



Bruker AXS

# *Poly*SNAP M

High-Throughput Cluster Analysis of  
Powder Diffraction Data

## Program Manual and Tutorial

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UNIVERSITY  
of  
GLASGOW

WestCHEM 

The WestCHEM logo features the word "WestCHEM" in a red and black sans-serif font, followed by a graphic of four interlocking hexagons in shades of grey and red.

## **Credits**

### ***PolySNAP M***

#### ***Systematic Non-parametric Analysis of Patterns***

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## **References**

- Barr, G., Dong, W. & Gilmore, C.J (2004). *J. Appl. Cryst.* **37**, 658-664.  
Gilmore, C.J., Barr, G. & Paisley, J. (2004). *J. Appl. Cryst.* **37**, 665-668.  
Gilmore, C.J., Barr, G. & Paisley, J. (2004). *J. Appl. Cryst.* **37**, 231-242.  
Barr, G., Dong, W. & Gilmore, C.J (2004). *J. Appl. Cryst.* **37**, 243-252.  
Barr, G., Dong, W. & Gilmore, C.J (2004). *J. Appl. Cryst.* **37**, 635-642.  
Barr, G., Dong, W. & Gilmore, C.J (2004). *J. Appl. Cryst.* **37**, 874-882

## **Documentation Production Notes**

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## **1.1 Program Overview**

PolySNAP M is a software package designed to match and analyse powder diffraction patterns utilising their full profiles. The use of the full-profile allows for more flexible and accurate identification of samples, even when data quality is low or preferred orientation effects are significant.

The software provides an easy to use interface to several powerful and novel statistical methods to rank patterns in order of their similarity to any selected sample, allowing unknowns to be quickly identified. In quantitative mode, given a mixture pattern and potential pure phase patterns, it can identify which patterns are in the mixture, and quantify their proportions quickly and easily using a non-Rietveld based approach.

The matching procedure can be automated for high-throughput analysis. PolySNAP M allows for datasets of up to 96 patterns to be analysed in a single run, and provides highly flexible graphical output to summarise and visualise the results. This highlights any unusual data, and means that time is not wasted looking at the very many patterns that behave exactly as expected. It can work with or without the provision of reference patterns, and includes features such as an automated report writer and a time/date stamped logfile to assist with audit trail procedures.

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## 1.2 Introduction

Four main stages are involved in a standard program run:

1. Import and processing of data files.
2. Match all data files against all other data files.
3. Perform cluster, quantitative and other analyses if required.
4. Output results to file and graphically to screen.

A flowchart representation of the main PolySNAP M processes is shown overleaf.

## 1.3 Program Requirements

PolySNAP M requires a modern, high-specification PC running Microsoft Windows 2000 SP2 or XP SP1 or later. Additionally, a monitor with minimum 1024 x 768 resolution at 32 bit colour depth is needed, and an active connection to the Internet.

### 1.3.1 Note on run-times

On a 2.4Ghz Intel Xeon with 512 Mb RAM, running Windows 2000 Professional SP4, some approximate average program run-times are shown below.

Times are assuming there are no delays waiting for data, and are measured from launching the program to the results display screen being displayed:

No. of Patterns	Time
50	10 seconds
96	20 seconds

These times are approximate, and may vary depending on the analysis options selected for a given program run - in particular, allowing for an offset in the matching calculations will greatly add to the run time.

## 1.4 Installation

If there has been a previous version of the software installed, then it is recommended to install the new version in a different location than the older one; do not install a new version directly over the top.

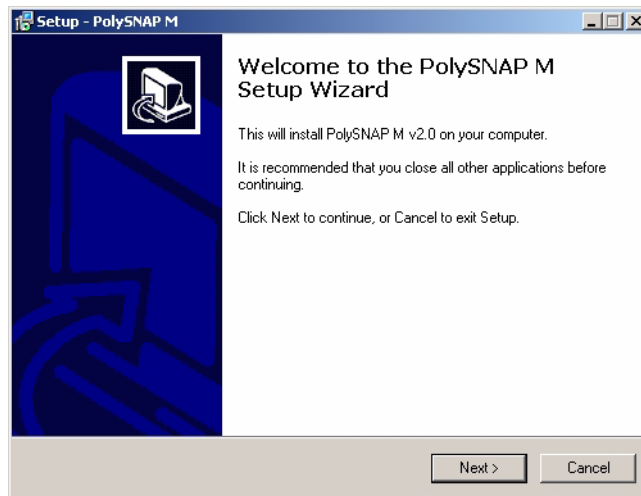
Insert the CD containing the software in the CD-ROM drive of your computer. On the CD (normally drive D:\ on most PCs), open the folder

*PolySNAP M Install*

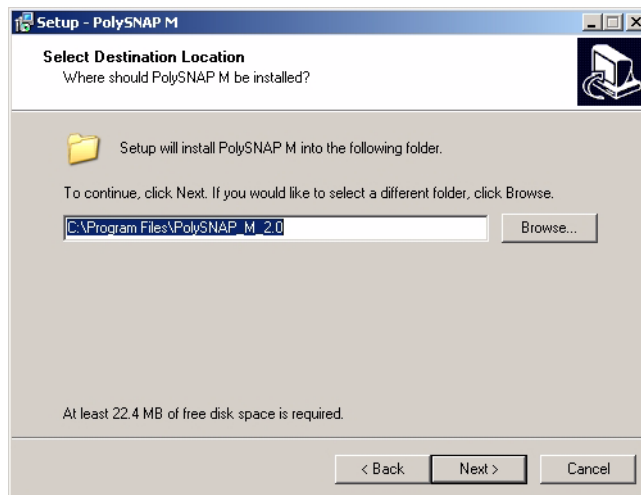
and launch the program *Setup.exe* by double-clicking it.

Note that to install software on Windows 2000/XP systems, the user must be logged on to an account with system administrator privileges.

It will display a welcome window:



Followed by a dialog box allowing the user to control where the program is installed:



The default path,

*C:\Program Files\PolySNAP M\*

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should be suitable for most environments, but a different location may be chosen if required by clicking on the *Change Directory* button (please note that installing or running PolySNAP M from a remote network drive is **not** a supported configuration).

The next two screens control if a shortcut to the software is added to the Start Menu and/or the Desktop. The final screen displays a summary of the selected options; click *Install* to start the installation process.

Installation should then proceed automatically, and once completed, the installer will quit. Depending on the version of Windows, a restart may be required at this point; if so the installer will notify that this is the case.

## 1.5 Launching PolySNAP M

Assuming a default installation, the program may be accessed in one of the following two ways:

- Run the shortcut to *PolySNAP M* which the installer will have placed on the desktop by double-clicking its icon.



- From the Start Menu, select the *Programs* sub-menu, followed by the *PolySNAP M folder*, and then the *PolySNAP M* option. (It is usually installed at the very bottom of the list of programs).

## 1.6 Registering PolySNAP

The copy of PolySNAP that is now installed needs to be registered before it can be used. A dialog box will appear asking for a Product Key.

You will have been provided with a product code of the form:

*SNAPx-xxxx-xxxx-xxxx*

Enter this code now (case-sensitive, including dashes), and click OK.

The program will now try to connect to the internet to validate the registration. It will display a message warning you of this, and a progress dialog box will appear letting you know that this is happening.

You will then be asked to fill in some registration details. If you have purchased a license, you will only be asked for your name and email address. If you are running in a Trial mode, you will be asked for some more details. Click OK when complete.

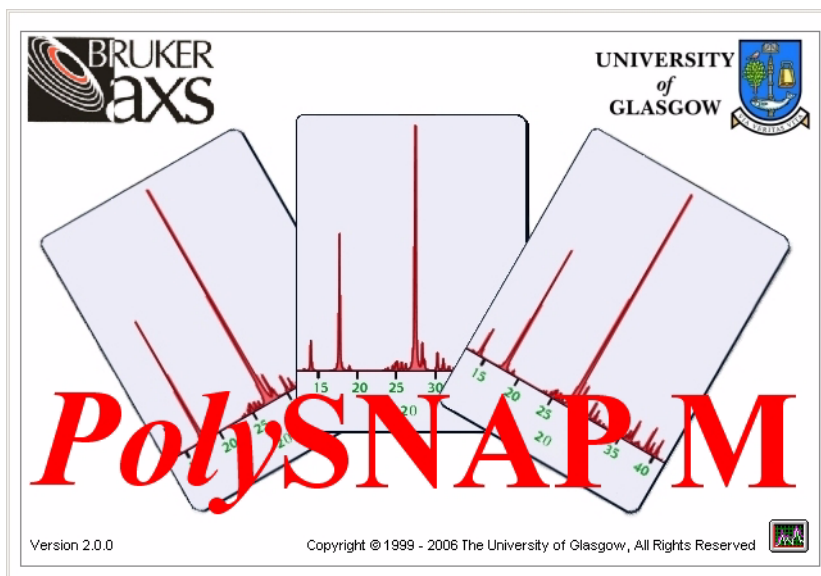


*NB: your email address and other information will not be passed to any third party and will not be used for any other purpose.*

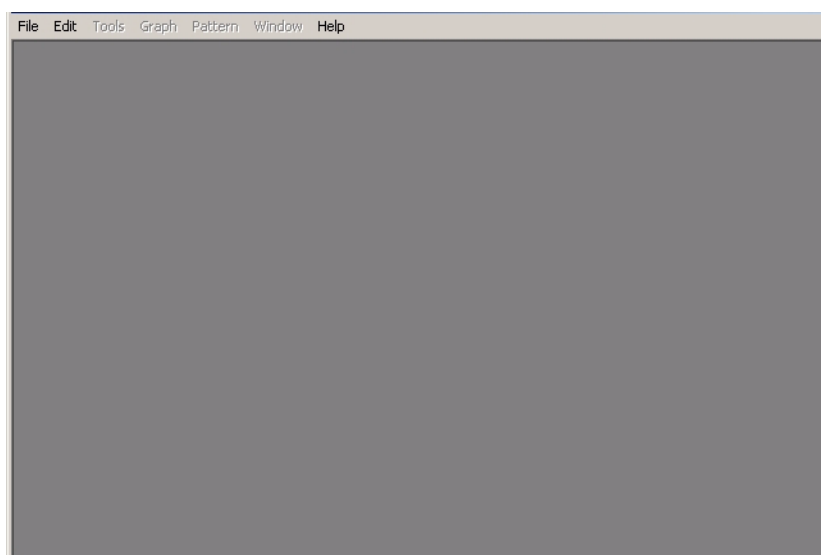
If you have any problems with the process, or are unable to connect to the internet, please contact us directly at

**snap@chem.gla.ac.uk**

Once this registration process is complete, the program logo screen will appear for a few seconds, before being automatically dismissed:



The main PolySNAP M window will then appear, and will by default fill the entire screen:



You are now ready to begin working with the software.

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Please note that a searchable PDF on-line version of this manual can be viewed at any time during the program by selecting *View Manual* from the *Help* menu.

## **1.7 Installation Troubleshooting**

### **Problem**

Program registration was not completed, because PolySNAP was unable to connect to the internet.

### **Solution**

If the registration process could not connect to the internet to validate the install, then it will have displayed an error and a corresponding unique Installation Code for your copy. Please either email this number, along with your Product Code, to [snap@chem.gla.ac.uk](mailto:snap@chem.gla.ac.uk) or using another computer visit

[www.copyminder.com/activate.php](http://www.copyminder.com/activate.php)

to obtain an activation code manually.

### **Problem**

A message box displaying an error '51' is displayed during program installation. The program will not launch correctly and may display further errors after this occurs.

### **Solution**

Search the Windows System Folder and its subfolders (usually *C:\WINNT* for Windows 2000, or *C:\Windows\* for Windows XP), for copies of the file *CCMOVE32.DLL*. Move this file to a different location (e.g. *C:\temp*), then re-run the program installer.

### **Problem**

When PolySNAP M is launched, a Microsoft Office Installer window keeps repeatedly appearing and cannot easily be dismissed.

### **Solution**

This problem occurs on a system where the currently logged in user has never previously run any of the installed Microsoft Office applications on this machine. Keep clicking *Cancel* until the window finally goes away, and then quit PolySNAP M. Launch any installed Office application, e.g. Word, and the same installer window will probably appear. This time allow it to run to completion, and click *OK* when requested. Once Word has fully loaded as normal, exit the program and then run PolySNAP M again. It should now run normally without any further interruptions from Office.

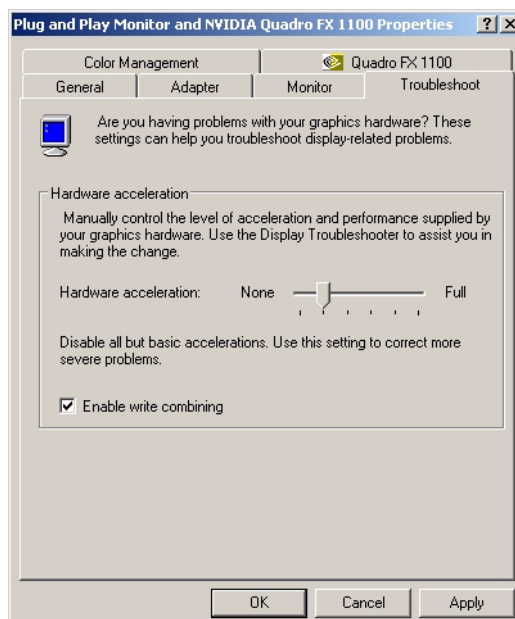
### Problem

Problems may occur with the graphics panes – for example, strange artefacts may appear on the graphics panes in the results display screen (such as some of the lines in the dendrogram not being visible), the program may freeze when a graphics pane is being interacted with (*e.g.* rotated, zoomed *etc.*) or the program may hang when attempting to first display the results screen at the end of a program run.

### Solution

This problem can occur on systems that have graphics cards that are not 100% compatible with the standard OpenGL libraries. As a workaround, first quit PolySNAP M, then go to

*Start Menu -> Settings -> Control Panel -> Display .*



Under the *Settings* tab, click the *Advanced* button on the bottom right of the pane. In the window that appears, select the *Troubleshooting* tab, and move the *Hardware Acceleration* slider down to one notch above the far left hand side (“None”). Click *OK*, then *OK* again. Restart PolySNAP M and see if the problem has been resolved

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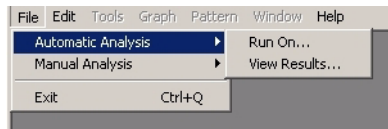
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## 2.1 Starting Automatic Mode

To run in automatic mode, select the *Automatic Analysis* option from the *File* menu (this is only available when no other databases or match windows are open).

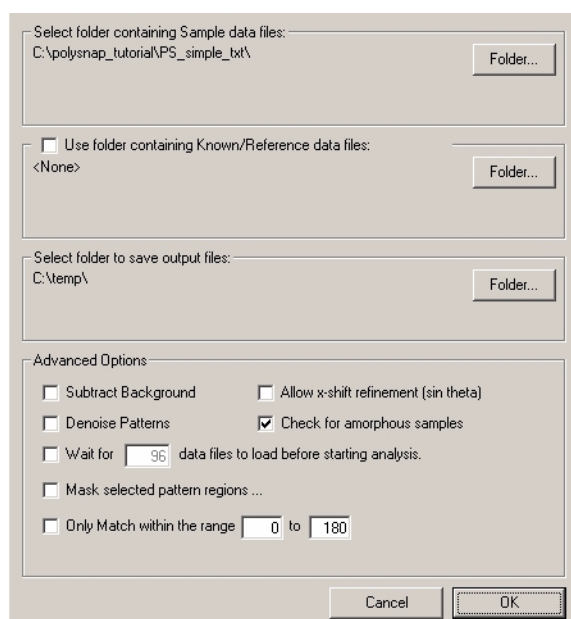


The options from which to choose are presented:

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### 2.1.0.1 Run on...

This menu item gives the following options:



This allows the location of the required files to be selected on a run-by-run basis, without having to change the default settings in the PolySNAP M program options.

Note that setting the input folder to be the same location as the output folder is not permitted.

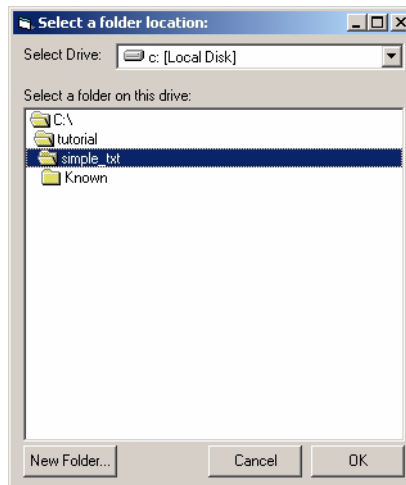
The initial paths listed in this window will correspond to those defaults found in the options window. The three main sections are as follows:

- *Select folder containing Sample data files*

This option allows the user to run PolySNAP M analysis on either a folder containing multiple individual data files.

*Folder Selection:*

Clicking on the *Folder...* button will open the following window:



This window allows selection of an entire folder, rather than a single file within a folder.

From the upper selection area any available local or network drives can be selected, and doing so updates the lower region to display all folders contained on that drive.

By double-clicking on a folder name, it may be opened, and any folders contained within that folder are then shown.

To select a folder to use as the main folder, double-click on it to open it. For example, in the screenshot above, the folder at *C:\tutorial\simple\_txt\* is selected.

Clicking *OK* results in the selected folder path being displayed in the settings window.

- *Use folder containing Known/Reference data files*

When importing files, new samples can be optionally compared to patterns of known samples. If known samples are available to be compared, their location may be set here after turning on the checkbox. In this case, two options are available to the user:

- to select a folder containing one or more individual pattern files, click on *Folder...* and select a folder as described above

or

- to not select any known phase source at all, turn the checkbox back off, and the location is set to *<None>*.

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Copies of the selected patterns are stored in a file *knownphaseDB.par* within the selected output directory. The original data files are left untouched.

- *Select folder to save output files*

The program has to be given a set location in which to save all of the output files created by an automatic run. This can be manually set to any folder as required by the user (although having the output and input locations the same is not permitted).

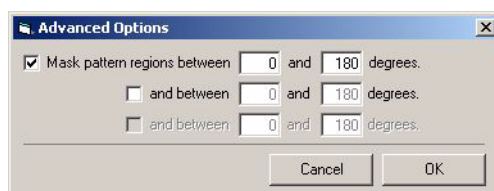
Note that if an output folder is selected that already contains files from a previous run, those files will be deleted prior to the new run starting.

Click on *Folder...* to open the folder selector as above. From here any output folder can be selected as required; note that a *New Folder* button is available to allow the creation of a new, empty folder if required.

- *Advanced Options*

The options here allow additional optional processing to be performed upon the data as it is imported. The options are to subtract background, de-noise the signal, check for amorphous samples, and to allow an x-shift between the patterns.

Additionally, when turned on, the checkbox *Mask Selected Pattern Regions...* brings up a dialog box allowing up to three independent regions of the pattern to be masked to zero intensity.



This allows for impurity peaks or problem background areas *etc.* to be removed prior to matching.

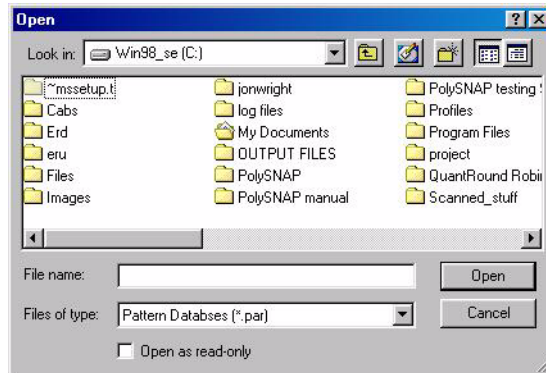
The final option, *Only match within the range [] to []*, allows a single subregion of the full angle range to be used for comparison. This can be useful to concentrate the analysis on a single area of interest within a larger pattern.

The processing options (Background subtraction, smoothing, shifting, etc.) available here are discussed in more detail in the *Options and Defaults* chapter.



