename given by the <a href="#">fillColorDictionary</a> setting.</p>

Example [38](#)

## FIT

Value	none (section heading)
Description	Optional section header
Aliases	
System default	
Use	Can be used in the input file to highlight the beginning of FIT keywords. There is no attribute associated with it.

## fitAdjustableParameters

Value	list of 0 or 1's
Description	Flags whether fit parameters are fixed (0) or adjustable (1)
Aliases	<a href="#">adjustableParameters</a>
System default	all 0
Use	The list should be of length given by the number of fit parameters. Each parameter has the value of 0 or 1 signifying whether it is fixed or adjustable.
Examples	<a href="#">80</a> , <a href="#">83</a>

## fitConvergenceCriterion

Value	positive number [ <i>rss</i>   <i>absdiff</i>   <i>function</i>   <i>L1</i>   <i>L2</i> ]
Description	Specifies the convergence criterion used during fitting and the type of objective function.
Aliases	<a href="#">fitConvergeCriterion</a> , <a href="#">convergenceCriterion</a> , <a href="#">RHOEND</a>
System default	1e-6 <i>rss</i>
Use	Controls when fitting is deemed to have converged and, optionally, the objective function used. <i>L1</i> is a synonym for <i>absdiff</i> and <i>L2</i> is a synonym for <i>rss</i> .

The default objective function is '*rss*' (the *L2* norm, least squares) unless one of the other options is specified and the fitting method is appropriate. '*absdiff*' uses the sum of the weighted absolute differences (the *L1* norm) whereas '*function*' simply uses the calculated value and can be used for finding the minimum in a '*function*'. The '*nlls*' and '*lm*' methods are specifically designed for the *L2* norm and cannot be used with the *L1* norm.

Interpretation depends on the algorithm chosen (see Section 12.5.5 and [Table 12.2](#)). For '*nlls*', a 'normal' termination is triggered when the objective function is predicted to be less than [fitConvergenceCriterion](#)<sup>2</sup>. Since the objective function is itself a summation this will depend on the

number of observations.

For the ‘trust region’ methods, [fitConvergenceCriterion](#) defines the radius of the final trust region, `RHOEND`. This should indicate the accuracy that is required in the final values of the parameters.

A value of 1e-6 (default) to 1e-3 is normally reasonable.

Small values will always provide more accurate fits but at a cost in terms of the number of iterations required.

Normally if this setting is set at a very small value, the lack of a significant change in parameter values will also trigger termination.

Examples [80](#), [83](#)

## fitFiniteDiffStepSize

Value	positive number
Description	Specifies the size of the interval that is used by the ‘ <code>n11s</code> ’ fitting routine to calculate numerical derivatives by finite differences.
Aliases	<a href="#">finiteDiffStepSize</a>
System default	1e-3
Use	The size should be sufficiently large to give rise to a significant change in the response of the dependent variable since each of the <code>n</code> adjustable parameters is adjusted by this amount during the first <code>n+1</code> iterations. However, if the setting is too large then the fitting may wander too far from the optimal solution, and possibly into territory where <b>PHREEQC</b> fails or where convergence of the fitting is not achieved.
Examples	<a href="#">80</a> , <a href="#">83</a>

## fitLogParameters

Value	a list of 0 and 1’s
Description	Specifies whether the fit parameters are to be log10 transformed (1) or not (0) during fitting.
Aliases	<a href="#">logParameters</a>
System default	all 0’s
Use	The list should be the same length as indicated by the number of fit parameters. Each parameter should have a 0 or 1 associated with it.  A value of 0 fits the parameter as given.  A value of 1 indicates that the parameter will be anti-logged ( $10^x$ ) before being substituted in the model so the parameter values specified by <a href="#">fitParameterValues</a> should be log10 values.  This option can be useful to: (i) restrict a parameter to positive values; (ii) fit parameters that can vary by orders of magnitude.  Although this option will not necessarily affect the final fit, it can affect it

because the rescaling will affect how the parameters are adjusted between steps. For example, the [fitFiniteDiffStepSize](#) applies to the parameters in the original log space as does the [fitStepSize](#).

Because these log/antilog transformations distort the parameter space, standard errors and the correlation matrix will not be given if any of the adjustable parameters have been fitted as log parameters. To get estimates of these errors, either turn off all the logging and re-run with the best fit parameters entered as non-logged values, or modify the **PHREEQC** code to accept log parameters directly.

Examples [80](#), [83](#)

---

## fitLowerParameterValues

Value	list of numbers
Description	Specifies the minimum allowable value of each adjustable parameter during fitting.
Aliases	<a href="#">lowerParameterValues</a>
System default	UNDEFINED UNDEFINED
Use	Used for constrained optimization (= 'bobyqa' only).  There should be one value for each parameter, corresponding one-to-one with the other parameter lists such as that of <a href="#">fitParameterValues</a> and length defined by <a href="#">numberOfFitParameters</a> . Values should be included for 'fixed' parameters to maintain the correspondence of the lists. These values will not be used.  A value of UNDEFINED (or -99999) means that no constraint will be applied (it is automatically set to a huge negative value).

---

## fitMaxIterations

Value	positive integer
Description	Controls the maximum number of iterations allowed during fitting
Aliases	<a href="#">fitMaxIteration</a> , <a href="#">maxIterations</a> , <a href="#">maxiteration</a>
System default	500
Use	An 'iteration' is one set of calculations of the residuals for all observations. <a href="#">fitMaxIterations</a> can be varied to either allow more time for convergence or to deliberately force an early exit, e.g. after one iteration.  <b>PhreePlot</b> will attempt to exit gracefully after the maximum iterations have been reached. This includes reporting the optimal parameter values (so far) and their errors, and plotting the results. A low-pitched beep will be given if the sound is on and an error message written to the log file and screen, if active.  Sometimes a few extra function calls are made after the maximum iterations have been reached in order to restore the previous best estimates of the fit.

Examples [80](#), [83](#)


---

## fitMethod

Value	List of one or more of 'nlls', 'lm', 'newuoa', 'bobyqa', 'subplx' or 'contour' (case is not significant)
Description	Specifies the optimization (fitting) procedure(s) used
Aliases	
System default	'nlls'
Use	Five optimization procedures are currently available: 'nlls', 'lm', 'newuoa', 'bobyqa', 'subplx'. These are all derivative-free methods. They are all unconstrained except 'bobyqa' which accepts lower and upper bounds on the parameters. See <a href="#">"Fitting and simulations", p. 151</a> .

If more than one optimization method is given, then the fit will be re-run with all settings the same except for the optimization method. A plot will be produced for each run. The method, e.g. "\_nlls", will be appended to the various output filenames to distinguish them. Beware that some of the stepping and convergence parameters have somewhat different meanings with the different methods and if this is important, run each fit with a separate file and adjust the parameters accordingly.

The 'contour' option is used to produce a contour plot of the objective function versus two user-defined variables, most usefully two of the model parameters being fitted. The objective function, defined by the [contourZvariable](#), is the z-variable and [xmin](#), [xmax](#), [ymin](#), [ymax](#) and the resolution drive the calculation of the objective function. The <x\_axis> and <y\_axis> tags must be present explicitly in the list of [fitParameterValues](#). These will be substituted at run time. If necessary, these values can be passed to other tags used in the model via the [numericTags](#) settings. They must also be given parameter names. The resolution, [nres](#), should be set to 2 or greater.

---

## fitnpt

Value	integer
Description	Specifies the number of conditions or interpolation points (NPT) used by the NEWUOA and BOBYQA optimization algorithms.
Aliases	
System default	UNDEFINED
Use	This value must be in the interval $[\lfloor n+2 \rfloor, (n+2) * (n+1) / 2]$ where $n$ = the number of adjustable parameters. A larger value will provide more accuracy but at a cost.  If the value is set to UNDEFINED, then the chosen value will depend on the value of $n$ :  if $n < 6$ , then $NPT = (n+2) * (n+1) / 2$ (the maximum)

else `NPT = 2*n+1` (the recommended value for large problems).

---

## fitParameterNames

Value	list of character strings (up to 30 characters)
Description	Specifies the names of each of the fit parameters
Aliases	<a href="#">parameterNames</a>
System default	""
Use	Specifies the names of the parameters (fixed or adjustable) used in the model. These names are used to make tags which can be used within the <code>CHEMISTRY</code> section (the <b>PHREEQC</b> code).  These names must not be used in other tag definitions, e.g. <a href="#">numericTags</a> .
Examples	<a href="#">80</a> , <a href="#">83</a>

---

## fitParameterValues

Value	list of numbers
Description	Specifies the initial values of each of the fit parameters.
Aliases	<a href="#">parameterValues</a>
System default	missing value
Use	A value must be assigned to each parameter. It will either be treated as fixed or adjustable depending on the values of <a href="#">fitAdjustableParameters</a> .  Normally during fitting, the optimizer takes complete control of setting these values so they cannot be manipulated from outside – you cannot assign tag values to them. The exception is with the <a href="#">fitMethod</a> 'contour' when you can – indeed, must – since in this case the optimizer is not being used. Rather the parameter values are being driven by the x- and y-axis variables and so their corresponding tags (<x_axis> and <y_axis>) are required here.
Examples	<a href="#">80</a> , <a href="#">83</a>

---

## fitStepSize

Value	positive number
Description	During fitting, controls the maximum size of a step that can be taken.
Aliases	stepSize, fitMaxStepSize, RHOBEG
System default	100
Use	The interpretation of this parameter depends on the <a href="#">fitMethod</a> used. With 'nlls', it controls the minimum size of the Marquardt parameter (along with the <a href="#">fitConvergenceCriterion</a> ) and so influences the size of the steps taken – the larger its value, the larger the step sizes. With the 'trust

region' methods, it defines `RHOBEQ`, the initial radius of the 'trust region'. This radius is subsequently reduced as the algorithm converges to a solution. `RHOBEQ` and so `fitStepSize` should be about one tenth of the expected greatest change to an adjustable parameter (hence the importance of some approximate scaling of the adjustable parameters).

This parameter should not be so small as to lead to an insignificant shift in the objective function during fitting or so small as to make progress painfully slow. Neither should it be so large that it allows the parameter values to wander into 'undesirable' territory causing **PHREEQC** to fail to converge.

Examples [80](#), [83](#)

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## fitUpperParameterValues

Value	list of numbers
Description	Specifies the maximum allowable value of each parameter during fitting.
Aliases	<a href="#">upperParameterValues</a>
System default	UNDEFINED UNDEFINED
Use	Used for constrained optimization (= 'bobyqa' only).  There should be one value for each parameter, corresponding one-to-one with the other parameter lists such as that of <a href="#">fitParameterValues</a> and length defined by <a href="#">numberOfFitParameters</a> . Values should be included for 'fixed' parameters to maintain the correspondence of the lists. These values will not be used.  A value of UNDEFINED (or -99999) means that no constraint will be applied (it is automatically set to a huge positive value).

---

## fitWeightingMethod

Value	0, 1 or 2
Description	Controls how the residuals are weighted in the objective function used by the fitting algorithms.
Aliases	<a href="#">weightingMethod</a> , <a href="#">weighting</a>
System default	0
Use	The objective function to be minimized, $s$ , is given by:

$$s = \sum_i [w_i \times (f_i - \hat{f}_i)]^2$$

where  $f_i$  = observed value for observation  $i$ ,  $\hat{f}_i$  = fitted value for observation  $i$ ,  $w_i$  = weight for observation  $i$ . Note  $w_i$  is inside the square.

The [fitWeightingMethod](#) setting can take the following values:

0 = unit weighting (all  $w_i = 1$ )

1 = relative error weighting ( $w_i = 1/\hat{f}_i$ )

2 = weights ( $w_i$ ) read from the data file

Ideally, the weights should be equal to the standard deviation of each observation. This can be estimated from repeat measurements. It may vary with the magnitude of  $f_i$ .

If `fitWeightingMethod` = 2 is used, then the column containing the weights is given by the `weightColumn` setting.

Examples

[80](#), [83](#)

## font

**Value** [font] [character encoding]  
**Description** Optionally one or both of, the name or number of the font family or font (up to 40 characters) and/or the character encoding to use, all case insensitive. The encoding must follow the font if present.

**Aliases**

**System default** Helvetica Latin-1

**Use** All 35 standard Postscript fonts are available. The font can be defined by its name, number or font family. Only one font family is used for the basic text in a plot (axis titles and numbering etc.). However, entries in [text](#) lines and [extraText](#) files can define which font to use.

The character encoding can be either 'Standard', 'Latin-1' (or 'Latin1') or 'ASCII' (see [Appendix 4](#)). See the discussion of how to input special characters in [Section 7.6.1](#).

Fonts are numbered consecutively based on their order of appearance in **PhreePlot**'s default font table, or in the `fonts.dat` file, if present, scanning across and down the table, i.e. 1 = Helvetica, 2 = Helvetica-Oblique, 3 = Helvetica-Bold, ..., 44 = Dingbats (see Table below). Font numbers outside this range lead to a fatal error.

The following eight font families are the default in **PhreePlot**: Helvetica, Helvetica-Narrow, Bookman, Avantgarde, Times, Palatino, NewCentury-Schoolbook and Courier. The Chancery (only the italic font), Symbol and Dingbats fonts are also defined. The Symbol font contains Greek characters and some common plotting symbols. The Ghostscript distribution normally contains all these fonts.

The principal text fonts look like this:

[Dingbats](#) are mostly iconic symbols and are only approximately centered.

The above font families and their various faces make up the 35 standard Postscript fonts.

The specified font is checked against the current fonts table first checking for a specific font and if this is not found, checking for the name of a font family. If a font family is found, the 'regular' face of this font is used as the base font (i.e. plain text). If the name of a specific font face is found, this

Helvetica: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Helvetica-Narrow: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Bookman: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Avantgarde: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Times: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Palatino: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 NewCenturySchoolbook: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Courier: The quick brown fox jumps over a lazy dog 0123456789 *italic bold*  
 Chancery: *The quick brown fox jumps over a lazy dog 0123456789 italic bold*

Standard fonts and their numbering as defined in `fonts.dat`

Font_family	Regular	Italic	Bold	Bold-italic
<b>Helvetica</b>	1. Helvetica	2. Helvetica-Oblique	3. Helvetica-Bold	4. Helvetica-BoldOblique
<b>Helvetica-Narrow</b>	5. Helvetica-Narrow	6. Helvetica-Narrow-Oblique	7. Helvetica-Narrow-Bold	8. Helvetica-Narrow-BoldOblique
<b>Bookman</b>	9. Bookman-Light	10. Bookman-LightItalic	11. Bookman-Demi	12. Bookman-DemiItalic
<b>Avantgarde</b>	13. AvantGarde-Book	14. AvantGarde-BookOblique	15. AvantGarde-Demi	16. AvantGarde-DemiOblique
<b>Times</b>	17. Times-Roman	18. Times-Italic	19. Times-Bold	20. Times-BoldItalic
<b>Palatino</b>	21. Palatino-Roman	22. Palatino-Italic	23. Palatino-Bold	24. Palatino-BoldItalic
<b>NewCenturySchoolbook</b>	25. NewCentury-Schlbk-Roman	26. NewCentury-Schlbk-Italic	27. NewCentury-Schlbk-Bold	28. NewCentury-Schlbk-BoldItalic
<b>Courier</b>	29. Courier	30. Courier-Oblique	31. Courier-Bold	32. Courier-BoldOblique
<b>Chancery</b>	33. ZapfChancery-MediumItalic	34. ZapfChancery-MediumItalic	35. ZapfChancery-MediumItalic	36. ZapfChancery-MediumItalic
<b>Symbol</b>	37. Symbol	38. Symbol	39. Symbol	40. Symbol
<b>Dingbats</b>	41. Dingbats	42. Dingbats	43. Dingbats	44. Dingbats

will be used as the ‘base font’. It is usually best to use the name of a font family or the name of the regular face font as the base font. Then bold and italic can be turned on with the tags `<b></b>` and `<i></i>`, respectively. If a bold font is chosen as the base font, then the bold cannot be turned off using the tags.

How software reacts to these fonts depends on whether the output device recognises the specified fonts either in terms of having the font of the exact same name available or being able to provide an appropriate substitution font (there is no standardization of font names and so similar fonts can have more, or less, different names).

The `fonts.dat` file contains the names of the 11 font families and the 35 fonts defined in **PhreePlot**. These are the names of the fonts actually written to the Postscript file. This file can be edited to give the required font names for the device of interest based on the available fonts

The `fonts.dat` file has a standard format and consists of eleven rows of data, each line containing the family name of the font (as used by [font](#))

and then the font names for the regular font, the italic (or oblique) font, the bold font and the bold, italic font. A blank string ("") is a placeholder that indicates that no such font is defined. This file is read in free format.

It is in principle possible to use different font families for plain text, italic, bold and italic-bold by editing the `fonts.dat` file.

The search path for the font file is the current directory followed by the system directory.

If `font` is not one of the specified font families, then a close match is sought – if the given font includes a font family name within it, this font family is chosen. Also if `font` contains any of the words below, the corresponding font family is selected:

<code>arial</code>	Helvetica font family
<code>roman</code>	Times font family

Text tags provide a way of specifying changes to the appearance of individual characters (bold, italic) and groups of characters. They can also specify Greek characters (these are converted to the Symbol font).

The 'standard' character encoding consists of the standard ASCII 7-bit character set ('ASCII' encoding, decimal codes 0-127) plus a variable range of extended characters often including the permil sign and the oe ligature. Not all codes are defined in Postscript fonts.

The 'Latin-1' character encoding consists of the ANSI (default for your system) 8-bit character set (decimal codes 0-255), often known as the ISO-8859-1 encoding. This includes most of the accented characters used in Western European languages (but not the euro sign or the oe ligature) and apart from these exceptions, is broadly similar to the commonly-used Windows-1252 character set.

A table of the current character set and font can be produced if `plotTitle` is set to 'character set', `labelSize` set to about 2 mm and 'A4' or 'letter' `paperSize` chosen. Most other settings are ignored.

Example

[66](#)

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## gridColor

Value	One to six Cohort or rgb colours
Description	Defines the colour of the grid lines for the six axes
Aliases	<a href="#">gridColors</a> , <a href="#">gridLineColor</a>
System default	<code>black</code>

Use Defines the colours used for drawing grid lines.

The six colours refer in order to the following six axes: major x, minor x, major y, minor y, major 2y and minor 2y.

If less than six colour are entered, then the missing colours are automatically filled in by recycling the colours given. See [tickSize](#) for the recycling rules that apply.

---

## gridDashesPerInch

Value	One to six non-negative numbers
Description	Defines the number of dashes per inch for the six grid lines
Aliases	
System default	20
Use	<p>The six numbers refer in order to the following six axes: major x, minor x, major y, minor y, major 2y and minor 2y.</p> <p>If less than six numbers are entered, then the missing numbers are automatically filled in by recycling the numbers given. See <a href="#">tickSize</a> for the recycling rules that apply.</p> <p>Grid lines are only drawn if the corresponding <a href="#">gridLines</a> setting is <code>TRUE</code> or the corresponding <a href="#">tickSize</a> is very large.</p> <p>See <a href="#">gridLineStyle</a> below for choosing the line style.</p>

---

## gridLines

Value	One to six logical values
Description	Defines whether a grid line is drawn or not
Aliases	<a href="#">gridline</a> , <a href="#">grid</a>
System default	<code>FALSE</code>
Use	<p>This keyword is used to determine if a grid line is drawn (<code>TRUE</code>) on a plot or not (<code>FALSE</code>). The values refer in order to the following six axes: major x, minor x, major y, minor y, major 2y and minor 2y.</p> <p>The major axes are where the major ticks and axis numbers are positioned; the minor axes are where the minor ticks are positioned.</p> <p>If less than six values are entered, then the missing values are automatically filled in by recycling the values given. See <a href="#">tickSize</a> for the recycling rules that apply.</p> <p>The 2y ticks and grid lines are only drawn if some 2y lines or points are actually plotted.</p> <p>Grid lines can also be set by specifying very large tick sizes (see <a href="#">tickSize</a>).</p> <p>Other settings (<a href="#">gridLineStyle</a>, <a href="#">gridDashesPerInch</a> and <a href="#">gridColor</a>) affect the appearance of the grid lines and even whether they are drawn. <a href="#">AxisLinewidth</a> controls the width of the grid lines.</p>

---

## gridLineStyle

Value	Form one to six integers in the range 0 to 20
-------	---

Description	Defines the styles of line drawn for the major and minor grid lines
Aliases	<a href="#">gridLineTypes</a>
System default	1
Use	<p>This keyword is used to determine the style of a grid line. The default (1) is for the grid lines <i>not</i> to be dashed. <a href="#">Line styles</a> can be solid, dashed, dotted and dot-dash.</p> <p>The six numbers refer in order to the following six axes: major x, minor x, major y, minor y, major 2y and minor 2y.</p> <p>If less than six numbers are entered, then the missing numbers are automatically filled in by recycling the numbers given. See <a href="#">tickSize</a> for the recycling rules that apply.</p> <p>Grid lines are only drawn if the corresponding <a href="#">gridLines</a> setting is <code>TRUE</code>.</p> <p>See <a href="#">lineType</a> for a full description of the 20 line types, e.g. useful styles are 0 = no line; 1 = full line; 6 = dashed line; 11 = dotted line; 15 = dash-dot line.</p>

## info

Value	Cohort or rgb colour for the info data block
Description	Sets the colour of the ‘info’ block printed at the bottom left-hand corner of the plot.
Aliases	<a href="#">infoColor</a>
System default	nd [nd]
Use	<p>One or two <a href="#">colours</a> must be specified: the first is for the whole ‘info’ block. The second is for the file path of the input file and is only used when the first colour is ‘nd’ or blank. If the second colour is omitted or the first colour is not ‘nd’ or blank, then the first colour is used for both.</p> <p>The info block contains summary information about the figure. The information given varies slightly depending on the type of calculation. An example is shown below for a ‘ht1’ calculation:</p>

```

1  Main species = Fe   Temperature = 25.0 °C
Resolution = 250   Speciation calculations = 2544; Time = 0.251 min
C:\Program Files\PhreePlot\0.01\demo\Fel\fo_Fe1.ps
PhreePlot version = Pre-release 0.01 (27 Jun 2008)
Speciation program = PHREEQC (4 April 2007)
Database = wateq4f.dat (8 Sept 2006)
12:25:47 27 June 2008

```

The printing of the ‘info’ block can be turned off by setting the first colour to ‘nd’ or blank and giving no second colour.

‘nd’ as the first parameter also turns off the printing of any “<input:” text specified in a [text](#) line or an [extraText](#) file (“<input:” enables a copy of all or some of the input file(s) to be printed with the plot). ‘nd’ overrides any input settings in this file and so can be used to produce ‘clean’ plots without editing the individual text lines. This can be set in the `override.set` file to ensure that this text is missing from all plot files whatever the input file states.

The size of the info text is automatically determined from the [labelSize](#) setting. If `labelSize` >= 0.1 inch (or the equivalent on other scales) then

the text size will be  $0.6 \times \text{labelSize}$ . If it is less than 0.1, then it is fixed at 0.05 inch.

Example [38](#)

## initialValue

Value	number
Description	Value given to all undefined numeric tags
Aliases	
System default	UNDEFINED (-99999)
Use	A numeric tag should normally be defined in terms of constants and other tag values that have already been defined, i.e. that precede the given tag in terms of evaluation order.  However sometimes this is not appropriate and it is necessary to set an initial value, e.g.

```
<n> = "<n> + 1"
```

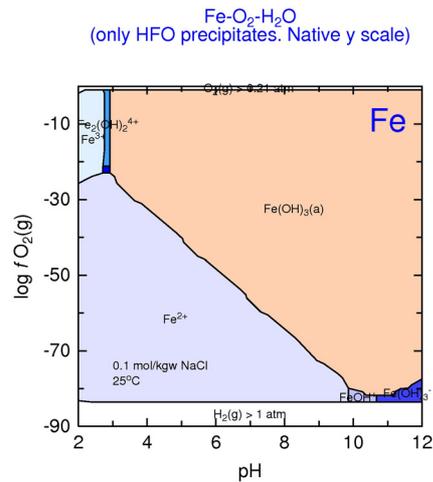
## jobTitle

Value	string
Description	Description of job
Aliases	<a href="#">job</a>
System default	""
Use	Free text used to describe the job (up to 400 characters long). This string is printed in the log file so can be used for comments about the job.

## jpg

Value	logical [[number] filename]
Description	Determines whether the plot output (if any) is converted to a file in the jpg format.
Aliases	
System default	F
Use	A jpg file can only be produced if Ghostscript/GSview is installed. <b>PhreePlot</b> makes use of the Ghostscript <code>jpeg</code> device to produce this file.  The second, optional parameter specifies the resolution (in dpi) to use when making the conversion. The default is 300 dpi.  If filename is present, this overrides the auto-generated filename.  An example of output in jpg format is given below (the resolution seen here has been reduced during conversion to pdf – the quality of the origi-

nal jpg was better than this).



Example [79](#)

## labelColor

Value	Cohort or rgb colour
Description	Sets the colour of labels in custom-type plots
Aliases	<a href="#">labCol</a>
System default	black
Use	Specify the <a href="#">colour</a> to be used for labels. Use 'nd' (not drawn) if no labels are wanted. This also controls the default color of the text used by the <code>&lt;input...&gt;</code> tag.  Colours should be chosen from the <a href="#">colour palette</a> .  If 'auto' is set as the colour, then the colour of the label in the plot and legend will match that of the line, or symbol rim color if the line has not been plotted. If the rim colour is not defined or is 'white' or 'nd', the point colour is chosen instead.  This setting does not apply to contour plots which have their own mechanism for labelling contours, and does not make much sense for predominance plots since the label will be largely hidden. It is principally of use for custom plots and their derivatives, e.g. species plots.

Example [51](#)

## labelEffort

Value	0, 1, 2 or 3 [number]
Description	Controls the amount of effort used and time taken to place the labels.
Aliases	<a href="#">effort</a>

System default	1
Use	<p>Controls the amount of effort (and time) used to optimize the placement of labels:</p> <ul style="list-style-type: none"> <li>0 No optimization; labels are placed half-way along the x axis</li> <li>1 Basic</li> <li>2 Moderate</li> <li>3 High</li> </ul> <p>This applies to the labelling of lines in custom and fit plots and fields in predominance plots. If the optional second parameter is present, the time taken for label placement in custom or fit plots will be at most this time in sec.</p> <p>The time taken varies greatly with the number of labels, their size and the degree of overlap found in the default placement (near the centre point of the curve). In order to reduce overlap, reduce the label size, change the axis scale, or reduce the number of curves plotted.</p> <p>With predominance plots having highly concave fields and labels on a polygon boundary, <code>labelEffort = 2</code> or greater may improve placement.</p> <p>The <code>ESC</code> key can be used to interrupt the labelling. If the plotting is stopped at this point, the best placement found so far is used.</p> <p>The labels can be repositioned manually by editing the line colour dictionary and using <a href="#">calculationMethod</a> 2. The line colour dictionary contains the position of the centre of each label and the line colour. <a href="#">useLineColorDictionary</a> should be set to 2 to give the dictionary priority over automatic labelling.</p> <p>A value of 0 rarely produces worthwhile output.</p> <p>The labels can be turned off altogether by setting <a href="#">labelColor</a> to 'nd' or <a href="#">labelSize</a> to be 0.</p>
Example	<a href="#">45</a>

---

## labelFile

Value	logical
Description	Now redundant.
Aliases	
System default	<code>&lt;inputfile_ending&gt;.lab T</code>
Use	<p>Originally a switch that controlled the creation and deletion of the labels (*.lab) file that is used by ht1. The labels file contains the name, position and angle of all of the labels used to label the fields in predominance plots.</p> <p>Since this file is essential for the operation of 'ht1' plots, the labels file is automatically created and retained with these plots.</p>

---

## labels

Value	list of strings (up to 30 characters each).
Description	Can be used to override the default names used for labelling the curves on custom and fit plots
Aliases	<a href="#">label</a> , <a href="#">loopNames</a> , <a href="#">loopName</a> , <a href="#">loopNumberNames</a>
System default	“ (use default names)

Use

A list of names to be associated with each set of data plotted in a multi-loop or multi-curve custom plot. The order in which the curves are plotted is in the order shown in the legend. This order is the order that the data have been written to the appropriate plot data file(s) (the ‘out’ file or ‘pts’ file depending on the type of plot, and any [extradat](#) files) and will run sequentially through each z-loop value for each of the variables to be plotted.

This list of labels can be used to rename the entries in a custom plot legend – the labels are simply picked from this list in turn and used in the legend.

A single curve is designated by a contiguous set of records in a single column in the data file being read. Multiple curves are designated by having one or more blank lines in a column of data or by the data being derived from several columns, or both of these.

Blank lines are normally inserted in ‘out’ files at each change in the value of the z-loop variable. The third and fourth [dataSeparators](#) settings control the insertion of line breaks in generated data files during looping.

If the data are derived from fit data files, then blank rows are copied across from the input files to the output files preserving the column breaks.

Names are picked off the [labels](#) list as needed, one by one, for each dataset. All curves for a given variable and a given z-loop variable will be plotted first, then curves with different values of the z-loop variable will be plotted. The labels list is recycled if short.

If the [labels](#) keyword is set blank, then the column headers of the data being read will be used to generate default label names. If more than one subset of data is being plotted, then a subset identifier will be appended to the label name. This takes the form *columnHeader\_subsetIdentifier*. The subset identifier is the subset number. This is often the z-loop number.

Labels set with the [labels](#) keyword take precedence over those set by specifying an alphanumeric variable as the first column of a [loopFile](#). These label names will always be used as is – they are never appended with the subset number, e.g. “\_1” and so on.

The loop names can be used to label each iteration of the loop variable, or in the case of a data file, each separate subset of data as indicated by a break (blank line) in the plot data file (the ‘out’ and ‘extradat’ files for custom plots and the ‘pts’ file for fit plots).

The [convertLabels](#) setting controls whether there is an attempt to convert the loop names to **PHREEQC** formulae for the label plotting, or not.

Examples [61](#), [84](#)

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## labelSize

Value	non-negative number
Description	Controls the size of the labels used in the plots and the size of the info text.
Aliases	<a href="#">textSize</a> , <a href="#">labelTextSize</a> , <a href="#">labelHt</a> , <a href="#">textHt</a>
System default	2
Use	Controls the size of the labels used in the ht1, fit and custom plots. The size of the text is also controlled by the units being used (default is mm). Also controls the size of the vertex number labels in a contour plot with the <a href="#">contourShiftLabel</a> 'n' option.  The size of the info text is also automatically set to 0.5 x <a href="#">labelSize</a> .
Example	<a href="#">40</a> , <a href="#">67</a> , <a href="#">74</a>

---

## legendBox

Value	number number number [colour [ colour [ 4 numbers]]]
Description	Adds a legend with a box around the legend
Aliases	
System default	<code>x y 0 black auto 0 0 0 0 0 0</code>
Use	<p>Adds a box around the legend in custom or contour plots. The format is:</p> <pre>x, y, box_line_width [, box_line_colour [, box_background_colour...]]</pre> <p><code>x</code> and <code>y</code> are the coordinates of the upper left-hand corner of the legend box in graph units (the <code>y</code> scale refers to the main <code>y</code> axis); 'auto' for <code>x</code> and <code>y</code> will give this default position. <code>box_line_width</code> is in the box line width in the units in force. Only the first three parameters are mandatory.</p> <p>The minimum requirement is to set <code>x</code>, <code>y</code> and the line width. The default line width is zero which means no box is drawn. 'auto' for line width uses the <a href="#">axisLineWidth</a>.</p> <p>The two colours are the box line colour and the background colour.</p> <p>The default line colour is black. The default background colour is 'auto' which gives the box background the same colour as that of the plotting area. To make the background transparent or to change the colour, choose a different colour, including 'white' or 'nd'.</p> <pre>legendBox auto auto auto</pre> <p>will draw a black border around the legend which will be on the right-hand side of the plot.</p> <p>The final six numbers adjust the position of the four legend box lines (hence the size of the box) and also the position of the box in relation to the main plot. These adjustments are in inches, and in the side order: bot-</p>

tom, right, top, left, xdistance and ydistance. The first four parameters control the position of the legend box lines and the last two control the overall position of the box from the plot. These adjustments are made to the calculated or specified positions and may be positive or negative.

The keywords [legendTitle](#) and [legendTextSize](#) set the default title and text size for the title and box contents.

Note that the x, y position of the legend box can also be set with the `<legend>` tag and the [text/extraText](#) keywords but this latter approach differs in that it is also possible to specify the plot number, i.e. the `<legend>` approach can give a different legend position for each plot. The `<legend>` setting takes precedence over any other setting.

## legendTextColor

Value	A Cohort or rgb colour.
Description	Determines the colour of the legend text in custom, contour and grid plots.
Aliases	<a href="#">keyTextColor</a> , <a href="#">keyTitleColor</a> , <a href="#">legendTitleColor</a>
System default	“auto”
Use	Enables the colour of the legend text to be changed. ‘auto’
Example	

## legendTextSize

Value	non-negative number
Description	Determines the size of the legend text in custom, contour and grid plots.
Aliases	<a href="#">keyTextSize</a> , <a href="#">keyText</a> , <a href="#">legendTitleSize</a>
System default	“auto”
Use	Enables the size of the legend text to be changed. The units are defined by the <a href="#">units</a> keyword. The default units are mm. “auto” sets the size to be the same as <a href="#">labelSize</a> or 0.0 if this is UNDEFINED. If set to zero, no legend is drawn providing that the legend properties have not been explicitly reset with the <code>&lt;legend&gt;</code> tag. <a href="#">legendBox</a> draws a box round the legend.
Example	<a href="#">74</a>

## legendTitle

Value	Character string or ‘auto’
Description	One way of specifying the legend title in custom, contour and grid plots.
Aliases	<a href="#">keyTitle</a> , <a href="#">key</a> , <a href="#">legendText</a>
System default	“”

Use	<p>Adds a title to the legend in custom plots. Maximum length is 400 characters. This can contain text enhancements such as <code>&lt;b&gt;...&lt;/b&gt;</code> and line breaks (<code>&lt;br&gt;</code>). It is justified to the left but this can be altered by adding leading spaces.</p> <p>The legend text can also be added with the <code>&lt;legend&gt;</code> tag in a <a href="#">text</a> line or <a href="#">extraText</a> file. If present, this will override any <a href="#">legendTitle</a> setting.</p> <p>By default, the legend is placed to the right of the plot. If you want to place it somewhere else, including inside the plot, use the <code>&lt;legend&gt;</code> approach. The colour of the legend title is controlled by <a href="#">legendTextColor</a>.</p> <p>The 'auto' option only applies to residual sum of squares plots. If used here, the legend title is taken from the <a href="#">contourZvariable</a> setting.</p>
Example	<a href="#">73</a>

---

## lineColor, lineColor2y

Value	list of one or more Cohort or rgb colours
Description	Controls the colours used for lines in ht1, custom and fit plots for the main y and 2y axes.
Aliases	<a href="#">col</a>
System default	black
Use	<p>In ht1 plots, <a href="#">lineColor</a>(1) controls the <a href="#">colour</a> of the line separating the fields. In custom, species and fit plots, the effect of <a href="#">lineColor</a> depends on the <a href="#">useLineColorDictionary</a> setting. If <a href="#">useLineColorDictionary</a> is 0, then <a href="#">lineColor</a> sets the colours for the first n lines plotted where n = length of the list colours set by <a href="#">lineColor</a>. Additional line colours are selected sequentially from the <b>PhreePlot</b> colour sequence (<a href="#">Line colours and auto line colouring</a>). In effect, <a href="#">lineColor</a> promotes the given colours up the colour sequence list.</p> <p>If <a href="#">useLineColorDictionary</a> is 1 or 2 and the species being plotted is specified in the line colour dictionary, then the dictionary colour is used in preference. If the species is not in the dictionary then the colour is chosen from the <b>PhreePlot</b> line colour sequence.</p> <p>Colours should be chosen from the <a href="#">colour palette</a>.</p>
Example	<a href="#">73</a>

---

## lineColorDictionary

Value	filename
Description	Specifies the filename for the line colour dictionary.
Aliases	<a href="#">linefile</a> , <a href="#">lineDict</a>
System default	lineColor.dat
Use	If the filename is blank or the specified file cannot be found, then the system default filename is used.

The line colour dictionary is used to record and, if specified, control the colour of points and lines in plots. It also stores the coordinates of any line labels.

The specified file is read and updated if found; otherwise it is created. Whether the colours and coordinates in the dictionary are used is determined by the [useLineColorDictionary](#) setting (see [Section 7.9](#)).

Example [73](#)

## lines, lines2y

Value	character list
Description	Specifies which columns should be plotted as lines for datasets plotted on the main y (left) and 2y (right) axes.
Aliases	<a href="#">plotLines</a> ; <a href="#">plotLines2y</a> , <a href="#">lines2y</a> , <a href="#">line</a> , <a href="#">line2y</a>
System default	""
Use	<p>The list should contain the column names or column numbers of columns for which the lines are to be plotted. The names are case dependent. The names or numbers refer to the column of the file being used for plotting, e.g. the 'out' file for custom plots or the 'pts' file for fit plots.</p> <p>The names can contain tags, most usefully character tags.</p> <p>The order of plotting the lines is determined by the column order in the 'out' file.</p> <p>Additional files can be added to the search path using the <a href="#">extradat</a> keyword. These files must be in tabular format with a single header row defining the column names. One of these columns must be the same as the <a href="#">customXcolumn</a> defined elsewhere.</p> <p>Additional lines can be added to predominance diagram plots as well as custom plots (including fit and species plots). No legend is produced for lines added to predominance plots.</p> <p>The 2y axis is the right-hand y axis which can have a different scale from the left-hand or main y axis.</p>
Examples	<a href="#">55</a> , <a href="#">65</a>

## lineType, lineType2y

Value	A list of numbers in the range 0 to 20
Description	Defines the styles of lines in predominance and custom plots
Aliases	
System default	1
Use	<p>This keyword is used to determine the <a href="#">style of lines</a> defined by <a href="#">lines</a> in custom plots. <a href="#">Line styles</a> can be solid, dashed, dotted and dot-dash.</p> <p>The default (1) is for the line to be a solid line. Styles in the range 2-10 give an increasing length of space to dash; style 11 is pure dots and styles</p>

12-20 are dot-dash style with an increasing length of dash.

By varying the [dashesPerInch](#), [lineWidth](#) and [lineColor](#) settings, a wide variety of line styles can be achieved.

The 2y version applies to the second y-axis.

These line styles can also be used for the grid lines of a plot. Here the corresponding [gridLineStyle](#) keyword is used.

Example See the `\demo\linetype\linetype.ppi` example.

## lineWidth, lineWidth2y

Value	list of numbers
Description	Controls the line widths in plots including custom plots with datasets plotted according to the main y (left) and 2y (right) axes.
Aliases	<a href="#">width</a> , <a href="#">lw</a>
System default	0.3
Use	<p>This keyword sets all line widths in the plot to the given values. The list controls the line widths for successive curves in a custom-based plot. The position of the entry used is based on the corresponding position of the variable name in the <a href="#">lines</a> keyword. The list is recycled as necessary. The actual line width drawn is determined by the units in operation. The system default units are mm.</p> <p>A value of 0.0 means that no line will be drawn.</p> <p>A negative value draws a dashed line of width <code>ABS(lineWidth)</code> with 10 dashes per inch by default.</p> <p>The number of dashes per inch to use for a dashed line is set by <a href="#">dashesPerInch</a>.</p> <p>The width of lines separating fields in predominance diagrams is 0.66 times <a href="#">lineWidth</a>(1).</p>
Examples	<a href="#">61</a> , <a href="#">55</a> , <a href="#">23</a>

## log

Value	logical
Description	Determines whether a log file is produced.
Aliases	<a href="#">logFile</a>
System default	T
Use	<p>The log file is a text file containing feedback about the run and is especially useful for debugging. The amount of information sent to the log file is controlled by the <a href="#">debug</a> parameter. This increases as <code>debug</code> is changed from -1 or 0, 1, 2 and 3. It can be a very large file when <a href="#">debug</a> = 3.</p> <p>The default value is <code>TRUE</code> and so some output may be sent to the log file before the redefined value comes into effect. Set the <a href="#">log</a> setting in the</p>

`pp.set` file to avoid this early output being sent to the log file.

---

## logDepVariable

Value	0 or 1 or -1
Description	During fitting, determines whether the calculated values of the dependent variable returned by <b>PHREEQC</b> should be log-transformed or un-log-transformed (exponentiated) before being used or not
Aliases	
System default	0
Use	<p>If <code>logDepVariable</code> is set to 1, then the calculated value of the dependent variable returned by <b>PHREEQC</b> is log-transformed before being used in the objective function. This option avoids having to store log-transformed values of the dependent variable in the data file. Similarly if <code>logDepVariable</code> is -1, the value of the dependent variable returned by <b>PHREEQC</b> is un-log-transformed, i.e. <math>10^x</math>.</p> <p>If <code>logDepVariable</code> is 0, the calculated value is used without transformation.</p> <p>Note that the observed values of the dependent variable must be on the transformed scale.</p> <p>log transforming the dependent variable has approximately the same effect as using a relative error weighting.</p> <p>It is possible to return log values of the dependent variable by using the <code>log10</code> function in the <b>USER_PUNCH</b> data block. In this case, <code>logDepVariable</code> should usually be set to zero since no further transformation needs to be applied.</p> <p>There are a number of examples of <code>logDepVariable</code> in the <code>\demo\iso\isologx.ppi</code> series of files.</p>

---

## logVariableIn

Value	A list of 0, 1, -1, -, X (or x)
Description	Determines the format by which to read columns of data from the data files used by <code>fit</code> and <code>simulate</code> , and whether to transform these data or not.
Aliases	
System default	'' (empty string)
Use	<p>The default, an empty list, means that the format is determined by the first row of data in the data file. This classifies each column as either numeric or character depending on the data found. If anything other than this is wanted, for example forcing a numeric value to be read as a character or transforming the data, or skipping columns, then the format must be specified explicitly. If the title of the column ends in a \$ symbol, it will always be defined as a character column.</p> <p>Format options for each column are:</p>

0=numeric data

1=numeric and positive data; apply a log10 transformation

-1=numeric data, apply an anti-log10 ( $10^{**x}$ ) transformation

X=character data (X is not case sensitive)

--skip column

The default empty list means that each column of data is read according to the formats derived from the header line and the first row of data.

Reading in character data with a numeric format will produce a fatal error (the first 10 such errors will be reported).

If a list of formats is given this overrides the format derived from the first data row. If this list contains  $n$  items and is shorter than the number of columns found then only the first  $n$  columns will be read. If  $n$  is greater than the number of columns found, then only the first  $n$  items in the format list will be used.

The above list will also determine which columns of data are transferred to the 'out' and 'pts' files.

If requested, the data are transformed immediately on reading in. No knowledge of this is used further on in the processing.

If the dependent variable is to be read in from the file (i.e. observations are present), then its column should be given by the [dependentVariableColumnObs](#) setting and the [logDepVariable](#) should be used to indicate whether this variable needs to be log-transformed or not. However, the appropriate [logVariableIn](#) setting should also be set correctly. Care should be taken to ensure that both the observations and the calculated values of the dependent variable are on the same scale. It is not possible for **PhreePlot** to check this at run time.

In a simulation ([calculationType](#) simulate), the dependent variable may or may not be present in the fit data file. If it is absent, then the [logDepVariable](#) will determine whether the calculated value is transformed or not.

There are a number of examples of different [logVariableIn](#) settings in the \demo\iso\isologx.ppi series of files.

## loopFile

Value	valid file path to an existing loop file [data separator]
Description	Optional name of a file containing a list or table of loop values.
Aliases	
System default	'' (empty string)
Use	<p>If <a href="#">loopFile</a> is defined and present, then loop values are read from this file, one or more values per line. If a header line is present in the file, this is used to name the tags that are created. These column headers must be unique – they should not clash with the names of other tags.</p> <p>If the data are all numeric and no header line is present, then the data associated with column 1, 2, ... are automatically labelled with loop tags, &lt;loop1&gt;, &lt;loop2&gt;, ... .This will take preference over the single &lt;loop&gt; tag</p>

generated from [loopMin](#), [loopMax](#) and [loopInt](#). In this case, <loop1> is copied to <loop> so that <loop> remains defined.

In general, for mixed tables with both numeric and character columns, **PhreePlot** attempts to determine the structure of the file based on the first two columns and first two rows of data. It is safest if the first row is a row of character values which serve as a header line and which are used to generate tag names for the columns of data below. Similarly, if the first column of data is all character values then this is treated as a column of row labels which can be used in plotting.

The header line (if present) and the remaining part of the file will be parsed, by default, according to the separator(s) specified by the first entry in the [dataSeparators](#) keyword. If the optional data separator string is specified with the loop file name, then this is used. The options for this separator are given in [Section 5.2.6](#).

Columns should consist of all numeric or all character data. If the analysis of the header line and the first row of data indicates that a row is numeric, then any subsequent reading of non-numeric data in this column will result in any error and the entire row of data are discarded. Any column with a column heading ending in a \$ symbol will be assumed to be a character column and if necessary, will generate character tags. It is best to always use this \$ convention for naming character columns since this will avoid any chance of the the first column being identified as row names (see below).

If the first two rows of the first column contains character variables (up to 30 characters and not ending in \$), the rows are assumed to contain row names in the first column. These are used for labelling any plot that is produced from this data. However, if label names have been assigned by the [labels](#) keyword then these are used in precedence over those defined by a loop file.

A special case is a single column of character variables. Here the normal rules are ambiguous and the following assumption is made: the first row is assumed to be the column name (and will be used as a tag name) and the remaining rows are character values. These are accessible by using the tag name. The loop tags, <loop1> etc, remain undefined since these are reserved for numeric variables.

If numeric values like 1, 2, 3... are wanted as label names, force them to be read as character strings by adding quotes, e.g. "1", "2" etc. This only applies to column 1. Alternatively, if the labels are just used for plotting, you can add a non-plotting character (ASCII encoding) to the string, e.g. 1↵ to force it to be read as a character variable.

Quotes tend to get stripped from variables when read or may need to be added when a substituted character tag is to be read by **PHREEQC** so it may be necessary to include the tag in quotes, e.g. "<description>" or even use the two types of quotes, ``<description>``.

The key feature of a loop file is that it 'loops'. A new row of loop values will be associated with the appropriate tags on each iteration of the z- loop variable. This includes row names (potential labels) if present.

[loopLogVar](#) operates as normal but it operates over all of the numeric variables.

The normal search path is used for locating the specified loop file.

If [loopFile](#) is defined but the specified file is not found, then this is treated as a fatal error.

[Normal conventions](#) for reading input files apply to the loop file. This includes not using # or ; in label names. Comment lines can be included and will be skipped.

The values of the loop variables read from the loop file will be written to the log file and can be checked there.

Example [65](#)

## loopIndexStartNumber

Value	positive integer
Description	The initial z-loop number used to define a filename
Aliases	<a href="#">zstart</a> , <a href="#">loopStartNumber</a>
System default	1
Use	By default this 1. This specifies the starting number used in the file extension when a series of files is output. This enables single plots to be created with any number, thus enabling the replotting of just one file when many were produced in a series (not tested).

## loopInt

Value	non-negative number
Description	The value of the z-loop interval ( $\geq 0$ ) used to calculate the value of the z-loop variable, $\langle \text{loop} \rangle$ .
Aliases	<a href="#">zint</a>
System default	UNDEFINED
Use	<p>If <a href="#">loopInt</a> <math>&gt; 0</math>, then the value of the <math>\langle \text{loop} \rangle</math> variable is varied from <a href="#">loopMin</a> to <a href="#">loopMax</a> in steps of <a href="#">loopInt</a>. For example, given the following loop parameters (<a href="#">loopMin</a>, <a href="#">loopMax</a>, <a href="#">loopInt</a>, the <math>\langle \text{loop} \rangle</math> values generated will be:</p> <p>262,loop values generated: 2, 4, 6</p> <p>263,loop values generated: 2, 5</p> <p>If <a href="#">loopInt</a>=0, then <math>\langle \text{loop} \rangle</math> is set to <a href="#">loopMin</a> and only one iteration is made. <a href="#">loopMax</a> is therefore not be used and should not be defined otherwise a fatal error will be signalled (unless <a href="#">loopMin</a> = <a href="#">loopMax</a>).</p> <p><math>\text{loopInt} &lt; 0</math> is incorrect if <math>\text{loopMax} &gt; \text{loopMin}</math> but will be corrected using:</p> <pre>LOOPINT = sign(LOOPINT, LOOPMAX-LOOPMIN).</pre> <p>The above assumes that <a href="#">loopLogVar</a> is 0 (linear scale). If <a href="#">loopLogVar</a>=1 then the loop variable will be set to <math>10^{\langle \text{loop} \rangle}</math>. <math>\langle \text{logloop} \rangle</math> always contains the current value of <math>\log_{10} \langle \text{loop} \rangle</math>.</p> <p>If <math>\langle \text{loop} \rangle</math> is used in an input file and if <a href="#">loopint</a> (or <a href="#">loopMin</a> or <a href="#">loopMax</a>)</p>

is undefined, then an error is reported.

Example [61](#)

## loopLogVar

Value	0 or 1
Description	Determines whether the z-loop variable and z-loop interval are based on a log10 scale or not
Aliases	<a href="#">zvar</a> , <a href="#">looplog</a> , <a href="#">logLoopVar</a>
System default	0
Use	Either has a value of 0 or 1.

0 = a linear scale; 1 = log10 scale.

The following examples show how [loopLogVar](#) controls the z-loop variable, <loop>, given the values of [loopMin](#), [loopMax](#), [loopInt](#) shown below:

[loopLogVar](#) = 0

0, 10, 2 will generate values of 0, 2, 4, 6, 8, 10

[loopLogVar](#) = 1

-2, 2, 1 will generate values of 0.01, 0.1, 1, 10, 100

Example [61](#)

## loopMax

Value	number
Description	Maximum value of the z-loop variable
Aliases	<a href="#">zmax</a>
System default	not defined
Use	Determines the finishing value of the z-loop variable. <a href="#">loopMax</a> must be defined if <a href="#">loopInt</a> is non-zero.

Example [61](#)

## loopMin

Value	number
Description	Minimum value of the z-loop variable
Aliases	<a href="#">zmin</a>
System default	not defined
Use	Determines the starting value of the z-loop variable.

Example [61](#)


---

## loopVal

Value	an array of numeric values
Description	A list of loop values.
Aliases	
System default	“ (empty string)
Use	<p>If present, this list of numeric values is used to control the z-loop values. It takes precedence over any values defined with a loop file or the <a href="#">loopMin</a> etc keywords.</p> <p>The generated z-loop value is accessible via the &lt;loop&gt; tag. The <a href="#">loopLog-Var</a> setting operates on these z-values.</p> <p>If the value is an empty string and no other mechanism defines the loop variable, the z-loop value is undefined and the z-loop is only executed once.</p>

---

## mainLoop

Value	integer or ‘auto’ or ‘last’ [logical]
Description	Defines the division, if any, between ‘pre-loop’ <b>PHREEQC</b> simulations and ‘main loop’ simulations and, optionally, the <a href="#">oneSimulationAtaTime</a> switch determines whether the main loop simulations should be executed as individual simulations one at a time or all together in one run.
Aliases	<a href="#">loopSimulationStartNumber</a> , <a href="#">simulationStartNumber</a> , <a href="#">simulationStart</a> , <a href="#">start</a>
System default	‘auto’ [FALSE]
Use	<p><a href="#">mainLoop</a> defines the division between ‘pre-loop’ simulations and ‘main loop’ simulations. The number given defines the first of the main loop <b>PHREEQC</b> simulations numbered from the top of the appropriate block of simulations downwards. Where a data file is used to specify a separate block of simulations for each line of data as in fitting, <a href="#">mainLoop</a> is always counted relative to the top of the block not the absolute simulation number, i.e. 1 will always point to the first simulation.</p> <p>‘auto’ is set by <b>PhreePlot</b>: normally it refers to the last simulation but for calculationType’s ‘fit’ and ‘simulate’ it is set to 1. ‘last’ refers to the last simulation.</p> <p>The optional second parameter is the <a href="#">oneSimulationAtaTime</a> switch which if set to TRUE will run each main loop simulation separately. The default is FALSE which means that all the main loop simulations are run in a single call to <b>PHREEQC</b>. Running each simulation separately enables tags to be defined and used between simulations.</p> <p>The <a href="#">mainLoop</a> simulation and all subsequent simulations will be ‘looped’ over by the x- and y-axis loops as controlled by the &lt;x_axis&gt; and</p>

<y\_axis> tags. These main loop iterations are intended to be run fast, with minimum overheads, trying to avoid the repeating of unnecessary calculations. This distinction also affects what output is stored and in particular eliminates the accumulation of unwanted output data in the 'out' file. The 'out' file has to be well-formed to go into the plotting or fitting phases successfully.

With the second [oneSimulationAtaTime](#) parameter set to `FALSE`, as by default, all simulations within the 'main loop', i.e. those simulations numbered [mainLoop](#) and greater, will be executed in one call to **PHREEQC**. Tags are only substituted before entering this block of code and only updated after exiting it. They cannot be updated between these simulations since execution is not returned from **PHREEQC** to **PhreePlot** until all the simulations sent for the run have been executed. If tag values need to be passed from one simulation to another, set [oneSimulationAtaTime](#) to `TRUE`.

Output is only sent to the 'out' file (the main plotting file) from the last simulation or set of simulation to be run. The number of lines sent from the chosen `SELECTED_OUTPUT` block is controlled by [selectedOutputLines](#). 'Pre-loop' **PHREEQC** simulations are processed one-by-one with tags generated between simulations but no pre-loop output is ever sent to the 'out' file.

'Pre-loop' simulations are intended to be one-off simulations in which solutions, equilibrium phases, surfaces, reactions, databases etc. are defined and initialised while the main loop is where the **PhreePlot**-style iterations are done.

This strategy gives the main loop advantages in terms of speed in that the overheads are reduced when as many **PHREEQC** simulations are executed in one **PHREEQC** run as possible and when calculations that do not need to be repeated are not. The price paid is that the tags are not updated between the individual simulations making up the main loop (just before and after) and so cannot be used to pass newly-acquired output data from one simulation to a later one. This type of calculation should be done wherever possible in the pre-loop section.

If there are no tags in an input file, the [mainLoop](#) setting should make no difference to the results although in principle the calculations should be somewhat faster with a setting of 1.

With fits and simulations, the [mainLoop](#) setting may be set individually for the blocks of simulations associated with each data point. This overrides any setting by [mainLoop](#) although the value of [oneSimulationAtaTime](#) is still inherited from [mainLoop](#). With fits and simulations, [mainLoop](#) refers to the position relative to the start of the specified block of simulations for an observation not to its position in the main input file.

---

## mainLoopColumn

Value	integer, string
Description	Defines the column number or name in the 'fit' data file which contains the <a href="#">mainLoop</a> number

Aliases	
System default	0
Use	Defines the column number or name in the 'fit' data file which contains the <a href="#">mainLoop</a> number. The string should refer to a column header in the 'fit' data file.

## mainspecies

Value	list of strings (maximum length 32 characters each), optionally in quotes
Description	Determines the 'main species' used in the calculation of predominance and species diagrams
Aliases	<a href="#">main</a>
System default	'' (empty string)
Use	This setting controls the outermost (slowest moving) loop in a <a href="#">predominance diagram</a> (ht1 and grid plots). This is a 'character loop' – the only one – and it uses each of the strings in the list in turn to set the <code>&lt;mainspecies&gt;</code> tag. The setting can be used to specify a list of main 'species', e.g. "Fe" "Mn" "Zn". This can also be input simply as Fe Mn Zn without the quotes. It also controls the 'element' analysed in a <a href="#">species plot</a> .

For parallel processing, where several main species need to be calculated for each speciation calculation, the main species would be entered as

Fe:Mn:Zn

where the end-of-input character, the colon (:) is used to separate the subspecies. The important point is that this so-called species is read by **PhreePlot** as a single species and so the main species loop will only go round once, i.e. one speciation calculation. This is fundamentally different from the 'Fe Mn Zn' approach which would be parsed as three separate items and hence go round this outer loop three times.

The 'main species' (or main subspecies) is the species for which predominance is to be calculated, e.g. Fe will give a diagram containing only Fe species while Cu would give a diagram with only Cu species.

At least one main species must be defined to create a predominance diagram. A list of up to 50 main species can be entered. They will be looped in the order given. Separate by spaces or commas.

A special main species is 'minerals' which acts as a 'superspecies' - actually more like a 'do nothing' species. If used in conjunction with an appropriate script, e.g. `minstabl.inc`, it can be used to produce a 'minerals only' or mineral stability plot. This will plot the most abundant mineral no matter what elements it contains.

The 'main species' do not have to refer to chemical species or master species but can be used for any list of character variables that define the number of iterations of the main species loop and the values of the `<mainspecies>` tag which are generated and which can then be used in an input file.

Examples [1](#), [3](#), [54](#)

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## minimumAreaForLabeling

Value	non-negative number
Description	Either defines the minimum percentage of the plot area that is necessary for a field to be labelled with <code>ht1</code> or defines the minimum y-value for a line to be plotted in a <code>species</code> or <code>custom</code> plot.
Aliases	<a href="#">minArea</a> , <a href="#">minimumArea</a>
System default	0.1
Use	<p>Sometimes some very small fields are found by the hunt and track algorithm either because they actually exist or because they are produced as a result of the numerical error inherent in the numerical method employed in calculating the speciation. This setting can be used to prevent them being labelled (but not from being plotted).</p> <p>In species plots, there may be many minor species present. These would obscure the plot so this setting can be used to ignore all species for which the maximum value (% species or log concentration) is less than the set value. Neither the line nor the label are plotted in such cases.</p>
Example	<a href="#">23</a>

---

## minimumYValueForPlotting

Value	number [number]
Description	Defines the minimum y-value for a dataset to be plotted in a <code>species</code> or <code>custom</code> plot. The optional second parameter applies the same test to datasets plotting according to the 2y axis.
Aliases	<a href="#">minY</a>
System default	UNDEFINED UNDEFINED
Use	<p>Points or lines datasets will only be plotted if the maximum value in the dataset is equal to or greater than this value. Each dataset is initially clipped to the plotting domain insofar as it is known at the time.</p> <p>A ‘dataset’ in this context is a whole column of data as read in from a data file. This dataset may contain line breaks (internally represented by <code>-99998</code>) and so may consist of more than one line (plotted curve). It is not possible to apply this criterion to each separate line in a dataset.</p> <p>This setting can be used to exclude the plotting of datasets where all the data are close to zero, for example.</p> <p>A setting of <code>UNDEFINED</code> means that no test is applied.</p>
Example	<a href="#">75</a>

---

## missingValue

Value	integer
Description	A value used in data files to signify a missing data value
Aliases	<a href="#">miss</a>
System default	-99999
Use	<p>Missing values are substituted as place markers in some data output files where a proper value is not available, e.g. because the speciation has failed so no valid concentration can be written.</p> <p><b>PhreePlot</b> also uses an <code>UNDEFINED</code> value in other places when it has to print a value without having a value. This is currently set as -99999 and cannot be changed.</p>

---

## multipageFile

Value	logical
Description	Where more than one plot is produced, determines whether a separate plot file is produced for each file or a single, multipage plot file is produced.
Aliases	<a href="#">multipage</a>
System default	F
Use	<p>Looping through multiple 'main species' produces multiple plots which can either be stored separately one file per plot or as a single multiple page file.</p> <p>This is also true for multiple predominance plots produced with the <code>&lt;loop&gt;</code> variable. However, for custom plots the <code>&lt;loop&gt;</code> variable is used to produce multiple curves per plot and so the <code>&lt;loop&gt;</code> variable does not trigger the production of a multipage file.</p> <p>Such files can be viewed with Ghostscript and Adobe Illustrator and can be translated to multiple page pdf files. These are very compact and can be viewed with Adobe Reader.</p> <p>Set to <code>TRUE</code> for a multipage file. It is often best to produce single page files initially as these will be stored as soon as they are produced in a run and can be viewed separately. It is also only possible to follow progress with a tracking plot if this setting is set to <code>FALSE</code>. Once the set of plots is complete, a multipage file can be generated quickly by setting <a href="#">calculation-Method 2</a> and <a href="#">multipageFile</a> to <code>TRUE</code> and replotting.</p> <p>This setting applies to <code>ps</code>, <code>pdf</code> and <code>png</code> files. It may not be possible to view multipage <code>png</code> (<code>mng</code>) files as most <code>png</code> viewers, including <code>GsView</code>, only render the first page.</p> <p>For an example of the making of a multipage file see <code>\demo\multipage-file\multipagefile.ppi</code>.</p>

---

## nameSpeciationProgram

Value	string
Description	The name of the speciation program being used
Aliases	<a href="#">program</a>
System default	PHREEQC
Use	Since the speciation program used is currently fixed, the default value should not be changed. It is only used in the log file as a matter of record.

---

## nudge

Value	A list of nudge parameters
Description	Final adjustments to label positions specified in length units, mm etc.
Aliases	
System default	""
Use	This can be used for all types of plots with automatically-generated labels. The list of nudge parameters are read in the order:

plot number, label number, label name, type of nudge, x coordinate in length units (e.g. mm), y coordinate, [angle, [pos]]

with the parameters defined as:

- (1) plot number for which this set of adjustments will be used. Use 'auto' (or -99999) or 0 for all plots.
- (2) label number. This is used to differentiate labels when the same label is used more than once. The number refers to the order in which the labels are printed and is slightly different for the different types of plots (see the log file or label file for predominance plots). The nudge file gives the label numbers in the 'num' column. Use 'auto' (or -99999) or 0 for all labels with the given label name. For non-zero numbers, only labels with this label number will be changed. The label number was introduced in March 2020 and so earlier files will need to have this parameter added.
- (3) label name exactly as given in the log file, labels file, fill color file etc. Don't include <sub> etc tags unless explicitly specified. Quotes are optional unless space in name. A blank name, "", matches any name.
- (4) type of nudge is either 'diff' or 'abs'. 'diff' shifts the default position by this amount whereas 'abs' resets the position to this position;
- (5) delta x ('diff') or x coordinate ('abs') in the distance units currently in force, e.g. mm.
- (6) delta y ('diff') or y coordinate ('abs') in the distance units currently in force, e.g. mm.

- (7) `angle` to rotate from the horizontal, measured clockwise (in degrees downwards from the horizontal). For example, to rotate the label for the water limits in predominance plots, a positive ‘`abs`’ number must be given. The absolute angle of the water line is given in the log file. Optional. Default = 0.0.
- (8) `pos` is x-justification of the ‘anchor’ point of the label given in (4) above with respect to the direction the text is being written, e.g. if the text is rotated 90°, then this justification will move the text in the vertical direction. 0 = beginning of label string (left justified), 1 = centre of string, 2 = end of string (right justified). The y-coordinate refers to the vertical centre position of the string (approximately), or the first line of a multi-line string. This parameter is not used for ‘`diff`’ shifts. Optional. Default = 0 except 1 for the inline labels of contour plots which are always centered.

Parameters can be set for multiple nudges on one line. An end-of-input character, namely a colon (:), is used to end a set of parameters. Precede the colon with `\` if the colon is part of the label name.

Default values are given for any unspecified parameters from ‘`angle`’ onwards. If in doubt, use ‘`auto`’ for the first two entries.

More specifically, a line could look like

```
nudge 1 0 "Zn+2" diff 2.0 0.0 : \
      1 0 "ZnCO3\ :H2O" abs 80.0 100.5
```

for two nudges on plot 1. Note that the continuation character `\` at the end of line 1 means that the text is read as a single long line, as required, whereas the `\` in `"ZnCO3\ :H2O"` allows the colon to be taken literally rather than as a line ending. This colon is the **PHREEQC** convention for a period (.) with a formula and is translated as such when plotted.

These inline `nudge` settings are read after any found in the labels file or a nudge file and for `diff` type nudges, operate cumulatively.

If you don't know the plot number or label number just use `auto` or 0. If there is only one label with the given label name, this will be fine. If not, you will have to choose which ones to nudge explicitly. The log file gives a table of the labels and their label number, and x, y positions so it should be possible to locate which label to nudge.

These nudge settings are temporary and always refer back to the original calculated positions not the positions accumulated after repeated nudges.

In predominance plots, the default labels for the water limits and methane (specifically for  $H_2(g)$ ,  $O_2(g)$  and  $CH_4(g)$ ) are automatically rotated if their rotation is set at exactly 0.0 degrees. To avoid this, set the rotation to some small value, e.g. 1e-6. The labels file will show the rotation, and any subsequent ‘nudge’ is from this position.

In custom plots, nudged labels do not show their ‘anchors’ since they are then not necessarily associated with a line. This is the easiest way to see if a label has been moved. ‘`abs`’ nudges are always assumed to be moves.

In contour plots, if the label is moved to a position on or very near the contour line, then the contour line will be broken and the label will be placed ‘in line’.

A label can be effectively deleted by nudging it off the plot. If an eps file is being created, set the x or y nudge to ‘`abs`’ and a negative value, e.g. -999.

Example See `\demo\ZnS\ZnS.ppi`, `demo\FeAsS2\FeAsS2.ppi`, `\demo\Hfo_titration\Hfo_titration3.ppi`, `\demo\contourFeAsS\contourFeAsS.ppi`

## nudgeFile

Value logical, or a filename [`data_separator`]  
 Description Either `TRUE` or `FALSE` to indicate whether a nudge file is to be automatically created or not, or, the name of a nudge file for adjusting the position of labels in a plot.  
 Aliases [nudgeLabelsFile](#), [nudgeLabels](#)  
 System default ""

Use If the option to create a nudge file is given and no such file already exists, then a template nudge file is created with a `'diff'` entry for all the available plot labels. This can then be edited as required. Alternatively if the name of a file is given, this is opened as an existing nudge file which is then used to adjust the label positions.

The second option, the filename option, has the option of an additional parameter, a [data separator](#) indicating how the nudge file should be read. Default is "" which specifies that the parameters are separated by whitespace or multiple commas.

The easiest approach is to create a 'do nothing' nudge file by first setting this switch to `TRUE`. If a nudge file of the default file name does not exist, a 'do nothing' nudge file called `<input_filename>_nudge.dat` will be automatically created containing all the labels found in all the plots. This can be edited and then used by specifying this file with the [nudgeFile](#) keyword. This creation only works for [calculationMethod](#) 1 and 3.

The format of a nudge file is:

line 1: a header line (compulsory). Its actual content is optional but would normally consist of the column headings, e.g.

```
plot num label type x y angle pos
```

Leave a blank line if no headings. The headings are for your help only.

line 2 and subsequent: a spreadsheet-like file with the columns consecutively given as above.

See [nudge](#) for details.

There can be any number of lines in a nudge file. Blank lines and comment lines will be ignored. The speciation calculations do not have to be redone – use [calculationMethod](#) 2 or 3 for simply replotting.

A graphics viewer like **GSview** is useful for getting precise coordinate positions from a ps file. Minor adjustments are most easily made using the `'diff'` option to nudge a label by a small amount.

## numberOfFitParameters

Value non-negative integer

Description	Defines the number of parameters specified in a 'fit' calculation (the number can also be implicitly defined by the length of the various fit parameter lists).
Aliases	
System default	0 (but set to 2 in the distributed <code>pp.set</code> file)
Use	This specifies the number of parameters, each with its own tag, that will be defined and which may be used in the Chemistry section of the input file. These parameters may be fixed or adjustable.  If this setting is used, it should precede all of the other fit parameter lists in the input file since if it has a positive value, it will reset the values of all the parameter lists to their system defaults. There are six such lists (all must have a length of <code>numberOfFitParameters</code> ): <a href="#">fitParameterNames</a> , <a href="#">fitLogParameters</a> , <a href="#">fitAdjustableParameters</a> , <a href="#">fitParameterValues</a> , <a href="#">fitLowerParameterValues</a> , and <a href="#">fitUpperParameterValues</a> .
Example	<a href="#">80</a>

## numericTags

Value	A list of tag definitions, all on one logical line
Description	Numeric tags can be used to substitute numeric values within the <b>PHREEQC</b> part of the input file, and used in plots.
Aliases	<a href="#">numericTag</a> , <a href="#">numberOfNumericTags</a>
System default	"
Use	The general form for the definition of a tag with the name 'mytag', say, is: <pre>&lt;mytag&gt; = "tag expression"</pre> <p>where the spaces surrounding the '=' are optional. The tag name is case dependent. The tag expression can itself contain numeric tags providing that they have already been defined. Tags are defined and evaluated in the order of their definitions, effectively 'top down'. Numeric tag names are case sensitive.</p> <p>The tag name must not be the same as the name of a fit parameter.</p> <p>Any number of tag definitions can be included on a line. While the tags and their definitions must all be on a single logical line, it improves legibility if they are split, one definition per physical line, e.g.</p> <pre>numericTags &lt;tag1&gt; = 20 \ &lt;tag2&gt; = "2*&lt;tag1&gt;"</pre> <p>The tag expression must be one 'word' so if it contains spaces, it should be embedded in quotes. Otherwise the quotes are optional. The tag expressions can contain the mathematical functions, <code>abs</code>, <code>exp</code>, <code>log10</code>, <code>log</code>, <code>sqrt</code>, <code>sinh</code>, <code>cosh</code>, <code>tanh</code>, <code>sin</code>, <code>cos</code>, <code>tan</code>, <code>asin</code>, <code>acos</code>, <code>atan</code>, <code>rand</code> and <code>nrand</code>.</p> <p>For historic reasons, the list of tag definitions may optionally be preceded by an integer giving the number of tag definitions to follow. This option will be removed at some date.</p> <p>This keyword can be repeated and each instance will be appended to the last rather than replacing it.</p>
Example	<a href="#">63</a>

---

## objectiveFunction

Value	L1   L2   RSS [value]
Description	Specifies the type of objective function and its termination value.
Aliases	
System default	RSS
Use	<p>Specifies whether to use the L1 norm (sum of absolute deviations) or L2 norm (sum of deviations squared or the residual sum of squares, RSS). Not all routines (e.g. nlls, lm) can compute the L1 norm.</p> <p>If the optional value is given and the objective function falls below this value, then the search will stop irrespective of the routines own convergence criteria.</p>

---

## omitAccumulate

Value	list of strings, each up to 32 characters long
Description	Filters out lines of <b>PHREEQC</b> input if it contains any of the strings (case sensitive).
Aliases	
System default	""
Use	<p>If any of the strings defined with this keyword is found in the <b>PHREEQC</b> input, then the entire logical line is omitted from input to the <b>PHREEQC</b> processor.</p> <p>Trailing blanks are not significant. Leading blanks are.</p> <p>This can be used to omit lines containing the word <code>UNDEFINED</code> which could have been introduced when a tag to be substituted is <code>UNDEFINED</code>.</p>

---

## onePass

Value	logical
Description	Used by 'fit' and 'simulate' to determine if the all the values of the dependent variable are calculated in one pass through the <b>PHREEQC</b> code or not.
Aliases	
System default	F
Use	<p>This keyword only has any effect during 'simulate' or 'fit' calculations.</p> <p>This switch affects how the simulations are run and how the selected output is read.</p>

If `onePass` is `TRUE`, the **PHREEQC** code should deliver at least  $n$  lines of selected output (excluding the header) where  $n$  = number of data points (the last  $n$  lines will be picked).

If `onePass` is `FALSE`, the **PHREEQC** code should deliver just 1 line of selected output (excluding the header). The code block is iterated  $n$  times to produce the required data.

`onePass` might be appropriate because internal **PHREEQC** looping produces multi-line selected output (e.g. the `KINETICS`, `REACTION` or `TRANSPORT` keyword data blocks) or because the **PhreePlot** `CHEMISTRY` section contains multiple simulations that between them produce the required number of lines of output.

The actual lines picked from the selected output produced by each simulation can be specified with the `selectedOutputLines` keyword. 'auto' will attempt to pick the correct number but if this does not work it should be entered explicitly.

Fitting is usually considerably faster with the `onePass` `TRUE` setting since this requires fewer calls to **PHREEQC** and less overheads. However, this is at the expense of a more complex set up. The `input file pre-processor` may reduce the effort in setting up repetitive parts of the input file.

Also since tag values can only be updated when execution is returned from **PHREEQC**, simulations containing tags that need to be updated every iteration must be included in the main loop simulations. It may therefore be necessary to use `mainLoop` (or `mainLoopColumn`) to ensure that the required simulations are included in the main loop and so updated on every iteration.

It is also possible to force **PhreePlot** to run each simulation within a block of simulations used to calculate a data point separately, even with the `onePass` set to `TRUE`. This is done by setting the optional `oneSimulationAtATime` switch of `mainLoop` to `TRUE`.

Example [81](#)

---

## out

Value	logical
Description	Determines if the out output file is created
Aliases	<code>outputFile</code> , <code>output</code> , <code>outFile</code>
System default	T
Use	This file contains the selected output from the last run, i.e. the last simulation or set of simulations run together. It is the main file for saving data for plotting and is always in a spreadsheet type format. Its precise form depends on the type of plot made.
	Output is only sent to the 'out' file for main loop simulations (not pre-loop simulations) and when there is more than one main loop simulation and these are executed <code>oneSimulationAtATime</code> (see <code>mainLoop</code> ), output is normally only sent from the very last simulation.
	In order to get all of the selected output sent to the 'out' file from all sim-

ulations, set [mainLoop](#) to 1, [oneSimulationAtATime](#) to `FALSE`, and [selectedOutputLines](#) to `'auto'`.

A new `'out'` file is started (or old file rewound) whenever the main loop value (`iz`) is 1. `'species'` calculations also begin a new file on every iteration of the z-loop.

With predominance plots, the `'out'` file contains the species–value pairs in the number and order specified by the five counts found at the end of the line. This is controlled by the `htl.inc` file or similar.

With custom and fit plots, the file contains the accumulation of the selected `'selected output'` with the headings that were sent to the selected output. A blank line separates custom datasets with different loop values. Other methods are available for inserting blank lines (see [dataSeparators](#)). The number of lines to be sent to the `'out'` file is controlled by the type of calculation and the [selectedOutputLines](#) keyword.

Example

---

## overlay

Value	list of filenames of <b>PhreePlot</b> -generated Postscript plot files
Description	Plots one of these files on top of the main plot
Aliases	
System default	""
Use	<p>This keyword provides the names of plot files to be added to the main plot(s) and so can be useful for combining several <b>PhreePlot</b> plots into one. The list of filenames should match the number of plots generated in the run. If there are not enough files in the list to match the number of plots, the list is recycled. The number of each plot can be seen by using the <a href="#">info</a> block.</p> <p>This list of files is used, one per <code>'page'</code> (or plot) in turn. This means that each of the individual plots produced can be overwritten with a different plot.</p> <p>A null string, <code>""</code>, means that no overlay is added to that plot for that position and so can act as an empty placeholder.</p> <p>This feature assumes a specific format for the ps file(s) to be overlaid. It only applies to ps files generated by <b>PhreePlot</b> in an earlier run. It does not apply to ps files in general or to <b>PhreePlot</b>-generated ps files that have been edited by other software.</p> <p>The overlay plot(s) will be drawn on top the main plot.</p> <p>The ps file to be overlaid should be a <code>'single page'</code> file. If a <code>'multipage file'</code> is specified, the overlay will only use the plot from the first page.</p> <p>The resulting plots are automatically named with the main filename and the suffix, <code>"_overlay.ps"</code>, e.g. <code>hfo_Fel_overlay.ps</code>. The original plot file, e.g. <code>hfo_Fel.ps</code>, without the overlay is generated as normal.</p> <p>If other format plot files, such as pdf, are generated these will include the overlay(s).</p>

Although **PhreePlot** does not support transparency (because **Postscript** has only limited transparency options), it is possible to produce some pseudo-transparency. For example, the colour 'nd' ('not drawn') can be useful for fill colours in overlay files since it allows other colours below to be seen. It is the default if no colour background for plots is specified. Note that 'nd' (100% transparent) is different from 'white' (100% opaque) in this respect.

The **overlay** option can be useful for adding more information (and complexity) to predominance plots, e.g. the underlying aqueous speciation. An example is shown in the figure below. This was produced in two stages: (i) prepare a 'bare' diagram showing just the boundaries for the aqueous speciation (no solid phases present), no axes drawn and a gray colour for the boundaries and labels; (ii) prepare a full diagram with the solid phases, axes, boundaries and labels in black and overlay with (i) above. Tweak the labelling.

An example of this is shown below where the aqueous speciation is overlaid on the main predominance diagram.

An overlay can also be used for 'watermarking' your plot.

Unlike most keywords, multiple instances of the **overlay** keyword in input files will not result in overwriting the earlier setting(s) but will enable multiple ps plot files to be overlaid on top of the main ps plot file. Each instance can have its own list of files to be picked one-by-one in sequence. This produces an  $n \times m$  matrix of filenames where  $n$  is the number of different files to add to a plot and  $m$  is the number of the plot produced in a multiplot file. This enables each file in a multiplot file to have multiple, but different, overlay plots for each plot (or page in a multipage file).

For example, if the input file produces four separate plots and the **overlay** keyword is used five times, namely

```
overlay  File1.ps
overlay  File2.ps  File3.ps
overlay  ""        File4.ps  ""        File5.ps
overlay  File6.ps  File7.ps  File8.ps  File9.ps
overlay  File10   ""        File11.ps
```

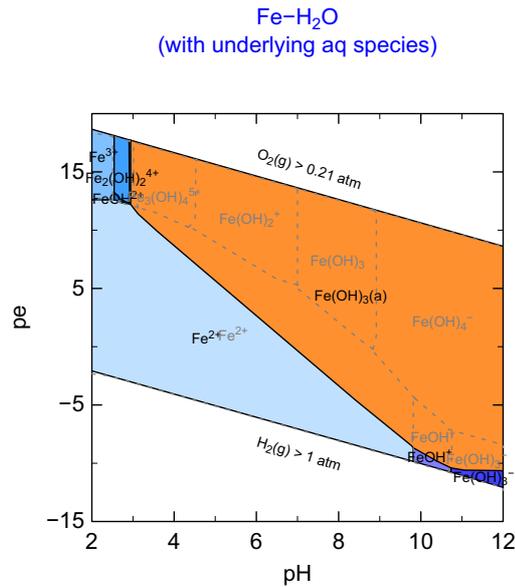
then applying the recycling rules, the four plots will be successively overlaid with the following overlay files:

	<b>Plot 1</b>	<b>Plot 2</b>	<b>Plot 3</b>	<b>Plot 4</b>
add file	File1.ps	File1.ps	File1.ps	File1.ps
add file	File2.ps	File3.ps	File2.ps	File3.ps
add file		File4.ps		File5.ps
add file	File6.ps	File7.ps	File8.ps	File9.ps
add file	File10.ps		File11.ps	File10.ps

The positioning of the 'overlaid' plot on the page will depend on their position in the originating Postscript file, i.e. it will depend on the offsets, axis lengths and orientation defined by the **PhreePlot** input file used to produce them. By varying the position of individual plots on a page, it is possible to produce complex page layouts with multiple plots.

Example

See `\demo\Fe\hfo_with_overlay\hfo-aq.bat` and the plot shown below.




---

## pageOrientation

Value	0 or 1
Description	Determines the page orientation of plot files.
Aliases	
System default	0
Use	0 signifies portrait mode while 1 signifies landscape mode.

---

## paperSize

Value	One of the standard paper sizes given by the codes below (case not significant).
Description	Determines the paper size written to the Postscript file.
Aliases	<a href="#">paper</a>
System default	a4
Use	Sets the paper size. The following paper sizes are available:

Example

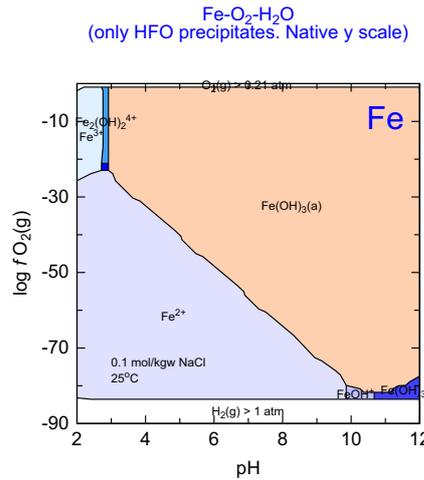
Table 14.3. Standard paper sizes

Code	Dimension (width x height)
11x17	11 x 17 inch
A0	841 x 1189 mm
A1	594 x 841 mm
A2	420 x 594 mm
A3	297 x 420 mm
A4	210 x 297 mm
A5	148 x 210 mm
B4	250 x 353 mm
B5	176 x 250 mm
Ledger	17 x 11 inch
Letter	8.5 x 11 inch
Legal	8.5 x 14 inch
Note	8.5 x 11 inch

---

## pdf

Value	logical [[logical] filename]
Description	Determines whether the plot output (if any) is converted to a file in the Adobe Portable Document (pdf) format.
Aliases	<a href="#">pdfFile</a>
System default	FALSE
Use	<p>The first logical switch determines if a pdf file is produced. The second, optional switch determines if the file is ‘linearised’ or not (aka ‘Fast web-view’). Both switches are FALSE by default.</p> <p>A <a href="#">pdf</a> file can only be produced if <b>Ghostscript/GSview</b> is installed and available.</p> <p><b>PhreePlot</b> makes use of <b>Ghostscript</b> to produce the pdf file. pdf files are compact graphics files that can be viewed using <b>GSview</b>, <b>Adobe Reader</b> and other software. The file created is given the extension pdf. It is also possible to create a pdf file from <b>GSview</b> directly using its Convert facility. An example of pdf output is given below.</p> <p>If filename is present, this overrides the auto-generated filename.</p>
Example	<a href="#">79</a>




---

## pdfMaker

Value	file path
Description	Path for the Ghostscript executable file used for converting the ps file to other graphical formats including pdf.
Aliases	
System default	“”
Use	Ghostscript is not strictly necessary for the operation of PhreePlot since PhreePlot produces native Postscript (.ps) files. However, Ghostscript is necessary for the automatic conversion to other formats such as png or eps.

The Ghostscript executable is named `gswin32c.exe` or `gswin64.exe` (older versions of **PhreePlot** used `ps2pdf14.bat`). Its location is set in one of three ways:

(i) if **Ghostscript** has been downloaded during installation, this version of **Ghostscript** is used by default. This can be found alongside the `pp` executable in the appropriate Program Files folder. It consists of two files: `gswinxxc.exe` and `gsdllxx.dll` where `xx = 32` or `64`. Replacing these two files with any other version of **Ghostscript** will cause these to be used;

(ii) if the **GSC** environment variable has been set to a valid path, then this is used;

(iii) if `pdfmaker` is not blank and has been set to a valid path, then this will be the version of **Ghostscript** used, e.g. `pdfMaker "C:\Program Files\gs\gs9.26\bin\gswin64c.exe"`.

After normal installation, the **Ghostscript** executable will be installed into the same folder as the **PhreePlot** executable, `pp.exe` or `pp`. For Windows, this will be in the Program Files (or Program Files (x86)) folder.

The embedded executable usually has a path such as `C:\Program Files\gs\gsx.xx\bin\gswin64c.exe` and is installed along with its associated dynamic link library `gsdll64.dll` (Windows), where `x.xx` is the version number.

The embedded version is usually the latest version of **Ghostscript**. In any

case, Version 9.16 or later is required for reliable use.

---

## PHREEQC.out

Value	'auto' or a logical (TRUE or FALSE)
Description	Switch to determine if the standard PHREEQC.[id].out file is written
Aliases	PHREEQC.0.out
System default	'auto'
Use	<p>Explicitly sets the switch that determines if the PHREEQC.[id].out file is definitely written (TRUE) or not (FALSE). This will be written on every iteration and can slow down execution times. FALSE will cause the file to be deleted on termination if present.</p> <p>The 'auto' value sets the PHREEQC.[id].out switch depending on the debug level, FALSE if ABS(debug) = 0 else TRUE. When TRUE, the PHREEQC.[id].out file will always be created.</p> <p>'auto' is the default setting.</p> <p>This file is copied to the *.all file if created and so may be temporarily created even when it is not wanted itself at the end.</p>

---

## PLOT

Value	none (section heading)
Description	Optional section heading for input file
Aliases	
System default	
Use	None other than to offer chance to structure file

---

## plotFactor

Value	non-negative number
Description	Scaling factor for all plot dimensions
Aliases	<a href="#">factor</a>
System default	1.0
Use	<p>All plot dimensions (titles, axis lengths, line widths, symbol sizes etc) but excluding <a href="#">xoffset</a> and <a href="#">yoffset</a> are scaled by this factor. This scaling is done just before plotting and so if more than one plotFactor has been specified, only the latest is used. A value of zero will prevent any plotting.</p>
Example	<a href="#">Z1</a>

---

## plotFrequency

Value	positive integer
Description	Frequency of automatically writing the <code>plot.ps</code> file during computations
Aliases	<a href="#">plotFreq</a> , <a href="#">plotx</a>
System default	1000000
Use	Determines the frequency with which the <code>plot.ps</code> file is automatically written during computations. The file is written every <a href="#">plotFrequency</a> 'th point calculated. This file can be used to view the status of the <code>ht1</code> and grid calculations. A large number means very infrequently; the default effectively means 'never'. This file can also be forced to be written using the interrupt key ( <code>ESC</code> ).

---

## plotOrder

Value	list of 'lines', 'lines2y', 'points', 'points2y' (or their singular), in any order
Description	Controls the general order of plotting lines and points in custom plots
Aliases	
System default	<code>lines lines2y points points2y</code>
Use	<p>The order of plotting of points and lines can be important since it controls the over-printing – the last feature plotted will appear on top. The default is for points to appear on top of lines.</p> <p>Within a given class, say 'points', the order of plotting is controlled by the order of definition in the keyword setting.</p> <p>Although <a href="#">plotOrder</a> does control the order of plotting of separate sets of lines and points, when the same variable is plotted as both a line and a set of points, the line is always plotted first. This means that the points will always overprint the line.</p>

---

## plotTitle

Value	string (maximum 400 characters)
Description	Title at the top of a plot
Aliases	<a href="#">title</a>
System default	'' (empty string)
Use	<p>Gives the title string placed at the top of the plot. This can contain text tags such as <code>&lt;sup&gt;...&lt;/sup&gt;</code>. Its placement is fixed. Use <a href="#">text</a> or <a href="#">extraText</a> for other placements.</p> <p>A blank string means that an auto-generated title will be used. Turn-off by setting <a href="#">plotTitleColor</a> to 'nd', <a href="#">plotTitleSize</a> to 0 or setting the title to a</p>

non-printing character such as ‘`\n`’ (ASCII encoding).

A special case is to set `plotTitle` to ‘`character set`’ and this will produce a plot of the current character set (see [Appendix 4](#)).

Example [55](#)

## plotTitleColor

Value	Cohort or rgb colour
Description	Colour of the plot title.
Aliases	<a href="#">titleColor</a>
System default	<code>blue4</code>
Use	<a href="#">Colour</a> of the plot title. Colours should be chosen from the <a href="#">colour palette</a> .

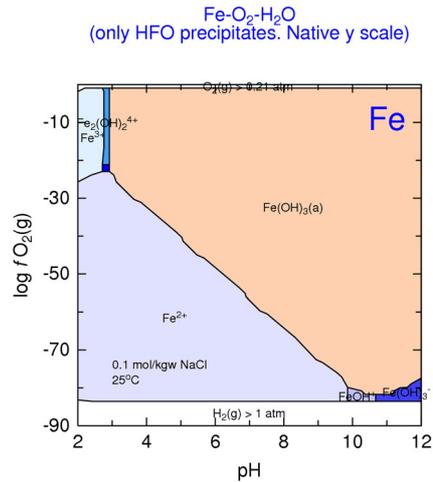
## plotTitleSize

Value	A non-negative number
Description	Size of the plot title
Aliases	<a href="#">titleSize</a>
System default	<code>3</code>
Use	Uses the length units in force at the time of plotting

## png

Value	logical [[number] filename]
Description	Make a png (portable network graphics) copy of the plot
Aliases	<a href="#">pngFile</a>
System default	<code>F</code>
Use	<p>Uses <b>Ghostscript</b> to convert from the ps file. The <b>Ghostscript</b> path for the conversion script is taken from <a href="#">pdfMaker</a> and assumes that the default <b>Ghostscript</b> directory structure given by the installation of a recent release Ghostscript is unchanged.</p> <p>The second, optional parameter specifies the resolution (in dpi) to use when making the conversion. The default is 300 dpi.</p> <p>An example of output in png format is given below.</p> <p>If filename is present, this overrides the auto-generated filename.</p>

Example [79](#)




---

## pointColor, pointColor2y

Value	list of colours
Description	Symbol colours used for plotting points
Aliases	<a href="#">symbolColor</a>
System default	red4

Use These define the [colour](#) of any points that are to be plotted. Colours should be chosen from the [colour palette](#).

If [pointsSameColor](#) is `TRUE` and a line has been drawn, uses the same colour for the points as for the line. Otherwise the point colour sequence is used.

Whether the colour changes for later datasets depends on the [changeColor](#) setting (q.v.). Point colours can be changed by editing the line colour dictionary and forcing the dictionary to be used by setting [useLineColorDictionary](#) to a value of 1 or more. The line colour dictionary is automatically written and updated as plotting takes place so it may be necessary to generate the plot first then edit the line colour dictionary and replot.

The colours specified by [pointColor](#) are promoted to be the first colours used. If further colours are needed, these are taken successively from the auto-generated list of colours (see [Section 7.9](#)).

If [useLineColorDictionary](#) is set to a value of 0, the line colour dictionary is not used and the colour sequence for points is either taken from the [pointColor](#) setting, or if that list is exhausted, automatically set by **PhreePlot**.

---

## points, points2y

Value	character list
Description	Specifies which columns should be plotted as points on the main y and 2y axes.
Aliases	<a href="#">plotPoints</a> , <a href="#">plotPoints2y</a> , <a href="#">2ypoints</a> , <a href="#">point</a> , <a href="#">point2y</a>
System default	''
Use	<p>The list should contain the column names or column numbers of columns for which the points are to be plotted. The names are case dependent. The names or numbers refer to the column of the file being used for plotting, e.g. the 'out' file for custom plots or the 'pts' file for species and fit plots.</p> <p>A special setting for <a href="#">points(2y)</a> is 'auto' by itself which means that points will be automatically plotted for all the plotted lines. These will inherit all the normal attributes of points such as <a href="#">pointType</a>, <a href="#">pointColor</a> etc. This only applies to custom-type plots and will only be activated if there are no other 'points' settings.</p> <p>The names can contain tags, most usefully character tags.</p> <p>Additional files can be added to the search path using the <a href="#">extradat</a> keyword. These files must be in tabular format with a single header row defining the column names. One of these columns must be the same as the <a href="#">customXcolumn</a> defined elsewhere.</p> <p>Points can be added to predominance diagram plots as well as custom plots (including fit and species plots).</p> <p>The 2y axis is the right-hand y axis which can have a different scale from the left-hand or main y axis.</p>
Examples	<a href="#">55</a> , <a href="#">80</a>

---

## pointsSameColor

Value	logical
Description	Determines if the colour used for points is the same as that use for the corresponding lines
Aliases	<a href="#">symbolSameColor</a> , <a href="#">sameColor</a>
System default	F
Use	<p>When both lines and points are drawn for a particular column/curve, setting this to TRUE will force the lines and points for a particular column to use the same <a href="#">colour</a>. This will be the colour of the lines irrespective of the <a href="#">pointColor</a> setting (see <a href="#">Section 7.9</a>).</p> <p>This only applies to datasets plotted on the same axis.</p>

---

## pointSize, pointSize2y

Value	list of non-negative numbers
Description	Sets the size of points (symbols) for each dataset plotted on the main y (left) and 2y (right) axes for custom plots
Aliases	<a href="#">symbolSize</a> , <a href="#">symbol</a>
System default	2
Use	<p>Symbols are used to plot points in custom plots (including fit plots) and their size, and that of all other symbols, are controlled by the <a href="#">pointSize</a> setting. The actual size of a plotted symbol depends on the length <a href="#">units</a> in force at plotting time and the way that the symbol fills the allotted symbol space.</p> <p>The <a href="#">rimFactor</a> and <a href="#">rimColor</a> settings, and their 2y counterparts, control the widths and colours of the rim around each filled circle, respectively. The rim factors are specified as a fraction of the corresponding symbol sizes.</p>
Example	<a href="#">55</a>

---

## pointType, pointType2y

Value	list of symbol numbers or names
Description	Used to define the symbols used in custom plots
Aliases	<a href="#">symbolType</a> , <a href="#">symbol</a>
System default	2
Use	<p>Symbols are used to plot points in custom plots (including fit plots) and the symbols used are controlled by the <a href="#">pointType</a> (main y axis) and <a href="#">pointType2y</a> (2y axis) settings.</p> <p>The y and 2y lists are maintained and used separately.</p> <p>Symbols can either be specified by their symbol numbers (see <a href="#">Figure 7.5</a>) or by their symbol names (<a href="#">Appendix 3</a>).</p>
Example	

---

## pol

Value	logical [exclude list]
Description	Determines if a polygon file is created during predominance plot and contour plot calculations, and whether any polygons should be excluded from plotting in predominance diagrams.
Aliases	<a href="#">polygonFile</a> , <a href="#">polygon</a>
System default	T

Use	<p>Controls the creation and deletion of the polygon (*.pol) file that is used by <code>ht1</code> and <code>grid</code>. The polygon file contains the x, y coordinates of field boundaries used to plot the predominance fields. The header also contains the resolution used to generate the file (e.g. <code>x500</code>) and the <code>pe</code> for each point.</p> <p>Since this file is essential for the operation of <code>ht1</code>, <code>grid</code> and <code>contour</code> plots, the polygon file is automatically created and saved for these plots. This means that the setting of this logical switch is ignored.</p> <p>The 'exclude list' is a list of polygon/species names (from the list of names appearing in the labels file) that are not to be infilled with colour.</p> <p>Contours fill areas are automatically named as "1", "2" etc. However, while contour fill areas can be excluded from filling with their ascribed colours, the areas may still be filled with an adjacent colour since the colouring of contour fill areas relies on the overprinting of larger areas by smaller areas. This is why the polygons are coloured strictly in order of decreasing polygon size and why this option is not recommended for contour plots.</p> <p>An alternative approach to excluding one or more polygons from plotting is to set the species numbers for the excluded polygons to 0 or less in the polygon file and replotting.</p> <p>The labelling of a polygon (but not the plotting of the polygon) can also be suppressed by using the <a href="#">minimumAreaForLabeling</a> criterion or more generally by setting the species number to a negative value in the plot file and replotting without recalculating the labels (<a href="#">calculationMethod</a> = 2).</p>
-----	---

## post

Value	<p>list of strings (up to 30 characters each) or a single column name from one of the plotting data files.</p> <p>If two strings are present and the second one is an integer, then this integer is interpreted as the number of significant figures to use when printing floating point numbers (see below).</p>
Description	Can be used to 'post' a numeric value or character string next to each plotted point in custom and fit plots.
Aliases	<a href="#">postName</a> , <a href="#">postNames</a>
System default	"" (use default names)
Use	<p>This only applies to variables plotted using the <a href="#">points</a> or <a href="#">point2y</a> keywords.</p> <p>The behaviour of this setting is somewhat similar to the <a href="#">labels</a> setting but it offers the possibility of posting values to individual points (symbols) in custom and fit plots, most commonly using another variable column to provide the posted character string.</p> <p>Posted values will always be written above and to the right of ('NE') of the associated symbol.</p> <p>If there is either one post name, or two with the second being an integer, then the first name is tested to see if it corresponds with a column name</p>

in one of the plot data files (the 'out' or 'pts' file or an [extradat](#) file). This test is case-sensitive.

If it does, then posted values for each point are taken from the specified column and the corresponding row of the identified file. Both posted variable and data variable must come from the same file, i.e. be of similar length. If the posted variable exists in more than one file, as would the x column, only the points from the post file are used.

The post column pointed to can be numeric or character.

If more than one post name is specified, then these are assumed to be a list of character strings to post against each point. These are recycled as necessary starting with the first string specified above always starting the cycle for each new dataset.

The interpretation of post strings as **PHREEQC** formulae is automatically turned off.

If multiple [points](#) data sets are defined from the same file as the posted column, each set is posted with the same list of posted values.

Floating point values are reduced to 3 significant figures unless the second (and last) item in the [post](#) list is an integer with an absolute value between 1 and 7 whereupon that value is used for the number of significant figures, e.g. if the `mass` value is 12.764897

`post mass` will print '12.8'

`post mass 2` will print '13'

Trailing zeros are removed to save space, even if deemed 'significant' by the above definition if the number of significant figures specified above is negative, i.e. between -1 and -7.

'Large' and 'small' numbers will be printed in E format. In this case, the second item absolute value if present will control the number of figures after the decimal point. For example, 1.2345678E-09 will print '1.235E-9' for a second item value of 3.

The size of the posted text is given by [postSize](#). The colour of the text is always black.

Posted text is always printed last and so will overprint any other text.

## postSize

Value	number
Description	The size of the posted text in the units of length in force at the time of reading.
Aliases	
System default	2
Use	Used with <a href="#">post</a> to post text alongside plotted symbols. The colour of the text is always black and the text is always placed to the top right of the symbol.

---

## pplog

Value	logical
Description	Controls whether a line is written to the <code>pp.log</code> file or not
Aliases	<a href="#">pplogFile</a>
System default	T
Use	<p>The <code>pp.log</code> file keeps a summary of each <b>PhreePlot</b> run. It is especially useful for seeing the results of multiple runs executed from a batch file, such as <code>demo.bat</code>.</p> <p>This setting should be set to <code>FALSE</code> if several instances of <b>PhreePlot</b> are run simultaneously to minimise interfering interactions.</p>

---

## prefix

Value	“auto” or directory name
Description	Redirects all output files to the given directory.
Aliases	
System default	‘auto’
Use	<p>Used to redirect all output files, including data and image files, to the specified directory (or folder). The default, ‘auto’, means that all these files will be in the same directory as the main input (.ppi) file. A blank value is the same as ‘auto’.</p> <p>The specified folder must exist before execution. The terminal directory separator is optional, e.g. “D:\PhreePlot\output\” or “D:\PhreePlot\output”.</p> <p>If a filename is specified with an image file’s logical switch, this takes precedence.</p> <p>The prefix setting is also used to locate data files (the <code>out</code> and <code>pts</code> files) for replotting and so the prefix should not be changed between the initial creation of the files and replotting.</p>

---

## printScreenFrequency

Value	integer
Description	Frequency of automatically writing a summary of the output to the screen during computations
Aliases	<a href="#">screenx</a>
System default	1
Use	The absolute value of <code>printScreenFrequency</code> determines the frequency with which summary results are automatically written to the screen dur-

ing computations. Output is written every `abs(printScreenFrequency)`'th point calculated. This output can be used to view the status of the ht1 and grid calculations, and to monitor progress during fitting. A large number means very infrequently.

A value of 0 during fitting means that the value is temporarily set to the number of adjustable parameters. This is because a new direction is only chosen every n'th function evaluation, where n is the number of adjustable parameters.

A negative value turns off the continual updating of the `pp.log` file that occurs on every iteration of a run.

## ps

Value	logical [filename]
Description	Turns on or off the output to the Postscript (ps) file
Aliases	<a href="#">psFile</a>
System default	T
Use	This is the native format for graphical output in <b>PhreePlot</b> .  Since several other file formats are derived from the ps file, this file will be produced as an intermediate file if necessary even when this parameter is set to F (FALSE). In such cases, the file is deleted at the end of the run.  If set to T (TRUE), a copy of the latest ps file is also stored as plot.ps.  If <a href="#">ps</a> is set to F (FALSE), then not only will the ps file not be produced but if a ps file of the same name is present, then this will be deleted. The same is true of the plot.ps file.  If filename is present, this overrides the auto-generated filename.

## pts

Value	logical
Description	Make (and deletes) a points file
Aliases	<a href="#">pointsFile</a>
System default	F
Use	The input value is overridden where a points file is necessary, e.g. in fit, species and ht1 plots.

## pxdec

Value	integer
Description	Determines the number of digits after the decimal point for x-axis numbers

Aliases	<a href="#">xaxisDecimalPts</a>
System default	auto
Use	Can be used to override the value automatically assigned. A value of -1 indicates that it will write a number without a decimal point (i.e. an integer). 'auto' supplies a default value (up to 6 decimal points).

---

## pxmajor

Value	number
Description	Plot x-axis interval between axis numbers
Aliases	<a href="#">pxint</a> , <a href="#">xaxisint</a>
System default	auto
Use	Defines the separation of the major tick (labelled) interval in plot units on the x axis. 'auto' supplies a default value.
Example	<a href="#">64</a>

---

## pxmax

Value	number
Description	Plot x-axis maximum value
Aliases	<a href="#">xaxismax</a>
System default	auto
Use	Defines the maximum value of the x axis. 'auto' supplies a default value.
Example	<a href="#">64</a>

---

## pxmin

Value	number [number]
Description	Plot x axis minimum value
Aliases	<a href="#">xaxismin</a>
System default	"auto" "undefined"
Use	<p>Defines the minimum value of the x axis. 'auto' supplies a default value. The optional second parameter (<code>pxminstart</code>) specifies the location of the first major tick mark (and axis numbering). <code>pxminstart</code> should always be greater than or equal to <a href="#">pxmin</a>.</p> <p>The first major tick is at <a href="#">pxmin</a> if <code>pxminstart</code> is not defined or at <code>pxminstart</code> if this is defined. This makes it easier to label the axis with 'pretty' numbers.</p>
Example	<a href="#">64</a>

---

## pxminor

Value	non-negative number
Description	Plot x-axis interval between minor (unlabelled) ticks
Aliases	<a href="#">xaxisMinorTickInt</a>
System default	auto
Use	Defines the axis interval of the minor ticks on the x axis. Choosing half the major tick interval is often sensible. 'auto' supplies a default value.  A value of 0 turns off the minor x-ticks.
Example	<a href="#">75</a>

---

## pydec, p2ydec

Value	positive integer
Description	Determines the number of digits after the decimal point for y(2y) axis numbers
Aliases	<a href="#">yaxisDecimalPts</a> , <a href="#">2yaxisDecimalPts</a>
System default	auto
Use	Can be used to override the value automatically assigned. A value of -1 indicates will write a number without a decimal point (i.e. an integer).  'auto' supplies a default value (up to 6 decimal points).  The 2y axis is the right-hand y axis which can be separately defined from the main y axis. The 2y axis is used for variables defined with <a href="#">points2y</a> and <a href="#">lines2y</a> .
Example	<a href="#">83</a>

---

## pymajor, p2ymajor

Value	number
Description	Plot y(2y)-axis interval between axis numbers
Aliases	<a href="#">pyint</a> , <a href="#">yaxisInt</a> , <a href="#">p2yInt</a> , <a href="#">2yaxisInt</a>
System default	auto
Use	Defines the separation of the major tick (labelled) interval in plot units on the y axis. 'auto' supplies a default value.  The 2y axis is the right-hand y axis which can be separately defined from the main y axis. The 2y axis is used for variables defined with <a href="#">points2y</a> and <a href="#">lines2y</a> .

---

## pymax, p2ymax

Value	number
Description	Plot y(2y)-axis maximum value
Aliases	<a href="#">yaxisMax</a> , <a href="#">2yaxisMax</a>
System default	auto
Use	<p>Defines the maximum value of the y axis. ‘auto’ supplies a default value.</p> <p>The 2y axis is the right-hand y axis which can be separately defined from the main y axis. The 2y axis is used for variables defined with <a href="#">points2y</a> and <a href="#">lines2y</a>.</p>

---

## pymin, p2ymin

Value	number [number]
Description	Plot y(2y)-axis minimum value
Aliases	<a href="#">yaxisMin</a> , <a href="#">2yaxisMin</a>
System default	“auto” “undefined”
Use	<p>Defines the minimum value of the yaxis. ‘auto’ supplies a default value. The optional second parameter (<code>pyminstart</code>, <code>p2yminstart</code>) specifies the location of the first major tick mark (and axis numbering). <code>pyminstart/p2yminstart</code> should always be greater than or equal to <a href="#">pymin/p2ymin</a>.</p> <p>The first major tick is at <a href="#">pymin</a> if <code>pyminstart</code> is not defined or at <code>pyminstart</code> if this is defined. This makes it easier to label the axis with ‘pretty’ numbers. The same applies to the 2y axis.</p> <p>The 2y axis is the right-hand y axis which can be separately defined from the main y axis. The 2y axis is used for variables defined with <a href="#">points2y</a> and <a href="#">lines2y</a>.</p>

---

## pyminor, p2yminor

Value	non-negative number
Description	Plot y(2y)-axis interval between minor (unlabelled) ticks
Aliases	<a href="#">yaxisMinorInt</a> , <a href="#">2yaxisMinorInt</a>
System default	auto
Use	<p>Defines the axis interval of the minor ticks of the y axis. Choosing half the major tick interval is often reasonable. ‘auto’ supplies a default value.</p> <p>A value of 0 turns off the minor y(2y)-ticks.</p> <p>The 2y axis is the right-hand y axis which can be separately defined from the main y axis. The 2y axis is used for variables defined with <a href="#">points2y</a></p>

and [lines2y](#).

---

## resolution

Value	non-negative integer
Description	Controls the x- and y axis step size used by the hunt and track algorithm and 'custom' calculations. When 'custom' calculations are made and no <code>&lt;x_axis&gt;</code> or <code>&lt;y_axis&gt;</code> tags are defined, the <code>resolution</code> defines the number of iterations of the CHEMISTRY section that are made. Also defines the resolution of the grid used to generate contour data.
Aliases	<code>res</code> , <code>nres</code>
System default	1
Use	The given x- and y-ranges are divided into a rectangular grid with <code>resolution-1</code> cells along each axis, i.e. <code>resolution</code> points or nodes on each axis. <code>ht1</code> uses a fixed step size (one grid cell) and so <code>resolution</code> is one of the primary determinants which determine the time to make a plot. The speed of the chemical calculations and the length of the boundaries are the others.

The larger the specified `resolution`, the more detailed the resolution of boundaries but the slower the calculations. Normally a resolution in the range 50-500 is reasonable. Although high resolutions produce more calculation points than lower resolutions, the number of points retained depends on the degree of simplification subsequently used and so will not necessarily lead to significantly larger file sizes.

Resolutions of less than 10 are not allowed by the hunt and track routine. Low resolutions may not be able to resolve certain junctions, particularly close to the domain edges, and may lead to a failure of the `ht1` algorithm to close all the polygons. If this happens, it is not possible to colour the polygons appropriately and so a black and white plot is produced from the vector file. Try increasing the resolution or altering the domain boundaries ([xmin](#), [xmax](#), [ymin](#) or [ymax](#)) to achieve polygon closure.

`resolution` also controls the number of iterations used in custom calculations and plots. If `<x_axis>` or `<y_axis>` are present in an input file, then `resolution + 1` iterations are made with the following values:

$$x_{\text{int}} = (x_{\text{max}} - x_{\text{min}}) / \text{resolution}$$

$$\text{for } (i \text{ in } 0:\text{resolution}) \{x_i = x_{\text{min}} + i * x_{\text{int}}\}$$

where `xint` is the `x` interval and `xi` is the value of `x` taken on successive iterations.

e.g. `xmin=0, xmax=10, resolution=5` will give values of `xi` = 0, 2, 4, 6, 8, 10.

If `<x_axis>` or `<y_axis>` are not defined, then the interval is set to 0.

Some **PHREEQC** keywords generate their own iterations internally and so produce a `SELECTED_OUTPUT` file with multiple lines of data suitable for plotting, e.g. the `REACTION` keyword can do this.

If a full listing of the normal **PHREEQC** output file is wanted, set the `PHREEQC.out` keyword to 'T'. This will write the output from the latest

simulation or set `all` to 'auto' and `debug>1`. This will then create the `*.all` file which contains the `PHREEQC.[id].out` output from all of the iterations.

`resolution = 1` will give a single iteration and automatically forces output of the `PHREEQC.out` file. This is useful for checking **PHREEQC** output. With predominance plot calculations, this will also produce a list of all possible mineral phases in the `PHREEQC.[id].out` file ready for pasting into the `CHEMISTRY` section of an input file. A resolution of 1 should normally be used when simple looping calculations are being undertaken and no plot is produced, i.e. when the `<loop>` tag has been used but the `<x_axis>` and `<y_axis>` tags have not and when `plotFactor` has been set to 0.

`resolution = 0` will cause an immediate exit from the calculations and will produce no plot and no error messages.

A contour plot must have a resolution of at least two. Normally a value of 10–100 provides reasonable plots, maybe higher for production plots.

Examples [3, 55](#)

## restartColorSequence

Value	logical
Description	When there are multiple plots/datasets per run, determines whether the line color sequence for auto-generated colours is restarted from the beginning of the sequence or not for each plot/dataset.
Aliases	
System default	FALSE
Use	<p>If the colours for auto-generated colours symbols and lines in multiple plots, or multiple line types within a single plot, need to follow the same sequence, then setting this keyword to <code>TRUE</code> ensures that the colour sequence is started at the beginning of the sequence defined by <code>lineColor</code> or <code>pointColor</code> for each plot.</p> <p>This also applies to whether the sequence should be restarted for any 2y plots or not. The default (<code>FALSE</code>) is to continue the y sequence. Set to <code>TRUE</code> to start 2y sequence with 'red'.</p> <p>If the various plots need lines and symbols to have different colours between plots, then this should be set to <code>FALSE</code>. This will ensure the continuation of the two sequences from where they left off in the previous plot.</p> <p>A more precise determination of colours can be made by editing the line colour dictionary and setting <code>useLineColorDictionary</code> to 1 or 2.</p>

## rimColor

Value	list of Cohort or rgb colors
-------	------------------------------

Description	Determines the rim colours for point (filled circles) symbols
Aliases	
System default	nd
Use	Each set of points (or ‘curve’) defined by <a href="#">points</a> can have its own symbol with a separate rim. The colour of the rim is defined by this list and the line width of the rim is given by <a href="#">rimFactor</a> .  Colours should be chosen from the <a href="#">colour palette</a> .  A rim is only drawn if the symbol itself is drawn.

## rimFactor

Value	list of non-negative numbers, normally less than one (fractional sizes)
Description	Determines the line width used for rim colours with point (filled circle) symbols
Aliases	
System default	0.08
Use	Each set of points (or ‘curve’) defined by <a href="#">points</a> can have its own symbol. If these are filled circles, they can have a separate rim. The line widths of the rims are defined by this list. The factor given represents the width as a fraction of the symbol size with the rim centered on the circumference of the original filled circle. Normally a value of 0.05 to 0.1 is about right.  If the list of rim sizes is shorter than required, the list is recycled.  The rim colour is defined by <a href="#">rimColor</a> . Open circles can be drawn by making the point colour white and the rim colour some other colour.  A rim is only drawn if the symbol itself is drawn.

## screen

Value	logical [non-negative integer]
Description	Turns on or off all screen output (except fatal errors during reading input files). The optional second argument is the close down time in seconds.
Aliases	
System default	T 5
Use	Set to <code>FALSE</code> to prevent any screen output. The system default is <code>TRUE</code> and so any output that is sent before a <code>FALSE</code> has been set will normally be output. This can be disabled by setting the <a href="#">screen</a> setting in <code>pp.set</code> to <code>FALSE</code> .  The optional integer value gives the close down time. This is the number of seconds counted down at the end of a run that has ‘failed’ for some reason. It allows the screen output to be inspected or paused before disappearing from sight. If the <code>ESC</code> key is pressed during closedown, then

**PhreePlot** will stop immediately.

The width of the console window is best set to at least 85 characters wide. This way the scrolling output during a predominance plot will not wrap. The defaults can be set by right-clicking on the top frame of the console window and changing the Defaults.

---

## selectedOutputFile

Value	logical [file open position]
Description	A logical switch which forces the selected output file to be written to a physical file or not, and optionally a setting to determine the file position when opening the file.
Aliases	
System default	FALSE
Use	<p>If this switch is set to <code>TRUE</code>, the selected output file(s) will be written to disk irrespective of the <code>debug</code> setting (normally it is only written for <code>debug &gt; 1</code>). The name of the file is taken from the file name defined by the <code>SELECTED_OUTPUT; -file</code> filename defined in the <b>PHREEQC</b> input file (or its default value) for the particular simulation.</p> <p>The amount of data sent to a selected output file(s) depends on many factors – the number of simulations executed, their <code>SELECTED_OUTPUT</code> and <code>USER_PUNCH</code> settings, the <code>selectedOutputLines</code> setting and whether all the simulations are executed in one block or one at a time (see <code>mainLoop</code>).</p> <p>The optional ‘file open position’ setting is either ‘<code>asis</code>’ (default) or ‘<code>append</code>’. ‘<code>asis</code>’ means that if the file is written, the file position when opening the file is set to the beginning of the file while with ‘<code>append</code>’, it is positioned at the end of the file if it already exists. Since the selected output file is opened and closed for each iteration, ‘<code>asis</code>’ means that only the last iteration will remain on the file at the end of the run whereas with ‘<code>append</code>’, the results from all iterations will accumulate in the file. This is especially useful for secondary <code>SELECTED_OUTPUT n/USER_PUNCH n (n&gt;1)</code> files. The setting applies to all secondary selected output files.</p> <p>The specified selected output files will always be deleted prior to the run if they exist.</p>

---

## selectedOutputLines

Value	a non-negative integer or <code>auto</code>
Description	This defines the number of lines to be copied from the chosen selected output to the ‘ <code>out</code> ’ file.
Aliases	<code>selectedOutput</code>
System default	1
Use	This figure gives the number of lines of selected output to be sent to the ‘ <code>out</code> ’ file and is counted backwards from the last (most recent) line. So the default value of 1 will pick off the last line. Any preceding lines are

ignored.

Sometimes more than one line must be sent to the 'out' file and [selected-OutputLines](#) enables this to be specified. The most important **PHREEQC** keywords generating such multiline files are `REACTION`, `KINETICS` and `TRANSPORT`.

The value of 'auto' means that all lines found in the selected output are sent to the 'out' file.

These setting does not affect the number of lines actually written to the selected output – this is controlled by `USER_PUNCH` and the `PRINT; -selected_output` switch – but rather it controls the number of such lines written to the 'out' file.

Setting a value to zero will turn off copying any selected output. If a value exceeds the number of lines produced, it will copy all the lines actually produced.

These data will be sent to the 'out' file, for plotting or use in fitting if, and only if, these data are part of main loop calculations. Data from any pre-loop calculations are never sent.

When there is more than one simulation in the main loop and [oneSimulationAtaTime](#) has been chosen (e.g. [mainLoop 1 TRUE](#)), then selected output is only written to the 'out' file from the last simulation.

The number of lines selected is set internally for 'simulate' and 'fit' calculations as there are only two possibilities. When [onePass](#) is `FALSE`, only one value must be exported per full iteration of the **PHREEQC** code; when [onePass](#) is `TRUE`, at least *n* lines must be sent where *n* is the number of observations. In this case, if there are more lines than needed only the last *n* are used. Given these limited options, the [selectedOutputLines](#) setting is ignored during fitting/simulations.

'ht' and 'grid' calculations automatically set [selectedOutputLines](#) to a value of 1 as this is what is expected by **PhreePlot**.

Where there are several `SELECTED_OUTPUT/USER_PUNCH` blocks defined in an input file, [selectedOutputLines](#) only applies to the blocks defined with the largest user number, *n*. This does not have to be the last to be executed though it often is. Giving any `SELECTED_OUTPUT/USER_PUNCH` block a high user number will force the 'out' output to come from this block.

It is often convenient to make sure that no redundant output is sent to the selected output in the first place. This can be done in the **PHREEQC** code by using

```
PRINT
-selected_output FALSE
```

for all simulations where no output is wanted and then by turning on the output for simulations where it is wanted

```
PRINT
-selected_output TRUE
```

---

## simplify

Value                    non-negative number

Description	Controls the degree of simplification of the field boundaries in predominance diagrams
Aliases	<a href="#">simplificationFactor</a> , <a href="#">simplification</a>
System default	1
Use	<p>This is mainly used to straighten ‘squiggly’ boundaries in <code>ht1</code> and <code>contour</code> plots. It only applies for <a href="#">calculationMethod</a> 1 or 3 and while plotting ‘vectors’ (line segments), not whole polygons. In grid plots, the only line simplification that is done is the removal of ‘in line’ or redundant vertices. It cannot be used to reduce the ‘steppiness’ of grid plots. The grid stepping is still retained.</p> <p>Line simplification is applied for all <a href="#">simplify</a>’s greater than 0.0.</p> <p>For <code>ht1</code> diagrams and contour plots, a value of <a href="#">simplify</a> of 1 often provides reasonable plots. Larger numbers, say 3, introduce more simplification and may be useful for removing low-angled, jagged boundaries. Smaller values, say 0.1, retain many more points. Somewhere in the range of 0.1 to 10 is usually reasonable.</p> <p>Simplification can significantly reduce the size of output files (data and plot files) and can produce more visually pleasing plots by eliminating unwanted noise. However, for the most accurate plots, it is usually better to reduce the ‘steppiness’ by increasing the resolution of the calculations rather than by increasing the simplification factor.</p> <p>The retained points can be viewed by making the track symbol viewable (<a href="#">trackSymbolSize(2)</a> &gt;0 and <a href="#">trackSymbolColor</a> not ‘nd’). Setting <a href="#">simplify</a> to 0.0 will show the result without any line simplification.</p> <p>You can change the simplification factor without recalculating the speciation by using <a href="#">calculationMethod</a> 3 (not 2).</p>

---

## skip

Value	non-negative integer
Description	Keep every <code>skips</code> data record when reading in data for fitting or simulation.
Aliases	<a href="#">numberOfSkipRecords</a>
System default	1
Use	<p>Used to select a small subset of the data for more rapid fitting. Useful when exploring the initial estimates of the adjustable parameters. The records to be skipped are calculated from <code>mod(ndatar-nstart, skip) /= 0</code> where <code>ndatar</code> is the number of data records read, <code>nstart</code> is the sequential number of the first record read (normally 1) of the data block and <code>skip</code> is the defined parameter.</p> <p>New data blocks begin after a blank line so the first record after a break is normally included providing the number of records in the block is equal to or greater than <a href="#">skip</a>.</p> <p>Only valid data lines are counted for skipping, i.e. blank and comment lines are filtered out first before counting for skip. To keep all data use <code>skip 1</code>. To keep roughly 1 in 10 use <code>skip 10</code>, etc.</p>

A [skip](#) value of zero is treated as 1.

---

## SPECIATION

Value	none (section heading)
Description	Section heading only
Aliases	
System default	
Use	Optional; does nothing.

---

## speciationProgram

Value	string
Description	The name of the speciation program to use
Aliases	<a href="#">program</a>
System default	PHREEQC
Use	The name of the speciation program to use for speciation calculations. Currently only PHREEQC.

---

## speciationProgramVersion

Value	string
Description	Specifies the current version of the speciation program being used
Aliases	<a href="#">dateProgram</a>
System default	''
Use	None specified by the program. The program version is now obtained directly from the library being used so this keyword is no longer necessary. Any text given here will be prepended to the rest of the version information. It is only used for printing in log file and info data block.

---

## startTemperature

Value	positive number
Description	The starting 'temperature' for the simulated annealing option for fitting (not implemented)
Aliases	
System default	100
Use	This is no longer used.

---

## stopOnFail

Value	0,1 or 2
Description	Determines whether calculations should continue after a failure in specification
Aliases	
System default	2
Use	<p>This keyword controls the behaviour after <b>PHREEQC</b> has failed as indicated by a non-zero error return.</p> <p>The default value is 2 which allows <b>PhreePlot</b> to decide whether to continue or not. For most types of calculations, <b>PhreePlot</b> will stop after a non-zero (error) return from <b>PHREEQC</b> but for predominance and contour plots with debug 0, it will continue - effectively mapping the NA area. To always continue, set to 0. To always stop on an error, set to 1.</p>

---

## svg

Value	logical string1 string2 [svgmaker]
Description	Turns on or off output to an svg-format file
Aliases	
System default	TRUE
Use	<p>If the switch is set to <code>TRUE</code>, then the <code>&lt;svgmaker&gt;</code> program is used to produce an svg file. The image converter program must already be installed and preferably with the path to the executable set in the <code>PATH</code> environment variable. It must be capable of doing a file conversion with a command line like:</p> <pre>&lt;svgmaker&gt; &lt;input file&gt; &lt;output file&gt;</pre> <p>where <code>&lt;svgmaker&gt;</code> is the path to the converter program, <code>&lt;input file&gt;</code> is the name of the input file plus any other options given by <code>string1</code> and <code>&lt;output file&gt;</code> is the name of the output svg file also including any switches or options given by <code>string2</code>. The use of both single and double quotes may be necessary to ensure that the input is correctly parsed into its components.</p> <p>With <b>ImageMagick</b>, this could be specified in <b>PhreePlot</b> as:</p> <pre>svg true plot.ps plot.svg magick.exe</pre> <p>With <b>Inkscape</b>, the required command line is a bit more complicated and the pdf file is best used as input, e.g.</p> <pre>svg true hfo_Fe1.pdf --export-filename="plot.svg" inkscape.exe</pre> <p><code>&lt;svgmaker&gt;</code> is the path to the program executable and needs to be defined somewhere. It could be specified in the <code>pp.set</code> file, for example, and then would not need to be specified with this keyword. The default is 'magick' (and so assumes the path has been set, but the full path can be included if</p>

necessary, with the two sets of quotes if necessary). This conversion can only be used for single page `ps` files.

The order of image file conversion from `ps` is: `pdf`, `png`, `eps`, `jpg`, `svg` and so for example, the `pdf` and `eps` files can be used for conversion to `svg`.

Observation - the `svg` files produced by **ImageMagick** work in most browsers but **Inkscape** produces more reliable output for importing into a document. This may be to do with the default settings.

Given the general nature of this command, it could be used to run all sorts of post-processing programs.

## symbolsLines

Value	A sequence of parameters in a defined order (see below).
Description	Adds one or more symbols or lines to a plot.
Aliases	<a href="#">symbols</a> <a href="#">symbol</a>
System default	""
Use	This keyword is useful for adding symbols and lines to a plot with more control than can be had by using ' <a href="#">points</a> ' and ' <a href="#">lines</a> '. For example, symbol and line properties can be varied from point to point, and tags can be used within the file.

For many new symbols or complex lines, create a file containing this data.

Many parameters (width, colour and type) persist unless redefined. This includes default values. Explicit inclusion of a parameter, resets it and this new value will then remain in effect until redefined.

The parameters are:

```
plotnumber,x,y,[lw,[linecol,[isymb,[sizesymb,[symbolcol,[rimcolor,[rimfactor,[linetype,[dashesperinch]]]]]]]]]]]
```

with the first three parameters being required and the remaining ones optional. For example, to add a symbol and give its colour, the first eight parameters must be defined. To plot a line without symbols, either ignore the symbol parameters or set them to null values: `isymb = 0`, `sizesymb = 0`, `symbolcol = ""`, `rimcolor = ""`.

To just plot a symbol, the line parameters should be set to null values, e.g.

```
symbolsLines 1 3 -10 0 nd 1 2 "red" "black"
```

The line parameters are taken from the second (end) point in a line segment – any given for the first (starting) point are ignored.

`plotnumber` (parameter 1) is the plot number (starts at 1) for which the data applies. The plot number is sequential and, if requested, is printed in the [info](#) at the bottom left-hand corner of each plot. `auto`, `0` or `'999'` means all plots. Out of range plot numbers are ignored.

`x` (parameter 2) and `y` (parameter 3) are the x- and y-coordinates for the points in plot coordinates (i.e. as seen on the screen or page).

`lw` (parameter 4) is the line width in whatever length units are in force. Negative line widths produce dashes if the `linetype` has not been explicitly defined. Default = [lineWidth](#).

`linecol` (parameter 5) is the [colour](#) of the line (including `nd`). Default = [lineColor](#).

`isymb` (parameter 6), `sizesymb` (parameter 7) and `symbolcol` (parameter 8) refer to the [symbol code number](#) or name, the symbol size and the symbol colour. Default = 1, 0.0 and [pointColor](#), respectively.

`rimcolor` (parameter 9), `rimfactor` (parameter 10) define the appearance of the rim for those symbols (1-6) that have one. Default = 'nd' and 0.05 respectively.

`linetype` (parameter 11), `dashesperinch` (parameter 12) are the line type (default = [lineType\(1\)](#)) and dashes per inch (default = [dashesPerInch\(1\)](#)).

The input for a given point is terminated by an end-of-line or by an end-of-input character, namely a colon (:). If the colon is used, parameters for additional points can be defined although the input must still be on a single logical line. It is possible to use the continuation character (\) to break the logical line into several physical lines.

By selecting the appropriate size and colour of the symbols and lines it is possible to have combinations of lines and symbols of any colour.

See [Section 7.12](#) for more details and a display of the available symbols and their symbol codes (`isymb`) and names.

The symbols and lines are normally clipped to the plot window. For complex examples, use an [extraSymbolsLines](#) file.

## text

Value	A sequence of parameters in a defined order (see below).
Description	The parameters contains the text to be added to a plot and its attributes.
Aliases	
System default	“
Use	<p>This is useful for adding extra text to a plot. The input line contains four or more parameters in a strict format which define various aspects of the text to be plotted.</p> <p>The input line has four compulsory parameters and up to seven optional ones:</p> <pre>plotnumber,x,y,"text"[[,size[,"colour"[,angle[,hjustify[,vjustify[,digits[,"font"]]]]]:]</pre> <p><code>plotnumber</code> is the plot number (starts at 1) for which the text applies. If the info block is printed, the plot number will be printed at the beginning. 'auto' or 0 means all plots. Any other out of range number, would suppress plotting.</p> <p>The <code>plotnumber</code> increments by one for each plot produced. The outer loop is the <code>z</code> loop and the inner (most rapidly changing) loop is the main species loop. so in a run with <code>m</code>-elements and <code>n</code>-loop (<code>z</code>) values, the order of plots will be:</p> <pre>z1-e11, z1-e12, ... z1-elm, z2-e11, z2-e12, ... z2-elm, ... zn-e11, zn-e12, ... zn-elm.</pre>

$x$  and  $y$  are the  $x$ - and  $y$ -coordinates for the text position in plotting coordinates (i.e. as seen on the screen or page).  $x$  and  $y$  can take on special values:  $x = \text{'auto'}$  (case insensitive) sets  $x$  just to the right of the  $x$  axis (at the start of the legend);  $y = \text{'auto'}$  sets  $y$  to just below the legend if printed. The text is horizontally justified according to the `hjustify` parameter (0=left, default; 1=centre; 2=right justification) and while the vertical justification parameter, `vjustify`, is read (0, 1, 2), the text is always vertically aligned such that  $y$  refers to the baseline of the first line of text. The default is therefore for  $x$  and  $y$  to refer to the bottom left (baseline) of the top line (if the text string contains any `<br>`'s). If  $x$  is set to `'last'` (case insensitive) then the last text  $x$  value is used. If  $y$  is set to `'last'` then  $y$  is set to one line below the last line. Setting both  $x$  and  $y$  to `'last'` means that the text is continued below where it previously finished. This is useful to overcome the 400 character limit to the length of a plotted text string.

`text` is the text string enclosed in quotes. It can be of any length but is truncated to a maximum length of 400 characters including tags when actually plotted. If a colon (:) is to be printed, precede it with a backslash otherwise it will be treated as an end-of-input (see below) even in a quoted a quoted string. The text can include tags including the normal text enhancement tags for sub- and superscripts, line breaks and so on ([Section 7.6.3](#)). In addition, there are two special tags to load variable text relating to the current simulation and plot. These are: `<input:s1,s2>` to echo lines of text from the all-inclusive input file to the plot, and `<legend>` to move the legend to a non-default position. `s1` and `s2` are the strings used to identify the starting and ending lines of input to be printed. A blank `s1` means beginning-of-file and a blank `s2` means end-of-file. The `CHEMISTRY` line is simply a placeholder for dividing the input file into two and cannot be used as a target in `s1` or `s2`. In `text` strings, a backslash preceding the colon is necessary to escape the colon which would otherwise be interpreted as an end-of-input marker, e.g. use `<input\SPECIATION, END>`. This is not necessary in an `extraText` file as a new line acts as the end-of-input marker. When these tags are used, they may impose their own layout rules which override the given ones. Normally the input text and legend are placed just to the right of the plot. Other tags can also be included and will be substituted at plot time if defined; if not defined, they will be plotted as a `'NA'` or *as is*.

`size` is the size of the text in the current [units](#).

`color` is the [colour](#) of the text enclosed in quotes.

`angle` is the angle of the text measured in degrees from the horizontal rotating clockwise. 0 is horizontal and upright. The text is rotated about the left, centre or right position of the baseline of the first line of text depending on justification.

`justify` is the justification with respect to the  $x, y$  coordinates. 0 = left-justified, 1 = centre, 2 = right-justified.

`digits` refers to the number of decimal places when substituting values for numeric tags ( $1 \leq \text{digits} \leq 16$ ). If `digits` is a negative number, then trailing zeros will also be removed. Exponential format is normally used when  $\text{abs}(\text{value})$  is less than 0.001. This value is ignored for non-numeric text strings.

`font` refers to the font (name in quotes or number) given by the [font](#) keyword, or `'Helvetica'` if undefined.

The special plot tags which are evaluated after computations are `<pxmin>`, `<pxmax>`, `<pymin>` and `<pymax>`. These contain the current values of [pxmin](#), [pxmax](#) etc and can be used to generalise plotting positions.

The size of the text, its colour, angle, justification and digits are optional though the order must be maintained. For example, if the `justify` parameter needs to be included, then all of the other preceding ones also do.

Default values for the parameters are:

```
size = labelSize
color = black
angle = 0 (horizontal and upright)
justify = 0 (= left)
digits = -3
```

#### *Multiple text strings on one line*

The input for a given text string is terminated by an end-of-line or by an end-of-input character, namely a colon (:). If the colon is used, parameters for additional strings can be defined although the input must still be on a single logical line. It is possible to use the continuation character (`\`) to break the logical line into several physical lines, e.g.

```
text auto, 7, 0, "Sample 1", 2.0, "red" :\
      auto, 9, 3, "Sample 2", 1.0, "blue"
```

To use a colon within the text string, escape it with a backslash, e.g. `"https\://phreeplot.org"`.

The default values defined above are used for the first entry if required, but after that, all existing values are used as the default for further entries until redefined. ‘auto’ for the optional parameters will normally not change the parameter from last time and can be used as a placeholder.

The background colour for all text inserts is defined by [background-Color\(3\)](#).

Examples            See `\demo\ZnS\ZnS.ppi`, `\demo\UPF\UPF.ppi`

---

## tickColor

Value	Cohort or rgb colour [colour [colour [colour [colour [colour ]]]]
Description	Specifies the colours of the major and minor axis ticks
Aliases	<a href="#">tickCol</a>
System default	auto
Use	From one to 6 colours need to be specified for the major x-axis, minor x-axis, major y-axis, minor y-axis tick marks, respectively ( <a href="#">tickSize</a> is similarly specified, see below). These can all be defined explicitly or implied as follows depending on the number of colours entered. See <a href="#">tickSize</a> for the recycling rules.
	If a colour is ‘auto’, it takes on the corresponding axis line colour.

The tick marks can also be used to produce a grid over the whole plot area (see [tickSize](#) below) but the preferred method is to use [gridLines](#), [grid-Color](#) etc.

The 2y colours are used for the ‘opposite y’ axis if the 2y-axis scale is specified by one of the sets of lines or points, else the tick colours are the same as the ‘normal’ y axis.

Colours should be chosen from the [colour palette](#).

**Example** [38](#)

## tickSize

Value	[number [number [number [number [number [number [inside or outside]]]]]] (but not completely blank)
Description	Sets the length of the major and minor ticks and their placement
Aliases	<a href="#">ticklength</a> , <a href="#">tick</a>
System default	2
Use	<p>From zero to six numbers plus an optional ‘inside’ or ‘outside’. There must be at least one number or inside/outside. Numbers are lengths in units in force, e.g. mm. Only positive values are used.</p> <p>Sets the length of the ticks and the placement of the ticks. Six tick lengths are defined, in order: major x-axis, minor x-axis, major y-axis, minor y-axis, major 2y-axis, and minor 2y axis. Tick marks are always the same on opposite sides. These lengths can all be defined explicitly or implied as follows depending on the number of numbers entered:</p> <p>one number:    defines major ticks on x-axis                          minor ticks on x-axis = <math>0.66 \times</math> major ticks on x-axis                          major ticks on y-axis = major ticks on x-axis                          minor ticks on y-axis = minor ticks on x-axis                          major ticks on 2y-axis = major ticks on x-axis                          minor ticks on 2y-axis = minor ticks on x-axis</p> <p>two numbers:    defines major and minor ticks on x-axes                          major ticks on y-axis = major ticks on x-axis                          minor ticks on y-axis = minor ticks on x-axis                          major 2 ticks on y-axis = major ticks on x-axis                          minor ticks on 2y-axis = minor ticks on x-axis</p> <p>three numbers:  defines major and minor ticks on x-axes, and major ticks on y-axis                          minor y-axis = minor x-axis                          major 2y-axis = major y-axis                          minor 2y-axis = minor x-axis</p> <p>four numbers:    defines major ticks on x-axis and minor ticks on x-axes, and major and minor ticks on y-axes                          major ticks on 2y-axis = major ticks on y-axis                          minor ticks on 2y-axis = minor ticks on y-axis</p> <p>five numbers:    defines major ticks on x-axis and minor ticks on x-axes,</p>

and major and minor ticks on y-axes, and major ticks on 2y-axis

minor ticks on 2y-axis = minor ticks on y-axis

six numbers: defines major and minor ticks on x-axes, major and minor y-axes, and major and minor ticks on 2y-axes

Ticks are always plotted with full lines not dashed lines. Zero tick size turns off the tick.

Minor ticks are by default placed half way between the major ticks but this can be changed with the [pxminor](#), [pyminor](#) and [p2yminor](#) keywords.

If the tick size is equal to 0.5 or more times the length of the shorter of the corresponding axis lengths ([xaxisLength](#) and [yaxisLength](#)), then grid lines will be plotted. Therefore using an arbitrary very large tick size makes that tick a grid line albeit normally ticks and grid lines are plotted independently. Using large negative values makes a dashed grid line. However, grid lines are preferably specified with [gridLines](#), [gridLineType](#) and [gridDashesPerInch](#).

If the tick marks are put on the outside, then both ticks and grid lines will be plotted. In this case, the major ticks will be based on `tickSize(1)` in the `pp.set` file with the minor ticks 0.66 times this size.

The line thickness of the major grid lines is given by [axisLineWidth](#) and the thickness of the minor grid lines is 0.5 x [axisLineWidth](#).

The default is for the tick marks to be placed inside the plotting area. This can be changed to outside by appending the word 'outside' to the end of the sequence of numbers entered above. 'inside' forces placement on the inside.

The 2y tick sizes are used for the 'opposite y' axis if the 2y-axis scale is specified by one of the sets of lines or points plotted, else the tick sizes are the same as the 'normal' y axis.

Example [38](#)

---

## trackSymbolColor

Value	Cohort or rgb colour
Description	The <a href="#">colour</a> of the tracking symbol.
Aliases	<a href="#">trackCol</a>
System default	<code>red4</code>
Use	Used for indicating visited sites in the intermediate <code>plot.ps</code> file produced when calculations are interrupted ( <code>ESC</code> ) during a predominance plot (see definition of <a href="#">plotFrequency</a> ).

Colours should be chosen from the [colour palette](#).

[trackSymbolColor](#) is also used for plotting the label anchor in custom plots and for showing the vector vertices in 'ht1' plots and contour plots with the [contourShiftLabel](#) option 'n'.

The track symbols can be turned off by setting the colour to 'nd' or the

size to zero.

---

## trackSymbolSize

Value	non-negative number [non-negative number]
Description	Size of the tracking symbol.
Aliases	<a href="#">tracksize</a>
System default	1.0 0.0
Use	<p>In custom plots, the track symbol shows the position of the label anchor. This only applies to labels that have been placed in the current plot (<a href="#">calculationMethod</a> 1). In contour plots and with <a href="#">contourShiftLabel</a> set to 'n' (for number), the track symbol (1) is drawn at all the vertices to aid deciding by how many vertices to shift the label.</p> <p>The track symbol is also used in the <code>plot.ps</code> file that is produced by pressing 'P' during predominance diagram calculations and shows the progress so far. In '<a href="#">grid</a>' mode, only the perimeter vertices of the visited cells are shown. A double-sized blue or red circle highlights the last calculated point.</p>

The first number, [trackSymbolSize\(1\)](#), gives the size of both of these symbols.

The second optional number, [trackSymbolSize\(2\)](#), either gives (i) the size of the symbols used to show the vertices that have been written to the polygon file for predominance plots, i.e. those vertices that remain after any line simplification, or (ii) the size of the anchor symbol (a filled circle) showing the centre of the plotted labels. These anchor symbols have the colour specified by [trackSymbolColor](#).

In a grid plot, the vertices on the domain boundary will be clipped since the grid is offset by half a cell and so extends beyond the domain boundaries. This means that the boundary vertices are not on the domain boundaries and consequently will not be shown.

Example [44](#)

---

## trk

Value	logical
Description	Determines if the 'track' file is retained or not
Aliases	<a href="#">track</a> , <a href="#">trackFile</a>
System default	F
Use	<p>The track file keeps a record of the summary results of each speciation calculation and records the top three species in terms of molar abundance for the purposes of predominance calculations. This is a more complete version of the summary output that is sent to the screen during a predominance plot calculation.</p> <p>Output is only sent to the track file for main loop simulations (not pre-loop simulations) and only one line of output is sent per main loop simulation, i.e. if there is more than one main loop simulation and these are</p>

executed `oneSimulationAtaTime` (see `mainLoop`), output is only sent from the last simulation.

The file also includes various system variables (x, y, pH, pe and temperature depending on the `calculationType`). If any 'carry variables' are specified, these are also appended.

The track file is the primary data file that is used to prepare a 'grid' type of predominance plot and is also used to store contour-generated data.

## units

Value	'mm', 'inch', 'pt'
Description	Units used for all length measurements (mm, inch, pt) that follow its definition.
Aliases	
System default	mm
Use	Choose between 'mm', 'inch' or 'pt' (one point = 1/72 inch). It is best to decide on the units at the outset and set this in the <code>pp.set</code> file or at the top of an input file.  All settings with a length dimension are read in as pure numbers without dimensions but are immediately converted to the units in force at the time of reading.  Unlike other keywords, the position of this keyword in the input file(s) is important since all length measurements following this keyword will be assumed to be specified using this length scale. This includes keywords, such as <code>extraText</code> , which read some parameters in terms of lengths or sizes from a file.  If a mixture of length units is required then they can be varied within an input file by using this keyword to redefine the units before the change is required.  Internally all dimensions are converted to inches for plotting but the default units in <b>PhreePlot</b> and its demo files is 'mm'.

## unrecognisedKeywordIsFatal

Value	logical
Description	Determines if an unrecognised keyword is treated as a fatal error or not.
Aliases	
System default	TRUE
Use	The default (TRUE) is to treat unrecognised keywords as fatal errors in which case they have to be corrected for <b>PhreePlot</b> to run.  Alternatively, by setting this switch to FALSE, the keyword and its arguments will be ignored. This could be useful in future when new keywords have been added to <b>PhreePlot</b> and a script using these keywords is run

with an older version of **PhreePlot**.

---

## updateFitParameters

Value	logical
Description	Determines whether after a successful optimization the updated parameter values are written back into the relevant input file ( <code>TRUE</code> ) or not ( <code>FALSE</code> ).
Aliases	
System default	F
Use	<p>If <code>updateFitParameters</code> is set to <code>TRUE</code> and if a line containing <code>fitParameterValues</code> was present in the original input file, as it normally would be for a fit, then the final fit values will be written back into the input file if the fit has been successful.</p> <p>The original input file is copied and saved with the template <code>***.bak.***</code> where the <code>***</code>'s are the original filename and extension providing that this backup file does not already exist.</p> <p>Clearly it is wise to make an independent backup of all important input files.</p>

---

## useLabelsFile

Value	logical
Description	Determines whether an existing labels file is used to position labels in a predominance plot particularly when the fields are being regenerated ( <code>calculationMethod = 1</code> ).
Aliases	<code>useLabelFile</code>
System default	<code>FALSE</code>
Use	<p>With predominance plots, the default behaviour (<code>FALSE</code>) is for <code>calculationMethod = 1</code> or <code>3</code> to recalculate the positions and orientation of labels each run. This keyword enables the readings in an existing labels file to take precedence and so preserve any editing. If <code>TRUE</code>, the labels file is read but not rewritten.</p>

---

## useLineColorDictionary

Value	0, 1 or 2
Description	Determines whether the line colour dictionary is used to determine the line and points (symbol) colours, and label positions, or not.
Aliases	<code>useColorDictionary</code> , <code>coldict</code>
System default	0
Use	Increasing numbers indicate increasing dependence on the line colour

dictionary, if present.

0 = do not use the line colour dictionary. Use the [lineColor](#) setting. If there is more than one line and [changeColor](#) is `FALSE`, use the auto-selected colour sequence defined by **PhreePlot** and the position of the [lineColor](#) variable in the list of variables.

1 = use the line colour dictionary if present but only for colours

2 = use the line colour dictionary if present for both colours and label positions. Labels are only used for lines. In multiplot files, the positions of the labels refer to the last positions recorded for each species. Use [post](#) for labelling points.

Example [83](#)

## vec

Value	logical
Description	Determines if a vector file created during 'hunt and track' calculations is retained at the end of computations.
Aliases	<a href="#">vectors</a> , <a href="#">vectorsFile</a>
System default	F
Use	The vectors file will always be created in ht1 calculations but this setting will determine if it is deleted at the end of the calculations. It can be regenerated from the points file using the re-process data option ( <a href="#">calculationMethod 3</a> ).

## weightColumn

Value	non-negative integer or column name (case sensitive)
Description	Column number of the weight variable for the fit method
Aliases	<a href="#">weightPosition</a>
System default	0
Use	Only used in fitting mode. If it is not a positive number, i.e. zero, then the default weighting (unit weighting) is used.

Example [81](#)

## writeAllInputFiles

Value	logical
Description	Controls whether only the main input files are printed to the log file (F) or all input files (T)
Aliases	<a href="#">writeInputFiles</a>
System default	FALSE

Use	<p>The main input file is the file named on the command line, usually having the <code>ppi</code> extension. Other input files are those ‘included’ in the main input file as well as the <code>override.set</code> file.</p> <p>Sometimes the include files are long and essentially constant and so would extend the log file unnecessarily if always printed. This setting provides the option to switch on or off the printing of these ancillary files.</p> <p><code>FALSE</code> only echoes the <code>ppi</code> and <code>override.set</code> files; <code>TRUE</code> echoes all the files.</p>
-----	--

## writePlaceholder

Value	logical
Description	Controls whether a placeholder (a blank line or one containing an UNDEFINED value) is written to the <code>out</code> and <code>trk</code> files when no output is produced by <b>PHREEQC</b>
Aliases	<a href="#">writePlaceholder</a>
System default	<code>TRUE</code>
Use	<p>The default value (<code>TRUE</code>) is useful when generating contour plots or grid-based predominance diagrams as it maintains the strict order required for plotting from these files even when there has been a failure of <b>PHREEQC</b> to converge. It can also be useful in other calculations to record where a failure has occurred.</p> <p>However, it may produce unwanted effects, for example, when the input script engineers that a failing calculation is repeated with a different input to produce the wanted output. Here the failing output placeholder would ‘contaminate’ the output files and so should not be written.</p>
Example	See the <code>demo\switch\switch1.ppi</code> example.

## xaxisLength

Value	positive number
Description	Length of x axis
Aliases	<a href="#">xlength</a>
System default	90
Use	The length is used to determine the length of the x axis in the units in operation (see <a href="#">units</a> ).
Example	

## xmax

Value	number
-------	--------

Description	Maximum value of the x-axis variable used during the calculations
Aliases	
System default	UNDEFINED
Use	Controls the final value for the <code>&lt;x_axis&gt;</code> variable.
Example	<a href="#">3</a>

---

## xmin

Value	number
Description	Minimum value of the x-axis variable used during the calculations
Aliases	
System default	UNDEFINED
Use	Controls the starting value for the <code>&lt;x_axis&gt;</code> variable.
Example	<a href="#">3</a>

---

## xoffset

Value	non-negative number
Description	Distance of the origin of the plot (lower left-hand corner) from the left side page margin
Aliases	
System default	30
Use	Distance of the origin of the plot (lower left-hand corner) from the left side page margin.
Example	<a href="#">40</a>

---

## xtitle

Value	string ([second string])
Description	Title of the x axis
Aliases	
System default	'auto' ''
Use	The first string is the main x-axis title.  The second string is appended to the first string with the 'exponential' scaling factor placed in between. For example if the x-data range from 0 to 1200 then the data could be automatically rescaled by dividing by 1e2. For example, <pre>xtitle 'Distance ( ' ` m)'</pre> gives Distance ( /102 m)

or in general, `trim(string)//trim(exptext)//trim(second string)` where `//` is the concatenation operator.

The title strings can be of any length but their maximum combined length including any text tags and the inserted scale factor is 400 characters.

'auto' gives a blank title for predominance and contour plots. For custom, fit and species plots 'auto' takes the value of [customXcolumn](#) label. For a residual sum of squares plot, it takes the title from the x-variable/parameter name.

A blank string means that an auto-generated title will be used. Turn-off by setting [axisTitleColor](#) to 'nd', [axisTitleSize](#) to 0 or setting the title to a non-printing character such as '↵' (ASCII encoding).

Example [66](#)

## yaxisLength

Value	non-negative number
Description	Length of x axis
Aliases	<a href="#">ylength</a>
System default	90
Use	The length is used to determine the length of the y axis in the units in operation (see <a href="#">units</a> ).

## ymax

Value	number
Description	Maximum value of the y-axis variable used during the calculations
Aliases	
System default	UNDEFINED
Use	Controls the final value for the <code>&lt;y_axis&gt;</code> variable.

## ymin

Value	number
Description	Minimum value of the y-axis variable used during the calculations
Aliases	
System default	UNDEFINED
Use	Controls the starting value for the <code>&lt;y_axis&gt;</code> variable.

Example

---

## yoffset

Value	non-negative number
Description	Distance of the origin of the plot (lower left-hand corner) from the bottom page margin
Aliases	
System default	140
Use	Distance of the origin of the plot (lower left-hand corner) from the bottom page margin.
Example	<a href="#">40</a>

---

## yscale

Value	character
Description	Determines the y-scale to use for predominance and contour plots
Aliases	
System default	“native”
Use	The y-scaling during the plotting of predominance and contour diagrams has the following three options: <ul style="list-style-type: none"> <li>“native” scale determined by the y-axis variable</li> <li>“pe” uses the pe scale</li> <li>“Eh” uses the Eh scale (in V)</li> <li>“mV” uses the Eh scale (in mV)</li> </ul>

If one of the pe-related scales is used, then the calculated pe-related value is used rather than the native y-axis variable.

This setting only applies to predominance and contour plots and is ignored by other plots. It only makes sense if the native y-scale is driven by a variable that directly controls the redox, most commonly O<sub>2</sub>(g) and a precondition for the conversion is that the pe must be known; for the Eh and mv scales, the temperature must also be known. These ‘system’ variables are always output in predominance plots via the `ht*.inc` files but these are not mandated in a contour plot. Therefore, in order to make a conversion to one of these pe scales, a column with the heading “pe” and values (-1a (“e-”)) must be PUNCH’ed to the output file, or read from an [extradat](#) file. Also for the Eh and mV conversions, a column with heading “TC” and values of temperature in Celsius (TC) must also be PUNCH’ed. These headings are case sensitive so must be exactly as indicated. Failure to specify the required columns will result in an error. Temperatures within a given plot must be constant for the pe to Eh (mV) conversion to be applied otherwise a warning is given and the first value used.

The calculated pe values, or the conversion parameters, are stored in all of the critical output files. Unknown pe/Eh/mV values are estimated from the known pe values just before plotting. For example, this may be neces-

sary to specify label positions.

The y-scale setting can be changed either before a plot is generated or before replotting. In predominance plots, use [calculationMethod](#) = 3 to recalculate the label positions, or for manual adjustment by editing the third column of the labels file, use [calculationMethod](#) = 2.

In order to make plots using one of the pe-related scales, it may be necessary to estimate the pe where the speciation has failed. This is not always possible to do reliably and it may therefore not be able to close the various polygons outlining the fields properly. Either reduce the domain to one where the pe can be estimated reliably at all times or drive the yaxis variable with the pe directly using the pe, i.e. use 'Fix\_e-' analogous to 'Fix\_H+'. If this is done, set the [yscale](#) to 'native'.

Example [18](#)

## ytitle, 2ytitle

Value	string [[second string] third string (max. 40 characters)]
Description	Title of the y(2y)-axis, its units and the character attached to label names to indicate that they refer to the 2y axis.
Aliases	<a href="#">title2y</a>
System default	'auto' '' '*'
Use	<p>The title strings can be any length but a maximum of 400 characters including any text tags are used for plotted.</p> <p>It behaves the same as for <a href="#">xtitle</a> except that for predominance plots, if <a href="#">yscale</a> is set to "pe" and <a href="#">ytitle</a> is 'auto', then <a href="#">ytitle</a> will be automatically set to "pe". Similarly for <a href="#">yscale</a> and "Eh" or "mV".</p> <p>For custom plots with <a href="#">ytitle</a> set to 'auto', the first label name is used for the y-title. Similarly for <a href="#">2ytitle</a>.</p> <p>The 2y axis is the right-hand y axis which can be separately defined from the main y axis. The 2y axis is used for variables defined with <a href="#">points2y</a> and <a href="#">lines2y</a>.</p> <p>See <a href="#">xtitle</a> for the meaning of the optional second string.</p> <p>A blank string means that an auto-generated title will be used. Turn-off by setting <a href="#">axisTitleColor</a> to 'nd', <a href="#">axisTitleSize</a> to 0 or setting the title to a non-printing character such as '¬' (ASCII encoding).</p> <p>The optional third parameter is a character string that is appended to all label names that refer to variables plotted according to the 2y axis. It is an asterisk by default but it can be set to null (') if no character is wanted or can include plot tags. This means that &lt;sup&gt;+&lt;/sup&gt; would be valid.</p>

Examples [3](#), [66](#)

# Examples

---

These examples are included in the `\demo` directory and can be run individually or they can all be run with the `demo.bat` file. The plot filename can be seen at the bottom left-hand corner of each plot.

The examples are arranged in sections based on the type of calculations undertaken. The sections are themselves ordered in terms of the [calculationType](#).

The **PhreePlot** code that produced each plot is shown below each plot. Note that long lines in the code may wrap to a second line so be careful if copying. If in doubt, refer to the original file in the `demo` directory.

The examples demonstrate many of the features built into **PhreePlot** and are intended as templates to be modified for your own particular problem. In most cases, the choice of concentrations etc. are arbitrary and are not intended to have any environmental significance.

The results of geochemical calculations are entirely dependent on the choice of thermodynamic database. **PHREEQC** makes it easy to select different databases, and to modify them either temporarily or permanently. In some cases, we have mixed databases in order to extend them. This can be dangerous and will almost certainly introduce inconsistencies. We have not made any effort to re-evaluate log *K*'s in order to achieve internal consistency though in any real application this should be seriously considered.

The other side of the coin is almost equally bad – to accept the *status quo* and to ignore a significant reaction because it cannot be modelled perfectly can also lead to serious errors – errors of omission rather than commission. If something is important to you, check it out carefully and if necessary, try and improve it. Pass your experiences on to others. Ultimately of course the database you use is your responsibility and you have to be able to defend its use – *caveat empor*.

## Predominance plots (grid approach)

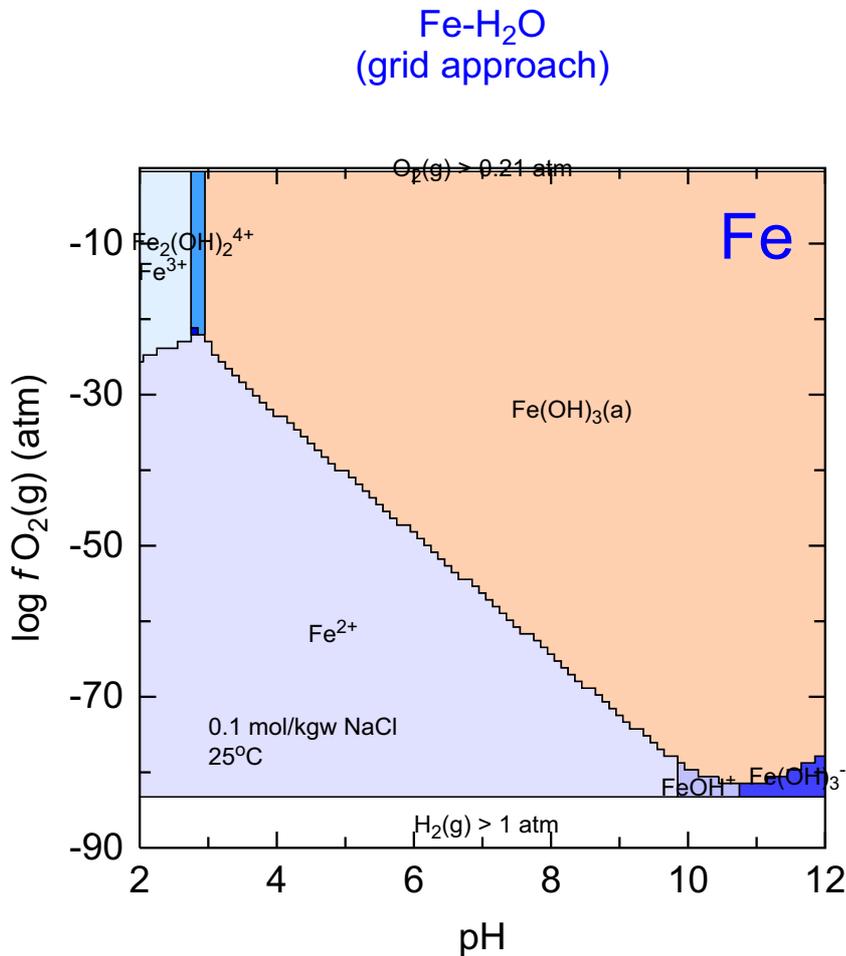
---

Predominance plots are a type of two-dimensional plot showing the predominant species as a function of two master variables plotted on the x- and y-axes.

**PhreePlot** uses a full speciation approach (based on **PHREEQC**) to calculate the predominant species. These examples use the 'grid' or brute force approach (Section 8.2).



# 1 Fe-H<sub>2</sub>O (grid approach)



C:\PhreePlot\demo\grid\gridhfo\_Fe1.ps

This is a predominance diagram for the Fe-H<sub>2</sub>O system. Only Fe(OH)<sub>3</sub>(a) (also known as hydrous ferric oxide and ferrihydrite) has been allowed to precipitate in this example – the more stable iron oxides such as goethite and hematite would take precedence if they were included in the list of minerals considered. The diagram shows that Fe(OH)<sub>3</sub>(a) dissolves under both acidic and reducing conditions.

The grid approach is the simplest way of calculating such predominance diagrams. Just calculate the speciation on a regular grid and plot the results directly, here on a 101 x 101 grid. However, there is much ‘wasted’ effort away from the boundaries and it takes quite a high grid resolution to make a good plot. The resultant plot file size is also quite large especially if the boundaries are not vectorised and simplified. Here the basic pixel map that is produced by the grid approach has been vectorised to give the polygon boundaries. This reduces the resultant file size. However, the boundaries have not been simplified, hence the ‘jaggies’.

It is natural to want to refine the boundaries with a finer grid. This can be done but is expen-

sive – the computational load increases with the square of the resolution. This logically leads to a search for a more efficient approach such as the ‘hunt and track’ approach. However, the grid approach is the most reliable approach (see the caution about the ‘hunt and track’ approach, Section 8.3). Its quality is only limited by the resolution

The main task of the input file is to define what **PHREEQC** calculations do and what and how the results are plotted. [calculationType](#) defines the type of calculations to be done, here ‘grid’ specifies a predominance diagram using the grid approach. [mainspecies](#) defines the ‘species’ or component for which the diagram is to be produced, here Fe. There could be a list of main species in multi-component systems, one for each ‘species’ present (other than H and O).

[xmin](#), [xmax](#), [ymin](#) and [ymax](#) define the range of the `<x_axis>` and `<y_axis>` tags, the domain of the calculations (not necessarily of the plotting - they are controlled by [pxmin](#) etc). resolution controls the size of the grid over which speciation calculations will be made, here 101 x 101.

The ‘title’ keywords control the various titles placed on the plot while [extraText](#) specifies a file which contains information from which to plot additional, user-supplied text anywhere on the page.

The **PHREEQC** code starts with the `ht1.inc` include file which writes data to the selected output ‘file’ in the format expected by **PhreePlot** for a predominance-type calculation. Note that while this file is called `ht1.inc`, it works equally well for both grid- and ht1-type calculations.

The rest of the code defines the total concentrations in the system and any minerals or gases that should be considered. Note that the initial pH of the solution (pH 1.8) is lower than the lowest pH of the plot (pH 2). This ensures that `Fix_H+` will be able to reach any required pH by the addition of NaOH. If the consequences of this are not wanted then the initial solution would need to have sufficient Na in it to support negative additions of NaOH.

The code is split into two simulations for speed. The first simulation does the initial solution calculation while the second simulation does the individual speciation calculations for each point on the plot. By default, **PhreePlot** only loops on the final simulation in a multi-simulation file. That is why `<x_axis>` and `<y_axis>` are found in the final simulation.

Note that the small, dark blue field ( $\text{FeOH}^{2+}$ ) at  $\text{pH} = 2.8$  and  $\log f\text{O}_2(\text{g}) = -22$  has not been labelled. This is because it occupies less than 0.1% of the plot area, the default value of [minimumAreaForLabeling](#).

```

# produces a predominance diagram for the Fe-H2O system using the grid approach

SPECIATION
  JobTitle                "Fe-H2O"
# uses the 'grid' or brute force approach - slow but more reliable than 'hunt and
track'
  calculationType         "grid"
  calculationMethod       1
# diagram is for Fe
  mainSpecies             Fe
# pH range
  xmin                    2.0
  xmax                    12.0
# fO2(g) range (controls the redox)
  ymin                    -90.0
  ymax                    0.0
# 101 x 101 grid
  resolution              101

PLOT
  plotTitle               "Fe-H<sub>2</sub><br>(grid approach)"
  xtitle                  pH
# this will produce a plot with the native y-scale, fO2(g)
  ytitle                  "log <i>f</i> O<sub>2</sub>(g) (atm)"
# can use the 'yscale' keyword to plot using pe, mV or Eh scales
  extraText               extratextFeOH.dat

CHEMISTRY

# standard file for calculating predominant species - from system directory
include 'ht1.inc'
# same as used by the hunt and track approach

SOLUTION 1
  pH      1.8
  units   mol/kgw
  Fe(3)   1e-2
  Na      1e-1
  Cl      1e-1
SAVE solution 1
END

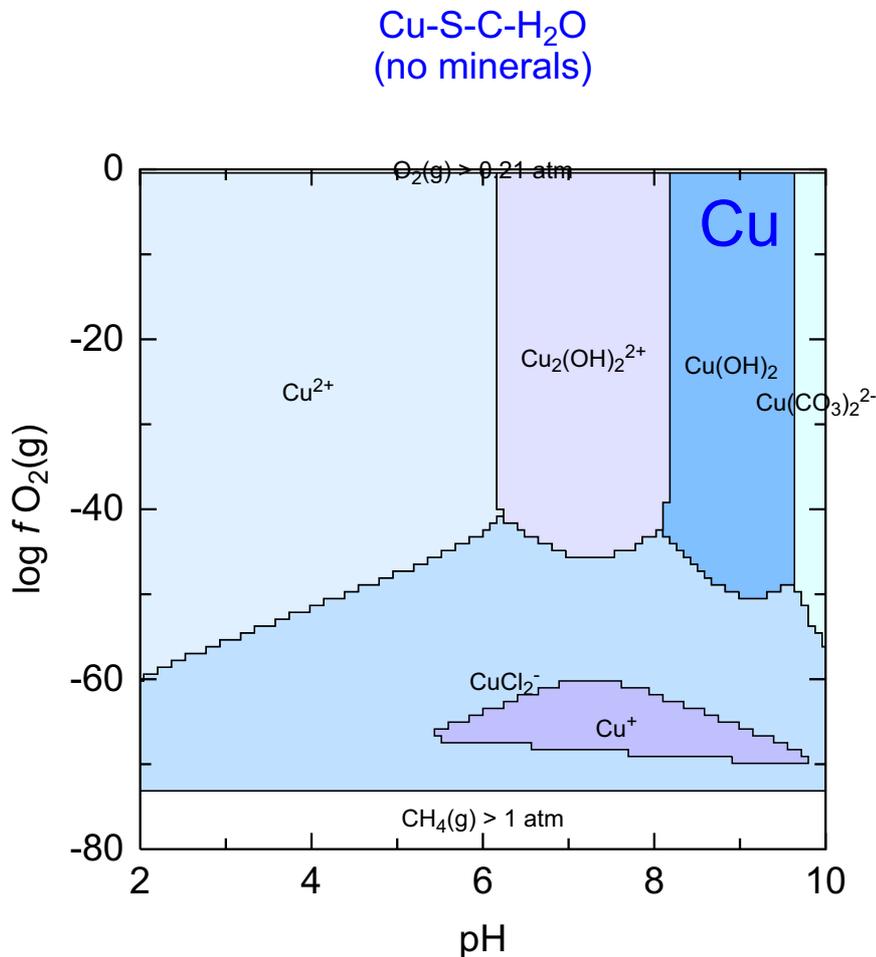
USE solution 1
EQUILIBRIUM_PHASES 1
# N.B. this works because <x_axis> is substituted without any leading spaces
  Fix_H+  -<x_axis> NaOH 10
# for negative values of <x_axis> would have to form a new tag to avoid --value
  -force_equality true
  O2(g)   <y_axis> 0.1

# the only mineral allowed to form - must be in the database used
  Fe(OH)3(a) 0 0
# 0 0 means achieve SI=0 and size of initial reservoir is 0 mol Fe(OH)3(a)
END
# i.e. allow to precipitate but none there to dissolve

```



## 2 Cu-S-C ('island' found with 'grid')



C:\PhreePlot\demo\island\CuSgrid\_Cu1.ps

This predominance diagram is for solution-only species; no minerals have been allowed to precipitate.

The diagram has been produced with the 'grid' approach. It illustrates an example where the 'hunt and track' approach fails to find all fields (see the next Example). The field not found is the Cu<sup>+</sup> field in the lower part of the diagram. This 'island' is not accessible from any of the domain boundaries and so the hunting part of the ht1 algorithm fails to find it.

Sections through the island at  $\log f_{\text{O}_2(\text{g})} = -63$  atm showing the Cu (Figure Ex2.1) and Cl (Figure Ex2.2) speciation as a function of pH indicate that the island occurs where the only two significant Cu species are Cu<sup>+</sup> and CuCl<sub>2</sub><sup>-</sup>. The Cl speciation is also dominated by the CuCl<sub>2</sub><sup>-</sup> species and so the Cl concentration fixes the CuCl<sub>2</sub><sup>-</sup> concentration which in turn fixes the Cu<sup>+</sup> concentration.

It appears in practice that such 'islands' are not that common. None of the other 'ht1' examples in this guide have an 'island'. Nevertheless, it is always wise to check an 'ht1' diagram

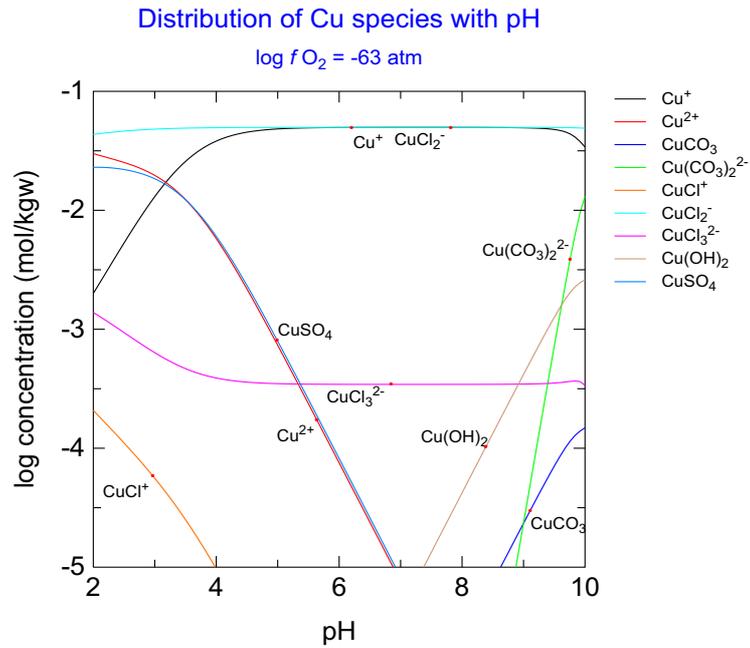


Figure Ex2.1. Variation of Cu speciation with pH. The pH section at  $\log f_{O_2}(g) = -63$  passes through the  $Cu^+$  'island' between pH 6.3 and pH 8.3.

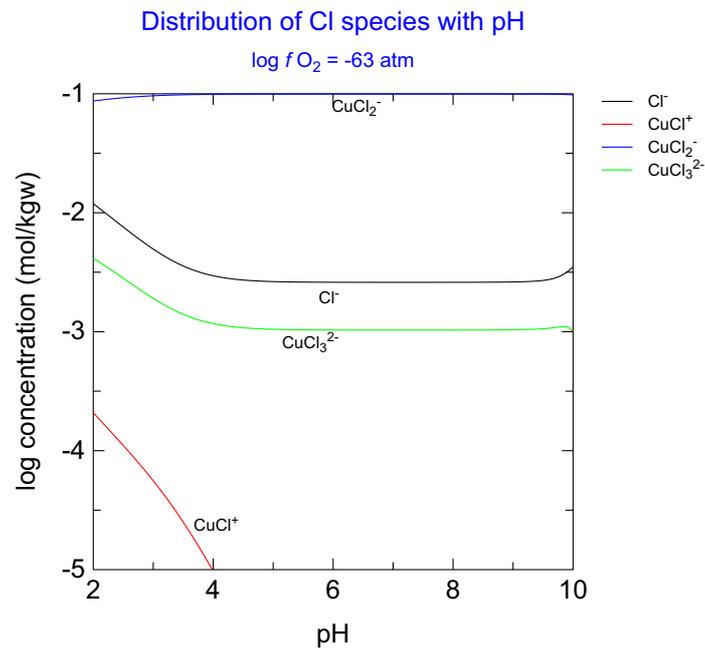


Figure Ex2.2. Variation of Cl speciation with pH. The pH section at  $\log f_{O_2}(g) = -63$  passes through the  $Cu^+$  'island' between pH 6.3 and pH 8.3.

using the 'grid' approach just to be sure.

Thanks to Hans Meeussen for finding this example.

```

SPECIATION
  calculationType      grid
  calculationMethod    1
  mainSpecies          Cu
  xmin                 2
# upper pH
  xmax                 10
  ymin                 -80.0
  ymax                 0.0
#
  resolution           100
PLOT
  plotTitle            "Cu-S-C-H<sub>2</sub><br>(no minerals)"
  xtitle               pH
  ytitle               "log <i>f </i><sub>2</sub>(g)"
  extraText            "extratextCuS.dat"

CHEMISTRY

# standard hunt and track file also works for grid plots
include 'ht1.inc'

SOLUTION 1
  Temp      20
# set just below lowest pH
  pH        1.8
  units     mol/kgw
# total concns
  Cu        1e-1
  S(6)      1e-1
# background electrolyte
  Na        1e-1
  Cl        1.032e-1
SAVE solution 1
END

# loop on last simulation by default
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis> 0.1
# N.B. no minerals
  CO2(g)    -3.5      1.0
END

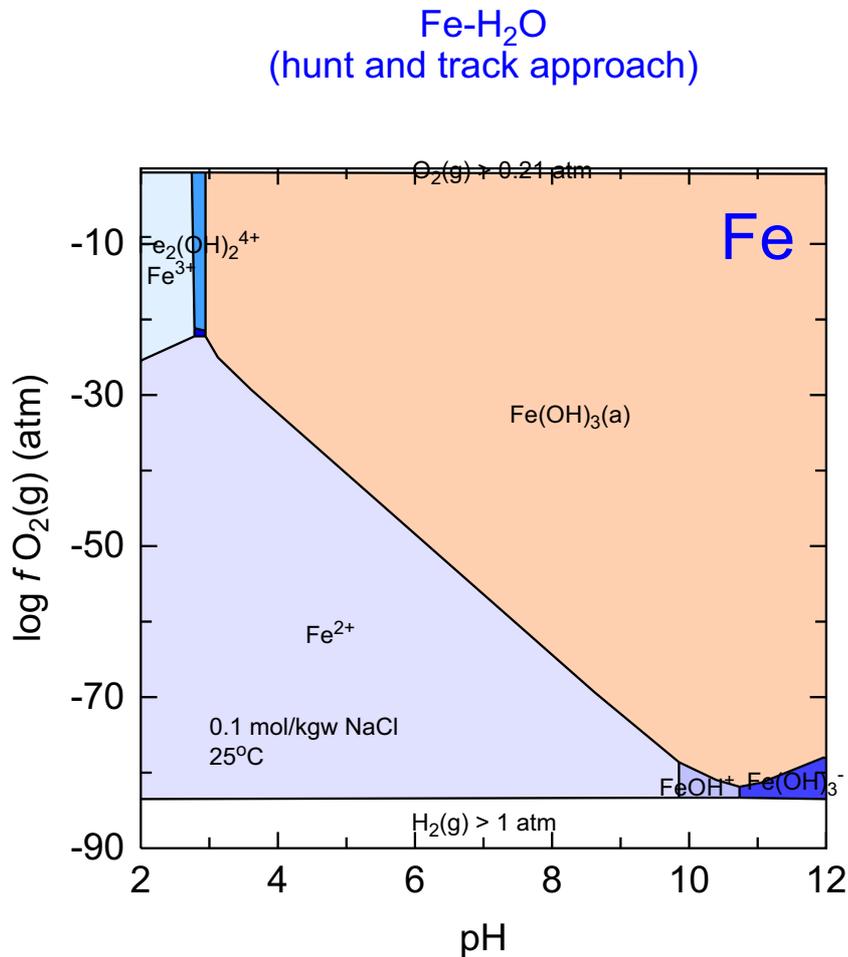
```

# Predominance plots (ht1 approach)

---

These examples use the 'ht1' or 'hunt and track' approach (Section 8.3) for calculating predominance diagrams.

### 3 Fe-H<sub>2</sub>O ('Hunt and track' approach)



This figure is for the same system as in the previous example but has been calculated using the 'hunt and track' approach rather than the 'grid' approach. This approach seeks out the change in predominant species along the domain boundaries (outside edges) and from these intersections tracks inside, bouncing along the boundary. Ultimately all the internal boundaries have been tracked and linked together to give the required polygons or fields. This approach assumes that there are no 'islands' – fields that cannot be reached from the edges – an assumption that is often but not always valid (see [Example 43](#)) so care is needed when applying this approach.

This approach is quicker than the grid approach for high quality plots. The effort depends on the length of the boundaries and varies more or less linearly with the resolution (not the square as with the grid approach).

The only change required from the previous example is to change the [calculationType](#) from 'grid' to 'ht1'.

```

# produces a predominance diagram for the Fe-H2O system using the hunt and track
# approach, uses native y-scale

SPECIATION
  JobTitle                "Fe-H2O"
# uses the 'hunt and track' approach - fast but not as reliable as the 'grid'
# approach
  calculationType         "ht1"
  calculationMethod       1
# diagram is for Fe
  mainSpecies             Fe
# pH range
  xmin                    2.0
  xmax                    12.0
# fO2(g) range (controls the redox)
  ymin                    -90.0
  ymax                    0.0
# jumps around on a 250 x 250 grid
  resolution              250

PLOT
  plotTitle               "Fe-H<sub>2</sub><br>(hunt and track
# approach)"
  xtitle                  pH
# this will produce a plot with the native y-scale, fO2(g)
  ytitle                  "log <i>f</i> O<sub>2</sub>(g) (atm)"
# can use the 'yscale' keyword to plot using pe, mV or Eh scales
  extraText               extratextFeOH.dat

CHEMISTRY

# standard file for calculating predominant species
include 'ht1.inc'
# same as used by the grid approach

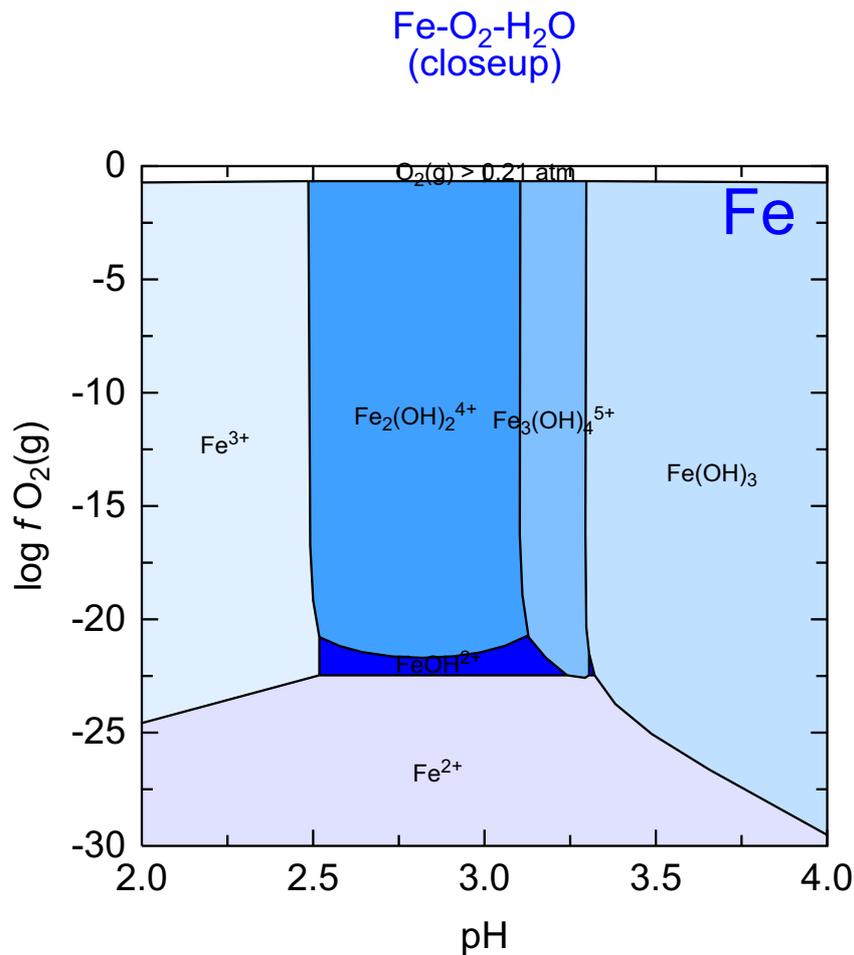
SOLUTION 1
  pH      1.8
  units   mol/kgw
  Fe(3)   1e-2
  Na      1e-1
  Cl      1e-1
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
# N.B. this works because <x_axis> is substituted without any leading spaces
  Fix_H+ -<x_axis> NaOH 10
# for negative values of <x_axis> would have to form a new tag to avoid --value
  -force_equality true
  O2(g) <y_axis> 0.1

# the only mineral allowed to form - must be in the database used
  Fe(OH)3(a) 0 0
# 0 0 means achieve SI=0 and size of initial reservoir is 0 mol Fe(OH)3(a)
END
# i.e. allow to precipitate but none there to dissolve

```

## 4 Fe-H<sub>2</sub>O: close-up (predominance criterion)



Close-up of a portion of an interesting part of the predominance diagram from the previous figure but this time using the `lnl1.dat` database.

This database file is specified with the `database` keyword. The database file should either be in the system directory or in the `ppi` directory or in a directory for which the full file path is specified with the keyword.

The `lnl1.dat` database has a more extensive set of polynuclear Fe species than `wateq4f.dat`. However, the larger database makes the calculations significantly slower.

Note the appearance of a second very small and unlabelled  $\text{FeOH}_2^+$  field to the right of the main  $\text{FeOH}_2^+$  field.