### 2.1.0.2 View results...

This option allows the results from a previous run of PolySNAP M to be displayed and examined without having to wait for all the analysis to re-run. Selecting it will open a standard file-selection dialog box:



Locate the folder containing all of the output files from a previous run. Inside this folder will be a database file, whose filename will be in a similar format to *Run\_09-11-2002.par* (the numbers refer to the date on which the run was performed).

Select this database file and click *Open*. The main PolySNAP M results window will appear and display the results - see Section 2.3.

Note that certain program options are not available in *View Results* mode.

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## 2.2 Running PolySNAP M

### 2.2.1 File formats that can be imported

*Text files (filename.txt) (filename.prn)*

These should be standard ASCII text files. The angle should be the x data, and the corresponding intensities the y data. The x-y data must be in the format:

```
x1      y1
x2      y2
.       .
.       .
```

*etc.*

***The fields must be tab-delimited.***

If the first line in the file begins with either a '#' or the string 'ID: ', the rest of that line is used as the 'Pattern Name' for the pattern.

Any subsequent lines beginning with the '#' character are ignored.

*Comma-separated value files (filename.csv)*

These should be standard ASCII CSV files, containing the x-y data in the format:

```
x1,y1
x2,y2
..
..
```

*etc.*

If the first line in the file begins with either a '#' or the string 'ID: ', the rest of that line is used as the 'Chemical Name' for the pattern.

Any subsequent lines beginning with the '#' character are ignored.

*CIF (Crystallographic Information Format) files  
(filename.cif)*

The program contains a CIF-format translator that reads standard version 2.0 Powder CIF files. Although the only data necessary for SNAP is the x-y intensity data, the rest of the CIF information - such as chemical names and formulae, author names and addresses *etc.* are also retained in the database for reference purposes, and may be viewed from the Pattern Editor window. Additionally, unit cell

dimensions and contents are read in if present for use in Quantitative Analysis mode.

For more information on CIF format files, see the IUCr website at:

*<http://www.iucr.org/iucr-top/cif/pd/index.html>*

#### *Bruker Raw Format files*

The program can import data from Bruker RAW format. This is a binary file-format, so cannot be edited or viewed in a conventional text editor. There are several different types of RAW format; PolySNAP M should be able to import all versions up to Version 4.

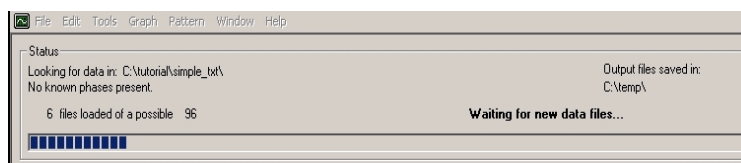
Although the only data necessary for PolySNAP M is the x-y intensity data, much of the rest of the information stored in the file - such as chemical names and formulae, author names and addresses etc. are also retained in the database for reference purposes, and may be viewed from the Pattern Editor window.

#### *PolySNAP M Pattern files (filename.pat)*

Patterns in PolySNAP M databases can be individually exported in the program's own .pat format. This format contains the original x-y raw data, any processed data - e.g. the profile after noise removal, marked peak positions and any other data fields present. Once saved as separate files, they can then be re-imported to the same or a different database at a later date.

### **2.2.2 Import all data files**

Assuming no data files are present when the automatic mode run is started, a screen similar to the following is displayed:



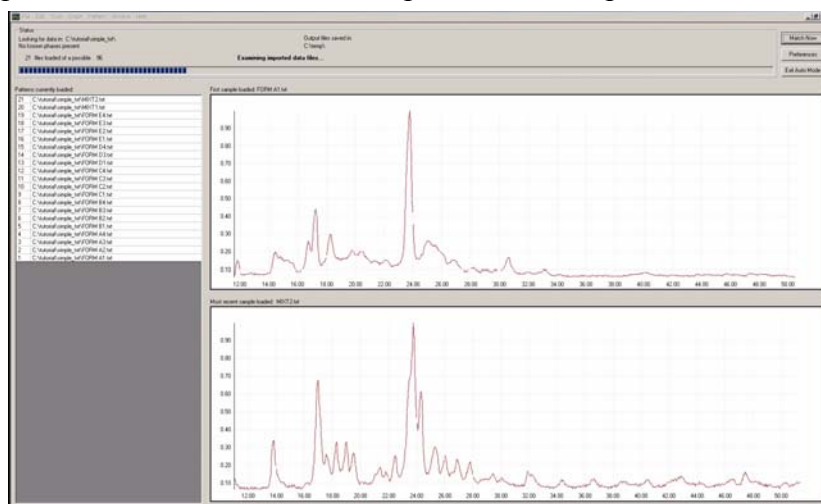
The location of the directory which the program is monitoring for input data is displayed. The number of files expected, and the number loaded so far are also given. It is possible to change these settings at this stage by clicking on the *Preferences* button to bring up the program options dialog described previously.

Clicking *Exit Auto Mode* returns the program to the usual interactive mode, and cancels the automatic run. The user will be asked to confirm that they did mean to select this option.

The *Match Now* option overrides any settings to wait for more patterns, and causes the program to proceed directly to the next phase. Again, the user is asked if they mean to pursue this course of action, as it may cause some data files to not be imported.

If all file locations were correctly set, a database file is created in the output folder defined earlier. This contains all the imported patterns. Any output from PolySNAP M is saved in this same directory, including the logfile, *SNAPlog.txt*, which describes the success or otherwise of importing each datafile, the results of the matching and clustering process, and other useful information.

Once files are found and imported, extra information is displayed at this stage in the form of a list of imported files, and a graphical representation of the most recent pattern to be imported:



The first file imported to the database is displayed by the top graph, the most recently imported file is represented by the lower graph. Other patterns imported can be displayed on the upper graph by selecting the pattern of interest from the list.

Any files which could not be imported are recorded in both the *SNAPlog.txt*, and the *errorlog.txt* file.

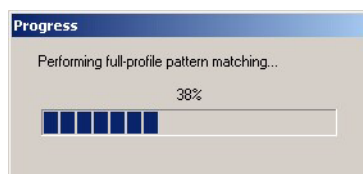
### 2.2.3 Examine the imported data files

Once all of the expected samples have been imported, the program examines the patterns. Several steps are performed at this stage (see also the flowchart in section 1.3 on page 5):

1. Patterns are checked to see if they may be amorphous. This involves calculating how much pattern would be left if all of the background areas were removed, as well as how many peaks of reasonable intensity there are superimposed on that background.
2. If known phase files were provided, the program compares each of the imported patterns to each of the known phases. Any good matches are recorded and will be displayed later.
3. For patterns that did not match any of the known phases sufficiently, quantitative analysis is performed to establish if they might possibly represent mixtures of more than one of the known phases provided. The quantitative analysis techniques described in the manual analysis section are performed with an additional step which removes each suggested component in turn, to establish if that improves or worsens the fit to the original pattern. In this way, patterns that are incorrectly included can be weeded out.

#### 2.2.4 Match all data files against all other data files

Upon commencement of this phase, a progress dialog is displayed:

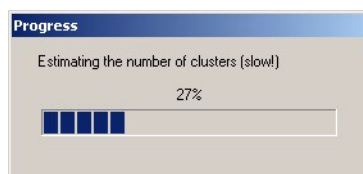


The various matching tests selected are then performed, and this may take some time, so patience is required.

#### 2.2.5 Perform cluster and quantitative analyses

Once the matching has been completed, the results are passed into the cluster analysis module, which then starts to try to group the data into similar clusters, and estimate their number. Again, this may take some time.

When more than 50 patterns are being examined, a progress bar is displayed to give some information about how far through the calculation is:



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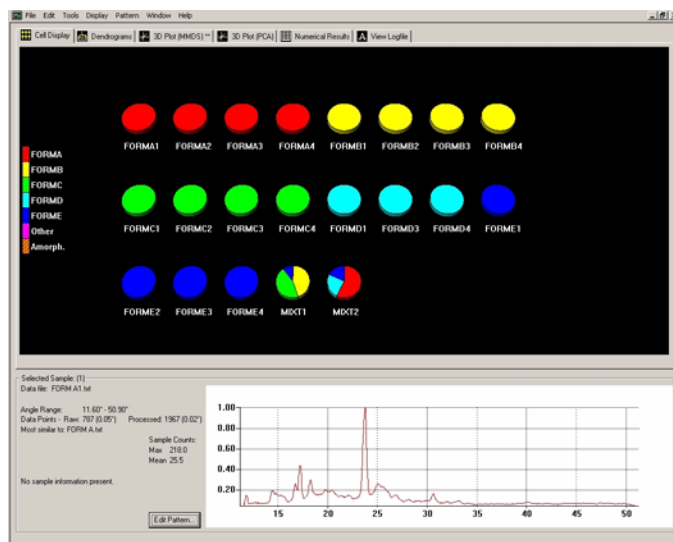
Note that while the clustering is underway, the main screen display is not updated in any way. Therefore, it may sometimes appear as if the program has crashed or frozen, as it will not respond to the mouse or keyboard during this process. Patience is recommended at this point.

### **2.2.6 Output results to file**

Once the clustering is complete, a copy of the raw numerical results from the matching is saved to the *PolySNAP M* output folder within the current working directory in the file *correlations.txt*; other output is saved to the logfile. Various other output files are also created, which are described in Section 2.5.

## 2.3 Results Display

Once the analysis is complete, the display screen is loaded and results can then be examined in a variety of ways.



In general the display consists of a display area at the top, in which the style of view can be altered by selecting the different tabs running along the top of the window.

The bottom half of the results display is an area giving information on the currently selected sample file or files. This comprises relevant textual information relating to the selected pattern, and a graphical representation of the pattern profile. By default, the first pattern to be imported is displayed at first. Note that the pattern information display is by default common to all display modes.

Additional controls are available from the menus at the top of the screen.

### 2.3.1 Display Options Overview

The various display modes available from the tab bar are as follows:



The first four displays each provide separate and different assessments of the number and types of groups of patterns presented, calculated using the various different methods described below. As a result, the groups suggested in each display mode may not correspond to the groups suggested by another. It is the responsibility of the user to determine which of the separate methods is providing the best results. The more the results from different methods are

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internally self-consistent, the more confidence there is in the overall result.

### *Cell Display*

This screen displays the results of comparing the samples with any known phases provided, and any resulting quantitative analyses of mixtures. (If no known phases are present, the *Cell Display* shows the *Dendrogram*-plotted results in a different form - see Section 2.3.5.1 for more information.).

### *Dendrogram*

This screen displays the results of the cluster analysis of the patterns provided.

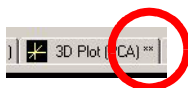
### *3D (MMDS)*

This screen shows the plotted results of performing metric multidimensional scaling upon the distance matrix.

### *3D (PCA)*

This screen shows the plotted results of performing principal component analysis upon the modified correlation matrix.

*N.B:* If either the 3D (MMDS) or 3D (PCA) have two stars next to their name, *e.g:*



then this informs the user which method of the two has produced markedly better results than the other for this particular run. If no stars are displayed, then the methods are producing relatively similar results, in terms of their reliability.

### *Numerical Results*

This tab displays the numerical values returned from the Match All process undertaken that compared each sample with every other sample.

### *View Logfile*

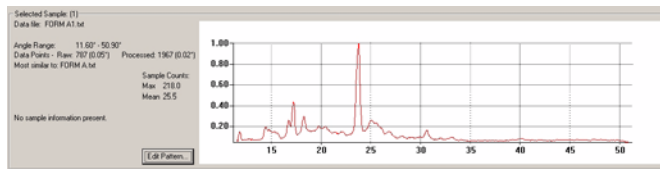
This tab displays all of the textual output written to the SNAPlog.txt file during the importing, processing and analysis undertaken by the program earlier. It is also updated automatically if the user manually overrides any of the PolySNAP M results.

Each of these options are described in detail later.



With the exception of the the *Logfile* pane, all of the displays above allow the selection of one or more sample data files; this is normally done by clicking once on the sample of interest, which will then become highlighted. Information regarding the selected sample will then be displayed in the Sample Information pane at the bottom left of the window.

### 2.3.2 Sample Information Pane



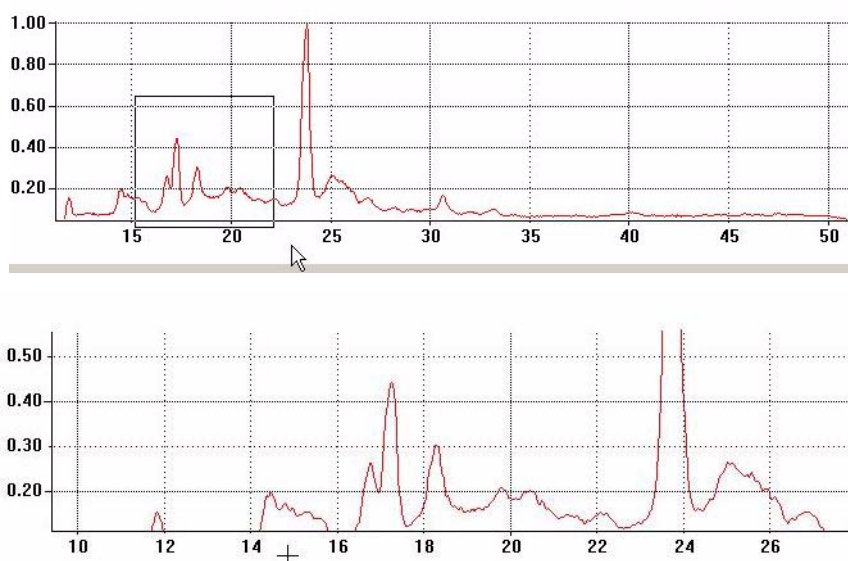
For a selected sample, the sample information pane displays relevant textual information on the left, and a graphical representation of the sample profile on the right. Although this information pane is always available by default, it is possible to hide it if more screen space is required to examine results in the graphical display areas of the window.

Selecting *Hide/Show Pattern Information* from the *Display* menu allows the information region to be hidden or shown as required.

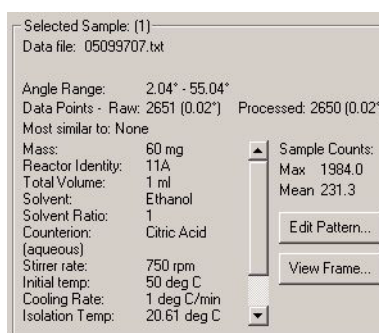


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The right-most region shows the current powder pattern profile; it can be zoomed in by using the mouse to drag a rectangle over the relevant area:



The graph pane is part of a larger area that shows information regarding the selected sample. To the left of the graph appears an area with text information associated with that sample:

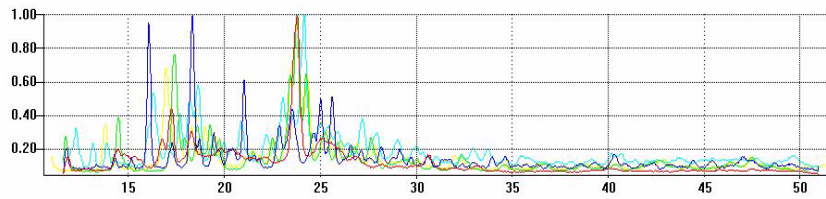


Typical information displayed includes the data file location, the angle range, the data points for the original raw data and once any processing has been performed, the known phase most similar to this pattern (if present), and finally other relevant information regarding the sample preparation, if saved in the data file headers.

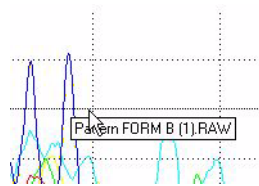
### 2.3.2.1 Multiple Selection

If more than one sample pattern has been selected in a given display screen, the pattern information pane displays a list of the patterns

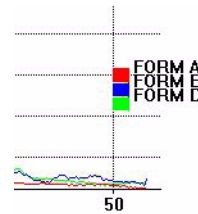
selected, and shows their profiles plotted on top of each other for easy comparison:



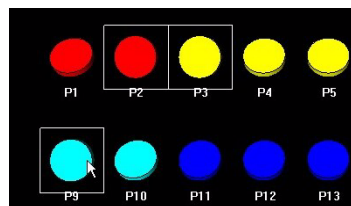
To identify which profile corresponds to which sample, hover the mouse over part of the line, until a tooltip appears containing the sample filename:



Alternatively, selecting the *Show Pattern Key on Graph* item in the *Display* menu brings up a visual colour-coded key:



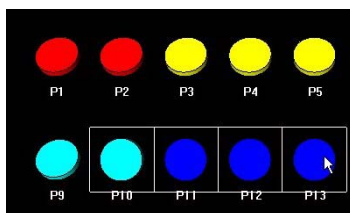
Multiple non-contiguous selection is achieved by clicking on multiple patterns with the *Control* key held down on the keyboard, for example:



Individual patterns can be de-selected in a similar manner, and their profiles will be removed from the graph.

---

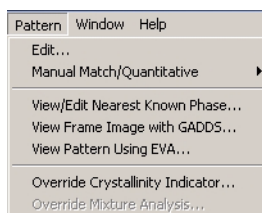
Alternatively, a continuous number of consecutively displayed patterns may be selected by holding the *Shift* key down and clicking on the first and then last pattern in the desired range, for example:



When multiple patterns are plotted, selecting *Toggle Mode* from the right-click menu displays all but the most recently selected pattern in the same colour, to allow easier comparison between one particular pattern and several others.

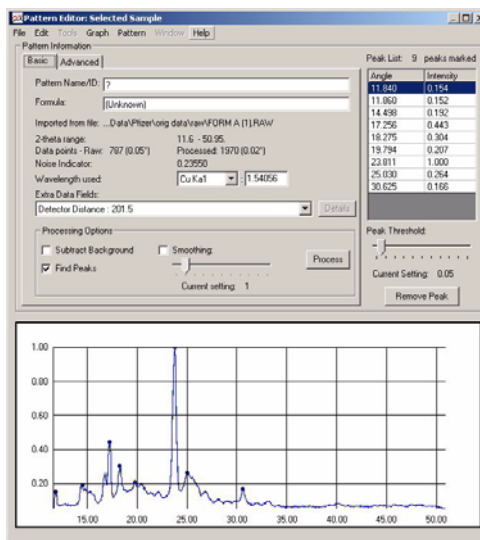
### 2.3.2.2 Additional Pattern Options

More options for examining and editing patterns and their assignments are available from the main program menubar. When an individual pattern is selected, the *Pattern* menu is available. It contains the following options:

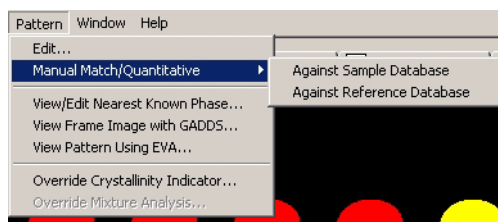


*Edit...*

Selecting this option, or clicking the *Edit Pattern* button causes the standard PolySNAP M pattern editor to appear with the current selected pattern loaded into it:



Refer section 3.3.1 on page 76 for full *Pattern Editor* description and functions.

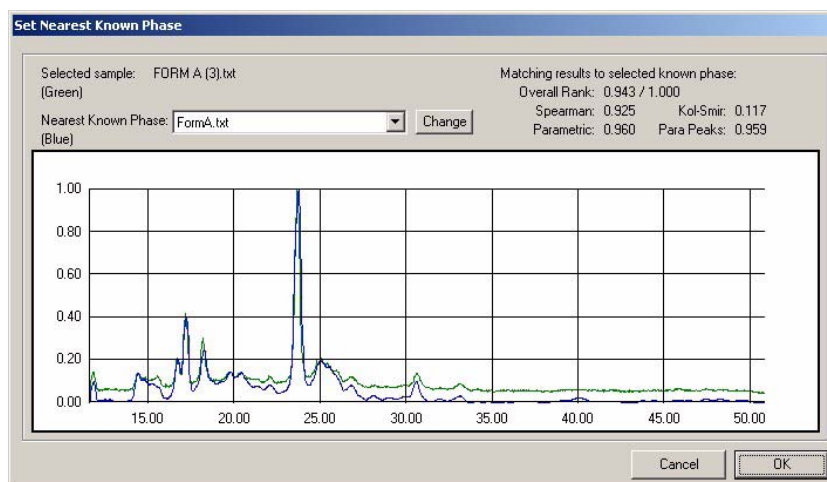
*Manual Match/Quantitative...*

This submenu has the options for matching the selected sample pattern to either the rest of the sample database, or the database of known phases (references), if present.