It is best to recalculate close-ups anew rather than merely replotting them by using a changed `pxmin` etc.

```

# closeup of the Fe-H2O system based on the llnl.dat database

SPECIATION
  JobTitle                "Fe-H2O-O2"
  calculationType         ht1
  calculationMethod       1
# species and their names vary with database
  database                llnl.dat
  fillColorDictionary     fillcolorllnl.dat
  mainSpecies             Fe
# pH range (x-axis) from 2-4 in 250 steps
  xmin                    2.0
  xmax                    4.0

# log f(O2(g)) range (y-axis) from -20 to 0 in 250 steps
  ymin                    -30.0
  ymax                    0.0
  resolution              250

PLOT
  plotTitle               "Fe-O<sub>2</sub>-H<sub>2</sub>O<br>(closeup)"
  xtitle                  pH
  ytitle                   "log <i>f</i> O<sub>2</sub>(g)"
  extraText                "extratextFeOHclose.dat"

CHEMISTRY

# first simulation - initial solution calculation

# special predominance diagram file that adds "(s)" to the names of all minerals
include 'htls.inc'
# this is helpful because in the llnl.dat database, "Fe(OH)3" could be confused

# with an aqueous species

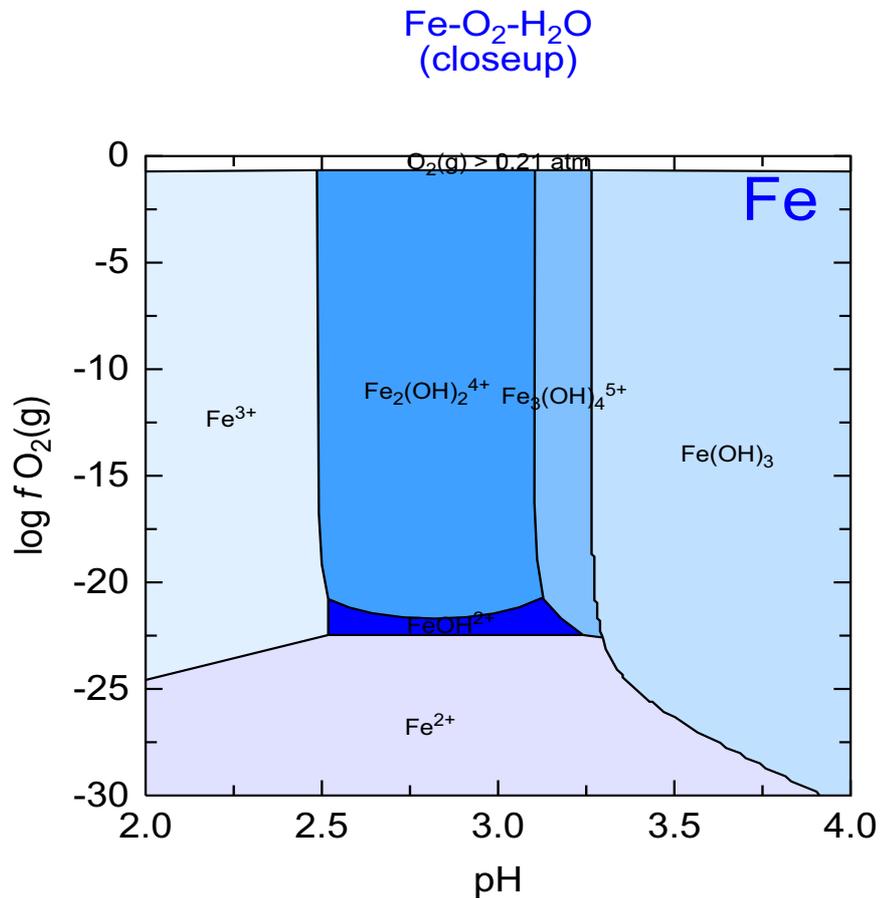
SOLUTION 1
# initial solution pH is less than pHmin
  pH          1.8
  units      mol/kgw
# total Fe
  Fe(3)      1e-2
# background electrolyte
  Na         1e-1
  Cl         1e-1
SAVE solution 1
END

# second simulation - iterate on this final simulation
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis>

# note the mineral is Fe(OH)3 not Fe(OH)3(a) in this database
  Fe(OH)3 0 0
END

```

## 5 Fe-H<sub>2</sub>O: close-up (stability criterion)



C:\PhreePlot\demo\Felhfocloseupstabiln\_Fe1.ps

This is the same as in the previous Example but calculated using the 'stability' criterion. Note the slightly different diagram with the appearance of an aqueous Fe(OH)<sub>3</sub> field.

```

# closeup of the Fe-H2O system based on the llnl.dat database

SPECIATION
  JobTitle                "Fe-H2O-02"
  calculationType         ht1
  calculationMethod       1
# species and their names vary with database
  database                llnl.dat
  fillColorDictionary     fillcolorllnl.dat
  mainSpecies             Fe
# pH range (x-axis) from 2-4 in 250 steps
  xmin                    2.0
  xmax                    4.0

# log f(O2(g)) range (y-axis) from -20 to 0 in 250 steps
  ymin                    -30.0
  ymax                    0.0
  resolution              250

PLOT
  plotTitle               "Fe-O<sub>2</sub>-H<sub>2</sub>O<br>(closeup)"
  xtitle                  pH
  ytitle                  "log <i>f</i> O<sub>2</sub>(g)"
  extraText                "extratextFeOHclose.dat"

CHEMISTRY

# first simulation - initial solution calculation
# standard stability diagram file
include 'htl1stability.inc'

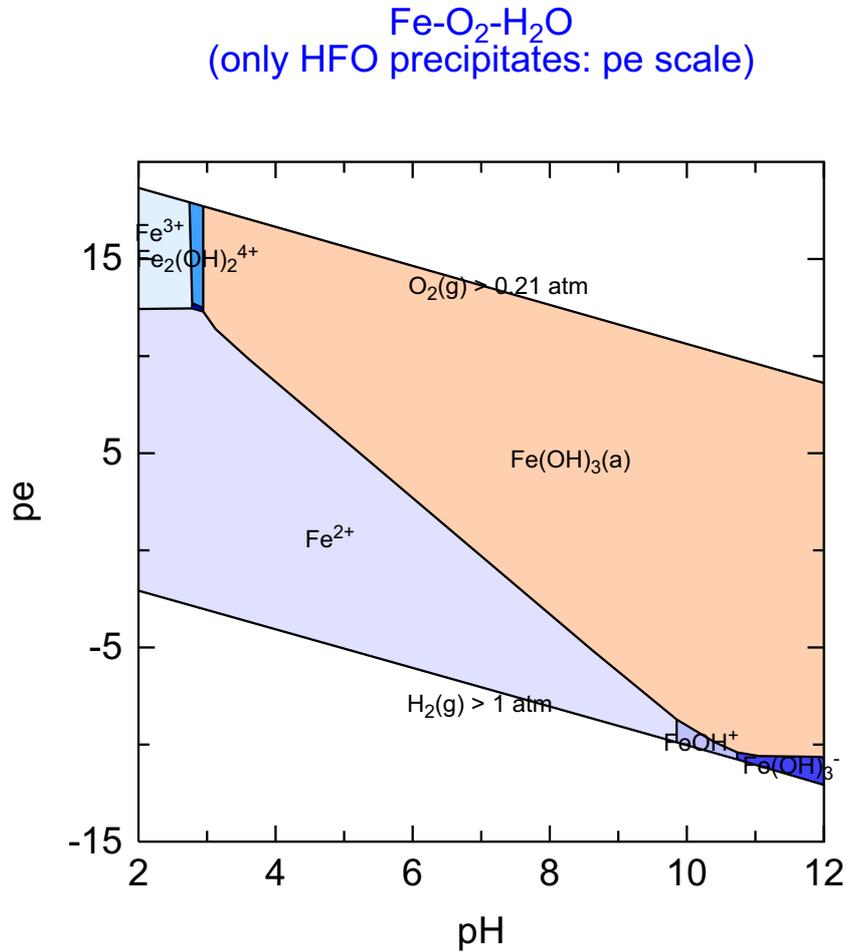
SOLUTION 1
# initial solution pH is less than pHmin
  pH          1.8
  units       mol/kgw
# total Fe
  Fe(3)       1e-2
# background electrolyte
  Na          1e-1
  Cl          1e-1
SAVE solution 1
END

# second simulation - iterate on this final simulation
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis>

# note the mineral is Fe(OH)3 not Fe(OH)3(a) in this database
  Fe(OH)3 0 0
END

```

## 6 Fe-H<sub>2</sub>O (pe scale)



C:\PhreePlot\demo\Fel\fope\_Fe1.ps

Same as in [Example 2](#) but plotted with the pe scale rather than the O<sub>2</sub>(g) fugacity scale. This is set with the `yscale` keyword. `pymin` and `pymajor` have also been set to ensure a reasonable y-scale. If `yscale` is set to “pe”, then the default y-axis title is automatically set to “pe”.

```

# produces a predominance diagram for the Fe-H2O system using the hunt and track
approach, pe scale
#

SPECIATION
  jobTitle                "Fe-H2O-O2"
# the 'hunt and track' method
  calculationType          ht1
# 1=calculate, 2=replot, 3=resimplify and replot
  calculationMethod        1
# make a Fe diagram
  mainSpecies              Fe

# pH range (x-axis) 2-12
  xmin                     2.0
  xmax                     12.0

# log f(O2(g)) range (y-axis) -90 to 0
  ymin                     -90.0
  ymax                     0.0
# searching takes place over a 250 x 250 grid
  resolution               250

PLOT
  plotTitle                "Fe-O<sub>2</sub>-H<sub>2</sub>O<br>(only HFO
precipitates: pe scale)"
  xtitle                   pH
# use pe scale - default title is 'pe'
  yscale                   pe
# min y value on plot scale
  pymin                    -15
# pymajor                   5                # interval between major
ticks and labels on y-scale
# make a pdf file (assumes Ghostscript installed)
  pdf                      T

CHEMISTRY

# first simulation - initial solution calculation only calculated once

include 'ht1.inc'

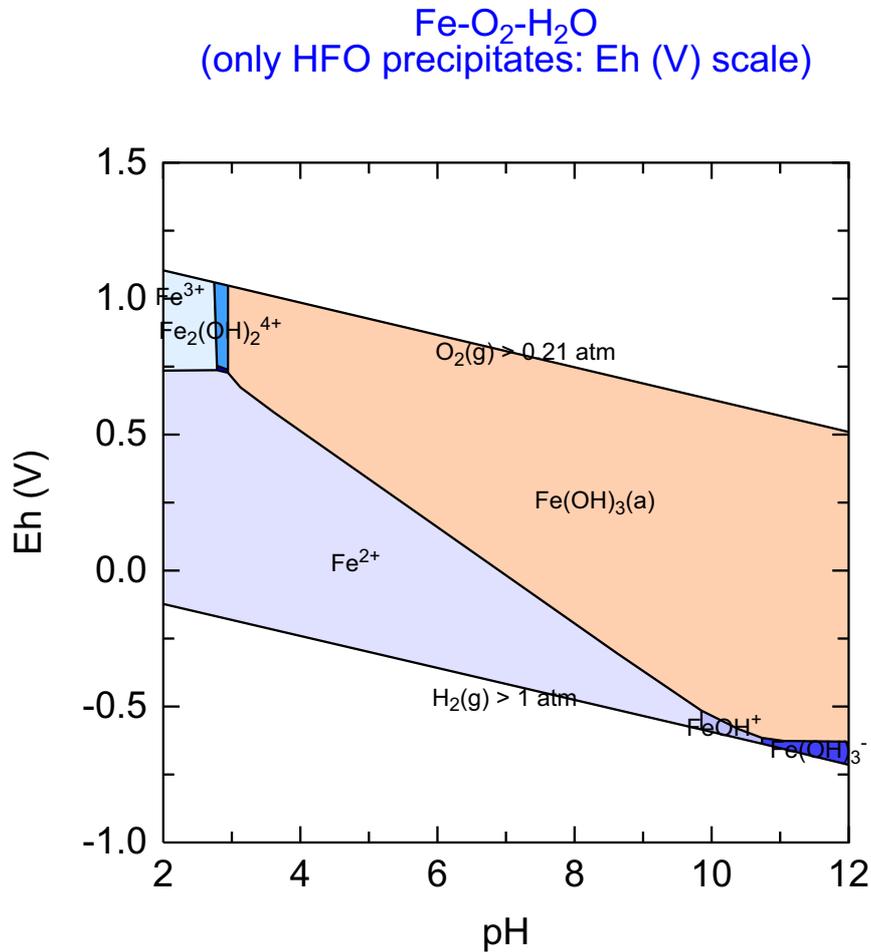
SOLUTION 1
  pH                       1.8
  units                     mol/kgw
# total Fe in system
  Fe(3)                    1e-2
  Na                       1e-1
  Cl                       1e-1
SAVE solution 1
END

# second (final) simulation - the final simulation is iterated many times as
required by the hunt and track procedure
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis>

# the only mineral considered
  Fe(OH)3(a) 0 0
END

```

## 7 Fe-H<sub>2</sub>O (Eh scale)



C:\PhreePlot\demo\Fe\hfoeh\_Fe1.ps

Same as in [Example 2](#) but plotted with an Eh scale rather than the O<sub>2</sub>(g) fugacity scale. This makes use of the [yscale](#) setting. [pymin](#) and [pymajor](#) have been set to ensure a reasonable y-scale. If yscale is set to “Eh”, then the default y-axis title is set to “Eh (V)”. If it is preferred to have the [yscale](#) in mV rather than ‘v’, set yscale to ‘mV’.

```

# produces a predominance diagram for the Fe-H2O system using the hunt and track
approach, Eh (V) scale
#

SPECIATION
  jobTitle                "Fe-H2O-O2"
# the 'hunt and track' method
  calculationType         ht1
# 1=calculate, 2=replot, 3=resimplify and replot
  calculationMethod       1
# make a Fe diagram
  mainSpecies             Fe

# pH range (x-axis) 2-12
  xmin                    2.0
  xmax                    12.0

# log f(O2(g)) range (y-axis) -90 to 0
  ymin                    -90.0
  ymax                    0.0
# searching takes place over a 250 x 250 grid
  resolution              250

PLOT
  plotTitle               "Fe-O<sub>2</sub>-H<sub>2</sub>O<br>(only HFO
precipitates: Eh (V) scale)"
  xtitle                  pH
# use Eh scale (V) - default title is 'Eh (V)'
  yscale                  Eh
# min y value on plot scale
  pymin                   -1
# interval between major ticks and labels on y-scale
  pymajor                 0.5
# make a pdf file (assumes Ghostscript installed)
  pdf                     T

CHEMISTRY

# first simulation - initial solution calculation only calculated once

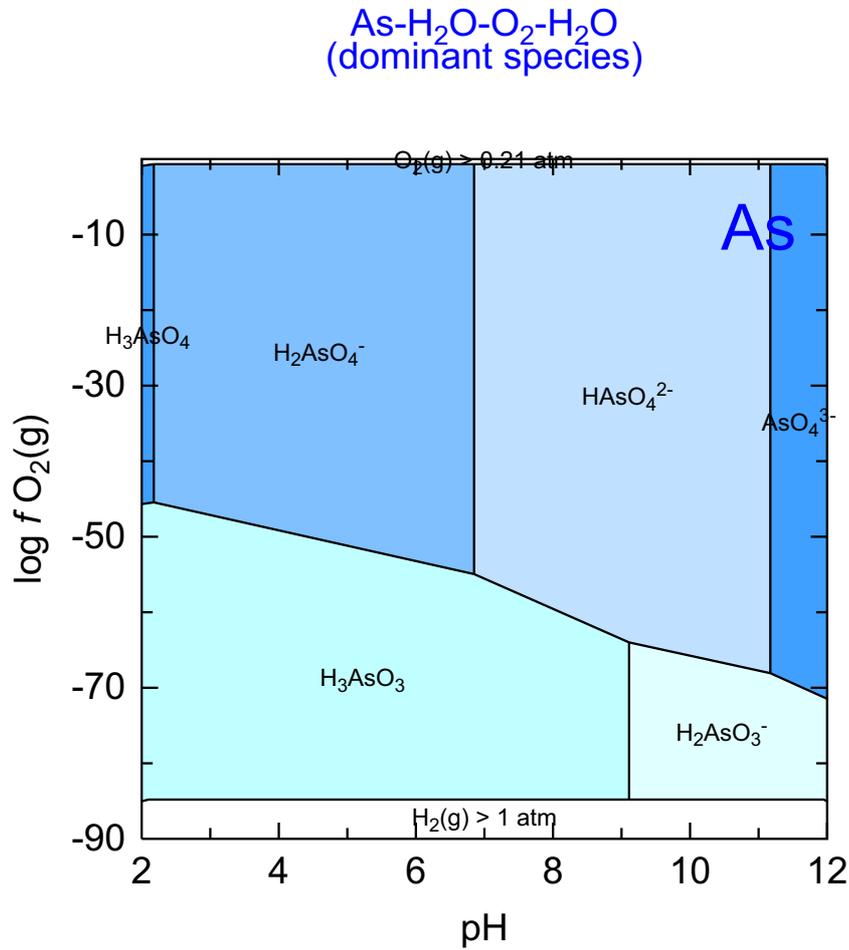
include 'ht1.inc'

SOLUTION 1
  pH          1.8
  units       mol/kgw
# total Fe in system
  Fe(3)       1e-2
  Na          1e-1
  Cl          1e-1
SAVE solution 1
END

# second (final) simulation - the final simulation is iterated many times as
required by the hunt and track procedure
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis>

# the only mineral considered
  Fe(OH)3(a) 0 0
END

```

8 As-O<sub>2</sub>(g)-H<sub>2</sub>O

C:\PhreePlot\demo\Assolution\As\_As1.ps

A classical predominance diagram for arsenic showing the change of arsenic species with both pH and redox. This diagram is only solution for solution species since no minerals have been included in the EQUILIBRIUM\_PHASES data block.

```

SPECIATION
  calculationType      ht1
  calculationMethod    1
  mainSpecies          As
  xmin                 2.0
  xmax                 12.0
  ymin                 -90.0
  ymax                 0.0
  resolution           200

PLOT
  plotTitle            "As-H<sub>2</sub>O<sub>2</sub>-H<sub>2</sub>O<sub>2</sub>(dominant species)"
  xtitle               pH
  ytitle               "log <i>f </i><sub>2</sub>(g)"
  extraText            "extratextAs.dat"

CHEMISTRY

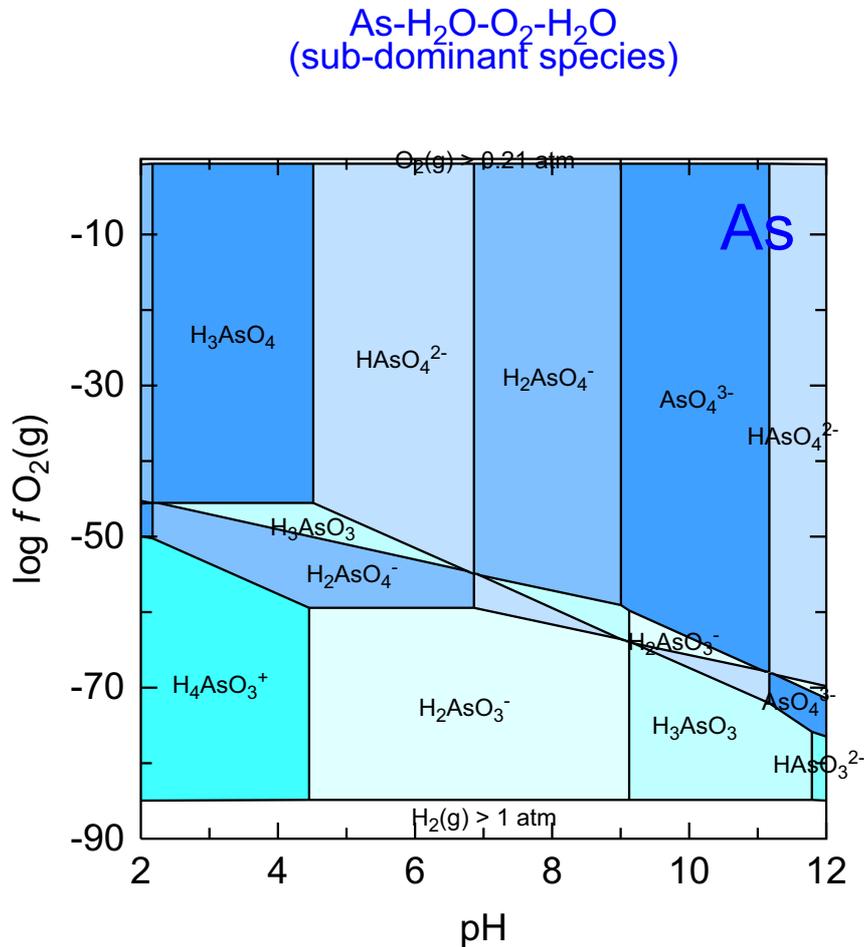
# standard 'hunt and track' file
include ht1.inc

SOLUTION 1
  temp      20
  units     mol/kgw
# total As
  As       1e-3
# background electrolyte
  Na       1e-1
  Cl       1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
# <x_axis> is pH so reverse sign
  Fix_H+    -<x_axis> NaOH
  -force_equality true
  O2(g)     <y_axis> 0.1
END

```

## 9 As-O<sub>2</sub>(g)-H<sub>2</sub>O (sub-dominant)



C:\PhreePlot\demo\Assolution\Assubdom\_As1.ps

This diagram has been calculated for the same system as for the previous diagram but this time the sub-dominant species (the second most abundant species) have been plotted.

The dominant species is still included in the calculations but it has been demoted so that it is not selected. Note that this often produces six-way intersections as opposed to the three-way intersections of the classical plots.

This type of plot may not be terribly enlightening but if the dominant species is of interest, then the sub-dominant species might also be of some interest. As with the normal predominance diagram, the diagram triggers questions about why particular fields are where they are and this in itself can aid understanding of the processes involved.

It is not possible to calculate this type of diagram with the classical (analytical) approach for calculating predominance diagrams.

```

# sub-dominant plot (second most abundant species - a bit different from normal!)
SPECIATION
  calculationType          ht1
  calculationMethod        1
  mainSpecies              As
  xmin                     2.0
  xmax                     12.0
  ymin                     -90.0
  ymax                     0.0
# need a high resolution to get good straight sloping lines - otherwise use 'simplify 10'
  resolution                500
# this picks the sub-dominant species
  dominant                  F

# three fields are not labelled since they are 'cross-over' fields of other fields
# and included in a single polygon sequence... and there is one label per polygon
# sequence
# some two-point segments are sent to the polygon file but are not plotted

PLOT
  plotTitle                "As-H<sub>2</sub>-O<sub>2</sub>-H<sub>2</sub>
sub>O<br>(sub-dominant species)"
  xtitle                   pH
  ytitle                   "log <i>f </i><sub>2</sub>(g)"
  extraText                "extratextAs.dat"

CHEMISTRY

# use standard predominance file which returns top three species - PhreePlot deals
# with this
include 'ht1.inc'

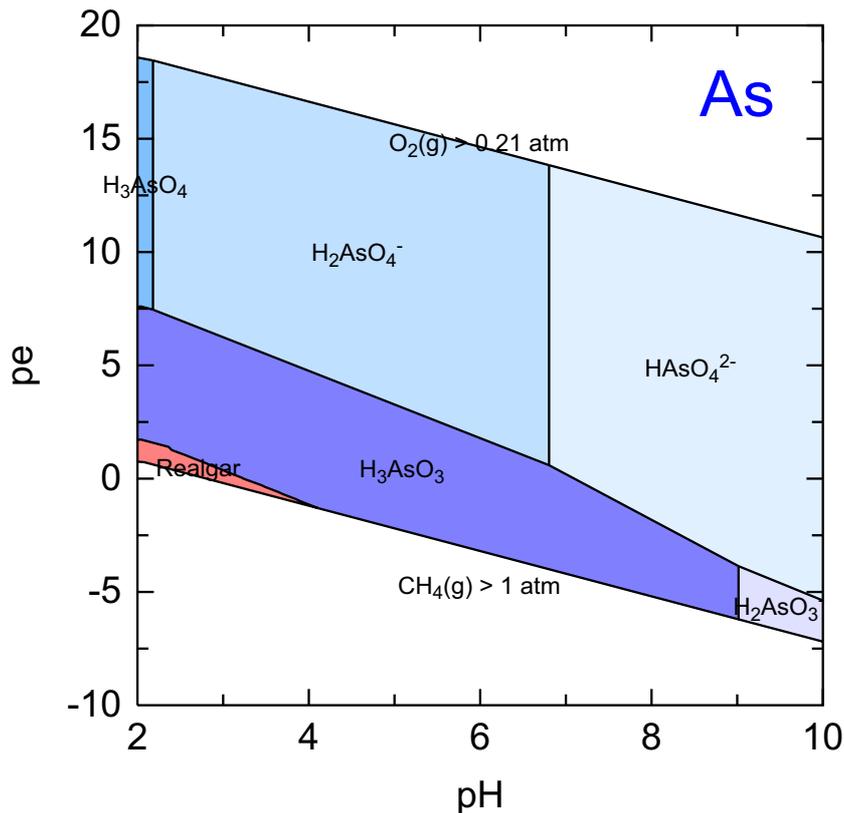
SOLUTION 1
  temp      20
  units     mol/kgw
  As        1e-3
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
# <x_axis> is pH so reverse sign
  Fix_H+      -<x_axis> NaOH
  -force_equality true
  O2(g)       <y_axis> 0.1
END

```

## 10 Fe-As-C-S

(minerals but no sorbed As)



C:\PhreePlot\demo\FEAsCS\FEAsCS\_As1.ps

This is the pe-pH diagram for As in a Fe-As-C-S system. This is a complex system with Fe, As, C and S minerals precipitating in various places.

Note that the ppi code (see next page) that produced this diagram actually produces diagrams for all four 'main species' or components (Fe, As, C and S). These are produced in a single ps file since [multipageFile](#) has been set to true. Looking at all four diagrams together gives a good indication of the interactions involved, and the reasons why the minerals predominate where they do.

For example, realgar is only stable in highly acidic and reducing systems where HS<sup>-</sup> and H<sub>3</sub>AsO<sub>3</sub> activities are relatively high. It does not therefore predominate when pyrite is present since this drops the sulphide activity too low or in oxidising conditions where SO<sub>4</sub><sup>2-</sup> and As(V) species predominate.

```

SPECIATION
  calculationType          ht1
  calculationMethod       1
# produce predominance diagrams for these four elements
  mainSpecies             Fe As C S
  xmin                    2.0
  xmax                    10.0
  ymin                    -85.0
  ymax                    0.0
  resolution              200

PLOT
  plotTitle                "Fe-As-C-S<br>(minerals but no sorbed As)"
  xtitle                   pH
  ytitle                   pe
  pymin                   -10.0
# this changes to the pe scale
  yscale                   pe
  extraText                "extratextFeAsCS.dat"

# put all the plots into a single file - only applies to ps and pdf
  multipagefile           t

CHEMISTRY

INCLUDE 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  S(6) 5e-3
  Fe 5e-3
  As 1e-2
  Na 1e-1
  Cl 1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 10

  Realgar                0 0
  Orpiment                0 0
  As2S3(am)              0 0
  Halite                  0 0
  Arsenolite              0 0
  Claudetite              0 0
  Pyrite                  0 0
  Mackinawite             0 0
  FeS(ppt)                0 0
  Sulfur                  0 0
  Fe(OH)2.7Cl.3          0 0
# Goethite                0 0
  Fe(OH)3(a)              0 0
# Hematite                0 0
  Greigite                0 0
  Magnetite               0 0
  Nahcolite               0 0
  Siderite                0 0
  Maghemite               0 0
  Siderite(d) (3)        0 0
  Scorodite               0 0
  Natron                  0 0
  Thermonatrite           0 0
  Fe3(OH)8                0 0

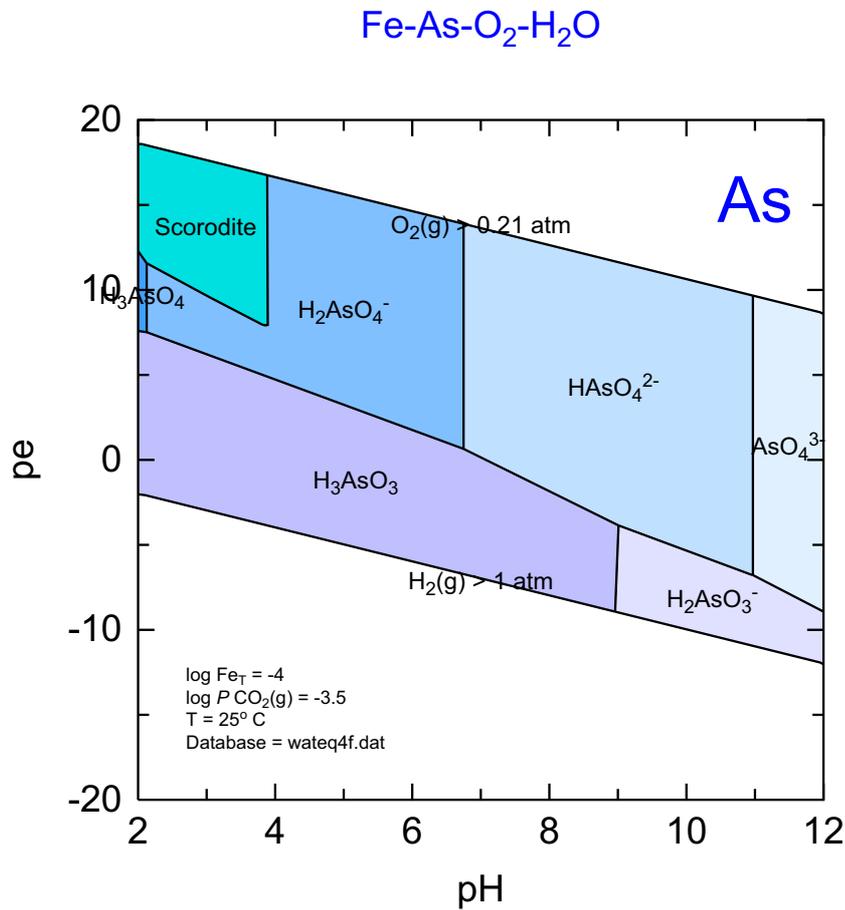
```

Thenardite	0 0
Melanterite	0 0
Mirabilite	0 0
As2O5(cr)	0 0
Trona	0 0
Jarosite-Na	0 0
JarositeH	0 0

END



# 11 Fe-As



C:\PhreePlot\demo\scorodite\scorodite\_As1.ps

This is the classical pe-pH diagram for As in Fe-As systems – it does not take into account any possible adsorption of As by Hfo which is precipitated above pH 4 and at high pe.

Scorodite is only stable below pH 4 and high pe since precipitation of Hfo reduces the Fe<sup>3+</sup> activity at higher pH values. Reduction of Fe<sup>3+</sup> to Fe<sup>2+</sup> reduces Fe<sup>3+</sup> activities at low pe and so scorodite is not stable there either.

```

SPECIATION
# aqueous and minerals
  jobTitle                "Fe-As-O2-H2O"
  calculationType         ht1
  calculationMethod       1
  mainSpecies             As
  xmin                    2.0
  xmax                    12.0
  ymin                    -85.0
  ymax                    0.0
  resolution              200

PLOT
  plotTitle               "Fe-As-O<sub>2</sub>-H<sub>2</sub>O"
  xtitle                  "pH"
# force the minimum axis y-scale
  pymin                   -20
  yscale                  pe
  extraText               "extratextscorodite.dat"

CHEMISTRY

# first simulation

include 'ht1.inc'

SOLUTION 1
# start at a low pH (less than xmin)
  pH      1.8
  units   mol/kgw
  Fe(3)   1e-1
  Na      1e-1
  Cl      1e-1
# total As
  As      1e-2
SAVE solution 1
END

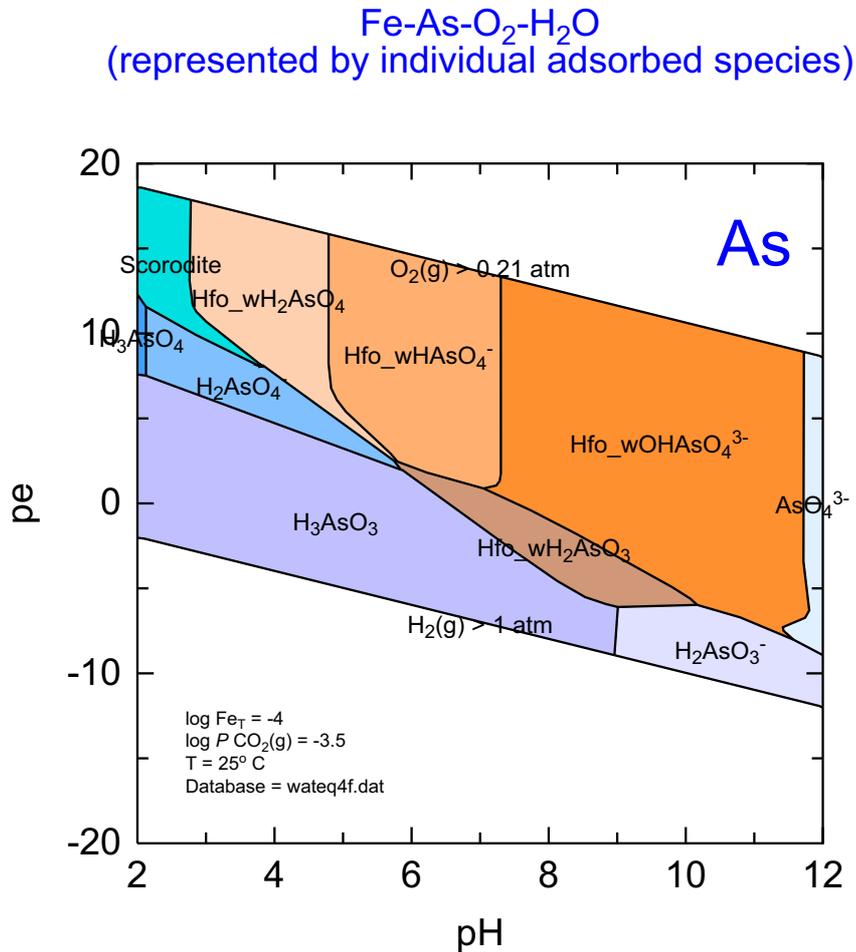
# second simulation

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
# but no adsorbed As
  Fe(OH)3(a) 0 0

# possible As minerals
  Arsenolite 0 0
  Claudetite 0 0
  Scorodite 0 0
  As2O5(cr) 0 0
END

```

## 12 Fe-As-Hfo (ht1.inc)



C:\PhreePlot\demo\scorodite\scoroditehfo3\_As1.ps

This diagram is for a similar chemistry to the previous example but uses the [Dzombak & Morel \(1990\)](#) DL model for Hfo to estimate As adsorption by Hfo. The adsorbed As consists of one As(III) and three As(V) species.

The adsorbed species have been included by using the `hfo.inc` file which links the precipitation of Fe(OH)<sub>3</sub>(a) to the Hfo surface.

In working out the predominant species, this example counts and displays each adsorbed species separately. This is how the `ht1.inc` include file has been coded.

```

SPECIATION
# aqueous, minerals and surface species
  jobTitle           "Fe-As-O2-H2O"
  calculationType    ht1
  calculationMethod   1
  mainSpecies        As
  xmin               2.0
  xmax               12.0
  ymin               -85.0
  ymax               0.0
  resolution         200

PLOT
  plotTitle          "Fe-As-O<sub>2</sub>-H<sub>2</sub>O<br>(rep-
resented by individual adsorbed species)"
  xtitle             pH
  pymin              -20
  yscale             pe
  extraText          "extratextscorodite.dat"

CHEMISTRY

# first simulation

# ht1.inc treats all Hfo-As surface species as separate species for plotting
include 'ht1.inc'

SOLUTION 1
  pH                1.8
  units              mol/kgw
  Fe(3)             1e-1
  Na                 1e-1
  Cl                 1e-1
# total As
  As                 1e-2
SAVE solution 1
END

# second simulation

# add Hfo surface
include 'hfo.inc'

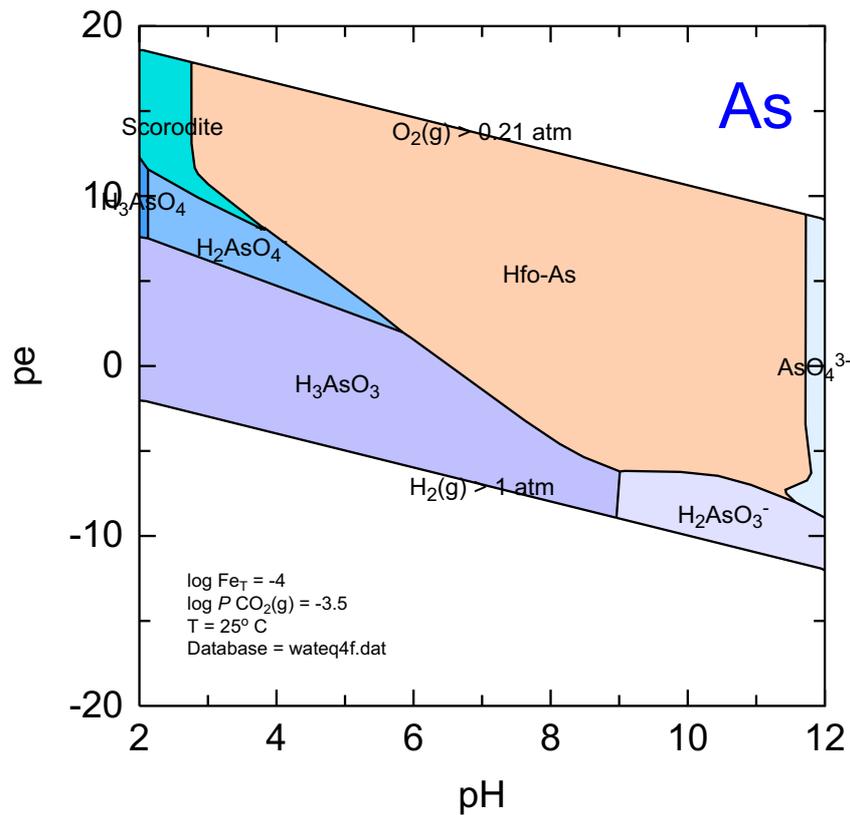
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
# only consider this oxide
  Fe(OH)3(a) 0 0

# possible As minerals
  Arsenolite 0 0
  Claudetite 0 0
  Scorodite 0 0
  As2O5(cr) 0 0
END

```

## 13 Fe-As-Hfo (ht1c.inc)

Fe-As-O<sub>2</sub>-H<sub>2</sub>O  
(represented by a single adsorbed species)



This is the same system as in the previous example but all the adsorbed As species have been lumped together into a single adsorbed species, Hfo-As. This change is made by using the `ht1combined.inc` include file rather than `ht1.inc` file.

The adsorbed species have been included by including the `hfo.inc` file which links the amount of Hfo surface to the amount of precipitated Fe(OH)<sub>3</sub>(a), as often occurs in nature.

The Hfo-As field closely follows the combined boundaries of the four adsorbed As species. It is actually very slightly larger than the sum of the four fields because of the larger number of moles of As in the combined Hfo-As field than in individual fields and hence its greater competitiveness against other As species.

```

SPECIATION
# aqueous, minerals and surface species
  jobTitle           "Fe-As-O2-H2O"
  calculationType    ht1
  calculationMethod  1
  mainSpecies        As
  xmin               2.0
  xmax               12.0
  ymin               -85.0
  ymax               0.0
  resolution         200

PLOT
  plotTitle          "Fe-As-O2-H2O (represented by a single adsorbed species)"
  xtitle             pH
  pymin              -20
  yscale             pe
  extraText          "extratextscorodite.dat"

CHEMISTRY

# first simulation

# treat all Hfo-As surface species as one 'super' species for plotting
include 'ht1combined.inc'

SOLUTION 1
  pH      1.8
  units   mol/kgw
  Fe(3)   1e-1
  Na      1e-1
  Cl      1e-1
# total As
  As      1e-2
SAVE solution 1
END

# second simulation

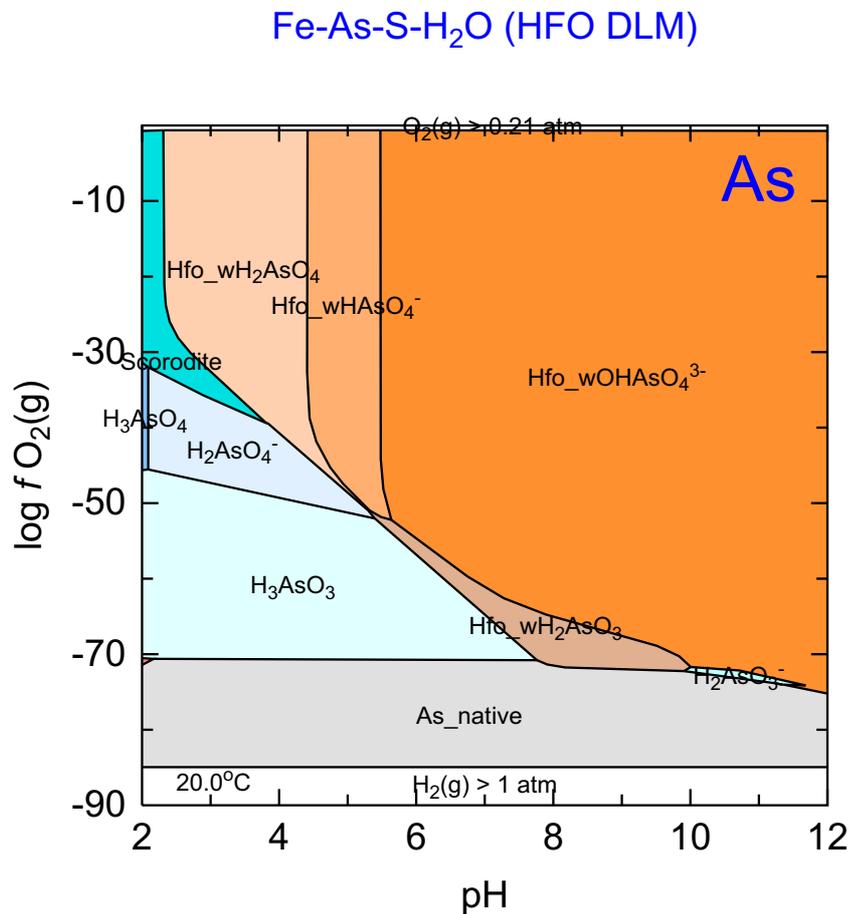
# add Hfo surface
include 'hfo.inc'

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
# only consider this oxide
  Fe(OH)3(a) 0 0

# possible As minerals
  Arsenolite 0 0
  Claudetite 0 0
  Scorodite 0 0
  As2O5(cr) 0 0
END

```

## 14 Fe-S-As (without sorption)



C:\PhreePlot\demo\FeAsS\FeAsS\_As1.ps

This example involves Fe-S-As and allows precipitation of the  $\text{Fe}(\text{OH})_3(\text{a})$  which is linked to the Hfo mineral phase. However, there is no code to link arsenic adsorption to this phase, i.e. no 'include hfo.inc' line, or similar. In this example, arsenic minerals only predominate under strongly reducing conditions.

There were a few 'beeps' when running this example with the default convergence parameters. **PHREEQC** repeatedly failed to converge at a point around pH 9.55 and  $\log f \text{O}_2(\text{g}) -84.7$ . No selected output was received by **PhreePlot** and the failed region was recorded as an 'NA' field. The problem was solved by relaxing the convergence tolerance from its default value of  $1\text{e-}12$  to  $1\text{e-}10$ . This was done by changing the `-convergence_tolerance` setting of the **KNOBS** keyword data block for the second simulation.

```
# predominance diagram for As in the presence of HFO which adsorbs As according to
the Dzombak & Morel DL adsorption model
```

```
SPECIATION
  calculationType          ht1
  calculationMethod        1
  mainSpecies              As
# range of pH
  xmin                     2.0
  xmax                     12.0
# range of log fO2(g) to control redox
  ymin                     -90.0
  ymax                     0.0
# controls the resolution (big resolution means small step size)
  resolution                500

PLOT
  plotTitle                "Fe-As-S-H<sub>2</sub>O (HFO DLM)"
  xtitle                   pH
  ytitle                   "log <i>f </i>O<sub>2</sub>(g)"
  extratext                extratextFeAsS.dat
```

```
CHEMISTRY
```

```
# simulation 1

# standard predominance-calculating file
include 'ht1.inc'

# initial solution calculation
SOLUTION 1
  Temp      20
  pH        1.8
  units     mol/kgw
# total concns
  Fe(3)     3.5e-1
  As        1e-2
# sulphide minerals can form but not adsorb
  S(6)      1e-2
  Na        1e-1
  Cl        1e-1
SAVE solution 1
END

include 'hfo.inc'

# simulation 2
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis>

# most likely minerals given the database
  As_native      0 0
# hematite, magnetite removed to make goethite stable
  Orpiment       0 0
  Realgar         0 0
  As2S3(am)      0 0
  Pyrite          0 0
  Arsenolite     0 0
  Claudetite     0 0
  Mackinawite    0 0
  FeS(ppt)       0 0
  Sulfur         0 0
  Fe(OH)3(a)     0 0
  Greigite       0 0
  Scorodite      0 0
  Mirabilite     0 0
  Melanterite    0 0
```

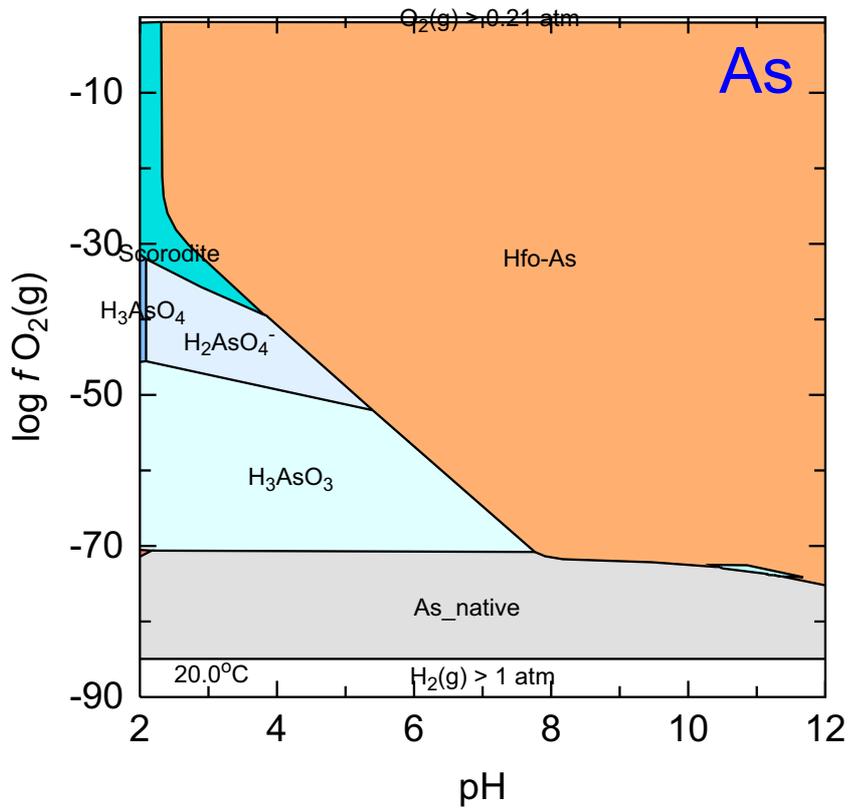
	Thenardite	0	0
	As2O5(cr)	0	0
	Jarosite-Na	0	0
	JarositeH	0	0
#	Goethite	0	0

END



# 15 Fe-S-As (low Fe, without surface speciation)

## Fe-As-S-H<sub>2</sub>O (HFO DLM)



C:\PhreePlot\demo\FeAsS\FeAsSall\_As1.ps

Similar to the previous example but calculated using the `ht1combined.inc` file which bulks together all As species adsorbed by Hfo into a single species, Hfo-As. This includes both As(V) and As(III) surface species.

```
# predominance diagram for As in the presence of HFO which adsorbs As according to
the Dzombak & Morel DL adsorption model
```

```
SPECIATION
  calculationType          htl
  calculationMethod        1
  mainSpecies              As
# range of pH
  xmin                     2.0
  xmax                     12.0
# range of log fO2(g) to control redox
  ymin                     -90.0
  ymax                     0.0
# controls the resolution (big resolution means small step size)
  resolution               500

PLOT
  plotTitle                "Fe-As-S-H<sub>2</sub>O (HFO DLM)"
  xtitle                   pH
  ytitle                   "log <i>f </i>O<sub>2</sub>(g)"
  extratext                 extratextFeAsS.dat

CHEMISTRY

# simulation 1

# standard predominance-calculating file
include 'htlcombined.inc'

# initial solution calculation
SOLUTION 1
  Temp      20
  pH        1.8
  units     mol/kgw
# total concns
  Fe(3)     3.5e-1
  As        1e-2
# sulphide minerals can form but not adsorb
  S(6)      1e-2
  Na        1e-1
  Cl        1e-1
SAVE solution 1
END

include 'hfo.inc'

# simulation 2
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis>      0.1

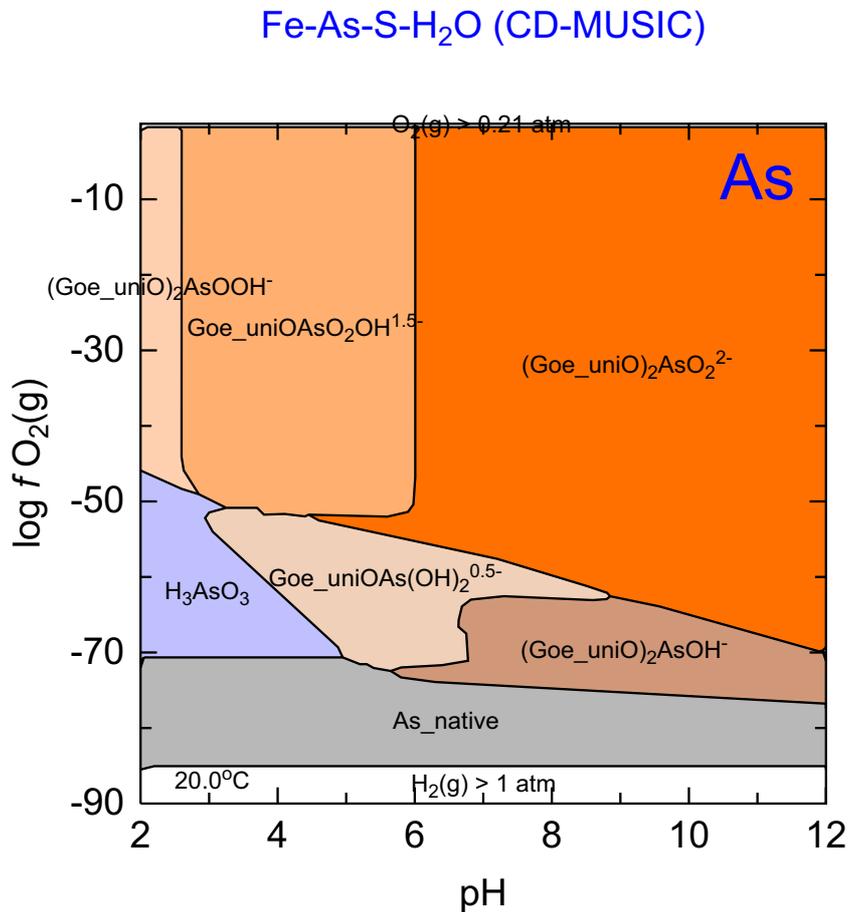
# most likely minerals given the database
  As_native      0 0
# hematite, magnetite removed to make goethite stable
  Orpiment       0 0
  Realgar        0 0
  As2S3(am)     0 0
  Pyrite         0 0
  Arsenolite    0 0
  Claudetite    0 0
  Mackinawite   0 0
  FeS(ppt)      0 0
  Sulfur        0 0
  Fe(OH)3(a)    0 0
  Greigite      0 0
  Scorodite     0 0
  Mirabilite    0 0
  Melanterite   0 0
```

	Thenardite	0	0
	As2O5(cr)	0	0
	Jarosite-Na	0	0
	JarositeH	0	0
#	Goethite	0	0

END



## 16 Fe-S-As (goethite, CD-MUSIC)



C:\PhreePlot\demo\FeAsS-cd-music\FeAsS(cd-music)\_As1.ps

An example of a predominance diagram for As in which the CD-MUSIC model has been used to calculate the adsorption of As(V) and As(III) species on goethite. The CD-MUSIC model parameters were taken from [Stachowicz et al. \(2006\)](#).

This diagram differs from the previous diagram in two main ways: (i) As adsorption has been calculated using the CD-MUSIC model rather than the diffuse layer model; (ii) adsorption is linked to goethite not HFO. Goethite is far less soluble than HFO.

The very insoluble nature of goethite and the strong adsorption of As species to goethite means that adsorbed As predominates throughout most of the domain, more so than for the more soluble HFO. Only under strongly reducing conditions at low pH, and at very high pH, do soluble As species predominate. Reducing conditions and a low pH leads to a marked increase in goethite solubility by reductive dissolution while a high pH leads to a strong electrostatic repulsion of the negatively-charged adsorbed As(V) species and the negatively-charged goethite surface at high pH. This reduces adsorption and so increases the apparent solubility.

```

# predominance diagram for As in the presence of goethite which adsorbs As \
    according to the CD-MUSIC adsorption model

SPECIATION
  calculationType          ht1
  calculationMethod        1
  mainSpecies              As
# range of pH
  xmin                     2.0
  xmax                     12.0
# range of log fO2(g) to control redox
  ymin                     -90.0
  ymax                     0.0
# controls the resolution (big resolution means small step size)
  resolution               101

PLOT
  plotTitle                "Fe-As-S-H<sub>2</sub>O \
                           (CD-MUSIC)"
  xtitle                   pH
  ytitle                   "log <i>f \
                           </i>O<sub>2</sub>(g)"
  extratext                extratextFeAsS.dat

CHEMISTRY

# simulation 1

# standard predominance-calculating file, also sets -high_precision true
include 'ht1.inc'

# CD-MUSIC database, resets convergence criterion, therefore must FOLLOW ht1.inc
include 'cdmusic_hiemstra.dat'

# initial solution calculation
SOLUTION 1
  Temp      20
  pH        1.8
  units     mol/kgw
# total concns
  Fe(2)    3.5e-1
  As       1e-2
# sulphide minerals can form but not adsorb
  S(6)     1e-2
  Na       1e-1
  Cl       8e-1  charge
END

# simulation 2
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis>      0.1

# most likely minerals given the database
  As_native      0 0
# hematite, magnetite removed to make goethite stable
  Orpiment       0 0
  Realgar        0 0
  As2S3(am)     0 0
  Pyrite        0 0
  Arsenolite    0 0
  Claudetite    0 0
  Mackinawite   0 0
  FeS(ppt)     0 0
  Sulfur        0 0
  Fe(OH)3(a)   0 0
  Greigite      0 0

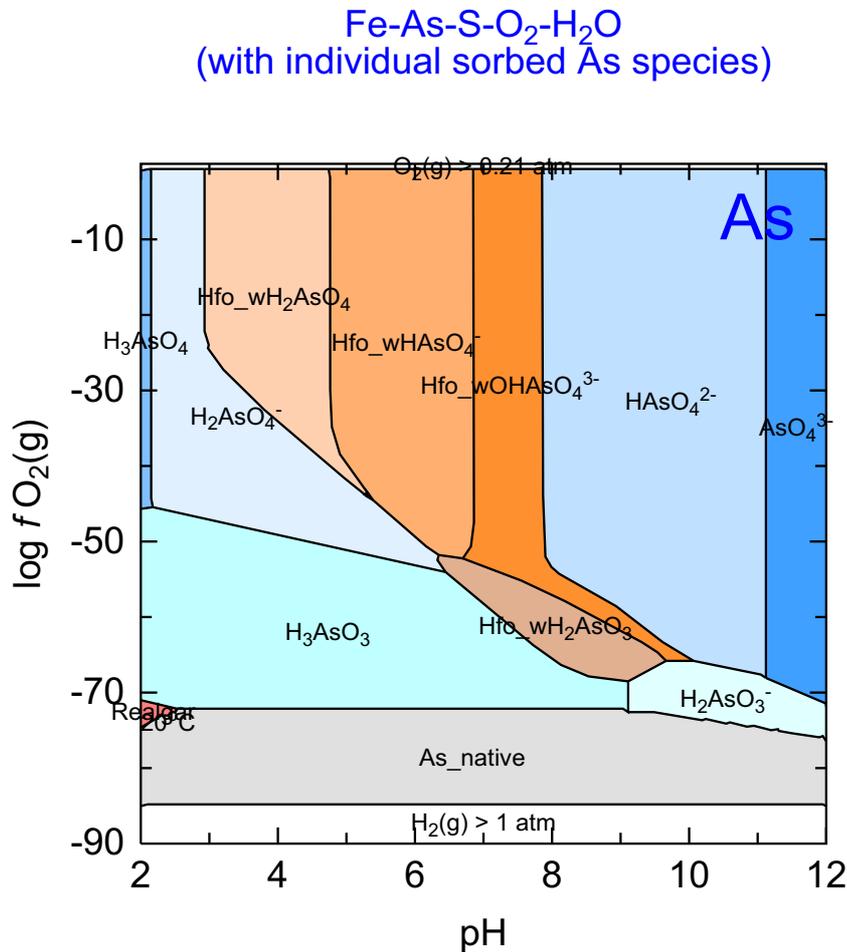
```

```
Scorodite          0 0
Mirabilite         0 0
Melanterite       0 0
Thenardite        0 0
As2O5(cr)         0 0
Jarosite-Na       0 0
JarositeH         0 0
# common Fe oxide under oxidising conditions
  Goethite         0 0
# Magnetite       0 0          # stable below log fO2(g) = -60 \
                             but not in cd-music database (yet) so ignore!!

SURFACE 1
# 3.5 sites/nm2, 98 m2/g, MWt = 88.855 g/mol
  Goe_uniOH1.5 Goethite 0.049886874 8707.79
# 2.7 sites/nm2
  Goe_triOH0.5 Goethite 0.039041901 8707.79
  -cd_music
# C1 C2- (in F/m2)
  -cap 0.85 0.75
  -equil 1
END
```



## 17 Fe-As-S (high Fe)



C:\PhreePlot\demo\FeAsS2\FeAsS2\_As1.ps

This is similar to [Example 13](#) except that the Fe/As mole ratio is 10:1 rather than 35:1 and the As, Fe and S concentrations are an order of magnitude lower. This means that the region where adsorbed As is a dominant species is much smaller and there is also insufficient  $\text{SO}_4^{2-}$  to lead to the precipitation of scorodite. However, realgar – an arsenic sulphide – has a small field at low pH and under strongly reducing conditions.

```

# predominance plot for As including As sorbed by Hfo

SPECIATION
  calculationType          ht1
  calculationMethod        1
# plots for these two species
  mainSpecies              As Fe
  xmin                     2.0
  xmax                     12.0
  ymin                     -90.0
  ymax                     0.0
  resolution               200

PLOT
  plotTitle                "Fe-As-S-O<sub>2</sub>-H<sub>2</sub>O<br>(with
  individual sorbed As species)"
  xtitle                    pH
  ytitle                    "log <i>f </i><sub>2</sub>(g)"
  extraText                 "extratextFeAsS2.dat"

CHEMISTRY

# first simulation

  SOLUTION 1
    Temp      20
    pH        1.8
    units     mol/kgw
    Fe        1e-2
# total concns
  As         1e-3
  S(6)       1e-3
  Na         1e-1
  Cl         1e-1
  SAVE solution 1
  END

# second simulation

# standard predominance plot file
include 'ht1.inc'
# this includes adsorbed species (calcd according to the D&M DLM)
include 'hfo.inc'

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+      -<x_axis> NaOH
  -force_equality true
  O2(g)       <y_axis>          0.1

  As_native          0 0
  Orpiment           0 0
  Realgar            0 0
  As2S3(am)         0 0
  Pyrite            0 0
  Arsenolite        0 0
  Claudetite        0 0
  Mackinawite       0 0
  FeS (ppt)         0 0
  Sulfur            0 0
  Fe(OH)3(a)        0 0
  Greigite          0 0
  Scorodite         0 0
  Mirabilite        0 0
  Melanterite       0 0
  Thenardite        0 0
  As2O5(cr)         0 0
  Jarosite-Na       0 0
  JarositeH         0 0
  END

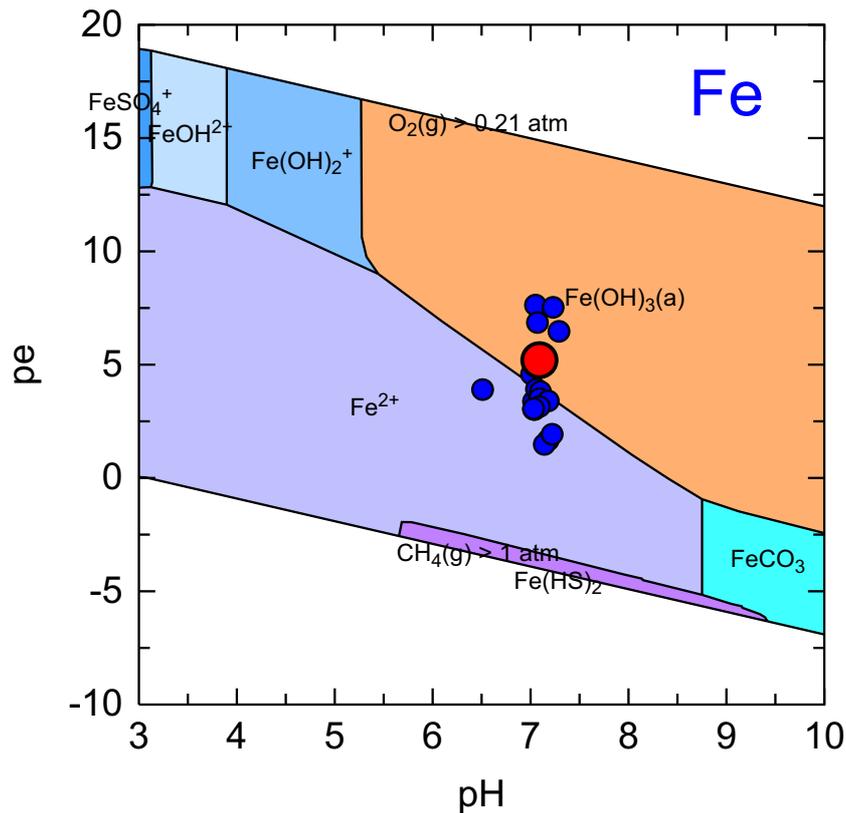
```





## 18 Fe-CO<sub>2</sub>-SO<sub>4</sub>-H<sub>2</sub>O with sample points

### Site 10



C:\PhreePlot\demo\samplepoints\Fesite10\_Fe1.ps

This is a customised predominance plot using the analytical concentrations of elements from a specific groundwater source (shown by the large red filled circle) to construct the predominance diagram. The diagram shows the stability fields for Fe for this water.

It is possible to overlay the plot with symbols designating the pe-pH location of a sequence of sample points, as here, using the [extra](#) keyword. This names a file containing the pH-pe coordinates of the groundwater source in question (in red) as well as of other sources in the same aquifer (displayed in blue).

Because the pH of the various sources is near neutral and the sodium concentration in many of the waters is low, it is necessary to add a source of Na in order to achieve the low pHs by subtracting NaOH. This is achieved by adding a nominal source of 'salt', NaCl. The code for this is in the `PHASES` and `EQUILIBRIUM_PHASES` data blocks. If the interactions of Na or Cl are important in defining the chemistry of interest, perhaps through an ionic strength effect, then non-interacting pseudo-elements can be used instead of Na and Cl (see [Section 6.5.5](#)).

```

# demonstrates how to add sample points to a predominance diagram

SPECIATION
  jobtitle                "Fe at Site 10 compared with other groundwater
sources"
  calculationType         ht1
  calculationMethod       1
  mainspecies             Fe
  xmin                   3
  xmax                   10
  ymin                   -80.0
  ymax                   0.0
  resolution              200

PLOT
  plottitle               "Site 10"
  xtitle                  pH
# tab-delimited
  extrasymbolslines       "extrasymbolslincs.lst.dat" "\t"
  extratext               "extratextmainspecies.dat" "\"
  yscale                  pe

  pxmin                   3
  pxmax                   10
  pxmajor                 1
  pymin                   -10
  pymax                   20

  debug 0

CHEMISTRY

# standard file for making a predominance plot
include 'ht1.inc'

PHASES
Salt
  NaCl = Na+ + Cl-
  log_k 0

# calculates predominance diagram according to these total concns - but only based
# on the 1 sample is not commented out
# this approach means that it is easy to calculate diagrams for the whole set by
# removing the comment from one sample at a time

SOLUTION_SPREAD
NumberDescriptiontempHpeBaCaClO(0)FFeC(4)KMgMnNaN(3)N(5)SiS(6)Sr
mg/kgwmg/kgwmg/kgwmg/kgwmg/kgwmg/kgw as HCO3mg/kgwmg/kgwmg/kgwmg/kgwmg/kgw
mg/kgwmg/kgwmg/kgw as SO4mg/kgw
#1Site 111.27.083.630.03691761140.30.2940.673443.45130.029475.30.120.0773.96166
0.816
#2Site 27.17.033.380.04222091020.170.2030.853554.5412.40.034793.50.09870.2653.7272
0.713
#3Site 310.27.043.020.040818986.20.170.1450.5583456.3611.20.030642.80.03230.264
3.382010.573
#4Site 410.17.014.580.009816855.90.110.2630.03383324.74110.007838.30.05122.553.37
1680.694
#5Site 510.07.063.920.013618459.50.110.3760.1233533.3612.10.011448.60.1230.3413.59
1960.947
#6Site 610.87.181.670.027213246.60.140.5580.4133122.8913.20.006651.90.239-0.054.02
1421.13
#7Site 79.97.141.480.016914246.30.170.2250.6433403.2524.60.006853.90.347-0.054.9
1991.85
#8Site 86.07.033.030.03892041020.310.210.8993794.4312.30.0406910.09750.2093.47262
0.695
#9Site 910.37.057.630.00717055.52.180.10.00253102.717.060.0006626-0.0074.53.22127
0.373
10Site 1010.07.095.200.008317855.62.820.0840.02523102.96.570.003926.7-0.0075.23
3.371310.348

```

```

#11Site 1110.37.296.470.0091176561.890.0950.00253152.857.370.0005327.50.01464.23
3.341340.39
#12Site 1210.27.13.810.006817371.61.340.1350.02513073.076.880.0009540.40.0194.49
3.111370.404
#13Site 1311.07.093.500.0123169588.740.0590.00252634.597.380.0000823.6-0.00716.3
2.91100.27
#14Site 1410.27.221.930.0132176420.210.2720.2093072.688.090.005622.30.0747-0.05
2.741710.679
#15Site 1510.27.183.400.014216845.10.210.3550.1323183.338.480.004729.90.0924-0.05
2.871630.698
#16Site 166.27.093.150.013516055.70.140.2534.233462.6215.10.065736.60.1-0.054.24
1530.81
#17Site 1710.26.513.900.012416645.20.210.3620.3363173.198.330.008429.30.0911-0.05
2.91590.708
#18Site 1810.47.033.060.015917346.70.220.3980.1543143.489.260.004733.20.106-0.05
3.11670.803
#19Site 199.37.237.530.007818145.40.10.2131.363113.17.040.018419.60.0232-0.052.92
1780.538
#20Site 2010.17.076.860.008918344.90.10.2410.1323173.097.390.005920.40.033-0.05
2.911750.602

```

## EQUILIBRIUM\_PHASES 1

```

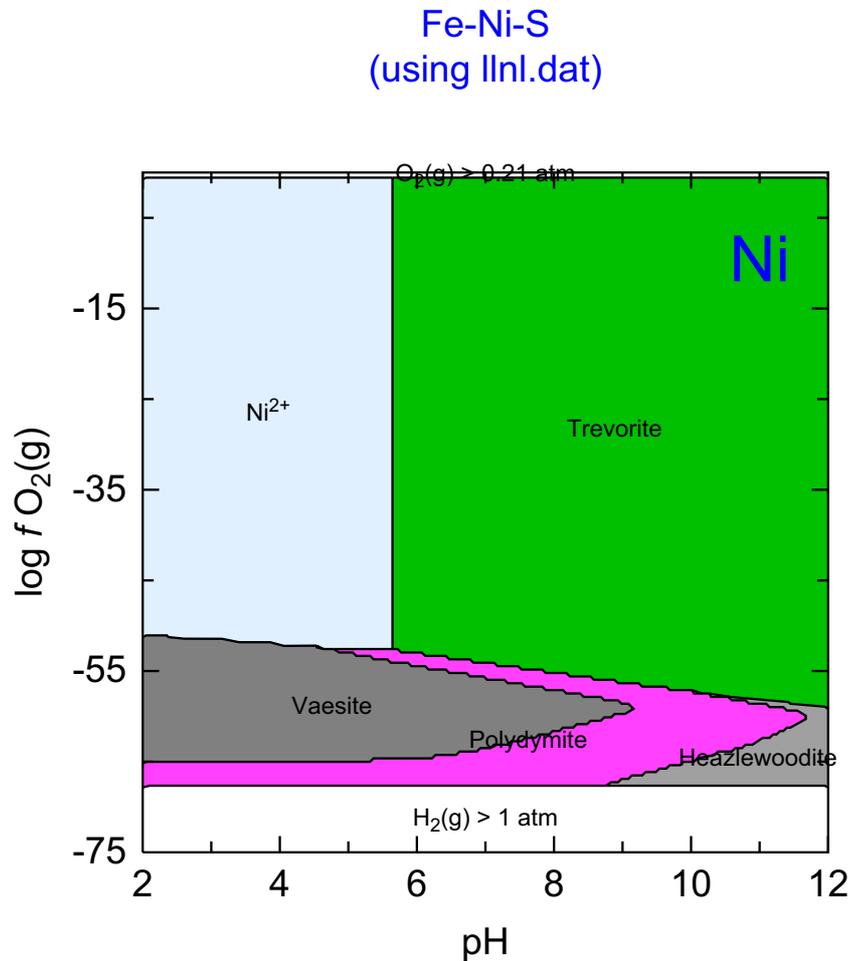
  Fix_H+ -<x_axis> NaOH 10
    -force_equality true
  O2(g) <y_axis> 10
# atmospheric CO2
  CO2(g) -3.5
# this ensures that Na does not run out when fixing low pH's
  Salt -12 10 dissolve

# list of the most probable minerals that might form
  Calcite      0 0
  Gypsum       0 0
  Dolomite     0 0
  Siderite     0 0
  Quartz       0 0
  Fe(OH)3(a)  0 0
  Hausmannite  0 0
  Pyrolusite   0 0
  Manganite    0 0
# disordered
  Rhodochrosite(d) 0 0
  Pyrochroite   0 0
# Birnessite           0 0 # more stable than
Pyrolusite -
  Bixbyite      0 0
  Fluorite      0 0
  Barite        0 0
END

```



# 19 Fe-Ni-S



C:\PhreePlot\demo\FeNiS\FeNiS\_Ni1.ps

This example shows an example of the Fe-Ni-S system with the low-angled wedges characteristic of predominance diagrams involving sulphide minerals.

The 'steppy' nature of the low-angled boundaries could be reduced either by increasing the resolution from 200 to say 500, or by increasing the simplification factor, say from 1 to 3.

If the resolution is increased then it is necessary to start the calculations from scratch.

If only the simplification factor is changed, then it is not necessary to recalculate the speciation rather change [calculationMethod](#) to 3 (resimplify and replot) and change [simplify](#) to 3.

```

SPECIATION
  Database                llnl.dat                # this is a
larger database, meaning more species, meaning slower
  calculationType        ht1
  calculationMethod      1
  mainSpecies            "Ni"
  xmin                   2.0
  xmax                   12.0
  ymin                   -75.0
  ymax                   0.0
  resolution             200

PLOT
  plotTitle              "Fe-Ni-S<br>(using llnl.dat)"
  xtitle                 pH
  ytitle                 "log <i>f </i><sub>2</sub>(g)"
  pointSize              1.5
  extraText              "extratextFeNiS.dat"      # file with
additional text to be added to plot

CHEMISTRY

include 'ht1.inc'                # standard
predominance plot file

# first simulation - initial colution calculation
PHASES
SOLUTION 1
  Temp      80
  pH        1.8
  units     mol/kgw
  density   1
  Fe(2)     1e-3
  Na        1e-1
  Ni        1e-3                # total concns
  S(6)      1e-2
  Cl        1e-1 charge
SAVE solution 1
END

# second simulation - only repeats this simulation while tracking
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH      # drives the x-axis
            -force_equality true
  O2(g)     <y_axis> 0.1        # drives the y-axis

  Polydymite          0 0      # list of possible
minerals
  Vaesite              0 0
  Pyrite               0 0
  Millerite            0 0
  Heazlewoodite       0 0
  Troilite             0 0
  Pyrrhotite          0 0
  Ni                   0 0
  S                    0 0
  Nickelbischofite    0 0
  NiCl2:4H2O          0 0
  NiCl2:2H2O          0 0
  FeO                  0 0
  Fe(OH)2              0 0
  Wustite              0 0
  Goethite             0 0
  Bunsenite            0 0
  Lawrencite           0 0
  Ni(OH)2              0 0
  Fe                   0 0
  NiCl2                0 0

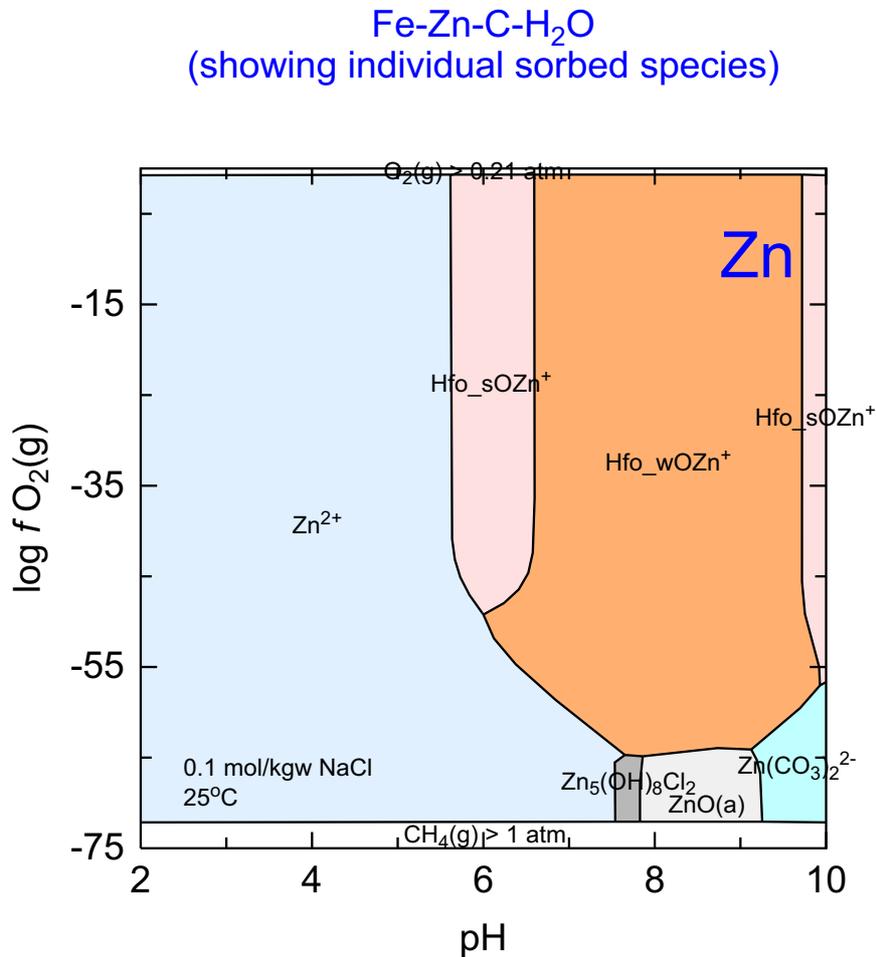
```

Fe(OH)3	0 0
Hematite	0 0
Magnetite	0 0
NaFeO2	0 0
Trevorite	0 0
Molysite	0 0
Melanterite	0 0
Mirabilite	0 0
Morenosite	0 0
NiSO4:6H2O(alpha)	0 0
Na	0 0
Thenardite	0 0
FeSO4	0 0
NiSO4	0 0
Na2O	0 0
Na3H(SO4)2	0 0
Jarosite-Na	0 0
Fe2(SO4)3	0 0

END



## 20 Fe-Zn-C-H<sub>2</sub>O (HFO)



C:\PhreePlot\demo\hfoZnC\hfoZnC\_Zn1.ps

This is a predominance diagram for the Zn-Fe-C-H<sub>2</sub>O system with adsorption of Zn by Hfo and precipitation of ZnO(a).

$\log f \text{CO}_2(\text{g})$  has been fixed at -3.5 subject to the constraint that not more than 1 mole of  $\text{CO}_2(\text{g})$  is used. Many minerals, including many more stable forms of iron oxide and siderite ( $\text{FeCO}_3$ ), have been suppressed for this example. Zn is adsorbed by the Hfo when it is stable. This example uses the 'ht1.inc' include file for sending **PHREEQC** output to **PhreePlot**. All Zn species adsorbed by Hfo have been treated as individual species for the purposes of ranking.

If a combined adsorbed Zn field had been wanted, then the 'ht1combined.inc' include file should have been used rather than 'ht1.inc' (see the next Example).

```

# Zn predominance diagram with Zn adsorbed onto Hfo
# all adsorbed Zn on Hfo are treated as separate species in terms of predominance
(mol) counting

SPECIATION
  pdf                      T
  calculationType          ht1
  calculationMethod        1
# diagram for Zn
  mainSpecies              Zn

# pH (x-axis) range 2-10
  xmin                     2.0
  xmax                     10.0
# log fO2(g) from -75 to 0
  ymin                     -75.0
  ymax                     0.0

# jumps about on a 500 x 500 grid when tracking
  resolution               500

PLOT
  plotTitle                "Fe-Zn-C-H<sub>2</sub><br>(showing individual
sorbed species)"
  xtitle                   pH
  ytitle                   "log <i>f</i> O<sub>2</sub>(g)"
  extraText                "extratexthfoZnC.dat"

CHEMISTRY

# this standard file calculates the predominant species based on
include 'ht1.inc'
# treating all sorbed species as separate species

SOLUTION 1
  pH          1.8
  units       mol/kgw
  Fe(3)       1e-1
  Zn          1e-3
  Na          1e-1
  Cl          1e-1
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
# driven by the x-axis parameters defined above
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
# driven by the y-axis parameters defined above
  O2(g) <y_axis>
# fix log PCO2(g) at -3.5 subject to the constraint that
  CO2(g) -3.5 1
# a maximum of 1 mol CO2 is supplied

# list of possible minerals (many are commented out)
  Fe(OH)3(a) 0 0
#Magnetite 0 0

#Hematite 0 0 # this is likely to be the
stable Fe(III)-oxide mineral

#Goethite 0 0

#Fe(OH)2.7Cl.3 0 0

#Fe3(OH)8 0 0

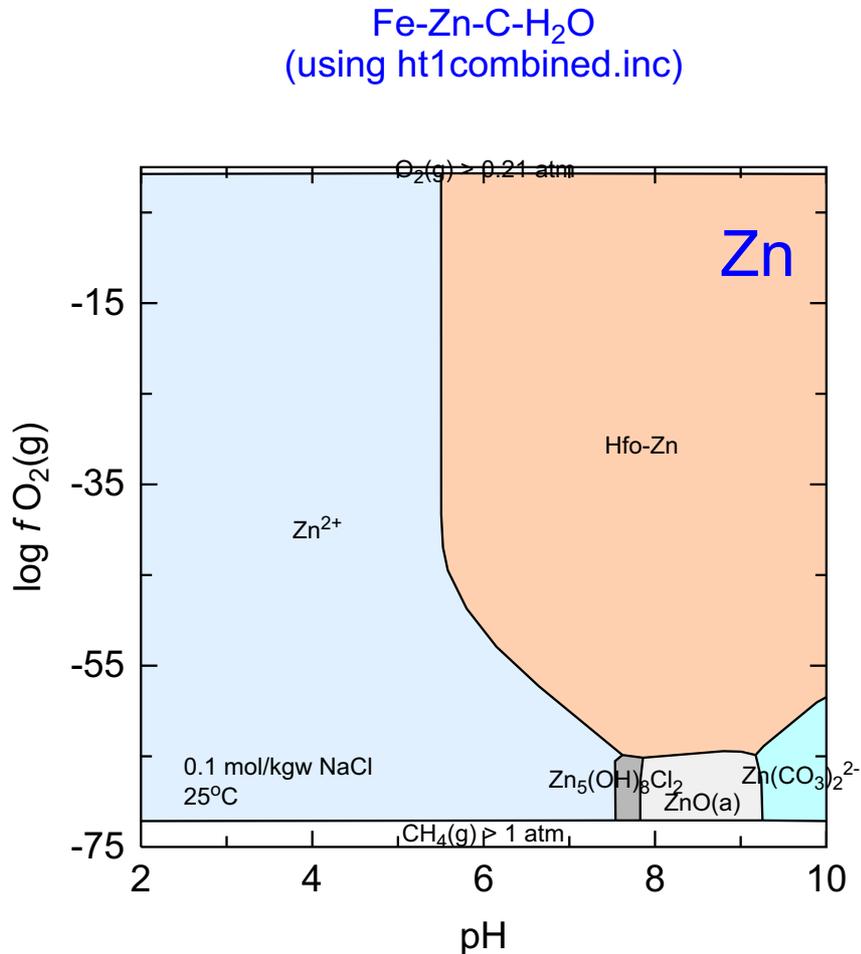
#Siderite 0 0

```

```
#Maghemite          0 0
#Siderite(d) (3)    0 0
  Trona              0 0
  Natron             0 0
  Thermonatrite     0 0
  Nahcolite         0 0
#Zincite(c)         0 0
  ZnO(a)            0 0
#ZnCO3:H2O          0 0
#Zn(OH)2-e          0 0
  Smithsonite       0 0
#Zn(OH)2-g          0 0
#Zn(OH)2-b          0 0
#Zn(OH)2-c          0 0
#Zn(OH)2-a          0 0
#Halite             0 0
  Zn2(OH)3Cl        0 0
  Zn5(OH)8Cl2       0 0
  ZnCl2             0 0
  ZnMetal           0 0
SURFACE 1
# Dzombak & Morel (1990) Hfo database
  Hfo_sOH Fe(OH)3(a)  equilibrium_phase 0.005 53300
  Hfo_wOH Fe(OH)3(a)  equilibrium_phase 0.2
END
```



## 21 Fe-Zn-C-H<sub>2</sub>O (HFO)



C:\PhreePlot\demo\hfoZnCl\hfoZnComb\_Zn1.ps

This is the same as the previous example except that all adsorbed Zn species have been combined into a single composite species, Hfo-Zn, for the purposes of ranking. This makes the diagram somewhat more straightforward in appearance and avoids the division into individual surface species which in many cases is poorly constrained and in any case may only be of interest to the surface chemist. This approach uses the 'ht1combined.inc' include file. The overall area of predominance of the adsorbed species is very similar.

The longer BASIC script required for this approach makes the calculations significantly slower per iteration (some 20% slower), but because the total length of the boundaries is less in the composite approach, the overall computation time is actually slightly faster

```

# Zn predominance diagram with Zn adsorbed onto Hfo
# all adsorbed Zn on Hfo are treated as separate species in terms of predominance
(mol) counting

SPECIATION
  pdf                      T
  calculationType          ht1
  calculationMethod        1
# diagram for Zn
  mainSpecies              Zn

# pH (x-axis) range 2-10
  xmin                     2.0
  xmax                     10.0
# log fO2(g) from -75 to 0
  ymin                     -75.0
  ymax                     0.0

# jumps about on a 500 x 500 grid when tracking
  resolution                500

PLOT
  plotTitle                "Fe-Zn-C-H<sub>2</sub><br>(showing individual
sorbed species)"
  xtitle                   pH
  ytitle                   "log <i>f</i> O<sub>2</sub>(g)"
  extraText                 "extratexthfoZnC.dat"

CHEMISTRY

# this standard file calculates the predominant species based on
include 'ht1.inc'
# treating all sorbed species as separate species

SOLUTION 1
  pH          1.8
  units       mol/kgw
  Fe(3)       1e-1
  Zn          1e-3
  Na          1e-1
  Cl          1e-1
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
# driven by the x-axis parameters defined above
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
# driven by the y-axis parameters defined above
  O2(g) <y_axis>
# fix log PCO2(g) at -3.5 subject to the constraint that
  CO2(g) -3.5      1
# a maximum of 1 mol CO2 is supplied

# list of possible minerals (many are commented out)
  Fe(OH)3(a) 0 0
#Magnetite                      0 0

#Hematite                        0 0      # this is likely to be the
stable Fe(III)-oxide mineral

#Goethite                        0 0

#Fe(OH)2.7Cl.3                   0 0

#Fe3(OH)8                        0 0

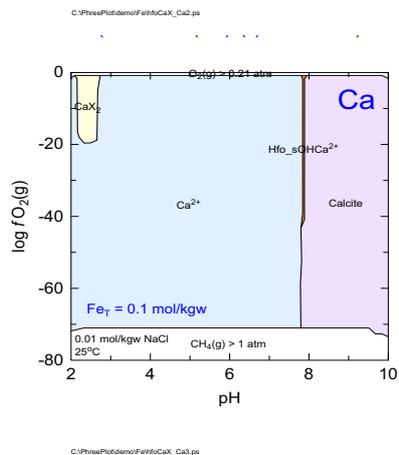
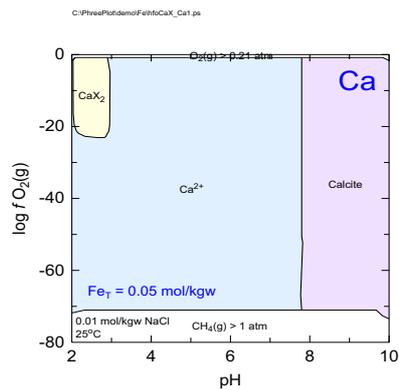
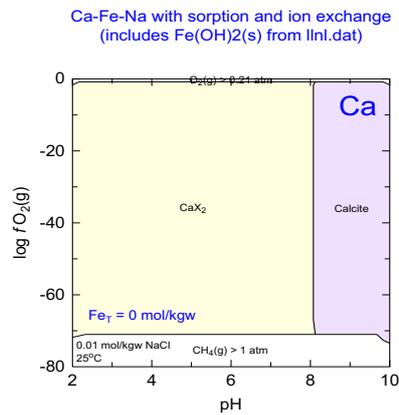
#Siderite                        0 0

```

```
#Maghemite                0 0
#Siderite(d) (3)          0 0
    Trona                  0 0
    Natron                  0 0
    Thermonatrite          0 0
    Nahcolite              0 0
#Zincite(c)               0 0
    ZnO(a)                 0 0
#ZnCO3:H2O                0 0
#Zn(OH)2-e                0 0
    Smithsonite            0 0
#Zn(OH)2-g                0 0
#Zn(OH)2-b                0 0
#Zn(OH)2-c                0 0
#Zn(OH)2-a                0 0
#Halite                   0 0
    Zn2(OH)3Cl             0 0
    Zn5(OH)8Cl2           0 0
    ZnCl2                  0 0
    ZnMetal                0 0
SURFACE 1
# Dzombak & Morel (1990) Hfo database
    Hfo_sOH Fe(OH)3(a)      equilibrium_phase 0.005 53300
    Hfo_wOH Fe(OH)3(a)      equilibrium_phase 0.2
END
```



## 22 Ca-Fe-Na-X-HFO (adsorption and ion exchange)



Shows how Fe, mostly as Fe<sup>2+</sup>, indirectly affects the dominant Ca speciation through Ca<sup>2+</sup>-Fe<sup>2+</sup> competition on the cation exchanger and on Hfo surface sites.

In principle, by combining one or more ion exchangers, some adsorbed species and some mineral species, it is possible to simulate the active species in many soils and sediments.

```

# produces a set of predominance diagrams for Ca using the <loop> variable to sys-
tematically vary the total Fe in the system
# system contains a reduced Fe mineral

# Ca is present in solution, on an ion exchanger (eg clay), sorbed by Fe(OH)3(a) and
potentially in a mineral (calcite)

SPECIATION
  jobTitle                "Fe-Ca-H2O redox"
  calculationType         ht1                                #
produce a predominance diagram using the hunt and track approach
  calculationMethod       1
  mainSpecies             Ca  Fe                            #
diagram for Ca
  xmin                    2.0                              # pH
range adjusted through the <x_axis> variable
  xmax                    10.0
  ymin                    -80.0                            #
f(O2(g)) range adjusted through the <y_axis> variable
  ymax                    0.0
  resolution               50                              # low
resolution - jumps around on a 50 x 50 grid

  loopMin                 0.0                              # min,
max and step size for FeT (the z-loop variable)
  loopMax                 0.1
  loopInt                 5.0E-02

PLOT
  plotTitle               "Ca-Fe-Na with sorption and ion
exchange<br>(includes Fe(OH)2(s) from llnl.dat)"
  xtitle                  pH
  ytitle                  "log <i>f</i> O<sub>2</sub>(g)"
  pxmax                   10.0
  extraText               "extratextFeOHCa.dat"           #
additional text on the plot

  multipageFile           F                                # each
plot in a separate file

CHEMISTRY

include 'ht1.inc'                                             #
standard predominance calculating file

PHASES                                                         #
temporarily add this to the database
Fe(OH)2(a) # from llnl.dat (NB approximate only - not checked for consistency)
  Fe(OH)2 + 2.0000 H+ = + 1.0000 Fe++ + 2.0000 H2O
  log_k              13.9045
  -delta_H           -95.4089 kJ/mol # Calculated enthalpy of reaction
  -analytic          -8.6666e+001 -1.8440e-002 7.5723e+003 3.2597e+001 1.1818e+002

SOLUTION 1
  temp              25
  pH                1.5
  units             mol/kgw
  Fe(3)            <loop>                                # FeT
is controlled by the <loop> variable
  Na               1e-2
  Cl               1e-2 charge
  Ca               1e-3                                    # CaT

EXCHANGE
  -equilibrate 1
  X 0.02                                                  # 0.02
equiv of an exchanger

EQUILIBRIUM_PHASES 1

```

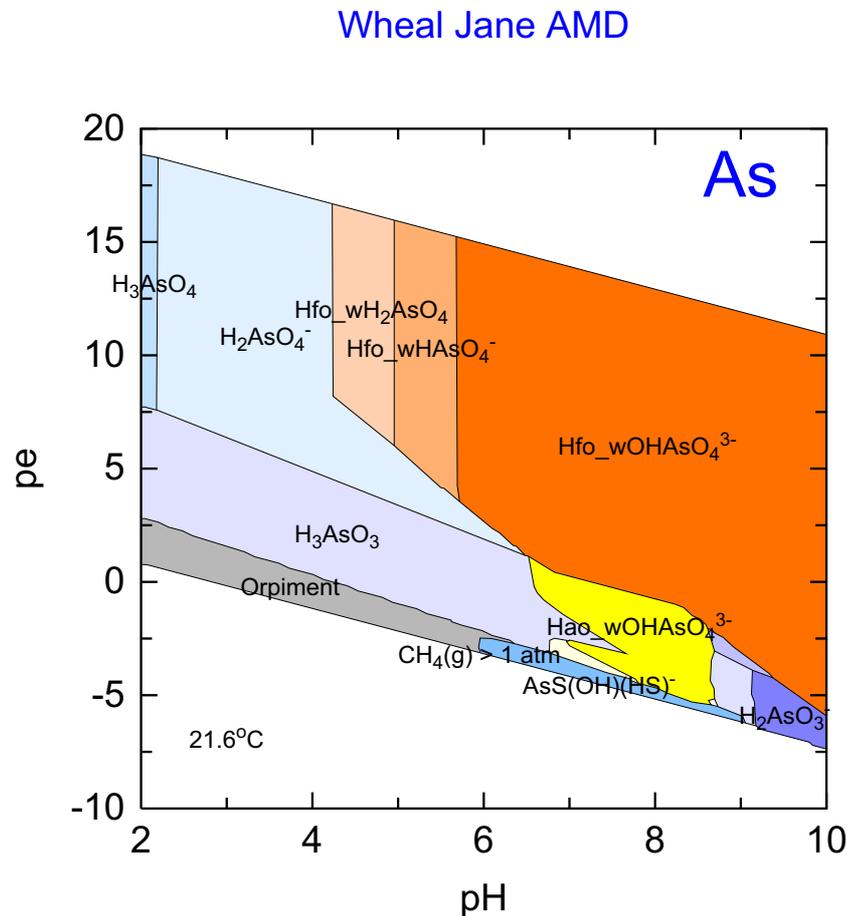
```
Fix_H+ -<x_axis> NaOH # x-
axis is pH
-force_equality true
O2(g) <y_axis> # y-
axis is log fO2(g)
CO2(g) -2 0.3 # soil
PCO2 - max CO2 supplied is 0.3 mol

Fe(OH)3(a) 0 0 #
possible minerals
Fe(OH)2(a) 0 0 # ...
added to database above
Calcite 0 0

SURFACE 1
Hfo_sOH Fe(OH)3(a) equilibrium_phase 0.005 53300
Hfo_wOH Fe(OH)3(a) equilibrium_phase 0.2
END
```



## 23 Acid mine drainage



C:\PhreePlot\demo\wjl\wjl\As\_As1.ps

This example shows the results of a predominance calculation starting with a water with a complex composition – it starts with some acid mine drainage (AMD). It is assumed that there is adsorption of As by HFO (hydrous ferric oxide) and HAO (hydrous aluminium oxide) and equilibrium with CO<sub>2</sub>(g) subject to a constraint on the total amount of CO<sub>2</sub>(g) used (simulating poor pathways for gas migration).

The `wateq4f.dat` database is used for most of the thermodynamic data. There is no established database for metal adsorption by HAO and so we have adjusted the HFO database for a higher pzc and reduced specific surface area. This is only very approximate but is included to show the possible impact of HAO. In this case, HAO becomes the dominant As species under reducing conditions where HFO is no longer stable. An optimised HAO database is required before taking the results of these calculations any further. This example is slow to calculate because of the complexity of the calculations – there are many mineral and adsorbed species.

This diagram is just for As but a better appreciation of the reactions can be achieved by viewing the diagrams for other elements. The following example is a diagram for C calculated for the same overall conditions as for As above.

```

SPECIATION
  jobTitle           "WJ AMD"
  Database           "wateq4fhao.dat"
  calculationType    ht1
  calculationMethod  1
  mainSpecies        As
  xmin               2.0
  xmax               10.0
  ymin               -80.0
  ymax               0.0
  resolution         200

PLOT
  plotTitle          "Wheal Jane AMD"
  xtitle             pH
  yscale             pe
  pymin              -10
  lineWidth          0.1
  minimumAreaForLabeling 1
  extraText          "extratextwj.dat"

CHEMISTRY

include 'ht1.inc'

PRINT
  -reset false

PHASES
Hydrozincite
  Zn5(OH)6(CO3)2 + 10H+ = 5Zn+2 + 2CO2 + 8H2O
#9.15
  log_k 45.75
#Preis & Gamsjager 2001
  -delta_H -256.5 kJ

# complex water chemistry
SOLUTION 1 WJ1
  temp      21.6
  pH        3.5
#100mV from other sample
  pe        1.69
# redox     pe
  units     mg/L
  density   1
# Alkalinity 12.7 as HCO3- #probably Al
  C      10 as H2CO3 CO2(g) -2
  Cl     179
  F      44
#reduction of this produces a lot of OH- 1390
  S(6) 1390 as SO4
  Ca    191
  Mg    43
  Na    93
  K     12
#25 really
  Al    25
  Si    11.0
  Sr    1.87
  Ba    0.052
  Li    2.7
  Fe    346
  Mn    19.7
  As    2.1
  Zn    125
# kg
  -water 1
SAVE solution 1
END

```

```

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+  -<x_axis> NaOH      10
          -force_equality true
  O2(g)   <y_axis> 0.1
# gives CH4 and can reduce to native As
  CO2(g)  -3.5  0.01
# maintains Na in the system for functioning of Fix_H+
  Halite  -6.34 10

Al(OH)3(a)0 0
As_native0 0
Ba3(AsO4)20 0
Barite 0 0
Calcite      0 0
Dolomite0 0
Fe(OH)3(a)0 0
Fluorite0 0
Halloysite0 0
Hausmannite0 0
Hydrozincite0 0
Jarosite(ss)0 0
JarositeH0 0
Jarosite-Na0 0
Manganite0 0
Orpiment0 0
Pyrite 0 0
Pyrochroite0 0
Pyrolusite0 0
Realgar0 0
Rhodochrosite0 0
Siderite0 0
Sphalerite0 0
Strontianite0 0
ZnO(a)0 0

SURFACE 1
# standard Hfo of D&M
  Hfo_sOH Fe(OH)3(a)      equilibrium_phase 0.005 53300
  Hfo_wOH Fe(OH)3(a)      equilibrium_phase 0.2

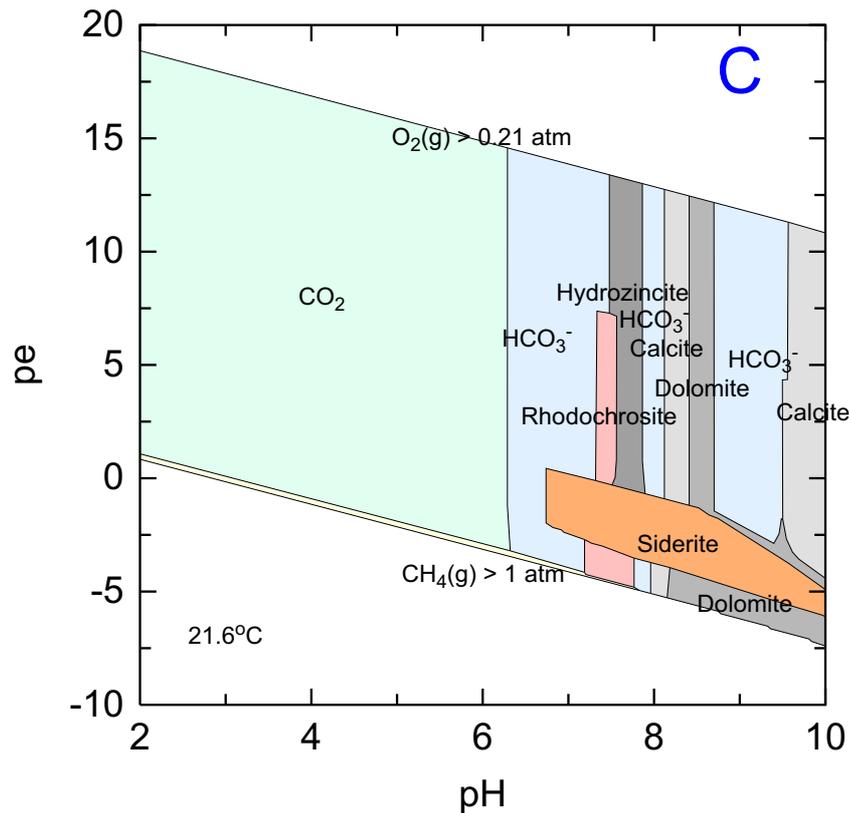
# glorified guesswork only
  Hao_sOH Al(OH)3(a)      equilibrium_phase 0.005 7800
  Hao_wOH Al(OH)3(a)      equilibrium_phase 0.2
END

```



## 24 AMD (carbon)

### Wheal Jane AMD



C:\PhreePlot\demo\wjl\wjc\_C1.ps

This diagram has been calculated for the same conditions as in the previous example but is for C rather than As. This has been done by changing the value of [mainspecies](#) from As to C.