This opens a standard PolySNAP M Match window, allowing a manual comparison or analysis to be performed on the selected pattern. See section 3.4.1 on page 92 for more information on the Match window.

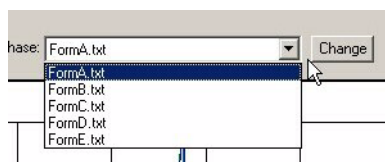
*View/Edit Nearest Known Phase...*

This option is only available if a comparison with a known-phase database was done during the analysis. If so, selecting a particular pattern and selecting this option brings up the following window:



The selected sample is plotted in green, and the known phase the program considers to be the best match to it is shown overlaid in blue. The actual matching statistics are displayed on the top right.

To see how well the sample compares to any of the other known phases provided, select the name of the phase from the pop-up list, and click *Change*:



The pattern overlay, and matching statistics, will update to represent the newly selected pattern.

To retain a changed assignment of a nearest known phase, click *OK*, and answer in the affirmative to the presented dialog box.

To keep the program-calculated nearest phase, click *Cancel*.

#### *View Frame Image...*

If the original GADDS frame file corresponding to the current pattern is available, and was saved in the same input data directory, clicking the *View Frame* button or selecting this menu item will open the Bruker GADDS software to display the frame image.

Note that this option requires both the GADDS software to be installed on the local computer, as well as a script file, *DisplayFrame.slm*, to be placed in the GADDS scripts directory. This should have been done by use of the option *Set GADDS...* in the

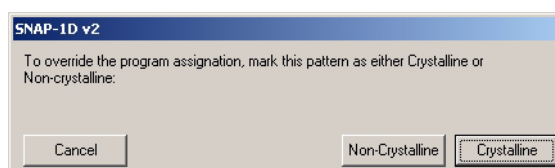
program options *Automatic: Advanced* tab, but if this menu item fails to work, check that this file is correctly placed.

#### *View Pattern Using EVA*

If the current pattern was imported from a RAW format file, this option allows it to be opened in the EVA software package for examination. Note that EVA must be set up as the default editing software for RAW files, and be installed on the local computer.

#### *Override Crystallinity Indicator...*

This brings up a dialog box allowing the user to manually override the program-calculated crystallinity marker setting:



The user can then choose to mark the currently selected pattern as either *Crystalline*, or *Non-crystalline*. (The criteria for what the program considers to constitute a non-crystalline phase were defined earlier in section 4.6 on page 144).

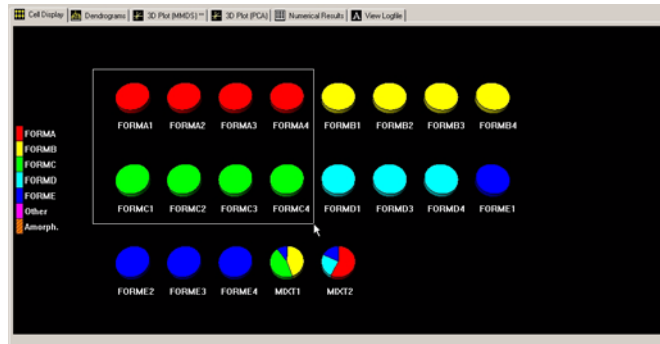
It may be useful to view a list of all samples from a current run that are marked as non-crystalline; this functionality is available from the *Tools* menu option *List Non-crystalline Patterns...* described in Section 2.3.15.1.

### **2.3.3 General Graphical Display Pane Options**

The various graphical display panes - the Cell Display, Dendrogram, Screen and two 3D plots - all share many similarities in their options and controls, and are hence initially described together here.

### 2.3.3.1 Display Controls Common to All Modes

To zoom in to a region of a graphical display, with the left mouse button held down, drag a rectangle over the region you wish to zoom:



The screen will then redraw with the contents of the rectangle filling the display area:



To move the contents of the display window, for example to move the contents up to see more results than will fit in the window by default, hold down the *Alt* key on the keyboard, and drag the mouse in the desired direction of movement.

### 2.3.3.2 Additional General Options of the Graphics Panes

Right clicking on the graphics pane causes the following menu to appear:





*Reset View* - This feature will return to the original view of the display if it has been moved or zoom has been activated.

*Zoom In* - Will zoom in on the centre area of the current display.

*Zoom Out* - Will zoom out from the centre of the current display.

*Toggle Mode* - This feature switches between viewing the patterns as Pie Charts or Stacks when in Cell Display mode, or between the full and simplified views of the Dendrogram in that mode.

*Centre Selection* - The currently selected item will be centred in the display.

*Deselect all* - Any patterns that have been highlighted in the display will be de-selected with this option.

*Show Toolbar* - The optional toolbar at the top of the graphics pane can be hidden or shown with this feature. The toolbar provides access to most of the options available through the right-click menu; for a full description see Section 2.3.3.3.

*Print* - The standard Windows print dialog box will appear, allowing the current graphics display region to be sent to a printer.

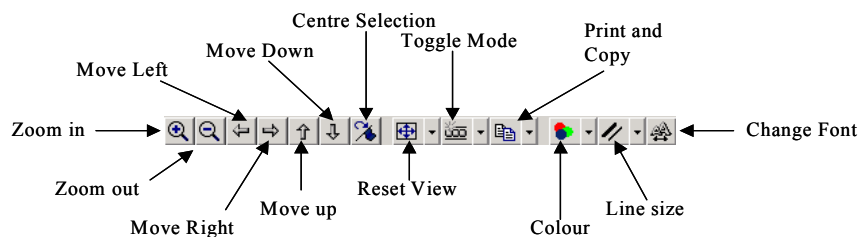
*Copy* - The whole of the current graphics display will be copied to the clipboard, and then can be pasted into any other standard Windows program - for example, *Microsoft Word*.

*Copy selection* - This option allows smaller specific regions of the graphic display to be copied. Click on *Copy Selection*, and then drag a rectangle over the area to be copied: This area only will now be copied to the clipboard, and can then be pasted in elsewhere as required.

Other mode-specific display options (e.g. *Show Grid/Show Labels/Show MRP Marks* are discussed under the relevant display section).

### 2.3.3.3 The Toolbar

The basic functions of the toolbar are illustrated below:



---

*Reset View* - This feature will return to the original view settings of the display.



Clicking on the small arrow next to the *Reset View* button allows access to the options for both *Reset View* and *Deselect All*.

*Zoom In* - Will zoom in on the centre area of the current display.

*Zoom Out* - Will zoom out from the centre of the current display.

*Toggle Mode* - This feature switches between viewing the results as Pie Charts or Stacks for Cell Display Mode.



Clicking on the small arrow next to the *Toggle Mode* button allows access to the options for use on graphics panes where there are a *Grid* or *Labels* displayed - these two options then allow them to be switched on or off as desired.

*Centre Selection* - The currently selected item will be centred in the display.

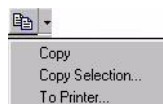
*Move Left* - The current display will move one unit to the left.

*Move Right* - The current display will move one unit to the right.

*Move Up* - The current display will move up one unit.

*Move Down* - the current display will move down one unit.

*Print* - The standard Windows print dialog box will appear, allowing the current graphics display region to be sent to a printer.



Clicking on the small arrow next to the *Print* button can be further used to access the *Copy* and *Copy Selection* options described above.

*Line size* - Clicking on the arrow next to the *Line Size* button opens a pull-down menu with a series of options for line size numbered 1 to 5, with 1 being the thinnest and 5 being the thickest. A dot appears next to the thickness currently selected. The line size options changes

the thickness of lines on the graphical displays which may be useful when preparing images for publication.

*Colour* - This option allows the colours of both the foreground and background to be altered to suit the user's requirements. Note that these will be reset on the next launch of PolySNAP M:

*Background:* The default colour is black, simply click on the down arrow next to the colour box and select *Background*:



This will now display the colour palette from which a colour can be chosen.



The colour selected here will then be applied to the background of the current view. Note that it may be useful to change the colour of the background to white before printing.

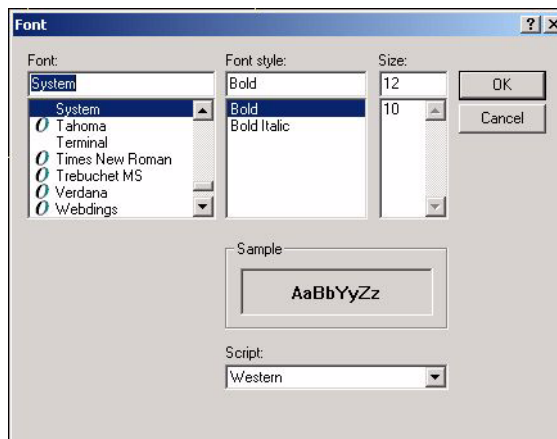
*Foreground:* The foreground selection is performed in the exact same way as the background, only this time selecting *Foreground* from the options presented:



The foreground option will alter the colour of the text or axes used in the current display.

---

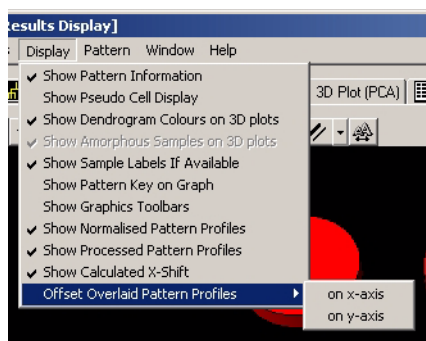
*Font* - Finally clicking on the *Font* button will open a standard font options dialog box:



This can be used to select the format of the text that will appear on axes labels, plot headers and pattern labels.

#### 2.3.3.4 The Display Menu

Further options to control the output screens are available from the *Display* menu:

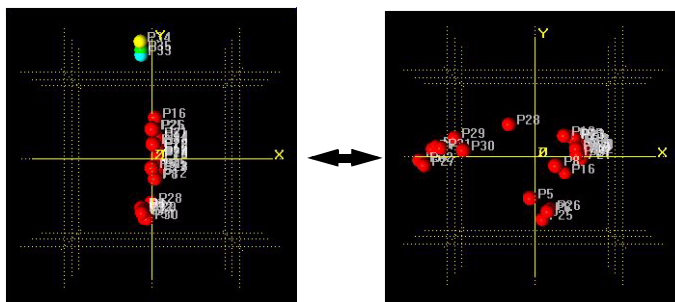


*Show Pattern Information*, *Show Pseudo Cell Display*, *Show Pattern Key on Graph* and *Show Dendrogram Colours on 3D plots* are discussed elsewhere.

#### *Show Amorphous Samples on 3D Plots*

This toggle determines if samples that are flagged by the program as being amorphous are shown or not on the standard 3D plots. It is only enabled when more than one pattern is labelled as amorphous. In

some cases, hiding such samples can make the plots appear quite different - this is often especially the case in the PCA plot.

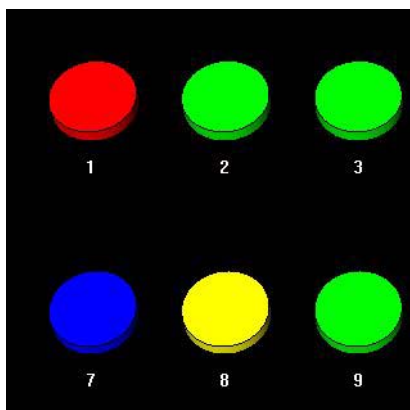


In the examples shown here the majority of the patterns are artificially 'flattened out' by the extreme distance between them and the amorphous; removing the amorphous allows for a better representation of the distances between the remaining patterns.

#### *Show Sample Labels if Available*

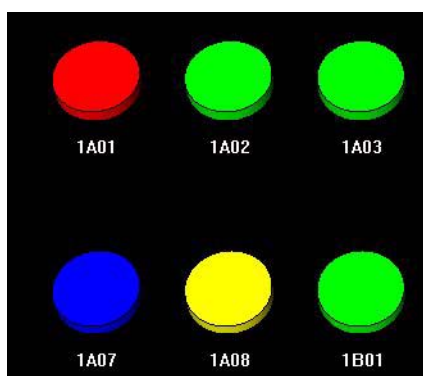
If the sample filenames are of the form where some form of sample ID is contained within the filename, then that information can be extracted and displayed to help identify the samples.

For example, with this option turned off, a typical display might resemble:



---

Whereas with the option turned on, the display would look like this:



The default for this toggle is on.

Note that all the files in a given dataset must have the same consistent format for Well IDs to be displayed. See the *Options and Defaults* section for details.

#### *Show Graphics Toolbars*

This toggles the toolbar displays which are available on some of the graphics panes. The setting is persistent for a given run, but may be overridden temporarily by means of the *Show Toolbar* option available in the right-click pop-up menu of most of the different displays.

#### *Show Normalised Pattern Profiles*

This option toggles the graph pane between displaying all profiles on a common intensity scale, where the maximum value is always 1.0, to displaying the profiles with their maximum intensities as recorded in the original data files. The default for this toggle is off.

#### *Show Processed Pattern Profiles*

This option toggles the graph pane between displaying all profiles with any processing - such as background subtraction or smoothing - or in their unprocessed original form. The default for this toggle is on.

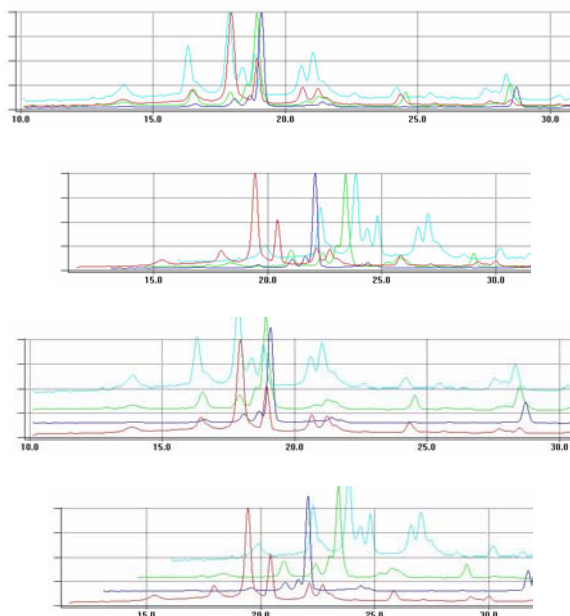
#### *Offset Overlaid Profiles -> on x-axis, on y-axis*

The two options in this submenu may be selected independently of one another. They control how patterns are displayed when more than one profile is shown on the graph pane at a time.

By default, overlaid profile traces are plotted directly on top of each other. By using these display toggles however, they may be plotted with a slight offset in either the x- or y-axes, or both. This may enable

differences or similarities between the patterns to be observed more clearly.

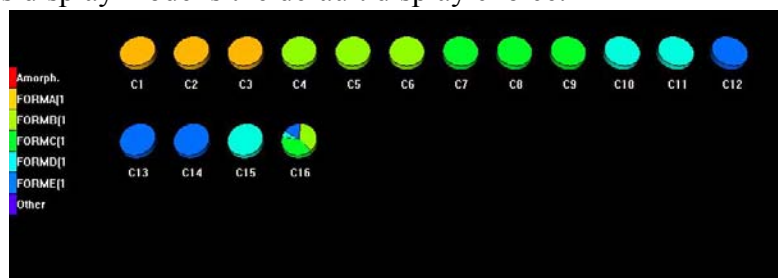
For example, the screenshots below show first, several directly overlaid patterns, then the same shifted in the x, and then in the y, and finally shifted with both options turned on:



*Note:* it is important to remember to check that the x-shift option is turned off when trying to see if the peak positions of two patterns coincide or not!

### 2.3.4 Cell Display

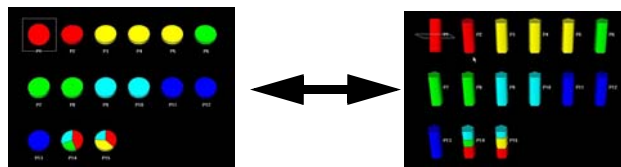
This display mode is the default display choice.



The Cell Display comprises of a pane in which the patterns loaded are each represented by an individual pie chart. Each pie chart is colour coordinated to group together similar patterns.

---

The cell display can be shown in either of two modes - as standard pie charts (the default), or as 'stacks':

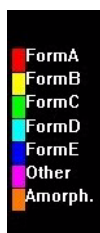


To switch between the two view modes, right-click on the display, and select *Toggle Mode* from the resulting menu.

Depending on the presence or absence of known phases for a given run, the colour-coding is obtained from two different sources.

*If known phases are available...*

When a database of known phases were provided to compare the new samples to, the 'key' on the left hand side of the display shows a list of those known phases, with the labels shown generated from the relevant pattern filenames:

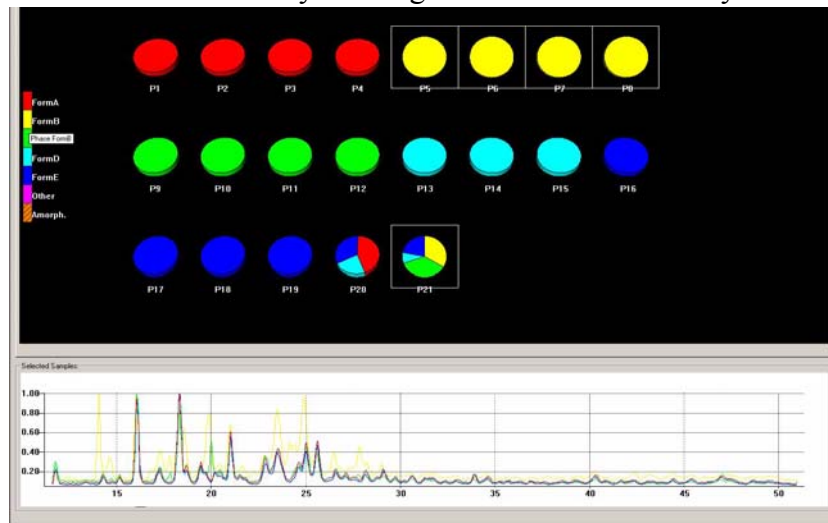


Each known phase has a unique colour assignment; and in addition colours are shown for patterns considered to be either non-crystalline/amorphous (*Amorph.*) or unlike any other known pattern provided (*Other*).