The computations are slow because of the large number of mineral boundaries and possible minerals.

There are many fields close together at high pH which makes labelling difficult. Some of the species have several fields, e.g. HCO<sub>3</sub><sup>-</sup> and the fields are small. Therefore the number of labels plotted has been reduced by changing the [minimumAreaForLabeling](#) from 0.1% (the default set in `pp.set`) to 1%.

```

SPECIATION
  jobTitle                "WJ AMD"
# includes Hao surface definitions
  Database                "wateq4fhao.dat"
  calculationType         ht1
  calculationMethod       1
  mainSpecies             C
  xmin                    2.0
  xmax                    10.0
# use PO2(g) to control redox
  ymin                    -80.0
  ymax                    0.0
  resolution              250

PLOT
  plotTitle               "Wheal Jane AMD"
  xtitle                  pH
# use pe scale
  yscale                  pe
# minimum pe on plot
  pymin                   -10
  lineWidth               0.1
# don't label small fields (diagram v complex)
  minimumAreaForLabeling 1
  extraText               "extratextwj.dat"

CHEMISTRY

include 'ht1.inc'

PRINT
  -reset false

PHASES
# a possibility
Hydrozincite
  Zn5(OH)6(CO3)2 + 10H+ = 5Zn+2 + 2CO2 + 8H2O
#9.15
  log_k 45.75
#Preis & Gamsjager 2001
  -delta_H -256.5 kJ

SOLUTION 1 WJ1
  temp      21.6
  pH        3.5
# 100 mV from other sample
  pe        1.69
# redox     pe
  units     mg/L
  density   1
# Alkalinity 12.7 as HCO3-
  C 10 as H2CO3 CO2(g) -2
  Cl 179
  F 44
#reduction of this produces a lot of OH- 1390
  S(6) 1390 as SO4
  Ca 191
  Mg 43
  Na 93
  K 12
# 25 really
  Al 25
  Si 11.0
  Sr 1.87
  Ba 0.052
  Li 2.7
  Fe 346
  Mn 19.7
  As 2.1
  Zn 125

```

```

# kg
-water 1
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+  -<x_axis> NaOH 10
  -force_equality true
  O2(g)  <y_axis> 0.1
# gets CH4 and native As
  CO2(g) -3.5 0.01
  Halite -6.34 10

# possible minerals
Al(OH)3(a) 0 0
As_native 0 0
Ba3(AsO4)20 0
Barite 0 0
Calcite 0 0
Dolomite 0 0
Fe(OH)3(a) 0 0
Fluorite 0 0
Halloysite 0 0
Hausmannite 0 0
Hydrozincite 0 0
Jarosite(ss) 0 0
JarositeH 0 0
Jarosite-Na 0 0
Manganite 0 0
Orpiment 0 0
Pyrite 0 0
Pyrochroite 0 0
Pyrolusite 0 0
Realgar 0 0
Rhodochrosite 0 0
Siderite 0 0
Sphalerite 0 0
Strontianite 0 0
ZnO(a) 0 0

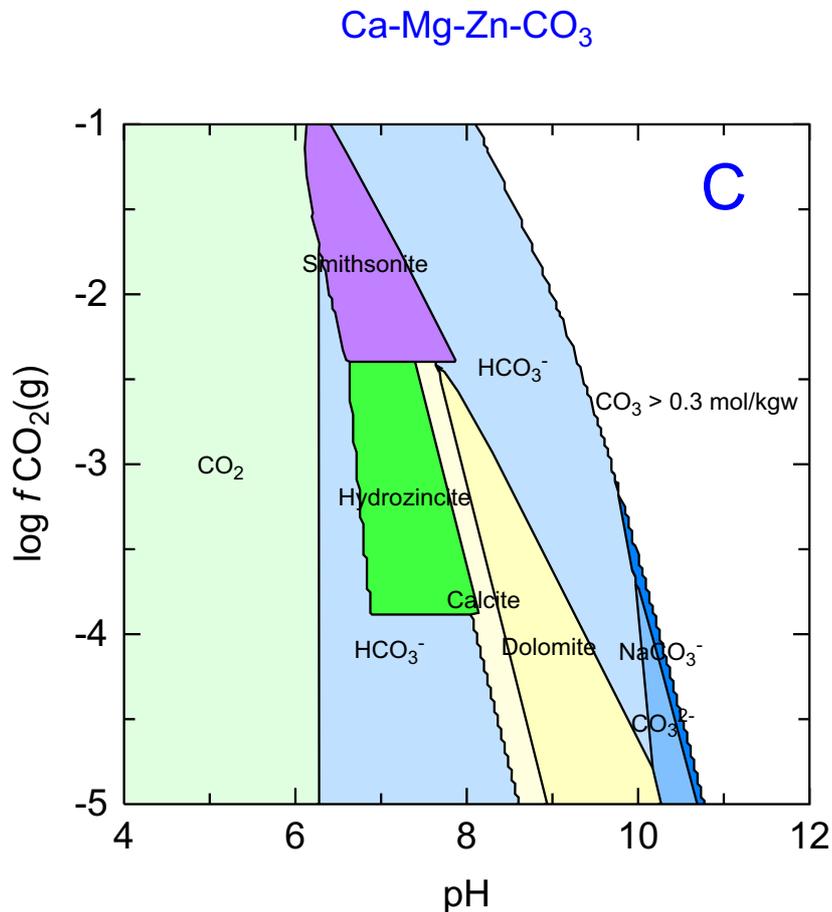
# two surfaces
SURFACE 1
  Hfo_sOH Fe(OH)3(a) equilibrium_phase 0.005 53300
  Hfo_wOH Fe(OH)3(a) equilibrium_phase 0.2

# mainly guesswork but would be wrong to ignore completely
  Hao_sOH Al(OH)3(a) equilibrium_phase 0.005 7800
  Hao_wOH Al(OH)3(a) equilibrium_phase 0.2
END

```



## 25 Ca-Mg-Zn-CO<sub>3</sub>



C:\PhreePlot\demo\CaMgZn\carbonates\_C1.ps

This example shows the use of a user-defined constraint to cut off part of the diagram, namely the region at high pH where the total carbonate concentration is greater than 0.3 mmol/kg water. This is done in the `ht1combinedCO3.inc` file by adding an additional constraint to the type 3 (constraints) section of the `ht1` code:

```
581 IF(TOT("C")/h2o > 0.3) THEN 582 ELSE 590
582 PUNCH "CO3 > 0.3 mol/kgw",TOT("C")/h2o
583 nout3 = nout3+1
```

This approach is exactly the same as that used for identifying the normal oxygen and hydrogen constraints for defining the 'water limits'. The area where the constraint applies is treated just like any other field. It inherits its name from the column heading written by the `ht1combinedCO3.inc` file and the colour from the fill colour dictionary.

The [simplify](#) keyword could be used to reduce the steps seen in some of the field boundaries. This is done by changing the `simplify` setting from its default value of 1 to a greater value, say 2.

```

SPECIATION
  jobTitle                "C predominance in the presence of selected
Ca, Mg and Zn carbonates"
  calculationType          ht1
  calculationMethod        1
  mainSpecies              C
  xmin                     4.0
  xmax                     12.0
  ymin                     -5.0
  ymax                     -1.0
  resolution                200
PLOT
  plotTitle                "Ca-Mg-Zn-CO<sub>3</sub>"
  xtitle                   pH
  ytitle                   "log <i>f</i> CO<sub>2</sub>(g)"
  simplify                  1.0
  extraText                 "extratextcarbonates.dat"

CHEMISTRY

PHASES
Fix_H+
  H+ = H+
  log_k 0.0
Hydrozincite
  Zn5(OH)6(CO3)2 + 10H+ = 5Zn+2 + 2CO2 + 8H2O
#9.0
  log_k 45.0
#Preis & Gamsjager 2001
  -delta_H -256.5 kJ
SELECTED_OUTPUT
  -high_precision true
  -reset false

# includes CO2 constraint
include 'ht1combinedCO3.inc'

SOLUTION 1
  temp      25
  pH        7
  pe        5
  redox     pe
  units     mmol/kgw
  density   1
# kg
  -water    1
  Ca        5
  Mg        2
  Zn        5
  Cl        24 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
# ... but no Na present as a background electrolyte
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) -0.68 0.1
# limit at high pH (corners)
  CO2(g) <y_axis> 2

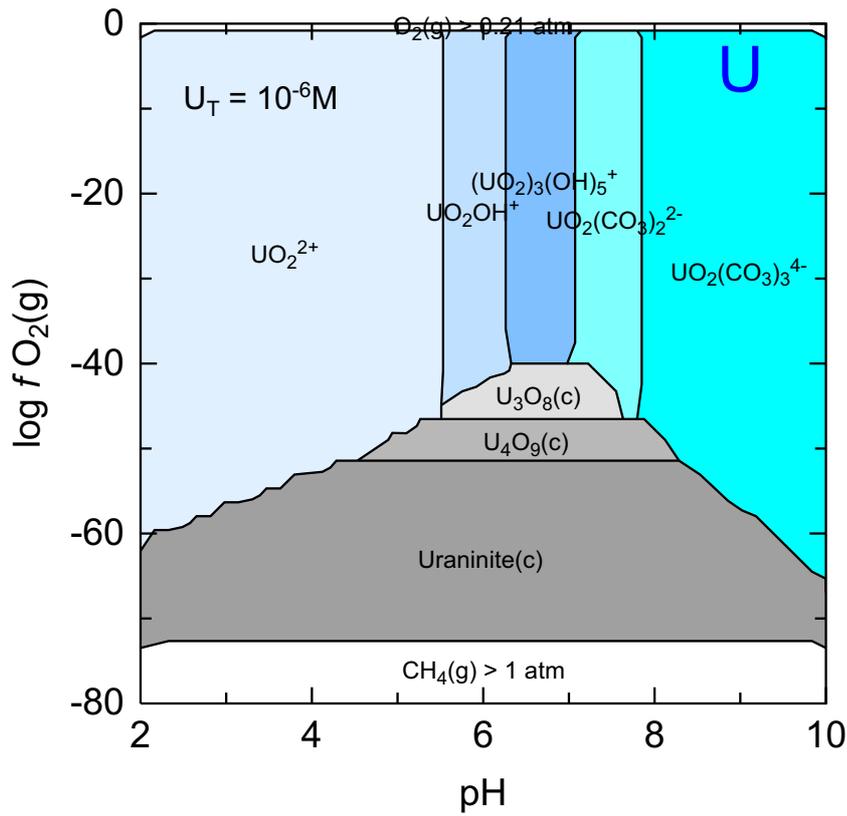
# This is necessary to provide a source of Na for Fix_H+ when it goes -ve
  Halite -12 0.1

#ZnCO3:H2O                0 0
Dolomite                   0 0
Calcite                     0 0
Smithsonite                 0 0
#Aragonite                  0 0

```

#Dolomite (d)	0 0
Magnesite	0 0
Zincite (c)	0 0
ZnO (a)	0 0
#Zn(OH)2-e	0 0
#Zn(OH)2-g	0 0
#Zn(OH)2-b	0 0
#Natron	0 0
#Zn(OH)2-c	0 0
#Nesquehonite	0 0
#Zn(OH)2-a	0 0
Hydrozincite	0 0
#Huntite	0 0
Brucite	0 0
#Artinite	0 0
Portlandite	0 0
#Zn2(OH)3Cl	0 0
#Hydromagnesite	0 0
#Zn5(OH)8Cl2	0 0
#ZnCl2	0 0
#ZnMetal	0 0
END	



26 U-CO<sub>3</sub>Uranium hydrolysis and redox  
(low resolution=50)

C:\PhreePlot\demo\UCO3\UCO3\_U1.ps

This is a low resolution plot (`resolution = 50`), hence the uneven boundaries. A low resolution is useful for quickly seeing what is involved before replotting at a higher resolution.

```

SPECIATION
  jobTitle          "Uranium redox and speciation"
  calculationType   "ht1"
  calculationMethod 1
  mainSpecies       "U"
  xmin              2.0
  xmax              10.0
  ymin              -80.0
  ymax              0.0
  loopmin           -6
  loopmax           -6
  loopint           0
  looplogvar        1
  resolution        50

PLOT
  plotTitle         "Uranium hydrolysis and redox<br>(low reso-
lution=50)"
  xtitle            "pH"
  ytitle            "log <i>f</i> O<sub>2</sub>(g)"
  extraText         "extratextUCO3.dat"

CHEMISTRY

include 'ht1.inc'

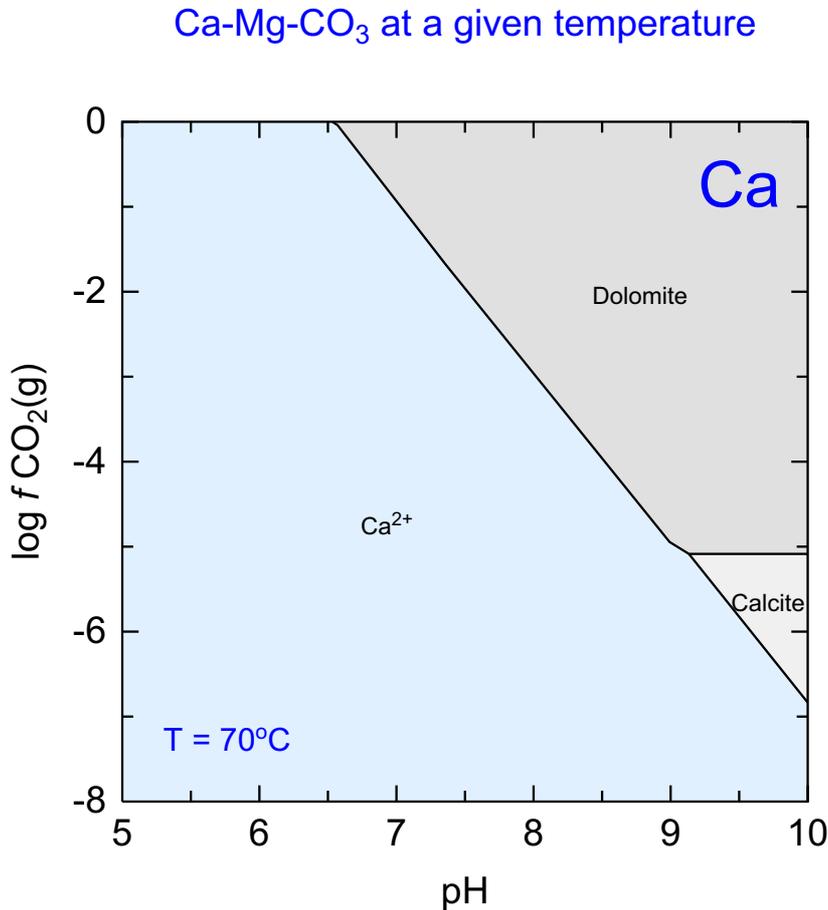
SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  U <loop>
  Na 1e-1
  Cl 1e-1
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ <x_axis> NaOH 10
    -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

  B-UO2(OH)2 0 0
  Gummite 0 0
  Na4UO2(CO3)3 0 0
  Nahcolite 0 0
  Natron 0 0
  Rutherfordine 0 0
  Schoepite 0 0
  Thermonatrite 0 0
  Trona 0 0
  U3O8(c) 0 0
  U4O9(c) 0 0
  UO2(a) 0 0
  UO3(gamma) 0 0
  Uraninite(c) 0 0
END

```

## 27 Ca-Mg-CO<sub>3</sub> at high T



This example shows how temperature affects calcite-dolomite stability as a function of pH and CO<sub>2</sub>(g) partial pressure. The results are shown as a series of predominance diagrams. The temperature varies from 0 to 80°C in increments of 10°C. This is achieved by using [loopMin](#), [loopMax](#) and [loopInt](#) to define the looping variable <loop>. This loop variable is then equated to <temp> in the [numericTags](#) definition (for convenience) and <temp> is substituted in the appropriate place in the SOLUTION definition below.

The [extraText](#) file includes a line which uses <temp> to write the current temperature in the bottom left of each plot.

The [multiPageFile](#) setting has been set to true so that only one plot file is recorded. This contains the nine plots, page by page. The plot above is for the eighth plot which is for 70°C.

```

SPECIATION
  calculationType          ht1
  calculationMethod        1
  mainSpecies              Ca
  xmin                     5.0
  xmax                     10.0
  ymin                     -8.0
  ymax                     0.0
  loopMin                  0
  loopMax                  80
  loopInt                  10
  resolution               200
# change this for different temperatures
  numericTags              <temp> = <loop>

PLOT
  multiPageFile            true
  plotTitle                "Ca-Mg-CO<sub>3</sub> at a given temperature"
  xtitle                   pH
  ytitle                   "log <i>f</i> CO<sub>2</sub>(g)"
# includes the <temp> tag for putting temperature on plot
  extraText                "extratextcalcite.dat"

CHEMISTRY

# standard 'hunt and track' file
include ht1.inc

SOLUTION 1
  temp                    <temp>
  pH                      7
  units                   mmol/kgw
  density                 1
# kg
  -water                  1
  Ca                      1
  Mg                      1
  Na                      100
  Cl                      100
SAVE solution 1
END

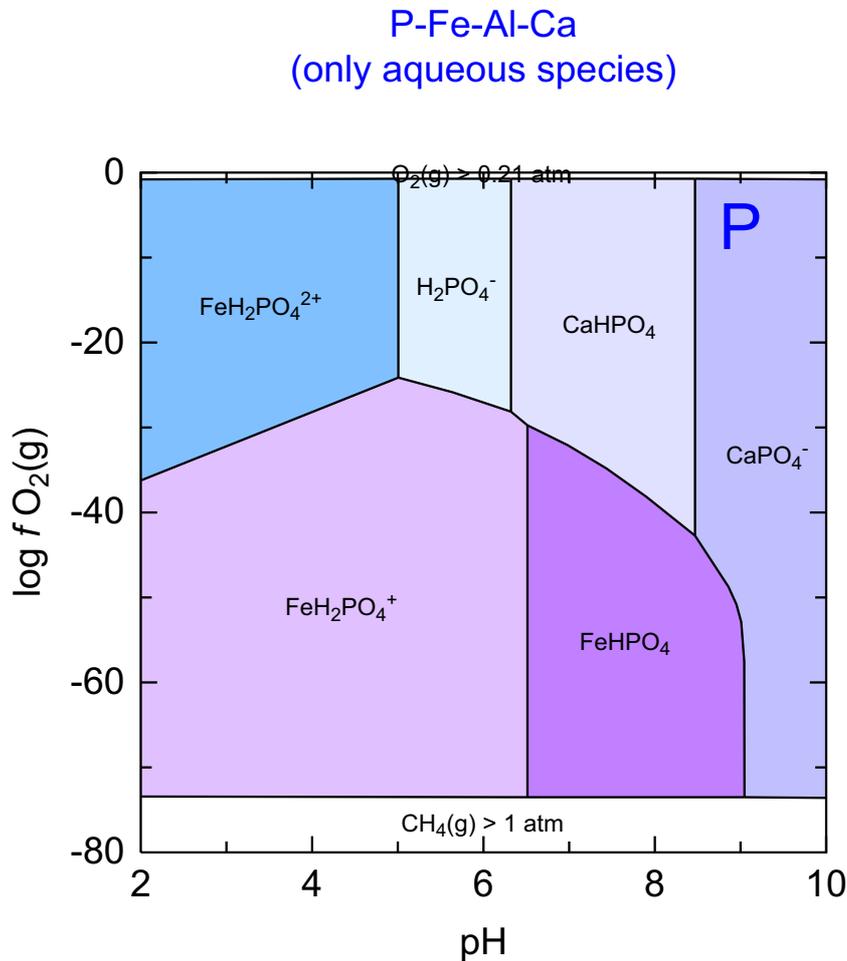
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+                  -<x_axis> NaOH 10
  -force_equality true
# limit CO2 supply at high pH
  CO2(g)                  <y_axis> 1

  Brucite                  0 0
  Calcite                  0 0
  Aragonite                0 0
  Magnesite                0 0
  Dolomite                 0 0
#Dolomite (d)             0 0

  Artinite                 0 0
  Nesquehonite             0 0
  Portlandite              0 0
  Huntite                  0 0
  Nahcolite                0 0
  Hydromagnesite           0 0
  Natron                   0 0
  Thermonatrite            0 0
  Trona                    0 0
END

```

## 28 P-Ca-Mg-CO<sub>3</sub>(aq)



C:\PhreePlot\demo\PIPaq\_P1.ps

A  $\log f_{\text{O}_2(\text{g})}$ -pH predominance diagram for phosphorus in the P-Fe-Al-Ca system. It is for aqueous species only – this is determined by the lack of any P (or other) minerals in the `EQUILIBRIUM_PHASES` data block. In that sense, the diagram is unrealistic since many minerals would precipitate at various places within the domain explored. This can be seen in the next example.

```

SPECIATION
  jobTitle           "Fe-Al-Ca-P"
  calculationType    ht1
  calculationMethod  1
  mainSpecies        "P"
  xmin               2.0
  xmax               10.0
  ymin               -80.0
  ymax               0.0
  resolution         500

PLOT
  plotTitle          "P-Fe-Al-Ca<br>(only aqueous species)"
  xtitle             pH
  ytitle             "log <i>f </i>O<sub>2</sub>(g)"
  extraText          "extratextP.dat"

CHEMISTRY

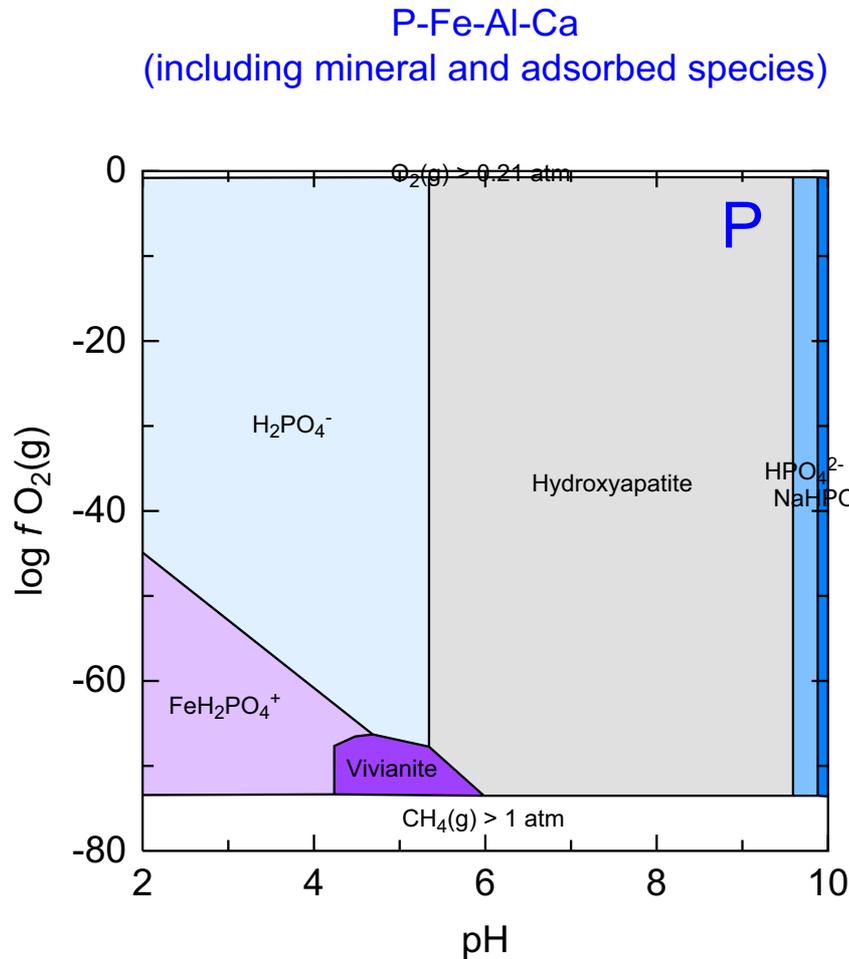
include 'ht1.inc'

# first simulation - initial solution calculation
SOLUTION 1
  Temp      20
  pH        1.8
  units     mol/kgw
  density   1
  P         1e-3
  Ca        1e-1
  Fe        1e-1
  Al        1e-1
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

# second simulation - reaction and equilibration
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis>
# no minerals - aqueous species only
  CO2(g)    -3.5
END

```

## 29 P-Ca-Mg-CO<sub>3</sub> (with solids)



This diagram is for similar conditions to the previous example but crucially a variety of minerals has been allowed to precipitate and P adsorption onto HFO has been taken into account. There has been a deliberate policy of only allowing the more soluble (less stable) minerals to precipitate so for example, the more stable iron oxides such as hematite and goethite have been removed from consideration by commenting them out.

Adsorbed P dominates in the region where  $\text{Fe}(\text{OH})_3(\text{a})$  is stable. Under acid, oxidising conditions where  $\text{Fe}(\text{OH})_3(\text{a})$  dissolves, strengite ( $\text{Fe}(\text{III})\text{PO}_4 \cdot 2\text{H}_2\text{O}$ ) is stable. Under reducing conditions, vivianite ( $\text{Fe}(\text{II})_3(\text{PO}_4)_2 \cdot 8\text{H}_2\text{O}$ ) and hydroxyapatite ( $\text{Ca}_5(\text{PO}_4)_3\text{OH}$ ) precipitate.

Dissolved P species only predominate under some of the most extreme conditions of high pH and strongly reducing conditions. The presence of  $\text{CO}_2(\text{g})$  leads to calcite precipitation above pH 7.6 which ultimately leads to the lowering of the  $\text{Ca}^{2+}$  activity to such an extent that hydroxyapatite becomes unstable.

```

SPECIATION
  jobTitle                "Fe-Al-Ca-P"
  calculationType         ht1
  calculationMethod       1
  mainSpecies             "P"
# x-axis calculation range
  xmin                    2.0
  xmax                    10.0
# y-axis calculation range
  ymin                    -80.0
  ymax                    0.0
# tracks on a 500 x 500 grid
  resolution              500
PLOT
  plotTitle               "P-Fe-Al-Ca<br>(including mineral and adsorbed
species)"
  xtitle                  pH
  ytitle                  "log <i>f </i><sub>2</sub>(g)"
  extraText               "extratextP.dat"

CHEMISTRY

include 'ht1.inc'

# first simulation - initial solution calculation
SOLUTION 1
  Temp      20
  pH        1.8
  units     mol/kgw
  density   1
  P         1e-3
  Ca        1e-1
  Fe        1e-1
  Al        1e-1
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

# second simulation - reaction and equilibration

USE solution 1

EQUILIBRIUM_PHASES 1
# fix the pH
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis>
# atmospheric PCO2(g)
  CO2(g)    -3.5

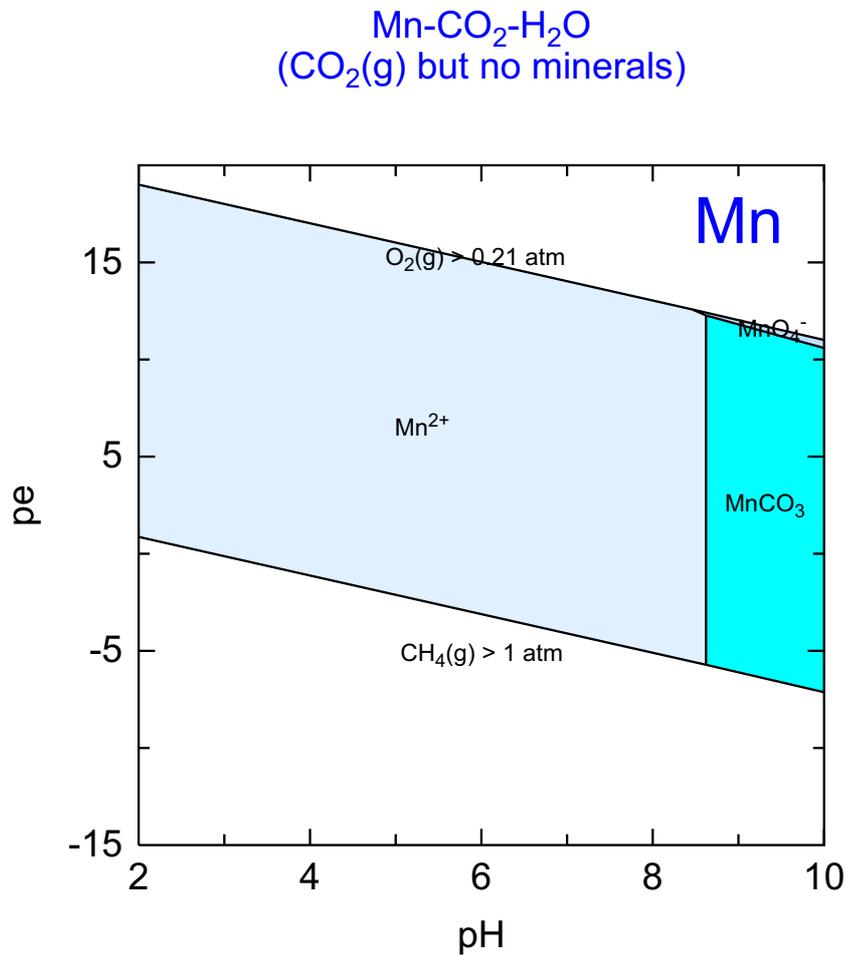
# choose the minerals you want (from the database)
  Hydroxyapatite      0 0
# Magnetite           0 0
  Hematite            0 0
  Vivianite           0 0
# Fe3(OH)8           0 0
# Goethite            0 0
# Fe(OH)2.7Cl.3      0 0
# Diaspore            0 0
# Gibbsite            0 0
# Maghemite           0 0
# Boehmite            0 0
  Al(OH)3(a)          0 0
# assumed the metastable Fe-oxide mineral
  Fe(OH)3(a)          0 0
  Portlandite         0 0
  Strengite           0 0
  Calcite             0 0
  Siderite            0 0

```

```
SURFACE
# phosphate adsorbed by Hfo
  Hfo_sOH Fe(OH)3(a)    equilibrium_phase 0.005 53300
  Hfo_wOH Fe(OH)3(a)    equilibrium_phase 0.2
END
```



## 30 Mn-CO<sub>2</sub>-H<sub>2</sub>O (no minerals)



This is a pe-pH predominance diagram for Mn in which no minerals have been allowed to precipitate. The system is in equilibrium with CO<sub>2</sub>(g) at close to its atmospheric partial pressure making MnCO<sub>3</sub>(aq) stable at high pH where carbonate activities are high.

Permanganate (MnO<sub>4</sub><sup>-</sup>) becomes stable in a small region at high pH and under strongly oxidising conditions.

This is an example where the hunt and track algorithm has to automatically readjust the resolution in order to track the boundaries properly. It increases the resolution from 400 to 746.

```

# Mn predominance diagram for aqueous species only - CO2 included

SPECIATION
  jobTitle                "Mn-CO2-H2O"
  calculationType         ht1
  calculationMethod       1
# diagram for Mn
  mainSpecies             "Mn"
# pH range 2-10
  xmin                    2.0
  xmax                    10.0
# log f(O2(g)) range -90 to 0
  ymin                   -90.0
  ymax                    0.0

# track on a 300 x 300 grid
  resolution              300

PLOT
  plotTitle               "Mn-CO<sub>2</sub>-H<sub>2</sub>"
  sub>0<br>(CO<sub>2</sub>(g) but no minerals)"
  xtitle                  pH
# drive redox with fO2(g) but use pe for plot yscale
  yscale                  pe
# force plot y min at pe = -15
  pymin                   -15
  extraText               "extratextMn.dat"

CHEMISTRY

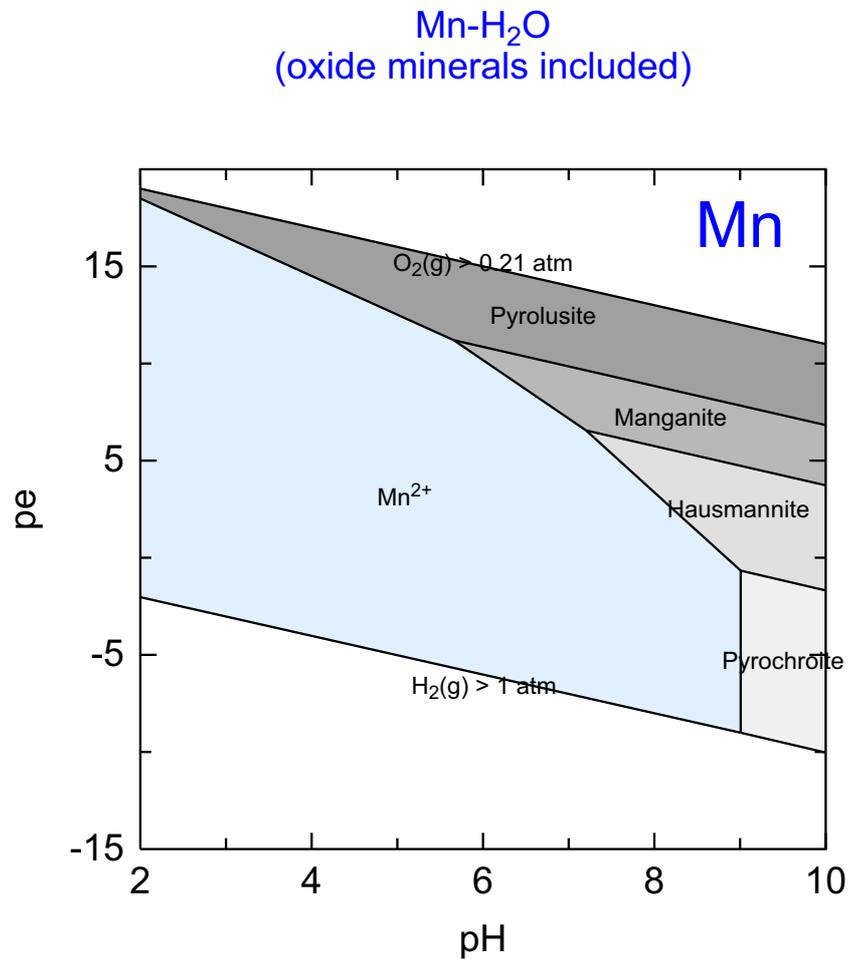
# standard predominance calculating code
include 'ht1.inc'

# first simulation - initial solution calculation
SOLUTION 1
  Temp                    20
# initial pH is less than pHmin so adding NaOH should always work
  pH                      1.8
  units                   mol/kgw
# total Mn
  Mn                      1e-2
# background electrolyte
  Na                      1e-1
  Cl                      1e-1 charge
SAVE solution 1
END

# second (final) simulation
USE solution 1
EQUILIBRIUM_PHASES 1
# add NaOH to get to specified logH
  Fix_H+                  -<x_axis> NaOH
  -force_equality true
  O2(g)                   <y_axis>
# NB no minerals specified
  CO2(g)                  -3.5      1
END

```

## 31 Mn-H<sub>2</sub>O (with minerals)



C:\PhreePlot\demo\Mn\Mnox1\_Mn1.ps

This is somewhat similar to the previous example except that minerals have been allowed to precipitate and no  $CO_2(g)$  is present. It shows the stability region of the various Mn oxides, some of which contain Mn in a mixed valence state.

```

# Mn predominance diagram including Mn oxide minerals (see Mn.ppi for aqueous species only)

SPECIATION
  jobTitle                "Mn-CO2-H2O"
  calculationType         ht1
  calculationMethod       1
# diagram for Mn
  mainSpecies             "Mn"
# pH range 2-10
  xmin                    2.0
  xmax                    10.0
# log f(O2(g)) range -90 to 0
  ymin                    -90.0
  ymax                    0.0

# track on a 400 x 400 grid
  resolution              400

PLOT
  plotTitle               "Mn-H<sub>2</sub>O<br>(oxide minerals included)"
  xtitle                  pH
# drive redox with fO2(g) but use pe for plot yscale
  yscale                  pe
# force plot y min at pe = -15
  pymin                   -15
  extraText               "extratextMn.dat"

CHEMISTRY

# standard predominance calculating code
include 'ht1.inc'

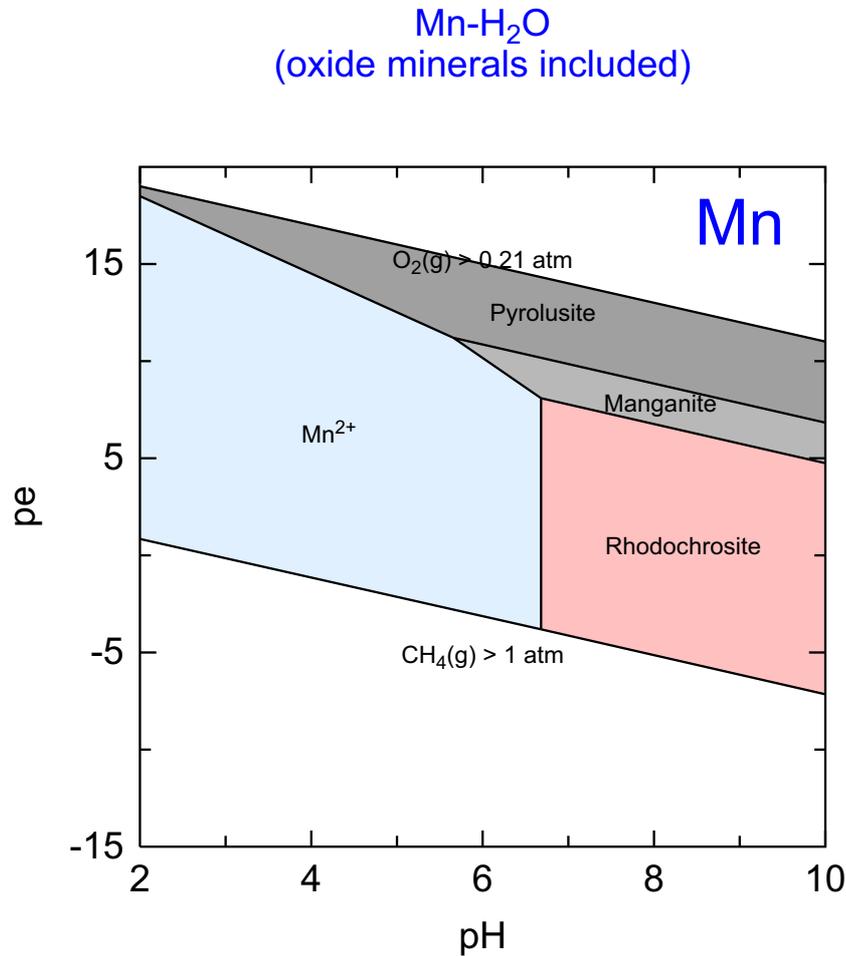
# first simulation - initial solution calculation
SOLUTION 1
  Temp                    20
# initial pH is less than pHmin so adding NaOH should always work
  pH                      1.8
  units                   mol/kgw
# total Mn
  Mn                      1e-2
# background electrolyte
  Na                      1e-1
  Cl                      1e-1 charge
SAVE solution 1
END

# second (final) simulation
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+                  -<x_axis> NaOH
  -force_equality true
  O2(g)                   <y_axis>

# this list of minerals is considered
  Pyrochroite             0 0
  Manganite               0 0
  Pyrolusite              0 0
  Nsutite                 0 0
  Birnessite              0 0
  Bixbyite                0 0
  Hausmannite             0 0
END

```

## 32 Mn-CO<sub>2</sub>-H<sub>2</sub>O



C:\PhreePlot\demo\Mn\Mnox2\_Mn1.ps

This is similar to the previous example but in this case, CO<sub>2</sub>(g) is present. This leads to the formation of rhodochrosite (MnCO<sub>3</sub>) at high pH and under moderately to strongly reducing conditions. In this case, Hausmannite and Pyrochroite are no longer predominant Mn minerals.

The CO<sub>2</sub>(g) is reduced to CH<sub>4</sub>(g) under strongly reducing conditions.

```
# Mn predominance diagram including Mn oxide and carbonate minerals (see Mn.ppi for
aqueous species only)
```

```
SPECIATION
  jobTitle           "Mn-CO2-H2O"
  calculationType    ht1
  calculationMethod  1
# diagram for Mn
  mainSpecies       "Mn"
# pH range 2-10
  xmin              2.0
  xmax              10.0
# log f(O2(g)) range -90 to 0
  ymin              -90.0
  ymax              0.0

# track on a 400 x 400 grid
  resolution        400

PLOT
  plotTitle          "Mn-H<sub>2</sub>O<br>(oxide minerals
included)"
  xtitle             pH
# drive redox with fO2(g) but use pe for plot yscale
  yscale             pe
# force plot y min at pe = -15
  pymin              -15
  extraText          "extratextMn.dat"
```

#### CHEMISTRY

```
# standard predominance calculating code
include 'ht1.inc'

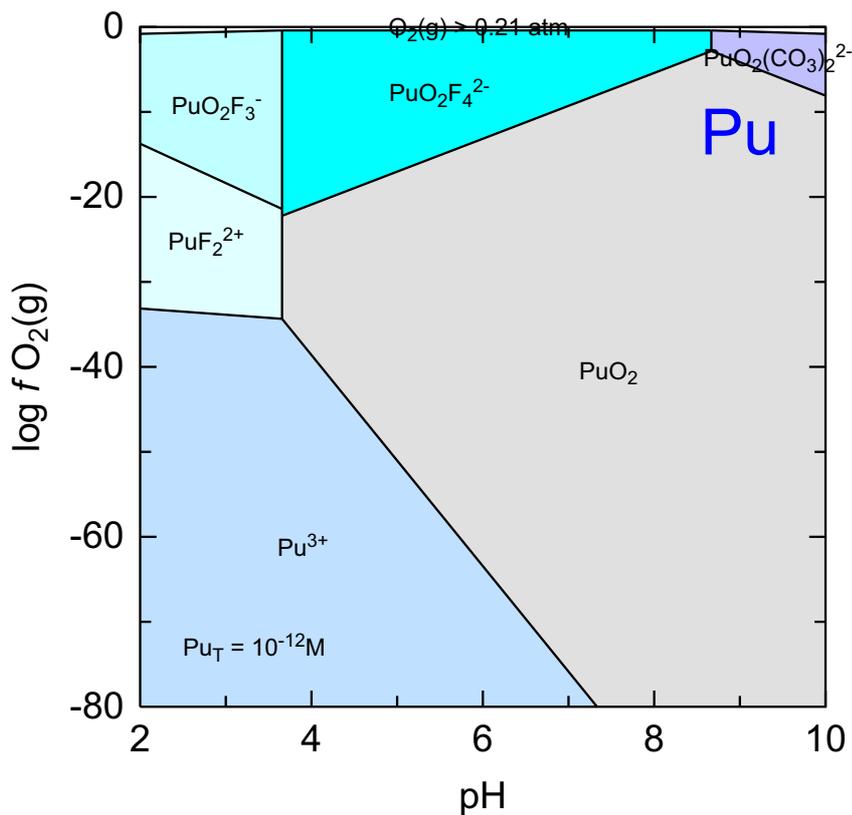
# first simulation - initial solution calculation
SOLUTION 1
  Temp      20
# initial pH is less than pHmin so adding NaOH should always work
  pH        1.8
  units     mol/kgw
# total Mn
  Mn        1e-2
# background electrolyte
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

# second (final) simulation
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis>
# atmospheric pCO2(g) - include up to 1 mole CO2 max
  CO2(g)    -3.5      1

  MnCl2:4H2O      0 0
  Pyrochroite     0 0
  Rhodochrosite   0 0
  Rhodochrosite(d) 0 0
  Manganite       0 0
  Pyrolusite      0 0
  Nsutite         0 0
  Birnessite      0 0
  Bixbyite        0 0
  Hausmannite     0 0
END
```

## 33 Pu-F-H<sub>2</sub>O

### Plutonium hydrolysis and redox (using Ilnl.dat database)



C:\PhreePlot\demo\Pu\Pu\_Pu1.ps

This  $\log f_{\text{O}_2(\text{g})}$ -pH predominance diagram for plutonium ( $10^{-12}$  mol/kgw  $\text{Pu}_T$ ) in the presence of fluoride and carbonate demonstrates the extreme insolubility of  $\text{PuO}_2$  under a wide range of conditions. It also shows that fluoride and carbonate form strong complexes with Pu(IV) and can maintain relatively high concentrations of Pu in solution. Reduction of Pu in solution from Pu(IV) to Pu(III) under reducing and acidic conditions also enhances Pu solubility.

```

SPECIATION
  jobTitle          "Plutonium redox and speciation"
  Database          llnl.dat
  epsi              T
  calculationType   ht1
  calculationMethod 1
  mainSpecies       "Pu"
  xmin              2.0
  xmax              10.0
  ymin              -80.0
  ymax              0.0
  resolution        100

PLOT
  plotTitle         "Plutonium hydrolysis and redox<br>(using
llnl.dat database)"
  xtitle            pH
  ytitle            "log <i>f</i> O<sub>2</sub>(g)"
  labelSize         2.0
  simplify          10
  extraText         "extratextPu.dat"

CHEMISTRY

include 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  Pu 1e-9
  Na 1e-1
  Cl 1e-1
  S 1e-3
  F 1e-3
SAVE solution 1
END

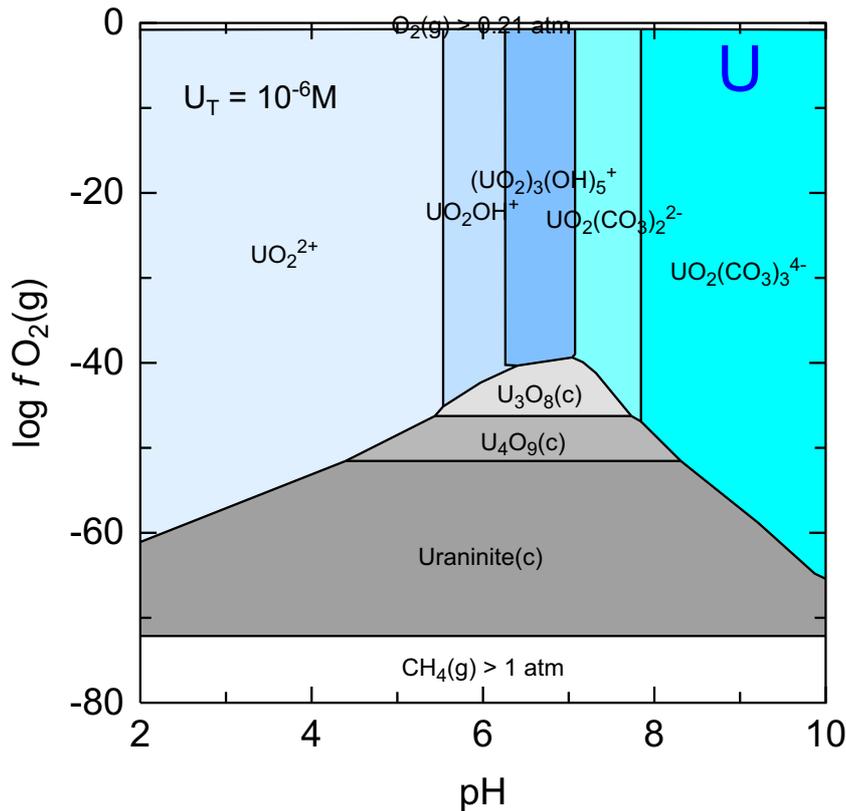
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

PuO2 0 0
Pu(OH)4 0 0
Nahcolite 0 0
Natron 0 0
Na2CO3:7H2O 0 0
Thermonatrite 0 0
Pu(OH)3 0 0
PuO2OH(am) 0 0
Na2CO3 0 0
PuO2(OH)2 0 0
C 0 0
Pu2O3 0 0
Na 0 0
Na2O 0 0
Pu 0 0
END

```

## 34 U-C-H<sub>2</sub>O (wateq4f.dat)

### Uranium hydrolysis and redox: wateq4f.dat



C:\PhreePlot\demo\UCO3\UCO3wq\_U1.ps

This is one of three log  $fO_2(g)$ -pH predominance diagrams for U ( $10^{-6}$  mol/kgw U<sub>T</sub>) which demonstrate how predominance diagrams provide a useful way of comparing thermodynamic databases, here made with `wateq4f.dat`.

Uranium speciation is strongly dependent on the pH and redox conditions with the highly insoluble mineral Uraninite dominating reducing conditions. Uranium(VI) forms strong complexes with carbonate which enhances U solubility in the presence of CO<sub>2</sub>(g) and high pH.

The extraText file, `extratextUCO3.dat`, also adds the text in the top left corner of the diagram and demonstrates features such as subscripts, superscripts, italics, line breaks (<br>) and the use of multiline input through the use of the \ continuation character.

```

SPECIATION
  jobTitle          "Uranium redox and speciation"
  Database          "wateq4f.dat"
  calculationType   "ht1"
  calculationMethod 1
  mainSpecies      "U"
  xmin             2.0
  xmax             10.0
  ymin             -80.0
  ymax             0.0
  loopmin          -6
  loopmax          -6
  loopint          0
  looplogvar       1
  resolution       500

PLOT
  plotTitle        "Uranium hydrolysis and redox: wateq4f.dat"
  xtitle           "pH"
  ytitle           "log <i>f</i> O<sub>2</sub>(g)"
  extraText        "extratextUCO3.dat"

CHEMISTRY

  include 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  U 1e-6
  Na 1e-1
  Cl 1e-1
SAVE solution 1
END

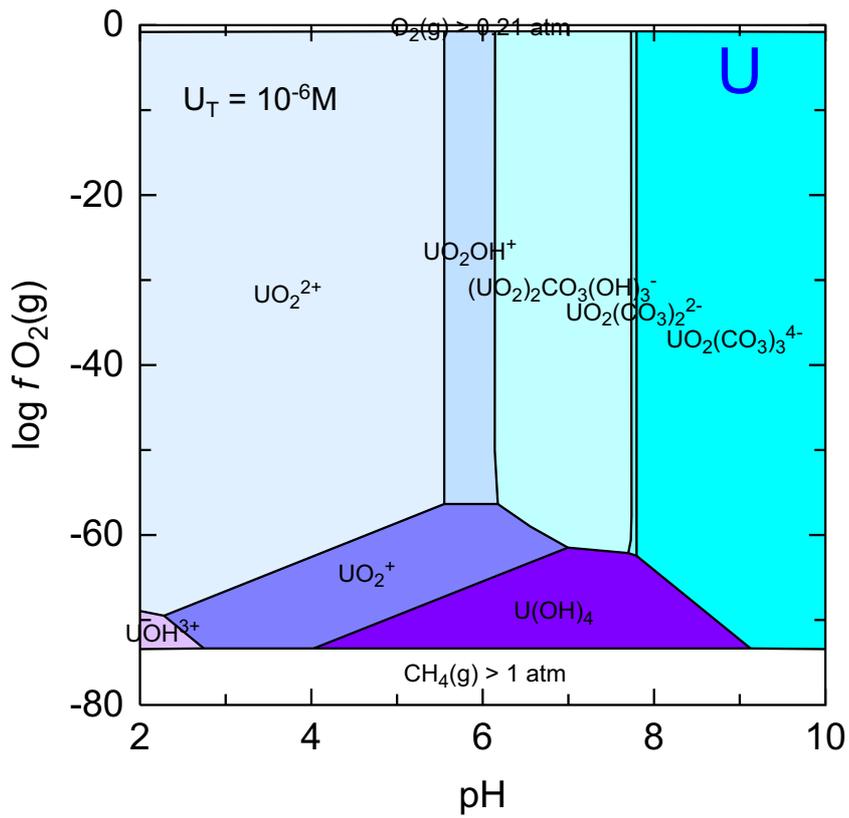
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

  Uraninite(c) 0 0
  UO2(a) 0 0
  U4O9(c) 0 0
  Schoepite 0 0
  B-UO2(OH)2 0 0
  UO3(gamma) 0 0
  Nahcolite 0 0
  Gummite 0 0
  Rutherfordine 0 0
  Natron 0 0
  Thermonatrite 0 0
  U3O8(c) 0 0
  Trona 0 0
  Na4UO2(CO3)3 0 0
END

```

# 35 U-C-H<sub>2</sub>O (NAPSI)

Uranium hydrolysis and redox (NAPSI)



C:\PhreePlot\demo\UCO3\UCO3psi\_U1.ps

The same as for the previous diagram but here made with the NAPSI database.

```

SPECIATION
  jobTitle          "Uranium redox and speciation"
  Database          "NAPSI_290502.DAT"
  calculationType   "ht1"
  calculationMethod 1
  mainSpecies       "U"
  xmin              2.0
  xmax              10.0
  ymin              -80.0
  ymax              0.0
  loopmin           -6
  loopmax           -6
  loopint           0
  looplogvar        1
  resolution        500

PLOT
  plotTitle         "Uranium hydrolysis and redox (NAPSI)"
  xtitle            "pH"
  ytitle            "log <i>f</i> O<sub>2</sub>(g)"
  extraText         "extratextUCO3.dat"

CHEMISTRY

include 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  U 1e-6
  Na 1e-1
  Cl 1e-1
SAVE solution 1
END

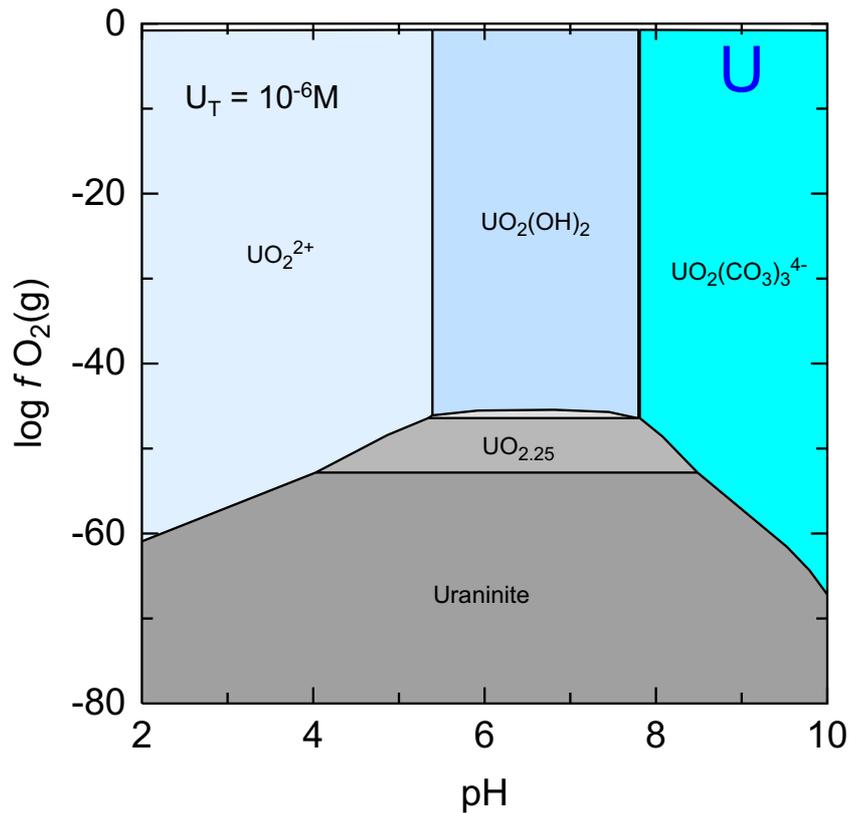
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ <x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

END

```

36 U-C-H<sub>2</sub>O (llnl.dat)

Uranium hydrolysis and redox: llnl.dat



C:\PhreePlot\demo\UCO3\UCO3\llnl\_U1.ps

The same as for the previous diagram but here made with the `llnl.dat` database.

Note that one of the fields in the centre of the diagram has not been labelled (light grey, `UO2.3333(beta)`) because it occupies less than the minimum area required to plot a label (as given by the keyword [minimumAreaForLabeling](#) which is 1% by default).

This sequence of diagrams demonstrates the quite large differences in speciation models for U in the various databases. This applies not only to the minerals but also the aqueous species.

```

SPECIATION
  jobTitle          "Uranium redox and speciation"
  Database          "llnl.dat"
  calculationType   "ht1"
  calculationMethod 1
  mainSpecies       "U"
  xmin              2.0
  xmax              10.0
  ymin              -80.0
  ymax              0.0
  loopmin           -6
  loopmax           -6
  loopint           0
  looplogvar        1
  resolution        500

PLOT
  plotTitle         "Uranium hydrolysis and redox: llnl.dat"
  xtitle            "pH"
  ytitle            "log <i>f</i> O<sub>2</sub>(g)"
  minimumAreaForLabeling 1.0
  extraText         "extratextUCO3.dat"

CHEMISTRY

include 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  U 1e-6
  Na 1e-1
  Cl 1e-1
SAVE solution 1
END

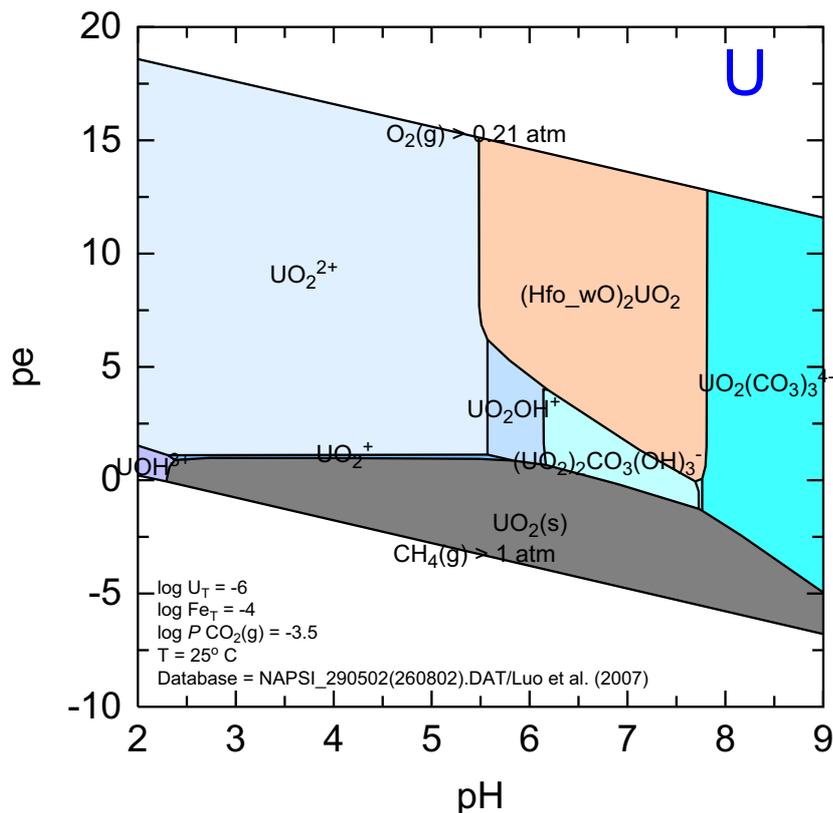
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

Ice 0 0
Uraninite 0 0
UO2.25 0 0
UO2.25(beta) 0 0
UO2.3333(beta) 0 0
UO2(am) 0 0
Schoepite 0 0
UO3:2H2O 0 0
UO2(OH)2(beta) 0 0
Schoepite-dehy(.9) 0 0
UO3:.9H2O(alpha) 0 0
Schoepite-dehy(.85) 0 0
Schoepite-dehy(1.0) 0 0
UO2ClOH:2H2O 0 0
Schoepite-dehy(.648) 0 0
UO2.6667 0 0
UO2Cl 0 0
Schoepite-dehy(.393) 0 0
UO3(gamma) 0 0
UO3(beta) 0 0
UO3(alpha) 0 0
UO2Cl2:3H2O 0 0
NaUO3 0 0
UOCl2 0 0
UO2Cl2:H2O 0 0
U5O12Cl 0 0

```

UO2C12	0 0
Na2U2O7	0 0
UOC13	0 0
Na2UO4 (alpha)	0 0
(UO2)2C13	0 0
UOC1	0 0
UC14	0 0
UC13	0 0
U2O2C15	0 0
Na	0 0
UC15	0 0
Na3UO4	0 0
Na2O	0 0
UC16	0 0
U	0 0
UH3 (beta)	0 0
END	



37 U-Fe-C-H<sub>2</sub>OU-Fe-C-H<sub>2</sub>O  
(with adsorbed speciation)

C:\PhreePlot\demo\Uhf\Uhf\_U1.ps

This is a uranium ( $\log U_T = -9$ ) pe-pH predominance diagram with mineral formation and adsorption of U and carbonate on hydrous ferric oxide (HFO). There is also competition from carbonate complexation in solution at high pH.

The U adsorption is approximate in the sense that the U adsorption parameters have been taken from a source that is not necessarily consistent with the aqueous speciation database used here (see the code below for details). In principle, consistent databases should be used although this is often not possible and can be difficult to maintain.

Carbonate species are also adsorbed by HFO although they never become the dominant C species in the system. Maximum carbonate adsorption is at about pH 6.5.

```

SPECIATION
  jobTitle                "Uranium redox and speciation"
  mainSpecies             "U"
  calculationType         htl
  calculationMethod       1
# relatively recently revised database for U
  database                 NAPSI_290502.DAT
  fillColorDictionary     "fillcolor.dat"
# minimum pH
  xmin                    2.0
# maximum pH
  xmax                    9.0
# minimum PO2(g) to generate variable redox
  ymin                    -75.0
# maximum PO2(g)
  ymax                    0.0
  resolution              400

PLOT
  plotTitle               "U-Fe-C-H<sub>2</sub><br>(with adsorbed spe-
  ciation)"
  xtitle                  pH
# use pe for the y-scale
  yscale                  pe
# on the pe scale
  pymin                  -10.0
  extraText               "extratextUhfo.dat"

CHEMISTRY

TITLE U Sorption to ferrihydrite according to DLM and database derived and used by
  Luo et al. Journal of Contaminant Hydrology 92, 129-148 (2007)

include 'U-Hfo.dat'
include 'htl.inc'

# first simulation - initial solution calculations
SOLUTION 1
  temp                   25
# initial pH is just less than pHmin
  pH                     1.8
  units                  mol/kgw
  Na                     0.1
  Fe                     1e-4
  U(6)                   1e-6
  Cl                     0.1   charge

EQUILIBRIUM_PHASES
# NB name of related mineral is different from wateq4f.dat
  Fe(OH)3(am) 0 0

SURFACE 1
  Hfo_sOH Fe(OH)3(am)      equilibrium_phase 0.005 53300
  Hfo_wOH Fe(OH)3(am)      equilibrium_phase 0.2

SAVE solution 1
SAVE surface 1
END

# second simulation - loops on the final simulation
USE solution 1
USE surface 1
EQUILIBRIUM_PHASES 1
  Fix_H+   -<x_axis> NaOH      10
           -force_equality true
  O2(g)    <y_axis> 0.1
  CO2(g)   -3.5 1.0

Graphite                0 0
UO2(s)                  0 0

```

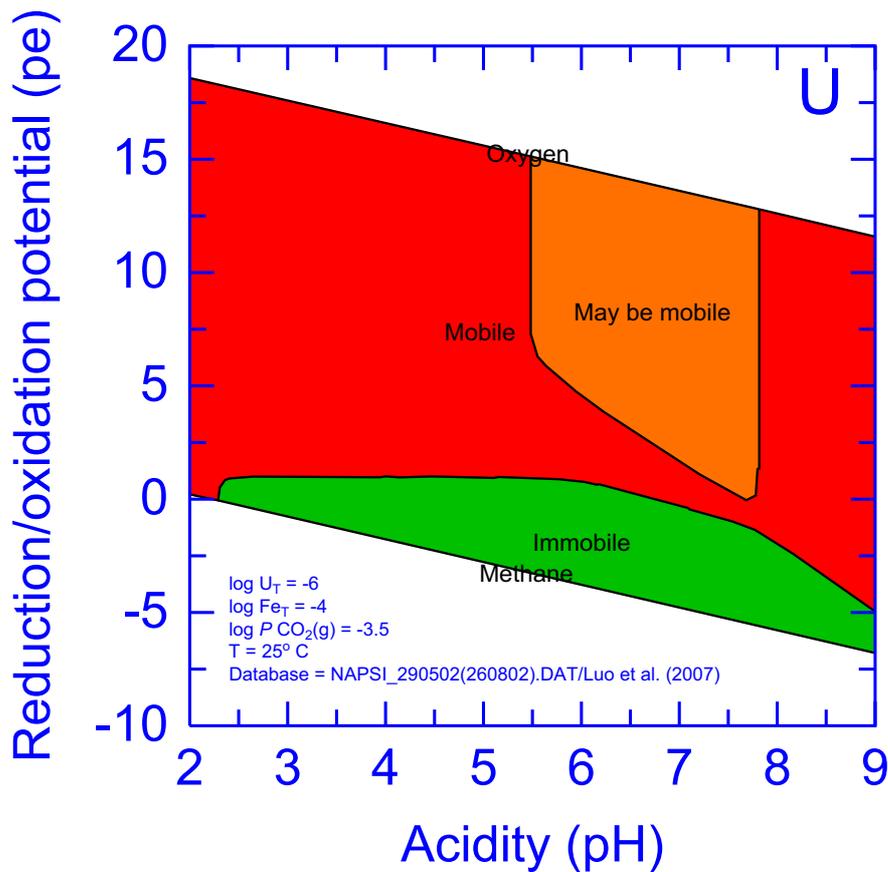
400 *PhreePlot Guide*

```
#Goethite          0 0
  Siderite         0 0
  FeCO3 (pr)      0 0
#Fe(OH)3 (mic)    0 0
  Schoepite       0 0
  Rutherfordine   0 0
  Fe(OH)3 (am)   0 0
#Fe(cr)           0 0
#Hematite         0 0
#Magnetite        0 0
END
```



## 38 U-Fe-C (risk colours)

### U-Fe-C-H<sub>2</sub>O (with adsorbed speciation)



C:\PhreePlot\demo\Uhf\Uhf(risk)\_U1.ps

The same as the previous example but with labelling and colouring more appropriate for conveying the risk of uranium mobilization to a non-technical audience.

Dissolved species are coloured red ('Mobile'); adsorbed species are coloured orange ('May be mobile') and the mineral species are coloured green ('Immobile'). The criteria for determining predominance are entirely set in the `USER_PUNCH` file, 'risk.inc', and can be changed to give whatever priorities you like – see the next example where the redox state is the defining criterion. In general, the `SYS()` function is your friend here.

Many of the axis settings have also been changed.

```

SPECIATION
  jobTitle                "Uranium redox and speciation"
  mainSpecies             "U"
  calculationType         ht1
  calculationMethod       1
# relatively recently revised database for U
  database                NAPSI_290502(260802).DAT
  fillColorDictionary     "fillcolor.dat"
# minimum pH
  xmin                   2.0
# maximum pH
  xmax                   9.0
# minimum PO2(g) to generate variable redox
  ymin                   -75.0
# maximum PO2(g)
  ymax                   0.0
  resolution             400

PLOT
  plotTitle              \
                        "U-Fe-C-H<sub>2</sub>O<br>(with adsorbed speciation)"
  xtitle                 "Acidity (pH)"
  ytitle                 "Reduction/oxidation potential (pe)"
# use pe for the y-scale
  yscale                 pe
# on the pe scale
  pymin                  -10.0

  plotTitleColor         red
  plotTitleSize          5

  axisNumberSize         4
  axisNumberColor        "blue"
  axisTitleSize          4
  axisTitleColor         "blue"
  axisLineWidth          0.4
  axisLineColor          "blue"

  tickSize               3
  tickColor              "blue"

  info                   "nd" "blue"

  extraText              "extratextUhfo(risk).dat"

CHEMISTRY

TITLE U Sorption to ferrihydrite according to DLM and database derived and used by
  Luo et al. Journal of Contaminant Hydrology 92, 129-148 (2007)

include 'U-Hfo.dat'
# this uses simple 'traffic light' classification for aqueous, adsorbed and mineral
# phases
include 'risk.inc'

# first simulation - initial solution calculations
SOLUTION 1
  temp      25
# initial pH is just less than pHmin
  pH        1.8
  units     mol/kgw
  Na        0.1
  Fe        1e-4
  U(6)      1e-6
  Cl        0.1  charge

EQUILIBRIUM_PHASES
# NB name of related mineral is different from wateq4f.dat
  Fe(OH)3(am)  0 0

```

#### 404 PhreePlot Guide

```
SURFACE 1
  Hfo_sOH Fe(OH)3(am)      equilibrium_phase 0.005  53300
  Hfo_wOH Fe(OH)3(am)      equilibrium_phase 0.2
SAVE surface 1
END
```

```
# second simulation - loops on the final simulation
```

```
USE solution 1
USE surface 1
EQUILIBRIUM_PHASES 1
  Fix_H+   -<x_axis>  NaOH 10
           -force_equality true
  O2(g)    <y_axis>   0.1
  CO2(g)   -3.5      1.0

  Graphite      0 0
  UO2(s)        0 0
#Goethite      0 0

  Siderite      0 0
  FeCO3(pr)    0 0
#Fe(OH)3(mic)  0 0

  Schoepite     0 0
  Rutherfordine 0 0
  Fe(OH)3(am)  0 0
#Fe(cr)        0 0

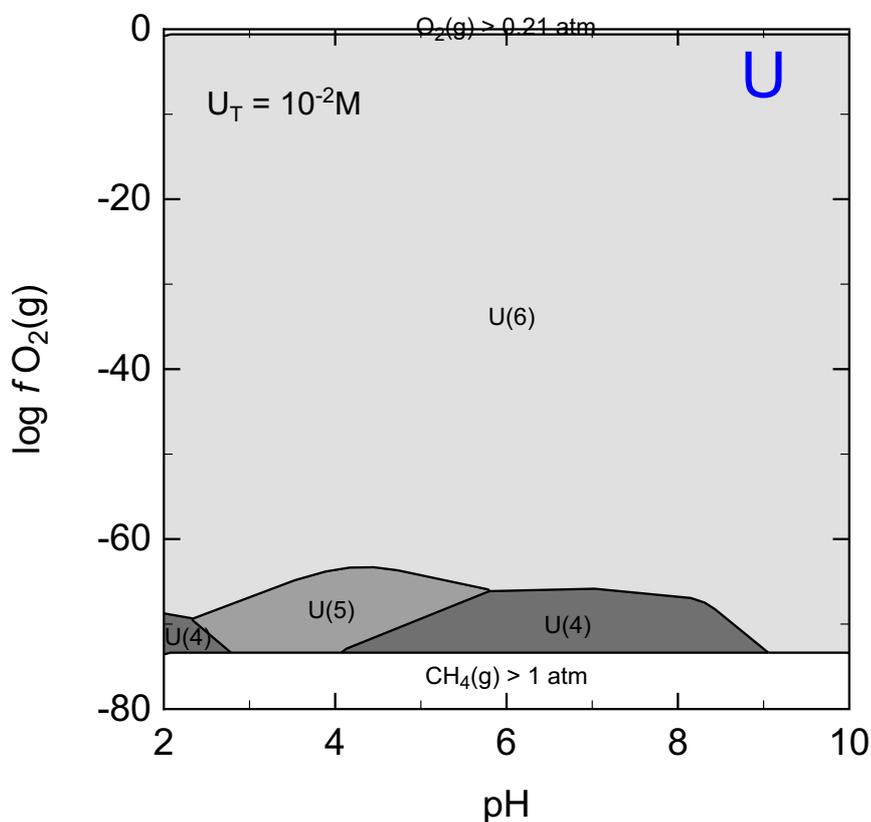
#Hematite      0 0

#Magnetite     0 0

END
```



## 39 U-H<sub>2</sub>O (redox state)



C:\PhreePlot\demo\redox\_predominance\Uredox.ps

This example shows a predominance diagram based solely on the redox state of the aqueous species for a given 'master species', here the element U. The example file loops over three total U concentrations and produces a multipage ps file.

This diagram has been produced by using the `SYS()` function within the `htlredox.inc` file to give the moles of all possible redox states from -8 to +8, sorting them, and then returning the top three of these to the tracking routine within **PhreePlot**. These figures define the predominant 'species', albeit an aggregation of all species with the given valence state.

This redox speciation can include, in principle, solid and adsorbed species based on the valence of the species given in their dissolution (mineral) or association (surface) reactions. For example, magnetite which contains both Fe(2) and Fe(3) will contribute to both of these 'super' species. For a mineral to be actually present depends on its inclusion within an `EQUILIBRIUM_PHASES` block; similarly, adsorbed phases depend on `SURFACE` blocks.

However, be aware that for some minerals, such as the strongly covalent arsenic sulphides, the valence state of the elements within the mineral phase is in reality rather poorly defined. Also some tabulated dissolution reactions, such as that for *Realgar*, *Manganite* and *CuMetal* in `wateq4f.dat`, involve release of an electron which means that the valence of these solid phases may be reported incorrectly.

```

# Predominance diagram for U in the presence of CO2(g).
# All species are aggregated into their valence states, e.g. U(4), U(5), U(6).
# Thanks to Remi Marsac (INE) for the suggestion.

```

```

SPECIATION
  Database                "NAPSI_290502.DAT"
  calculationType         "ht1"
  calculationMethod       1
  mainSpecies             "U"
  xmin                    2.0
  xmax                    10.0
  ymin                    -80.0
  ymax                    0.0
  loopmin                 -6
  loopmax                 -2
  loopint                 2
  looplogvar              1
  resolution              200
# used in extraText file
  numericTag              <logUt> = <logloop>

PLOT
  plotTitle               "Uranium redox states"
  xtitle                  "pH"
  ytitle                  "log <i>f</i> O<sub>2</sub>(g)"
  extraText               "extratextUredox.dat"
  multipagefile           t

CHEMISTRY

PHASES
  Fix_H+
  H+ = H+
  log_k 0.

#include 'ht1.inc'
include 'ht1redox.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  U <loop>
  Na 1e-1
  Cl 1e-1
SAVE solution 1
END

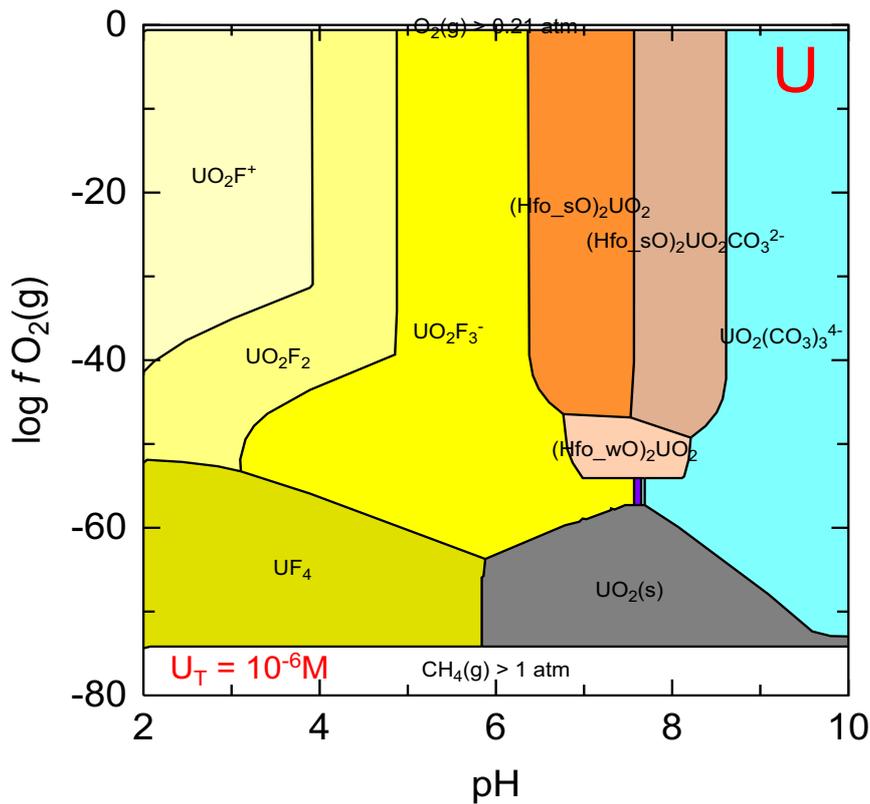
# main loop - iterate here
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

END

```

## 40 U-F-P (U)

### U complexation in the presence of F and P (loops on the main species)



C:\PhreePlot\demo\UPF\UPF\_U1.ps

This is an example of a predominance diagram for U in a system containing many U species including U adsorbed to HFO and other components. The input file also demonstrates how to generate a number of diagrams (U, P, F, Fe, C) for the same system. The next two examples give the corresponding fluoride and phosphorus outputs for this system.

The calculations were made using the `NAPSI_290502(260802).DAT` database for most species but since this does not include surface species, it was combined with a revised database for HFO-U surface species. This is found in `u.dat`. These data from [Luo et al. \(2007\)](#) use the [Dzombak and Morel \(1990\)](#) DLM but the surface reaction for U is described in terms of bidentate binding.

The NAPSI database does not include such an extensive set of minerals as the `wateq4f.dat` database and is completely lacking in some trace elements. Therefore some second order interactions may be missed.

The total uranium concentration is set by the loop variable although in this case only one

value is selected, -6. This is converted to  $10^{-6}$  before it is substituted by setting [loopLogVar](#) to 1. This value is then used in the SOLUTION data block with the <loop> tag.

```

SPECIATION
  jobTitle                "Uranium complexation"
  database                 NAPSI_290502.DAT
  calculationType          ht1
  calculationMethod        1
# calculate diagrams for these 5 elements
  mainSpecies              U P F Fe C
# minimum pH etc used to generate the plot
  xmin                     2.0
  xmax                     10.0
  ymin                     -80.0
  ymax                     0.0
  loopMin                  -6.0
  loopMax                  -6.0
  loopInt                  1
  loopLogVar               1
  resolution                200

PLOT
  plotTitle                "U complexation in the presence of F and
P<br>(loops on the main species)"
  xtitle                   pH
  ytitle                   "log <i>f</i> O<sub>2</sub> (g)"
  xoffset                   40.0
  yoffset                   150.0
  labelSize                1.7
  extraText                 "extratextUPF.dat"
# make one ps file per element not one file overall
  multiPagefile            f

CHEMISTRY

# revised database for U surface species - also other surface species
include 'U-Hfo.dat'
# standard code to generate predominance diagrams
include 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.3
  units mol/kgw
  U <loop>
  Na 1e-1
  Cl 1e-1
  F 1e-2
  S(6) 1e-2
  P 1e-4
  Fe 1e-2

EQUILIBRIUM_PHASES 1
  Fe(OH)3(am) 0 0

SAVE solution 1
END

# second simulation - loops on the final simulation

#PRINT; reset true
USE solution 1
USE surface 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1

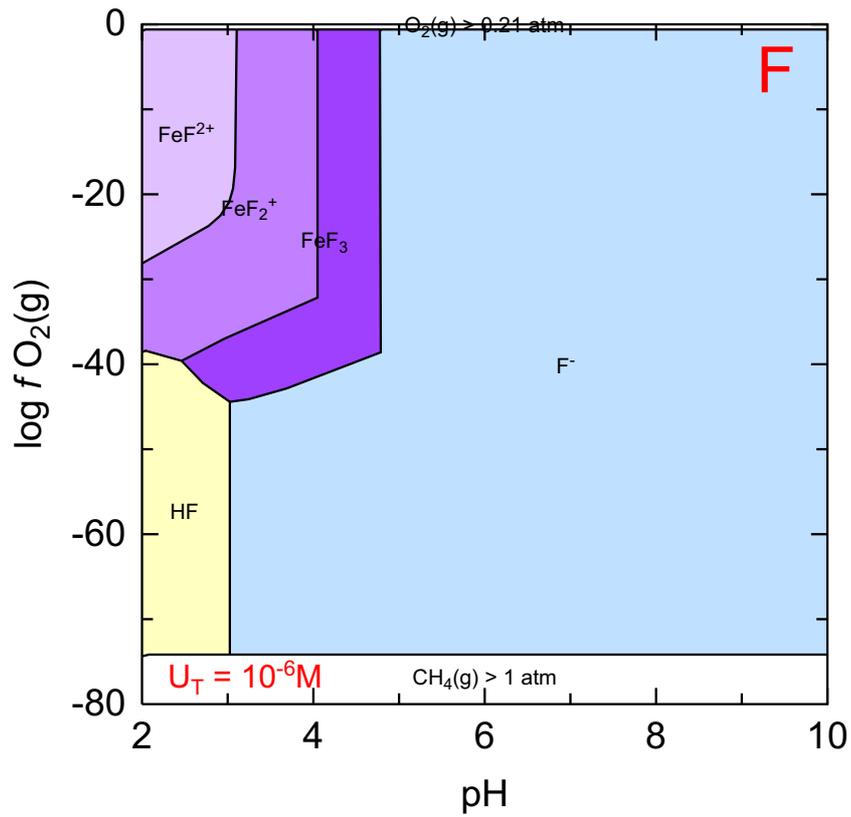
# PSI database
  Pyrite 0 0
  Troilite 0 0

```

UF <sub>4</sub> ·2.5H <sub>2</sub> O (cr)	0 0
Graphite	0 0
S (rhomb)	0 0
#Goethite	0 0
UO <sub>2</sub> (s)	0 0
#Fe (OH) <sub>3</sub> (mic)	0 0
Fe (cr)	0 0
Fe (OH) <sub>3</sub> (am)	0 0
Siderite	0 0
FeCO <sub>3</sub> (pr)	0 0
Chernikovite	0 0
#Hematite	0 0
Schoepite	0 0
#Magnetite	0 0
Melanterite	0 0
Rutherfordine	0 0
U (OH) <sub>2</sub> SO <sub>4</sub> (cr)	0 0
(UO <sub>2</sub> ) <sub>3</sub> (PO <sub>4</sub> ) <sub>2</sub> ·4H <sub>2</sub> O (cr)	0 0
END	

# 41 U-F-P (F)

U complexation in the presence of F and P  
(loops on the main species)



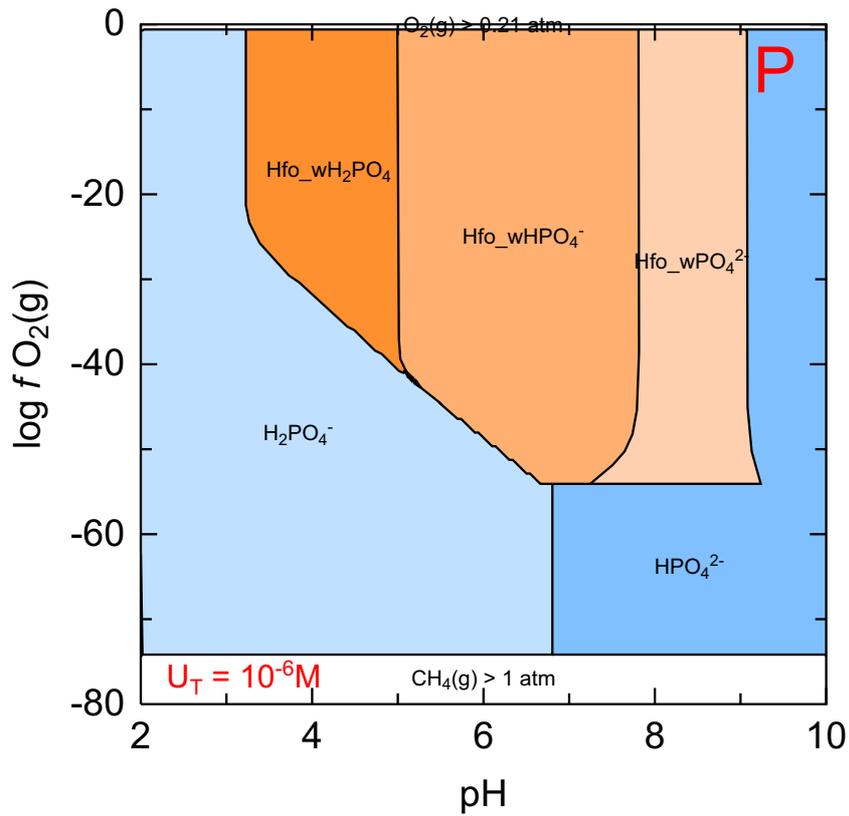
C:\PhreePlot\demo\UPF\UPF\_F1.ps

The fluoride view of the previous example.



## 42 U-F-P (P)

U complexation in the presence of F and P  
(loops on the main species)

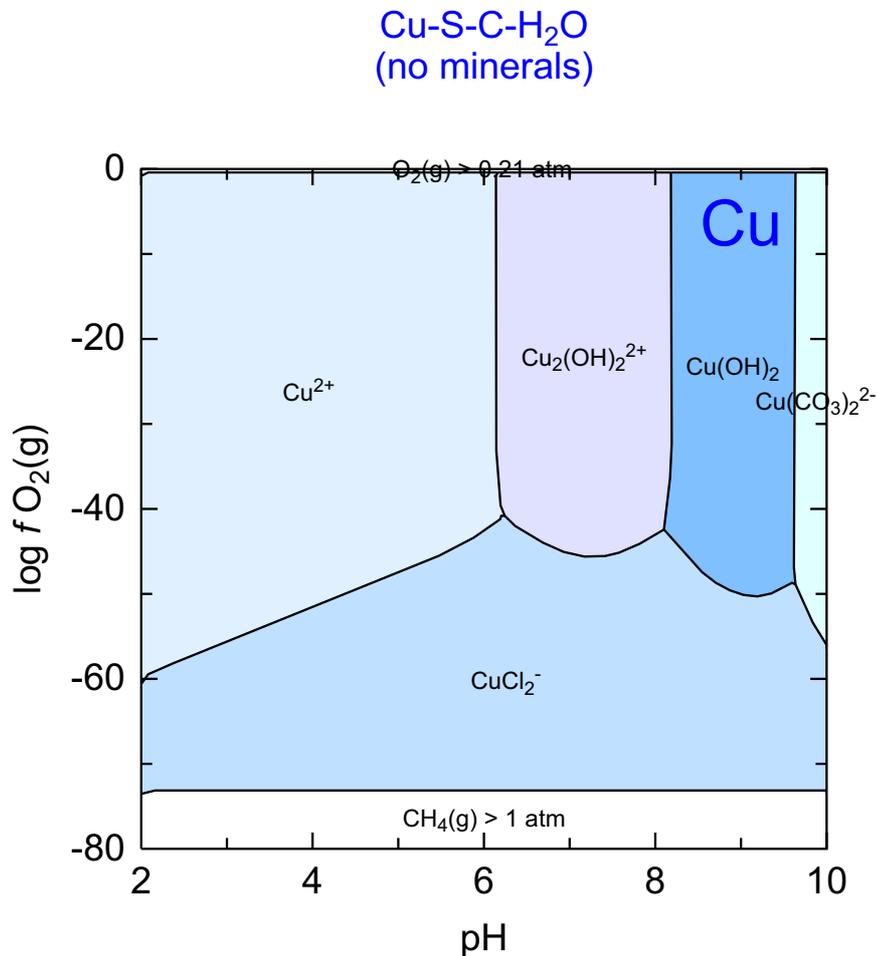


C:\PhreePlot\demo\UPF\UPF\_P1.ps

The phosphorus view of the previous example. Phosphorus adsorption is calculated using the DLM with default [Dzombak & Morel \(1990\)](#) model parameters.



## 43 Cu-S-C ('island' not found with 'ht1')



C:\PhreePlot\demo\island\CuSht1\_Cu1.ps

This example was computed with the same conditions as in the previous example but used the 'ht1' approach rather than the 'grid' approach (the only difference was in the [calculation-Method](#) setting; the same ht1.inc file was used for generating the predominant boundaries in both diagrams.

This diagram has failed to identify the Cu<sup>+</sup> field since it is an 'island' and is not accessible by hunting along the domain boundaries or tracking internal boundaries. This field is found using the 'grid' approach which provides a more reliable but slower approach.