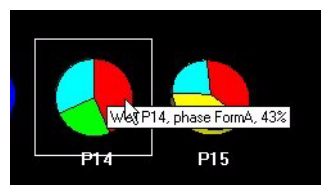
Each individual pattern that corresponds to a known phase (*i.e.* one that gave good matching statistics when being compared to a known phase) is given the same colour as that known phase - for example, in the screenshot above, the patterns that matched well to Form B are all



the same colour of yellow. All of the patterns that match to Form B can be selected at once by clicking on the colour in the key:

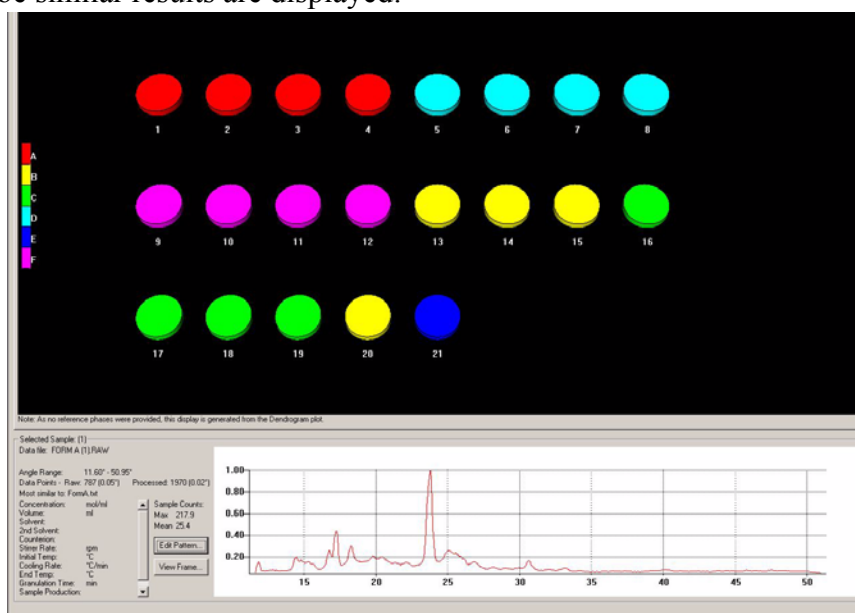


A pie that contains multiple colours (*e.g.* sample P21 above) represents a pattern which is thought to be a mixture of two or more of the known patterns, and the colours within the pie-chart again correspond to the phases thought to comprise it. Allowing the cursor to hover over a particular component of a mixture brings up a tooltip describing which phase and in what amount:



*If no known phases are available...*

On the other hand, if no known phases are available what *appear* to be similar results are displayed:



However, there are subtle and very important differences. The colour of the pies obviously no longer correspond to those of known phases, the colours are now merely representative of patterns which are similar to each other. In the example above Pies 1, 2, 3 and 4 are similar to each other as are 5, 6, 7 and 8. Pattern 21 is dissimilar to all the other samples, as it is a colour not shared by any other samples.

This information is generated from the cluster analysis results as presented in the dendrogram view (see the next section). As a result of this, a warning message is displayed that the results shown are no longer determined separately, but are merely clustering results presented differently:

Note: As no reference phases were provided, this display is generated from the Dendrogram plot, at cut-level 0.4601

Because clustering results are being used, the groups shown are entirely dependant on the cut-level used on the dendrogram display. The cut-level is discussed in more detail in Section 2.3.5.1, but it is important to note that when no known phases are present, altering the cut-level or otherwise editing the dendrogram display will cause the cell display colours to be altered and updated accordingly.

This display mode can also be accessed when known phases are present, by means of the *Show Pseudo Cell Display* option in the *Display* menu.

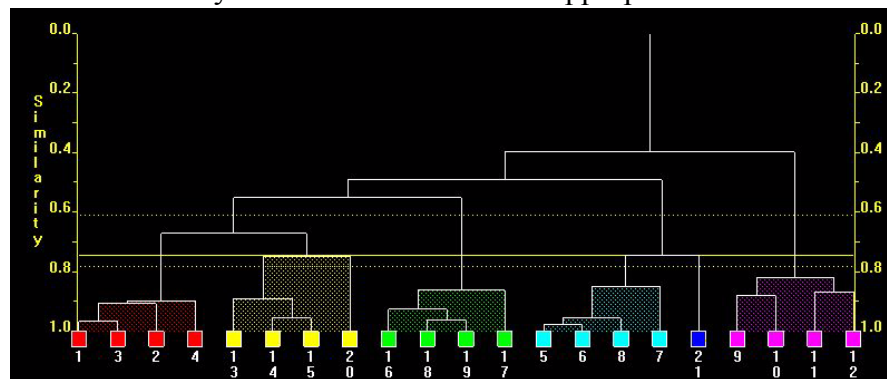
Note that once a particular well is selected, the wells on either side can be selected in turn by means of the left and right arrow keys, thus allowing for quickly scanning through multiple patterns.

### 2.3.5 The Dendrogram

The dendrogram display can be accessed by clicking on the Dendrogram tab along the top of the display window.

The dendrogram provides a visual means to display the results of the hierarchical method of data classification using cluster analysis. The dendrogram itself takes the form of a tree-diagram in which each single terminal branch is representative of a single object (in this case an individual pattern from the data input).

The initial cut point is set by the program, and is shown by the yellow horizontal line. Upper and lower confidence limits on this cut-level are shown with yellow dotted lines where appropriate.



Each pattern is numbered along the bottom axis of the dendrogram. Each number is the same as in the other displays - for example, number 1 on the dendrogram is the same pattern as number 1 in the cell display.

Each pattern can be selected by clicking on the box above its number. When a pattern is selected, the sample information along with its pattern profile is displayed in the bottom half of the display window. Multiple patterns can be selected by holding down the *Control* key and clicking on different patterns.

Note that once a particular pattern is selected, the patterns on either side can be selected in turn by means of the left and right arrow keys, thus allowing for quickly scanning through multiple patterns.

The view of the dendrogram can be zoomed in on by dragging a rectangle over the relevant area with the left-hand mouse button down as with the graph and cell displays.

---

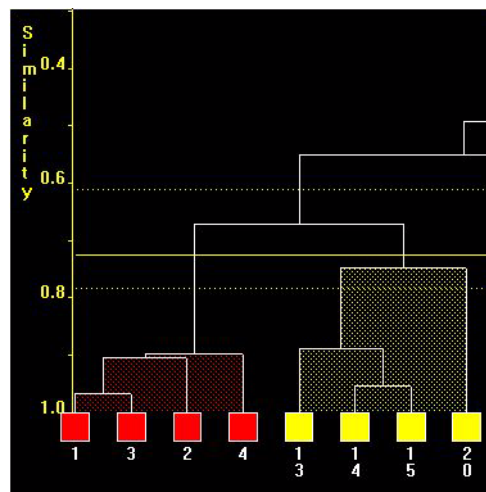
The position of the dendrogram position on the horizontal axis can be altered by holding down the *Alt* key and moving the mouse left or right. This can be useful if the zoom has been used and the whole tree no longer fits on the screen at one time.

Patterns are joined together by a series of lines. The further up the similarity axis (y-axis) the patterns are joined, the less similar they are. Therefore, in the screenshot above, patterns 1 and 3 are joined at a high level of similarity (nearly 1.0), and are therefore very similar, whereas patterns 1 and 12 are not joined until a similarity of less than 0.4, indicating a large difference between them.

Given the calculated similarity between patterns, it is then possible to categorise similar patterns as belonging to the same cluster. This is done by drawing a horizontal line across the display at a given similarity level - this is called the cut-level.

The optimum cut-level is determined by PolySNAP M using a combination of several different techniques in order to determine the number of clusters that statistically best represents the data given. These techniques include principle component analysis, metric multidimensional scaling, the C-H test, gamma statistics, *etc.*

The cut-level is then drawn on the dendrogram, and different patterns which are grouped together below this line are considered to be similar enough to be thought of as being in the same cluster:



In the screenshot above, the horizontal cut-point is set at around 0.72, and is therefore considering patterns 1, 3, 2 and 4 to be in one cluster, whereas 13,14, 15 and 20 are in a separate and distinct one.

The different clusters are colour coded, and if no known phases are present, these dendrogram results are used to generate a pseudo-cell display (see Section 2.3.4). In this case the colours used here will correspond to the colours in that display. Optionally, the same colour-

coding can be used to help interpret the results in the various 3D plots.

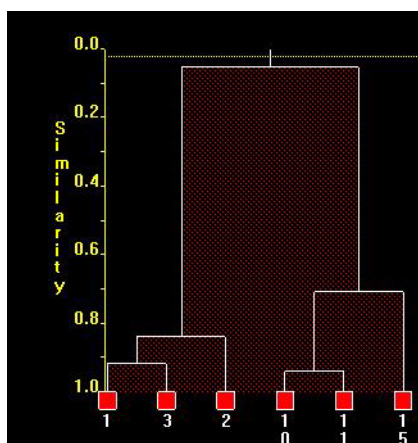
The *Toggle Mode* option, accessed through the right-click menu, redraws the dendrogram with only the first, last and middle patterns of each cluster shown. This allows easier interpretation of a crowded display when many patterns are being analysed. Note that while showing the simplified dendrogram, the cut-level and other modifications cannot be made. A label is displayed on the top-left of the display to indicate that the display is in simplified mode.

It is possible to toggle the showing of the axes on and off using the *Show Axes* option, accessed through the right-click menu.

### 2.3.5.1 Modifying the Dendrogram

#### -Changing the Cut-level

If the program-calculated cut-level is not considered to be correct, it can be overridden by the user. This is done by holding down the *Shift* key and left mouse button, while dragging the mouse up or down. The cut-line on the dendrogram display will move, and the cluster colouring will update in real time. For example, moving the cut-level up to around 0.1 results in the following:



Note that the colour assignments have updated accordingly. If the user chooses to retain this change when closing the dendrogram display or switching to another display pane, then the pseudo-cell display will be updated accordingly, and the modification noted in the program logfile. If the change is not retained, the previous value is kept.

[In addition to this method, if a mouse with a scroll wheel is used, it is possible to just click once in the display area with the left mouse

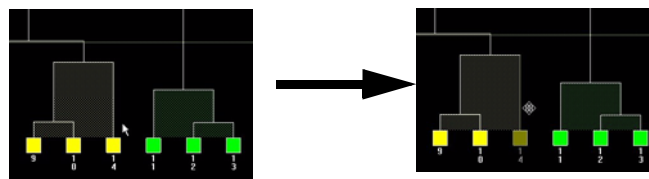
---

button, and then move the mouse wheel up or down to move the cut-level indicator.]

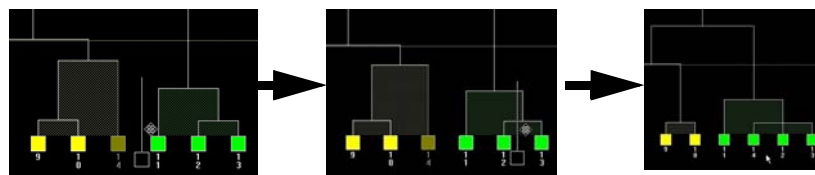
-Manually changing the contents of clusters

PolySNAP M makes its assignment of the contents of clusters using a combination of powerful statistical techniques. It should not normally be necessary to override its results, but for the occasions when this is necessary, it is possible to reassign either a single pattern or group of patterns manually.

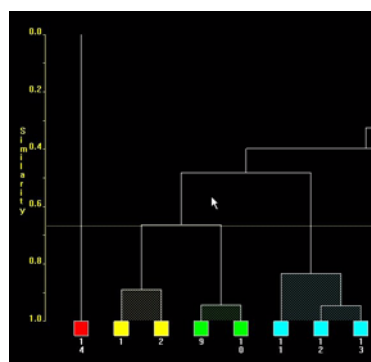
To do this, hold down the *Shift* key and click and hold down on the vertical line attached to the pattern or sub-cluster required to be moved:



Continuing to hold both the *Shift* key and mouse button, drag the unit to the desired location. To add it to an existing cluster, release the mouse when the cursor is over the area the sample is to be added to:



To create an entirely new, separate cluster, drag it to an empty space between existing clusters:



To cancel a drag operation part-way through, it is only necessary to release the *Shift* key.

A one-step *Undo* is available for this method of altering the dendrogram, if for example a user changes their mind, or a cluster is incorrectly joined. To do this, right click on the dendrogram, and

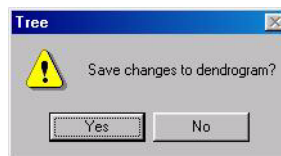
select *Undo* from the pop-up menu. Note that only the most recent operation can be undone.

The only way to be able to undo multiple operations is to choose not to save the changes to the dendrogram when closing or switching the window; that way the original dendrogram will be retained and shown the next time the results are examined.

When changes to the dendrogram are saved, the changes and the resulting new clusters and corresponding component patterns are listed in the program logfile.

### 2.3.5.2 Saving and Reverting Changes

When another tab is clicked on after the dendrogram has been altered in one of the ways described above, the following message is displayed:



Selecting *No* will cause any changes to be discarded, and the previous version of the dendrogram, prior to any manual changes, will be retained.

Selecting *Yes* causes the changes made to the dendrogram to be kept, and also be recorded in the program logfile. Changes to the dendrogram can also be saved at any point using the *Save Modified Tree* option in the right-click menu.

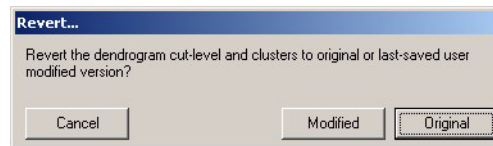
#### *Reverting to a previous dendrogram:*

Because the program retains earlier saved versions of the dendrogram, it is possible to revert to them if required at a later stage. This function is accessed through the *Tools* menu option *Undo dendrogram modifications...* Selecting this option brings up the following dialog box.

If more than one set of changes to the dendrogram have been saved, the user is offered the choice between the original, program

---

generated tree, and the most-recently saved previously modified version of the dendrogram:



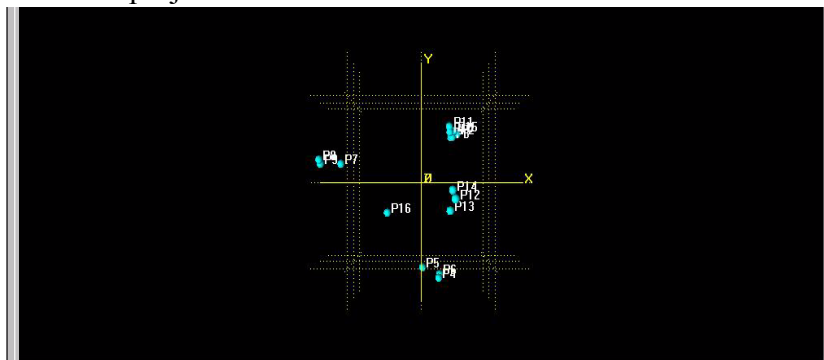
Selecting *Cancel* retains the current version with no changes. Selecting *Original* reverts to the original version. Selecting *Modified* causes the current, modified dendrogram to be replaced with the most recently modified saved changes.

### 2.3.6 3D Plot (MMDS)

This option displays the results of metric multidimensional scaling which make use of distances between objects calculated from the correlation matrix generated by the matching process to produce a three-dimensional spatial representation of the samples. Each point which appears on this spatial representation corresponds to one of the patterns. The closer two points appear on the plot, the more similar the patterns are, and the more different an object is to another the further apart they will appear. Therefore groups of similar patterns appear to cluster together.

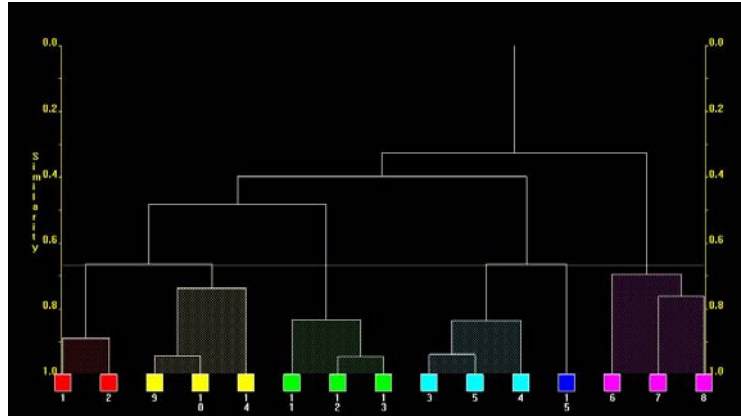
The multidimensional scaling performed is based on calculated proximities rather than observations. First for  $n$  patterns, we generate an  $(n \times n)$  distance matrix  $D$  based on dissimilarities,  $\delta_{rs} = 1, 2, \dots, n$ , computed from the correlation matrix. Each object is compared against itself and every other object. The result of an object being paired against itself gives a dissimilarity of zero, which corresponds to the diagonal of the matrix. The goal of this method is to derive a set of underlying dimensions, with co-ordinates that should create a Euclidean distance matrix, which in turn should be the same or very close to the  $\delta_{rs}$  of the original  $D$ .

The initial view of the 3D plot shows only the X and Y axis - the Z axis lies in projection.

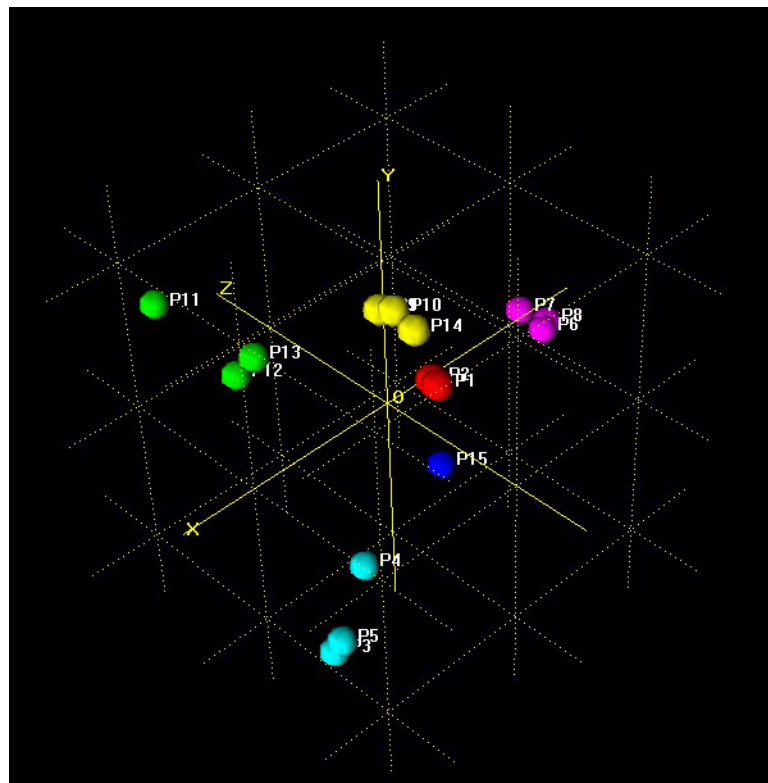




In the *Display* menu, the option *Use Dendrogram Colours on 3D Plots* is available. When this item is selected, a check mark appears next to it in the menu, and the individual points plotted on either of the 3D plots are coloured to correspond to the colour groupings shown in the Dendrogram plot - e.g. if samples 11, 12 and 13 are all in the same cluster according to the dendrogram, they will all be the same colour - green:



In the 3D plot, they will all still be coloured similarly:



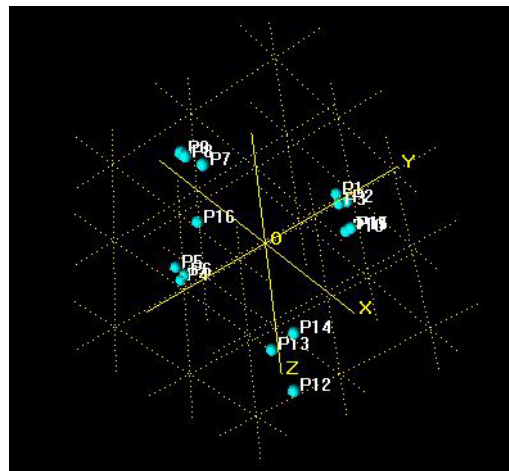
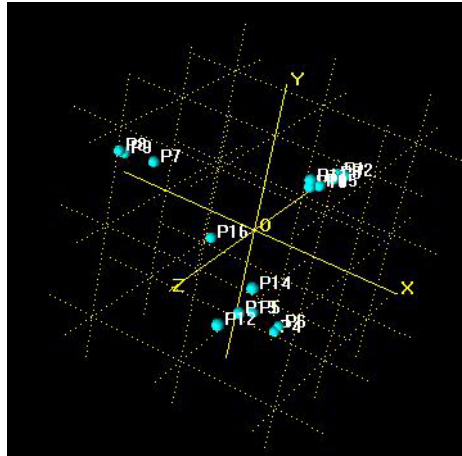
Changing the dendrogram cut-level causes the colours in the 3D plots to be updated.. A small numerical label in the top-left corner of the display gives an indication as to the goodness of fit of these results. Numbers close to 1.0 suggest that it is a good fit, and low numbers

---

suggest that caution may be required, or that the program had trouble adequately partitioning the data.