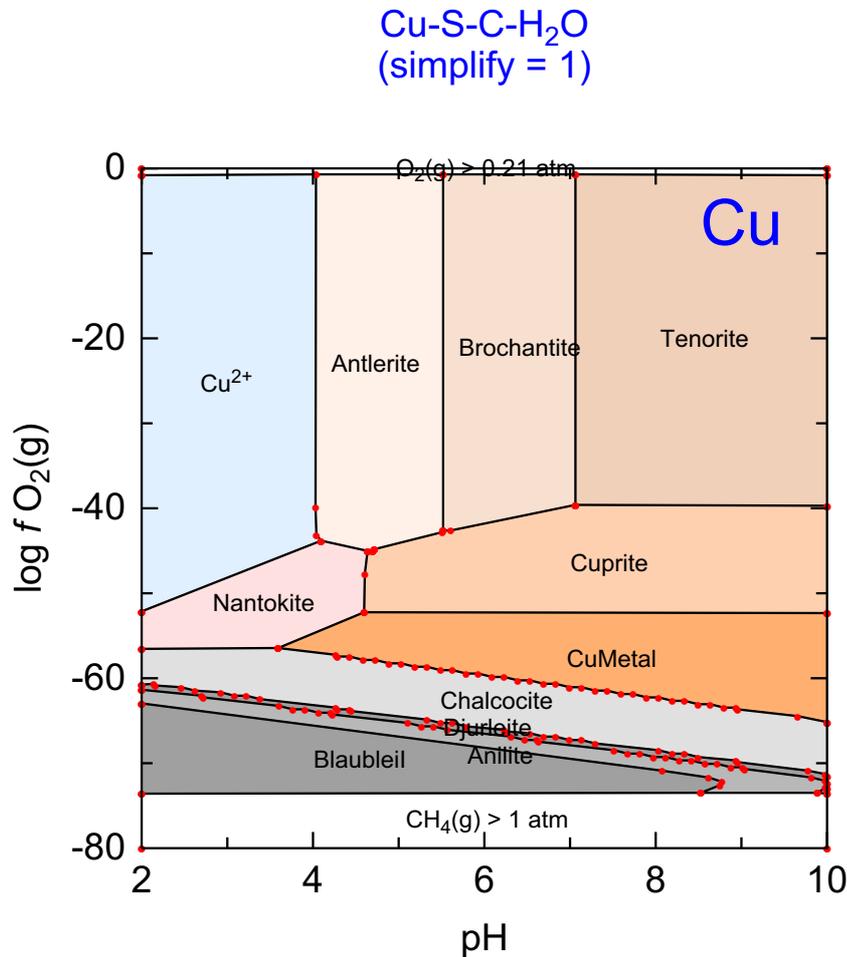
```

SPECIATION
  calculationType      ht1
  calculationMethod    1
  mainSpecies          Cu
  xmin                 2
  xmax                 10
  ymin                 -80
  ymax                 0
  resolution           100
PLOT
  plotTitle            "Cu-S-C-H<sub>2</sub><br>(no minerals)"
  xtitle               pH
  ytitle               "log <i>f </i><sub>2</sub>(g)"
  extraText            extratextCuS.dat
CHEMISTRY
  include 'ht1.inc'
  SOLUTION 1
    Temp      20
    pH        1.8
    units     mol/kgw
    Cu        1e-1
    S(6)      1e-1
    Na        1e-1
    Cl        1.032e-1
  SAVE solution 1
  END

  USE solution 1
  EQUILIBRIUM_PHASES 1
    Fix_H+    -<x_axis> NaOH
              -force_equality true
    O2(g)     <y_axis> 0.1
    CO2(g)    -3.5      1.0
  END

```

## 44 Cu-S-C (simplification factor = 1)



C:\PhreePlot\demo\CuS\CuS\_Cu1.ps

The regular 'jagged' lines for the Chalcocite-Djurleite and other boundaries, highlighted by the red symbols (`pointSize = 1.5`), are because of the low angle of the slopes of the boundaries in relation to the chosen resolution (`resolution = 400`). The resolution controls the spacing of the imaginary grid where evaluations take place. Straight boundaries with a low angle therefore tend to result in regular steps. This is not a property of the underlying speciation program but of the hunt and track algorithm used. The regular steps can be eliminated by increasing the simplification factor (see the next example). This does not require recalculation of the data just replotting (`calculationType = 3`) with a larger value of the simplification factor, `simplify` which is set to 1 here. Alternatively, recalculating with a higher resolution will reduce the step size.

Sometimes boundaries, especially mineral boundaries, can be 'noisy'. This is a reflection of the speciation program but again the boundaries can be smoothed by increasing the simplification factor.

```

SPECIATION
  calculationType          ht1
  calculationMethod        1
  mainSpecies              Cu
  xmin                     2.0
  xmax                     10.0
  ymin                     -80.0
  ymax                     0.0
  resolution               400
PLOT
  plotTitle                "Cu-S-C-H<sub>2</sub><br>(simplify = 1)"
  xtitle                   pH
  ytitle                   "log <i>f </i><sub>2</sub>(g)"
# sets the sizes of the symbols used for an intermediate plot and
  trackSymbolSize          1.5 1.5
# custom plot label anchor symbols

# normal default of 1 - but note the jaggies in some of the low-angled boundaries
  simplify                 1
  extraText                "extratextCuS.dat"

CHEMISTRY

# standard hunt and track file
include 'ht1.inc'

SOLUTION 1
  temp      20
  pH        1.8
  units     mol/kgw
# total concns
  Cu        1e-1
  S(6)      1e-1
# background electrolyte
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis> 0.1
# includes carbonate species
  CO2(g)    -3.5      1.0

# permitted minerals
  Chalcocite          0 0
  Djurleite           0 0
  Anilite             0 0
  BlaubleiIII         0 0
  BlaubleiI           0 0
  Covellite          0 0
  CuMetal             0 0
  Sulfur              0 0
  Nantokite           0 0
  Cuprite             0 0
  Tenorite            0 0
  Cu(OH)2             0 0
  Melanothallite     0 0
  Nahcolite           0 0
  Atacamite           0 0
  CuCO3               0 0
  Natron              0 0
  Thermonatrite       0 0
  Thenardite          0 0
  Mirabilite          0 0
  Chalcanthite        0 0
  Malachite           0 0

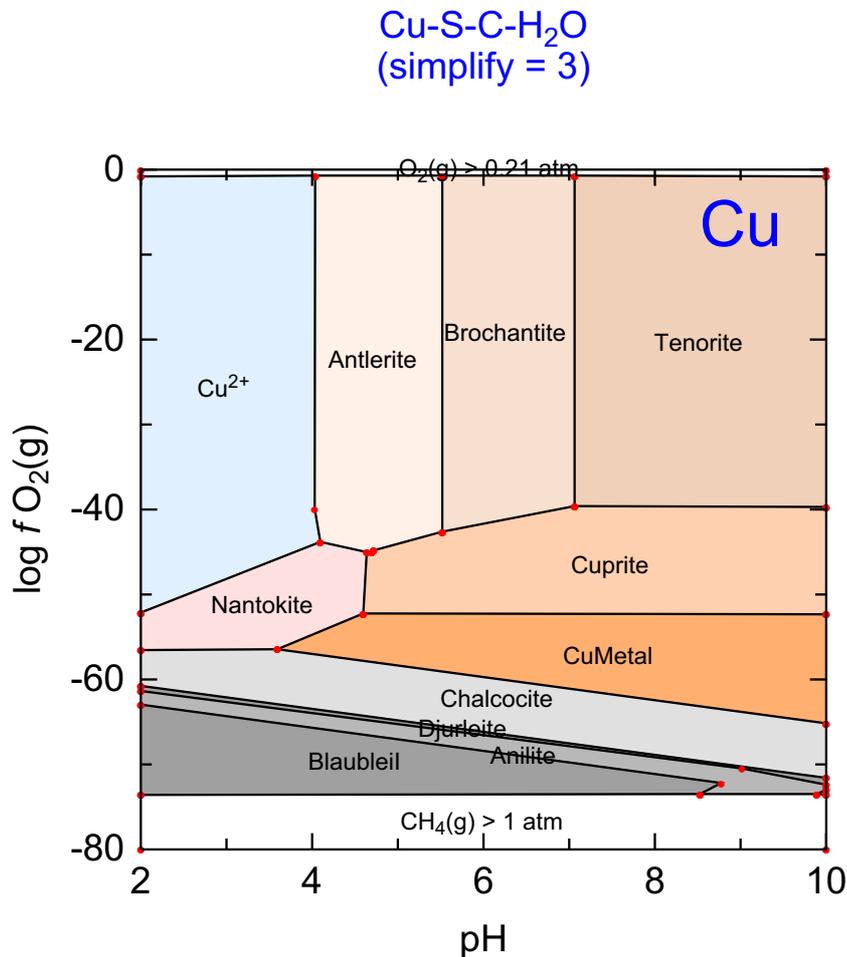
```

CuSO4	0 0
Cu2SO4	0 0
Trona	0 0
CuOCuSO4	0 0
Antlerite	0 0
Azurite	0 0
Brochantite	0 0
Langite	0 0

END



## 45 Cu-S-C (simplification factor = 3)



C:\PhreePlot\demo\CuS\CuS2\_Cu1.ps

This is the same example as the previous example except that it uses a greater value of the simplification factor, [simplify](#), compared with the previous example has eliminated the obvious stepping. The value of 'simplify' is normally set to 1. Values greater than 1 reduce the number of vertices used to draw the polygons while a value less (normally in the range 0.1 to 1) will give more. A value of 0 does no line simplification at all.

A value of 3 was chosen here which almost completely eliminates the intermediate points although some of the boundaries seem unnaturally sharp suggesting that a greater resolution would also help. Note that it is not necessary to recalculate the points in order to change the simplification but it is necessary to use [calculationMethod](#) 3 not 2.

```

SPECIATION
  calculationType          ht1
  calculationMethod        1
  mainSpecies              Cu
  xmin                     2.0
  xmax                     10.0
  ymin                     -80.0
  ymax                     0.0
  resolution               400
PLOT
  plotTitle                "Cu-S-C-H<sub>2</sub><br>(simplify = 3)"
  xtitle                   pH
  ytitle                   "log <i>f </i><sub>2</sub>(g)"
# sets the sizes of the symbols used for an intermediate plot and
  trackSymbolSize          1.5 1.5
# custom plot label anchor symbols

# increase smoothing of field boundaries above normal default of 1
  simplify                 3
  extraText                "extratextCuS.dat"

CHEMISTRY

# standard hunt and track file
include 'ht1.inc'

SOLUTION 1
  temp      20
  pH        1.8
  units     mol/kgw
# total concns
  Cu        1e-1
  S(6)      1e-1
# background electrolyte
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis> 0.1
# includes carbonate species
  CO2(g)    -3.5      1.0

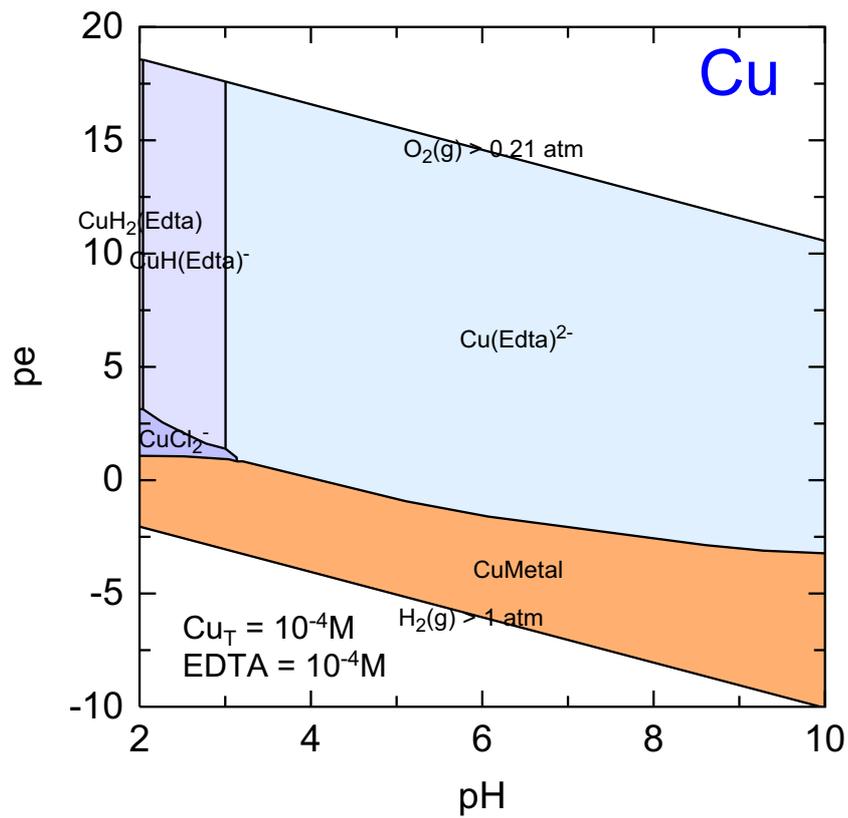
# permitted minerals
  Chalcocite          0 0
  Djurleite           0 0
  Anilite             0 0
  BlaubleiIII         0 0
  BlaubleiI           0 0
  Covellite           0 0
  CuMetal             0 0
  Sulfur              0 0
  Nantokite           0 0
  Cuprite             0 0
  Tenorite            0 0
  Cu(OH)2             0 0
  Melanothallite     0 0
  Nahcolite           0 0
  Atacamite           0 0
  CuCO3              0 0
  Natron              0 0
  Thermonatrite       0 0
  Thenardite          0 0
  Mirabilite          0 0
  Chalcanthite        0 0
  Malachite           0 0

```

CuSO4	0 0
Cu2SO4	0 0
Trona	0 0
CuOCuSO4	0 0
Antlerite	0 0
Azurite	0 0
Brochantite	0 0
Langite	0 0

END



46 Cu-EDTA-H<sub>2</sub>OCu-EDTA  
(using minteq.v4.dat)

C:\PhreePlot\demo\Cuedta\Cuedta\_Cu1.ps

The `wateq4f.dat` database does not contain any data for EDTA so it is necessary to use the `minteq.v4.dat` database which does. However, it is also necessary to add data for the aqueous solubility of  $\text{H}_2(\text{g})$  since this is not included in the `minteq.v4.dat` database.

```

SPECIATION
# for EDTA
  Database                "minteq.v4.dat"
  calculationType         ht1
  calculationMethod       1
  mainSpecies             Cu
# pH range
  xmin                    2.0
  xmax                    10.0
# O2(g) range
  ymin                    -85.0
  ymax                    0.0
  resolution              300
PLOT
  plotTitle               "Cu-EDTA<br>(using minteq.v4.dat)"
  xtitle                  pH
  pymin                   -10.0
# use pe scale even though redox controlled by PO2(g)
  yscale                  pe
# omit domain boundary lines
  domain                  F
  extraText               "extratextCuedta.dat"

CHEMISTRY

SOLUTION_SPECIES
# can help convergence (see Phreeqc_3 manual, KNOBS p 117)
  H2O + 0.01e- = H2O-0.01; log_k -9.0

PHASES
# not in minteq.dat
H2(g)
  H2 = H2
# solubility of H2(g)
  log_k   -3.150
  delta_h -1.759 kcal

# standard hunt and track file
include 'ht1.inc'

# initial solution calculation
SOLUTION 1
  temp 25
# start ing pH below minimum pH cos adding NaOH
  pH 1.8
  units mol/kgw
# total concentrations
  Cu 1e-4
  Edta 1e-4
# background electrolyte
  Na 1e-1
#
  Cl 1e-1
SAVE solution 1
END

# faster split into two simulations as here
USE solution 1
# - only loops on last simulation by default

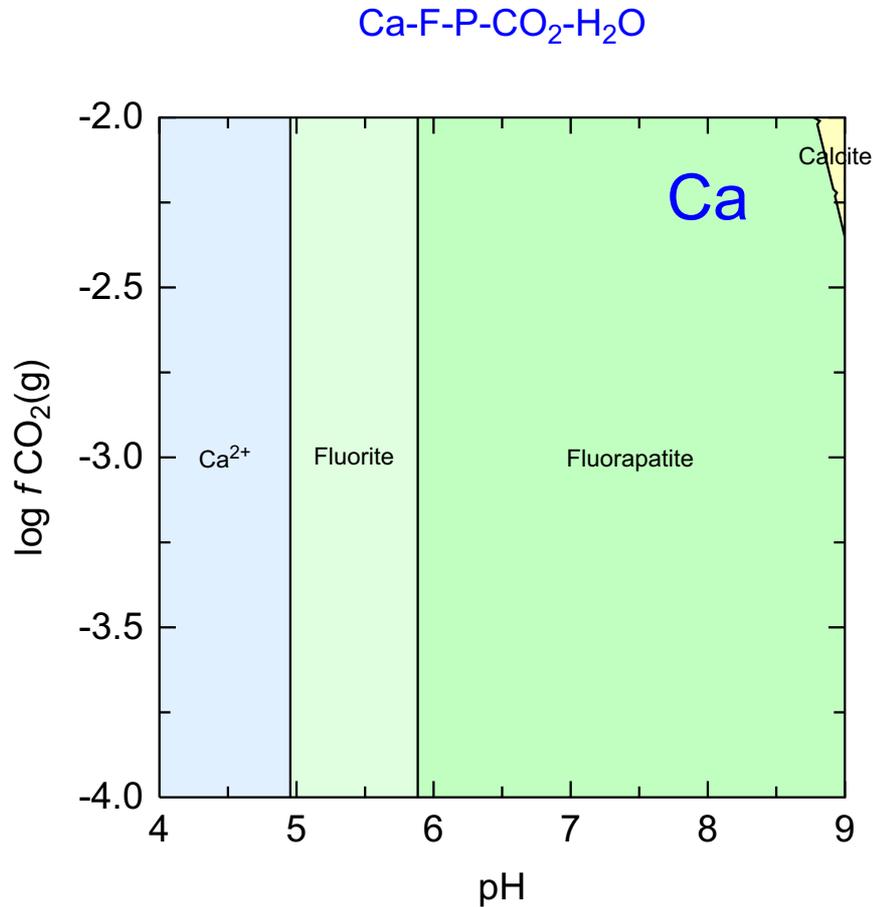
EQUILIBRIUM_PHASES 1
# negative sign converts pH to logH
  Fix_H+ <-x_axis> NaOH 10
  -force_equality true
# limit to 0.1 mol O2 max
  O2(g) <y_axis> 0.1

# possible minerals
  Atacamite 0 0
  Cu(OH)2 0 0

```

```
CuMetal      0 0
Cuprite      0 0
Melanohallite 0 0
Nantokite    0 0
Tenorite     0 0
END
```



47 Ca-F-P-C-H<sub>2</sub>O

C:\PhreePlot\demo\CaF\CaF2\_Ca1.ps

In this example, a predominance diagram is drawn but the y-axis is not related to redox but is the partial pressure of CO<sub>2</sub>(g). The diagram is one way of showing the competition between three Ca minerals as a function of CO<sub>2</sub>(g) and pH – at different points, a fluoride, a phosphate and a carbonate predominate.

```

SPECIATION
  jobTitle          "Calcium in the presence of fluoride, phosphate
and bicarbonate"
  calculationType   ht1
  calculationMethod 1
  mainSpecies       Ca
  xmin              4.0
  xmax              9.0
  ymin              -4.0
  ymax              -2.0
  resolution        200
PLOT
  plotTitle         "Ca-F-P-CO<sub>2</sub>-H<sub>2</sub>O"
  xtitle            pH
  ytitle            "log <i>f</i> CO<sub>2</sub>(g)"
  extraText         "extratextCaF.dat"

CHEMISTRY

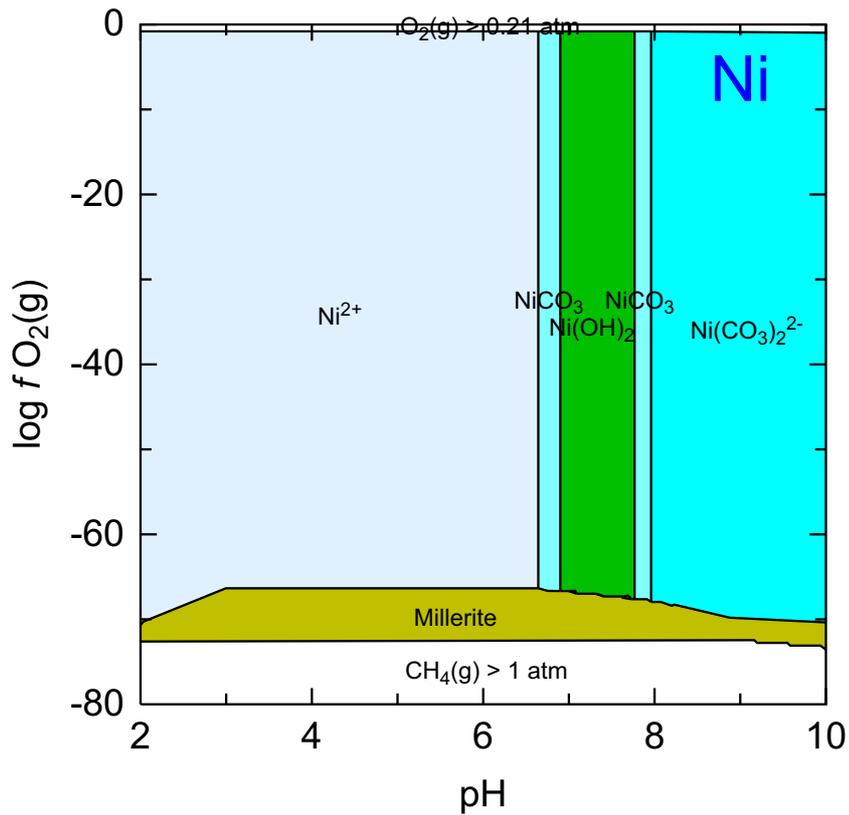
# standard 'hunt and track' file
include 'ht1.inc'

SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  Ca 1e-2
  F 1e-2
  P 3e-3
  Na 1e-1
  Cl 1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 1
  -force_equality true
  CO2(g) <y_axis> 1
  -force_equality true

  Calcite 0 0
  Fluorite 0 0
  Fluorapatite 0 0
  Calcite 0 0
  Aragonite 0 0
END

```

48 Ni-S-C-H<sub>2</sub>ONi-S-C-O<sub>2</sub>-H<sub>2</sub>O at 20°C

C:\PhreePlot\demo\NiS\NiS\_Ni1.ps

A redox-pH predominance diagram for Ni in the presence of C and S. Since some of the Ni minerals do not have mineral names in the database (e.g. Ni(OH)<sub>2</sub>), the `ht1s.inc` include file has been used rather than `ht1.inc` file. This is the same as the `ht1` file except that it appends '(s)' to mineral names making it clear that Ni(OH)<sub>2</sub>(s) is a mineral whereas NiCO<sub>3</sub> is not.

```

# predominance diagram for Ni in the presence of S and C (employing the Halite ploy)

SPECIATION
  jobTitle           "Ni-S-C-H2O"
  calculationType    ht1
  calculationMethod  1
  mainSpecies        "Ni"
# calculate pH 2-10
  xmin               2.0
  xmax               10.0
# calculate log f(O2(g)) -80 to 0
  ymin               -80.0
  ymax               0.0

# track on a 250 x 250 grid
  resolution         250

PLOT
  plotTitle          "Ni-S-C-O<sub>2</sub>-H<sub>2</sub>O at
20<sup>o</sup></sup>C"
  xtitle             pH
  ytitle             "log <i>f</i> O<sub>2</sub>(g)"
  extraText          "extratextNiS.dat"

CHEMISTRY

# first simulation - initial solution calculation

# standard predominance diagram code
include 'htls.inc'

SOLUTION 1
  Temp              20
# initial pH less than pHmin to hope that Fix_H+ works (but see below)
  pH                1.8
  units             mol/kgw
# total Ni etc
  Ni                1e-2
  S(6)              1e-2
# background electrolyte
  Na                1e-1 charge
  Cl                1e-1
SAVE solution 1
END

# second simulation

USE solution 1
EQUILIBRIUM_PHASES 1
# Fix_H+ defined in ht1.inc
  Fix_H+           -<x_axis> NaOH
  -force_equality true
  O2(g)            <y_axis>
# limit max CO2 supplied to 1 mol
  CO2(g)           -1.5      1

# list of possible minerals
  Millerite        0 0
  Sulfur           0 0
  Ni(OH)2          0 0
# reduction of S(6) produces a lot of OH- so may actually need HCl
  Halite           -12 1 dis
# (or -NaOH) to adjust pH - can't specify +NaOH and +HCl so use -NaOH.
  Bunsenite        0 0
# This Halite phase ensures that there will always be some Na to take away.
  NiCO3            0 0
# To avoid this, either reduce initial pH to pH 1 or add more Na(Cl) or add less
S(6).

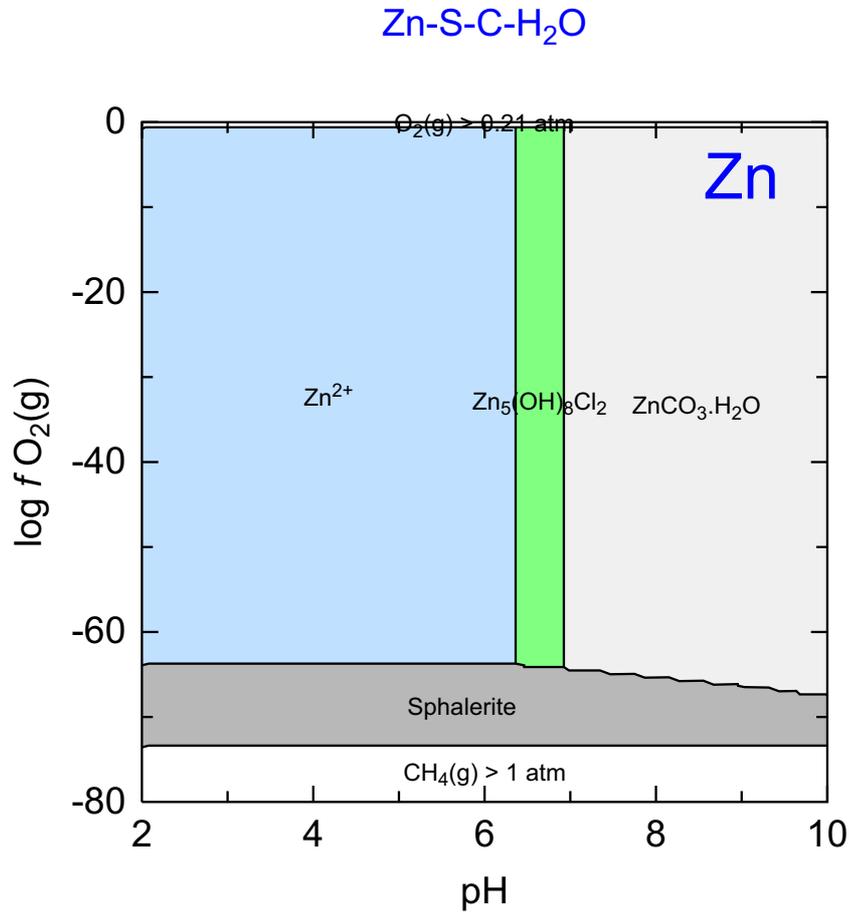
```

434 *PhreePlot Guide*

Nahcolite	0 0
Morenosite	0 0
Retgersite	0 0
Natron	0 0
Thermonatrite	0 0
Thenardite	0 0
Mirabilite	0 0
Ni <sub>4</sub> (OH) <sub>6</sub> SO <sub>4</sub>	0 0
Trona	0 0

END



49 Zn-S-C-H<sub>2</sub>O

C:\PhreePlot\demo\ZnS\ZnS\_Zn1.ps

This is similar to the previous example except that it is for Zn not Ni. As before, the 'htls.inc' file was used so that '(s)' has been appended to the mineral names, which in this case included Zn<sub>5</sub>(OH)<sub>8</sub>Cl<sub>2</sub>.

```

SPECIATION
  jobTitle           "Zn-C-H<sub>2</sub>O"
  calculationType    ht1
  calculationMethod   1
  mainSpecies        Zn
  xmin               2.0
  xmax               10.0
  ymin               -80.0
  ymax               0.0
  resolution         200

PLOT
  plotTitle          "Zn-S-C-H<sub>2</sub>O"
  xtitle             pH
  ytitle             "log <i>f</i> O<sub>2</sub>(g)"
  extraText          "extratextZnS.dat"

CHEMISTRY

include 'ht1s.inc'

PHASES
Hydrozincite
  Zn5(OH)6(CO3)2 + 10H+ = 5Zn+2 + 2CO2 + 8H2O
#9.0
  log_k 45.0
#Preis & Gamsjager 2001
  -delta_H -256.5 kJ

SOLUTION 1
  Temp      20
# start at pH less than pHmin for Fix_H+
  pH        1.8
  units     mol/kgw
# total Zn
  Zn        1e-1
# also redox sensitive
  S(6)      1e-1
  Na        1e-1
  Cl        1e-1 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis> 0.1
  CO2(g)    -3      1.0

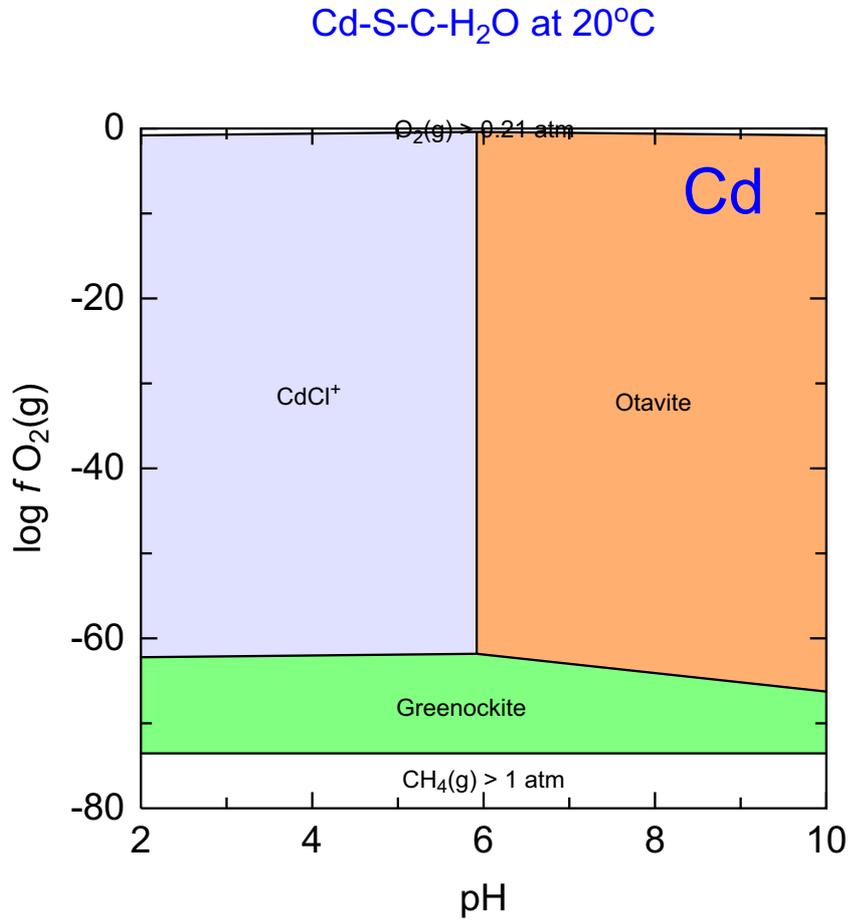
# minerals that could ppt
  Sphalerite      0 0
  Wurtzite        0 0
  ZnS(a)          0 0
# to maintain some Na at all times
  Halite          -10 1 dis
  Sulfur          0 0
  ZnO(a)          0 0
  Zincite(c)     0 0
  Zn(OH)2-e      0 0
  Zn(OH)2-g      0 0
  Zn(OH)2-b      0 0
  Zn(OH)2-c      0 0
  Zn(OH)2-a      0 0
  ZnCl2          0 0
  Zn2(OH)3Cl     0 0
  ZnCO3:H2O      0 0
  Smithsonite    0 0
  Nahcolite      0 0

```

ZnMetal	0 0
Natron	0 0
Goslarite	0 0
Thermonatrite	0 0
Bianchite	0 0
ZnSO4:H2O	0 0
Thenardite	0 0
Mirabilite	0 0
Zn5(OH)8Cl2	0 0
Zincosite	0 0
Zn2(OH)2SO4	0 0
Trona	0 0
Zn4(OH)6SO4	0 0
Zn3O(SO4)2	0 0

END



50 Cd-S-C-H<sub>2</sub>O

C:\PhreePlot\demo\CdS\CdS\_Cd1.ps

In this example, [simplify](#) was set to a high value (10) in order to eliminate the 'steppiness' of the low-angled Greenockite-Otavite boundary.

```

SPECIATION
  jobTitle                "Cd in the presence of sulphur"
  calculationType         ht1
  calculationMethod       1
  mainSpecies            Cd
# logH range
  xmin                    2.0
  xmax                    10.0
# O2(g) range
  ymin                    -80.0
  ymax                    0.0
  resolution              100
# straightens out the low-angled boundary
  simplify                10

PLOT
  plotTitle               "Cd-S-C-H<sub>2</sub>O at 20<sup>o</sup>C"
  xtitle                  pH
  ytitle                  "log <i>f </i>O<sub>2</sub>(g)"
  extraText               "extratextCdS.dat"

CHEMISTRY

# standard 'hunt and track' file
include ht1.inc

SOLUTION 1
  Temp      20
  pH        1.8
  units     mol/kgw
# total Cd
  Cd        1e-1
  S(6)      1e-1
# background electrolyte
  Na        1e-1
  Cl        1e-1
SAVE solution 1
END

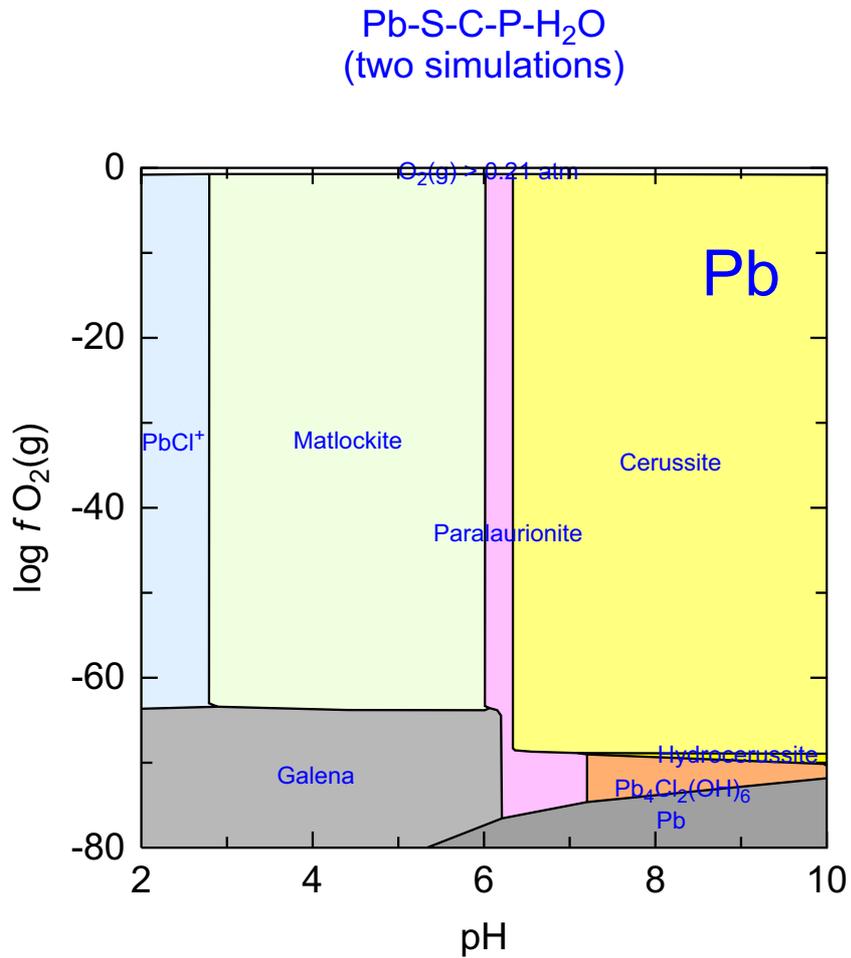
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+    -<x_axis> NaOH
            -force_equality true
  O2(g)     <y_axis> 0.1
  CO2(g)    -3.5      1.0

Greenockite          0 0
CdCl2:2.5H2O         0 0
CdCl2:H2O            0 0
CdCl2                0 0
Sulfur               0 0
CdOHCl               0 0
Cd(OH)2              0 0
Monteponite          0 0
Cd(OH)2(a)           0 0
CdMetal              0 0
Cd(gamma)            0 0
Otavite              0 0
Nahcolite            0 0
Natron                0 0
Thermonatrite        0 0
CdSO4:2.7H2O         0 0
CdSO4:H2O            0 0
Thenardite           0 0
Mirabilite           0 0
CdSO4                0 0
Trona                0 0
Cd3(OH)4SO4          0 0
Cd4(OH)6SO4          0 0
Cd3(OH)2(SO4)2       0 0

```





51 Pb-S-C-P-H<sub>2</sub>O

C:\PhreePlot\demo\Pb\Pb\_Pb1.ps

This is quite a ‘challenging’ diagram to generate. It has with competing mineral phases and some close, low-angled boundaries.

The colour of the info text and the field labels have been set to blue with `info` and `labelColor`, respectively.

```

SPECIATION
  jobTitle                "Lead speciation"
# large database
  Database                llnl.dat
# hunt and track approach
  calculationType         ht1
  calculationMethod       1
  mainSpecies             "Pb"
  xmin                    2.0
  xmax                    10.0
  ymin                    -80.0
  ymax                    0.0
# tracks on a 500 x 500 grid
  resolution              500

PLOT
  plotTitle               "Pb-S-C-P-H<sub>2</sub>0<br>(two simulations)"
  xtitle                  pH
  ytitle                  "log <i>f</i> O<sub>2</sub>(g)"
# colour of the field labels
  labelColor              blue
# colour of the info and filename
  info                    nd blue
  extraText               "extratextPb.dat"

CHEMISTRY

  include 'htl.inc'

# first simulation - initial solution calculation only
SOLUTION 1
  temp 25
  pH 1.8
  units mol/kgw
  Pb 5e-4
  S 2e-4
  F 5e-4
  P 1e-5
  Na 1e-1
  Cl 1e-1 charge
SAVE solution 1
END

# second simulation - equilibrate

# saves recalculation
USE solution 1

EQUILIBRIUM_PHASES 1
  Fix_H+ <x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3 1.0

# these minerals were obtained by first running with resolution = 1 & PRINT -true
Pb(H2PO4)2 0 0
# this special case produces a list of all the possible mineral species
Pb4O(PO4)2 0 0
Pyromorphite-OH 0 0
Pb3(PO4)2 0 0
PbHPO4 0 0
Galena 0 0
#Ice 0 0

  Matlockite 0 0
  PbFCl 0 0
#Halite 0 0

  Cotunnite 0 0

```

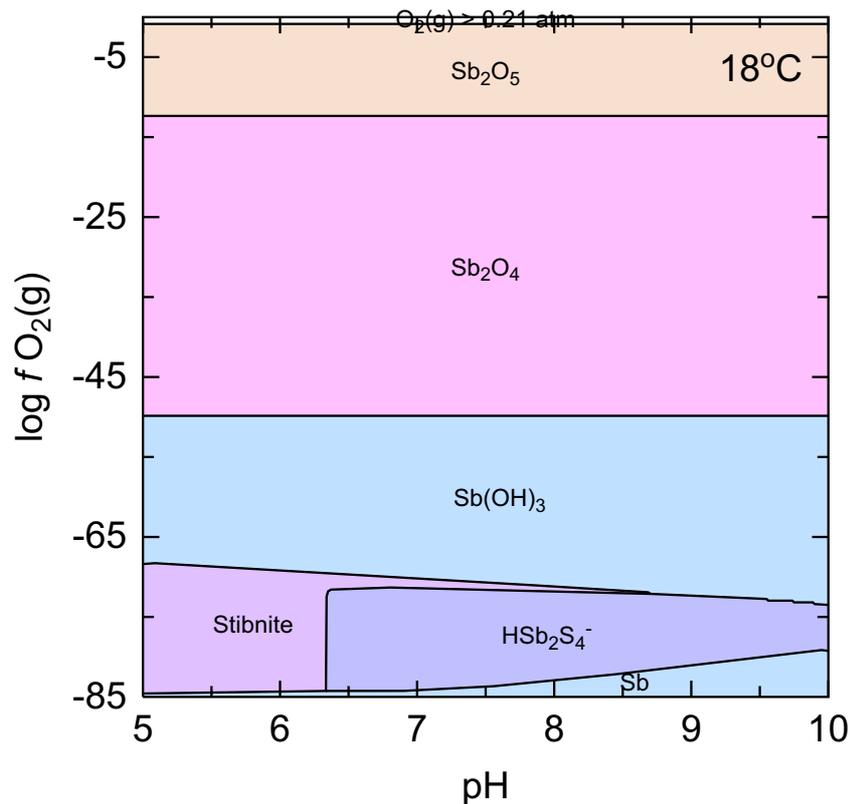
Paralaurionite	0 0
S	0 0
Pb	0 0
PbF2	0 0
C	0 0
Litharge	0 0
Massicot	0 0
Nahcolite	0 0
Cerussite	0 0
Anglesite	0 0
Phosgenite	0 0
Pb2Cl2CO3	0 0
Mirabilite	0 0
Pb4Cl2(OH)6	0 0
Thenardite	0 0
Natron	0 0
Na2CO3:7H2O	0 0
Thermonatrite	0 0
Na2CO3	0 0
Lanarkite	0 0
PbCO3.PbO	0 0
Na	0 0
Plattnerite	0 0
Pyromorphite	0 0
Pb3SO6	0 0
Na2O	0 0
Pb4SO7	0 0
Na3H(SO4)2	0 0
Hydrocerussite	0 0
Minium	0 0
Burkeite	0 0

END



## 52 Sb-S

Sb-S-O<sub>2</sub>-CO<sub>2</sub>-H<sub>2</sub>O  
(demonstrates increased weighting of Fix\_H+)



C:\PhreePlot\demo\SbS\SbS\_Sb1.ps

This is also an awkward example to specify properly because  $\text{Sb(OH)}_3$  is present as both a solution species and a mineral species in the `11nl.dat` database. It is necessary to ensure that the species names are actually different not just for plotting but also so that the tracking is able to differentiate between them. As before, this is achieved by using the `ht1s.inc` include file which appends '(s)' to all mineral species names. In this case, the differentiation is not just useful for making the plot more legible but is also important for actually generating the proper boundaries.

The resolution has been set at 400 which produces the plot without problems. However, **PhreePlot** fails to converge at some lower resolutions such as 100 because of problems in the lower left-hand corner. There is a narrow sliver of  $\text{Sb(s)}$  which is uncomfortably close to the lower axis boundary. **PhreePlot** therefore automatically increases the resolution until it converges. The 'steppiness' of the low-angled boundaries at low resolutions can be reduced or eliminated by increasing the [resolution](#) or the simplification factor using [simplify](#).

```

SPECIATION
  jobTitle          "Sb-O2-H2O"
# has Sb data
  Database          llnl.dat
  calculationType   ht1
  calculationMethod 1
  mainSpecies       "Sb"
  xmin              5.0
  xmax              10.0
  ymin              -85.0
  ymax              0.0
# need an even higher resolution to get smooth low-angled boundaries
  resolution        400

PLOT
  plotTitle         "Sb-S-O<sub>2</sub>-CO<sub>2</sub>-H<sub>2</sub>O<br>(demonstrates increased weighting of Fix_H+)"
  xtitle            pH
  ytitle            "log <i>f</i> O<sub>2</sub>(g)"
  extraText         "extratextSbS.dat"

CHEMISTRY

# first simulation

# adds "...(s)" for mineral phases to avoid confusion with aq species
include 'htls.inc'

PHASES

Fix_H+
  H+ = H+
  log_k 0.0

# Kerfoot, GWB 15 Dec 2005
SOLUTION 1
  Temp      18
  pH        3.00
  units     mol/kgw
# total Sb
  Sb        3e-7
  S(6)      4.4e-4
  Na        0.0027
  K         0.00020
  Mn        1e-4
  Ca        9.93e-4
  Fe(2)     1e-4
  Cl        5e-5
SAVE solution 1
END

# second simulation
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+  -<x_axis> NaOH
  -force_equality true
  O2(g)   <y_axis> 0.1
  CO2(g)  -3.523 1.0

  Pyrite      0 0
  Stibnite    0 0
  Sb          0 0
  Sb(OH)3     0 0
  S           0 0
  Fe(OH)2     0 0
  Mn(OH)2(am) 0 0
  Sb2O3       0 0
  Fe(OH)3     0 0
  Sb2O4       0 0

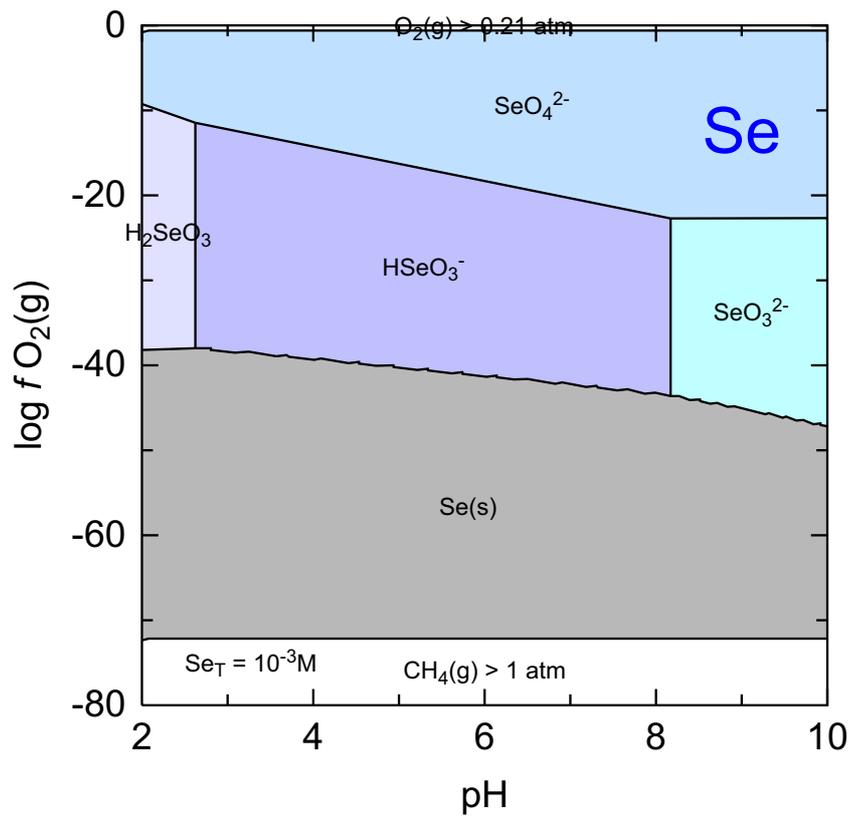
```

450 *PhreePlot Guide*

```
Sb406 (cubic)      0 0
Rhodochrosite     0 0
Siderite          0 0
Calcite           0 0
Sb406 (orthorhombic) 0 0
Sb205             0 0
END
```



## 53 Se-S

Selenium protonation and redox  
(no adsorption)

This plot was produced with the `wateq4f.dat` database. The low-angled boundaries for  $\text{Se}(\text{s})$  was rather 'steppy' and so `simplify` was set to 3. Selenium metal is stable under a wide range of reducing conditions.

```

SPECIATION
  jobTitle                "Plutonium redox and speciation"
# contains Se species
  Database                wateq4f.dat
  calculationType         ht1
  calculationMethod       1
  mainSpecies             "Se"
# pH 2 to 10
  xmin                    2.0
  xmax                    10.0
# redox
  ymin                    -80.0
  ymax                    0.0
# some low-angled boundaries could benefit from higher resolution or more smoothing
  resolution              200

PLOT
  plotTitle               "Selenium protonation and redox<br>(no adsorp-
tion)"
  xtitle                  pH
  ytitle                  "log <i>f</i> O<sub>2</sub>(g)"
  labelSize               2.0
  extraText               "extratextSe.dat"

CHEMISTRY

# first simulation - initial solution calculation

# each adsorbed species is counted separately
include 'ht1.inc'

SOLUTION 1
  temp 25
# start out at pH<xmin
  pH 1.8
  units mol/kgw
# total Se
  Se 1e-3
  Na 1e-1
  Cl 1e-1
  S 1e-3
SAVE solution 1
END

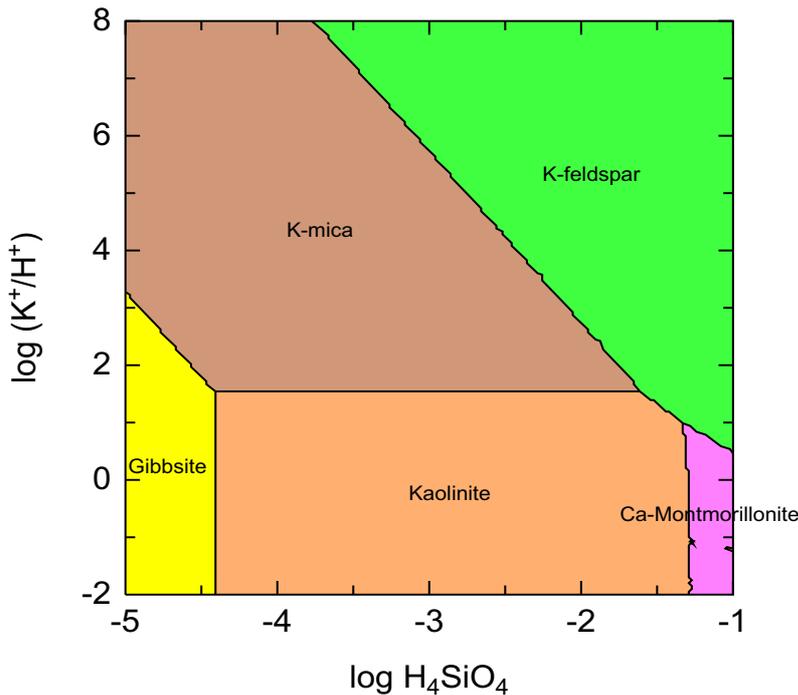
# second simulation - equilibrate
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  CO2(g) -3.5 1.0

# possible Se minerals
  Se(s) 0 0
  Mirabilite 0 0
  Thenardite 0 0
  Sulfur 0 0
  SeO2 0 0
END

```

## 54 Clay mineral stability diagram

Clay mineral stability diagram  
(using mainSpecies = minerals)



C:\PhreePlot\demo\minstab\minstab\_minerals1.ps

**PhreePlot** is not recommended for drawing the type of mineral stability diagrams often used in mineral geochemistry as the large range of activities often involved can lead to problems of convergence. However, in principle, such diagrams can be calculated and this example is one such calculated using the 'ht1' procedure. It plots the most abundant mineral at any particular point. The logic for determining the boundaries is in the include file 'minstab1.inc'.

The main species has been set to 'mineral' as it is counting all minerals, not just minerals of a particular element. The x- and y-axes are driven by 'fixing' the  $H_4SiO_4$  activity and the  $K^+/H^+$  activity ratio, respectively, using fictitious phases defined in the PHASES keyword block.

The diagram shows the predominant mineral species (in terms of moles). Pure phases fix the activity or activity product of their constituent species. The indicated mineral is often the only mineral present (except on the phase boundaries). This is reflected by the NA code that appears on the screen for the sub-dominant species. If no mineral is stable, the field is labelled 'No minerals present'. This can be demonstrated in this example by changing the units of concentration from mol/kgw to umol/kgw.

It can be difficult to fix the activity ratios over a wide range of values using the present approach and numerical errors can mean that the boundaries are rather ragged (see bottom right-hand corner). In such cases, the 'grid' approach may be a better option. An alternative is to plot the mineral with the largest *theoretical* supersaturation (see the minstab2.ppi demo).

```
# an example of a classical mineral stability diagram - diagram only includes min-
erals (not aqueous etc species)
```

```
SPECIATION
  jobTitle                "Clay mineral stability diagram"
  Database                 "phreeqc.dat"
# use this approach for finding field boundaries of most abundant minerals
  calculationType         ht1
  calculationMethod        1
# NB "minerals" is a special case that invokes this type of plot
  mainSpecies              "minerals"
  xmin                     -5.0
  xmax                     -1.0
  ymin                     -2.0
  ymax                     8.0
  resolution               200
PLOT
  plotTitle                "Clay mineral stability diagram<br>(using
mainSpecies = minerals)"
  xtitle                   "log H<sub>4</sub>SiO<sub>4</sub>"
  ytitle                   "log (K<sup>+</sup>/H<sup>+</sup>)"
```

#### CHEMISTRY

```
# first simulation - initial solution calculation

# special file for generating mineral stability diagrams
include 'minstabl.inc'
```

#### PHASES

```
# used for driving the x-axis variable
Fix_Si
  H4SiO4 = H4SiO4
  log_k 0.0

# used for driving the y-axis variable
Fix_H/K
  KOH = K+ + H2O - H+
  log_k 0.0
```

#### PRINT

```
  reset FALSE
SOLUTION 1
# this also controls the diagram
  pH          7
  units       mol/kgw
# added by reaction
  K           0
  Na          1e-2
  Cl          1e-2
  Al          1e-2
# added by reaction
  Si          0
  Ca          1e-2
SAVE solution 1
END
```

```
# second (final) simulation - iterates on this simulation when driving the x- and y-
axes
```

```
USE solution 1
EQUILIBRIUM_PHASES 1
# fix H4SiO4 activity
  Fix_Si <x_axis> H4SiO4 10
# fix H/K activity ratio
  Fix_H/K <y_axis> KOH 10

# list of minerals considered
```

```
Kaolinite          0 0
K-feldspar         0 0
K-mica             0 0
Gibbsite           0 0
# SiO2(a)          0 0          # can't add this
cos Si activity fixed by Fix_Si
  Ca-Montmorillonite 0 0
END
```

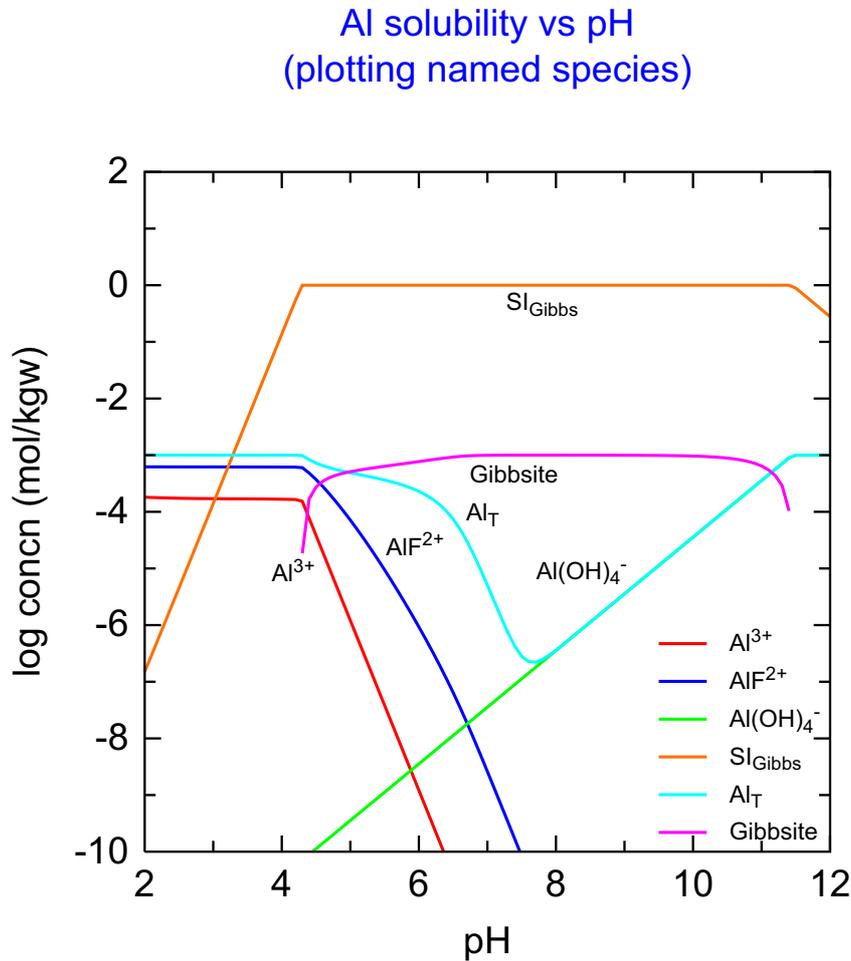
# Custom plots

---

Custom plots refer to plots created directly from `USER_PUNCH` code. **PHREEQC** provides a very versatile mechanism for writing output to the selected output 'file' using `BASIC` code within `USER_PUNCH` keyword data blocks. This output is accumulated in the 'out' file which is then used for plotting.

The following examples give a guide as to how to create custom plots.

## 55 Gibbsite solubility vs pH



C:\PhreePlot\demo\Alvsph\Alvsph.ps

A custom plot showing the concentration of Al complexes as a function of pH. The species plotted have been explicitly defined in the input file. The saturation index for gibbsite has also been plotted.

This example demonstrates simple looping using the x axis variable. [Xmin](#) and [xmax](#) control the range of values taken by the `<x_axis>` tag. [Resolution](#) determines the number of sub-divisions within the x-axis and so directly controls the number of points calculated for each curve. Here the resolution is 200 which is more than enough to get smooth curves.

Species names and plot labels have been defined by the headings given in the `USER_PUNCH` keyword data block. This writes the headings to the selected output file which are then copied to the 'out' file which is then used for plotting. Note that text enhancement tags such as subscript can be used in the headings and passed through to the plot.

The curves plotted have been defined with the [lines](#) keyword and have auto colour selection. The order of plotting and the order in which the labels are printed in the legend is determined

by the order `PUNCHED` in the selected output file. The legend has been moved from its default position to the right of the plot into the plot area using the `<legend>` tag in the `extraText` file.

```

SPECIATION
  calculationType          custom
  calculationMethod        1
  xmin                     2.0
  xmax                     12.0
# determines the number of 'points' on the curves (i.e. PHREEQC runs)
  resolution               101

PLOT
# <br> causes a line break
  plotTitle                "Al solubility vs pH<br>(plotting named spe-
cies)"
  xtitle                   pH
  ytitle                   "log concn (mol/kgw)"
# force the y-axis range
  pymin                    -10.0
  pymax                    2.0
# in the units currently in force
  lineWidth                0.4
# x-axis variable -'pH' must match the name of one of the punched columns below
  customXcolumn            pH
# y-axis variables in legend order
  lines                    Al+3 AlF+2 Al(OH)4- SI<sub>Gibbs</sub>
Al<sub>T</sub> Gibbsite
  extraText                "extratextAlvsph.dat"
# turns off the little red label 'anchors'
  trackSymbolSize          0

CHEMISTRY

SELECTED_OUTPUT
  reset false
  high_precision true

PHASES
Fix_H+
  H+ = H+
  log_K 0.0
SOLUTION 1 Total Al
  units mol/kgw
  Al 1e-3
  F 1e-3
  S(6) 1e-3
  Na 1e-1
  Cl 1e-1

USER_PUNCH
# this is where 'pH' and all the y-axis variables are defined
headings pH Al+3 AlF+2 Al(OH)4- SI<sub>Gibbs</sub> Al<sub>T</sub> Gibbsite
-start
10 totel = SYS("Al",n,n$,t$,c)
20 mol_gibbsite = equi("Gibbsite")
30 REM -99999 is PhreePlot's UNDEFINED value
40 IF (mol_gibbsite > 0) THEN log_gibbsite = log10(mol_gibbsite) ELSE log_gibbsite
= -99999
50 PUNCH -la("H+"), lm("Al+3"), lm("AlF+2"), lm("Al(OH)4-"), SI("Gibbsite"),
log10(tot("Al")), log_gibbsite
-end
END

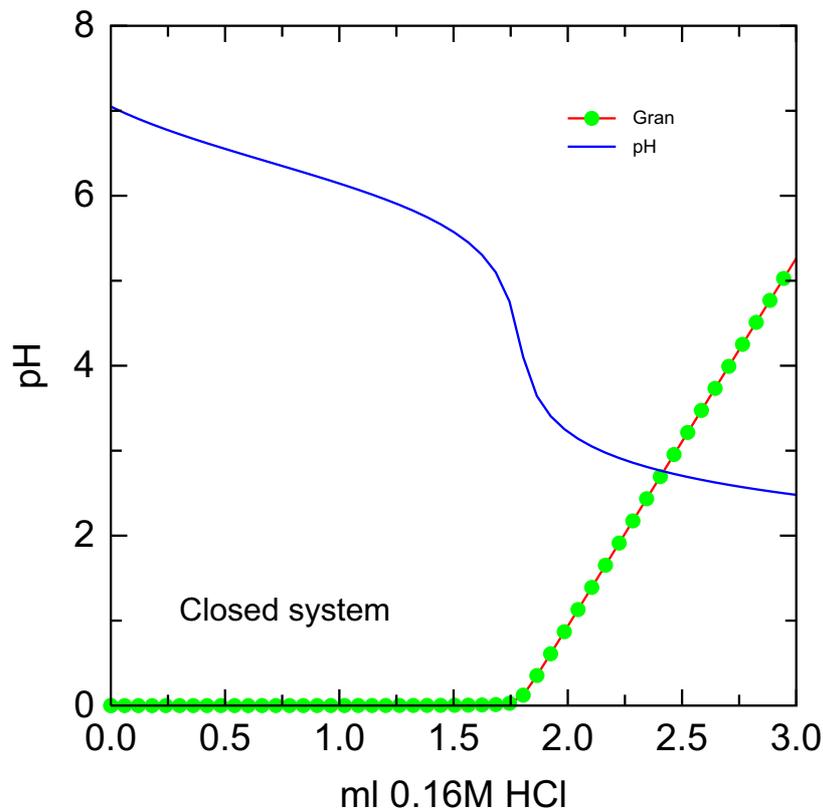
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
# these are the possible minerals considered
  Gibbsite 0 0
# Al(OH)3(a) 0 0
  Basaluminite 0 0
  Boehmite 0 0
  Jurbanite 0 0
END

```



## 56 Acid titration of groundwater (using 'REACTION')

Acid titration of 50 mL of groundwater  
(using REACTION keyword)



C:\PhreePlot\demo\titration\titration.ps

This example demonstrates how a single iteration of **PHREEQC** can generate a multiline `SELECTED_OUTPUT` file. Each of the `REACTION` steps produces a line of output. `RXN` gives the moles of reactant used at each step and this is converted to mmoles for plotting. [resolution](#) has been set to 1 because only iteration is used.

The [selectedOutputLines](#) setting has been set to `auto` which signals that all lines in the selected output are transferred to the 'out' file rather than just the last line.

The labels normally attached to each line have been suppressed by setting [labelSize](#) to 0. The legend has been moved inside the plot with the [<legend>](#) tag in the [extraText](#) file.

It is much faster to use **PHREEQC**'s internal looping like this compared with **PhreePlot**'s looping mechanisms. Having said that, calculation times are often so short that speed is not an issue for simple calculations like this.

```

SPECIATION
  calculationType          custom
  calculationMethod        1
# get as many lines as there are -> out file
  selectedOutputLines      auto

PLOT
  plotTitle                "Acid titration of 50 mL of groundwa-
ter<br>(using REACTION keyword)"
  xtitle                   "ml 0.16M HCl"
  ytitle                   pH
  customXcolumn            ml
  pxmax                    3
# from selected output
  lines                    pH Gran
# from selected output
  points                   Gran
# suppress curve labels inside plot
  labelSize                0
  lineColor                blue
  pointColor               green
  extraText                extratexttitration.dat

CHEMISTRY

SELECTED_OUTPUT
  -reset false

# Groundwater                                # the groundwater to titrate with HCl
SOLUTION 1
  pH      7.05
  units mg/L
# temp 10.5
  water 0.050 kg
  Na     6
  K      0.6
  Ca     124
  Mg     1.6
  Cl     11
  Alkalinity 348 as HCO3
  S(6)   3 as SO4
  Si     5.8

REACTION 1 Add HCl to the soln
# 1 mL of 0.16M HCl                                # this takes into account the dilu-
tion since it includes water
  HCl    0.16e-3
  H2O    55.5e-3
  3 in 50 steps

USER_PUNCH
  -headings ml pH water Gran
# assumes density = 1
10 VT = TOT("water")*1000
20 V = VT-50
30 pH = -la("H+")
40 Gran = VT*(10^-pH)*30
50 punch V, pH, VT, Gran

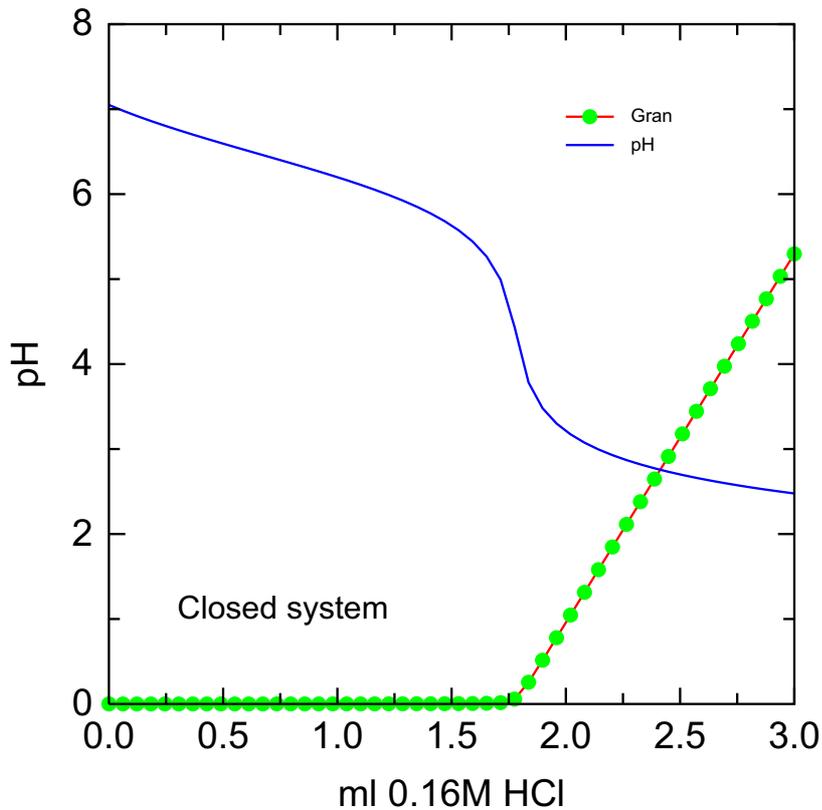
GAS_PHASE
  -fixed_volume
# 10 mL gas + 50 mL solution
  -volume      0.01
# equilibrate with solution 1 to begin with - this leads to some initial degassing
  -equilibrate 1
  CO2(g)

END

```

## 57 Acid titration of groundwater (using PhreePlot looping)

Acid titration of 50 mL of groundwater  
(using MIX keyword)



C:\PhreePlot\demo\titration\titration2.ps

This is essentially the same example as the previous example but has been calculated using one of **PhreePlot**'s own looping mechanisms. This involves using a 1 mol/kgw solution of HCl to titrate the groundwater. The titration is achieved using the `MIX` keyword.

This approach includes the dilution brought about by the titration (the `REACTION` approach essentially titrates with 'solid' HCl). In this case, the dilution is very small.

## SPECIATION

```

calculationType          custom
calculationMethod        1
xmin                     0.0
xmax                     3.0E-03
resolution               50
numericTags              <titre> = "<x_axis>"

```

## PLOT

```

plotTitle                "Acid titration of 50
mL of groundwater<br>(using MIX keyword)"
xtitle                   "ml 0.16M HCl"
yttitle                  pH
lineColor                blue
customXcolumn           ml
lines                   pH Gran
points                   Gran
pointColor               green
labelSize                0
extraText                "extratexttitration.dat"

```

## CHEMISTRY

## SELECTED\_OUTPUT

```
-reset false
```

TITLE Acid titration of groundwater (assumes no CO2 loss)

## SOLUTION 1 # Groundwater

```

pH      7.05
units mg/L
temp    10.5
water   0.050 kg
Na      6
K       0.6
Ca     124
Mg     1.6
Cl     11
Alkalinity 348 as HCO3
S(6)   3 as SO4
Si     5.8

```

## SOLUTION 2

```

units mol/kgw
pH    1 charge          # 0.16 mol/
kgw HCl
Cl    0.16
END

```

```

MIX 1 Add 0.1M HCl to the soln          # mix two
solutions, the sample and the acid
1    1
2    <titre>                          # driven by
x loop parameters, see above

```

## USER\_PUNCH

```

-headings ml pH VT Gran
1 pH = -la("H+")
10 V = <titre>*1000
11 VT = (0.05 + <titre>)*1000
20 Gran = VT*(10^-pH)*30
30 punch V, pH, VT, Gran

```

## GAS\_PHASE

```

-fixed_volume
-volume      0.01          # 10 mL gas
+ 50 mL solution
-equilibrate 1            # equilibrate
with solution 1 to begin with - this leads to some initial
degassing
CO2(g)

```

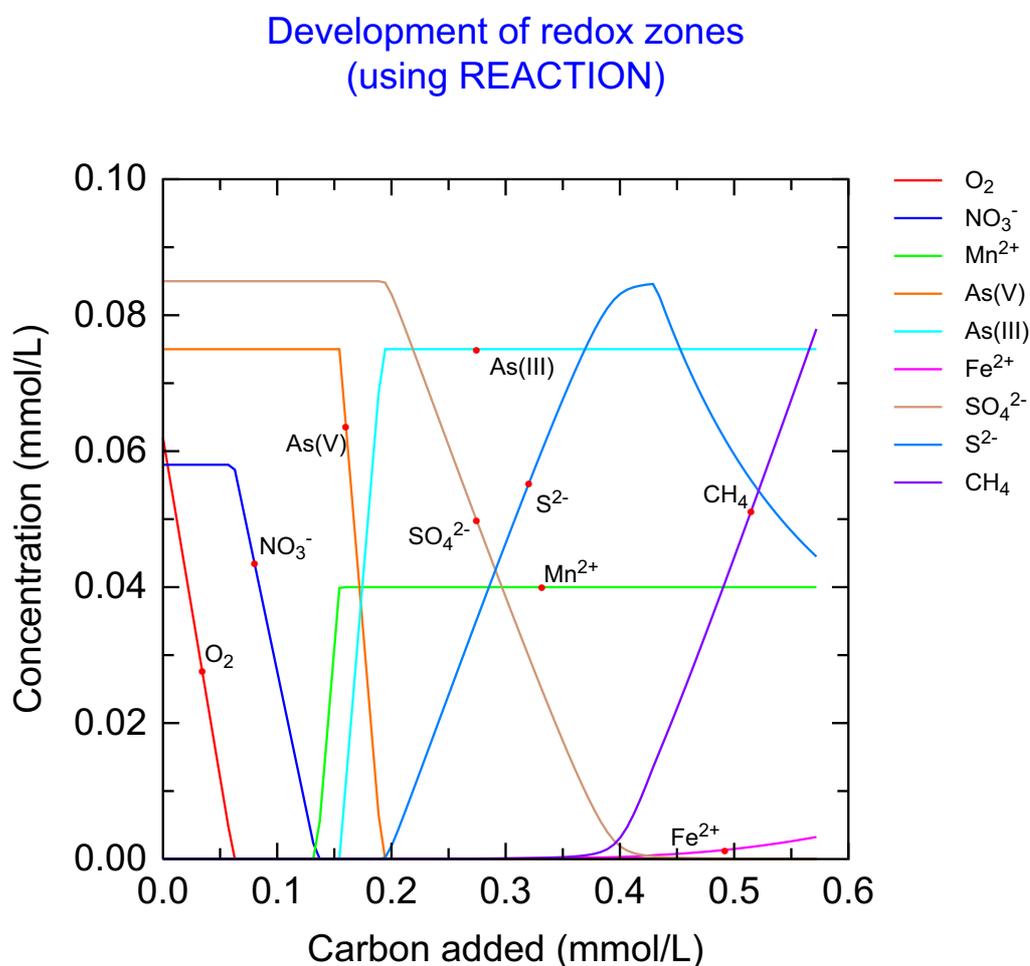
```

END

```



## 58 Redox sequence



This example (from [Appelo and Postma, 2005](#), Fig. 9.17) shows how a single iteration of **PHREEQC** (using the `REACTION` keyword) can generate a series of points that can be assembled to give the 'redox ladder' plot indicated. The `REACTION` keyword generates its own internal looping and so there is no need for **PhreePlot** loops.

The curves show the successive reduction of various solutes as the groundwater is titrated with C (as in organic matter) in the presence of a small amount of goethite and pyrolusite.

The label names have been set explicitly by making them the names for the headings in the selected output. These names get passed to the 'out' file which is then used for plotting. Note that the default assumes that all labels are species names and so are interpreted with superscripts etc. accordingly. This behaviour can be suppressed by setting `convertLabels` to `FALSE`.

The order of species plotted and in the legend is determined from the order `PUNCHED` to the selected output. `FeS(ppt)` is the only mineral that is allowed to form.

The script could be generalised by using tags to define the number of steps used, the mol of C

added and the initial solution concentrations. For example, to define just the first two of these, the following changes could be made:

(i) add to the **PhreePlot** section

```
numericTags                <steps> = 100 \  
                           <molCadded> = 0.572e-3
```

(ii) change line 10 in the **USER\_PUNCH** data block

```
10 addedc=step_no*<molCadded>*1e3/<steps>
```

(iii) change the **REACTION** data block

```
REACTION 1  
  CH2O; <molCadded> in <steps> steps  
INCREMENTAL_REACTIONS true  
END
```

```

# titrate with C (like glucose)

SPECIATION
  jobTitle           "Development of redox zones (A&P, Fig 9.17)"
  calculationType    custom
  calculationMethod  1
# just one iteration since REACTION has its own looping mechanism
  resolution        1
# copy all lines in selected.out to out file
  selectedOutputLines auto

PLOT
  plotTitle          "Development of redox zones<br>(using REAC-
TION)"
  xtitle             "Carbon added (mmol/L)"
  ytitle             "Concentration (mmol/L)"
# heading from out file (derived from selected.out)
  customXcolumn      C
# headings from out file (derived from selected.out)
  lines              O2 NO3- Mn+2 As(V) As(III) Fe+2 SO4-2 S-2 CH4

CHEMISTRY

SELECTED_OUTPUT
  -reset false
  -high_precision true
USER_PUNCH
  headings C O2 NO3- Mn+2 Fe+2 SO4-2 S-2 CH4 As(V) As(III)
-start
10 addedc=step_no*0.572/100
20 punch addedc, 1000*tot("O(0)"/2, 1000*tot("N(5)"), 1000*tot("Mn"),
1000*tot("Fe(2)"), \
1000*tot("S(6)"), 1000*tot("S(-2)"), 1000*tot("C(-4)"), 1000*tot("As(5)"),
1000*tot("As(3)")
-end

SOLUTION 1
  pH      7.1
  Na      1.236
  K       0.041
  Mg      0.115
  Ca      0.067
  Cl      1.467
  N(5)    0.058
  S(6)    0.085
  As(5)   0.075
  Alkalinity 0.26
  O(0)    0.124

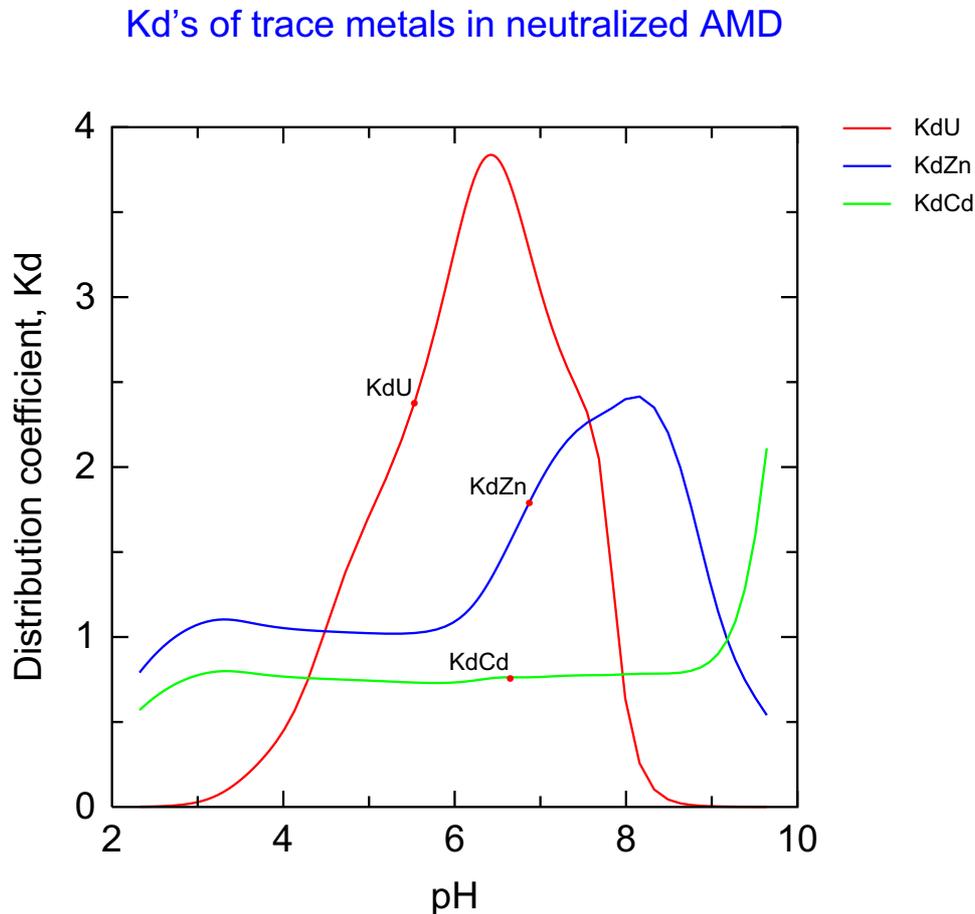
EQUILIBRIUM_PHASES
# start with some
  Goethite 0 2.5e-3
# start with none
  FeS(ppt) 0 0
# start with some
  Pyrolusite 0 4e-5

REACTION 1
# internal looping by REACTION data block
  CH2O; 0.572e-3 in 100 steps
INCREMENTAL_REACTIONS true
END

```



## 59 Kd's for trace metals as a function of pH



C:\PhreePlot\demo\kd\kd.ps

This example (from [Appelo and Postma, 2005](#), Fig. 11.19) also uses the `REACTION` keyword to generate a series of curves showing the variation of solid/solution partition coefficient ( $K_d$ ) as a function of pH for U, Zn and Cd.

It uses the `SURF()` function to get the total number of moles of each element adsorbed to a particular mineral surface (here `HfO`) and `TOT()` to get the total number of moles of each element remaining in solution. Cd and Zn are also bound by ion exchange reactions on kaolinite. The total bound includes both adsorbed and exchanged species so these must be added together to calculate the  $K_d$ .

The initial solution is a sample of acid mine drainage in equilibrium with a quartz-rich sediment. This is progressively neutralized with NaOH. The trace metals are bound to Hfo and kaolinite and the  $K_d$ 's reflect how binding to these two surfaces changes with pH. Cd and Zn are mostly bound to kaolinite at low pH and this is modelled as a simple pH-independent cation exchange reaction. At high pH, binding to ferrihydrite becomes important. U sorption is out-competed by other trace metals on ferrihydrite at low pH. At high pH, various negatively charged U species dominate in solution which works against their sorption at high pH.

```

# plots the solid/solution partition coefft (Kd) for the sorption of metals by HFO
as a function of pH

SPECIATION
  jobTitle                "Kd's of trace metals in neutralized AMD (A&P,
Fig 11.19)"
  calculationType          custom
  calculationMethod        1                # 1 = calculate
and plot
  resolution              1                # just one
iteration of x- and y-axis variables
  selectedOutputLines     auto             # auto = results
will be on the last line of the selected output

PLOT
  plotTitle               "Kd's of trace metals in neutralized AMD"
  xtitle                  pH
  ytitle                  "Distribution coefficient, Kd"
  customXcolumn           pH              # from the out file
  lines                   KdU KdZn KdCd   # from the out
file - plot these three as lines
  extraText               "extratextkd.dat" # additional
text on/by plot

CHEMISTRY

SELECTED_OUTPUT
  reset false
  high_precision true
USER_PUNCH
  headings pH KdU KdZn KdCd             # these columns
of data accumulate in the out file
  -start
10 IF (STEP_NO = 0) THEN 70             # don't output
any data for plotting for initial solution calculations
20 PUNCH -la("H+")
30 KdU = SURF("U","Hfo")/TOT("U")      # NB TOT("U")
is total dissolved U
40 KdZn = (SURF("Zn","Hfo") + mol("ZnX2"))/TOT("Zn") # solid phase
= adsorbed + cation exchanged
50 KdCd = (SURF("Cd","Hfo") + mol("CdX2"))/TOT("Cd")
60 PUNCH KdU,KdZn,KdCd                 # this outputs
the data to selected output and then the out file
70 END
  -end

SOLUTION 1 AMD
  -temp 10
  -units mmol/kgw
  pH 2.3                                # analysis from
some Acid Mine Drainage
  Na 23.8
  K 0.1
  Mg 2.0
  Ca 11.6
  C 1.7e-4
  Cl 13
  P 0.08
  S(6) 52.8
  Al 6.5
  Cd 0.01
  Fe(3) 10.7
  Fe(2) 0.27
  U(6) 0.18
  Zn 1.5

SURFACE 1
  Hfo_w 2e-3 600 0.89
  Hfo_s 5e-5
  -equil 1

```

```
EXCHANGE_SPECIES  
H+ + X- = HX  
log_k 1.0  
-gamma 9.0 0.0
```

```
EXCHANGE 1  
X 50e-3  
-equil 1
```

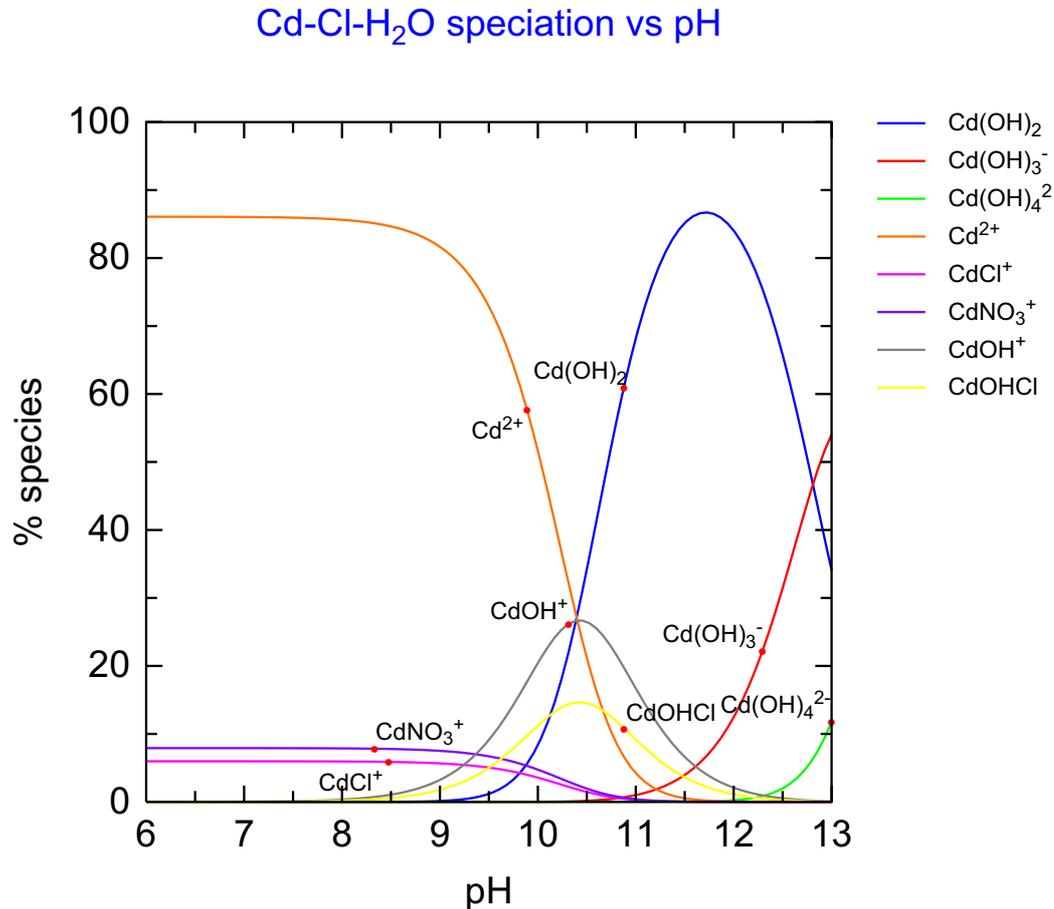
```
REACTION 1  
NaOH 1  
105e-3 in 100 steps  
steps controls the resolution of the plot  
INCREMENTAL_REACTIONS
```

# the number of

```
END
```



## 60 Cd speciation vs pH



C:\PhreePlot\demo\Cdspeciation\Cdspeciation.ps

**PHREEQC** cannot automatically generate column headings containing the species names. This means that it is not possible to automatically write the correct header in the 'out' file when writing species that are generated automatically, for example, by the `SYS()` function.

However, a custom plot needs to be able to pick up the correct label names from the header line in order to be able to label the plot properly. Communicating the species names to the plot file therefore becomes a problem. There are two ways round this: (i) put the label names explicitly (manually) in the `-headings` line of a `USER_PUNCH` block, or (ii) write them as a separate data column in the 'out' file, i.e. as name-value pairs.

The first approach is illustrated in this example. This requires that you know which species will be output in the first place. The `SYS()` function in the `Cdvsph.inc` file makes it easy to output all of the species involved automatically. These are output in descending amount order (largest amounts first) and so this order will change with pH. The species therefore need to be sorted. This is done with the `sort.inc` file. The species will then always be output in ascending alphabetic order (ignoring parentheses) and the `-heading` list should reflect this order. It is normally necessary to run a problem like this twice: firstly to get the species involved, and sec-

only to make the plot. This example also illustrates the use of nested include files. The [minimumYValueForPlotting](#) keyword eliminates all curves which do not rise above 5%.

The next example illustrates the second approach which is normally easier to implement.

```

SPECIATION
  jobTitle                "Cd speciation vs pH<br>(using \
                           explicit \
                           naming of species to plot)"

  calculationType         custom
  calculationMethod       1
  xmin                    -13.0
  xmax                    -6.0
# determines the number of points at which speciation is calculated
  resolution              100

PLOT
  plotTitle               "Cd-Cl-H<sub>2</sub>/sub>O \
                           speciation vs pH"

  xtitle                  pH
  ytitle                  "% species"
  pxmax                   13
# explicit naming of species - order defined in user_punchCd.inc
  lines                   Cd(OH)2 Cd(OH)3- Cd(OH)4-2 Cd+2 Cd2OH+3 \
                           CdCl+ CdCl2 CdCl3- CdNO3+ CdOH+ CdOHC1

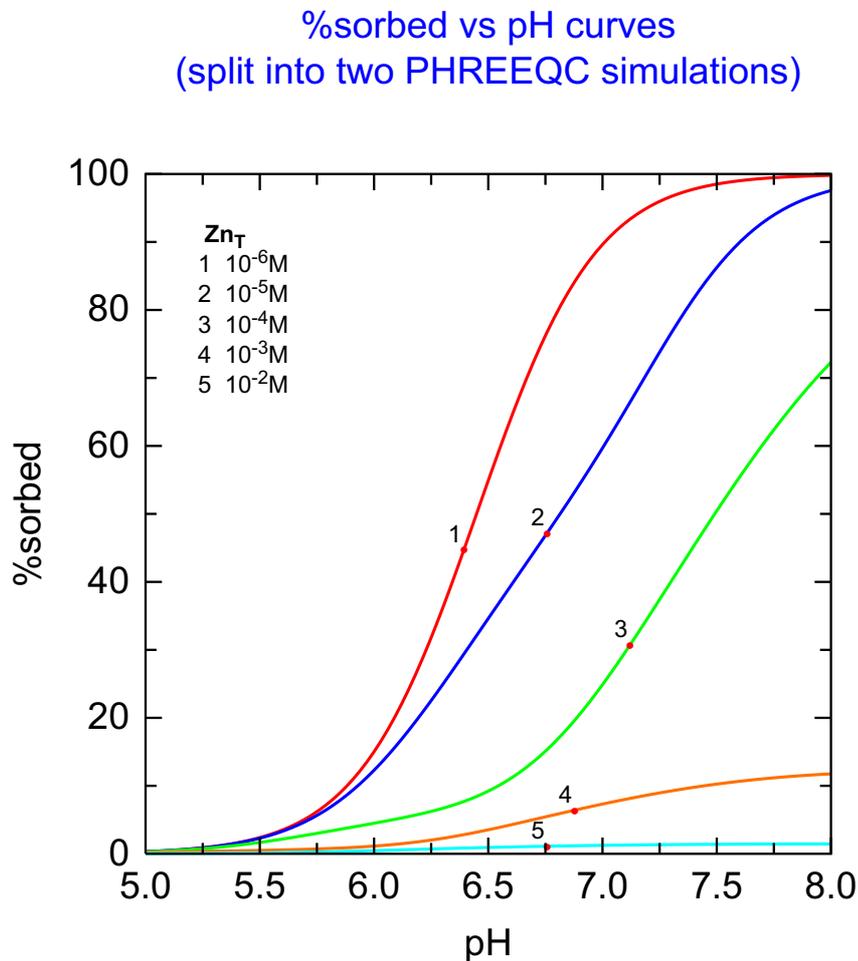
  lineColor               "blue"
  pointSize               5.0
# use first column as defined by include files - this is pH
  customXcolumn           1
# this prevents minor species being plotted
  minimumYValueForPlotting 5.0
  extraText               "extratextCdspeciation.dat"

CHEMISTRY
include 'Cdvsph.inc' # nested includes

```



## 61 Zn-HFO: %sorption vs pH curves



This example, based on Example 8 in the **PHREEQC** distribution, demonstrates the use of the `<x_axis>` tag to loop over a range of pH and the loop variable to loop over a range of Zn concentrations. The `logLoopVar` has been used to transform the loop variable to  $10^z$ . The plot shows the percentage of Zn adsorbed as a function of pH in 0.1M NaNO<sub>3</sub>.

The `<x_axis>` tag and the `resolution` determine the range and step size for the x-axis variable (pH). The `USER_PUNCH` data block produces a block of selected output for each pH-Zn combination. With the default setting of `selectedOutputLines`, the last line of this block of output is copied to the 'out' file for plotting. A blank line is written to the 'out' file for each new value of the loop variable but not for each new value of the x-axis variable. The data are therefore plotted as a series of curves with a new curve after each change of the loop variable.