Note that as the number of samples increases, the average GOF score will decrease.

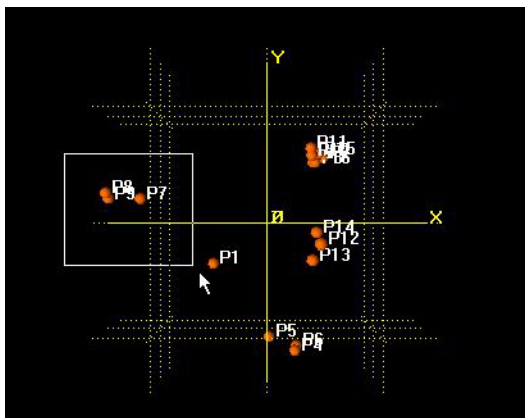
The orientation of the 3D plot can be altered by holding down the *Shift* key and dragging the mouse in any direction as desired; the plot rotates as shown below:



In the above plots it can be seen that there are 4 or 5 clusters depending on P16 and whether it can be considered to belong to an adjacent cluster or not.

A variety of views can be achieved to gain a better understanding of the distribution of the pattern data points in the three-dimensional space.

As in the other graphics screens, any particular area of the 3D view can be zoomed in by dragging a rectangle over the relevant region:

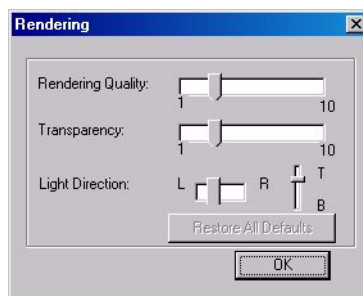


The powder pattern corresponding to each display point can be selected by clicking on it, this in turn updates the pattern information display in the lower portion of the window.

The points representing the patterns can be enlarged or shrunk to suit any zoom level by holding down the *Ctrl* key and moving the mouse either up or down. An upward movement will reduce the size of the spheres, a downward movement will increase the size.

The 3D plot position itself can be translated by holding down the *Alt* key and then moving the mouse in any direction as required.

The drawing quality of the spheres can be altered if needed - with many points plotted, working with the display can be much faster if the rendering quality is reduced (this is especially the case with lower-powered graphics cards). To do this, with the 3D display visible, press the *F2* button on the keyboard:

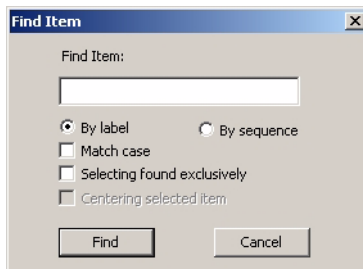


Moving the slider causes the drawing of the spheres to update in real time, so the effects of a particular setting can be easily seen. The chosen quality setting is saved and used from that point on. The higher quality settings can be useful when preparing screenshots for use in reports or for publication.

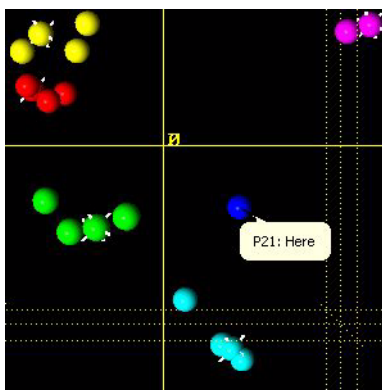
---

Further options can be accessed by right clicking on the display area to show the standard pop-up menu. Options relevant to the 3D plot include:

*Find Item...*



This brings up a dialog box allowing a particular pattern of interest to be located on the display by means of its index number, or label as appropriate.

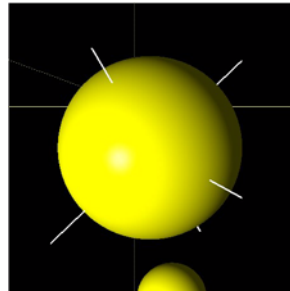


Additional options allow the pattern to become automatically selected when found - thus updating the pattern information display, and optionally centred in the display. This is useful when dealing with large numbers of patterns, as locating an individual pattern of interest on a crowded plot can be difficult.

*Show Grid* - the grid which appears in the 3D plot can be hidden or displayed.

*Show Labels* - the labels which appear next to the plotted points can be turned on or off with this option. This may aid in seeing an overall clustering pattern when the display is crowded with many points.

*Show MRM Marks* - the Most Representative Member in each cluster can be highlighted if required with this option. It appears on the display as a normal pattern with several 'spikes' coming out of it:



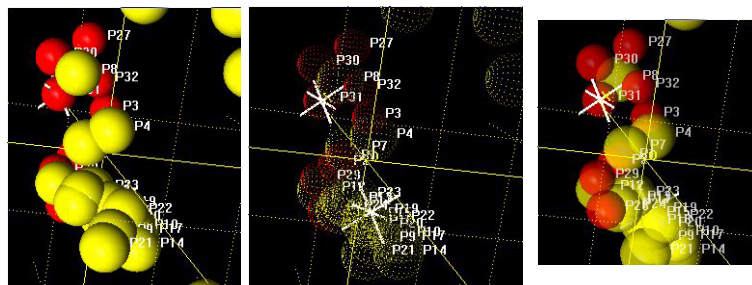
These spikes can be hidden or shown by means of this menu option. Clicking on an MRM sphere brings up a dialog box containing information about the mean pattern-pattern distance for that particular cluster. The smaller the distance, the tighter the cluster.



*Show Top View* - this option brings up a small simplified overview of the plot in the lower right hand corner. It can be useful for orientating yourself when zoomed into the display:



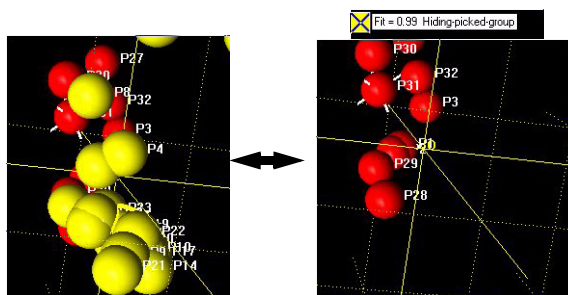
*Render as Dots* and *Transparent* alter the way the spheres are plotted as shown in the diagrams below. This can be useful to identify if for example, a single pattern of one colour is hidden within a group of another patterns:



*Mask Group*

---

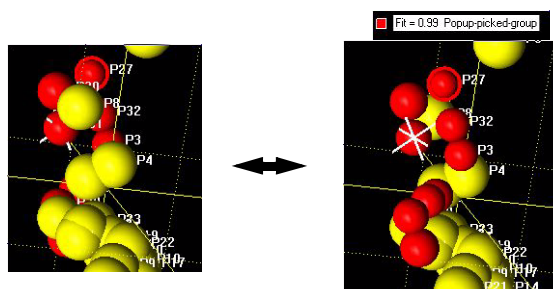
This option is useful in a crowded display with lots of different clusters overlapping each other - select the *Mask Group* option, and the next cluster you click on is temporarily removed from the display. A key in the top left corner shows the colour of the hidden cluster. To restore the cluster, deselect the option from the menu. Alternatively, click on a different colour, and that will be hidden instead. Only one cluster at a time can be hidden.



With the *Mask Group* option selected, pressing the spacebar toggles between hiding the selecting group and showing everything else, and hiding everything else and showing just the selected group. The left and right arrow keys can also be used at this point to cycle through and have each group selected in turn.

#### *Popup Group*

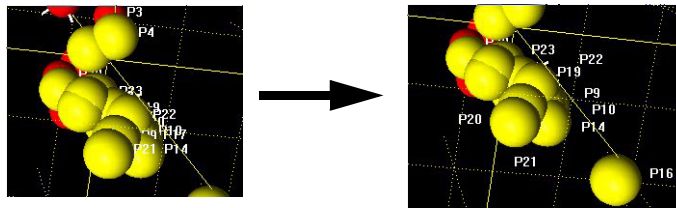
This option can be used to bring the whole of a particular coloured cluster to the front of the display, so it can all be seen at one time. A key in the upper left shows the colour of the selected group. Deselecting this option returns the display to normal.



#### *Drag Labels*

With this option toggled on, the display is fixed and cannot be rotated or zoomed. Therefore, it is necessary to use the normal zooming and rotation controls to select a suitable view angle before selecting this option. Once selected, all of the pattern labels on the display can be moved individually by clicking on them and dragging to the required

new location. This allows for neater diagrams to be created when required for a report.



### 2.3.7 3D Plot (PCA)

The plot drawn here is based on the results from principle component analysis of the modified correlation matrix. The use and interaction options available for this plot are identical to those for the 3D Plot (MMDS) described in Section 2.3.6.

### 2.3.8 Numerical Results

This pane is used to display the pattern correlation matrix. If there are a large number of patterns then the entire matrix may not fit within the display, and scroll bars will be displayed along the side and bottom of the table.

Row\Col	FORM A1 ne	FORM A2 ne	FORM A3 ne	FORM A4 ne	FORM B1 ne	FORM B2 ne	FORM B3 ne	FORM B4 ne	FORM C1 ne	FORM C2 ne	FORM C3 ne	FORM C4 ne	FORM D1 ne	FORM D2 ne	FORM D3 ne	FORM D4 ne	FORM E1 ne	FORM E2 ne	FORM E3 ne	FORM E4 ne	MCCT 1 ne	MCCT 2 ne	
FORM A1 ne	1	0.0903	0.1903	0.0824	0.4519	0.4428	0.6234	0.4871	0.3803														
FORM A2 ne	0.0903	1	0.3103	0.0958	0.4824	0.4563	0.5688	0.4853	0.381														
FORM A3 ne	0.1903	0.3103	1	0.3094	0.4422	0.5929	0.4844	0.3411															
FORM A4 ne	0.0824	0.0958	0.3094	1	0.4414	0.413	0.5346	0.4563	0.3795														
FORM B1 ne	0.4519	0.4824	0.4422	0.4414	1	0.9752	0.9931	0.9513	0.9272														
FORM B2 ne	0.4428	0.4563	0.4422	0.413	0.9752	1	0.9425	0.9594	0.9266														
FORM B3 ne	0.6234	0.6234	0.5622	0.5346	0.9931	0.9425	1	0.938	0.9602														
FORM B4 ne	0.4871	0.4853	0.4844	0.4563	0.9513	0.9594	0.938	1	0.9266														
FORM C1 ne	0.3803	0.381	0.3411	0.3795	0.9272	0.9266	0.9602	0.9266	1														
FORM C2 ne	0.417	0.4507	0.409	0.4102	0.9241	0.9292	0.4409	0.9215	0.9267														
FORM C3 ne	0.4826	0.4224	0.4676	0.5626	0.9222	0.9299	0.9224	0.9295	0.9602														
FORM C4 ne	0.3749	0.3863	0.3959	0.3712	0.9292	0.9262	0.4631	0.438	0.9297														
FORM D1 ne	0.6463	0.5872	0.6161	0.5222	0.9292	0.9483	0.9802	0.9632	0.4119														
FORM D2 ne	0.7962	0.6962	0.7091	0.7622	0.4929	0.9272	0.9696	0.4209	0.9892														
FORM D3 ne	0.7422	0.6441	0.7344	0.6595	0.3843	0.9262	0.4909	0.3874	0.9662														
FORM D4 ne	0.5418	0.4749	0.5959	0.4961	0.5003	0.4752	0.5631	0.4822	0.9297														
FORM E1 ne	0.4269	0.3807	0.4624	0.4622	0.3809	0.9266	0.4616	0.3844	0.9496														
FORM E2 ne	0.6274	0.5071	0.6032	0.4449	0.9262	0.9299	0.9262	0.9291	0.9292														
FORM E3 ne	0.6271	0.6172	0.6491	0.6772	0.5461	0.5254	0.6815	0.5412	0.9212														
MCCT 1 ne	0.9596	0.6075	0.969	0.963	0.7626	0.7421	0.946	0.7642	0.6312														
MCCT 2 ne	0.6379	0.6498	0.6279	0.5826	0.9297	0.9842	0.4113	0.3827	0.9096														

If the program was run with the *Allow Offsets* option turned on, an additional file, *correlations\_offsets.txt* will also be created in the output folder. The results from it can be seen by selecting a particular cell, and then allowing the mouse to hover over that cell for a second, until a 'tool-tip' appears. This contains two numbers in the form  $(a_0, a_1)$ , where  $a_0$  is the amount of linear offset applied, and  $a_1$  the amount of non-linear offset applied.

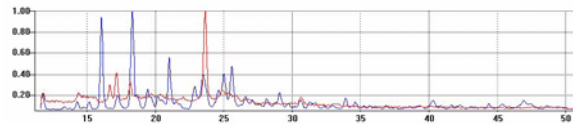
A diagonal line of 1 should be present to show the result of each pattern matched against itself. Clicking on the 1 for each pattern will produce the profile and information for that pattern in the relevant area below.

---

For comparison purposes two patterns can be overlaid on each other by clicking on a number above or below the line of *I*.

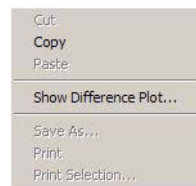
Rank:	FORM A (2)	FORM A (3)	FORM A (4)	FORM B (2)	FORM B (3)
FORM A (2)	1	0.8592	0.9038	0.3387	0.4366
FORM A (3)	0.8592	1	0.8885	0.3184	0.4531
FORM A (4)	0.9038	0.8885	1	0.2914	0.4855
FORM B (2)	0.3387	0.3184	0.2914	1	0.8482
FORM B (3)	0.4366	0.4531	0.4855	0.8482	1

For example if 0.2914 is clicked on as highlighted above, the graph of FORM A (4) and FORM B (2) will be displayed, one overlaid on the other in the graph pane:



This allows a visual comparison to help decide if the matching results displayed are sensible or not.

Right clicking on the matrix of results will produce the following options:

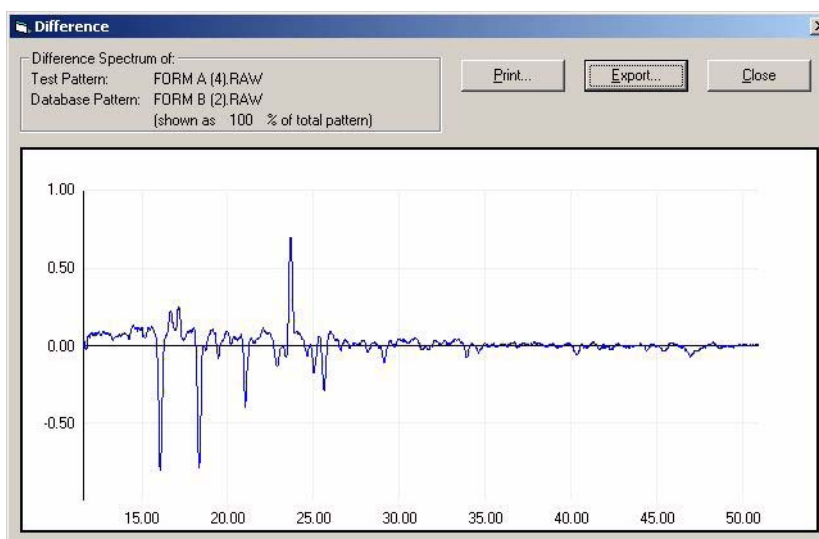


Clicking on *Copy* (or alternatively selecting *Copy* from the *Edit* menu) will copy the contents of any selected cells to the clipboard. To copy only part or all of the results, drag a rectangle over the desired numbers, a blue highlight region will appear indicating the numbers selected. Now right click to produce the options and click on *Copy*.

Note that the numbers in this window are not editable in any way.



The *Show Difference Plot...* option brings up a new window with a plot showing the difference trace between the two currently selected patterns, for example:



### 2.3.9 View Logfile

The results of the file import, processing, pattern matching, clustering *etc.*, and any subsequent changes to the results are written to a file in the output folder named *SNAPlog.txt*. It is the contents of this file which are displayed in the View Logfile Pane:

```

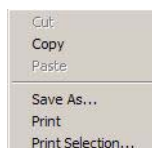
Cell Display | Dendrogram | 3D Plot (MMG) | 3D Plot (PCA) | Numerical Results | View Logfile
SNAP-ID v2 Auto-mode run started at 20/11/2005 16:03:51
Started by user 'sbey' on computer 'FITZG0' in domain 'WORKGROUP'
Data loaded from 'C:\tutorial\vsnapie.txt'
SNAP-ID v2 working & output directory: 'C:\temp'
Known phases data directory: 'c:\tutorial\vsnapie.txt\Known'

Looking for known phase data...
Files will be added to database 'C:\temp\KnownPhaseDB.par'
Known phase file FORM A.txt was successfully imported.
Known phase file FORM B.txt was successfully imported.
Known phase file FORM C.txt was successfully imported.
Known phase file FORM D.txt was successfully imported.
Known phase file FORM E.txt was successfully imported.
Looking for new data files to import.
Files will be added to database 'C:\temp\Run 11-30-2005.par'
Data will be processed as follows:
Automatic peak picking applied, using minimum peak threshold 0.05
Pattern FORM A1.txt loaded successfully at 20/11/2005 16:03:52
Pattern FORM A2.txt loaded successfully at 20/11/2005 16:03:52
Pattern FORM A3.txt loaded successfully at 20/11/2005 16:03:52
Pattern FORM A4.txt loaded successfully at 20/11/2005 16:03:52
Pattern FORM B1.txt loaded successfully at 20/11/2005 16:03:53
Pattern FORM B2.txt loaded successfully at 20/11/2005 16:03:53
Pattern FORM B3.txt loaded successfully at 20/11/2005 16:03:53
Pattern FORM B4.txt loaded successfully at 20/11/2005 16:03:54
Pattern FORM C1.txt loaded successfully at 20/11/2005 16:03:54
Pattern FORM C2.txt loaded successfully at 20/11/2005 16:03:54
Pattern FORM C3.txt loaded successfully at 20/11/2005 16:03:54
Pattern FORM C4.txt loaded successfully at 20/11/2005 16:03:54
Pattern FORM D1.txt loaded successfully at 20/11/2005 16:03:56
Pattern FORM D2.txt loaded successfully at 20/11/2005 16:03:56
Pattern FORM D3.txt loaded successfully at 20/11/2005 16:03:56
Pattern FORM D4.txt loaded successfully at 20/11/2005 16:03:56
Pattern FORM E1.txt loaded successfully at 20/11/2005 16:03:57
Pattern FORM E4.txt loaded successfully at 20/11/2005 16:03:59
Pattern M1T1.txt loaded successfully at 20/11/2005 16:03:58
Database M1T1.txt loaded successfully at 20/11/2005 16:03:58

```

A scroll bar appears on the right hand side of the pane to allow the user to view all of the text, as the output is normally quite long.

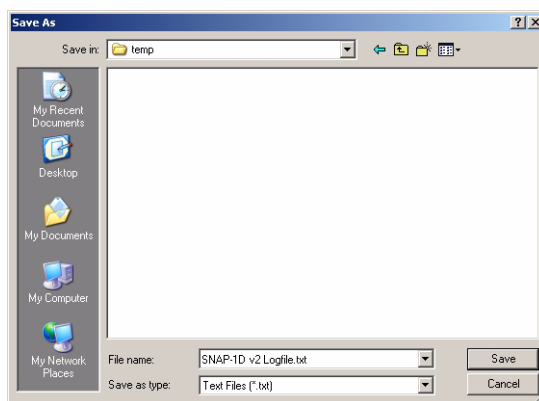
The text can be copied to the clipboard and pasted to other applications by selecting the relevant text to highlight it and then right-clicking in the text pane:



---

Click on *Copy* to copy the text (alternatively choose the *Edit* menu and click on *Copy*). Note that the *Cut* and *Paste* options are unavailable, as the logfile cannot be edited manually.

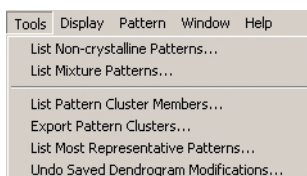
The *Save As...* option causes a standard file saving dialog box to appear



This allows a copy of the current logfile to be saved to a new file. Select the desired location for the file, edit the filename if required. The format for saving is an ASCII text file (\*.txt)

The *Print...* option brings up the standard Windows print dialog box, allowing the current selection of the logfile output to be printed.

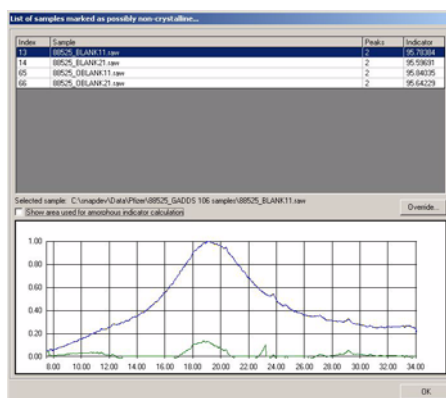
### 2.3.10 Other Display Tools



#### 2.3.10.1 List Non-crystalline Patterns...

This option, accessed through the *Tools* menu, allows the user to examine a list of any patterns that the program has marked as being possibly non-crystalline when it has examined them.

Selecting it brings up a display window:



The upper region is a grid showing the pattern names, number of peaks, and approximate percentage amorphous content. The larger this value, the more likely the pattern is to have an amorphous content.

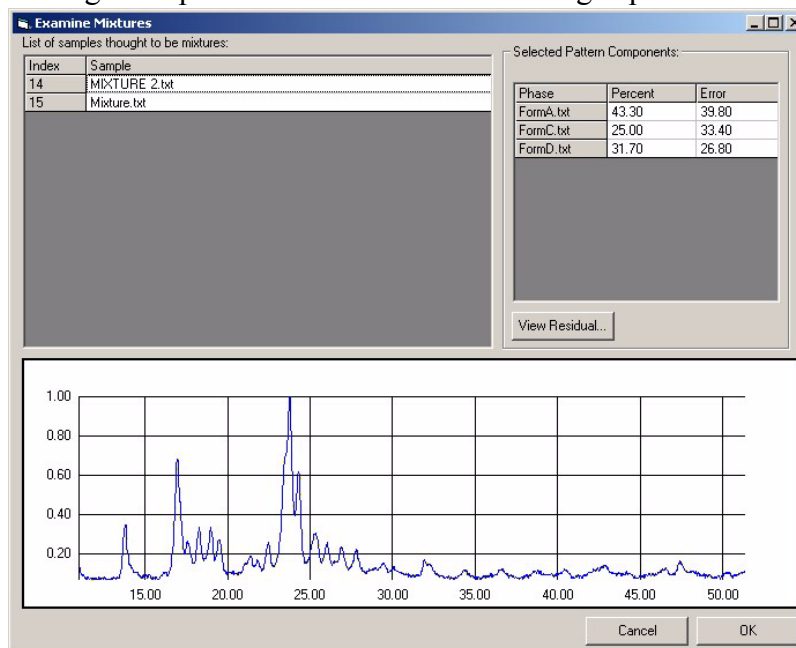
Selecting a pattern in the list (by clicking on it once) updates the profile display in the lower region of the window to show what the pattern profile actually looks like. If the *Show area used for amorphous indicator calculation* checkbox is selected, then a second, green trace shows the rough profile that would be left if the program subtracted out everything it thought was amorphous from the pattern.

If the user considers that the program has made an error in marking a particular pattern as non-crystalline, they may override this by clicking the *Unmark* button on the lower left. This action is recorded in the program logfile.

It is also possible to do the opposite, and mark a pattern as amorphous; for information on how to do this, see Section 2.3.2.2.

### 2.3.10.2 List Mixture Patterns...

Selecting this option from the *Tools* menu brings up a new window:



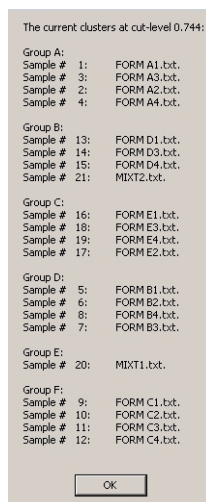
This consists of an upper region listing all of the patterns marked as mixtures, and a lower graph-pane region. Selecting a particular pattern from the list causes it to be displayed in the graph pane, and a list of which known phases are thought to make it up are listed in the display area. Clicking the *Residual* button opens a PolySNAP M window to allow comparison of a simulated pattern created from the suggested phase components, and the original sample.

*N.B.* this option is only available when powder patterns for known phases were provided.

### 2.3.10.3 List Pattern Cluster Members...

This option is available only when the dendrogram is being displayed, and generates a list of the current members of each cluster suggested by the cluster analysis, according to the current saved dendrogram cut-level.

If the list of cluster members is short enough, it is displayed as a message box, which can then be dismissed:



If the list of members is too long for a standard message box, it is automatically added to the end of the program logfile, from where it can be copied into a report or other program as required.

#### 2.3.10.4 *Export Pattern Clusters...*

This option brings up a dialog box allowing the list of pattern clusters to be saved to a text file for use elsewhere.

#### 2.3.10.5 *List Most Representative Patterns...*

This option is only available when either the MMDS or PCA plots are being displayed. Note that the calculation of MRPs is specific to the type of plot displayed, so different results may be obtained from each of the two methods. Different results will also be obtained if the dendrogram cut-level is adjusted manually.

A list of the pattern indexes and filenames for the most representative patterns in each cluster to have 3 or more members is shown in a dialog box on the screen. A copy of the list is also automatically added to the logfile when this option is selected.

---

## 2.4 Other Menu Items

*Close Window* in the *File* menu closes the automatic analysis results window. The user will be asked if they wish to retain any unsaved changes to either the dendrogram.

The *Edit* menu, in addition to giving access to the standard text editing controls (*Cut, Copy, Paste, etc.*) also allows access to the program defaults and preferences through the *Options* item.

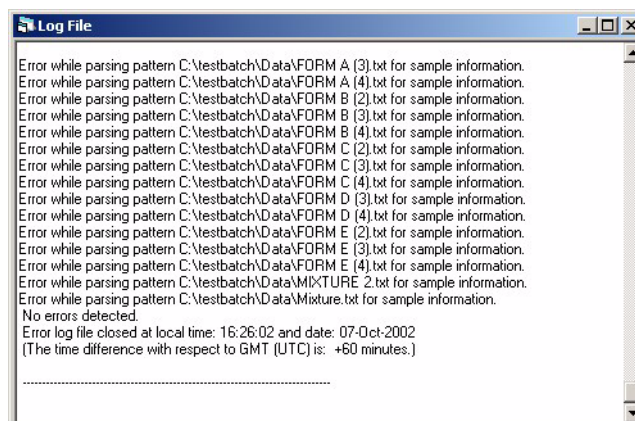
The *Window* menu contains the following items:

### *Window List* (submenu)

This submenu lists all of the currently open windows within the PolySNAP M program. Selecting a window from the list brings it to the front.

### *View Error Log*

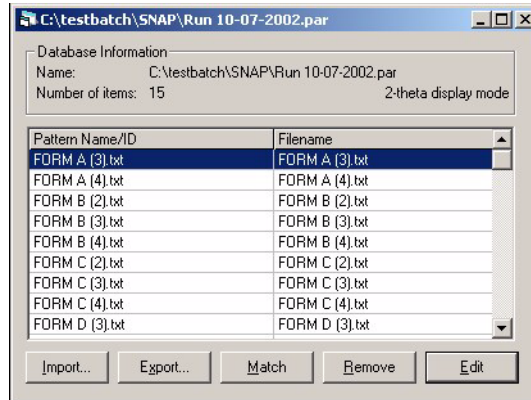
This option opens a new window containing an edited version of the PolySNAP M logfile, which contains only lists of errors or problems that have occurred during a run of the program:



It may be a useful aid in the determination of where any problems are occurring.

### *View/Edit Reference Database*

This option opens the current database of known or reference patterns (if present) in a standard PolySNAP M database window:



It can then be examined, edited or used as a basis for a manual match or analysis procedure as required. For more details see section 3.4 on page 92.

### *View/Edit Sample Database*

This option opens the current database of imported patterns in a standard database window. It can then be examined, edited or used as a basis for a manual match or analysis procedure as required.

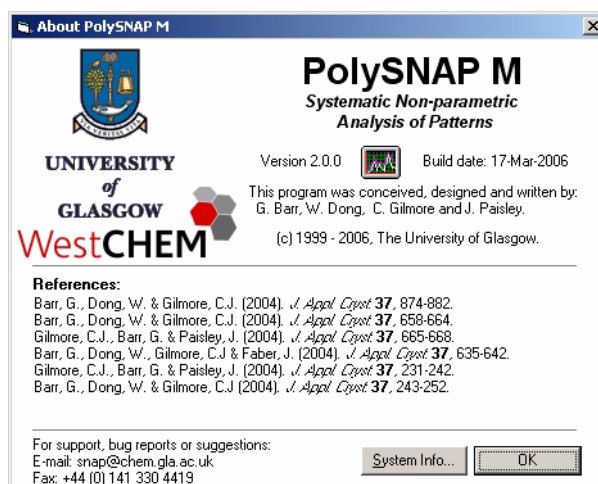
The *Help* menu contains the following relevant items:

### *View Manual*

This option opens a new window containing a PDF version of this manual that can be searched, displayed or printed as required.

### *About PolySNAP M*

Selecting this menu item brings up a screen describing the running version of PolySNAP M, and includes useful information such as the version number and build date:





## 2.5 Output Files

An average run of PolySNAP M creates a variety of different files in the selected output folder. This section lists and describes the most important of them:

### *Run\_xx-yy-zz.par*

This is the database file containing copies of all of the original data files. It can be opened and examined manually in manual analysis if required. The file was created on the date *xx-yy-zz*.

### *Known\_phases\_xx-yy-zz.par*

This is the database file containing copies of any individual known phase files. It can be opened and examined manually in manual analysis. This file only appears if known phases are being used, and they are not already in a database file. The file was created on the date *xx-yy-zz*.

### *SNAPlog.txt*

This file is added to continually while the program is running. It consists of a record of program operations and any user alterations to the program-generated results. It can be viewed from within the program, or in any text editor.

### *Errorlog.txt*

This file is a very abbreviated version of the logfile, containing only records of problems or difficulties encountered during data import, processing, or pattern analysis. It can be viewed from within the program, or using any text editor.

### *correlations.txt*

These files contains the numerical values from the sample matching process, where every individual pattern is compared to every other pattern. It is these numbers which are displayed in the Numerical Results pane of the Display window. Values can also be examined by viewing this file in a spreadsheet program such as Microsoft Excel.

### *Dendrogram.dat*

### *Dendrogram\_modified.dat*

### *Dendrogram\_original.dat*

### *Dendrogram\_disused.dat*

The output file containing data for the dendrogram display is saved as *Dendrogram.dat*. If the user then makes and saves changes to the dendrogram, the original output file is renamed

---

*Dendrogram\_original.dat*. If further changes are made and saved, the previous version of the file is renamed *Dendrogram\_modified.dat*. Should the user later choose to revert to an earlier version of the dendrogram, the appropriate file is renamed to *Dendrogram*, and the current, unwanted version renamed as *Dendrogram\_disused.dat*. Both *Dendrogram\_disused.dat* and *Dendrogram\_modified.dat* retain only the most recent changes, and may be overwritten. The original results file is never overwritten, and can be returned to at any time.

#### *Pie.dat* and *Pseudo\_pie.dat*

If known phases were provided, *Pie.dat* contains information used by the cell display to show colour-coding and mixtures compared to known-phase patterns. If no known phase files were provided, *Pseudo\_pie.dat* contains the current dendrogram groupings reformatted for display in the cell context. If filename information was used to label the cells with the correct well identity number, then an additional file *pie\_index.dat* is used to store the original output file.

#### *mmds.dat* and *mmds\_coloured.dat*

This file contains display information used to display the 3D (MMDS) plot, using either the default colour scheme (*3dmmds.dat*) or the colour scheme utilised by the current saved version of the dendrogram (*3dmmds\_coloured.dat*).

#### *pca.dat* and *pca\_coloured.dat*

This file contains display information used to display the 3D (PCA) plot, using either the default colour scheme (*pca.dat*) or the colour scheme utilised by the current saved version of the dendrogram (*pca\_coloured.dat*).

#### *QuantitativeResults.dat* *correlations\_offsets.txt*

The first file contains the output from the quantitative analysis of any suspected mixture patterns. The second file contains the output of the best calculated shift for each pattern matched.

#### *amorphous.dat* *membership.dat*

#### *mmds\_na.dat* *pca\_na.dat*

#### Various files ending in *.tmp*

These are various internal files used by the program.

---

# Using PolySNAP M: Manual Analysis

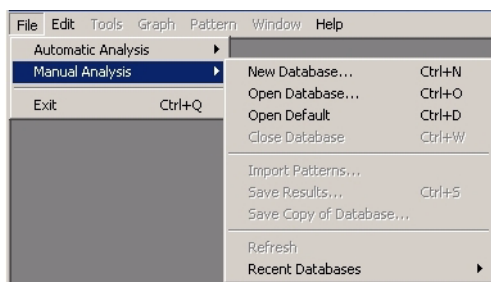
---

## 3.1 Database and File Handling

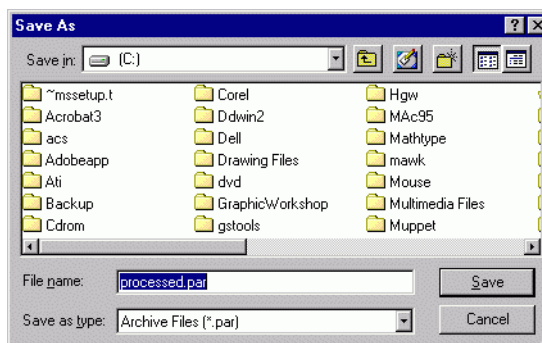
In order to use PolySNAP M in manual analysis mode, the user must first either create a new, empty database and load some patterns into it, or open an existing database. This chapter describes both these processes.

### 3.1.1 Database creation

Having launched the program, select *New Database...* from the *Manual Analysis* section of the *File* menu.



A standard Windows file dialog will appear:

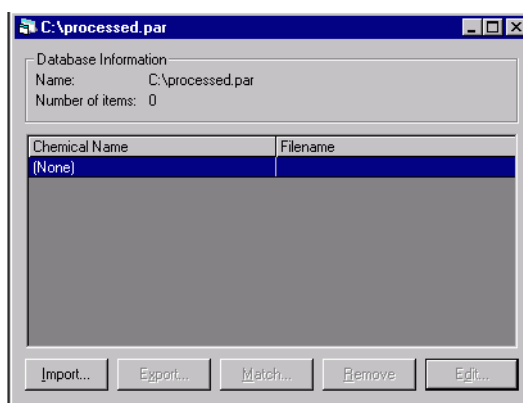


---

This will initially suggest the filename *processed.par* and a location at the root directory of the C:\ drive. The filename and location can be changed in the normal Windows manner.

Note that the *.par* suffix indicates the database being is saved in the standard PolySNAP M database format.

Once created, the database will be opened in a new window:



The top portion of the window provides some basic information on the database, including its name and location, and the number of patterns stored in it. Initially, of course, it is empty.

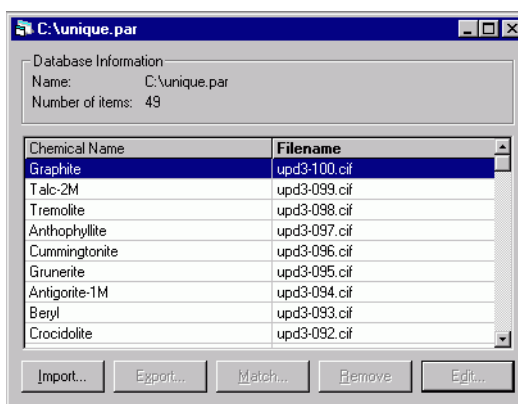
The central portion of the window will list the patterns included in it. It will be described in more detail on page 70.

The lower region consists of 5 buttons, used to access the main functions of the program. The buttons all have corresponding entries in the program menus.

### 3.1.2 Opening an Existing Database

To open a pre-existing database, select *Open...* from the *File* menu. A standard Windows file browser will appear. Locate the database, and either double-click on it, or click once to select it, and then click the *Open* button.

A database window will open, and the patterns loaded. Depending on the number of patterns in the database, this may take some time. Progress is indicated *via* a progress bar at the top of the window:

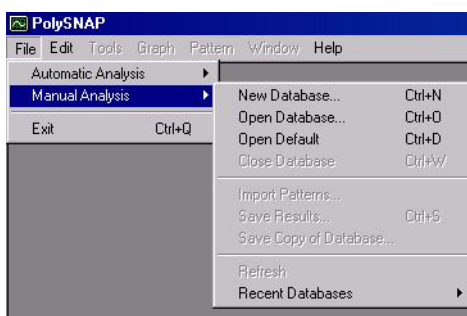


### 3.1.3 Default Databases

If you commonly open the same database each time you launch the program, this process can be speeded up by defining the path of your database as the program's default. This can then be opened directly by use of the *Open Default* option in the *File* menu, or by the keyboard short-cut Option-D.

The default default database is *C:/processed.par*. This can be changed in the Program Options dialog, accessed through the *Edit* menu's *Options...* entry.

### 3.1.4 Recent Databases



The four most recently opened databases are stored in the *Recent Databases* submenu for easy access. Selecting one of the entries automatically causes that particular database to be re-opened.

Note that if you have moved the file since it was last opened you will have to open it manually.

---

### 3.1.5 Importing Files into a New Database

Once a new, empty database has been created and opened, the next stage is to import some patterns into it. This is achieved by clicking on the *Import...* button at the bottom of the database window (or using the *Alt-I* short-cut, or choosing *Import Patterns...* from the *File* menu).

A standard Windows file selection dialog will appear, and either single or multiple pattern files can be selected for import. Multiple files of different types can be easily selected using the shift or option keys, or by dragging the mouse across the names to select them.

Click *Open* to begin the data importation process.

This version of the program can import pattern files in one of 4 formats:

#### 3.1.6 Text files (*filename.txt*) (*filename.prn*)

These should be standard ASCII text files. The angle should be the x data, and the corresponding intensities the y data. The x-y data must be in the format:

```
x1      y1
x2      y2
.       .
.       .
```

*etc.*

***The fields must be tab-delimited.***

If the first line in the file begins with either a '#' or the string 'ID: ', the rest of that line is used as the 'Pattern Name' for the pattern.

Any subsequent lines beginning with the '#' character are ignored.

#### 3.1.7 Comma-separated value files (*filename.csv*)

These should be standard ASCII CSV files, containing the x-y data in the format:

```
x1,y1
x2,y2
..
..
```

*etc.*

If the first line in the file begins with either a '#' or the string 'ID: ', the rest of that line is used as the 'Chemical Name' for the pattern.

Any subsequent lines beginning with the '#' character are ignored.

### **3.1.8 CIF (Crystallographic Information Format) files (*filename.cif*)**

The program contains a CIF-format translator that reads standard version 2.0 Powder CIF files. Although the only data necessary for SNAP is the x-y intensity data, the rest of the CIF information - such as chemical names and formulae, author names and addresses *etc.* are also retained in the database for reference purposes, and may be viewed from the Pattern Editor window (see Section 3.3.1). Additionally, unit cell dimensions and contents are read in if present for use in Quantitative Analysis mode.

For more information on CIF format files, see the IUCr website at:

*<http://www.iucr.org/iucr-top/cif/pd/index.html>*

### **3.1.9 Bruker Raw Format files**

The program can import data from Bruker RAW format. This is a binary file-format, so cannot be edited or viewed in a conventional text editor. There are several different types of RAW format; PolySNAP M should be able to import all versions up to Version 4.