The normal legend or key has been suppressed by setting `legendTextSize` to zero. A new legend has been placed in the top-left corner using a line of the `extraText` file. The new 'legend' text has been placed on a series of lines using the continuation character, `\`, to concatenate lines and give the single text string required. Note that the maximum total length of the text string,

including any text enhancement tags such as `<sub>`, is 200 characters. [labels](#) have been used to number the curves.

```

# %sorption vs pH for Zn on Hfo
# Modelled after 'Example 8' from the PHREEQC example set

SPECIATION
  calculationType          custom
  calculationMethod        1
# x-axis (pH) range
  xmin                     5.0
  xmax                     8.0
# z-loop (log ZnT), one curve for each ZnT
  loopMin                  -6.0
# from -6 to -2 in steps of +1
  loopMax                  -2.0
  loopInt                  1.0
# l = value of loop variable is exponentiated (=10^<loop>) before use
  loopLogVar               1
# number of calculations (PHREEQC simulations) for each curve
  resolution               100

PLOT
  plotTitle                "%sorbed vs pH curves<br>(split into two PHRE-
EQC simulations)"
  xtitle                   pH
  ytitle                   "%sorbed"
# this variable in the 'out' file is plotted as a line (%sorbed is a valid column
header)
  lines                    %sorbed
  lineWidth                0.4
  changeColor              T
# used in order for label names on the plots
  labels                   1 2 3 4 5
  labelSize                2.0
  legendTextSize           0.0
  customXcolumn            pH
# adds customised legend text
  extraText                "extratextpcSORPTION.dat"

CHEMISTRY

# simulation 1 - initial surface calculation is run but no selected output is pro-
duced or read
TITLE Example 8.--Sorption of zinc on hydrous iron oxides.
SURFACE_SPECIES
  Hfo_sOH + H+ = Hfo_sOH2+
  log_k 7.18

  Hfo_sOH = Hfo_sO- + H+
  log_k -8.82

  Hfo_sOH + Zn+2 = Hfo_sOZn+ + H+
  log_k 0.66

  Hfo_wOH + H+ = Hfo_wOH2+
  log_k 7.18

  Hfo_wOH = Hfo_wO- + H+
  log_k -8.82

  Hfo_wOH + Zn+2 = Hfo_wOZn+ + H+
  log_k -2.32
SURFACE 1
  Hfo_sOH          5e-6    600.    0.09
  Hfo_wOH          2e-4

PHASES
Fix_H+
  H+ = H+
  log_k 0.0

# first simulation

```

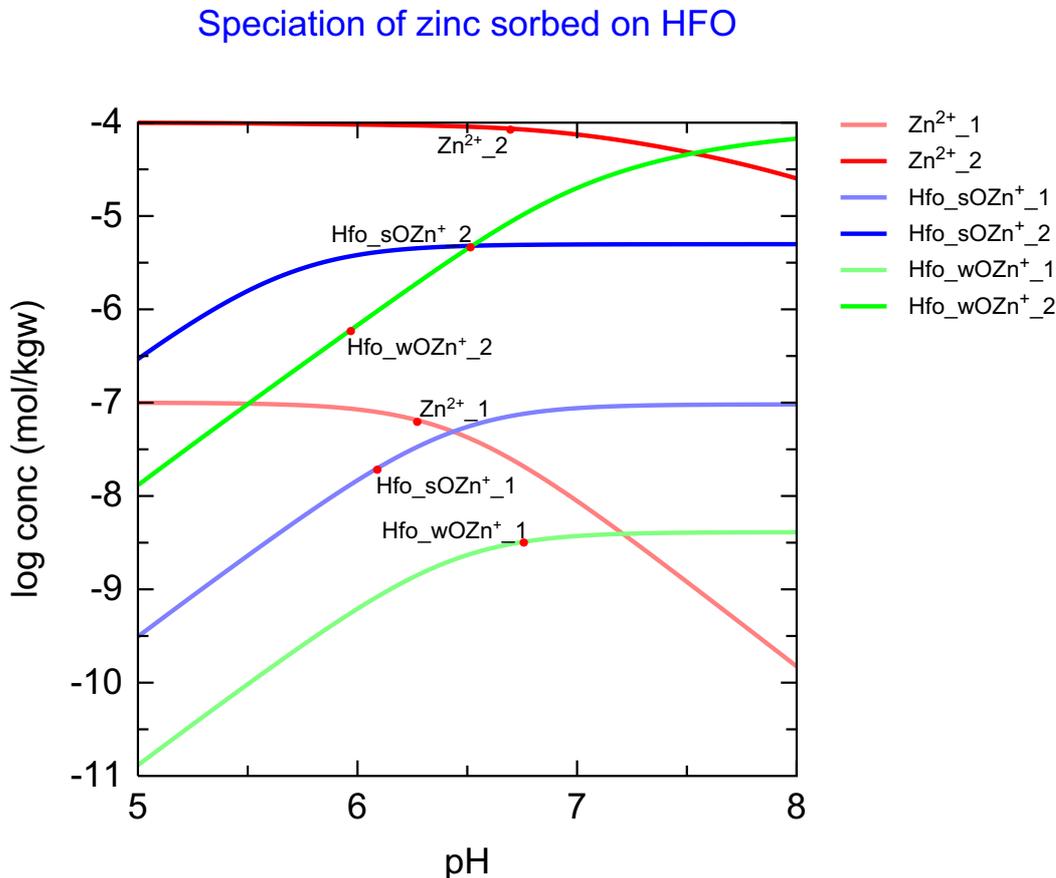
```
USE solution none

SELECTED_OUTPUT
  -reset false
USER_PUNCH
# determines column headers in the 'out' file
  -heading pH %sorbed sorbed
  10 sorbed = SURF("Zn","Hfo")
  20 totZn = SYS("Zn")
  30 pcsorbed = 100*sorbed/totZn
  40 punch -la("H+"), pcsorbed, sorbed
END

# simulation 2 - loops on this simulation to produce the output required for graph-
# ing

USE surface 1
SOLUTION 1
  -units mol/kgw
  pH      8.0
# ZnT
  Zn      <loop>
  Na      0.1
  N(5)    0.1 charge
EQUILIBRIUM_PHASES 1
# fixes the pH
  Fix_H+  -<x_axis> NaOH 10.0
  -force_equality true
END
```

## 62 Zn-HFO: Surface speciation



C:\PhreePlot\demo\example8\speciation.ps

This example shows the surface speciation for Zn adsorbed to Hfo in the same system as that of the previous example. Curves are produced for total Zn concentrations of  $10^{-7}$ M and  $10^{-4}$ M. Adsorbed speciation is calculated by PUNCHING the log concentrations of the adsorbed species directly. A similar plot could also be made using the 'species plot' procedure (see the demo\example8 directory) with the logadsspeciesvsph.inc include file.

Since there are two loops for each species, the labelling appends an underscore and the loop number to the species name to help to differentiate between the curves.

[pxmajor](#) has been set to one since the auto setting would produce major tick marks (and axis labels) at every 0.5 pH unit.

The legend has been suppressed by setting the legend text size to 0 and the colour to 'nd' in the <legend> line of the extraText file. It could also have omitted by setting the [legend textSize](#) to 0.

[changeColor](#) is by default false and [useLineColorDictionary](#) has been set to 0 (the default) so that the default colour sequence is automatically used starting at red2, blue2 etc as given by

their respective positions in the [lineColor](#) list in the input file. On the second loop, the colours are kept the same but the density is increased to 4, e.g. red4, blue4, ... .

```

SPECIATION
  calculationType          custom
  calculationMethod        1
  xmin                     5.0
  xmax                     8.0
# minimum value of <loop> tag
  loopMin                  -7.0
# maximum value of <loop> tag
  loopMax                  -4.0
# increment of <loop> tag per iteration
  loopInt                  3.0
# 1 = antilog loop value, ie <loop> = 10^<loop>
  loopLogVar               1
  resolution               100

PLOT
  plotTitle                "Speciation of zinc sorbed on HFO"
  xtitle                   pH
  ytitle                   "log conc (mol/kgw)"
  pxmajor                  1.0
  customXcolumn            pH
# lines to plot from out file - headings defined below
  lines                    Zn+2 Hfo_sOZn+ Hfo_wOZn+
  lineWidth                0.6
# starting colours and colour densities
  lineColor                red2 blue2 green2
  labelSize                1.8
  trackSymbolSize          2.0

CHEMISTRY

# Similar to PHREEQC Example 8
TITLE Example 8.--Sorption of zinc on hydrous iron oxides.
# <loop> iterates on all simulations - this is the outer loop

SELECTED_OUTPUT
  -reset false
  -high_precision true
SURFACE_SPECIES
  Hfo_sOH + H+ = Hfo_sOH2+
  log_k 7.18

  Hfo_sOH = Hfo_sO- + H+
  log_k -8.82

  Hfo_sOH + Zn+2 = Hfo_sOZn+ + H+
  log_k 0.66

  Hfo_wOH + H+ = Hfo_wOH2+
  log_k 7.18

  Hfo_wOH = Hfo_wO- + H+
  log_k -8.82

  Hfo_wOH + Zn+2 = Hfo_wOZn+ + H+
  log_k -2.32
SURFACE 1
  Hfo_sOH          5e-6   600.   0.09
  Hfo_wOH          2e-4
PHASES
Fix_H+
  H+ = H+
  log_k 0.0
# Initial setup simulation
SOLUTION 1
  -units mol/kgw
# only for the initial solution calculation
  pH 8.0
  Zn <loop>
# background electrolyte

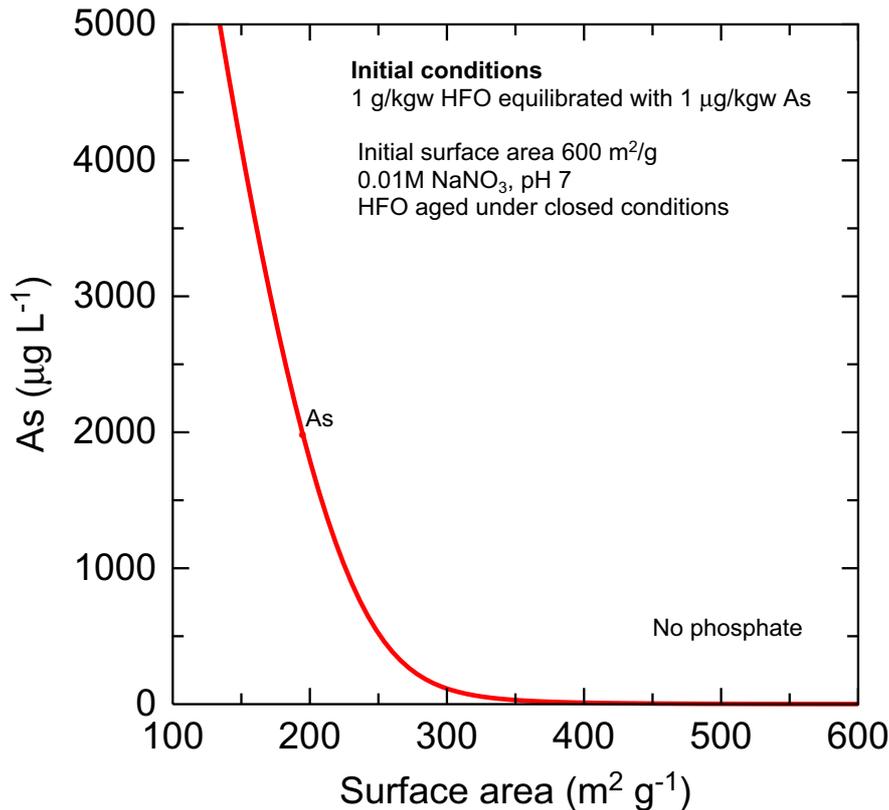
```

```
Na      0.1    charge
N(5)    0.1
USER_PUNCH
-heading pH Zn+2 Hfo_wOZn+ Hfo_sOZn+
10 punch -la("H+"), lm("Zn+2"), lm("Hfo_wOZn+"), lm("Hfo_sOZn+")
END

# <x_axis> iterations only execute the last iteration by default
USE solution 1
USE surface 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10.0
END
```

## 63 As-HFO: reduction in surface area

### As desorption as the surface area decreases



C:\PhreePlot\demo\surfacearea\surfacearea.ps

This example shows how the dissolved As concentration could evolve as the surface area of HFO declines (ageing). The example demonstrates the use of user-defined tags to pass information from one simulation to the next. An alternative approach involves using the `PUT()` and `GET()` BASIC functions

The total amount of As is defined by the first simulation and then the adsorbed As (and any adsorbed P) is redistributed in the second simulation assuming closed conditions (apart from H<sup>+</sup>). The dissolved As (and P) from the first simulation is discarded and the adsorbed As redistributed as the surface area decreases. It is assumed that while the surface area of the HFO decreases, the surface properties of the HFO remain unchanged (unlikely to be true in practice).

The various tag definitions in [numericTags](#) calculate the number of sites at any particular stage based on the given initial surface characteristics. These values are substituted in the **PHREEQC** code during each iteration.

The **PhreePlot** looping is only over the second (final) simulation.

```

# calculates how the solution concn of As changes as the surface area of Hfo
# (but not the surface properties) is reduced in a closed system.
SPECIATION
  JobTitle                "Diagenesis"
  calculationType         custom
  calculationMethod       1
  xmin                    10.0 # minimum surface area, see below
  xmax                    600.0 # maximum surface area
  resolution              100

  numericTags             &lt;mass&gt; = 1 \
                          &lt;molecular_wt&gt; = 89 \
                          &lt;initial_site_density_per_mol&gt; = 0.2 \
                          \
                          &lt;initial_surface_area&gt; = 600 \
                          &lt;initial_site_density_per_g&gt; = \
&lt;initial_site_density_per_mol&gt;/&lt;molecular_wt&gt; \
                          &lt;initial_sites&gt; = \
                          &lt;initial_site_density_per_g&gt;*&lt;mass&gt; \
                          &lt;site_density_per_m2&gt; = \
&lt;initial_site_density_per_g&gt;/&lt;initial_surface_area&gt; \
                          &lt;surface_area&gt; = &lt;x_axis&gt; \
                          &lt;sites&gt; = \
&lt;surface_area&gt;*&lt;site_density_per_m2&gt;*&lt;mass&gt;

PLOT
  plotTitle               "As desorption as the surface area \
                          decreases"
  xtitle                  "Surface area (m<sup>2</sup> \
                          g<sup>-1</sup>)"
  ytitle                  "As (mg L<sup>-1</sup>)"
  pymax                   5000.0 # truncate the highest values
  customxColumn           surface_area
  lines                   As
  lineWidth               0.6
  lineColor                red
  legendTextSize          0.0
  extraText               "extratextsurfacearea.dat"

CHEMISTRY

PRINT
# -reset false
PHASES
Fix_H+
  H+ = H+
  log_k 0.0

SELECTED_OUTPUT
  -high_precision        true
  -reset                  false

USER_PUNCH
-headings totAs totP
-start
10 totAs=SYS("As",n,n$,t$,c)
20 totP=SYS("P",n,n$,t$,c)
30 punch totAs, totP
-end

# first simulation - set up initial conditions
SOLUTION 1
  temp      25
  pH        7.0
  units     mol/kgw
  density   1
  Na        1e-2
  N(5)      1e-2
# Equilibrate Hfo with low As and P
As          1 ug/kgw
P           0 ug/kgw # P has an important effect
-water     1 kg

```

```

EQUILIBRIUM_PHASES 1
  Fix_H+   -7.0 NaOH 10
    -force_equality true
  O2(g)    -0.67 10

SURFACE 1
  Hfo_w <initial_sites> <initial_surface_area> <mass>;
    -equilibrate 1
END

# second simulation - now start reducing surface area always starting from the \
                                                                initial state

USER_PUNCH
  -headings  surface_area As
  -start
  10 As=tot("As")*74.9216*1e6
  20 punch <surface_area>; As
  -end

SOLUTION 1
  temp      25
  pH        7.0
  units     mol/kgw
  density   1
  Na        1e-2
  N(5)     1e-2
  As       <totAs>; # tag name from selected output file headings above
  P        <totP>; # mol/kgw
  -water    1 # kg

EQUILIBRIUM_PHASES 1
  Fix_H+   -7.0 NaOH 10 # keep a constant pH
  O2(g)    -0.67 10

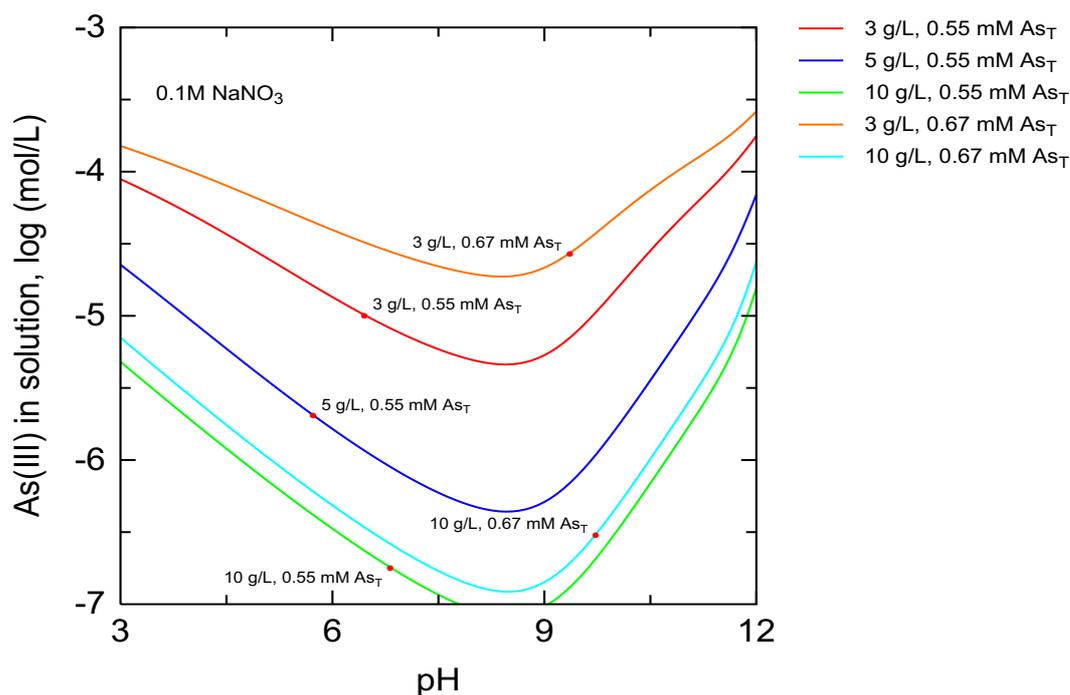
SURFACE 1
  Hfo_w <sites> <surface_area> <mass>;
END

```



## 64 CD-MUSIC: As(III) adsorption on goethite

CD-MUSIC: As(III) remaining in solution  
(after Stachowicz et al., 2006, Fig. 4)



C:\PhreePlot\demo\As-cd-music\As3-shvrfig4.ps

This example shows the calculated concentration of As(III) remaining in solution after adsorption of As(III) on goethite (98 m<sup>2</sup>/g) as a function of pH. Calculations are based on the CD-MUSIC model and parameters of [Stachowicz et al. \(2006\)](#) and reproduces their Figure 4. As(III) loadings were varied by varying the solid/solution ratio and the initial As(III) concentration.

Thermodynamic data for the aqueous As species are retrieved from the `ecosat.inc` include file. The arsenic species in the default database have been removed from consideration by defining all As(III) reactions in terms of a new element, [As3]. The CD-MUSIC model is defined in the `cdmusic.inc` include file. Many parameter values are set with tags in the main input file for convenience.

`pxmin` and `pxmajor` override the default x-axis scaling which would give an x-axis ranging from 2 to 12 with labelling every 2 units. `pxmin` forces the x-axis to start at 3 while `pxmajor` forces the axis labelling to be every 3 pH units. Similarly `pymin` and `pymax` force the y-axis scaling to the desired range.

The label names are derived from the loop names which themselves are defined in column 1 of the loopfile. `changeColor` has been set to `TRUE` to ensure that the different curves of the same data column have different colours.

```

SPECIATION
  calculationType          custom
  calculationMethod        1
  xmin                     3.0
  xmax                     12.0
  resolution               100
  loopFile                 "loopfig4.dat"
  numericTags              <mass>      = <loop1> \
                          <AsT>       = <loop2>

PLOT
  plotTitle                "CD-MUSIC: As(III) remaining in solu-
tion<br>(after Stachowicz et al., 2006, Fig. 4)"
  xtitle                   pH
  ytitle                   "As(III) in solution, log (mol/L)"
  pxmin                   3
  pxmajor                  3
  pymin                   -7
  pymax                   -3
  customxcolumn            pH
  lines                    As3
  changeColor              T
  labelsize                1.5
  extratext                "extratextfig4.dat"

CHEMISTRY

include 'cdmusic_hiemstra.dat'

SELECTED_OUTPUT
  -reset false

SOLUTION 1
  Temp      25
  pH        2.9
  units     mol/kgw
# total As
  As(3)     <AsT> mmol/kgw
# background electrolyte
  Na        1e-1
# N(5) is not thermodynamically stable with As(3)
  [N5]     1e-1

USER_PUNCH
-headings pH As3
10 PUNCH -la("H+"), log10(tot("As"))

PHASES ; Fix_H+; H+ = H+ ; log_k 0

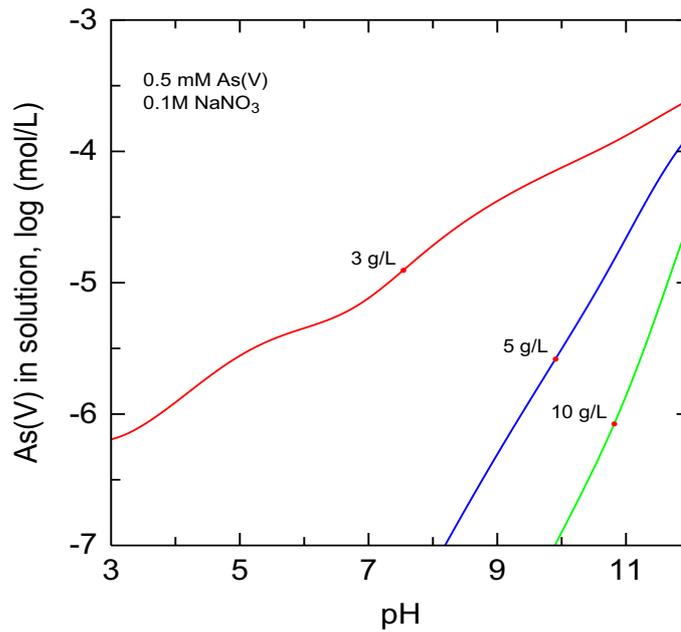
SURFACE 1
# sites/nm2 m2/g g
  Goe_uniOHH0.5 3.45 98 <mass>
# C1 C2 (in F/m2)
  -cap 0.85 0.75
  Goe_triOH0.5 2.7
  -cd_music
  -sites_units density

EQUILIBRIUM_PHASES 1
# to ensure all As(3)
  O2(g) -70
  Fix_H+ -<x_axis> NaOH
  -force_equality true
END

```

## 65 CD-MUSIC: As(V) adsorption on goethite

CD-MUSIC: As(V) remaining in solution (3 species)  
(after Stachowicz et al., 2006, Fig. 6)



C:\PhreePlot\demo\As-cd-music\As5-shvrfig6.ps

This is similar to the previous example except it is for the adsorption of As(V) rather than As(III). The figure shows the calculated amount of As(V) remaining in solution after adsorption on goethite (98 m<sup>2</sup>/g) as a function of pH. The calculated curves were based on the CD-MUSIC model and the parameters of [Stachowicz et al. \(2006\)](#). This figure replicates the calculated curves of their Fig. 6.

```

SPECIATION
  calculationType          custom
  calculationMethod        1
  xmin                    3.0
  xmax                    12.0
  resolution              100
# defines <loop1> and <loop2> tags for mass and AsT
  loopfile                "loopfig6.dat"
  numericTags             <mass> = <loop1> \
                        <AsT> = <loop2>

PLOT
  plotTitle               "CD-MUSIC: As(V) remaining in solution (3
species)<br>(after Stachowicz et al., 2006, Fig. 6)"
  xtitle                  pH
  ytitle                  "As(V) in solution, log (mol/L)"
# plot limits
  pxmin                   3
  pxmax                   12
  pymin                   -7
  pymax                   -3
# column name from selected output file: see below
  customxcolumn           pH
# ibid
  lines                   As5
  changeColor             T
# removes legend (key) from plot
  legendTextSize          0
# additional text for plot
  extratext               "extratextfig6.dat"

CHEMISTRY

SELECTED_OUTPUT
  -reset false

SOLUTION 1
  Temp      25
  pH        3
  units     mol/kgw
  As(5)     <AsT> mmol/kgw
  Na        1e-1
  N(5)     1e-1

# the results here differ slightly from the published ones due to small differences
# in the databases used
# note particularly the sensitivity of the 3 g/L curve at low pH

include 'cdmusic_hiemstra.dat'

USER_PUNCH
# column names used above
-headings pH As5
10 PUNCH -la("H+"), log10(tot("As"))

PHASES ; Fix_H+; H+ = H+ ; log_k 0

SURFACE 1
# sites/nm2 m2/g g
  Goe_uniOHH0.5 3.45 98 <mass>
# C1 C2 (in F/m2)
  -cap 0.85 0.75
  Goe_triOH0.5 2.7
  -cd_music
  -sites_units density

EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH
  -force_equality true
# As(5) please
  O2(g) -0.67

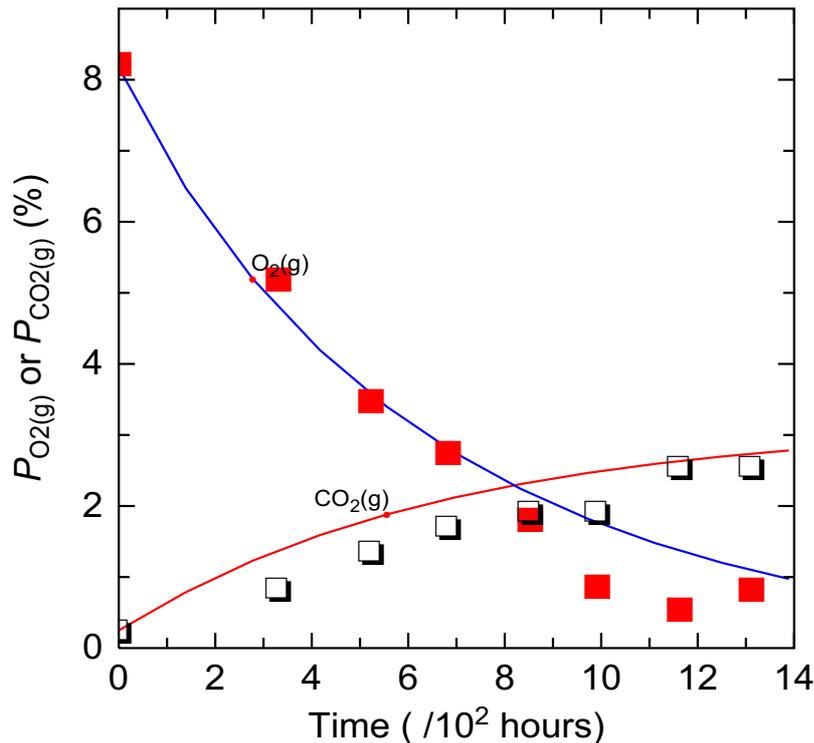
```

END



## 66 Kinetics of pyrite oxidation

### Pyrite oxidation kinetics (Appelo and Postma, 2005)



C:\PhreePlot\demo\pyritekinetics\pyritekinetics.ps

This example shows the kinetics of the oxidation of pyrite from [Appelo and Postma \(2005\)](#), p 455-456, Fig. 9.28 (the calculated  $O_2(g)$  curve here does not quite agree with A&P's because of small changes in the `PHREEQC.dat` database used).

The resolution only has to be set to 1 since the `KINETICS` data block has an internal looping mechanism (like `REACTION`) which produces a multi-lined selected output 'file'. [selectedOutputLines](#) has therefore been set to `auto` so that all the lines in the selected output are picked up.

The calculated points are plotted as a continuous curve using the [lines](#) keyword with two variable (column) names, namely `O2(g)` and `CO2(g)`. These names are defined in the `USER_PUNCH` headings line and are automatically passed through to the 'out' file which is then used for the plotting.

The data points are plotted using an [extra](#) file. [legendTextSize](#) has been set to 0 to eliminate the legend. The Times-Roman font has been selected with the [font](#) keyword.

The x-axis scaling and title includes a scaling factor ( $\times 10^2$ ) which indicates that the true scale actually varies from 0–1400 hours.

```

SPECIATION
  jobTitle                "Pyrite oxidation kinetics, A&P (2005) p 455-6"
  database                phreeqc.dat
  calculationType         custom
  calculationMethod       1
# only need to do one calculation as KINETICS block has its own looping
  resolution              1
# multiline selected.out so copy all the lines produced into the out file
  selectedOutputLines     auto

PLOT
  plotTitle               "Pyrite oxidation kinetics<br>(Appelo and
Postma, 2005)"
  xtitle                  "Time (\" \" hours)"
  ytitle                  "<i>P</i><sub>O2(g)</sub> or <i>P</i>"
i><sub>CO2(g)</sub> (%)"
# fix upper limit of y-axis
  pymax                   9
# omit legend
  legendTextSize          0.0
# from out file
  customXcolumn           Time
# modelled results - labels from USER_PUNCH block -> out file
  lines                   CO2(g) O2(g)
# plot experimental data points
  extraSymbolsLines       "pyritekineticsdata.dat"

CHEMISTRY

SELECTED_OUTPUT
  -reset false
  -high_precision true

USER_PUNCH
# defines column heading in out file
  -headings Time CO2(g) O2(g)
  -start
  10 PUNCH total_time/3600
  20 PUNCH 100*10^si("CO2(g)"), 100*10^si("O2(g)")
  -end

RATES
# the kinetic model
  Pyrite
  -start
  1 A=15e3*m0
  10 if SI("Pyrite")>0 then goto 100
  20 fH=mol("H")
  30 fFe2=(1+tot("Fe(2)"))/1e-6
  40 if mol("O2")<1e-6 then goto 80
# rate with oxygen
  50 rO2=10^-8.19*mol("O2")*fH^-0.11
  60 rO2_Fe3=6.3e-4*tot("Fe(3)")^0.92*fFe2^-0.43
  70 goto 90
  80 rem
# rate without oxygen
  81 rFe3=1.9e-6*tot("Fe(3)")^0.28*fFe2^-0.52*fH^-0.3
  90 rate=A*(m/m0)^0.67*(rO2+rO2_Fe3+rFe3)*(1-SR("Pyrite"))
# must include this
  100 save rate*time
  -end

SOLUTION_SPECIES
# force one way - dissolved N2(g) does not make nitric acid!
  2NO3- + 12H+ + 10e- = N2 +6H2O; log_k 500

SOLUTION 1
# kg
  -water 0.0069239
  -temp 20

```

500 *PhreePlot Guide*

```
pH 7 charge; pe 14 O2(g) -1.0878  
Ca 1 Calcite; C 1 CO2(g) -2.6021  
Fe 1e-3 Goethite 2; N 1.3 N2(g) -0.0382
```

EQUILIBRIUM\_PHASES

```
Goethite 2; Calcite 0; Gypsum 0 0
```

GAS\_PHASE 1

```
-fixed_pressure  
-volume 0.02127; temp 20  
CO2(g) 0.0025; O2(g) 0.0817; N2(g) 0.9157
```

KINETICS 1

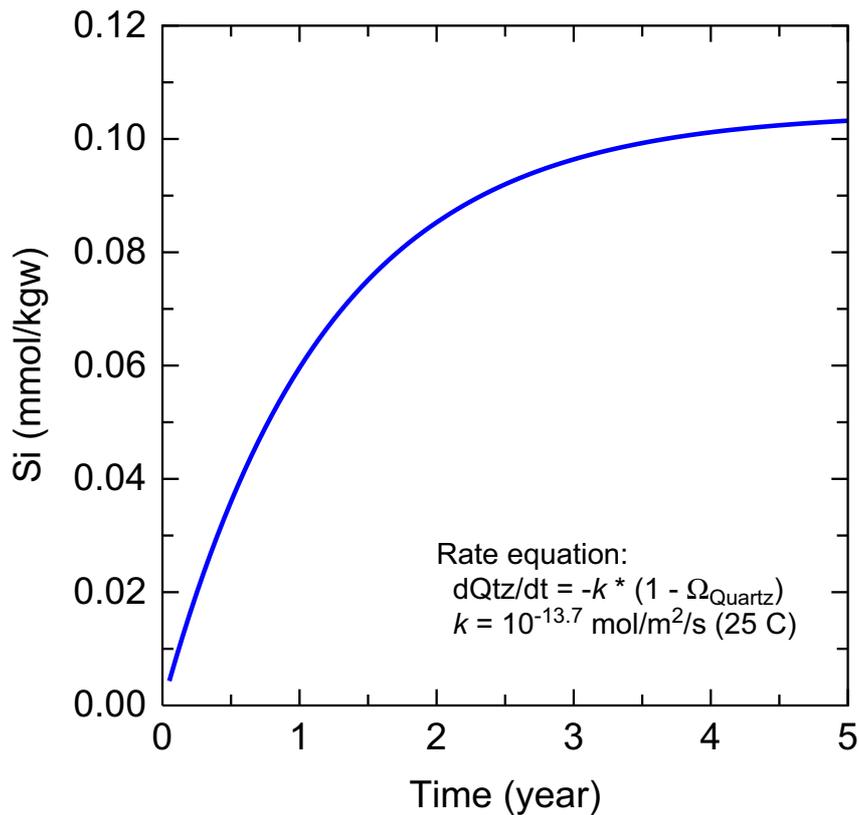
```
Pyrite; -m0 1.32e-4; -step 0 5e5 5e5 5e5 5e5 5e5 5e5 5e5 5e5 5e5  
INCREMENTAL_REACTIONS true
```

END



## 67 Kinetics of quartz dissolution

Kinetics of quartz dissolution  
(from Appelo 'Get-going' sheet 11)



C:\PhreePlot\demo\kineticsSi\kineticsSi.ps

This example demonstrates how a single iteration of the `KINETICS` data block generates a multiline selected output file which is read in with `selectedOutputLines` set to `auto`.

The label in the plot and the key to the right of the plot have been suppressed with `labelSize` and `legendTextSize` both set to 0.

The `extraText` file also includes the use of various text enhancements – italics, subscripts, superscripts and a Greek character.

```

# plot of the dissolution of quartz vs time based on the PHREEQC kinetics model

SPECIATION
  calculationType          custom
  calculationMethod        1
  selectedOutputLines      auto

PLOT
  plotTitle                "Kinetics of quartz dissolution<br>(from Appelo
'Get-going' sheet 11)"
  xtitle                   "Time (year)"
  ytitle                   "Si (mmol/kgw)"
# plot x = time
  customXColumn            time
# plot y(line) = Si
  lines                    Si
  linecolor                blue
  linewidth                0.6
# suppresses label
  labelSize                0
# suppresses key
  legendTextSize           0
  numericTags              <log_k> = -13.7
# additional text (including some Greek symbols)
  extraText                extratextkinetics.dat

CHEMISTRY
# Kinetics of quartz dissolution
# from Appelo 'Get-going sheet #11'

RATES
#1 dQu/dt = -k * (1 - SR(Quartz)). k = 10^-13.7 mol/m2/s (25 C)
#2 parm(1) = A (m2), parm(2) = V (dm3) recalculate to mol/dm3/s

# rate name
Quartz
-start
10 moles = parm(1) / parm(2) * (m/m0)^0.67 * 10^<log_k> * (1 - SR("Quartz"))
# integrate. save and time must be in rate definition
20 save moles * time
# moles count positive when added to solution
-end

# Sediment: 100% qu, grain size 0.1 mm, por 0.3, rho_qu 2.65 kg/dm3
KINETICS
# rate name
Quartz
-formula SiO2
# initial moles of quartz
-m0 102.7
# parameters for rate eqn. Here:
-parms 22.7 0.162
# Quartz surface area (m2/kg sediment), water filled porosity (dm3/kg sediment)

# 1.5768e8 seconds = 5 years
-step 1.5768e8 in 100 steps
# integration tolerance, default 1e-8 mol
-tol 1e-8

# start integration from previous step
INCREMENTAL_REACTIONS true

SOLUTION 1

SELECTED_OUTPUT
  -reset FALSE

USER_PUNCH
# these are accumulated in the out file ready for plotting
-heading time Si SIQtz

```

```
-start  
10 IF (step_no>0) THEN punch total_time/3.1536e7, tot("Si")*1e3, SI("Quartz")  
-end  
  
END
```





```

SPECIATION
  calculationType      custom
  calculationMethod    1

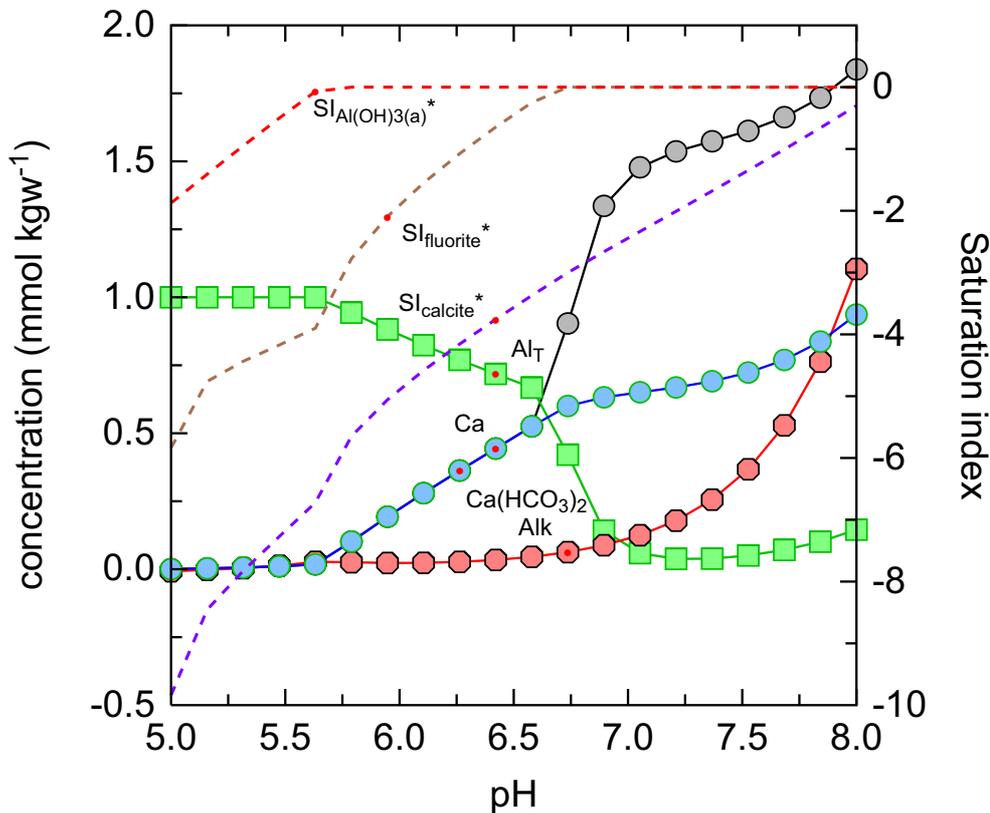
PLOT
# make bigger
  plotfactor           2
  xaxislength          90
  yaxislength          110
  units                "mm"
  plotTitle            "Symbols, dingbats and lines"
# it should not look like an x-y plot
  xtitle              ""
  ytitle              ""
# plot area large enough not clipped gray border
  pxmin               -2
  pxmax               17
  pxmajor             1
  pxminor             1
  pymin               -100
  pymax               120
  pymajor             10
  pyminor             5
  xoffset             7.5
  yoffset             10
  tickSize            0
  axisNumberSize      0
  axisLineWidth       0
# contains the list of symbols and their positions etc
  extraSymbolsLines   "symbols.dat"
# number the positions
  extraText           "extratextsymbols.dat"

# gridlines           t

# axislinewidth       0.05

```

## 69 Varying symbols and lines in plots



C:\PhreePlot\demol\symbols\plotsymbols.ps

This example demonstrates how different lines and sets of points of custom plots can have different attributes associated with them. Some acidic, Al-F-containing water is titrated with Ca(HCO<sub>3</sub>)<sub>2</sub>. Eight variables are PUNCHED to the selected output. pH is used as the x-axis and the other variables are plotted on the y- and 2y-axes according to the lists given in [points](#), [lines](#) and [lines2y](#). Attributes are pulled off the associated lists ([pointColor](#), [pointType](#), [pointSize](#) etc.) until exhausted in which case the list is automatically extended (colours) or recycled (other attributes). There is a default sequence of 15 colours (red, blue, green, orange, cyan, magenta, brown, sky, purple, gray, yellow, maroon, lawn, spring, black) for each type of list (points and lines, y and 2y axes). These lists are rearranged according to the individual input colour lists which effectively promote their members to the top of the respective sequence. If there are more than one subsets of data, the colour density is cycled (not here).

The attributes chosen for a particular dataset depend on the position of that dataset in the input list. For example, ALK is third in the points list so will pick up the third [pointColor](#), third [pointType](#), third [pointSize](#), and so on. Symbol types are defined either by number (see the preceding Example) or name (see [Appendix 3](#)). The first six symbols can have a separate [rimColor](#). The width of the rim is defined in terms of the fraction of the overall symbol width ([rimFactor](#)). Dashed lines are signified by negative line widths and here are on the 2y axis (\*).

This is the basic method of assigning attributes. Colour selection can be modified from this by using [changeColor](#), [pointsSameColor](#) and [restartColorSequence](#). The colours and other attributes can also be set using the line colour dictionary and ensuring its use with [lineColorDictionary](#) <sup>1</sup> or <sup>2</sup>.

```

# demonstrates the use of different symbols, colours and line types in a plot.

# For reference, the 15 auto color sequence is:
#   red, blue, green, orange, cyan, magenta, brown, sky,
#   purple, gray, yellow, maroon, lawn, spring, black

SPECIATION
calculationMethod 1
calculationType   custom
xmin              5
xmax              8
resolution        20

PLOT
xtitle            pH
ytitle            "concentration (mmol kgw<sup>-1</sup>)"
2ytitle           "Saturation index"
# this is used as the x-axis
customXcolumn     pH
p2ymax            1
# these will be plotted as points
points            Ca(HCO3)2 Al<sub>T</sub> Alk Ca
# these will be plotted as lines
lines             Ca(HCO3)2 Al<sub>T</sub> Alk Ca
lines2y           SI<sub>calcite</sub> SI<sub>fluorite</sub> SI<sub>Al(OH)3(a)</sub>
sub>
# symbols to use in sequence for 'points' datasets, recycled
pointType         1 2 6
# colors to use in sequence for 'points'
pointColor        gray2 green2 red2 sky2
# size of symbols, recycled
pointSize         3
# explicit rim color for first 2 datasets then recycle
rimColor          black green6
# fractional rim width, recycled
rimFactor         0.08
# colors to use in sequence for 'lines'
lineColor         black green6 red blue
# colors to use in sequence for 'lines2y' then auto sequence
lineColor2y       purple brown6
# line width to use for 'lines2y', negative for dashed, recycled
lineWidth2y       -0.4
changeColor       f

CHEMISTRY

# titrate acidic Al-rich water with Ca(HCO3)2

PHASES
Fixed_H+
H+ = H+
log_k 0.

SOLUTION
-units mmol/kgw
pH 4.5
Al1
F2
C13 charge
SAVE solution 1
END

USE solution 1
EQUILIBRIUM_PHASES
Fixed_H+ -<x_axis> Ca(HCO3)2
Al(OH)3(a) 0 0
Fluorite 0 0
Calcite 0 0
CO2(g) -3.5

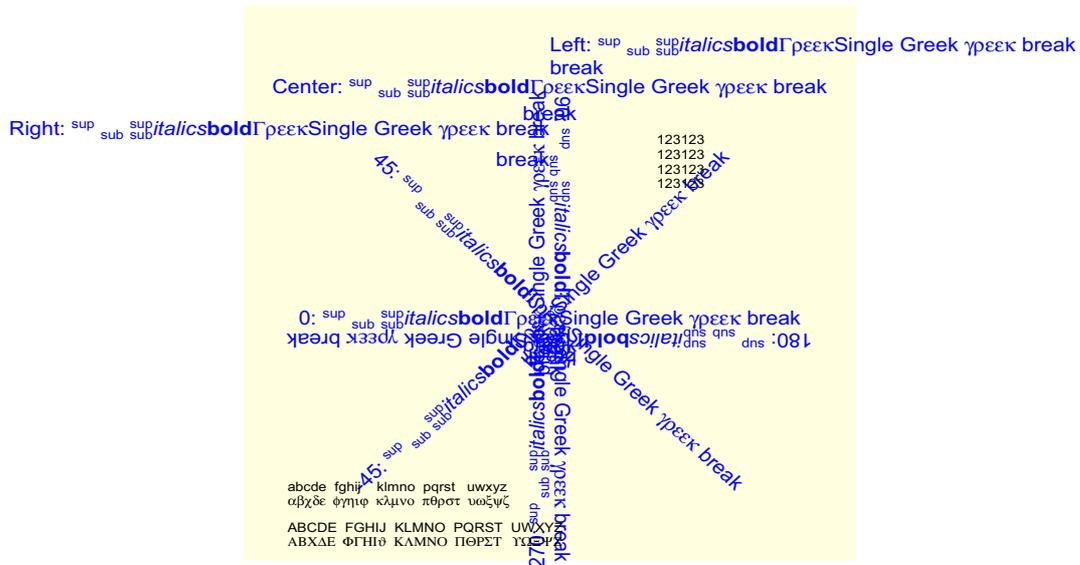
```

```
SELECTED_OUTPUT
  -reset FALSE

USER_PUNCH
  -headings Ca(HCO3)2 pH Al<sub>T</sub> Alk Ca SI<sub>calcite</sub> SI<sub>fluorite</sub> SI<sub>Al(OH)3(a)</sub>
10 IF (STEP_NO = 1) THEN PUNCH (10-EQUI("Fixed_H+"))/TOT("water")*1e3, -la("H+"),
TOT("Al")*1e3, \
      Alk*1e3, TOT("Ca")*1e3, SI("Calcite"), SI("Fluorite"), SI("Al(OH)3(a)")
END
```

## 70 Text

### Text: demonstrating *justification*, *orientation* and *character sets*



C:\PhreePlot\demosymbols\text.ps

This example also does no geochemistry but demonstrates some of the capabilities of justifying and rotating text as well as enhancing it with subscripts and superscripts and Greek characters and text. These are all defined in the [extraText](#) file `extratexttext.dat`.

The light yellow background colour has been set with the [backgroundColor](#) setting. It only occupies the 'plot' area.

```
SPECIATION
  calculationType          custom
  calculationMethod        1

PLOT
  backgroundColor          "yellow0"
  plotTitle                "<b>Text: demonstrating <i>justification</i>,"
  <i>orientation</i> and <i>character sets</i></b>"
# not supposed to look like an x-y plot
  xtitle                   ""
  ytitle                   ""
  xoffset                  60
  pxmin                    -2.0
  pxmax                    12.0
  pxmajor                  1.0
  pymin                    -20.0
  pymax                    100.0
  pymajor                  10.0
  tickSize                 0.0
  axisNumberSize           2
  axisLineWidth            0.05
  pointSize                0.0
# file containing special text
  extraText                "extratexttext.dat"

  gridlines T
  gridlinecolor gray4

  font Bookman

# font Latin-1

CHEMISTRY
```

## 71 Simple PHREEQC looping

**PhreePlot** does not have to be used to produce plots. It also provides a simple way of looping around a **PHREEQC** input file automatically substituting a different value during each iteration. The input file in `demo\PHREEQC_looping\Fespecies` demonstrates this. It speciates a trace Fe-containing solution that is adjusted to various pHs. It is split into two simulations so that the initial solution calculations can be omitted from the `PRINT` output.

The pH is generated from `xmin`, `xmax` and `resolution`. There are always `resolution` iterations of **PhreePlot** during looping of the x or y axes. Hence with `xmin` = -10, `xmax` = -4 and `resolution` = 3, the x-values of -10, -7 and -4 will be generated. These values are automatically associated with the `<x_axis>` tag which is used in the penultimate line of code to 'fix' the pH.

```
# Simple looping on one variable, log (H+) activity
# Fe speciation at pH 4, 7, 10
SPECIATION
  calculationType      "custom"
  xmin                 -10
  xmax                 -4
  resolution            3      # i.e. pH 10, 7, 4
  all                  t      # writes the *.all file
  selectedOutputLines  1 0 0  # no SELECTED_OUTPUT expected
CHEMISTRY
PRINT
  -reset FALSE        # don't output initial solution calculation
PHASES
Fix_H+
  H+ = H+
  log_k 0
SOLUTION 1
  pH      2
  units   mol/kgw
  Fe(3)   1e-6
  Na      1e-2
  Cl      1e-2
# no reaction so no need to SAVE solution 1
END

USE solution 1
PRINT
  -equilibrium_phases true
  -species TRUE
EQUILIBRIUM_PHASES
  Fe(OH)3(a) 0 0
  Fix_H+ <x_axis> NaOH
END
```

and the output from the three iterations of **PHREEQC** are accumulated in `*.all` which, when using the `wateq4f.dat` database looks like this:

```
===== Simulation 1 =====
-----
Reading input data for simulation 1.
-----

      PRINT
        reset FALSE      # don't output initial solution calculation
-----Phase assemblage-----

Phase              SI log IAP  log KT      Moles in assemblage
                   -0.00  17.91   17.91  Initial      Final      Delta
Fe(OH)3(a)         -0.00  17.91   17.91  0.000e+000  7.572e-007  7.572e-007
Fix_H+             -10.00 -10.00    0.00
```

NaOH is reactant 1.000e+001 9.989e+000-1.124e-002

-----Distribution of species-----

Species	Molality	Activity	Log Molality	Log Activity	Log Gamma
OH-	1.134e-004	1.001e-004	-3.945	-4.000	-0.054
H+	1.113e-010	1.000e-010	-9.953	-10.000	-0.047
H2O	5.551e+001	9.995e-001	1.744	-0.000	0.000
Cl	9.998e-003				
Cl-	9.998e-003	8.798e-003	-2.000	-2.056	-0.056
FeCl+	4.580e-018	4.042e-018	-17.339	-17.393	-0.054
FeCl+2	3.414e-026	2.071e-026	-25.467	-25.684	-0.217
FeCl2+	9.221e-028	8.138e-028	-27.035	-27.090	-0.054
FeCl3	7.134e-031	7.160e-031	-30.147	-30.145	0.002
Fe (2)	1.872e-015				
FeOH+	1.192e-015	1.052e-015	-14.924	-14.978	-0.054
Fe+2	5.487e-016	3.328e-016	-15.261	-15.478	-0.217
Fe (OH) 2	8.916e-017	8.949e-017	-16.050	-16.048	0.002
Fe (OH) 3-	3.765e-017	3.323e-017	-16.424	-16.478	-0.054
FeCl+	4.580e-018	4.042e-018	-17.339	-17.393	-0.054
Fe (3)	2.427e-007				
Fe (OH) 4-	2.213e-007	1.953e-007	-6.655	-6.709	-0.054
Fe (OH) 3	2.135e-008	2.143e-008	-7.671	-7.669	0.002
Fe (OH) 2+	1.886e-011	1.664e-011	-10.724	-10.779	-0.054
FeOH+2	8.290e-018	5.029e-018	-17.081	-17.299	-0.217
Fe+3	2.400e-025	7.793e-026	-24.620	-25.108	-0.488
FeCl+2	3.414e-026	2.071e-026	-25.467	-25.684	-0.217
FeCl2+	9.221e-028	8.138e-028	-27.035	-27.090	-0.054
FeCl3	7.134e-031	7.160e-031	-30.147	-30.145	0.002
Fe2 (OH) 2+4	5.027e-033	6.807e-034	-32.299	-33.167	-0.868
Fe3 (OH) 4+5	0.000e+000	0.000e+000	-40.269	-41.626	-1.357
H (0)	2.347e-030				
H2	1.173e-030	1.178e-030	-29.931	-29.929	0.002
Na	2.124e-002				
Na+	2.124e-002	1.877e-002	-1.673	-1.726	-0.054
O (0)	5.983e-033				
O2	2.991e-033	3.002e-033	-32.524	-32.523	0.002

===== Simulation 2 =====

-----Phase assemblage-----

Phase	SI	log IAP	log KT	Moles in assemblage		
				Initial	Final	Delta
Fe (OH) 3 (a)	0.00	17.91	17.91	0.000e+000	9.596e-007	9.596e-007
Fix_H+	-7.00	-7.00	0.00			
NaOH				1.000e+001	9.989e+000	-1.113e-002

-----Distribution of species-----

Species	Molality	Activity	Log Molality	Log Activity	Log Gamma
OH-	1.133e-007	1.001e-007	-6.946	-7.000	-0.054
H+	1.113e-007	1.000e-007	-6.954	-7.000	-0.046
H2O	5.551e+001	9.995e-001	1.744	-0.000	0.000
Cl	9.998e-003				
Cl-	9.998e-003	8.802e-003	-2.000	-2.055	-0.055
FeCl+	1.181e-016	1.043e-016	-15.928	-15.982	-0.054
FeCl+2	3.410e-017	2.071e-017	-16.467	-16.684	-0.216
FeCl2+	9.225e-019	8.144e-019	-18.035	-18.089	-0.054
FeCl3	7.143e-022	7.168e-022	-21.146	-21.145	0.002
Fe (2)	1.428e-014				
Fe+2	1.413e-014	8.584e-015	-13.850	-14.066	-0.216
FeCl+	1.181e-016	1.043e-016	-15.928	-15.982	-0.054
FeOH+	3.073e-017	2.713e-017	-16.512	-16.567	-0.054
Fe (OH) 2	2.300e-021	2.308e-021	-20.638	-20.637	0.002
Fe (OH) 3-	9.708e-025	8.571e-025	-24.013	-24.067	-0.054
Fe (3)	4.043e-008				
Fe (OH) 3	2.135e-008	2.143e-008	-7.671	-7.669	0.002
Fe (OH) 2+	1.885e-008	1.664e-008	-7.725	-7.779	-0.054
Fe (OH) 4-	2.212e-010	1.953e-010	-9.655	-9.709	-0.054
FeOH+2	8.278e-012	5.029e-012	-11.082	-11.299	-0.216
Fe+3	2.392e-016	7.793e-017	-15.621	-16.108	-0.487
FeCl+2	3.410e-017	2.071e-017	-16.467	-16.684	-0.216
FeCl2+	9.225e-019	8.144e-019	-18.035	-18.089	-0.054
Fe2 (OH) 2+4	4.997e-021	6.806e-022	-20.301	-21.167	-0.866
FeCl3	7.143e-022	7.168e-022	-21.146	-21.145	0.002
Fe3 (OH) 4+5	5.332e-026	2.367e-027	-25.273	-26.626	-1.353
H (0)	1.561e-039				
H2	7.807e-040	7.835e-040	-39.108	-39.106	0.002
Na	2.113e-002				
Na+	2.113e-002	1.868e-002	-1.675	-1.729	-0.053
O (0)	1.352e-014				
O2	6.760e-015	6.784e-015	-14.170	-14.169	0.002

```

===== Simulation 3 =====
-----Phase assemblage-----
Phase                SI log IAP  log KT      Moles in assemblage
                   log IAP  log KT      Initial    Final      Delta
Fe(OH)3(a)          -1.44  16.47  17.91  0.000e+000          0.000e+000
Fix_H+              -4.00  -4.00   0.00
   NaOH              is reactant  1.000e+001  9.989e+000-1.102e-002
-----Distribution of species-----
Species              Molality    Activity    Log Molality  Log Activity  Log Gamma
H+                   1.113e-004  1.000e-004  -3.954       -4.000       -0.046
OH-                  1.133e-010  1.001e-010  -9.946       -10.000      -0.054
H2O                  5.551e+001  9.995e-001  1.744        -0.000       0.000
Cl
  9.998e-003
Cl-                  9.998e-003  8.802e-003  -2.000       -2.055       -0.055
FeCl+2              1.243e-009  7.551e-010  -8.906       -9.122       -0.216
FeCl2+              3.363e-011  2.969e-011  -10.473      -10.527      -0.054
FeCl+               5.990e-013  5.288e-013  -12.223      -12.277      -0.054
FeCl3               2.604e-014  2.613e-014  -13.584      -13.583      0.002
Fe (2)
  7.224e-011
Fe+2                7.164e-011  4.352e-011  -10.145      -10.361      -0.216
FeCl+              5.990e-013  5.288e-013  -12.223      -12.277      -0.054
FeOH+              1.558e-016  1.376e-016  -15.807      -15.861      -0.054
Fe(OH)2            1.166e-023  1.170e-023  -22.933      -22.932      0.002
Fe(OH)3-           4.922e-030  4.346e-030  -29.308      -29.362      -0.054
Fe (3)
  9.997e-007
Fe(OH)2+           6.872e-007  6.067e-007  -6.163       -6.217       -0.054
FeOH+2            3.017e-007  1.833e-007  -6.520       -6.737       -0.216
Fe+3              8.718e-009  2.841e-009  -8.060       -8.547       -0.487
FeCl+2            1.243e-009  7.551e-010  -8.906       -9.122       -0.216
Fe(OH)3           7.784e-010  7.812e-010  -9.109       -9.107       0.002
FeCl2+            3.363e-011  2.969e-011  -10.473      -10.527      -0.054
Fe2(OH)2+4        6.640e-012  9.045e-013  -11.178      -12.044      -0.866
FeCl3             2.604e-014  2.613e-014  -13.584      -13.583      0.002
Fe(OH)4-          8.065e-015  7.120e-015  -14.093      -14.147      -0.054
Fe3(OH)4+5        2.583e-015  1.146e-016  -14.588      -15.941      -1.353
H (0)
  0.000e+000
H2                 0.000e+000  0.000e+000  -40.821      -40.819      0.002
Na
  2.101e-002
Na+               2.101e-002  1.858e-002  -1.677       -1.731       -0.053
O (0)
  3.613e-011
O2                1.806e-011  1.813e-011  -10.743      -10.742      0.002

```

The output for pH 10, 7 and 4 shows that Fe(OH)<sub>3</sub>(a) is precipitated at pH 10 and 7 but not at pH 4.

More flexible control of the <loop> variable can be had by reading in the values from a file using the [loopFile](#) keyword. The `FespeciesLoopFile.ppi` example in the `demo` directory provides an example of this approach.



## 72 PHREEQC mineral species

By default and for good reason, **PHREEQC** does not automatically precipitate all minerals for which the saturation index exceeds zero. Nor is it possible easily to encourage it to do so. The mineral species must be explicitly included in an `EQUILIBRIUM_PHASES` block. The actual mineral species that need to be considered will depend on the database being used (even the name of the same mineral species can vary between databases).

The following input file from `demo\PHREEQC_minerals\FeZnminerals` demonstrates how a list of all possible minerals can be created in the normal **PHREEQC** output file and used for pasting into the input file. The `printphases.inc` include file is used. This makes use of the **PHREEQC** `SYS()` function for enquiring about the status of the system:

```
# runs a single iteration of PHREEQC to generate a list of all possible Fe and Zn
mineral phases
SPECIATION
  calculationType          "custom"
  resolution                0 # 1 iteration only
  PHREEQC.0.out            t # writes PHREEQC.0.out file
  selectedOutputLines      0 # tells PhreePlot not to expect any
SELECTED_OUTPUT
CHEMISTRY
include 'printphases.inc'
SOLUTION 1
  pH          1.95
  units       mol/kgw
  Fe          0.01
  Zn          1e-6
  Na          1e-1
  Cl          1e-1
END
```

and `printphases.inc` looks like this:

```
PRINT
  -reset false
  -user_print true
USER_PRINT
-start
10 totm = SYS("phases", nm, nm$, tm$, cm)
20 FOR i = 1 TO nm
30   k = INSTR(nm$(i), "(g)")
40   k = k+INSTR(nm$(i), "Fix")+INSTR(nm$(i), "FIX")+INSTR(nm$(i), "fix")
50   IF(k > 0) THEN 70
60   PRINT " ", CHR$(35)+PAD(nm$(i), 30), "0", "0"
70 NEXT i
-end
```

`CHR$(35)` is a convenient way of including the `#` symbol.

The output in `PHREEQC.out` using the `wateq4f.dat` database looks like this:

```
-----
Reading input data for simulation 1.
-----

      PRINT
      reset false
-----User print-----

#Fe(OH)2.7Cl.3          0 0
#Halite                 0 0
#Goethite               0 0
#Hematite               0 0
#Fe(OH)3(a)            0 0
#Magnetite              0 0
```

```

#Zincite(c)           0 0
#ZnO(a)               0 0
#Zn(OH)2-e           0 0
#Zn(OH)2-g           0 0
#Zn(OH)2-b           0 0
#Zn(OH)2-c           0 0
#Zn(OH)2-a           0 0
#ZnCl2                0 0
#Maghemite            0 0
#Zn2(OH)3Cl          0 0
#Fe3(OH)8             0 0
#ZnMetal              0 0
#Zn5(OH)8Cl2         0 0

```

The output for the minerals given above can be pasted into an input file and the required minerals un-commented. '0 0' indicates that the mineral should precipitate when the saturation index exceeds 0 (first 0) but will not dissolve since the initial abundance is 0 (second 0) in all cases.

Therefore in order to find out all the possible mineral species in your system, edit the SOLUTION block of this file to include the components of interest, rename and run. Then look at the PHREEQC.out file.

## Species plots

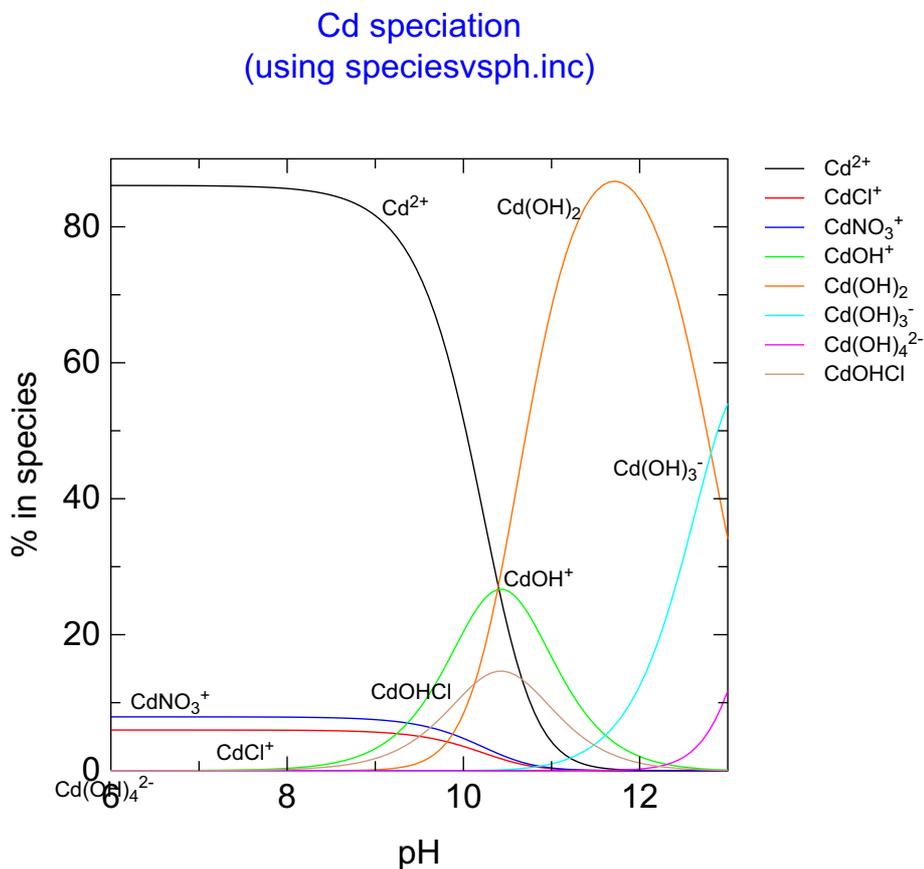
---

It is often useful to know the relative abundance of all the chemical species in a system. ‘species’ plots are a special type of custom plot that produce plots of the distribution or abundance of all the species for a particular element as a function of some master variable, often set to pH.

There are two variants of this plot in **PhreePlot**, one produces a percentage distribution and the other plots the log concentration. While these plots could be produced using the normal custom plot approach, the species plot approach does not require any prior knowledge of the names of the species present and is therefore usually easier to setup.



## 73 Cd speciation vs pH (species plot)



C:\Program Files\PhreePlot\0.01\demo\Cdspeciation(species1)\Cdspeciation(species1).ps

This produces similar output to the previous example but uses the ‘species’ [calculationType](#) to label the curves automatically. It uses the species-value paired output approach.

A `species` plot automatically generates a % species versus pH plot. This is a special type of `custom` plot in which **PhreePlot** expects the ‘out’ file to contain a succession of species name-%distribution pairs. It ignores any headings. Rather it gets the species name from the preceding column. It also expects the x-axis variable to be sent as the first pair of values. This is pH in this example but by changing the include file, any variable can be used.

The `speciesvsph.inc` include file specifies the ‘out’ or plot file. Pure phases (assumed to be mineral species) are appended with ‘(s)’ to distinguish them from aqueous species.

In order to generate the above type of plot, it is necessary to specify: (i) “species” as the plot type; (ii) a main species, here ‘cd’; (iii) an initial chemistry and any equilibrium phases, and (iv) the x-axis variable and its range. It is also necessary to indicate with an `<x_axis>` tag how the x-axis variable changes the chemistry (here pH) and point [customXcolumn](#) to the pH column.

If any of the following plot titles are blank, they are set as follows: (i) `xtitle` = name accompanying the x-axis value (position defined by [customXcolumn](#)); (ii) `ytitle` = “% species”, and (iii) `plotTitle` = “Distribution of <main-species> with <xtitle>” where the angle brackets indicate

the substitutions to be made. To omit, set the appropriate colour to 'nd'.

```

SPECIATION
  jobTitle                "Speciation vs pH using 'species' plot \
                           type"
  calculationType          species
  calculationMethod        1
  mainSpecies              Cd
# logH range
  xmin                    -13.0
  xmax                     -6.0
  resolution               100

PLOT
  plotTitle                "Cd speciation<br>(using \
                           speciesvsph.inc)"
# x-axis value is the second column - the first column is 'pH' (see out file)
  customXcolumn            2
# default is 14
  pxmax                    13
# eliminates minor species
  minimumYValueForPlotting 5.0
  legendTitle              "Cd species"
  extraText                "extratextCdspeciation.dat"

CHEMISTRY

# contains the logic for outputting the expected x-axis, y-axis (%distr) pairs
# expected by 'species' plot type
include 'speciesvsph.inc'

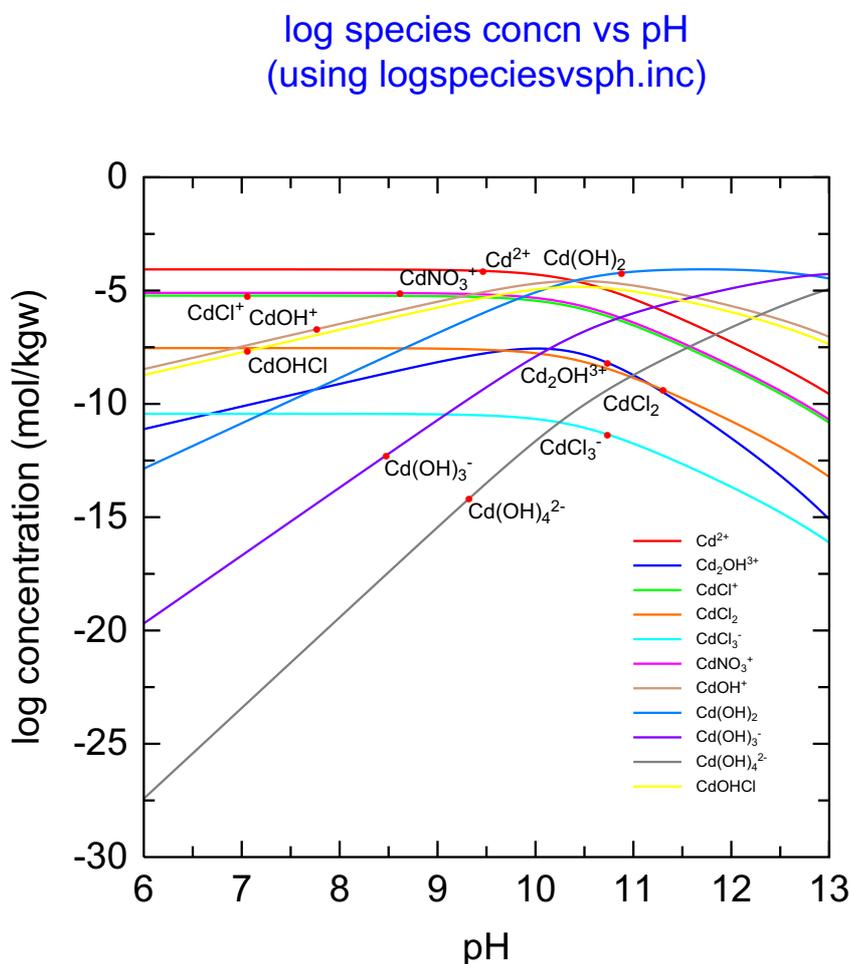
PHASES
Fix_H+
  H+ = H+
  log_k 0.0
SOLUTION 1
  temp      25
  pH        7
  units     mol/kgw
  density   1
  Cd        1e-4
  Cl        2e-3
  Na        0.1
  N(5)     0.1 charge
END

USE solution 1
EQUILIBRIUM_PHASES
  O2(g)      -0.677  0.1
  Fix_H+    <x_axis> NaOH 10
            -force_equality true
END

```



## 74 Cd speciation vs pH (log species plot)

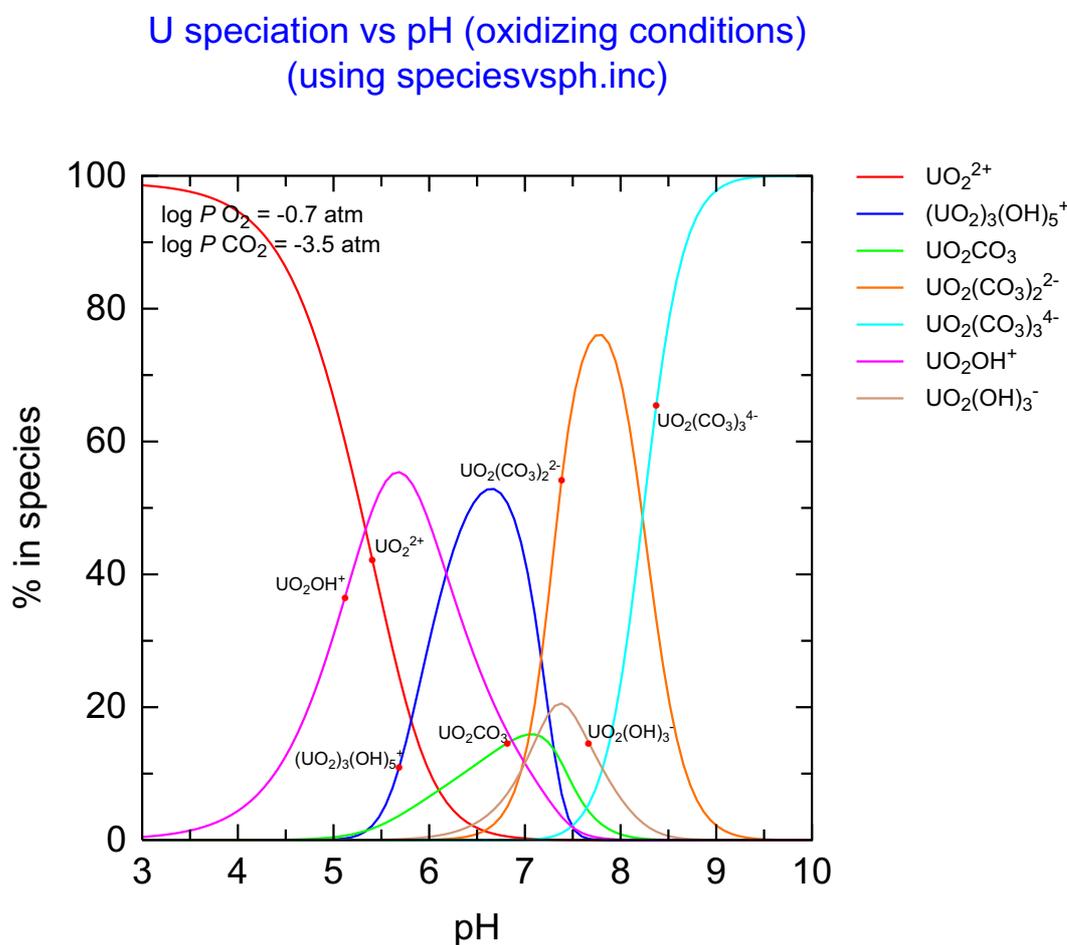


This is a variant of the previous example but plots the log of the species concentrations vs pH rather than the %distribution. This change is made entirely within the include file which controls the values sent to the 'out' file.. The include file has been changed to output log concentrations (see `logspeciesvsph.inc`) and `ytitle` has been given explicitly to override the default '% species' title.

The size of the legend (key) text has been reduced using `legendTextSize` and its placement has been set in the `extraText` file.



## 75 U species plot (oxidizing)



C:\PhreePlot\demo\Uspeciation\Uspeciationox\_U.ps

Another example of a 'species' plot. Oxidising conditions have been maintained by equilibrating with a high partial pressure of oxygen. This is set by the `<pO2>` tag. Similarly the  $CO_2(g)$  partial pressure is set with the `<pCO2>` tag.

The U speciation is dominated by U(VI) species under these conditions. Note the carbonate species at high pH.

[useLineColorDictionary](#) has been set to 1 to force the colour dictionary (`linecolor.dat`) to be read. This is where the colour of each of the lines is defined.

The [minimumYValueForPlotting](#) has been set to 5% so that minor species are not plotted.

The [labelSize](#) has been set to 1.5 mm. The label anchors shown as red dots by each of the labels can be removed by setting [trackSymbolColor](#) to 'nd'.

```

SPECIATION
  jobTitle           "Speciation vs pH using 'species' plot type"
  calculationType    species
  calculationMethod  1
  mainSpecies        "U"
  xmin               3.0
  xmax               10.0
  resolution         100
  numericTags        <pCO2> = "-3.5" \
# atmospheric PO2    <pO2> = "-0.677"

PLOT
  plotTitle          "U speciation vs pH (oxidizing condi-
tions)<br>(using speciesvsph.inc)"
  pxmin              3.0
  pxmajor            1.0
  labelSize          1.5
# only plot species with max(conc)>5%
  minimumYValueForPlotting 5.0
  extraText          "extratextUspeciation_ox.dat"

CHEMISTRY

# PHREEQC code for outputting species-concn pairs
include 'speciesvsph.inc'

PHASES
Fix_H+
  H+ = H+
  log_k 0.0

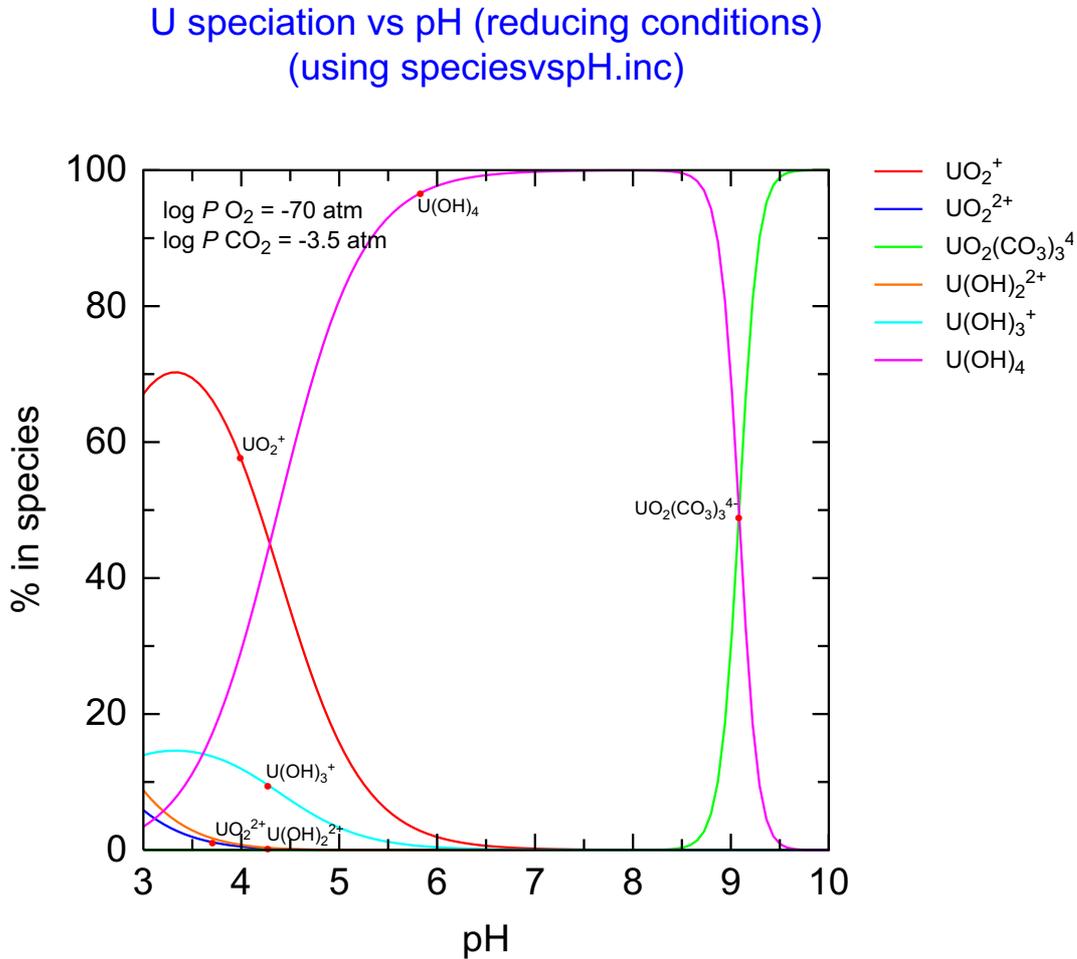
SELECTED_OUTPUT
# omit all default output
  -reset                false

SOLUTION 1
  temp      25
  pH        7
  pe        4
  units     mol/kgw
# total U
  U         1e-6
# background electrolyte
  Cl        0.01
  Na        0.01
END

# second (final) simulation - loops on this one
USE solution 1
EQUILIBRIUM_PHASES
  O2(g)     <pO2> 0.1
  Fix_H+   -<x_axis> NaOH 1
            -force_equality true
# Uraninite(c) 0 0 # omit for
solution only
  CO2(g)    <pCO2> 1.0
END

```

## 76 U species plot (reducing)



C:\PhreePlot\demo\Uspciation\Uspciationred\_U.ps

This is similar to the previous plot but  $\langle p_{O_2} \rangle$  has been set to a low oxygen fugacity  $\log P_{O_2}(g) = -70$ . Most of the plotted species are U(IV) species but  $UO_2(CO_3)_3^{4-}$  is a U(VI) species and  $UO_2^+$  is a U(V) species.

It would be necessary to go to an even lower  $\langle p_{O_2} \rangle$  value (-75) to ensure that no U(VI) species are plotted.

```

SPECIATION
  jobTitle                "Speciation vs pH using 'species' plot type"
  calculationType         species
  calculationMethod       1
  mainSpecies            "U"
  xmin                   3.0
  xmax                   10.0
  resolution             100
  numericTags            <pCO2> = "-3.5" \
# quite strongly reducing
                        <pO2> = "-70"

PLOT
  plotTitle              "U speciation vs pH (reducing condi-
tions)<br>(using speciesvsph.inc)"
  pxmin                  3.0
  pxmajor                1.0
  labelSize              1.5
# only plot species with max(conc)>5%
  minimumYValueForPlotting 5.0
  extraText              "extratextUspeciation_red.dat"

CHEMISTRY

# PHREEQC code for outputting species-concn pairs
include 'speciesvsph.inc'

PHASES
Fix_H+
  H+ = H+
  log_k 0.0

SELECTED_OUTPUT
# omit all default output
  -reset                false

SOLUTION 1
  temp      25
  pH        7
  pe        4
  units     mol/kgw
# total U
  U         1e-6
# background electrolyte
  Cl        0.01
  Na        0.01
END

# second (final) simulation - loops on this one
USE solution 1
EQUILIBRIUM_PHASES
  O2(g)     <pO2> 0.1
  Fix_H+   -<x_axis> NaOH 1
            -force_equality true
# Uraninite(c) 0 0 # omit for solution only
  CO2(g)    <pCO2> 1.0
END

```

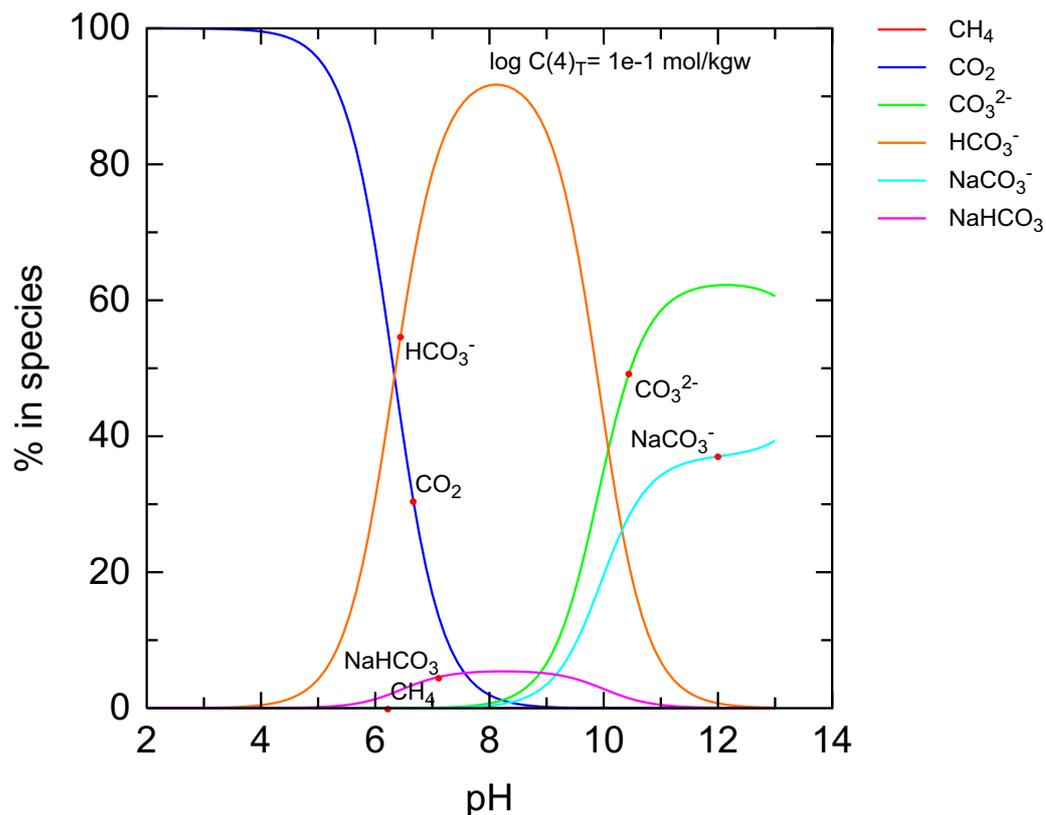
## 77 Carbon speciation vs pH

This uses a 'species' plot to show the variation in carbon species with pH in an oxidising environment. It uses the 'speciesvsph.inc' include file and so plots % in species vs pH.

The PHREEQC output is accumulated in 'species name, species concentration' pairs, one line per pH. The order of the species output is based on decreasing C concentration (i.e. highest concentration first) and so the order changes as the pH changes. Because it is a 'species' plot, **PhreePlot** expects this type of paired output and sorts the data so that the column positions for all species are fixed. This enables them to be plotted.

With the given include file and input file setup, the first column is defined as the x-axis variable and so the value of [customXcolumn](#) is ignored.

C speciation vs pH  
using speciesvsph.inc



```

SPECIATION
# plot %C species vs pH
  calculationType          species
  calculationMethod        1
  mainSpecies              C
# controls the range of pH plotted
  xmin                     2
  xmax                     13
# controls the number of points on each curve
  resolution               100
PLOT
  plotTitle                "C speciation vs pH<br>using \
                           speciesvsph.inc"
  extraText                "extratextcarbonspeciation.dat"
# pxmax                    13

CHEMISTRY

# this file exports the required x-axis(pH), y-axis (%) value pairs. Edit as
# required.
include 'speciesvsph.inc'

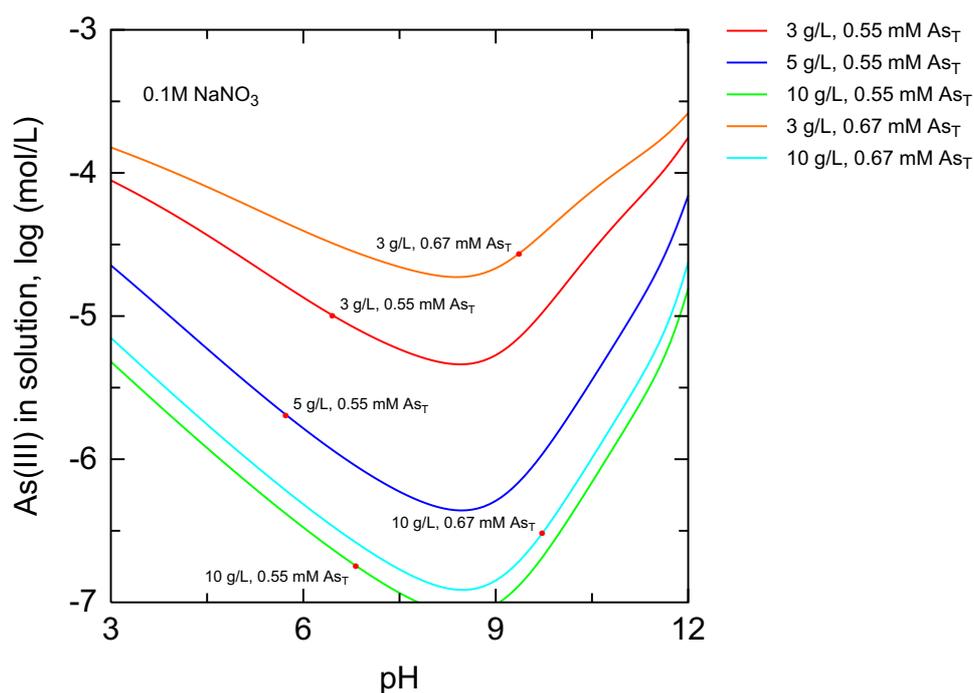
PHASES
Fix_H+
  H+ = H+
  log_k 0.0
SOLUTION 1
# carbonate speciation at least depends on temperature
  temp      10
  pH        7
  units     mol/kgw
# total C
  C(4)      1e-1 as HCO3
# background electrolyte
  Na        0.1 charge
  Cl        0.1
END

USE solution 1
EQUILIBRIUM_PHASES
  Fix_H+  -<x_axis> NaOH 10
          -force_equality true
END

```

## 78 CD-MUSIC: As(V) surface speciation on goethite

CD-MUSIC: As(III) remaining in solution  
(after Stachowicz et al., 2006, Fig. 4)



C:\PhreePlot\demo\As-cd-music\As3-shvrfig4.ps

This figure shows the surface speciation of As(V) adsorbed on goethite as a function of pH. The calculated curves were based on the CD-MUSIC model and the parameters of [Stachowicz et al. \(2006\)](#). This figure replicates the calculated curves of their Fig. 7 for one of the three surface loadings (1.70  $\mu\text{m}^2$ , 3 g/L) studied. The input file generates plots for the other two surface loadings as separate files and the [extraText](#) file picks off the appropriate text based on the plot number.

In the other plots, the contribution of several of the species is everywhere less than 10%. These curves could be omitted by setting the [minimumYValueForPlotting](#) setting to 10.

```

SPECIATION
# plot all As species f(pH) including adsorbed species
  calculationType      species
  calculationMethod    1
#
  mainSpecies          "As"
  xmin                 3.0
  xmax                 12.0
# controls the number of points at which speciation is calculated
  resolution           100
# defines <loop1> and <loop2> which are used below
  loopFile             "loopfig7.dat"
  numericTags          <AsT> = <loop1> \
                      <mass> = <loop2>

PLOT
  plotTitle            "CD-MUSIC: As(V) surface speciation<br>(after
  Stachowicz et al., 2006, Fig. 7)"
  xtitle               pH
# 2nd column in selected output created by adsspeciesvsph.inc
  customxcolumn        2
# plot xmin
  pxmin                3
  labelSize            1.5
# can be used to omit plotting of species that are always below this value
  minimumyvalueforplotting 0.1
# here the As(3) species

  extratext            "extratextfig7.dat"
# turn off legend to the right of the plot
  legendTextSize       0

CHEMISTRY

# this controls exactly what is plotted (see the system directory for the file)
include 'adsspeciesvsph.inc'
# must 'punch' x-axis, y-axis pairs

SELECTED_OUTPUT
  -reset false

SOLUTION 1
  Temp      25
  pH        2.9
  units     mol/kgw
# total As(5) concn
  As(5)     <AsT> mmol/kgw
# background electrolyte
  Na        1e-1
# N(5) only stable in oxidising environments
  N(5)     1e-1

include 'cdmusic_hiemstra.dat'

#
# Arsenate - these are the actual figures used in the SHR2006 paper and change the
# speciation from the above database slightly
#

SURFACE_SPECIES

  Goe_uniOH-0.5 + 2H+ + AsO4-3 = Goe_uniOAsO2OH-1.5 + H2O
# SHR2006 26.60 # SHR2008
  log_k      26.62
  -cd_music  0.30 -1.30 0 0 0

  2Goe_uniOH-0.5 + 2H+ + AsO4-3 = (Goe_uniO)2AsO2-2 + 2H2O
# SHR2006 29.77 # SHR2008
  log_k      29.29
  -cd_music  0.47 -1.47 0 0 0

```

```
2Goe_uniOH-0.5 + 3H+ + AsO4-3 = (Goe_uniO)2AsOOH- + 2H2O
# SHR2006 33.00 # SHR2008
    log_k      32.69
    -cd_music  0.58 -0.58 0 0 0

PHASES
Fix_H+; H+ = H+ ; log_k 0

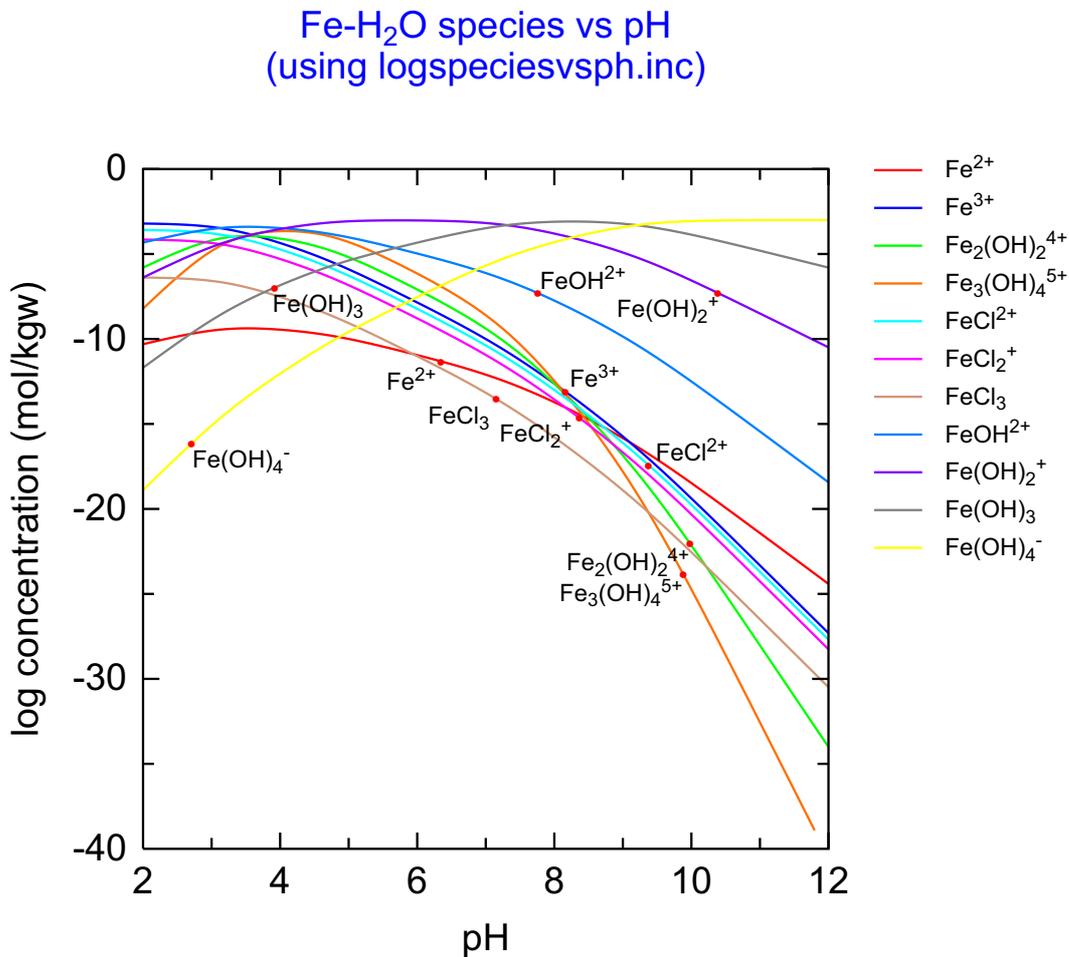
SURFACE 1
# sites/nm2 m2/g g
Goe_uniOHH0.5 3.45 98 <mass>
# C1 C2 (in F/m2)
    -cap      0.85 0.75
Goe_triOH0.5 2.7
    -cd_music
    -sites_units density

EQUILIBRIUM_PHASES 1
    Fix_H+ -<x_axis> NaOH
    -force_equality true
    O2(g) -0.67

END
```



## 79 Test plot output formats



C:\PhreePlot\demo\testplotformats\testplotformats\_Fe.ps

This example is primarily to demonstrate how plot files can be created in different formats: `ps`, `eps`, `jpg`, and `pdf`. The conversions from the native `ps` format are all carried out by [Ghostscript](#) and so can only be produced if **Ghostscript** is properly installed and the [pdfMaker](#) setting is pointing to a valid directory and file.