Although the only data necessary for PolySNAP M is the x-y intensity data, much of the rest of the information stored in the file - such as chemical names and formulae, author names and addresses *etc.* are also retained in the database for reference purposes, and may be viewed from the Pattern Editor window (see Section 3.3.1).

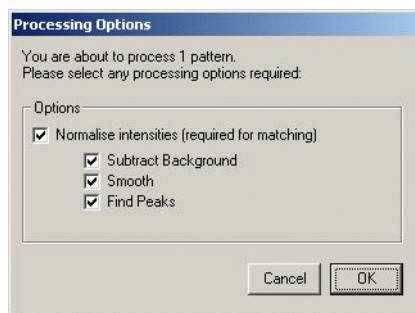
### **3.1.10 PolySNAP M Pattern files (*filename.pat*)**

Patterns in PolySNAP M databases can be individually exported in the program's own *.pat* format. This format contains the original x-y raw data, any processed data - *e.g.* the profile after noise removal, marked peak positions and any other data fields present. Once saved as separate files, they can then be re-imported to the same or a different database at a later date.

---

### 3.1.11 Processing

Once files have been selected for import, a dialog box will then appear, informing you how many patterns will be imported, and offering several data processing options:



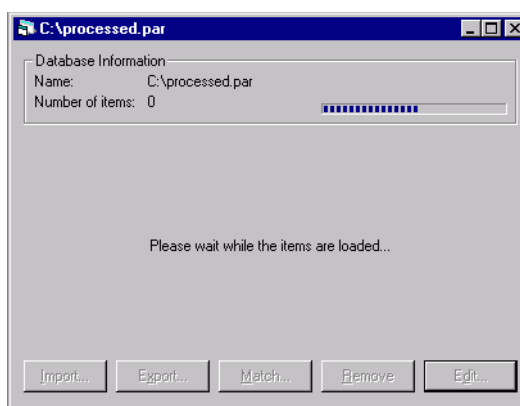
Normally, the default settings at this stage are to perform all three options:

- Background subtraction
- Smoothing and noise removal
- Peak finding.

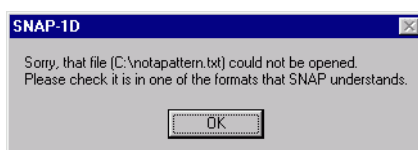
All of the processing choices are optional, although in order to perform basic matching operations, at least the main '*Normalise intensities (required for matching)*' checkbox should be selected.

Selecting *OK* will begin the import process.

A progress bar indicates progress through the processing:



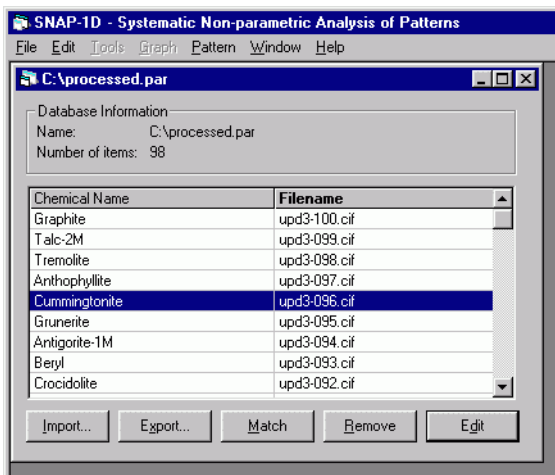
If any selected patterns cannot be loaded - for example if they are not in the correct format, or a file is corrupted, a warning will be shown:





In such a case, the rest of the selected patterns should still load correctly.

Once the import procedure is completed, the list of patterns contained in the database will appear in the centre of the database window:



Each entry in this list corresponds to one imported pattern. The left-most column contains the pattern name or ID associated with that pattern, if one is known. (This is either read from the CIF data field if present, or can be entered manually in the pattern editor - see Section 3.3.3) If no name is known, this column shows the filename.

The rightmost column lists the filename from which each pattern was loaded.

### 3.1.12 Sorting Database Entries

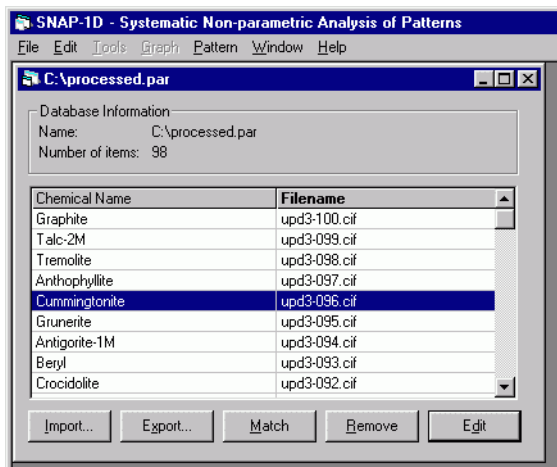
Initially, this list of patterns is shown in the order that patterns were added to the database. It is often more useful to see the list of patterns sorted in order of either chemical name/ID, or individual filenames. This is done by clicking once on the relevant column header. Clicking again on the same header will reverse the order of the sorting, *e.g.* from ascending to descending, or *vice versa*.

### 3.1.13 Exporting patterns

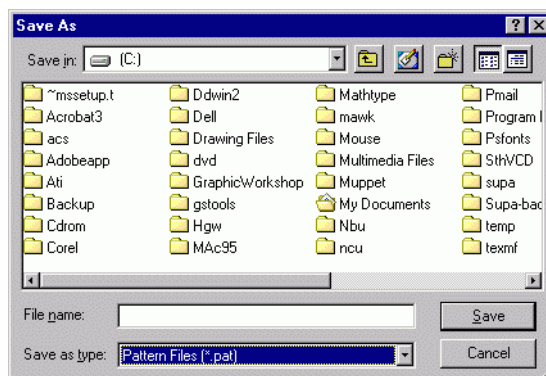
Individual patterns contained within a PolySNAP M database can be exported to either text or pattern format files, for easy viewing or editing in other programs, or for transferring to other PolySNAP M databases. This means PolySNAP M can be used as a general purpose pre-processing tool for patterns that are to be used in other programs.

---

Click once on the pattern you wish to export. It should become highlighted in the list:



Then click once on the *Export...* button (or use the *Export...* option under the *Pattern* menu). A standard file saving dialog box appears:



Select the desired location for the file, and edit the filename if required. The default format for export is a *.pat* pattern file, but a *.txt* text file format option can also be selected from the *Save as type* drop-down menu at the bottom of the dialog box.

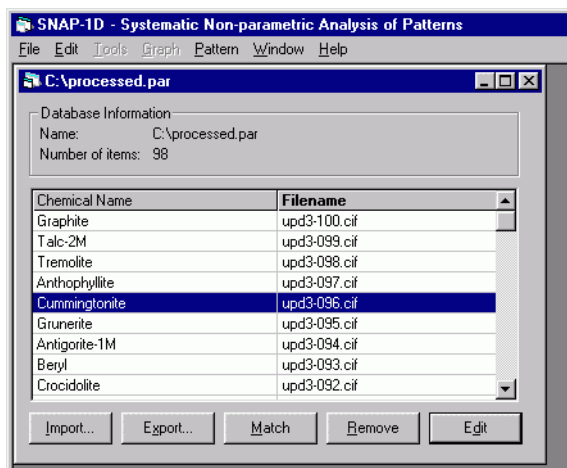
Click *Save*, and the file will be saved to the chosen location.

*Note:* This process saves a copy of the selected pattern to a separate file, it does not remove the original pattern entry in the database.

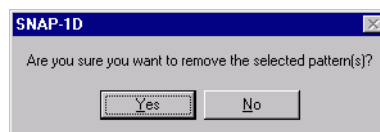
This option saves the *processed* version of the pattern (*i.e.* the version with smoothing, background subtraction *etc.* applied) if one is present, so if the raw pattern is required, remove any processing using the *Edit* window before exporting.

### 3.1.14 Removing Patterns

Select the pattern or patterns you wish to delete from a database. They should become selected in the list:



Then click once on the *Remove* button (or select *Remove* from the *Pattern* menu, or press the *Delete* key on the keyboard). A warning appears:

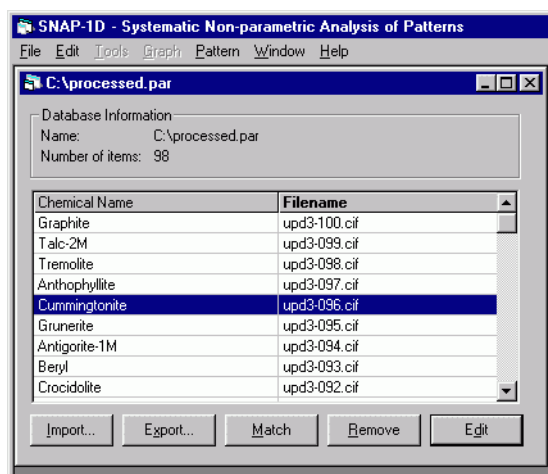


If you change your mind, select *No*. Selecting *Yes* removes the selected pattern(s) from the database permanently. To retrieve them, you would then have to re-import the pattern from the original data file. (The original data files are not affected in any way by the *Remove* command.)

---

### 3.1.15 Viewing and Editing Patterns

Click once on the pattern you wish to examine. It should become selected in the list:



Then click once on the *Edit* button (or select *Edit Pattern* from the *Pattern* menu).

The Pattern Editor window should appear. This is described in detail in section 3.3.1 on page 76.

## 3.2 Matching and Analysing Patterns

If you have a new, unknown pattern you wish to analyse or compare to entries in an existing database, the first step is to import the new pattern to the existing database.

Having done this, select it in the list of patterns, and click *Match* (or select *Open in Match Window* from the *Pattern* menu).

The matching window is described in detail in Section 3.4, Pattern Matching and Analysis.

### 3.2.1 Refresh Database

This feature is accessed through the menu item *Refresh* found in the *Manual Analysis* section of the *File* menu. This option updates the local copy of the database in memory by reloading all pattern information from the copy on disc.

### 3.2.2 Save Copy of Database

This feature, accessed through the *Save Copy of Database...* Menu item located in the *Manual Analysis* section of the *File* menu, brings up a standard Windows *Save As* file dialog. The process asks for a

new database name, and copies the pattern contents of the existing database into the new one. Note that you cannot use the existing database name as that file remains open during the process.

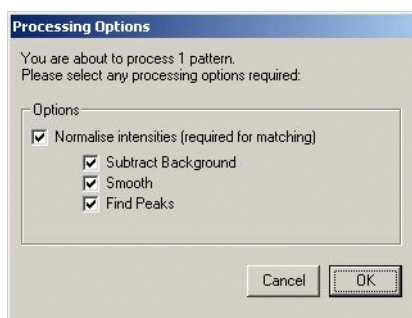
Once completed, the resulting database will be saved with the name selected and can then be opened by PolySNAP M in the usual manner.

### 3.2.3 Apply Processing to Database

This feature is accessed through the *Tools* menu item *Apply Processing...*

If you wish to change the way in which all of the patterns are processed at once, it is possible to do so without having to change them individually, or having to re-import them from the original files.

Select *Process*, then select the new required processing options as required from the resulting dialog:

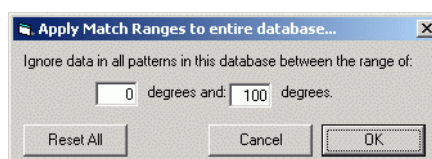


The selected processing will then be applied, which for a large database may take some time.

### 3.2.4 Mask Regions

This option, accessed under the *Tools* menu, is used to mask a particular region of the diffraction pattern to zero for every pattern in a database. (For more information on masking regions, section 3.3.10 on page 86)

Selecting this option brings up a window which asks for the start and end angles of the region to be masked:



Enter the values, and click Apply. The region selected will be set to zero for *all* of the patterns in the current database. Depending on the size of the database, this may take some time.

Multiple regions can be masked by repeating this process.

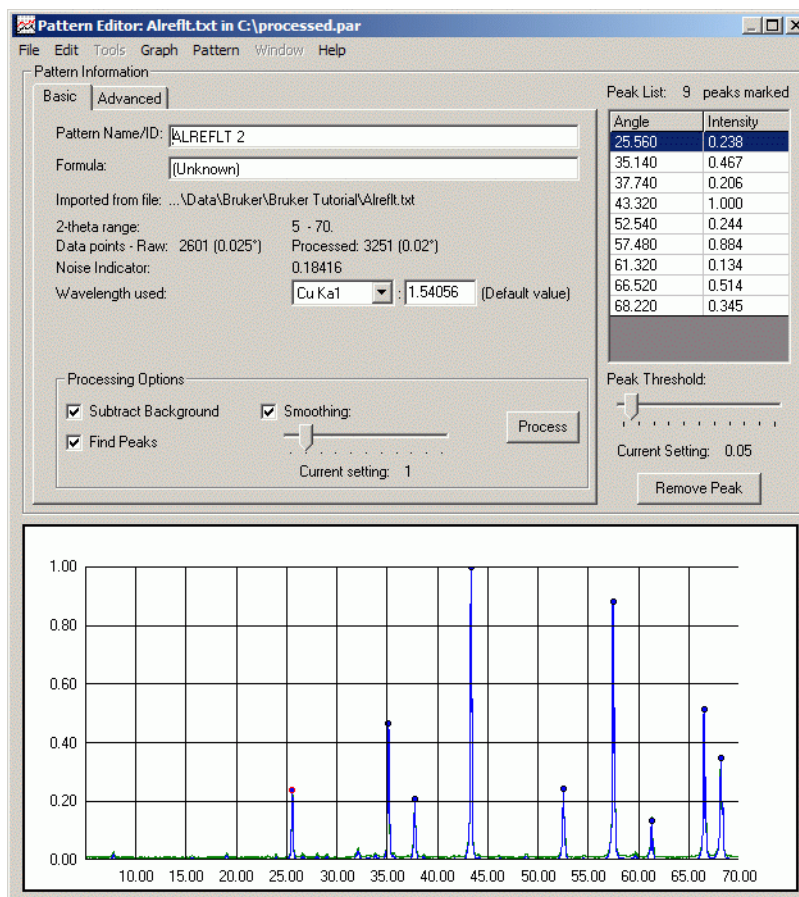
Note that applying any additional processing to a pattern after this point will remove any masked regions. Masking can be re-applied or changed for an individual pattern in the Pattern Editor (see Chapter 3).

To remove all masking from all patterns for a particular database, select the *Mask Regions* menu option, and click the *Reset All* button. Again, this may take some time.

### 3.3 Pattern Editing and Processing

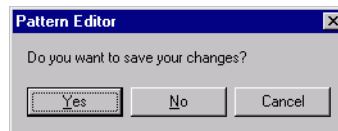
#### 3.3.1 The Pattern Editor

After selecting a pattern in the database, and selecting the *Edit* option, the Pattern Editor window will appear:



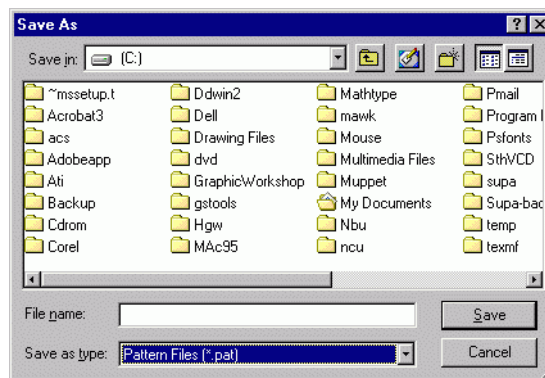
Note that while the editor window is open, no other changes can be made to the open database.

The *File* menu option, *Close Window*, closes the editor and returns to the main database window. (The same result is achieved by clicking the close box on the titlebar of the window.) If any changes to the pattern have been made, a dialog box will appear asking if those changes should be retained or not:



Selecting *Yes* saves the changes and returns to the database listing window, *No* discards any changes made and *Cancel* returns to the Pattern Editor.

One of the other *File* menu option available, *Export...*, performs the same function for the pattern currently being edited as the *Export...* button in the main database window. Selecting it causes a standard file saving dialog box to appear:



Select the desired location for the file, and edit the filename if required. The default format for export is a *.pat* pattern file, but a *.txt* text file format option can also be selected from the pop-up menu at the bottom of the dialog box.

Click *Save*, and the file will be saved to the chosen location.

*Note:* This process saves a copy of the selected pattern to a separate file, it does not remove the original pattern entry in the database.

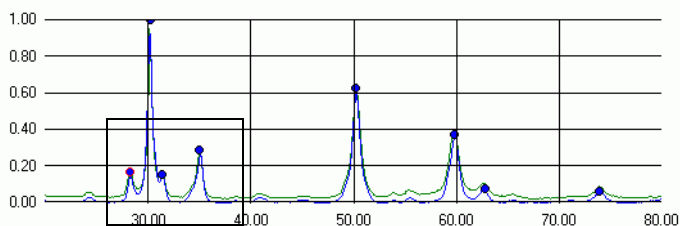
This option saves the *processed* version of the pattern (*i.e.* the version with smoothing, background subtraction *etc.* applied) if one is present, so if the raw pattern is required, remove any processing by turning off all processing options and clicking *Process* before exporting.

---

Finally, the option *Export Peak List* brings up a save dialog box, allowing the peak list for the current pattern to be saved to an ASCII text file for use in other programs.

### 3.3.2 Graph Pane

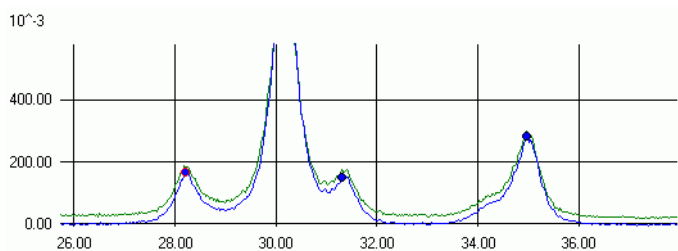
The lower part of the window, where the pattern is displayed, is called the graph pane:



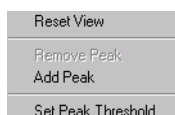
The x-axis is normally displayed as a  $2\theta$  range and the y-axis an intensity. For positive data, all values are normally scaled to between 0.0 and 1.0 for use in PolySNAP M, unless no processing has been performed at all upon the data.

Individual peaks in the graph pane are marked by peak markers, which are seen as a single large dot at the top of the peak. (For more information on peak markers, See “Find Peaks” on page 84.)

Clicking and dragging to draw a rectangular box on the graph pane using the left mouse button causes the graph to zoom in into the selected region, for example:



It is possible to zoom in repeatedly using this method. Clicking on the graph with the right mouse button causes a pop-up menu to appear:



Options in this menu are:

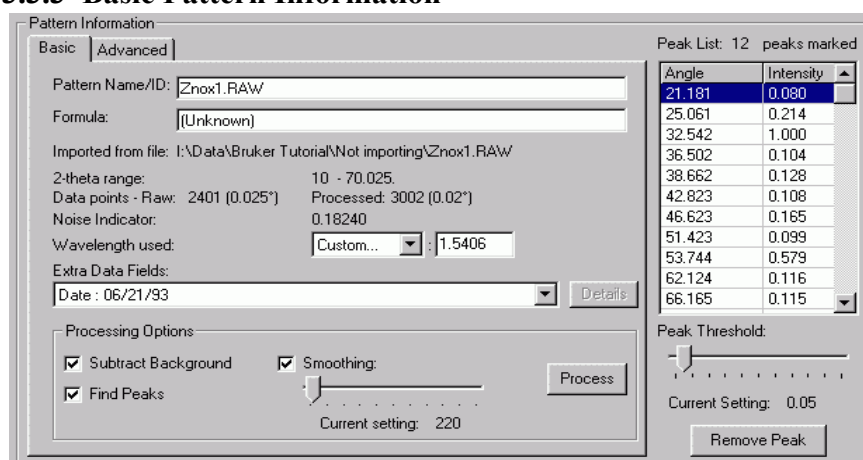
- Reset View - selecting this after the graph scale has been changed returns to the default zoom level.