The example shows a species distribution plot for aqueous Fe species in the Fe-Cl-H<sub>2</sub>O system as a function of pH.

The [minimumYValueForPlotting](#) has been set to -10 to eliminate minor species from the plot.

```

SPECIATION
  jobTitle          "log speciation vs pH using 'species' plot type"
# plots concn/% of all species containing the main species
  calculationType   species
  calculationMethod 1
  mainSpecies       Fe
  xmin              -12.0
  xmax              -2.0
  resolution        100
  minimumYValueForPlotting -10
  pdf               T
  png               T
  epsi              T
  jpg               T
  eps               T

PLOT
  plotTitle         "Fe-H<sub>2</sub>O species vs pH<br>(using logspeciesvsph.inc)"

CHEMISTRY

# this controls exactly what is plotted (see the system directory for the file)
include 'logspeciesvsph.inc'
# must 'punch' x-axis, y-axis pairs

PHASES
Fix_H+
  H+ = H+
  log_k 0.0
SOLUTION 1
  temp          10
# pH for initial solution calculations only. Changed by <x_axis>
  pH            7
  units         mol/kgw
# background electrolyte
  Na            0.1 charge
  Cl            0.1
# total concn of element
  Fe(3)         1e-3
END

USE solution 1
EQUILIBRIUM_PHASES
  O2(g)         -0.677 0.1
# controls logH from xmin to xmax
  Fix_H+ <x_axis> NaOH 10
  -force_equality true
END

```

## Fitting models to data

---

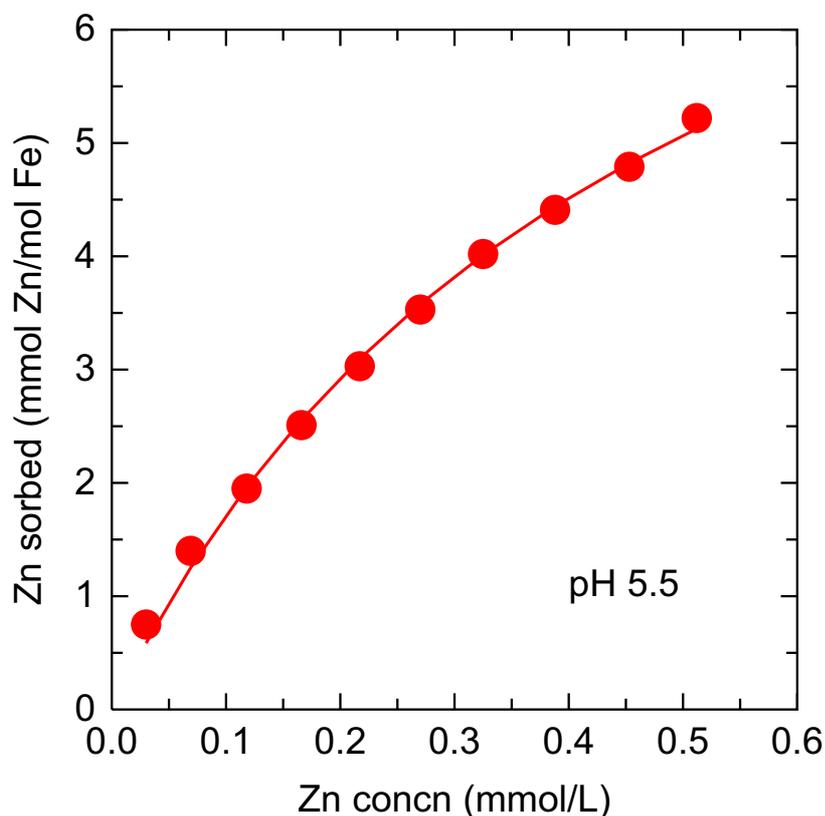
**PhreePlot** provides quite a versatile method for fitting chemical models to data (observations). This is sometimes called ‘optimization’ or ‘parameter identification’.

Other methods of optimizing **PHREEQC** models have been used, e.g. **PEST**, but the integration within **PhreePlot** is tight and the additional learning step is a relatively small one once the basics of producing custom plots have been mastered.

Nevertheless successful optimization, whatever the software used, is always a bit of an art that takes some time and experimentation to become proficient. The examples included here can be used as a starting point to experiment with. The golden rule is to start out simple.



## 80 Langmuir isotherm (1)



C:\PhreePlot\demo\fit\iso.ps

This example demonstrates the fitting of adsorption data to a Langmuir isotherm. Only one point is calculated per speciation calculation. This approach therefore requires  $n_{data} \times n_{iterations}$  **PHREEQC** runs. The [onePass](#) setting is set to `FALSE` in order to tell **PhreePlot** that it will require more than pass through the **PHREEQC** code in order to calculate dependent variable values for the complete set of data. The next example shows how to calculate all data points in one **PHREEQC** run thus reducing the number of **PHREEQC** runs to  $n_{iterations}$ . This latter approach speeds up the calculations at the expense of a more complex input file.

The input file must describe how to read in values for the dependent variable and all independent variables from the fit data file. The columns can be specified by column number or column name (from the header).

Fine tuning of the fitting parameters often helps convergence. The choice of [fitFiniteDiffStep-Size](#) is often critical to get the fitting started. It is also important to decide how the residuals are going to be weighted (the error model), here unit weighting has been used.

The plot can use any column from the 'pts' file. This includes special columns labelled 'observed', 'calculated', 'residuals' and 'weightedResiduals' as well as all the columns from the fit data file and from the selected output.

```

# simple example of fitting to a Langmuir isotherm using unit weighting
# basic fit with isotherm plot

SPECIATION
  jobTitle                "Test fitting: absolute errors (unit weight-
ing)"
  calculationType         fit
  calculationMethod       1
FIT
# contains a list of observations and independent variables
  dataFile                iso.dat
# does a separate PHREEQC simulation for each observation -
  onepass                 FALSE
# slow but easy to set up

# name of column in fit data file containing the observations (dep variable)
  dependentVariableColumnObs  Znsorbed
# name of column in selected output file containing the calcd values of the dep
variable
  dependentVariableColumnCalc  sorbZn
# 0 = unit weights
  fitWeightingMethod          0
# initial step size for each adjustable parameter
  fitFiniteDiffStepSize      1.0E-3
# column header in fit data file for which PHREEQC simulation(s) to use for each
observation
  mainLoopColumn             sim
  numberOfFitParameters      2
  fitParameterNames         log_k M1
# 0 = parameters on a linear scale, 1 = log10 parameters before fitting
  fitLogParameters           0 0
# 1 = adjustable
  fitAdjustableParameters   1 1
# initial values (starting point)
  fitParameterValues         3.0 1.0

PLOT
  plotTitle                 "Zn sorption on Hfo"
  xtitle                    "Zn concn (mmol/L)"
  ytitle                     "Zn sorbed (mmol Zn/mol Fe)"
# plot isotherm (x = Znconcn, y = sorbed)

# y = line from calculated values from out file with column heading = 'calculated'
lines                        calculated
# y = points from observed values from out file with column heading = 'observed'
points                       observed

  lineWidth                 0.4
  lineColor                 red
# no labels on plot
  labelSize                 0.0
# no legend (key)
  legendTextSize            0.0
  pointSize                 4.0
# x = Znconcn column in out file
  customXcolumn             Znconcn
# extra text on plot
  extraText                 "extratextiso.dat"

CHEMISTRY

PHASES
Fix_H+
  H+ = H+
  log_k 0.0

SURFACE_MASTER_SPECIES
  Surf Surf
SURFACE_SPECIES

```

```
Surf = Surf
log_k 0.0
# Langmuir model
Surf + Zn+2 = SurfZn+2
# this is where log_k (updated parameter value) is substituted
log_K <log_k>

SELECTED_OUTPUT
-high_precision true
-reset false
PRINT
-reset false

USER_PUNCH
# fit Langmuir isotherm
# these are the column headings used for tag names: NB this is the output pH not the
input pH
-headings sorbZn pH mmolZn step_no
10 sorbedZn=SURF("Zn","Surf")
# NB variable name (used internally) is distinct from column header
20 if sorbedZn>0 THEN punch sorbedZn, -la("H+"), tot("Zn")*1e3, step_no

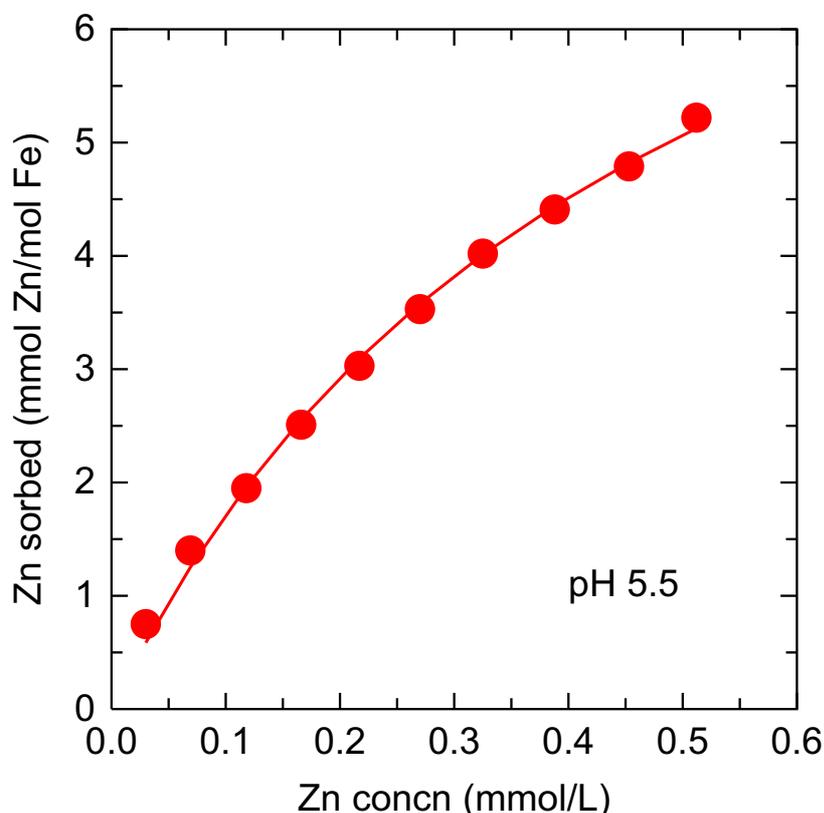
SOLUTION 1
-pH <pHobs>
-units mmol/L
# 1 M NaNO3 background electrolyte
Na 1000
N(5)1000
# <Znconcn> from iso.dat
Zn <Znconcn>

SURFACE
# this is where the max number of sites (updated parameter) is substituted
Surf <M1>
-equil 1
-no_edl

EQUILIBRIUM_PHASES
# pHobs from the fit data file
Fix_H+ -<pHobs> NaOH
-force_equality true
END
```



## 81 Langmuir isotherm (n)



C:\PhreePlot\demo\fitison.ps

This is exactly the same as the previous example except that all 10 points are calculated in a single pass of **PHREEQC**. This requires the [onePass](#) setting to be set `TRUE`. It also requires some rearrangement of the way that the input data are presented. There are two critical differences compared with the ‘one point per pass’ approach:

(i) in the ‘one point per pass’ approach, the **CHEMISTRY** part of the input file has just one **PHREEQC** simulation (one `END` at the end of the file) whereas in the ‘calculate all points in one pass’ approach there is one simulation for each data point, i.e. multiple `END`'s;

(ii) in the first approach, [selectedOutputLines](#) points to just the last line, e.g.

```
selectedOutputLines 1
```

whereas with the ‘calculate all points at once’ it points to many lines with the ‘auto’

```
selectedOutputLines auto
```

where ‘auto’ selects all the lines found in the selected output which should therefore contain one line per point. Each line of output represents one simulation.

Note that the **PHREEQC** setup in the input file contains many simulations which are near-repeats. This could become tedious to setup for large datasets and would probably require some form of automatic generation. **PhreePlot** includes a simple input file [pre-](#)

[processor](#) which can generate the necessary input file (see `demo\fitpreprocessor\ppiso.ppi`) from a simplified skeleton file.

```

SPECIATION
  jobTitle           "Test fitting"
  calculationType    fit
  calculationMethod  1

FIT
# fit data file
  dataFile          ison.dat
# says that all dependent variable values output in one PHREEQC pass (see below)
  onePass           TRUE
# NB no half way house - either one calculation per pass or the whole lot

  mainloop          2
# selectedOutputLines      0 1 1 1   1 1 1 1   1 1 1   # not necessary
since pre-loop doesn't write selected output
# observations from the fit data file
  dependentVariableColumnObs      Znsorbed
# from selected output
  dependentVariableColumnCalc     sorbZn
# initial step size
  fitFiniteDiffStepSize          1.0E-3
# from the fit data file
  weightColumn                    wt
# blockRangeColumn                sim           # from the fit
data file - defaults ok
# mainLoopColumn                  main         # from the fit
data file - defaults ok
  numberOfFitParameters           2
  fitParameterNames               log_k  M1
# 0 = linear parameters
  fitLogParameters                0 0
# 1 = adjustable, 0 = fixed
  fitAdjustableParameters         1 1
# starting values
  fitParameterValues              3.0 1.0

PLOT
  plotTitle                    "Zn sorption on Hfo<br>(onePass = TRUE)"
  xtitle                       "Zn concn (mmol/L)"
  ytitle                       "Zn sorbed (mmol Zn/mol Fe)"
# from the out file
  lines                         calculated
# from the out file
  points                        observed
  lineWidth                     0.4
  lineColor                      red
  labelSize                      0.0
  legendTextSize                 0.0
  pointSize                      4.0
# from the out file
  customXcolumn                  Znconcn
  extraText                      extratextiso.dat

CHEMISTRY

#1
PHASES
Fix_H+
H+ = H+
log_k 0.0

SURFACE_MASTER_SPECIES
  Surf Surf
SURFACE_SPECIES
  Surf = Surf
  log_k 0
END

#2

```

```

SURFACE_SPECIES
  Surf + Zn+2 = SurfZn+2
# <log_k> is binding constant - substituted from the parameters defined above
  log_K <log_k>

PRINT
  -selected_output true
#   -reset false
SELECTED_OUTPUT
  -high_precision true
  -reset false
# -state true
# -m Zn+2 SurfZn+2

SOLUTION_SPREAD
-pH <pHobs>
# this is an easy way to put in data - paste in here from a spreadsheet etc
-units mmol/L
# strictly PHREEQC names, separated by tabs
NumberNaN(5)ZnpH
# this is the pH used
1100010000.035.5
# data separated by tabs
2100010000.0695.5
3100010000.1185.5
4100010000.1665.5
5100010000.2175.5
6100010000.275.5
7100010000.3255.5
8100010000.3885.5
9100010000.4535.5
10100010000.5125.5

USER_PUNCH
# fit Langmuir isotherm
# this is the output pH
-headings sorbZn pH molZn step
# dependent variable calculated here
10 sorbedZn=SURF("Zn","Surf")
20 if sorbedZn>0 THEN punch sorbedZn, -la("H+"), tot("Zn")*1e3, step_no

END

#3
SURFACE
# <M1> is the number of sites - substituted from the parameters defined above
Surf <M1>
-no_edl
# this uses solution Number 1 above
-equil 1
END

#4
SURFACE
Surf <M1>
-no_edl
# this uses solution Number 2 above etc
-equil 2
END

#5
SURFACE
Surf <M1>
-no_edl
-equil 3
END

#6
SURFACE
Surf <M1>
-no_edl

```

```
-equil 4  
END
```

```
#7  
SURFACE  
Surf <M1>  
-no_edl  
-equil 5  
END
```

```
#8  
SURFACE  
Surf <M1>  
-no_edl  
-equil 6  
END
```

```
#9  
SURFACE  
Surf <M1>  
-no_edl  
-equil 7  
END
```

```
#10  
SURFACE  
Surf <M1>  
-no_edl  
-equil 8  
END
```

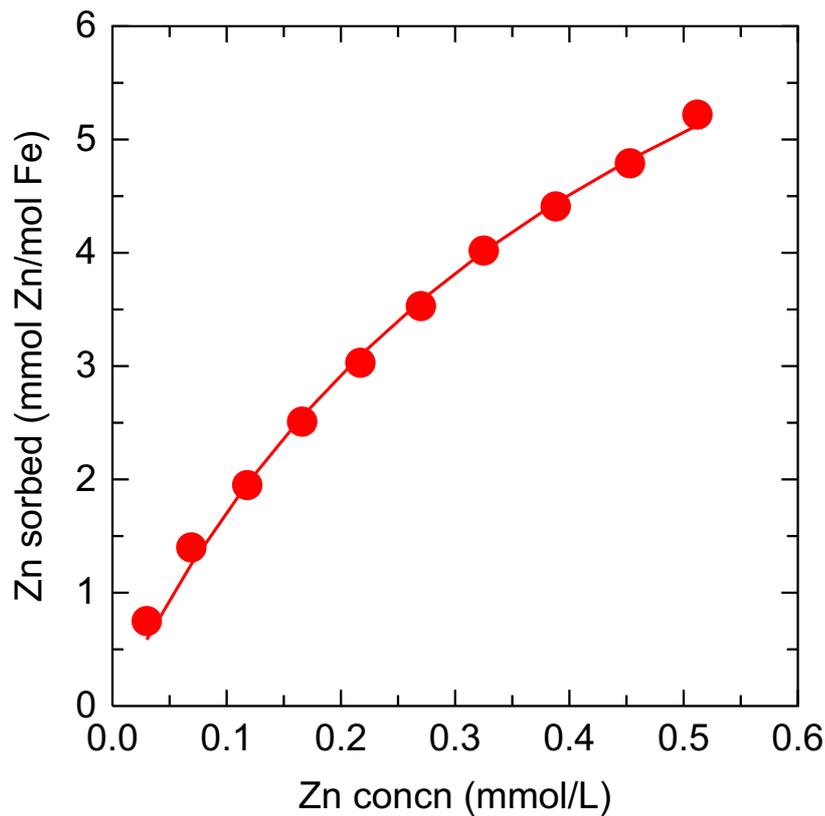
```
#11  
SURFACE  
Surf <M1>  
-no_edl  
-equil 9  
END
```

```
#12  
EQUILIBRIUM_PHASES  
  Fix_H+ -<pHobs> NaOH  
SURFACE  
Surf <M1>  
-no_edl  
-equil 10  
END
```



## 82 Langmuir isotherm (pre-processor)

Zn sorption on Hfo  
(all in one pass of the input preprocessor)



C:\PhreePlot\demo\fitpreprocessor\isopp.ps

This is similar to the `\demo\iso\ison.ppi` except that the near-repetitive blocks are generated automatically by invoking the **PhreePlot** pre-processor ([Section 13](#)) to expand the various blocks containing `<repeatStartn>` and `<repeatEndn>` tags where  $n$  is a positive integer.

```
# This demonstrates an efficient (fast) method of fitting data to a PHREEQC model.
# It uses the PhreePlot pre-processor which replicates blocks of PHREEQC code with
# minor changes.
# This enables the 'one pass' option to be used and avoids the copying normally nec-
# essary (cf ison.ppi).
# The expanded input file is written to the log file.
```

```
SPECIATION
  jobTitle           "Test fitting"
  calculationType    "fit"
  calculationMethod  1
```

```

FIT
# fit data file - has observations
  dataFile          "isopp.dat"
# this produces a block of selected output with 10 lines of data (not 1)
  onePass           TRUE
  mainLoop          1
# column in isopp.dat
  dependentVariableColumnObs      sorbed
# column in selected output
  dependentVariableColumnCalc     Znsorbed
# initial step size for parameter adjustment
  fitFiniteDiffStepSize          1.0E-03
# column in fit data file with the weights
  weightColumn                   wt
  numberOfFitParameters          2
  fitParameterNames              "log_k" "M1"
  fitLogParameters                0 0
# 1= adjustable, 0 = fixed
  fitAdjustableParameters        1 1
# initial values
  fitParameterValues             3. 1.

PLOT
  plotTitle                  "Zn sorption on Hfo<br>(all in one pass of
the input preprocessor)"
  xtitle                     "Zn concn (mmol/L)"
  ytitle                     "Zn sorbed (mmol Zn/mol Fe)"
# plot this column from the out file as lines
  lines                      calculated
  points                      observed
  lineWidth                   0.4
  lineColor                   "red"
  labelSize                   0.0
  legendTextSize              0.0
  pointSize                   4.0
  customXcolumn               Znconcn

# debug 3 # to see input and selected output on screen

CHEMISTRY

PRINT
  -reset false
  -selected_output false
SURFACE_MASTER_SPECIES
  Surf Surf

SURFACE_SPECIES
  Surf = Surf
  log_k 0

  Surf + Zn+2 = SurfZn+2
# from fitParameterNames
  log_k <log_k>

SELECTED_OUTPUT
  -high_precision true

USER_PUNCH
  -headings Znsorbed pH molZn step
  10 sorbedZn=SURF("Zn","Surf")
  20 if (step_no = 0) THEN punch sorbedZn, -1a("H+"), tot("Zn")*1e3, step_no

SOLUTION_SPREAD
DescriptionZnpHNaN(5)
mmol/kgwmmol/kgwmmol/kgw
13.00E-025.510001000
26.90E-025.510001000
31.18E-015.510001000
41.66E-015.510001000
52.17E-015.510001000

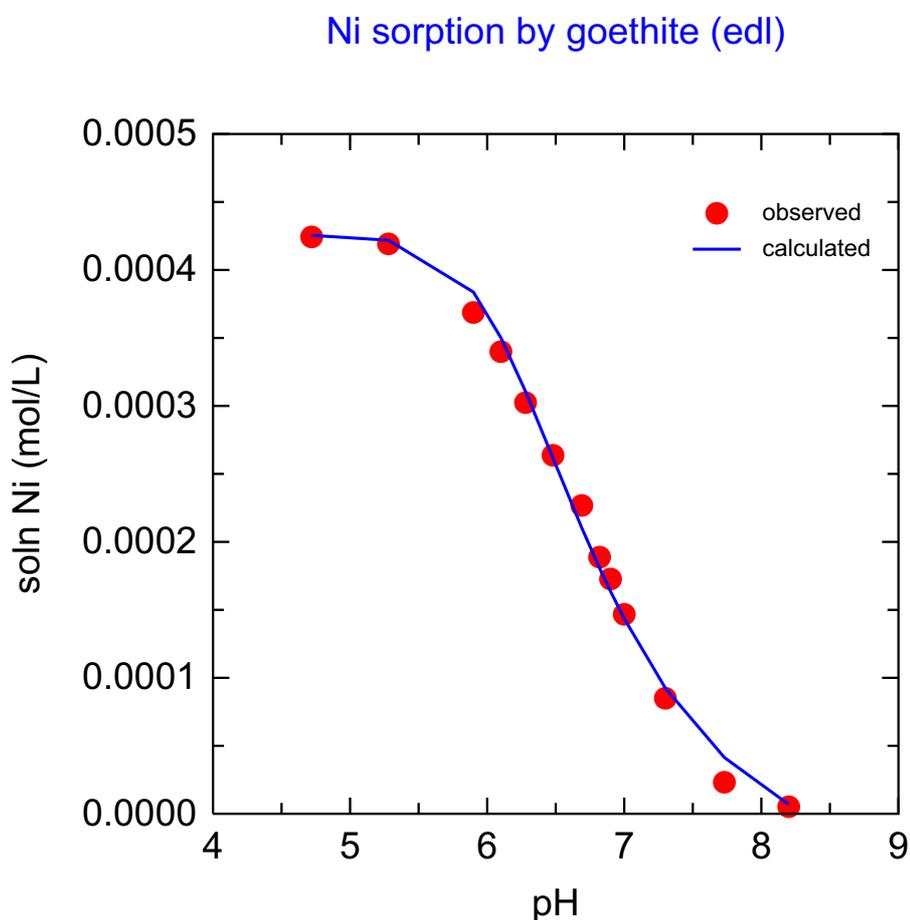
```

```
62.70E-015.510001000  
73.25E-015.510001000  
83.88E-015.510001000  
94.53E-015.510001000  
105.12E-015.510001000  
END
```

```
PRINT  
  -selected_output true  
  
<repeatStart1> 1 10  
SURFACE  
# from fitParameterNames  
  Surf <M1>  
  -no_edl  
  -equil <repeatValue1>  
END  
<repeatEnd1>
```



## 83 Ni sorption by goethite



C:\PhreePlot\demo\fitNi\Niedl.ps

This example fits sorption data for Ni sorption by goethite from data by Sherman and Peacock (unpublished). Ni sorption was measured as a function of pH at a constant solid solution ratio of goethite and constant background electrolyte concentration (0.1M NaNO<sub>3</sub>). The dependent variable was the final solution Ni concentration after sorption. The independent variable was the final pH.

The data were fitted to the [Dzombak and Morel \(1990\)](#) diffuse double layer model as implemented in **PHREEQC** (surface activities are defined in terms of mole fractions). The Ni was assumed to bind to two types of bidentate surface sites as inferred from EXAFS data. The `edl SURFACE` option was used. Two log K values were fitted.

The `finiteDiffStepSize` was set to 1e-2 which is a large enough shift in the log K's to give a small but significant change in the objective function while still giving reliable derivatives.

The fit is good but there is really not enough data to provide a convincing test of the model.

The line colour (blue) and points colour (red) are both determined by the line colour dictionary since `useLineColorDictionary` has been set to 1. This means 'use the dictionary if present and if the species are defined', which they are.

```

# fit some Ni sorption to goethite data

SPECIATION
  calculationType          fit
  calculationMethod        1

FIT
# fit data file - fit the final Ni concn not the amount sorbed
  dataFile                  "Nisolnfresh.dat"
# final Ni concn is in column 2 of fit data file
  dependentVariableColumnObs 2
# NB this is often a good way of fitting sorption data where possible

# calcd final Ni concn in column 2 of selected output
  dependentVariableColumnCalc 2
# size of initial adjustment of parameters when fitting
  fitFiniteDiffStepSize      1.0E-02
  fitConvergenceCriterion    1.0E-12
  fitStepSize                 1.0
# 0 = unit weighting for all points
  fitWeightingMethod         0
  numberOfFitParameters      2
  fitParameterNames          "log_k1" "log_k2"
# 0 = linear parameters
  fitLogParameters           0 0
# 1 = adjustable
  fitAdjustableParameters    1 1
# initial values of log_k1 and log_k2
  fitParameterValues         8.  0

PLOT
  plotTitle                  "Ni sorption by goethite (ed1)"
  xoffset                     60
  xtitle                      pH
  ytitle                       "soln Ni (mol/L)"
# p or plot limits
  pxmin                       4.0
  pxmax                       9.0
  pymin                       0
  pymax                       5.E-04
# number of decimal places
  pydec                       4
  lineColor                   blue
  lineWidth                   0.4
# calculated column from out file
  lines                       calculated
# observed column from out file
  points                      observed
# key size
  legendTextSize              1.9
  pointSize                   3.0
# suppress labelling
  labelSize                   0
# column 6 of out file
  customXcolumn               6
  extraText                   "extratextfitNi.dat"

CHEMISTRY

TITLE Goethite surface 1pK model, Ni sorption 1 site.
PHASES
Fix_H+
  H+ = H+
  log_k 0.

SURFACE_MASTER_SPECIES
  Fes_ Fes_OH-0.5
SURFACE_SPECIES
# surface charging
  Fes_OH-0.5 = Fes_OH-0.5
  log_k 0.0

```

```

Fes_OH-0.5 + H+ = Fes_OH2+0.5
log_k 8.50

# bidentate model
2Fes_OH-0.5 + Ni+2 = (Fes_OH)2Ni+
log_k <log_k1>

2Fes_OH-0.5 + Ni+2 + H2O = (Fes_OH)2NiOH + H+
log_k <log_k2>

SELECTED_OUTPUT
  high_precision true
  reset false
USER_PUNCH
headings pH Ni
-start
# pH and total dissolved Ni (calcd)
10 punch -la("H+"), TOT("Ni")
# fitting compares TOT("Ni") with obsd total, eg by ICP-AES
-end

SURFACE 1
# -diffuse_layer
# -no_edl
# goethite parameters
Fes_OH-0.5 1.09e-3 32.7 3.33

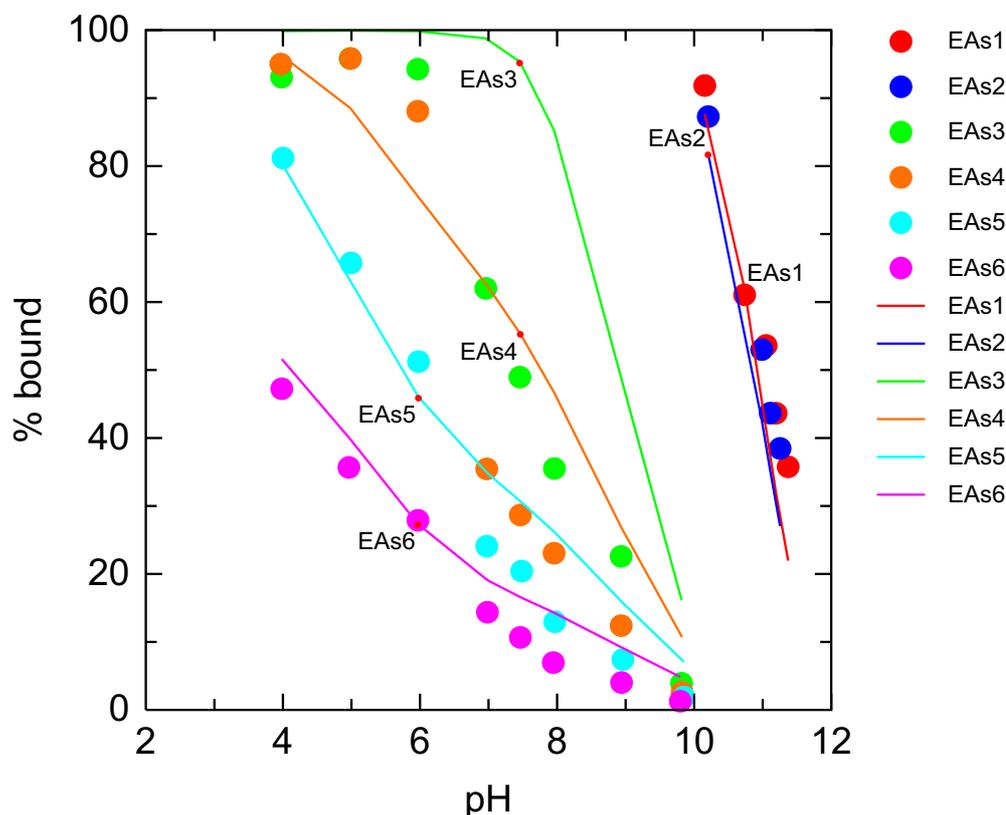
SOLUTION 1
  units mol/kgw
# NiT
Ni 0.4258e-3
# background electrolyte
Na 0.1
N(5) 0.1 charge

EQUILIBRIUM_PHASES
O2(g) -0.67 0.1
Fix_H+ -<pHobs> NaOH
-force_equality true
Ni(OH)2 0 0
END

```



## 84 As(V) sorption on hydrous ferric oxide



C:\PhreePlot\demo\fitfoAs\fitfoAsv.ps

This example uses the As data used by [Dzombak and Morel \(1990\)](#) to fit the three surface log K's for As(V) sorption by HFO. A global fit has been used. The weighting factors have all been set to one.

Line breaks in the input data file are used to defined line breaks in the plots – essentially six different data sets. The line and point colours are read from the line colour dictionary.

Some of the fits are not very good - EAs4 (orange points, orange line), for example, shows quite a large deviation between observations and fitted values.

Note that the in-plot labels are only plotted for the lines not the points. The lines and points for each dataset could be given the same colour by editing the line colour dictionary and replotting. [convertLabels](#) has been set to false to prevent the labels being interpreted as species names and therefore subscripting the final number.

[changeColor](#) has been set to `TRUE` to ensure that the various curves, which are all subsets of data from the same column, are given separate colours. This applies equally to both the [points](#) and [lines](#) sets of data – hence they follow the same colour sequence.

```

# Example of fitting some As sorption on Hfo data from Dzombak and Morel (1991)

SPECIATION
  calculationType          fit
  calculationMethod        1
  labels                   "EAs1" "EAs2" "EAs3" "EAs4" "EAs5" "EAs6"
"EAs1" "EAs2" "EAs3" \
# used in turn for labelling points then curves in plot
                                "EAs4" "EAs5" "EAs6"

FIT
# file containing observations and independent variables
  dataFile                 "1eAsv.dat"
# dep variable is in column 6
  dependentVariableColumnObs 6
# this where the calcd values are found in selected output - see below
  dependentVariableColumnCalc 4
# size of initial shift in parameter values looking for response
  fitFiniteDiffStepSize     1.0E-02
# controls when convergence has been achieved
  fitConvergenceCriterion   1.0E-03
  fitStepSize               1.0
# 2 = take weights from fit data file
  fitWeightingMethod        2
# weights in column 7 in fit data file
  weightColumn              7
# column 8 defines which PHREEQC simulation (see below) to use for each point
  blockRangeColumn         8
  numberOfFitParameters    3
  fitParameterNames        "log_K1" "log_K2" "log_K4"
# 0 = linear parameter values (ie don't use log param)
  fitLogParameters         0 0 0
# 1 = adjustable (0 = fixed)
  fitAdjustableParameters  1 1 1
# initial values
  fitParameterValues       29.31 23.51 10.58

PLOT
  plotTitle                "Refitting As(V) sorption data for
Hfo<br>(1eAsv.dat)"
  xtitle                   pH
  ytitle                   "% bound"
# the 'calculated' column in the 'out' file is plotted as a line
  lines                    calculated
# the 'observed' column in the 'out' file is plotted as points
  points                   observed
# prevents the labels being interpreted as species
  convertLabels            F
# give subsets a sequence of diff colours
  changeColor              T
# 0 = do NOT use the line colour dictionary for colours
  useLineColorDictionary  0
# symbols will be 3 mm (nominal)
  pointSize                3.0
# x-axis variable is in column 8 of the 'out' file
  customXcolumn            8
# can use this to scale whole plot
  plotFactor               1.0
# additional text for plot
  extraText                "extratextfithfoAsv.dat"

CHEMISTRY

PHASES
Fix_H+
  H+ = H+
  log_k 0.
Fe(OH)3(a) 112
  Fe(OH)3 + 3H+ = Fe+3 + 3H2O
  log_k 4.891

```

```

# prevents Fe(OH)3(a) from dissolving
  -add_constant -10

SURFACE_SPECIES
#  Arsenate
    Hfo_wOH + AsO4-3 + 3H+ = Hfo_wH2AsO4 + H2O
# the first parameter is substituted here
    log_k <log_K1>

    Hfo_wOH + AsO4-3 + 2H+ = Hfo_wHAsO4- + H2O
    log_k <log_K2>

    Hfo_wOH + AsO4-3 = Hfo_wOHAsO4-3
    log_k <log_K4>

SELECTED_OUTPUT
  high_precision true
  reset false

USER_PUNCH
# fourth column (%sorbed) is compared with observations
-headings pH Hfo AsT %sorbed
10 Hfo=equi("Fe(OH)3(a)")
20 totAs=SYS("As")
30 pcsorb=100*SURF("As","Hfo")/totAs
40 PUNCH -la("H+"), Hfo, totAs, pcsorb
SURFACE 1
# D&M Hfo parameters
    Hfo_sOH Fe(OH)3(a)      equilibrium_phase 0.005 53300
    Hfo_wOH Fe(OH)3(a)      equilibrium_phase 0.2

SOLUTION
  units mol/kgw
# <I>, <FeT> and <AsT> are from the fit data file
  Na <I>
  N(5) <I> charge
  Fe <FeT>
  As <AsT>
EQUILIBRIUM_PHASES
  O2(g) -0.67 0.1
# <pH> from the fit data file
  Fix_H+ -<pH> NaOH
  -force_equality true
  Fe(OH)3(a) 0 0
END

```

# Contour plots

---

Contour plots provide a way of viewing the variation of some factor in two dimensions. The contour plots generated by **Phreeplot** are simple, classical 2D views of the surface. The viewing angle of the generated surface is always looking down directly from above.

The user has control over many of the plotting parameters such as the choice of the contour levels, and the size and colour of many of the plot attributes.

The challenge is to generate a set of data and choose a set of contour levels that produces a good-looking plot while avoiding trying to trace numerical noise. This is largely controlled by the choice of resolution used to generate the regular grid of values, and the choice of the contour values. Plots based on geochemical data can produce areas with both extremely large and extremely low gradients, both of which can be challenging to contour.

## 85 Contour two metals at three resolutions

---

Besides demonstrating the generation of contour plots, this example (`demo\contour\contour_hfo-metalx.ppi`) shows the use of tags in the **PhreePlot** section of the main input file. These are used to produce contour plots for two metals, Zn and Pb, at three resolutions, 10, 25 and 100. The data contoured are the percentage of metal adsorbed by HFO in the presence of a fixed amount of metal, Fe and background electrolyte. The two variables, pH and  $O_2(g)$  fugacity, change over a wide range leading to the variable dissolution/precipitation of HFO on which the Zn and Pb are adsorbed. This combination produces a total of six plots.

The [calculationType](#) keyword is set to 'contour'. The <mt> tag defined in [numericTags](#) defines the total concentration of metal in the system and the system-defined <mainSpecies> tag defines the metals of interest. This tag is generated from the mainSpecies keyword list.

The **PHREEQC** calculations are relatively straightforward. A solution of either Zn or Pb plus 0.01 mol/kgw Fe and 0.1 mol/kgw NaCl background electrolyte is brought to a particular pH and  $\log f_{O_2(g)}$  using NaOH and  $O_2(g)$ , respectively, as defined by the `EQUILIBRIUM_PHASES` keyword data block. This uses the <x\_axis> and <y\_axis> tags. The values of these are generated on a regular grid by the 'contour' routine using [xmin](#), [xmax](#), [ymin](#), [ymax](#) and [resolution](#). The 'hfo.inc' include file is retrieved from the system directory and adds the Hfo surface and the DLM adsorption model.

The `USER_PUNCH` block calculates the % adsorbed using `TOT()` for the total dissolved metal concentration and `SYS()` for the total number of moles of the metal in the system. The total dissolved concentration has to be multiplied by the total amount of water (in kg) in the system to convert it to the number of moles of dissolved metal. The pH and percent adsorbed (%s) are output to the selected output once per iteration.

The selected output results accumulate in the 'out' file based on the `USER_PUNCH` selected output. It is this file that provides the z-data to contour. Note that the x- and y-data are not output – they are defined implicitly by their position in the 'out' file, the calculation domain and the grid resolution. The [contourZvariable](#) is defined as '%s'. The heading of the outfile is searched for this string to determine the column position of the z-variable used in contouring. The contour levels chosen are set to 1, 10, 20, 50, 80, 90 and 99% using the [contours](#) keyword.

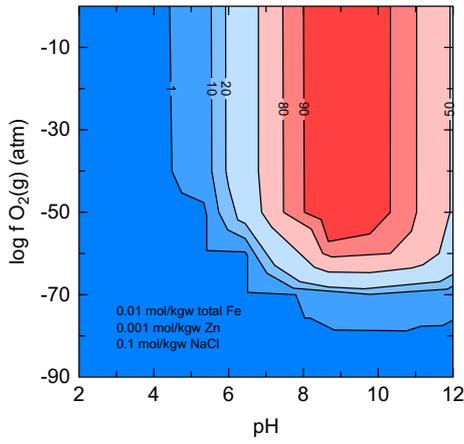
A loopfile, `loopmetalx.dat`, defines a loop variable, `res`, which in turn defines a corresponding <res> tag which successively takes on the values 10, 25 and 50. Note that a loop value derived from a loopfile overrides any setting of the loop variable using [loopMin](#) etc.

Four **PhreePlot** loops are involved in the calculations, each based on a generated tag value. These are (from the least rapidly changing outermost loop to the most rapidly changing innermost loop): <mainSpecies>, <res>, <y\_axis> and <x-axis>. The <res> tag is used in the **PhreePlot** section of the input file and is updated once per loop iteration.

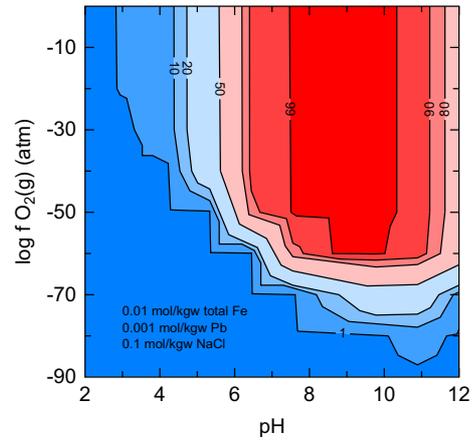
The [plotTitle](#) uses the <mainSpecies> and <res> tags and these are substituted in the title just before plotting. Similarly, the [extraText](#) file contains the <mt> and <mainSpecies> tags and these are substituted just before use.

Each mainSpecies-res combination generates its own outfile so there are six such outfiles. The [multipageFile](#) t setting means that each of the six plots is written to a single multi-page ps file, one plot per page. The six plots are shown in Figure Ex85.1. Pb is adsorbed more strongly than Zn resulting in a larger area with >99% adsorption. There is no adsorption at low pH or low  $f_{O_2(g)}$  due to the instability of HFO under those conditions. As the resolution increases, the clarity of the boundaries increase. The default placement of the labels is acceptable so there is no need to move them.

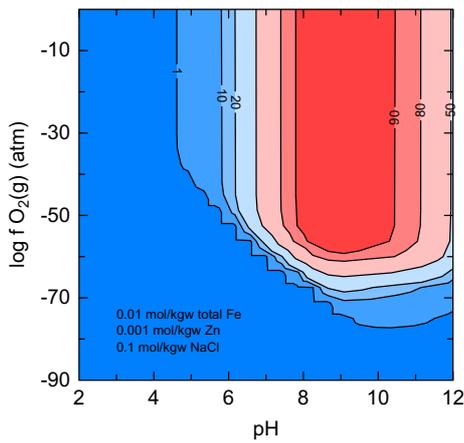
%Zn adsorbed by HFO  
resolution = 10



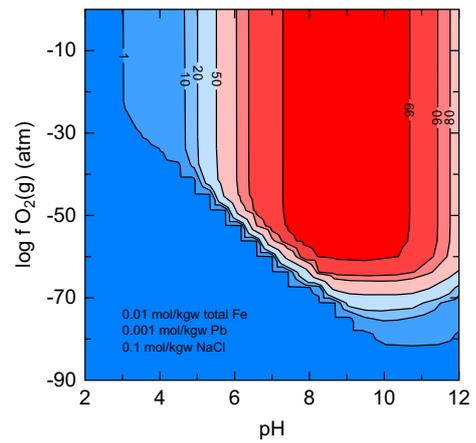
%Pb adsorbed by HFO  
resolution = 10



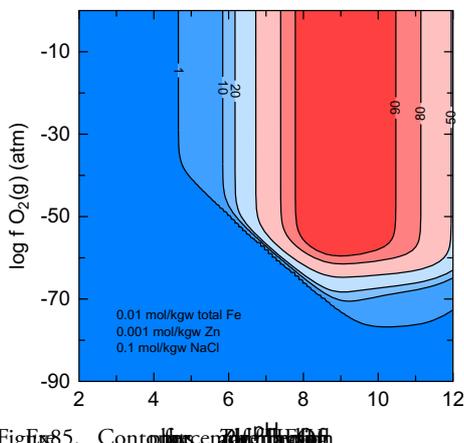
%Zn adsorbed by HFO  
resolution = 25



%Pb adsorbed by HFO  
resolution = 25



%Zn adsorbed by HFO  
resolution = 100



%Pb adsorbed by HFO  
resolution = 100

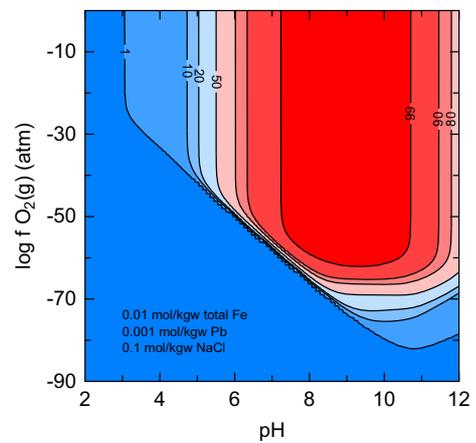


Figure Ex85. Contour plots of %Zn and %Pb adsorbed by HFO as a function of pH and log f O<sub>2</sub>(g) (atm) for various chemical concentrations. Figure Ex85.

```

# produces a contour plot for the Fe-H2O system with FeT = 0.01 mol/kg
# and Fe(OH)3(a) as a possible mineral phase
SPECIATION
  loopfile                loopmetalx.dat
  calculationType         "contour"
  calculationMethod       1
# see USER_PUNCH
  contourZvariable        %s
  mainspecies             Zn Pb
  xmin                    2.0
  xmax                    12.0
  ymin                    -90
  ymax                    0
# updated from loop file once per z-loop
  resolution              <res>

  numerictags             <Fet> = 0.01 \
                          <mt>=10^<M>

PLOT
  plotTitle               "%<mainspecies> adsorbed by HFO<br>resolution
= <res>"
  xtitle                  pH
  ytitle                  "log <i>f</i> O<sub>2</sub>(g) (atm)"
  contours                 1 10 20 50 80 90 99
  extraText               extratextmetalx.dat
  multipagefile           t

CHEMISTRY

# one simulation

# add standard Hfo DLM model
include hfo.inc

PHASES
Fix_H+; H+ = H+; log_k 0.

SELECTED_OUTPUT
-reset FALSE
-high_precision TRUE

USER_PUNCH
-headings pH %s
10 PUNCH -la("H+"), 100*(1 - TOT("<mainspecies>")*TOT("water"))/(SYS("<mainspe-
cies>"))

SOLUTION 1
  pH          1.8
  units       mol/kgw
  Fe(3)       <Fet>
  <mainspecies> <mt>
  Na          1e-1
  Cl          1e-1

EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g)   <y_axis>
  Fe(OH)3(a) 0 0
END

```



## 86 Contour Fe solubility as a function of Eh-pH

It is possible to produce a contour plot with Eh-pH axes rather like a predominance plot. It provides a useful alternative view of the behaviour over the domain of interest. As with predominance plots, it is best to vary the redox by varying the O<sub>2</sub>(g) fugacity and to use the yscale setting to convert from the O<sub>2</sub>(g) fugacity to the Eh scale.

The main requirements are that the parameter being contoured is output with a USER\_PUNCH block and identified with the [contourZvariable](#) setting. In order to convert from O<sub>2</sub>(g) fugacity to Eh, it is also necessary to explicitly output fields with the headings 'pe' for pe and 'TC' for temperature (Celsius). Also the [yscale](#) setting should be set to 'Eh'. The following example can be found in `demo\contour\contour_hfo_Eh_basic.ppi`.

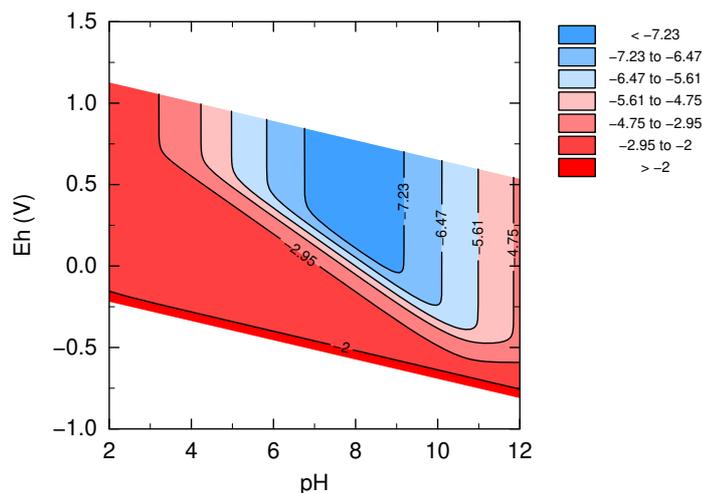
```
SPECIATION
  calculationType          "contour"
  calculationMethod        1
  contourZvariable         FeT # plot is for FeT defined in USER_PUNCH
  xmin                     2.0 # pH range
  xmax                     12.0
  ymin                     -90 # fO2(g) range (controls the Eh)
  ymax                     1
  resolution               100 # calculate with a 100 x 100 grid

PLOT
  xtitle                   "pH"
  ytitle                   "Eh (V)"
  yscale                   Eh
  contours                 auto 8 p
  pdf                      t

CHEMISTRY

# first simulation
PHASES
Fix_H+; H+ = H+; log_k 0.
SELECTED_OUTPUT 1
-reset FALSE
-high_precision TRUE
USER_PUNCH 1
  -headings FeT pH O2(g) pe Eh TC
10 R = 8.314462
20 F = 96485.33
30 pe = -LA("e-")
40 eh = pe*LOG(10)*R*TK/F
50 IF(TOT("Fe") > 0) THEN PUNCH LOG10(TOT("Fe")) ELSE PUNCH -99
60 PUNCH -LA("H+"), SI("O2(g)"), pe, eh, TC
70 END
SOLUTION 1
  pH          1.8
  units       mol/kgw
  Fe(3)       1e-2
  Na          1e-1
  Cl          1e-1
END

# last simulation - loop on this
USE solution 1
EQUILIBRIUM_PHASES 1
  Fix_H+ -<x_axis> NaOH 10
  -force_equality true
  O2(g) <y_axis> 0.1
  Fe(OH)3(a) 0 0
END
```



The above figure shows the output with maximum Fe solubility as expected at low pH and low Eh. The data were generated over the pH domain 2–12 and  $\log_{10}(f \text{O}_2(\text{g}))$  from -90 to +1 with 8 auto-generated classes based on percentiles. Two of these classes were deemed too close together and so have been removed. The white area is the area outside the original calculating domain before yscale transformation. Notice how the required output,  $\text{Fe}_T$ ,  $p_e$  and  $\text{TC}$  have been supplemented with columns  $p\text{H}$ ,  $\text{O}_2(\text{g})$  and  $\text{Eh}$ . These are just for additional information and can be seen in the ‘out’ file. The Eh is calculated internally from  $p_e$  and  $\text{TC}$  in the same way as indicated in the `USER_PUNCH` block and so does not have to be output here.

The plot is sufficient to show the principal features but can be improved in the following ways: (i) add the ‘water limits’ of choice; (ii) choose a more uniform set of contour values; (iii) change the y-scale to make better use of the plot area; (iv) add a plot title and a legend title. See `\demo\contour\contoure_hfo_Eh_pretty.ppi` for the revised plot.

The main challenge is to show the water limits properly bearing in mind that the contouring routine does not accept missing data. One approach would be to specify the calculation domain to be very close to the chosen water limits (best not to be the exact value as this would create the dilemma of is it in or out, subject to the usual numerical uncertainties). The data in the ‘out’ file generated above can help to identify the limiting  $f \text{O}_2(\text{g})$  values required, the greater the resolution, the more accurate these estimates will be. Alternatively it can be calculated by **PHREEQC** explicitly, e.g. for the lower limit by using `H2(g) <log_lower_limit> O2(g)` within an `EQUILIBRIUM_PHASES` block where `<log_lower_limit>` would be 0.0 for 1 atm  $\text{H}_2(\text{g})$ .

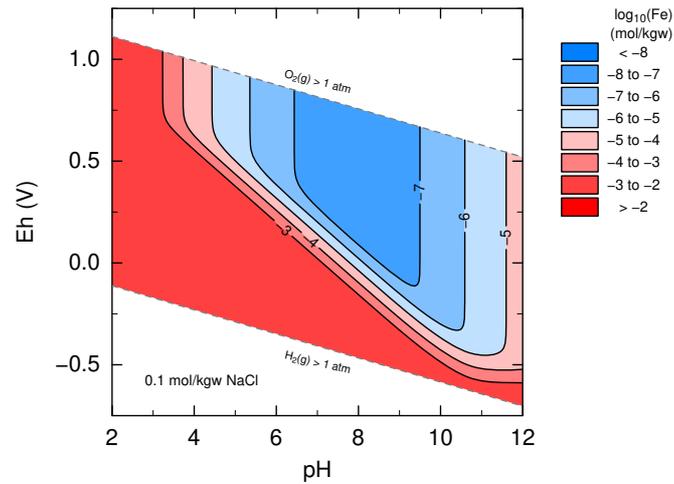
Alternatively, the  $f \text{O}_2(\text{g})$  can be tested by **PHREEQC** within the **Basic** code and a very small dummy  $\text{Fe}_T$  value (far below a realistic minimum value) inserted, e.g. -999, -99999, etc, for all values outside the water limits. This maintains the appearance of a continuous set of data over the whole domain but will produce a ‘cliff edge’ in the contour plot that will be easily identifiable. The lower water limit was set at 1 atm  $\text{H}_2(\text{g})$  and the upper one at 1 atm  $\text{O}_2(\text{g})$ .

The ‘pretty’ file shows the basics of both of these approaches as well as the other minor adjustments. The critical changes for the calculations are:

```
ymin          -82.7
ymax          -0.01
```

and

```
USER_PUNCH 1
-headings  FeT pH O2(g) pe Eh TC
# Calculate Eh (optional - it is calculated from pe & TC internally)
```

Fe solubility with  $\text{Fe}(\text{OH})_3(\text{a})$ 

```

10 R = 8.314462
20 F = 96485.33
30 pe = -la("e-")
40 eh = pe * log(10)*R*TK/F
# artificially add a 'cliff' at the water limits
50 IF (SI("O2(g)") > 0 OR SI("H2(g)") > 0) THEN PUNCH -999, -la("H+"),
SI("O2(g)"), pe, eh, TC : GOTO 100
60 IF (TOT("Fe") > 0) THEN PUNCH log10(TOT("Fe")) ELSE PUNCH -99999
70 PUNCH -la("H+"), SI("O2(g)"), pe, eh, TC
100 END

```

and to add the dashed lines and the text for the water limits:

```

symbolsLines 1 2 -0.112 0.3 gray4 1 0 "" "" 0.1 5 10 : \
              1 12 -0.7032 : : \
              1 2 1.112 : 1 12 0.520
text          1 7 0.88 "O<sub>2</sub>(g) > 1 atm" 1.5 black 13 1 : \
              1 7 -0.5 "H<sub>2</sub>(g) > 1 atm" 1.5 black 13 1 : \
              1 2.8 -0.6 "0.1 mol/kgw NaCl" 2 black

```

# The wateq4f . dat database

---

log  $f_{\text{O}_2}$ -pH predominance diagrams were calculated using the `ht1` approach for each of the 32 components (excluding `H`, `O` and `Humate`) in the `wateq4f.dat` database.

`Humate` was not included since `Fulvate` was included and all of the entries for `Humate` match those of `Fulvate`.

The total amount of each of the 32 components was set to  $1e-2$  mol/kgw.

Each of the possible 311 mineral species present in the database was allowed to precipitate if its saturation index indicated such. In practice, only 54 minerals actually did so.

The calculation is not meant to be particularly significant in terms of environmental chemistry. However, it is a fairly demanding test for the speciation program (**PHREEQC**) since the whole sequence of diagrams originally needed more than one week of continuous computing to calculate (more recent runs are considerably faster due to improvements in processor speed and in the **PhreePlot** and **PHREEQC** code).

These calculations also provide a unique insight into the essential character of the `wateq4f.dat` database, something that is remarkably difficult to achieve by simply staring at a table of numbers.

The following 32 components were considered: Ag, Al, As, B, Ba, Br, C, Ca, Cd, Cl, Cs, Cu, F, Fe, Fulvate, I, K, Li, Mg, Mn, N, Na, Ni, P, Pb, Rb, S, Se, Si, Sr, U and Zn.

The following 311 minerals were considered: Acanthite, Adularia, Ag<sub>2</sub>CO<sub>3</sub>, Ag<sub>2</sub>O, Ag<sub>2</sub>SO<sub>4</sub>, Ag<sub>3</sub>PO<sub>4</sub>, AgF·4H<sub>2</sub>O, AgMetal, Al(OH)<sub>3</sub>(a), AlAsO<sub>4</sub>·2H<sub>2</sub>O, Albite, AlumK, Alunite, Analcime, Anglesite, Anhydrite, Anilite, Annite, Anorthite, Antlerite, Aragonite, Arsenolite, Artinite, As<sub>native</sub>, As<sub>2</sub>O<sub>5</sub>(cr), As<sub>2</sub>S<sub>3</sub>(am), AsI<sub>3</sub>, Atacamite, Autunite, Azurite, Ba<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>, BaF<sub>2</sub>, Barite, Basaluminite, BaSeO<sub>3</sub>, Bassetite, Beidellite, Bianchite, Birnessite, Bixbyite, BlaubleiI, BlaubleiII, Boehmite, Brochantite, Bromyrite, Brucite, Bunsenite, B-UO<sub>2</sub>(OH)<sub>2</sub>, Ca<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>:4w, Calcite, CaSeO<sub>3</sub>, Cd(BO<sub>2</sub>)<sub>2</sub>, Cd(gamma), Cd(OH)<sub>2</sub>(a), Cd(OH)<sub>2</sub>, Cd<sub>3</sub>(OH)<sub>2</sub>(SO<sub>4</sub>)<sub>2</sub>, Cd<sub>3</sub>(OH)<sub>4</sub>SO<sub>4</sub>, Cd<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>, Cd<sub>4</sub>(OH)<sub>6</sub>SO<sub>4</sub>, CdBr<sub>2</sub>·4H<sub>2</sub>O, CdCl<sub>2</sub>, CdCl<sub>2</sub>:2.5H<sub>2</sub>O, CdCl<sub>2</sub>:H<sub>2</sub>O, CdF<sub>2</sub>, CdI<sub>2</sub>, CdMetal, CdOHCl, CdSiO<sub>3</sub>, CdSO<sub>4</sub>, CdSO<sub>4</sub>:2.7H<sub>2</sub>O, CdSO<sub>4</sub>:H<sub>2</sub>O, Celestite, Cerargyrite, Cerrusite, Chalcantite, Chalcedony, Chalcocite, Chalcopyrite, Chlorite14A, Chlorite7A, Chrysotile, Claudetite, Clinoenstatite, Clpyromorphite, Coffinite, Cotunnite, Covellite, Cristobalite, Cu(OH)<sub>2</sub>, Cu<sub>2</sub>(OH)<sub>3</sub>NO<sub>3</sub>, Cu<sub>2</sub>SO<sub>4</sub>, Cu<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>:6w, Cu<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>, Cu<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>:3H<sub>2</sub>O, CuBr, CuCO<sub>3</sub>, CuF, CuF<sub>2</sub>, CuF<sub>2</sub>:2H<sub>2</sub>O, CuI, CuMetal, CuOCuSO<sub>4</sub>, CupricFerrite, Cuprite, CuprousFerrite, CuSO<sub>4</sub>, Diaspore, Diopside, Dioptase, Djurleite, Dolomite(d), Dolomite, Epsomite, FCO<sub>3</sub>Apatite, Fe(OH)<sub>2</sub>.7Cl.3, Fe(OH)<sub>3</sub>(a), Fe<sub>2</sub>(SeO<sub>3</sub>)<sub>3</sub>, Fe<sub>3</sub>(OH)<sub>8</sub>, FeS(ppt), FeSe<sub>2</sub>, Fluorapatite, Fluorite, Forsterite, Galena, Gibbsite, Goethite, Goslarite, Greenalite, Greenockite, Greigite, Gummite, Gypsum, Halite, Halloysite, Hausmannite, H-Autunite, Hematite, Hindsalite, Huntite, Hxypyromorphite, Hydrocerrusite, Hydromagnesite, Hydroxyapatite, Illite, Iodyrite, Jarosite(ss), JarositeH, Jarosite-K, Jarosite-Na, Jurbanite, Kaolinite, K-Autunite, Kmica, Langite, Larnakite, Laumontite, Laurionite, Leonhardite, Litharge, Mackinawite, Magadiite, Maghemite, Magnesite, Magnetite, Malachite, Manganite, Massicot, Matlockite, Melanothallite, Melanterite, Millerite, Minium, Mirabilite, Mn<sub>2</sub>(SO<sub>4</sub>)<sub>3</sub>, Mn<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>:8H<sub>2</sub>O, Mn<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>, MnCl<sub>2</sub>:4H<sub>2</sub>O, MnHPO<sub>4</sub>, MnS(Green), MnSO<sub>4</sub>, Montepomite, Montmorillonite-Aberdeen, Montmorillonite-BelleFourche, Montmorillonite-Ca, Morenosite, Na<sub>4</sub>UO<sub>2</sub>(CO<sub>3</sub>)<sub>3</sub>, Na-Autunite, Nahcolite, Nantokite, Natron, Nesquehonite, Ni(OH)<sub>2</sub>, Ni<sub>2</sub>SiO<sub>4</sub>, Ni<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>:8H<sub>2</sub>O, Ni<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>, Ni<sub>4</sub>(OH)<sub>6</sub>SO<sub>4</sub>, NiCO<sub>3</sub>, Ningyoite, Nsutite, Orpiment, Otavite, Pb(BO<sub>2</sub>)<sub>2</sub>, Pb(OH)<sub>2</sub>, Pb<sub>2</sub>(OH)<sub>3</sub>Cl, Pb<sub>2</sub>O(OH)<sub>2</sub>, Pb<sub>2</sub>O<sub>3</sub>, Pb<sub>2</sub>O<sub>3</sub>CO<sub>3</sub>, Pb<sub>2</sub>SiO<sub>4</sub>, Pb<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>, Pb<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>, Pb<sub>3</sub>O<sub>2</sub>CO<sub>3</sub>, Pb<sub>3</sub>O<sub>2</sub>SO<sub>4</sub>, Pb<sub>4</sub>(OH)<sub>6</sub>SO<sub>4</sub>, Pb<sub>4</sub>O<sub>3</sub>SO<sub>4</sub>, PbBr<sub>2</sub>, PbBrF, PbF<sub>2</sub>,

PbHPO<sub>4</sub>, PbI<sub>2</sub>, PbMetal, PbO:0.3H<sub>2</sub>O, PbSiO<sub>3</sub>, Phillipsite, Phlogopite, Phosgenite, Plattnerite, Plumbogummite, Portlandite, Prehnite, Przhevalskite, Pyrite, Pyrochroite, Pyrolusite, Pyrophyllite, Quartz, Realgar, Retgersite, Rhodochrosite(d), Rhodochrosite, Rutherfordine, Saleeite, Schoepite, Scorodite, Se(s), SeO<sub>2</sub>, Sepiolite(d), Sepiolite, Siderite(d)(3), Siderite, Silicagel, SiO<sub>2</sub>(a), Smithsonite, Sphalerite, Sr-Autunite, SrF<sub>2</sub>, Strengite, Strontianite, Sulfur, Talc, Tenorite, Thenardite, Thermonatrite, Torbernite, Tremolite, Trona, Tsumebite, U(HPO<sub>4</sub>)<sub>2</sub>:4H<sub>2</sub>O, U(OH)<sub>2</sub>SO<sub>4</sub>, U<sub>3</sub>O<sub>8</sub>(c), U<sub>4</sub>O<sub>9</sub>(c), UF<sub>4</sub>(c), UF<sub>4</sub>:2.5H<sub>2</sub>O, UO<sub>2</sub>(a), UO<sub>2</sub>HPO<sub>4</sub>:4H<sub>2</sub>O, UO<sub>3</sub>(gamma), (UO<sub>2</sub>)<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>:4w, Uramphite, Uraninite(c), Uranocircite, Uranophane, Vivianite, Wairakite, Willemite, Witherite, Wurtzite, Zincite(c), Zincosite, Zn(BO<sub>2</sub>)<sub>2</sub>, Zn(NO<sub>3</sub>)<sub>2</sub>:6H<sub>2</sub>O, Zn(OH)<sub>2</sub>-a, Zn(OH)<sub>2</sub>-b, Zn(OH)<sub>2</sub>-c, Zn(OH)<sub>2</sub>-e, Zn(OH)<sub>2</sub>-g, Zn<sub>2</sub>(OH)<sub>2</sub>SO<sub>4</sub>, Zn<sub>2</sub>(OH)<sub>3</sub>Cl, Zn<sub>3</sub>(AsO<sub>4</sub>)<sub>2</sub>:2.5w, Zn<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>:4w, Zn<sub>3</sub>(SO<sub>4</sub>)<sub>2</sub>, Zn<sub>4</sub>(OH)<sub>6</sub>SO<sub>4</sub>, Zn<sub>5</sub>(OH)<sub>8</sub>Cl<sub>2</sub>, ZnBr<sub>2</sub>:2H<sub>2</sub>O, ZnCl<sub>2</sub>, ZnCO<sub>3</sub>:H<sub>2</sub>O, ZnF<sub>2</sub>, ZnI<sub>2</sub>, ZnMetal, ZnO(a), ZnS(a), ZnSiO<sub>3</sub> and ZnSO<sub>4</sub>:H<sub>2</sub>O.

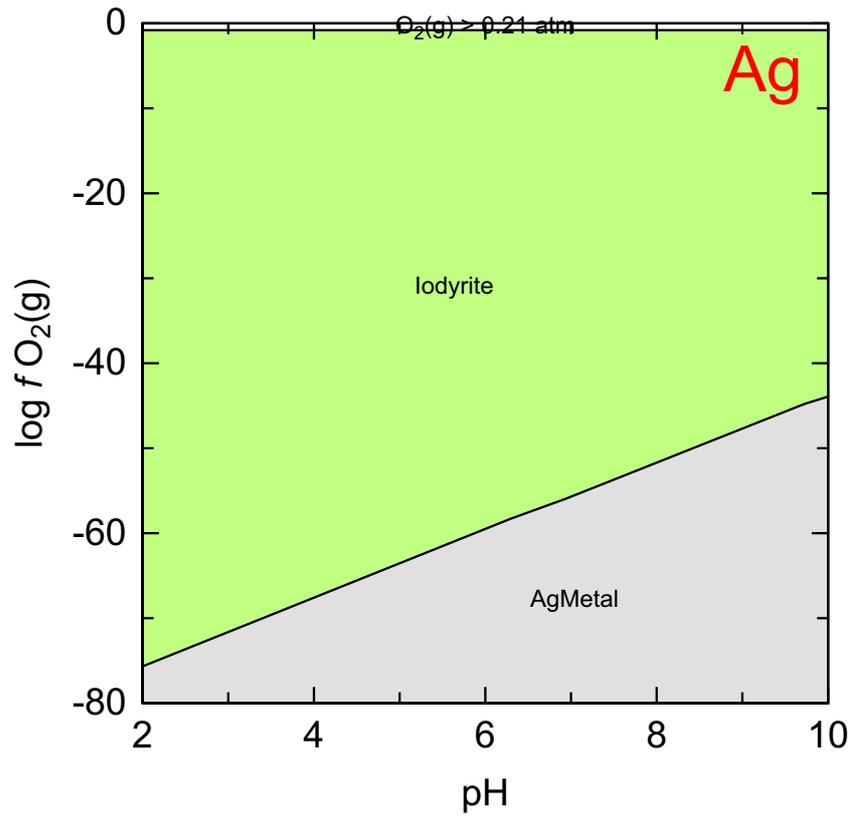
The usual 'water limits' of 0.21 atm O<sub>2</sub>(g) and 1 atm H<sub>2</sub>(g) were used. All calculations were carried out for a temperature of 25°C.

In practice, given the conditions used, only 54 of the 311 possible minerals precipitated somewhere within the range of conditions imposed. Inclusion of the other 257 minerals therefore has no impact on the predominance diagrams produced and in principle could be excluded. This results in approximately a four-fold increase in calculation speed illustrating that the number of pure phases considered can have a strong impact on the speed of **PHREEQC** calculations.

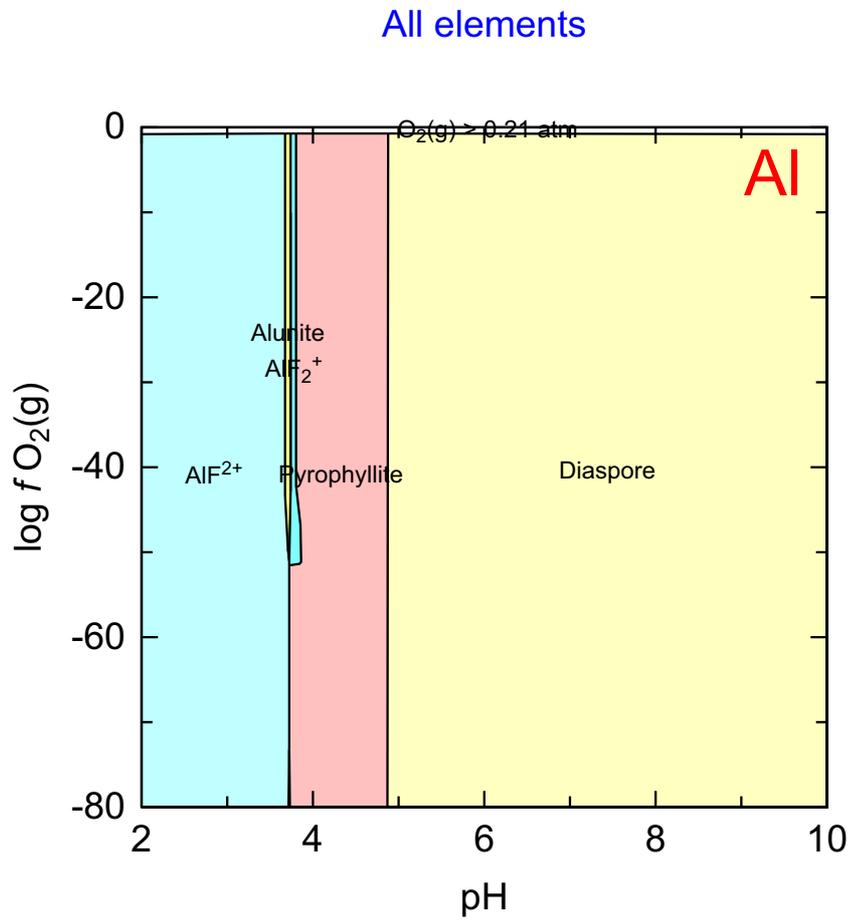
In these examples, we found that on average, about half the time was spent hunting along the domain boundaries and half was spent tracking along the internal boundaries. Of course this varies considerably from diagram to diagram.

# 1 Ag

All elements

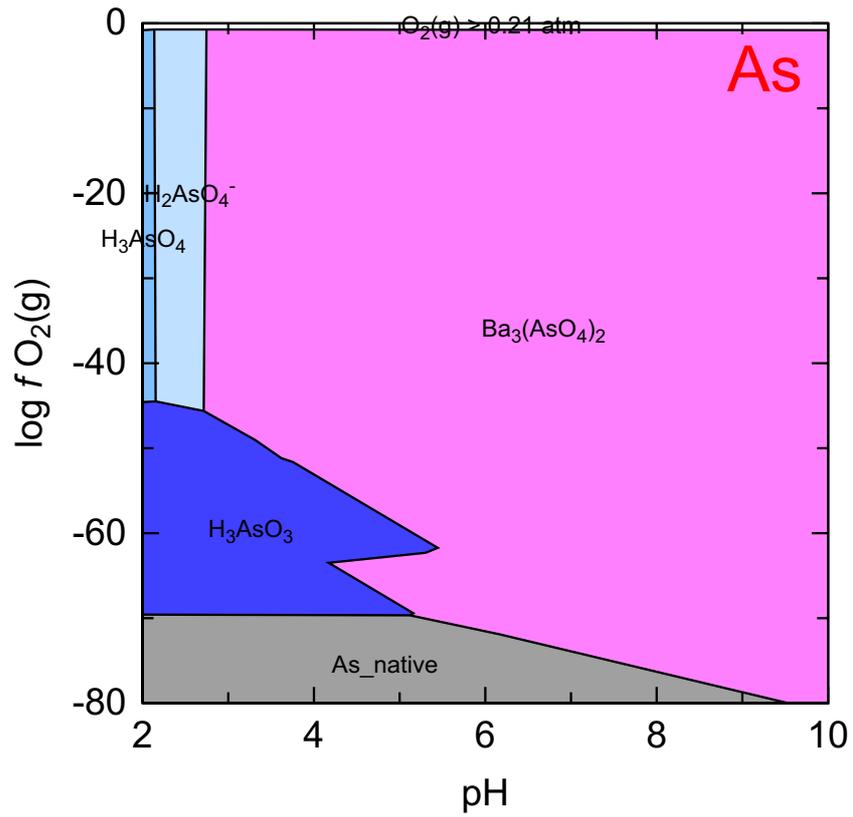


## 2 Al



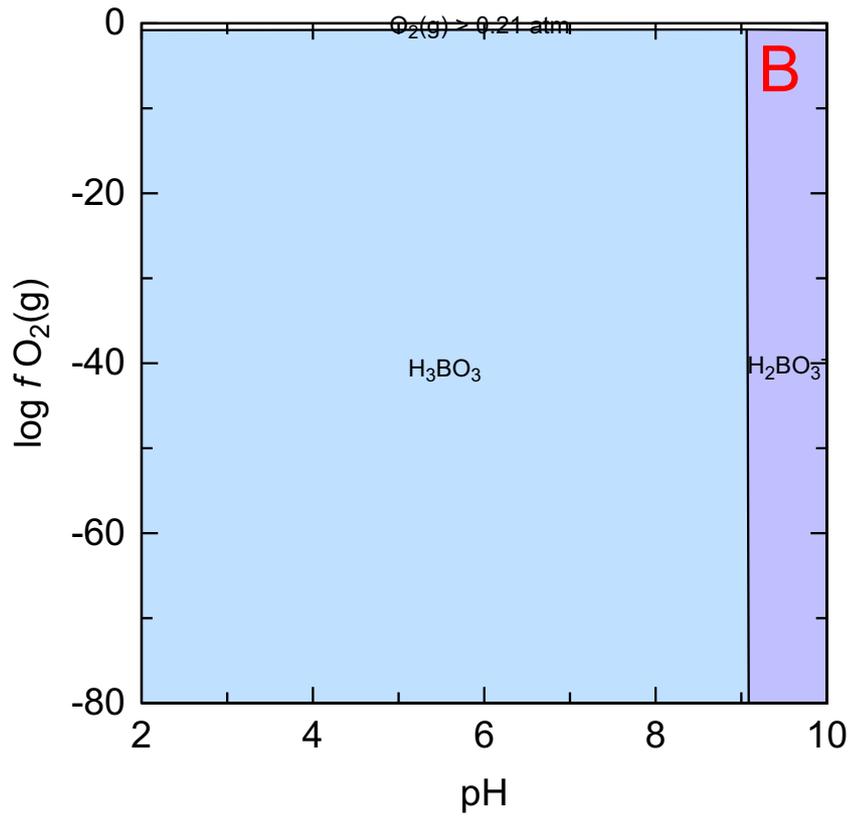
## 3 As

All elements

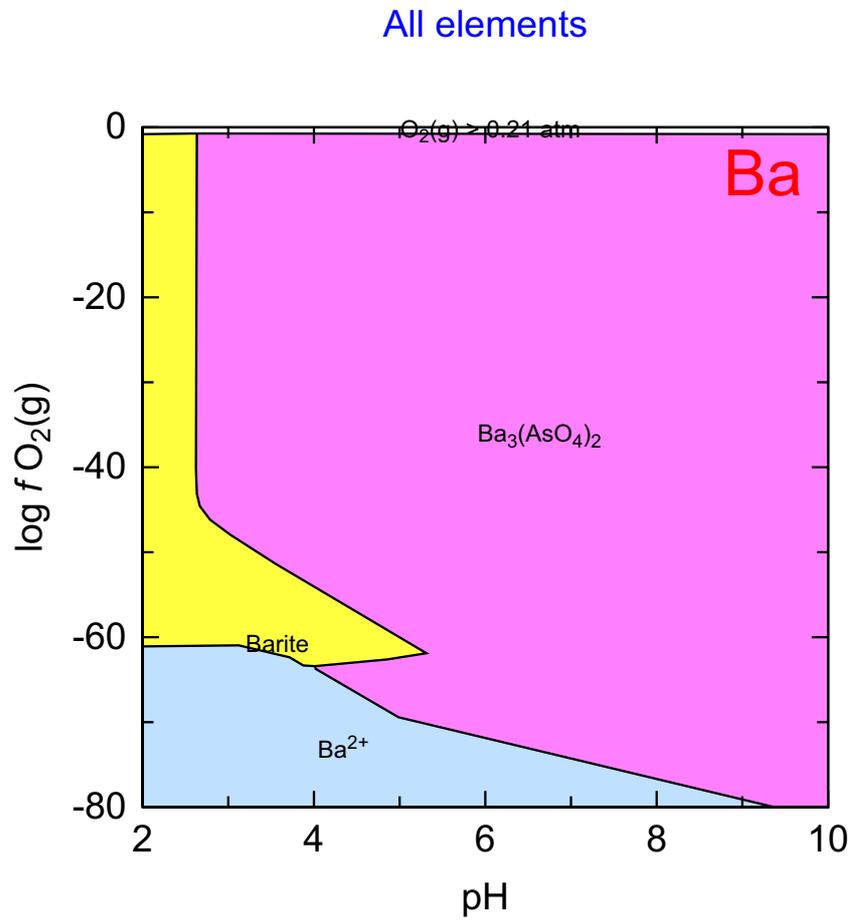


# 4 B

All elements

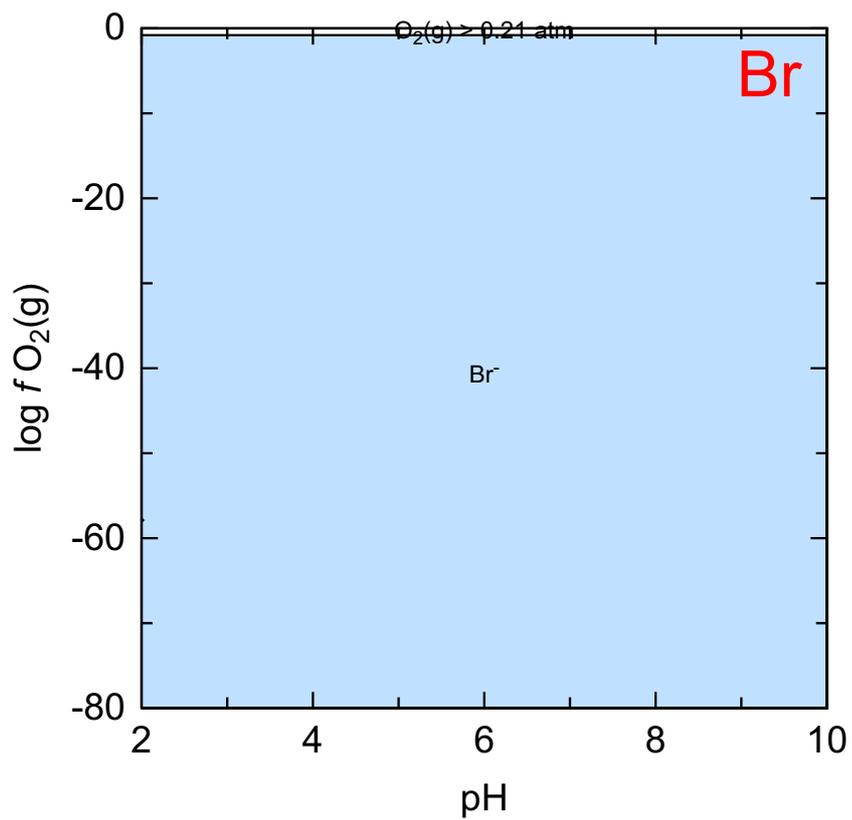


## 5 Ba



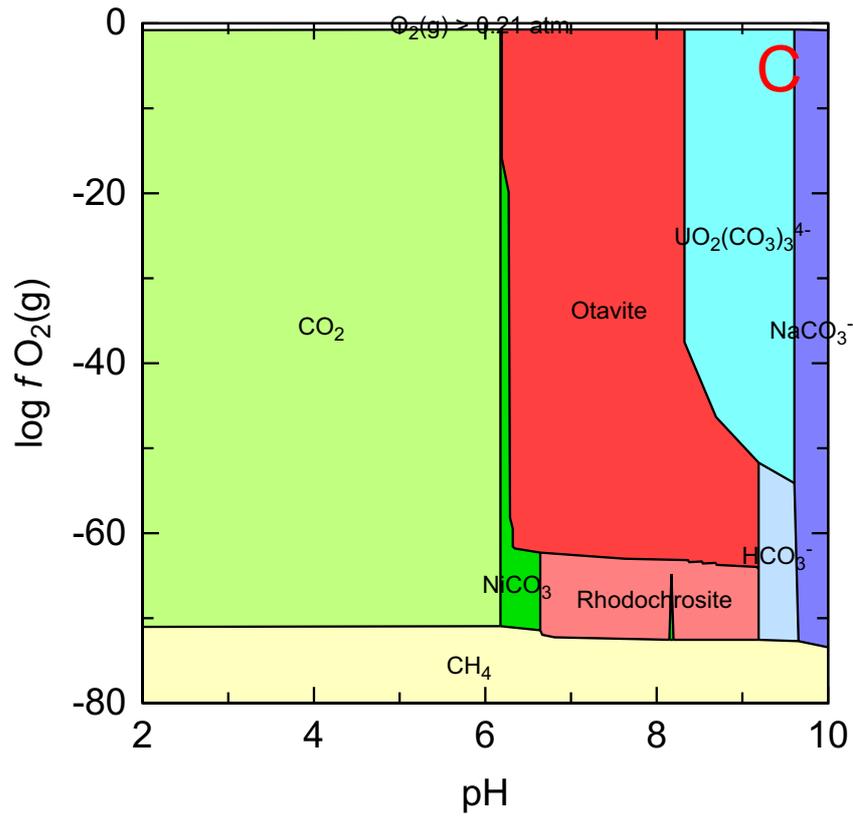
# 6 Br

All elements



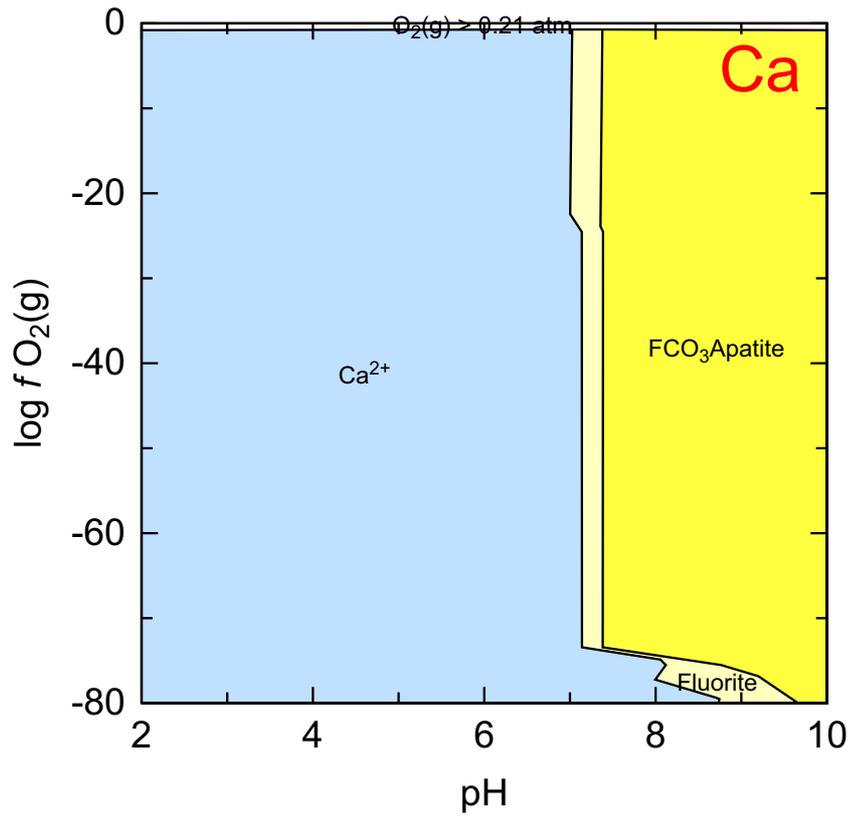
7 C

All elements

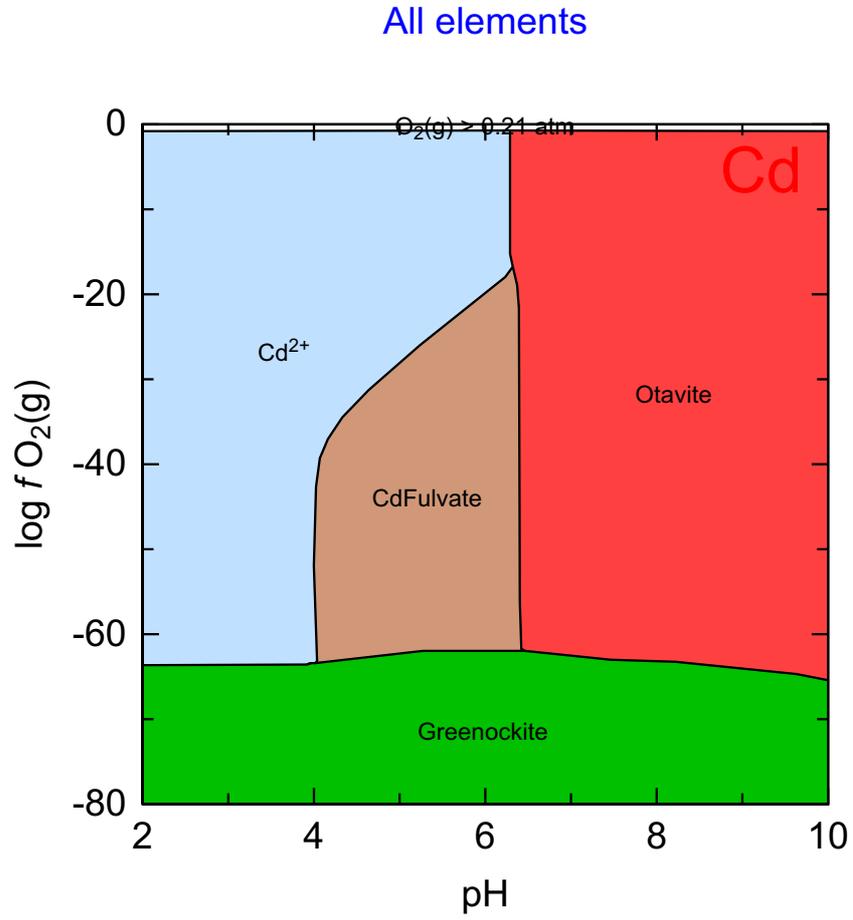


# 8 Ca

All elements

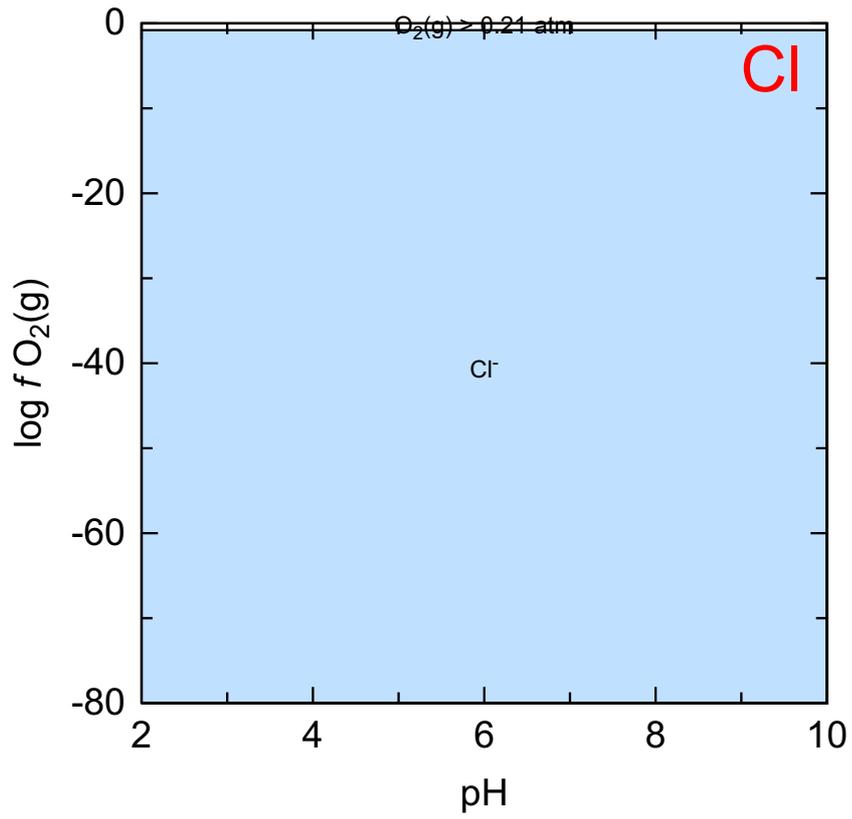


# 9 Cd



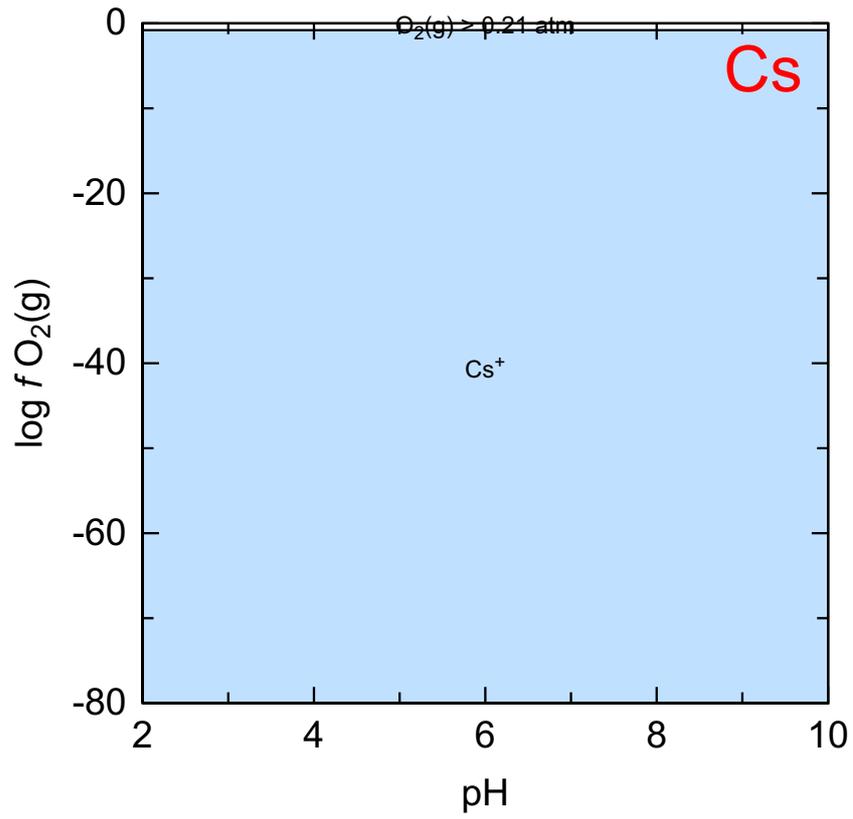
# 10 Cl

All elements



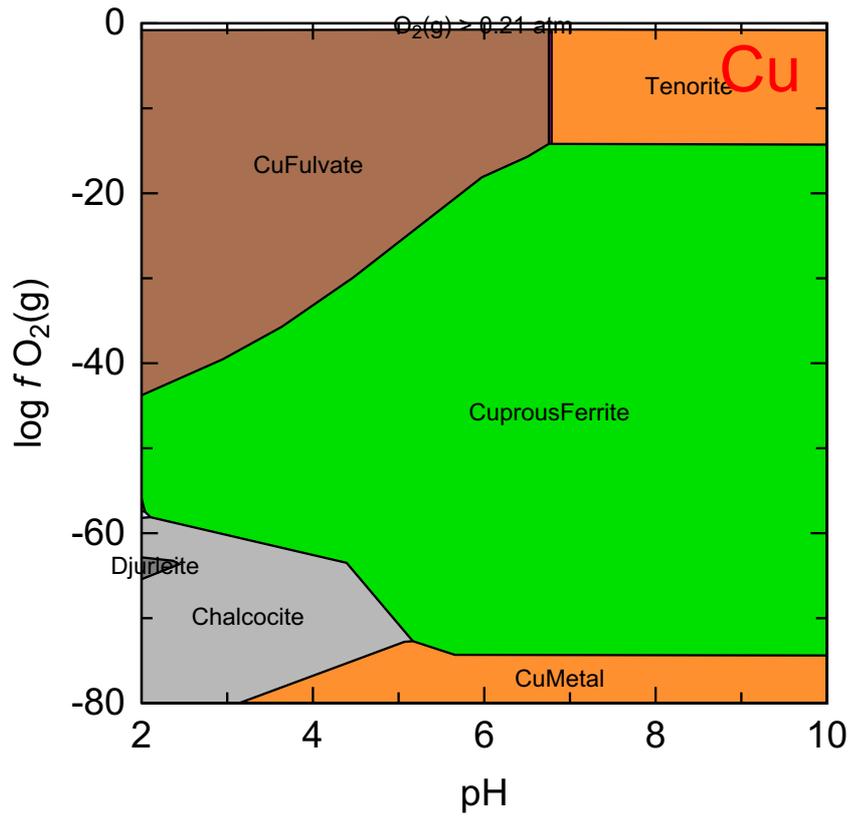
# 11 Cs

All elements



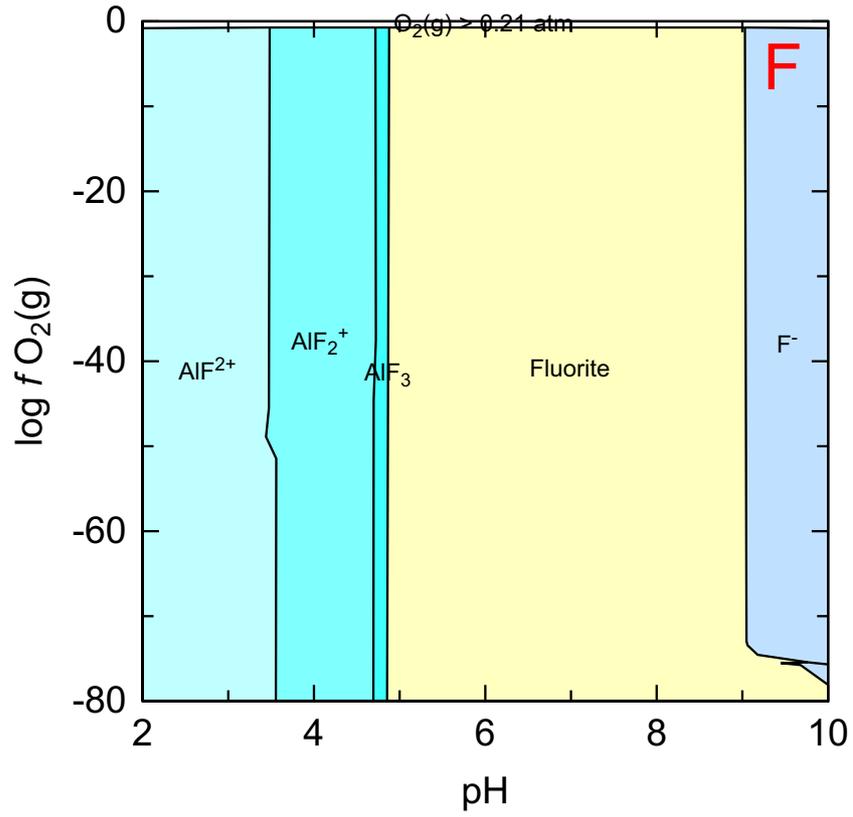
# 12 Cu

All elements



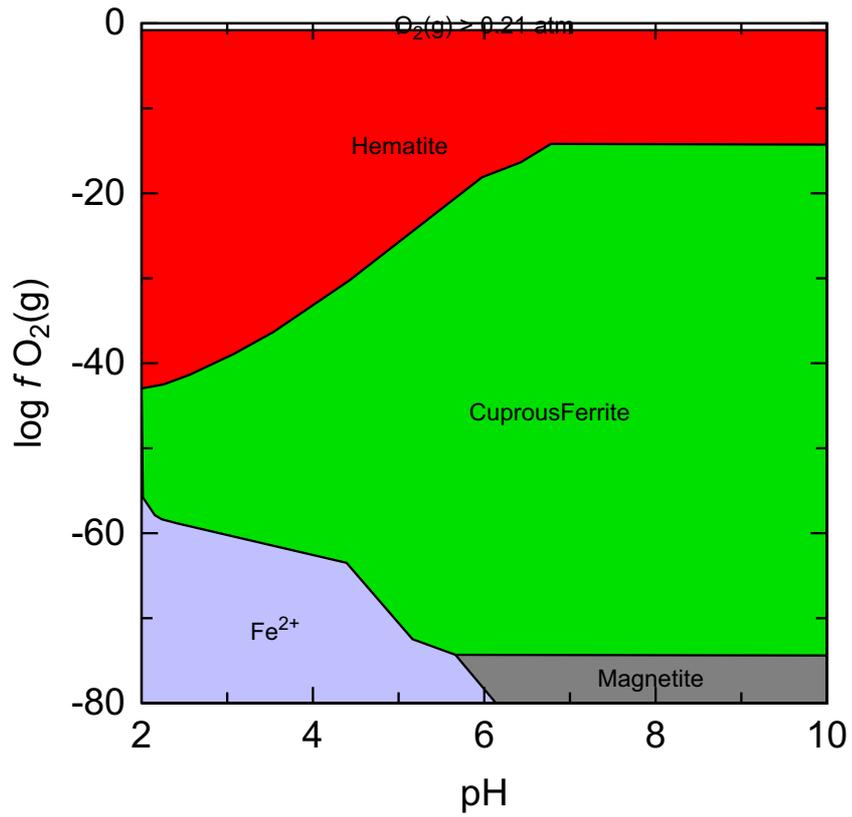
# 13 F

## All elements



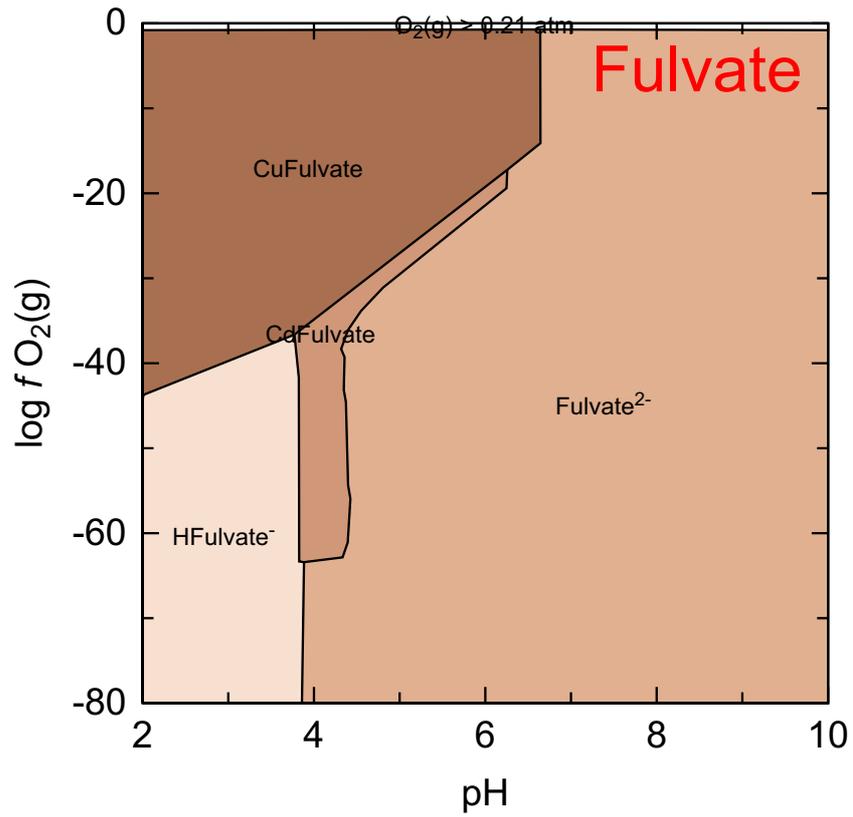
# 14 Fe

All elements



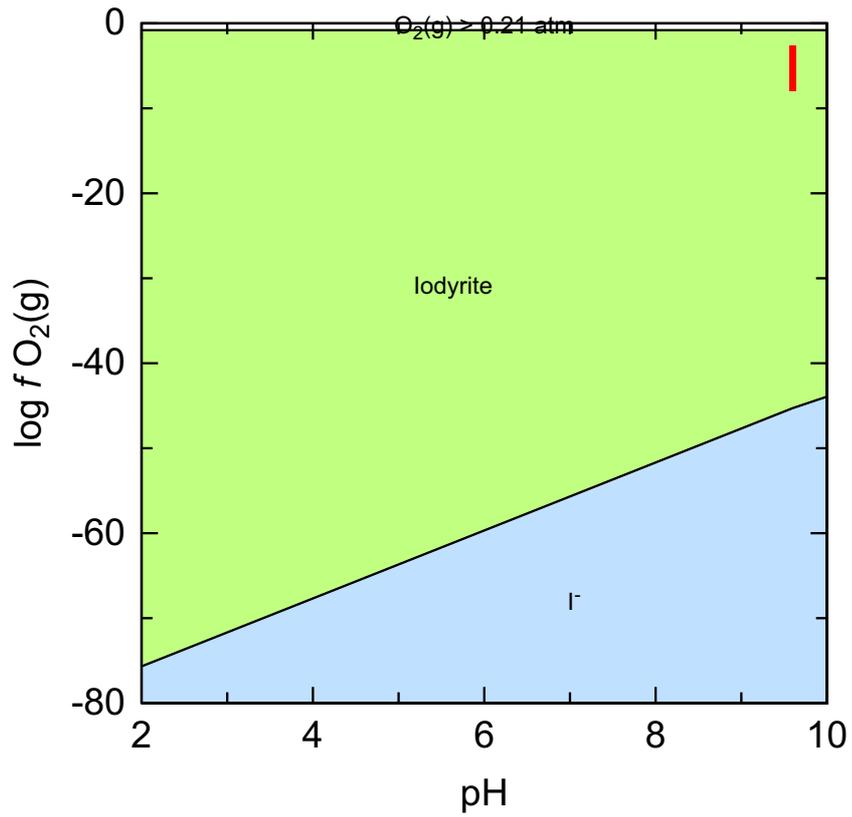
# 15 Fulvate

All elements



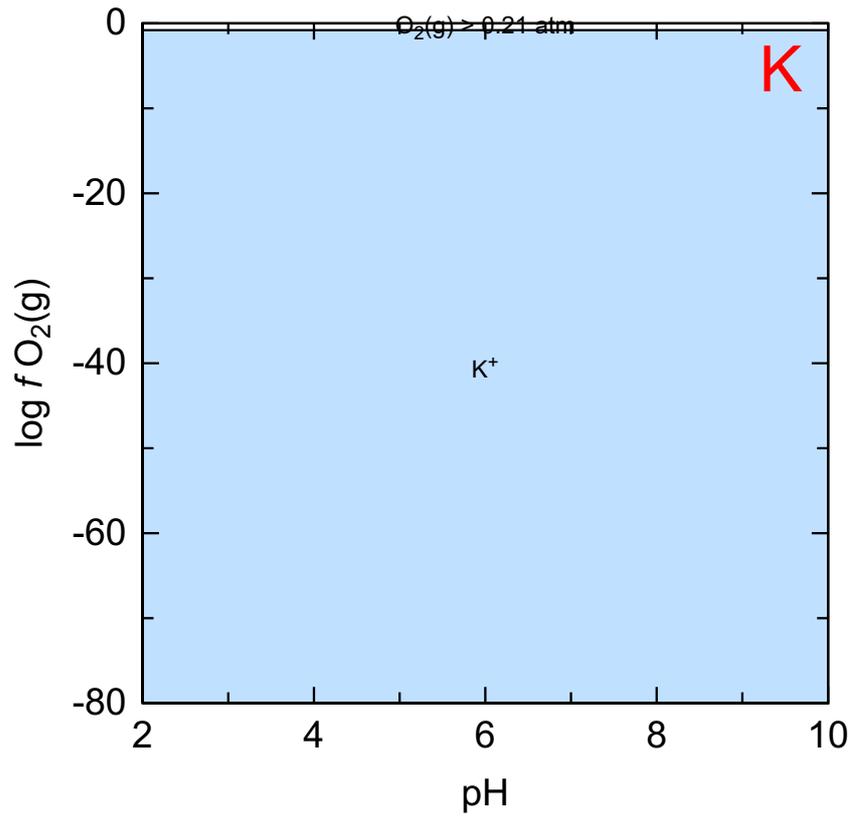
# 16 I

## All elements



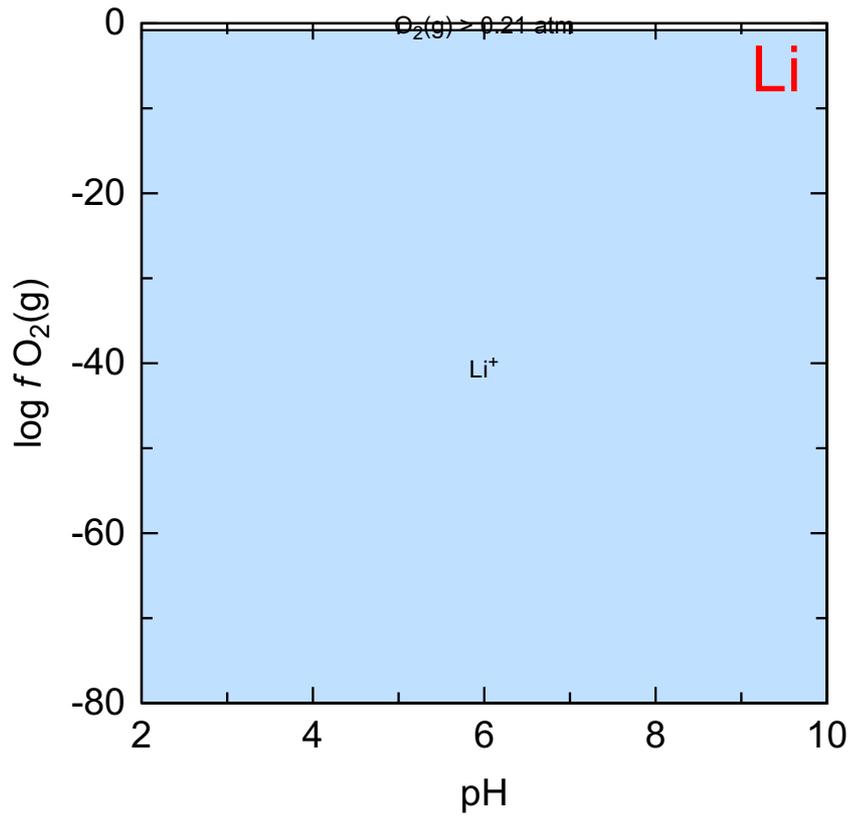
# 17 K

All elements



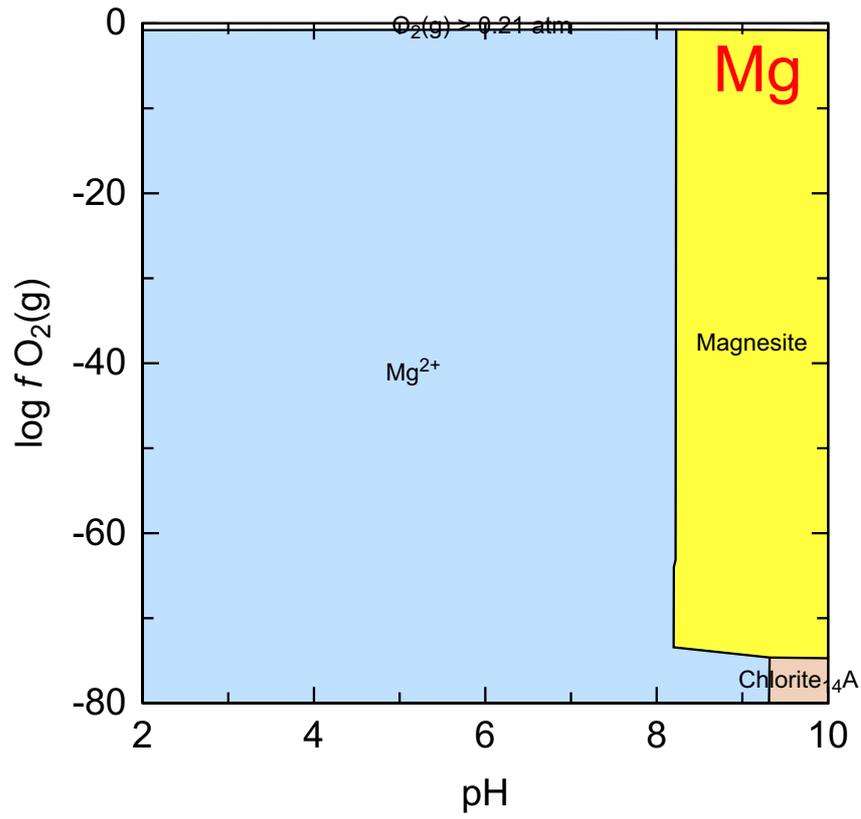
# 18 Li

All elements



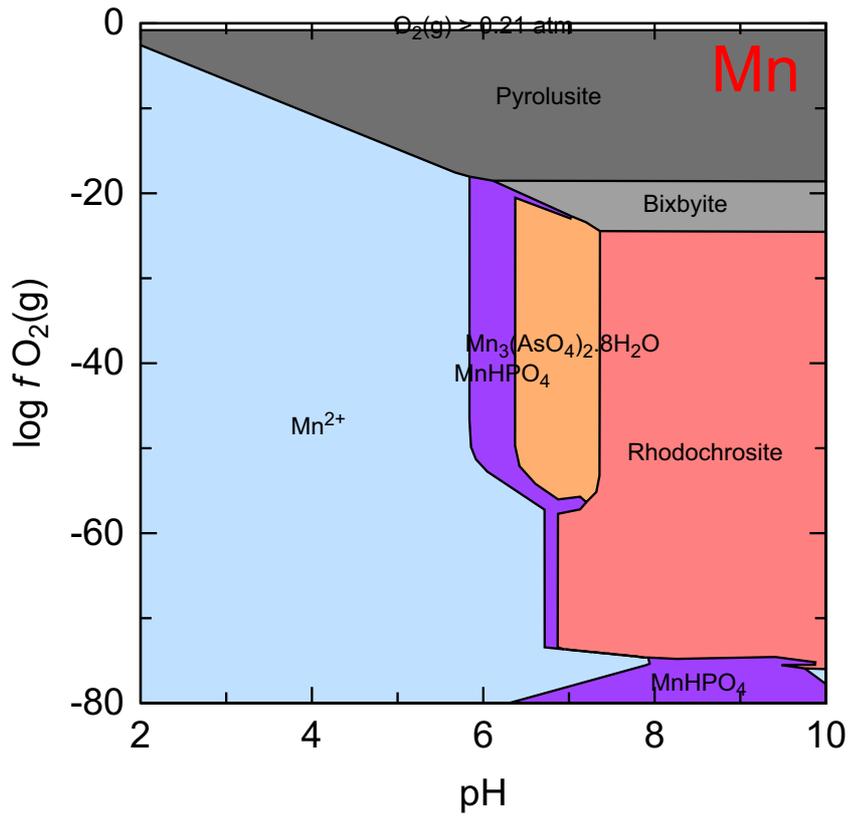
# 19 Mg

All elements



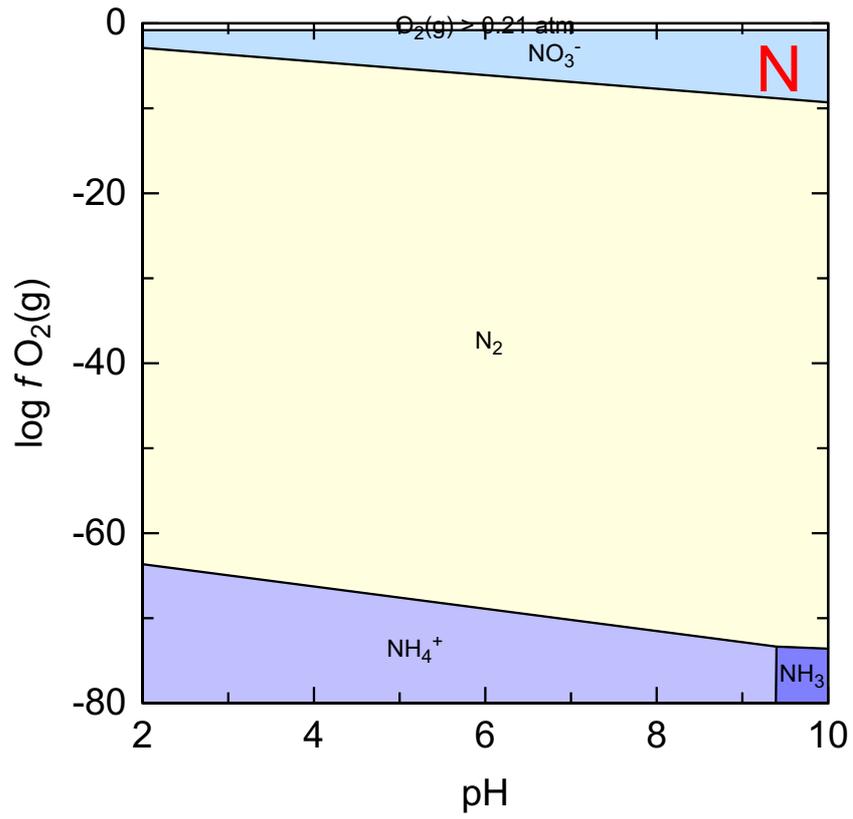
# 20 Mn

All elements



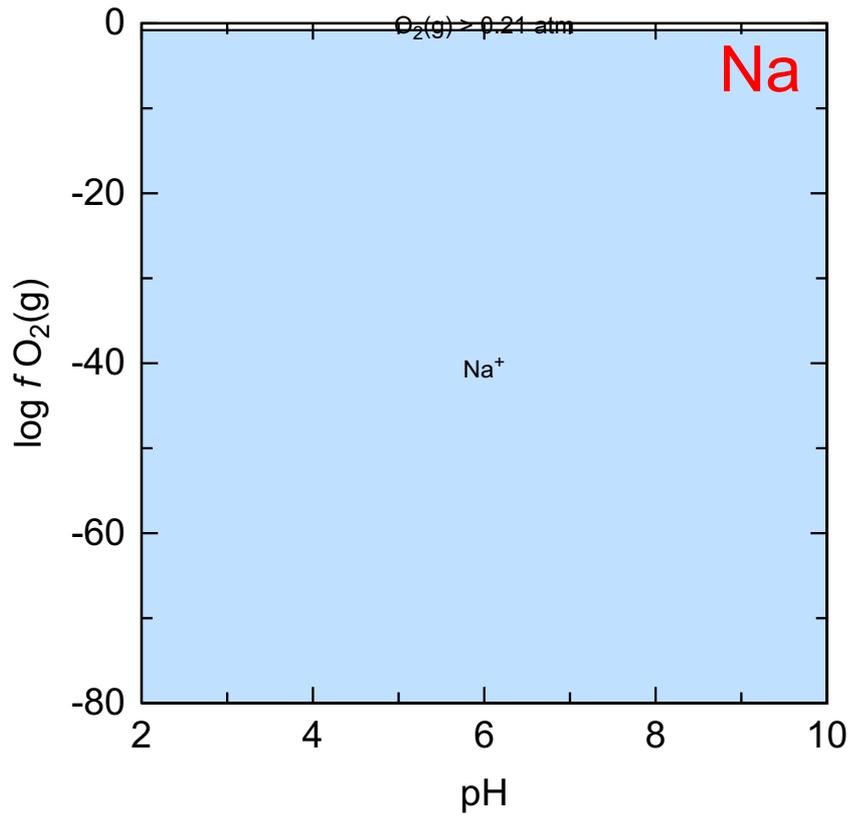
# 21 N

All elements



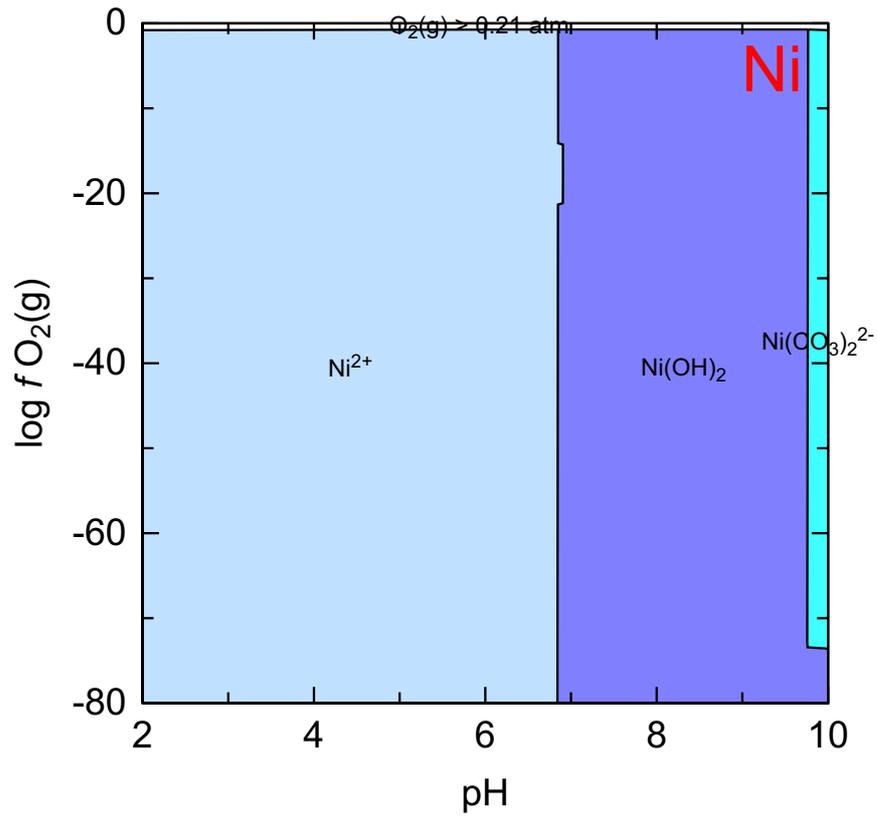
## 22 Na

All elements



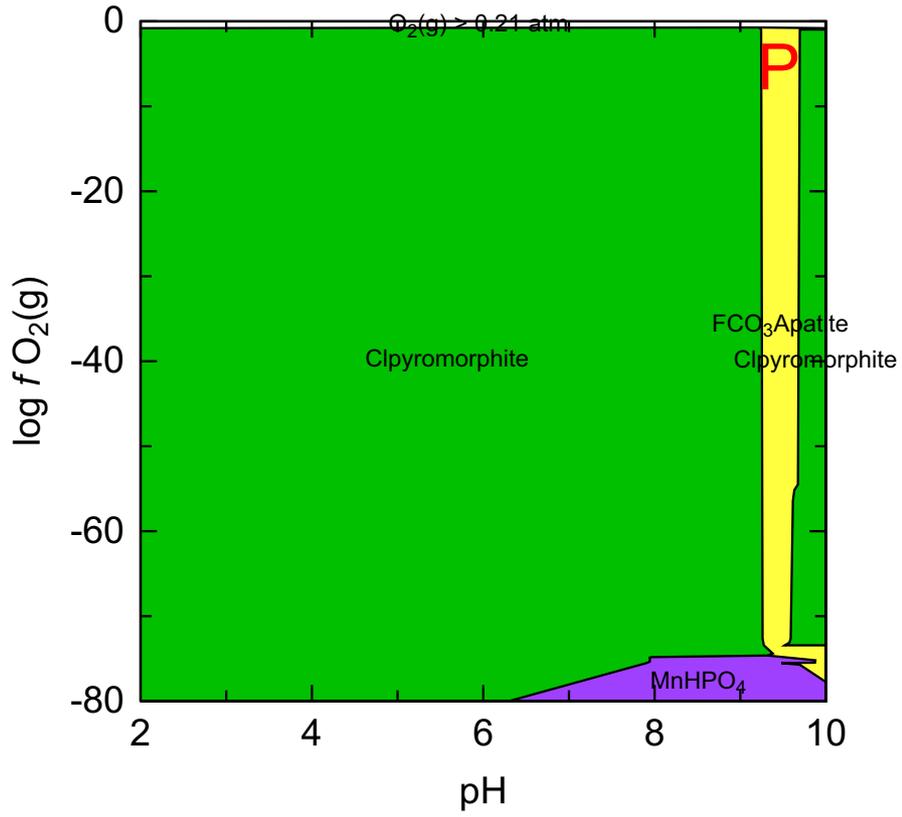
# 23 Ni

All elements



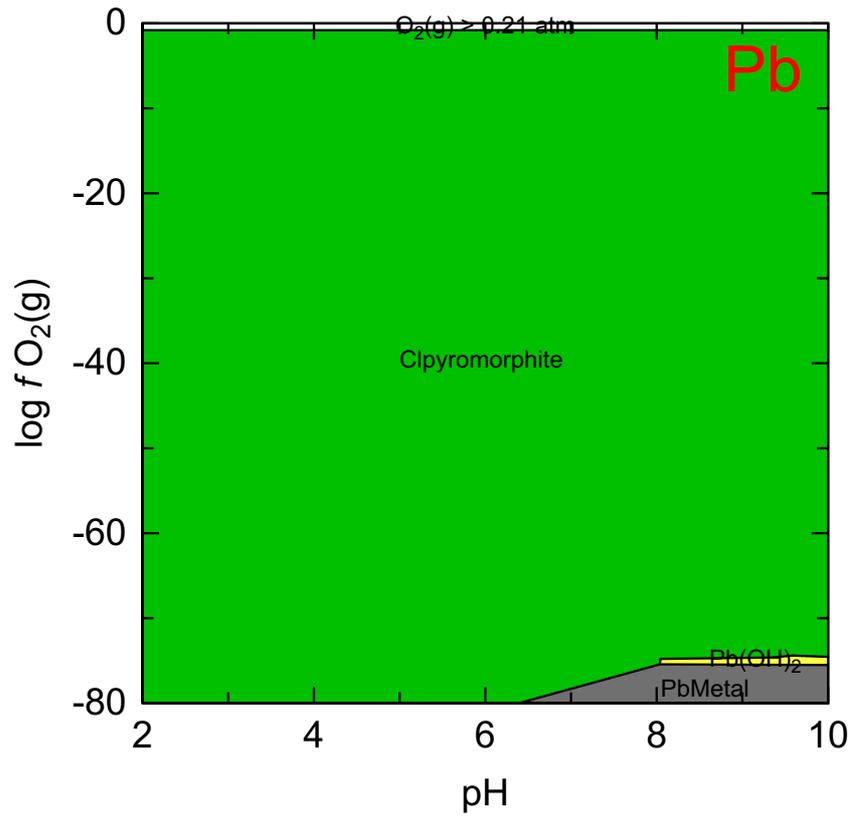
# 24 P

All elements



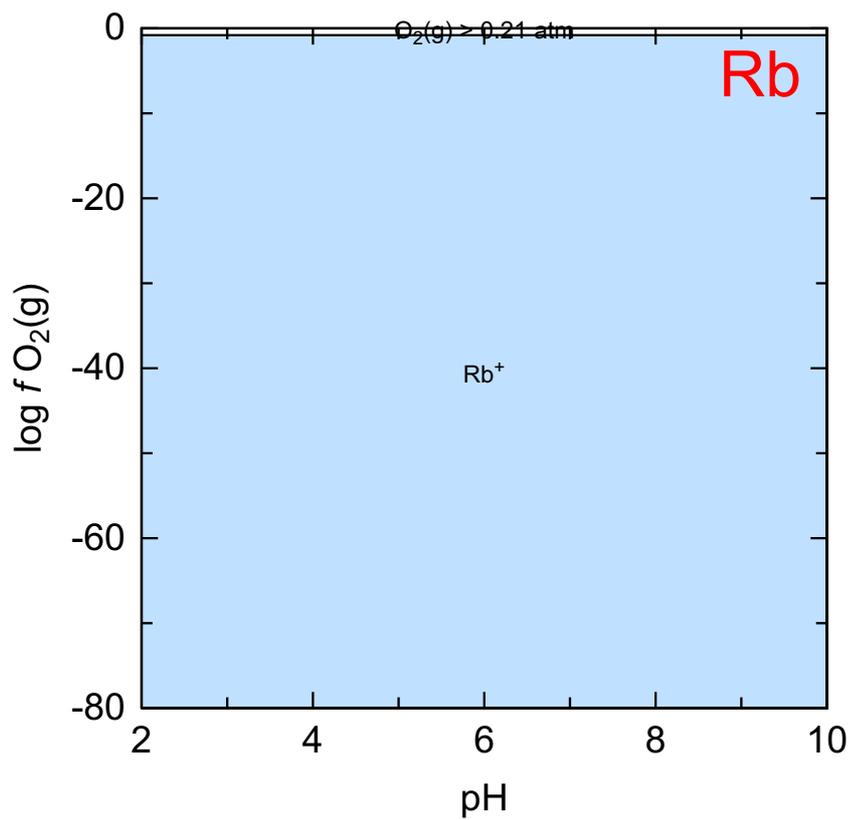
# 25 Pb

All elements



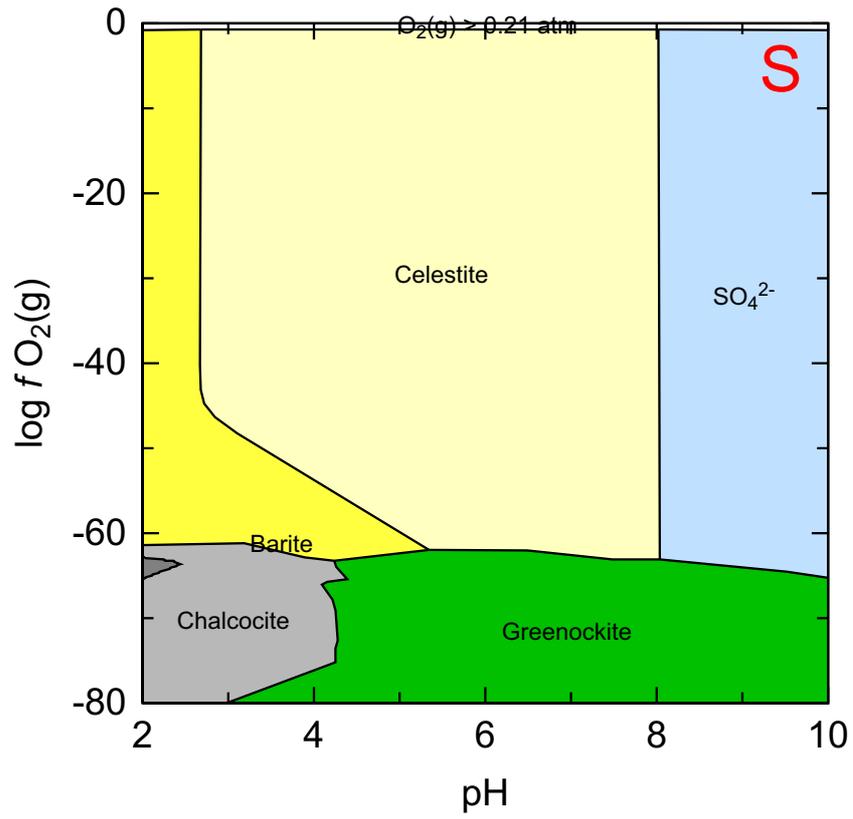
# 26 Rb

All elements



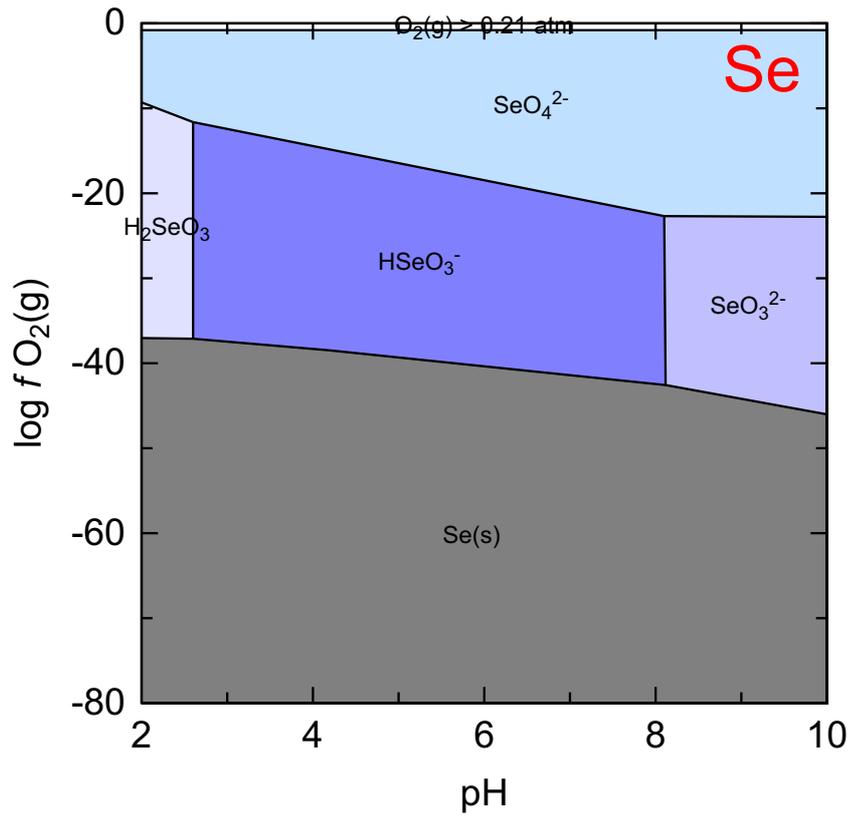
# 27 S

## All elements



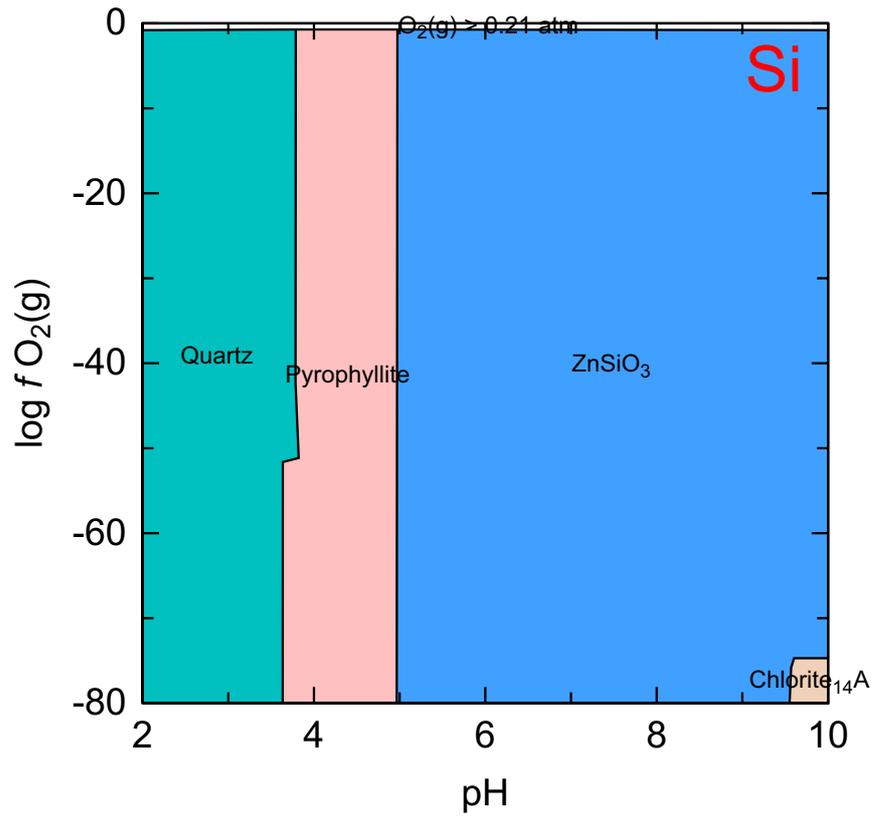
# 28 Se

All elements



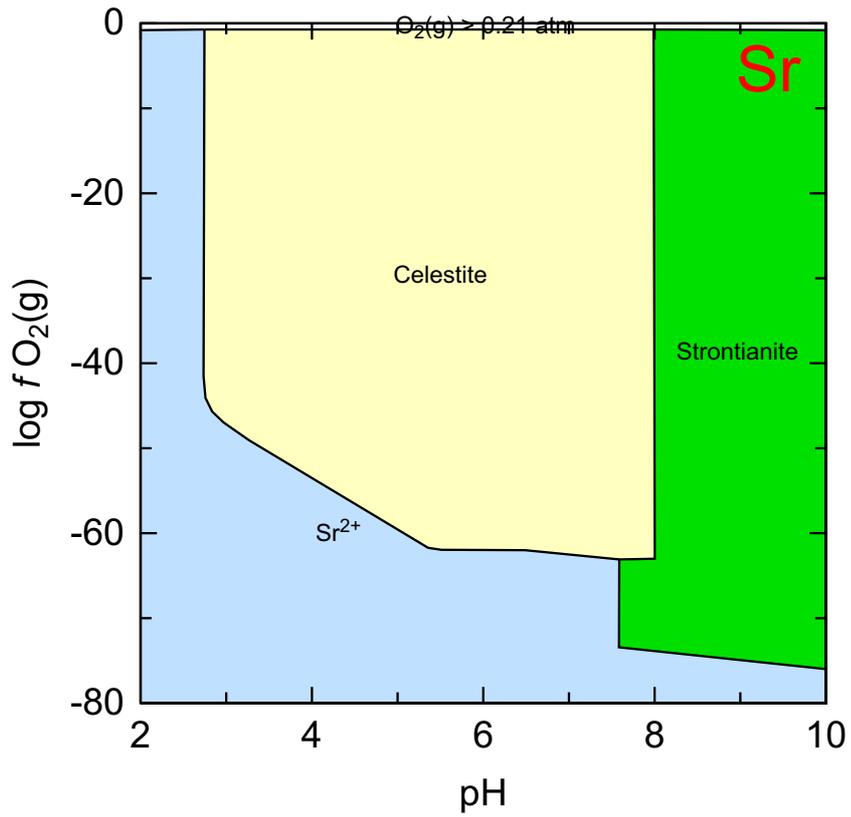
# 29 Si

All elements



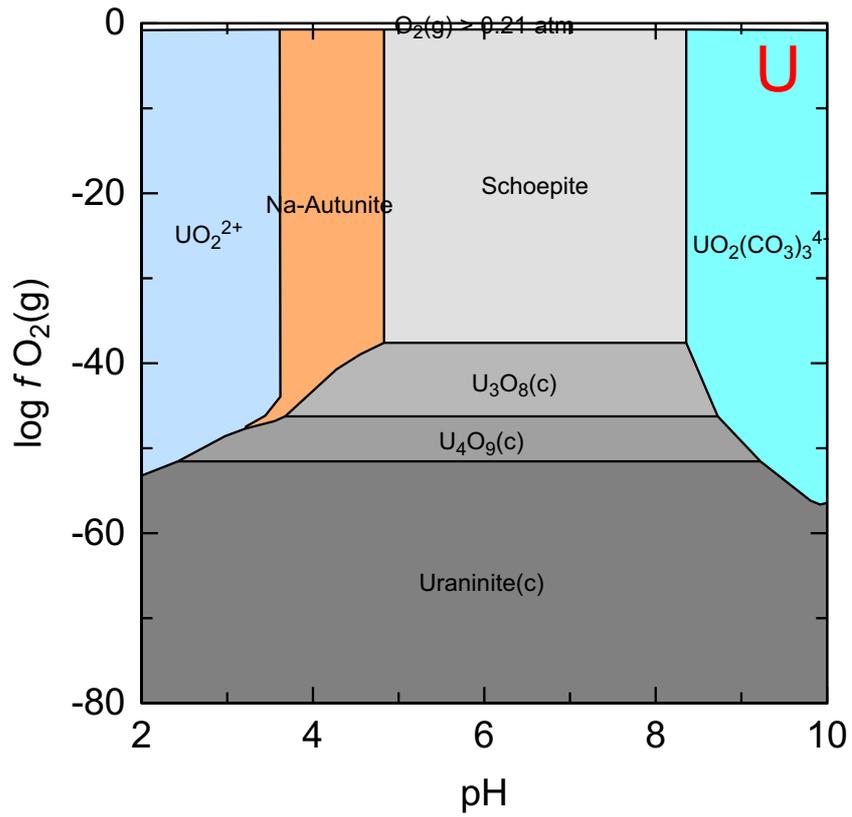
# 30 Sr

All elements



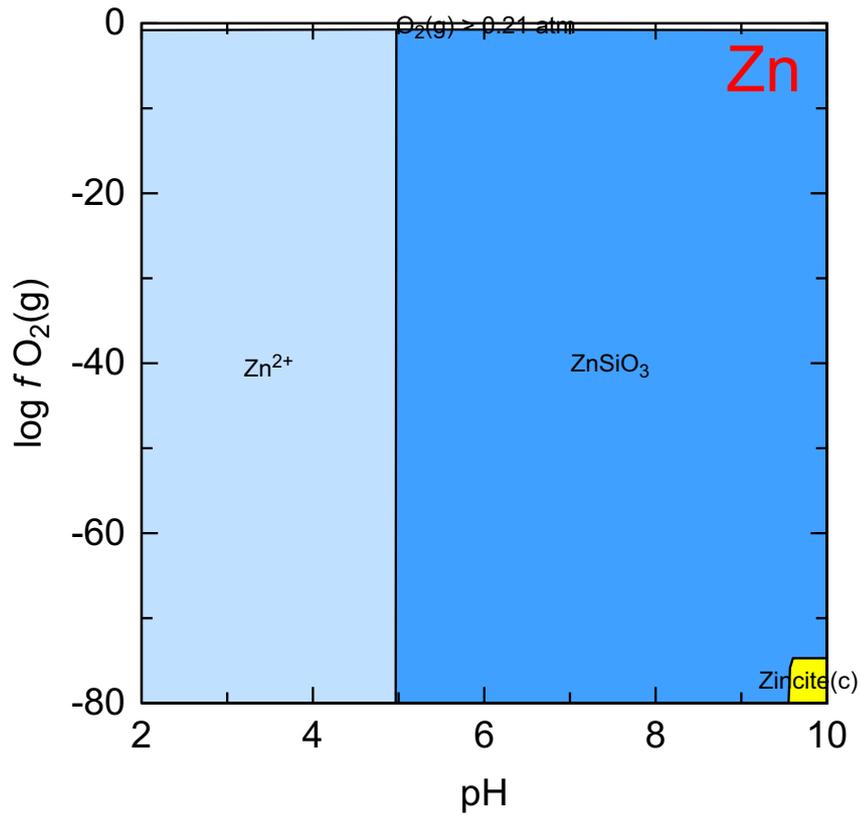
# 31 U

All elements



# 32 Zn

All elements



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## Acknowledgements

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**PhreePlot** inherits most of the hard work from others. **PHREEQC** does all of the geochemical calculations and is the work of David Parkhurst, Tony Appelo and Scott Charlton. Scott Charlton and David Parkhurst prepared the **PHREEQC** module that is embedded in **PhreePlot**. **PHREEQC** has become ever more powerful over the years and is a model of stability and reliability. It also comes with its own excellent documentation and databases.

The Postscript plotting library embedded in **PhreePlot** is from the late Kevin Kohler. This library enables **PhreePlot** to produce high quality, fully scalable plots. **Ghostscript** and **GSview** provide the perfect companions for rendering these files. **Ghostscript** provides a range of format conversions (pdf, png etc.) and can be configured to run directly from within **PhreePlot**.

Three of the fitting routines are by the late Mike Powell. The non-linear least squares routine ('nlls') has proved an invaluable and reliable assistant over many years, and his two newer routines are expected to be equally reliable and helpful. We also thank Tom Rowan for his 'subplx' code.

The contouring routine is from Paul Bourke. After quite a lot of testing, we found that this rather simple and elegant algorithm proved the most reliable for contouring geochemical data. It has been slightly modified here to enable the contour regions to be filled with colour.

Geochemical modelling is nothing without the databases that go with it and so we would like to thank all of those who have helped to painstakingly prepare these for use in **PHREEQC** and elsewhere. David Parkhurst deserves special praise here for designing the **PHREEQC** database format and for converting several important databases to this format. The **PHREEQC** format is now a standard format for many thermodynamic databases.

A number of smaller contributions have also been included. These are listed below with details of the sources and Conditions of Use.

Development of **PhreePlot** was begun while dgk was a full-time member of the [British Geological Survey](#) (Wallingford) and dmc was a member of the [Centre of Ecology and Hydrology](#) (Wallingford), both [NERC](#) Research Centres. We are grateful to these two institutions for their early support.

We are also grateful to the many users who have sent in bug reports and recommendations. In particular, many thanks to John Mahoney for his many useful contributions.

Function/software	Owner/source/Conditions of Use
<b>PHREEQC</b>	David Parkhurst, Scott Charlton (USGS), Tony Appelo, Free source code, libraries and binaries; license file. <a href="https://www.usgs.gov/software/PHREEQC-version-3/">https://www.usgs.gov/software/PHREEQC-version-3/</a> .
Fitting	Harwell Subroutine Library (HSL Archive), VA05 routine by M J D Powell, <a href="http://www.hsl.rl.ac.uk/archive/index.html">http://www.hsl.rl.ac.uk/archive/index.html</a> . Free source code after registering; can freely distribute binaries derived from this but not the source itself; license file. Also from Powell: BOBYQA ( <a href="http://www.damtp.cam.ac.uk/user/na/NA_papers/NA2009_06.pdf">http://www.damtp.cam.ac.uk/user/na/NA_papers/NA2009_06.pdf</a> ) and NEWUOA ( <a href="http://www.damtp.cam.ac.uk/user/na/NA_papers/NA2004_08.pdf">http://www.damtp.cam.ac.uk/user/na/NA_papers/NA2004_08.pdf</a> ). For original sources see Zhang ( <a href="https://www.zhangzk.net/software.html">https://www.zhangzk.net/software.html</a> ). For reformulated BOBYQA source, also see <a href="https://github.com/jacobwilliams/PowellOpt/blob/master/src/bobyqa.f90">https://github.com/jacobwilliams/PowellOpt/blob/master/src/bobyqa.f90</a> . Also thanks to Tom Rowan for SUBPLX from <a href="https://www.netlib.org/opt/subplex.tgz">https://www.netlib.org/opt/subplex.tgz</a> .
Postscript plotting	Kevin Kohler. <b>PSPLOT</b> subroutine plotting library. Available for download from <a href="http://www.nova.edu/ocean/psplot/">http://www.nova.edu/ocean/psplot/</a> . Egon Szondi has updated (2012) and ported the library to Fortran 95; follow the <b>PSPLOT</b> link given here.
Simulated annealing	William L Goffe (1996) subroutine simann.f, <a href="http://www.netlib.no/netlib/opt/simann.f">http://www.netlib.no/netlib/opt/simann.f</a> . Free source code.
Douglas-Peucker line simplification	P R Wade (1984), Department of Computer Science, University of Hull. Also see Whyatt, J D and Wade P R (1988) "The Douglas-Peucker Line Simplification Algorithm". Society of University Cartographers Bulletin 22 (1), 17 - 25. Free source code. <a href="https://hull-repository.worktribe.com/OutputFile/459247">https://hull-repository.worktribe.com/OutputFile/459247</a> .
Function parser	Roland Schmehl, University of Karlsruhe, Germany. Open source code. <a href="http://sourceforge.net/projects/fparser/">http://sourceforge.net/projects/fparser/</a> .
Hash function	Rich Townsend, <a href="https://groups.google.com/group/comp.lang.fortran/browse_frm/thread/456a07645b77f678">groups.google.com/group/comp.lang.fortran/browse_frm/thread/456a07645b77f678</a> . Free source code.
Contouring	Paul Bourke, <b>CONREC</b> , <a href="http://paulbourke.net/papers/conrec/">http://paulbourke.net/papers/conrec/</a> . Free source code.
The following may be used but are not necessarily embedded in <b>PhreePlot</b> :	
Windows installer	Inno Setup, Copyright © 1997-2020 Jordan Russell. All rights reserved. <a href="http://www.jrsoftware.org/isinfo.php">http://www.jrsoftware.org/isinfo.php</a> . Open source code (Delphi) and binaries; license file. Free to use but copyrighted.
Ghostscript (optional install)	Peter Deutsch, Ralph Levien and the Ghostscript team, <a href="https://www.ghostscript.com/download/gsdnld.html">https://www.ghostscript.com/download/gsdnld.html</a> . Opensource code and binary distributed under GPL conditions.
GSview (user install)	Russell Lang, <a href="http://www.ghostgum.com.au/">http://www.ghostgum.com.au/</a> . Very useful and reliable but new registrations are no longer being accepted. (P.S. GSView was a different program from Aladdin but it is no longer available).
wget for Windows	<a href="http://wget.exe">wget.exe</a> is used to check the PhreePlot server for the date of the latest version (see <a href="http://check-for-update.com/">check-for-update.com/</a> ). It is part of the GnuWin package and is distributed under the GNU GPL ( <a href="http://www.gnu.org/copyleft/gpl.html">http://www.gnu.org/copyleft/gpl.html</a> ).
agrep	<a href="http://agrep.exe">agrep.exe</a> is used as an 'approximate' grep to assist with correcting keyword entry errors. It was developed by Sun Wu and Udi Manber at the University of Arizona. It is distributed with its own license conditions ( <a href="http://www.tgries.de/agrep/#COPYRIGHT">http://www.tgries.de/agrep/#COPYRIGHT</a> ) as given below: <small>Copyright 1996, Arizona Board of Regents  on behalf of The University of Arizona.  Permission to use, copy, modify, and/or distribute this software for any purpose with or without fee is hereby granted, provided that the above copyright notice and this permission notice appear in all copies.  THE SOFTWARE IS PROVIDED "AS IS" AND THE AUTHOR DISCLAIMS ALL WARRANTIES WITH REGARD TO THIS SOFTWARE INCLUDING ALL IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS.  IN NO EVENT SHALL THE AUTHOR BE LIABLE FOR ANY SPECIAL, DIRECT, INDIRECT, OR CONSEQUENTIAL DAMAGES OR ANY DAMAGES WHATSOEVER RESULTING FROM LOSS OF USE, DATA OR PROFITS, WHETHER IN AN ACTION OF CONTRACT, NEGLIGENCE OR OTHER TORTIOUS ACTION, ARISING OUT OF OR IN CONNECTION WITH THE USE OR PERFORMANCE OF THIS SOFTWARE.</small>
libiomp5md.dll	This is the OMP runtime library distributed by Intel (used by the compiler).

# Appendix 1. Glossary of terms

Table A1. A glossary of terms used in this Guide

Term	Meaning
batch file	a text file containing batch commands that is executed by the command line interpreter (e.g. cmd.exe)
Chemistry section	all statements in the main input file following the line containing the word CHEMISTRY. This is made up of slightly modified PHREEQC code
custom plot	a type of xy-plot that is fully defined by the user
environment variable	a variable that is set and retrieved through the operating system and can be used by programs such as PhreePlot to configure the way in which they run. PhreePlot uses environment variables to define where the PhreePlot system directory is located and for defining the Paths to certain executable files such as the PhreePlot executable and Ghostscript executable
(fit) data file	a data file in tabular format that provides data (observations, independent variables) used in fit and simulate calculations
Ghostscript	Long-standing open source software for interpreting Postscript files under a number of operating systems and in many popular graphic file formats
grid approach	a way of calculating predominance and stability diagrams that simply calculates the speciation on a square grid of points
GSview	software that provides a pleasant user interface for running Ghostscript under Windows
hunt and track approach	a way of calculating predominance and stability diagrams that works by finding and then tracking the field boundaries from the domain boundaries inwards
include file	a file containing text that will be inserted into the Chemistry section at the point given by the include 'filename' statement
input file	a file containing PhreePlot keywords and settings
interrupt	the result of pressing the 'Esc' key during calculations. This enables the calculations to be paused, stopped or a keyword setting to be changed
job	a block of one or more runs
log file	a file that is normally generated by a PhreePlot run containing details of the run. The level of detail is controlled by the debug keyword
loop file	a data file in tabular format in which a row of data is read from the file for every iteration of the z-loop. Tags based on the column headings are generated from the line of data and may be used in the Chemistry section.
main input file	the principal file containing PhreePlot keywords and settings. It will also contain the Chemistry section, if present. It normally has the extension .ppi and is used to launch a job
main loop simulations	all simulations numbered mainLoop or greater. Used for iterating with the least overheads and with constant updating of the <x_axis> and <y_axis> tags
main species	a character string representing a main species variable that is controlled by the main species loop. Often used for a list of elements but can be used for a list of any character strings
mainspecies loop	the outermost alphanumeric loop controlled by the <mainspecies> tag and list of mainspecies
outfile or 'out' file	the selected output file. It is the default file used by custom calculations to make a plot
override file	an input file that contains PhreePlot keywords that is read immediately after the main input file and will override any settings in force at that point
PhreePlot environment variable	the PhreePlot environment variable (PHREEPLOT) is required to tell your computer where to find the PhreePlot system directory. It is set during installation, through the Control Panel or with a program such as setx.exe. It should end in a backslash
PhreePlot executable	the file that contains the executable code for PhreePlot, normally called pp.exe

Table A1. A glossary of terms used in this Guide (contd)

Term	Meaning
PhreePlot system directory	The directory containing many of the files needed by PhreePlot to run. It is normally called something like ...\\PhreePlot\\x.xx\\system\\ where x.xx is the PhreePlot version number; it is normally stored in the PHREEPLOT environment variable
PHREEQC	a popular geochemical speciation program (pH-redox equilibrium calculations in C) from the USGS that does all the geochemical calculations in PhreePlot
Postscript	a page description language noted for its ability to produce scalable text and vector graphics of high quality. Postscript is the code that PhreePlot uses to define its plots. It can be rendered with the Ghostscript/GSview software combination and is readily converted to other formats. pdf is a popular descendant of Postscript and was also developed by Adobe. Postscript files normally have the extension .ps
pp.log file	a file that contains a one-line entry for each PhreePlot run. It is automatically generated and is located in the PhreePlot system directory
pp.set file	an input file that contains user-defined default settings for all the PhreePlot keywords. This is the first input file to be read and overwrites the program defaults
pre-loop simulations	All simulations preceding the main loop simulation(s). Used for initialization calculations. Not repeated during execution of the x- and y-axis loops
predominance diagram	a diagram, normally in two-dimensions, that shows the dominant chemical species for a particular 'component' over the domain of interest. The 'predominant' species is defined in PhreePlot as the most abundant species in terms of moles of component, irrespective of whether it is a solution, mineral or adsorbed species
run	a block of one or more simulations that are executed in a single call to PHREEQC
selected output	tabular output generated by PHREEQC following some calculations. The output can be controlled using keywords such as SELECTED_OUTPUT and USER_PUNCH
selected output file	a 'file' created by PHREEQC that is used to communicate between PHREEQC and PhreePlot. The actual name of the file is defined by the -file identifier in the SELECTED_OUTPUT keyword data block of PHREEQC. The default name is selected_1.0.out but it can be an unnamed virtual file in PhreePlot when there is minimal debugging taking place
simulation	a block of one or more PHREEQC keywords ending with an END or the end-of-file
simulation number	the sequence number of a simulation counted from the top
stability diagram	similar to a predominance diagram except that a mineral species, if present, always take precedence over any solution species
tag	a character string (here 30 characters or less) that is enclosed by angle brackets, e.g. <x_axis>. Tags are used as placeholders in the Chemistry section and in certain PhreePlot keyword settings such as the plot title. They can be defined in a number of ways and can refer to either numeric or character variables. Tags are substituted by their current values before code is submitted either to PHREEQC for processing or to the in-built plotting routines for writing the plot file
x-axis loop	the third innermost loop controlled by the <x_axis> tag
y-axis loop	the fourth innermost (and most rapidly changing) loop controlled by the <y_axis> tag
z-loop	the second innermost loop controlled by the <loop> tag

## Appendix 2. Thermodynamic databases

The following tables show which elements are found in the various **PHREEQC**-format thermodynamic databases distributed with **PhreePlot**. The included elements are shown in red. Additional elements may be added by editing the databases or including the necessary code in an input file.

These database files can be found in the **PhreePlot** 'system' directory.

The 'Summary of inorganic species' for each database has been generated with the `count_database_species` demo.

Table A2a. Elements available in the `PHREEQC.dat` (USGS) database.<sup>†</sup>

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 <b>H</b>																	2 He	
2	3 <b>Li</b>	4 Be												5 <b>B</b>	6 <b>C</b>	7 <b>N</b>	8 <b>O</b>	9 <b>F</b>	10 Ne
3	11 <b>Na</b>	12 <b>Mg</b>												13 <b>Al</b>	14 <b>Si</b>	15 <b>P</b>	16 <b>S</b>	17 <b>Cl</b>	18 Ar
4	19 <b>K</b>	20 <b>Ca</b>	21 Sc	22 Ti	23 V	24 Cr	25 <b>Mn</b>	26 <b>Fe</b>	27 Co	28 Ni	29 <b>Cu</b>	30 <b>Zn</b>	31 Ga	32 Ge	33 As	34 Se	35 <b>Br</b>	36 Kr	
5	37 Rb	38 <b>Sr</b>	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 <b>Cd</b>	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 <b>Ba</b>	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 <b>Pb</b>	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids				57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu	
** Actinoids				89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr	

<sup>†</sup> These files are included with the standard **PHREEQC** distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

### Summary of inorganic species (elements) included

number of primary master species	=	25
number of secondary master species	=	18
number of minerals	=	57
number of gases	=	8
number of aqueous species	=	184

Table A2b. Elements available in the `Amm.dat` database.<sup>†</sup>

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

<sup>†</sup> This file is included with the standard **PHREEQC** distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

This database is similar to the original `PHREEQC.dat` except that `Amm.dat` also includes `Amm` as a master species and so breaks the assumed redox equilibrium between ammonium ( $N(-3)$ ) and other  $N$  species. Unlike the latest (2.17) version of `PHREEQC.dat`, it also excludes diffusion coefficients for some aqueous species.

### Summary of inorganic species (elements) included

Summary of inorganic species (elements)

number of primary master species	=	25
number of secondary master species	=	17
number of minerals	=	56
number of gases	=	6
number of aqueous species	=	180

Table A2c. Elements available in the wateq4f.dat (USGS) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

† This file is included with the standard PHREEQC distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

### Summary of inorganic species (elements) included

number of primary master species	=	33
number of secondary master species	=	29
number of minerals	=	311
number of gases	=	8
number of aqueous species	=	346

Table A2d. Elements available in the 11n1.dat (Lawrence Livermore National Laboratory) database.<sup>†</sup>

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Period																		
1	1 H																	2 He
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn
7	87 Fr	88 Ra	**															
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu	
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr	

<sup>†</sup> This file is included with the standard PHREEQC distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

### Summary of inorganic species (elements) included

number of primary master species	=	81
number of secondary master species	=	137
number of minerals	=	1120
number of gases	=	91
number of aqueous species	=	1186

Table A2e. Elements available in the minteq.dat (USEPA) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

† This file is included with the standard PHREEQC distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

This database includes cyanide, DOM and some 30 organic ligands including EDTA, citrate and acetate.

#### Summary of inorganic species (elements) included

number of primary master species	=	38
number of secondary master species	=	41
number of minerals	=	478
number of gases	=	14
number of aqueous species	=	484

Table A2f. Elements available in the minteq.v4.dat (USEPA) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

† This file is included with the standard PHREEQC distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

This database includes cyanide, cyanate and some 31 organic ligands including EDTA, citrate and acetate.

#### Summary of inorganic species (elements) included

number of primary master species	=	40
number of secondary master species	=	45
number of minerals	=	541
number of gases	=	15
number of aqueous species	=	609

Table A2g. Elements available in the `pitzer.dat` (USGS) database.<sup>†</sup>

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

<sup>†</sup> This file is included with the standard **PHREEQC** distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/).

This database includes Pitzer coefficients and is designed to be used with the Pitzer model.

#### Summary of inorganic species (elements) included

number of primary master species	=	16
number of secondary master species	=	4
number of minerals	=	45
number of gases	=	2
number of aqueous species	=	26

Table A2h. Elements available in the NAPSI\_290502 (260802) .DAT (Nagra-PSI) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Period																		
1	1 H																	2 He
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn
7	87 Fr	88 Ra	**															
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu	
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr	

† See <http://les.web.psi.ch/TDBbook/index.htm> for a description of the associated publication and here for [downloading](#) the data. Also see Duro L., Grivé M., Cera E., Domènech C., Bruno J. [Update of a thermodynamic database for radionuclides to assist solubility limits calculation for performance assessment](#). Technical Report TR-06-17 (2006), Svensk Kärnbränslehantering AB (Swedish Nuclear Fuel and Waste Management Co.).

### Summary of inorganic species (elements) included

number of primary master species	=	39
number of secondary master species	=	37
number of minerals	=	91
number of gases	=	6
number of aqueous species	=	391

Table A2i. Elements available in the sit.dat (ANDRA) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

† This file is included with the standard PHREEQC distribution. See [http://wwwbrr.cr.usgs.gov/projects/GWC\\_coupled/PHREEQC/](http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/PHREEQC/). It is based on the ThermoChimie v.7.b database, developed by Amphos 21, BRGM and HydrAsa for ANDRA, the French National Radioactive Waste Management Agency.

This database has been especially prepared for dealing with problems in radioactive waste management. It includes a table of SIT epsilon parameters for use with the Specific Interaction Theory (SIT) activity coefficient model of Grenthe et al. (1997).

#### Summary of inorganic species (elements)

number of primary master species	=	54
number of secondary master species	=	55
number of minerals	=	775
number of gases	=	10
number of aqueous species	=	1013

Table A2j. Elements available in the 050000c0.tdb (NEA) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne	
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar	
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

† See <http://migrationdb.jaea.go.jp/english.html> for the download home page and links to the privacy policy and copyright, and here for [downloading](#) this data. A variety of other related PHREEQC-format databases are available from the home page.

### Summary of inorganic species (elements) included

number of primary master species	=	54
number of secondary master species	=	4
number of minerals	=	404
number of gases	=	148
number of aqueous species	=	387

Table A2k. Elements available in the 011213c2.tdb (JAEA) database.<sup>†</sup>

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
Period																			
1	1 H																	2 He	
2	3 Li	4 Be												5 B	6 C	7 N	8 O	9 F	10 Ne
3	11 Na	12 Mg												13 Al	14 Si	15 P	16 S	17 Cl	18 Ar
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn	
7	87 Fr	88 Ra	**																
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu		
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr		

<sup>†</sup> See <http://migrationdb.jaea.go.jp/english.html> for the home page and links to the privacy policy and copyright, and here for [downloading](#) this data. A variety of other databases are available from the home page.

This database also includes definitions for the organic ligands: oxalate, citrate and EDTA.

#### Summary of inorganic species (elements) included

number of primary master species	=	48
number of secondary master species	=	39
number of minerals	=	368
number of gases	=	72
number of aqueous species	=	497

Table A2k. Elements available in the 011213c2.tdb (JAEA) database.<sup>†</sup>

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Period																		
1	1 H																	2 He
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn
7	87 Fr	88 Ra	**															
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu	
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr	

<sup>†</sup> See <http://migrationdb.jaea.go.jp/english.html> for the home page and links to the privacy policy and copyright, and here for [downloading](#) this data. A variety of other databases are available from the home page.

This database also includes definitions for the organic ligands: oxalate, citrate and EDTA.

#### Summary of inorganic species (elements) included

number of primary master species	=	48
number of secondary master species	=	39
number of minerals	=	368
number of gases	=	72
number of aqueous species	=	497

Table A21. Elements available in the PCHatches .dat (NEA18, formerly Serco now Amec) database.†

Group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Period																		
1	1 H																	2 He
2	3 Li	4 Be											5 B	6 C	7 N	8 O	9 F	10 Ne
3	11 Na	12 Mg											13 Al	14 Si	15 P	16 S	17 Cl	18 Ar
4	19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr
5	37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe
6	55 Cs	56 Ba	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn
7	87 Fr	88 Ra	**															
* Lanthanoids			57 La	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu	
** Actinoids			89 Ac	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr	

† This file is available from <http://www.hatches-database.com/main.htm>.

Although originally compiled for use in radiochemical modelling work, the HATCHES database also includes data suitable for many other applications e.g. toxic waste disposal, effluent treatment, chemical processing. It contains data for nearly 40 organic ligands.

#### Summary of inorganic species (elements) included

number of primary master species	=	59
number of secondary master species	=	96
number of minerals	=	946
number of gases	=	7
number of aqueous species	=	876

## Appendix 3. Symbol numbers and names

The following symbols are available for use in **PhreePlot**. Symbols can be specified either by their symbol code or by their name (case independent). Enclose the name in quotes if it contains a space. See [Figure 7.5](#) for a display of all of the symbols.

Table A3. Table showing the symbols available for plotting arranged by symbol code and name.

font	symbol code	symbol name
native	1	FILLED CIRCLE
	2	FILLED SQUARE
	3	FILLED TRIANGLE
	4	FILLED UPSIDE DOWN TRIANGLE
	5	FILLED DIAMOND
	6	FILLED OCTAGON
	7	OPEN CIRCLE
	8	PLUS
	9	MULTIPLY
	10	STAR
Symbol font	11	NUMBER SIGN
	12	PERCENT SIGN
	13	ASTERISK
	14	PLUS
	15	MINUS
	16	PERIOD
	17	QUESTION MARK
	18	PERPENDICULAR
	19	UNDERSCORE
	20	OVERSCORE
	21	BAR
	22	MINUTE
	23	LESSEQUAL
	24	CLUB
	25	DIAMOND
	26	HEART
	27	SPADE
	28	ARROWLEFTRIGHT
	29	ARROWLEFT
	30	ARROWUP
	31	ARROWRIGHT
	32	ARROWDOWN
	33	SIMILAR
	34	COPYRIGHTSANS

font	symbol code	symbol name
	41	UPPER BLADE SCISSORS
	42	BLACK SCISSORS
	43	LOWER BLADE SCISSORS
	44	WHITE SCISSORS'
	45	BLACK TELEPHONE
	46	TELEPHONE LOCATION SIGN
	47	TAPE DRIVE
	50	AIRPLANE
	51	ENVELOPE
	52	BLACK POINTING RIGHT INDEX
	53	WHITE POINTING RIGHT INDEX
	54	VICTORY HAND
	55	WRITING HAND
	56	LOWER RIGHT PENCIL
	57	PENCIL
	60	UPPER RIGHT PENCIL
	61	WHITE NIB
	70	HEAVY BALLOT X
	71	OUTLINED GREEK CROSS
	72	HEAVY GREEK CROSS
	73	OPEN CENTRE CROSS
	74	HEAVY OPEN CENTRE CROSS
	75	LATIN CROSS
	76	SHADOWED WHITE LATIN CROSS
	77	OUTLINED LATIN CROSS
	100	MALTESE CROSS
	101	STAR OF DAVID
	102	FOUR TEARDROP-SPOKED ASTERISK
	103	FOUR BALLOON-SPOKED ASTERISK
	104	HEAVY FOUR BALLOON-SPOKED ASTERISK
	105	FOUR CLUB-SPOKED ASTERISK
	110	BLACK FOUR POINTED STAR
	111	STRESS OUTLINED WHITE STAR
	112	CIRCLED WHITE STAR
	113	OPEN CENTRE BLACK STAR
	114	BLACK CENTRE WHITE STAR
	115	OUTLINED BLACK STAR
	116	HEAVY OUTLINED BLACK STAR
	117	PINWHEEL STAR
	120	SHADOWED WHITE STAR
	121	HEAVY ASTERISK
	122	OPEN CENTRE ASTERISK
	123	EIGHT SPOKED ASTERISK
	124	EIGHT POINTED BLACK STAR
	125	EIGHT POINTED PINWHEEL STAR
	126	SIX POINTED BLACK STAR
	127	EIGHT POINTED RECTILINEAR BLACK STAR
	130	HEAVY EIGHT POINTED RECTILINEAR BLACK STAR
	131	TWELVE POINTED BLACK STAR
	132	SIXTEEN POINTED ASTERISK
	133	TEARDROP-SPOKED ASTERISK
	134	OPEN CENTRE TEARDROP-SPOKED ASTERISK
	135	HEAVY TEARDROP-SPOKED ASTERISK
	136	SIX PETALLED BLACK AND WHITE FLORETTE
	137	BLACK FLORETTE
	140	WHITE FLORETTE
	141	EIGHT PETALLED OUTLINED BLACK FLORETTE
	142	CIRCLED OPEN CENTRE EIGHT POINTED STAR
	143	HEAVY TEARDROP-SPOKED PINWHEEL ASTERISK
	144	SNOWFLAKE
	145	TIGHT TRIFOLIATE SNOWFLAKE
	146	HEAVY CHEVRON SNOWFLAKE
	147	SPARKLE

Zapf Dingbat  
font

font	symbol code	symbol name
Zapf Dingbat font	150	HEAVY SPARKLE
	151	BALLOON-SPOKED ASTERISK
	152	EIGHT TEARDROP-SPOKED PROPELLER ASTERISK
	153	HEAVY EIGHT TEARDROP-SPOKED PROPELLER ASTERISK
	154	BLACK CIRCLE
	155	SHADOWED WHITE CIRCLE
	156	BLACK SQUARE
	157	LOWER RIGHT DROP-SHADOWED WHITE SQUARE
	160	UPPER RIGHT DROP-SHADOWED WHITE SQUARE
	161	LOWER RIGHT SHADOWED WHITE SQUARE
	162	UPPER RIGHT SHADOWED WHITE SQUARE
	163	BLACK UP-POINTING TRIANGLE
	164	BLACK DOWN-POINTING TRIANGLE
	165	BLACK DIAMOND
	166	BLACK DIAMOND MINUS WHITE X
	167	RIGHT BLACK SEMICIRCLE
	170	LIGHT VERTICAL BAR
	171	MEDIUM VERTICAL BAR
	172	HEAVY VERTICAL BAR
	173	HEAVY SINGLE TURNED COMMA QUOTATION MARK ORNAMENT
	174	HEAVY SINGLE COMMA QUOTATION MARK ORNAMENT
	175	HEAVY DOUBLE TURNED COMMA QUOTATION MARK ORNAMENT
	176	HEAVY DOUBLE COMMA QUOTATION MARK ORNAMENT
	241	CURVED STEM PARAGRAPH SIGN ORNAMENT
	242	HEAVY EXCLAMATION MARK ORNAMENT
	243	HEAVY HEART EXCLAMATION MARK ORNAMENT
	244	HEAVY BLACK HEART
	245	ROTATED HEAVY BLACK HEART BULLET
	246	FLORAL HEART
	247	ROTATED FLORAL HEART BULLET
	250	BLACK CLUB SUIT
	251	BLACK DIAMOND SUIT
	252	BLACK HEART SUIT
	253	BLACK SPADE SUIT
	254	DINGBAT CIRCLED DIGIT ONE
	255	DINGBAT CIRCLED DIGIT TWO
	256	DINGBAT CIRCLED DIGIT THREE
	257	DINGBAT CIRCLED DIGIT FOUR
	260	DINGBAT CIRCLED DIGIT FIVE
	261	DINGBAT CIRCLED DIGIT SIX
	262	DINGBAT CIRCLED DIGIT SEVEN
263	DINGBAT CIRCLED DIGIT EIGHT	
264	DINGBAT CIRCLED DIGIT NINE	
265	DINGBAT CIRCLED NUMBER TEN	
266	DINGBAT NEGATIVE CIRCLED DIGIT ONE	
267	DINGBAT NEGATIVE CIRCLED DIGIT TWO	
270	DINGBAT NEGATIVE CIRCLED DIGIT THREE	
271	DINGBAT NEGATIVE CIRCLED DIGIT FOUR	
272	DINGBAT NEGATIVE CIRCLED DIGIT FIVE	
273	DINGBAT NEGATIVE CIRCLED DIGIT SIX	
274	DINGBAT NEGATIVE CIRCLED DIGIT SEVEN	
275	DINGBAT NEGATIVE CIRCLED DIGIT EIGHT	
276	DINGBAT NEGATIVE CIRCLED DIGIT NINE	
277	DINGBAT NEGATIVE CIRCLED NUMBER TEN	
300	DINGBAT CIRCLED SANS-SERIF DIGIT ONE	
301	DINGBAT CIRCLED SANS-SERIF DIGIT TWO	
302	DINGBAT CIRCLED SANS-SERIF DIGIT THREE	
303	DINGBAT CIRCLED SANS-SERIF DIGIT FOUR	
304	DINGBAT CIRCLED SANS-SERIF DIGIT FIVE	
305	DINGBAT CIRCLED SANS-SERIF DIGIT SIX	
306	DINGBAT CIRCLED SANS-SERIF DIGIT SEVEN	
307	DINGBAT CIRCLED SANS-SERIF DIGIT EIGHT	
310	DINGBAT CIRCLED SANS-SERIF DIGIT NINE	

font	symbol code	symbol name
Zapf Dingbat font	311	DINGBAT CIRCLED SANS-SERIF NUMBER TEN
	312	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT ONE
	313	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT TWO
	314	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT THREE
	315	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT FOUR
	316	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT FIVE
	317	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT SIX
	320	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT SEVEN
	321	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT EIGHT
	322	DINGBAT NEGATIVE CIRCLED SANS-SERIF DIGIT NINE
	323	DINGBAT NEGATIVE CIRCLED SANS-SERIF NUMBER TEN
	324	HEAVY WIDE-HEADED RIGHTWARDS ARROW
	330	HEAVY SOUTH EAST ARROW
	331	HEAVY RIGHTWARDS ARROW
	332	HEAVY NORTH EAST ARROW
	333	DRAFTING POINT RIGHTWARDS ARROW
	334	HEAVY ROUND-TIPPED RIGHTWARDS ARROW
	335	TRIANGLE-HEADED RIGHTWARDS ARROW
	336	HEAVY TRIANGLE-HEADED RIGHTWARDS ARROW
	337	DASHED TRIANGLE-HEADED RIGHTWARDS ARROW
	340	HEAVY DASHED TRIANGLE-HEADED RIGHTWARDS ARROW
	341	BLACK RIGHTWARDS ARROW
	342	THREE-D TOP-LIGHTED RIGHTWARDS ARROWHEAD
	343	THREE-D BOTTOM-LIGHTED RIGHTWARDS ARROWHEAD
	344	BLACK RIGHTWARDS ARROWHEAD
	345	HEAVY BLACK CURVED DOWNWARDS AND RIGHTWARDS ARROW
	346	HEAVY BLACK CURVED UPWARDS AND RIGHTWARDS ARROW
	347	SQUAT BLACK RIGHTWARDS ARROW
	350	HEAVY CONCAVE-POINTED BLACK RIGHTWARDS ARROW
	351	RIGHT-SHADED WHITE RIGHTWARDS ARROW
	352	LEFT-SHADED WHITE RIGHTWARDS ARROW
	353	BACK-TILTED SHADOWED WHITE RIGHTWARDS ARROW
	354	FRONT-TILTED SHADOWED WHITE RIGHTWARDS ARROW
	355	HEAVY LOWER RIGHT-SHADOWED WHITE RIGHTWARDS ARROW
	356	HEAVY UPPER RIGHT-SHADOWED WHITE RIGHTWARDS ARROW
	357	NOTCHED LOWER RIGHT-SHADOWED WHITE RIGHTWARDS ARROW
	361	NOTCHED UPPER RIGHT-SHADOWED WHITE RIGHTWARDS ARROW
	362	CIRCLED HEAVY WHITE RIGHTWARDS ARROW
	363	WHITE-FEATHERED RIGHTWARDS ARROW
	364	BLACK-FEATHERED SOUTH EAST ARROW
	365	BLACK-FEATHERED RIGHTWARDS ARROW
	366	BLACK-FEATHERED NORTH EAST ARROW
	367	HEAVY BLACK-FEATHERED SOUTH EAST ARROW
	370	HEAVY BLACK-FEATHERED RIGHTWARDS ARROW
	371	HEAVY BLACK-FEATHERED NORTH EAST ARROW
	372	TEARDROP-BARBED RIGHTWARDS ARROW
373	HEAVY TEARDROP-SHANKED RIGHTWARDS ARROW	
374	WEDGE-TAILED RIGHTWARDS ARROW	
375	HEAVY WEDGE-TAILED RIGHTWARDS ARROW	
376	OPEN-OUTLINED RIGHTWARDS ARROW	

## Appendix 4. The Standard and Latin-1 character sets

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The following tables show the characters, and their decimal and octal codings, that are available with the Latin-1 (ISO-8859-1) (default in **PhreePlot**) and ‘Standard’ encodings. The Latin-1 encoding is often named ‘ANSI’ (c.f. ASCII) although it is not actually a proper ANSI standard. These character sets are enabled with the [font](#) keyword either

```
font Standard
or
font Latin-1
```

The font can also be changed at the same time, e.g.

```
font Roman Latin-1
```

The following tables show the character sets available on a ‘typical’ PC (mine!). It is possible to reproduce the tables to show your particular setup by setting `plotTitle` to ‘character set’ and using ‘A4’ or ‘letter’ size paper and using the `font` keyword to select the encoding. The following input should produce a character table for Latin-1:

```
calculationType      custom
plotTitle            "character set" # special case
labelsize            2 # sets text size in mm
font                 Latin-1 # or Standard
```

See [“Accented and other ‘foreign’ characters - the Latin-1 encoding”, p. 91](#) for how to enter characters not present on your keyboard.

The ASCII encoding points to the 7-bit ASCII character set and consists of only the first two columns in the tables below (decimal codes 0-127). This was the character set used in earlier versions of **PhreePlot**.

The extended characters with decimal codes 129-137 are used internally by **PhreePlot** to code subscripts, superscripts etc and should not be used in text strings.

### Greek characters

There are a couple of Greek characters in the Latin-1 character set but a full set can be found in the symbols font. These are entered singly with the backslash-character format, e.g. `\p` for  $\pi$ , or using the Greek pair of tags, `<g>...</g>`, for one or more characters. The codes used to specify the Greek characters are given below.

```
αβχδε φγηιφ κλμνο πθρστ υωξψζ
abcde fghij klmno pqrst uwxvz
```

```
ΑΒΧΔΕ ΦΓΗΙΘ ΚΛΜΝΟ ΠΘΡΣΤ ΥΩΞΨΖ
ΑΒCDE FGHIJ KLMNO PQRST UWXYZ
```

# 'Standard' encoding

dec	oct	chr									
000	000		064	100	@	128	200		192	300	
001	001		065	101	A	129	201		193	301	,
002	002		066	102	B	130	202		194	302	'
003	003		067	103	C	131	203		195	303	^
004	004		068	104	D	132	204		196	304	~
005	005		069	105	E	133	205		197	305	_
006	006		070	106	F	134	206		198	306	˘
007	007		071	107	G	135	207		199	307	˙
008	010		072	110	H	136	210		200	310	˚
009	011		073	111	I	137	211		201	311	°
010	012		074	112	J	138	212		202	312	°
011	013		075	113	K	139	213		203	313	˘
012	014		076	114	L	140	214		204	314	˙
013	015		077	115	M	141	215		205	315	˚
014	016		078	116	N	142	216		206	316	˘
015	017		079	117	O	143	217		207	317	˙
016	020		080	120	P	144	220		208	320	_
017	021		081	121	Q	145	221		209	321	
018	022		082	122	R	146	222		210	322	
019	023		083	123	S	147	223		211	323	
020	024		084	124	T	148	224		212	324	
021	025		085	125	U	149	225		213	325	
022	026		086	126	V	150	226		214	326	
023	027		087	127	W	151	227		215	327	
024	030		088	130	X	152	230		216	330	
025	031		089	131	Y	153	231		217	331	
026	032		090	132	Z	154	232		218	332	
027	033		091	133	[	155	233		219	333	
028	034		092	134	\	156	234		220	334	
029	035		093	135	]	157	235		221	335	
030	036		094	136	^	158	236		222	336	
031	037		095	137	˘	159	237		223	337	
032	040		096	140	˙	160	240		224	340	
033	041	!	097	141	a	161	241	i	225	341	Æ
034	042	"	098	142	b	162	242	ç	226	342	
035	043	#	099	143	c	163	243	£	227	343	a
036	044	\$	100	144	d	164	244	/	228	344	
037	045	%	101	145	e	165	245	¥	229	345	
038	046	&	102	146	f	166	246	f	230	346	
039	047	'	103	147	g	167	247	§	231	347	
040	050	(	104	150	h	168	250	¤	232	350	Ł
041	051	)	105	151	i	169	251	'	233	351	Ø
042	052	*	106	152	j	170	252	"	234	352	Œ
043	053	+	107	153	k	171	253	«	235	353	°
044	054	,	108	154	l	172	254	<	236	354	
045	055	-	109	155	m	173	255	>	237	355	
046	056	.	110	156	n	174	256	fi	238	356	
047	057	/	111	157	o	175	257	fl	239	357	
048	060	0	112	160	p	176	260		240	360	
049	061	1	113	161	q	177	261	—	241	361	æ
050	062	2	114	162	r	178	262	†	242	362	
051	063	3	115	163	s	179	263	‡	243	363	
052	064	4	116	164	t	180	264	·	244	364	
053	065	5	117	165	u	181	265		245	365	ı
054	066	6	118	166	v	182	266	¶	246	366	
055	067	7	119	167	w	183	267	•	247	367	
056	070	8	120	170	x	184	270	,	248	370	ı
057	071	9	121	171	y	185	271	„	249	371	ø
058	072	:	122	172	z	186	272	"	250	372	œ
059	073	;	123	173	{	187	273	»	251	373	ß
060	074	<	124	174		188	274	...	252	374	
061	075	=	125	175	}	189	275	‰	253	375	
062	076	>	126	176	~	190	276		254	376	
063	077	?	127	177		191	277	˘	255	377	

# 'Latin-1'

dec	oct	chr	dec	oct	chr	dec	oct	chr	dec	oct	chr
000	000		064	100	@	128	200		192	300	À
001	001		065	101	A	129	201		193	301	Á
002	002		066	102	B	130	202		194	302	Â
003	003		067	103	C	131	203		195	303	Ã
004	004		068	104	D	132	204		196	304	Ä
005	005		069	105	E	133	205		197	305	Å
006	006		070	106	F	134	206		198	306	Æ
007	007		071	107	G	135	207		199	307	Ç
008	010		072	110	H	136	210		200	310	È
009	011		073	111	I	137	211		201	311	É
010	012		074	112	J	138	212		202	312	Ê
011	013		075	113	K	139	213		203	313	Ë
012	014		076	114	L	140	214		204	314	Ì
013	015		077	115	M	141	215		205	315	Í
014	016		078	116	N	142	216		206	316	Î
015	017		079	117	O	143	217		207	317	Ï
016	020		080	120	P	144	220	!	208	320	Ð
017	021		081	121	Q	145	221	, ' , ^	209	321	Ñ
018	022		082	122	R	146	222	~	210	322	Ò
019	023		083	123	S	147	223	~	211	323	Ó
020	024		084	124	T	148	224	~	212	324	Ô
021	025		085	125	U	149	225	~	213	325	Õ
022	026		086	126	V	150	226	~	214	326	Ö
023	027		087	127	W	151	227	~	215	327	×
024	030		088	130	X	152	230	~	216	330	Ø
025	031		089	131	Y	153	231	~	217	331	Ù
026	032		090	132	Z	154	232	~	218	332	Ú
027	033		091	133	[	155	233	~	219	333	Û
028	034		092	134	\	156	234	~	220	334	Ü
029	035		093	135	]	157	235	~	221	335	Ý
030	036		094	136	^	158	236	~	222	336	ß
031	037		095	137	_	159	237	~	223	337	ƒ
032	040		096	140	̀	160	240	~	224	340	à
033	041	!	097	141	a	161	241	~	225	341	á
034	042	"	098	142	b	162	242	~	226	342	â
035	043	#	099	143	c	163	243	~	227	343	ã
036	044	\$	100	144	d	164	244	~	228	344	ä
037	045	%	101	145	e	165	245	~	229	345	å
038	046	&	102	146	f	166	246	~	230	346	æ
039	047	'	103	147	g	167	247	~	231	347	ç
040	050	(	104	150	h	168	250	~	232	350	è
041	051	)	105	151	i	169	251	~	233	351	é
042	052	*	106	152	j	170	252	~	234	352	ê
043	053	+	107	153	k	171	253	~	235	353	ë
044	054	,	108	154	l	172	254	~	236	354	ì
045	055	-	109	155	m	173	255	~	237	355	í
046	056	.	110	156	n	174	256	~	238	356	î
047	057	/	111	157	o	175	257	~	239	357	ï
048	060	0	112	160	p	176	260	~	240	360	ð
049	061	1	113	161	q	177	261	~	241	361	ñ
050	062	2	114	162	r	178	262	~	242	362	ò
051	063	3	115	163	s	179	263	~	243	363	ó
052	064	4	116	164	t	180	264	~	244	364	ô
053	065	5	117	165	u	181	265	~	245	365	õ
054	066	6	118	166	v	182	266	~	246	366	ö
055	067	7	119	167	w	183	267	~	247	367	÷
056	070	8	120	170	x	184	270	~	248	370	ø
057	071	9	121	171	y	185	271	~	249	371	ù
058	072	:	122	172	z	186	272	~	250	372	ú
059	073	;	123	173	{	187	273	~	251	373	û
060	074	<	124	174		188	274	~	252	374	ü
061	075	=	125	175	}	189	275	~	253	375	ý
062	076	>	126	176	~	190	276	~	254	376	þ
063	077	?	127	177		191	277	~	255	377	ÿ