- Remove Peak - if the click was in the vicinity of a marked peak, the marker will be removed.
- Add Peak - the nearest maxima to the click location is marked as a peak on the graph.
- Set Peak Threshold - sets the y-value of the current mouse position to the minimum allowed peak height.

The same options are also available from either the *Graph* or *Pattern* menus respectively. The central region of the Pattern Editor contains the pattern information controls in two tabs: *Basic* and *Advanced*.

### 3.3.3 Basic Pattern Information



At the top left corner is the pattern name/ID text box. If no name has been read in for the pattern from the data file, this will normally read "(Unknown)". This name can be edited by clicking in the text box, and deleting or adding text as required. It is recommended that pattern names do not exceed 256 characters. Standard text-editing commands, such as *Cut*, *Copy* and *Paste* are all available from the *Edit* menu. This field is used by default to identify different patterns in the database and match windows.

Below this is the *Formula* field, which is also an editable text field. If formula information is present in the datafile, it will be read in and displayed automatically. Otherwise, it would need to be entered manually. This field is not required for operation of the program, but may be useful for reference.

Below that is a text field displaying the path and filename of the original data file the pattern was obtained from. If this path is longer than 100 characters, it will be truncated, and only the right-most 100 characters will be displayed. To see the entire path, leave the mouse

---

cursor hovering over the text for a few seconds to see a 'tool tip' containing the full path.

Next is the range the current pattern spans on the x-axis (normally in degrees.)

Following this is the number of raw data points in the pattern: this corresponds to the number of data points read from the original data file.

The number in brackets after this is the resolution of the raw data calculated using:

$$\frac{(\text{End angle} - \text{Start angle})}{\text{No. of raw data points}}$$

This corresponds to the magnitude of the x-difference of the difference between two adjacent data points.

Next to this is a similar indicator for the processed data. The processing referred to is the basic processing undergone by every pattern imported into a PolySNAP M database. This involves scaling the intensity data between 0.0 and 1.0, and interpolating the data (using 5th order polynomials) so that all of the patterns in the database are the same standard data resolution. This is normally 0.02 degrees per datapoint, or 50 data points per degree.

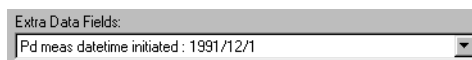
Below this is *noise indicator* for the pattern calculated in the wavelet domain, using the MAD estimator (see section 3.3.8, References). A larger number corresponds to a more "noisy" pattern.

The *wavelength* field reads in a value for the wavelength at which the data was recorded, either from a CIF or RAW data file. If another import format was used, or the information was not present in the file, the default value is used. In this situation, the legend 'Default Used' appears next to the wavelength value to warn the user that it may require to be changed manually.

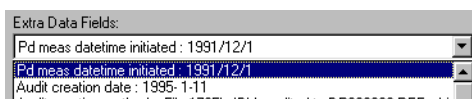


This can be done by either selecting a standard value from the scrolling list, or by choosing the '*Custom*' option at the bottom of the list of choices, and entering a numerical value in the adjacent text box. The pattern display is updated for a new standard wavelength immediately, and for a custom one after the changes to the pattern have been saved.

The final pattern information display only appears when the pattern is being edited was originally imported from a CIF or RAW data file.



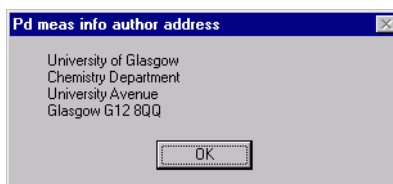
Any other data fields that were imported with the data are able to be examined *via* the list obtained by clicking on the small disclosure triangle:



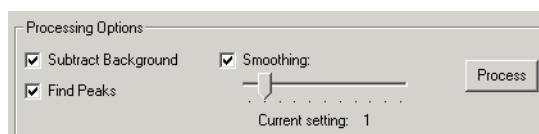
Only the first line of each data field is displayed in the list; if viewing of a multiple line field is required (for example, an author's address), select it from the list. A button will be enabled beside the pop-up region, labelled *Details*:



Clicking this produces a dialog box containing the full text of the field:



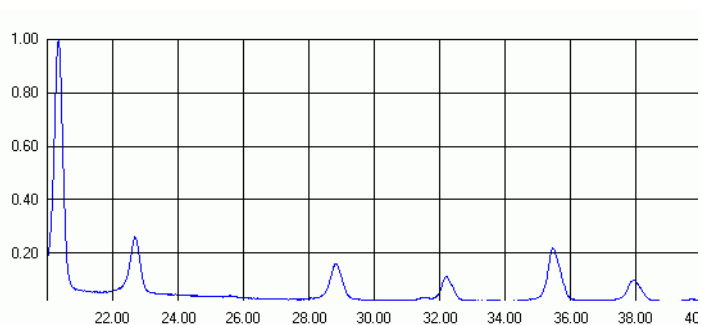
The final region of the of this pane contains the pattern processing options:



Although patterns will normally have been processed automatically upon import, it is easy to override those general processing options for an individual pattern using these controls.

---

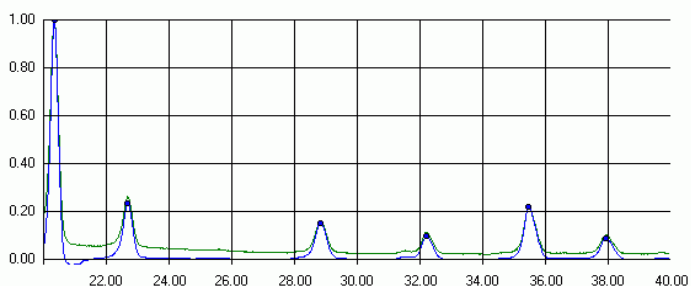
The operation of these controls maybe most easily illustrated upon a pattern that had no processing performed upon import. Such data would look something like the diagram below:



A raw data plot is generally shown in green on the graph pane when processing has been applied. Blue represents the processed profile. It is this processed profile that is used throughout the rest of the program for matching and analysis.

### 3.3.4 Background Subtraction

Checking the *Subtract Background* option under Processing Options, followed by clicking the *Process* button, causes a second pattern to appear on the graph pane, generally in blue:

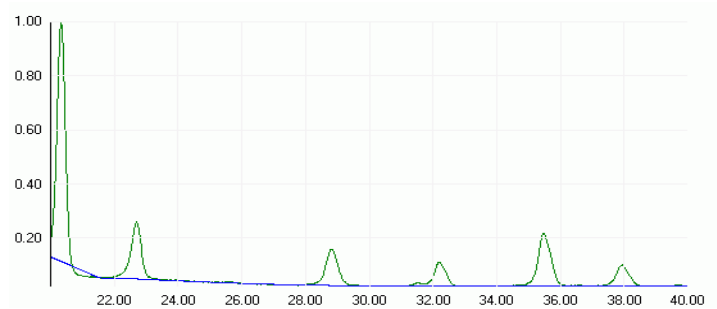


This is the same pattern as the raw data one, but with any unwanted background removed. This process is achieved by best-fitting several linked polynomials to the base of the raw data pattern, and then subtracting them from it.

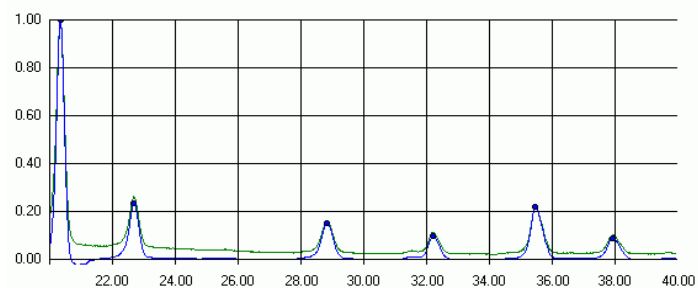
If results from this are unsatisfactory, this processing option can be switched off by simply unchecking the box, and clicking the *Process* button again.

If the actual curve that has been subtracted is required to be examined, select the *Show Background Curve* option in the *Pattern*

menu. A new window opens, and the calculated background region is then outlined in blue above the green raw pattern data.



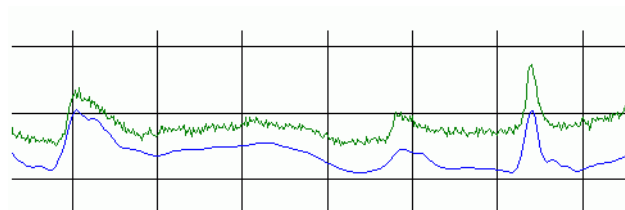
The same pattern with background subtracted:



### 3.3.5 Smoothing

Selecting the *Smooth* option, and clicking *Process* causes the pattern to be smoothed using a wavelet-based SURE thresholding procedure (see section 3.3.8, References). This allows obvious noise to be removed without the loss of small or fine peaks.

For example, a detail is shown below of the same region of the same pattern, before and after smoothing has taken place.



The upper green line is the original unsmoothed profile, and the lower blue is the same after smoothing has been performed.

To alter the amount of smoothing applied to the individual pattern being examined, move the slider to the right to increase, or to the left to decrease it. The display is updated automatically.

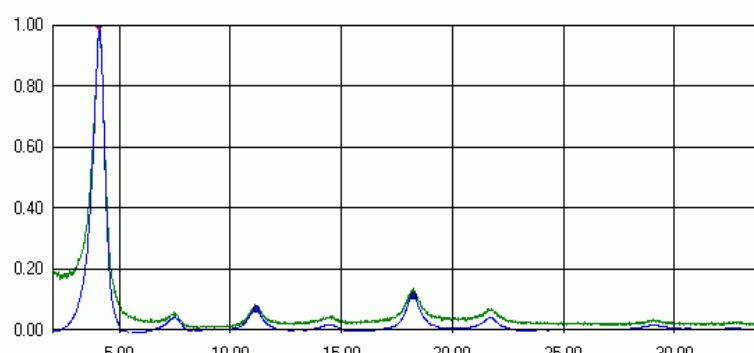
---

The amount of smoothing performed by default can be controlled by changing the 'Smoothing Factor' value in the program *Options* dialog.

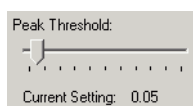
### 3.3.6 Find Peaks

Finally, selecting the *Find Peaks* option, followed by clicking the *Process* button tells the program to use a simple first-derivative peak search algorithm to locate the main peak maxima in the pattern. These are then marked with coloured circles on the graph pane.

For example:

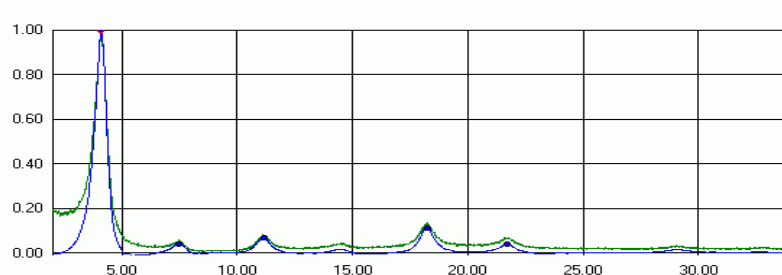


In order to stop small, unwanted peaks being marked, a peak threshold level can be set, *via* the slider on the right hand side of the window:



The default value is 0.05, meaning that no peaks will be marked below 5% of the maximum peak height. A global default value for the peak threshold can be set in the *Options* dialog (see Chapter 4.6, Matching Options). This value is used when processing multiple patterns automatically on import. Changes made to the threshold level in the pattern editor override the global value for the individual pattern in question.

For example, note the differences in the number of marked peaks for the same pattern as above, but with the peak threshold level set to zero:

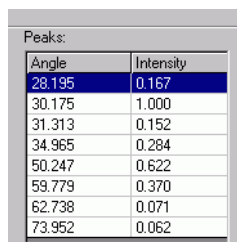


Individual peak markers can be removed by clicking on them once to select them (a differently coloured border will appear round the spot on the graph pane), followed by either clicking the *Remove Peak* button, or by selecting the *Remove Peak* option from the *Pattern* menu. After a peak is removed, the peak immediately to the right of it becomes automatically selected.

It is also possible to remove a peak by clicking on its entry in the Peak List box to select it, and then clicking the *Remove Peak* button.

The number of peaks field reports how many points in the pattern have been marked as peaks. These are shown by round dots on the profile displayed on the graph pane.

A scrolling list of all the marked peaks showing their x-position and corresponding y-value is displayed on the right-hand side of the pattern editor window:



Angle	Intensity
28.195	0.167
30.175	1.000
31.313	0.152
34.965	0.284
50.247	0.622
59.779	0.370
62.738	0.071
73.952	0.062

Clicking on a particular peak in this list causes it to become selected, and the corresponding peak marker to be highlighted on the pattern itself to aid in identification.

### 3.3.7 Notes on processing

Although the processing options (such as subtracting the background) can be made on a pattern by pattern basis, best results are obtained in the matching and analysis sections of the program with databases whose constituent patterns are all processed in a consistent manner. For example, two otherwise identical patterns may appear very different if one has been smoothed and background-subtracted, and the other has not. Consistency in how patterns are processed generally leads to the best matching and analysis results.

### 3.3.8 References

Wavelet SURE thresholding is discussed in:

Donoho, D.L.; Johnstone, I.M.; (1994). Adapting to Unknown Smoothness via Wavelet Shrinkage. *Technical Report, Department of Statistics, Stanford University.*

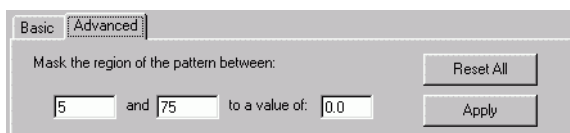
---

### 3.3.9 Advanced Pattern Information

The advanced tab has two main regions: one allowing the ability to mask sub-regions of the pattern, and the other to enter additional information and thus calculate various constants for the pattern.

#### 3.3.10 Masking

The upper section in the advanced pane contains the controls to mask selected regions of a pattern.

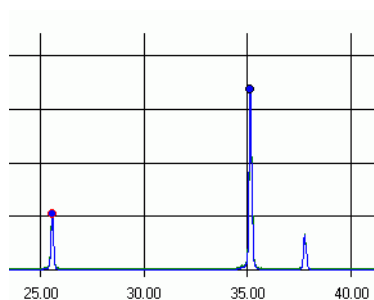


If a pattern contains a spurious peak or unwanted standard, or for some reason the user wishes to only compare a certain region from the pattern, this option allows a chosen sub-range to be set to a particular value. (This is generally zero, although non-zero values may be useful when a high background signal is present.)

To use this option, first decide on the angle range to be masked. Enter the start and end angles in the relevant boxes. The value in the magnitude box sets the signal to that value over that range.

Masked regions can also be applied in one step to every pattern in a database using the *Mask Regions...* option. This can be found under the *Tools* menu, when the database window is frontmost. See Section 3.2.4, Mask Regions.

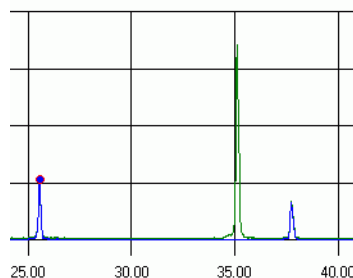
In the example below, the user wishes to mask the central of the three main peaks:



As it is at approximately  $35^{\circ} 2\theta$ , the start angle could be  $34^{\circ}$ , and the end angle  $36^{\circ}$ . There is no noticeable background, so the mask value can remain as zero.



Clicking the *Apply* button results in the following:



Notice that the peak is still visible in green. This shows that the original data - the unprocessed pattern - has not been modified. However, there is no peak visible in blue - it has been removed from the processed pattern. It will not appear in the Match window or other regions of the program which only make use of the processed pattern profile.

Multiple regions in the same pattern can be masked by repeated application of the same technique.

To reset all masking, and make the processed profile available again, click the *Reset All* button. The same effect is obtained by re-processing the pattern using any of the standard controls in the Basic tab.

### 3.3.11 Additional Pattern Information

Please enter additional known information:

Unit cell contents:  a:  b:  c:

Z:  alpha:  beta:  gamma:

Using the above information, the following have been calculated:

Unit cell volume: <Not enough information>

Formula Mass: <Not enough information>

Density [g cm<sup>3</sup>]: <Not enough information>

Linear Abs. Coeff. [cm<sup>-1</sup>]: <Not enough information>

Mass Abs. Coeff. [cm<sup>2</sup>/g]: <Not enough information>

This section of the pattern editor contains fields for entering other information that is known about the sample.

This information is used to calculate various useful constants and numbers about the pattern. The information calculated here is required if you wish quantitative analysis to return results as a weight fraction.

The first time the Advanced tab is used for a pattern, the *Unit Cell Contents* field is taken to be the same as the *Formula* field from the Basic tab. However, they are saved separately in the pattern, and changes to one do not affect the other. The *Formula* field is

---

completely free format, whereas the *Unit Cell Contents* field has a fairly strict format, as described below.

The unit cell contents should be entered in the form:

<Atom Symbol><No. of that atom><Space or comma><Next atom symbol ... etc.

For example, the following entries would be valid:

C3 H8 O2  
C3,H8,O2  
Al O3 H  
c3 H8 o2

Non-integer values are permitted.

The following entries would not be valid, for the reasons described:

C 3 H 8 O 2

-has spaces between the element types and the number.

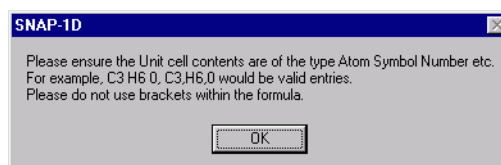
C3H8O2

-has no spaces at all between each separate entry!

Al(OH)3

-Contains brackets.

Any invalid entries should result in an error:



Note however that it is possible to enter a string that does not generate an error message, but that does not produce correct results. *For this reason, entries in this field should be checked carefully.* Also please note that entries are **not** checked for chemical sense during calculation.

The field *Z* represents the number of formula units per unit cell. It should be a numerical value greater than zero. It can be non-integer.

The fields for unit cell dimensions ( *a*, *b*, *c*,  $\alpha$ ,  $\beta$ ,  $\gamma$  ) all expect numerical non-zero entries. The angles should be in degrees, and the lengths in angstroms (Å).

Once all known information is entered, click the *Update* button. Depending on what information was provided, some or all of the text fields at the bottom of the pane will update with new values.

For example, with the following information entered:

Please enter additional known information:

Unit cell contents:	<input type="text" value="Al2O3"/>	a:	<input type="text" value="4.758"/>	b:	<input type="text" value="4.758"/>	c:	<input type="text" value="12.98"/>
Z:	<input type="text" value="1"/>	alpha:	<input type="text" value="90"/>	beta:	<input type="text" value="90"/>	gamma:	<input type="text" value="90"/>

Clicking *Update* results in the following results:

Using the above information, the following have been calculated:

Unit cell volume:	293.85	<input type="button" value="Update"/>
Formula Mass:	101.96	<input type="button" value="Enter manually"/>
Density (g cm <sup>3</sup> ):	0.58	
Linear Abs. Coeff. (cm <sup>-1</sup> ):	18.21	
Mass Abs. Coeff. (cm <sup>2</sup> /g):	31.4	

As in this case all of the fields have been successfully calculated, this pattern could potentially be used as part of a quantitative analysis resulting in a weight fraction being calculated.

### 3.3.12 Additional Calculation Information

For reference, the items above are calculated as follows:

- Unit Cell Volume:  
Given unit cell lengths a, b and c in Å, the volume  $V$  is then:
- Density:  
Given the molecular weight  $MW$  in atomic mass units, the number of formula units per unit cell  $Z$ , and cell volume  $V$  in cubic angstroms, the density  $\rho$  may be calculated by:

$$\rho = \frac{MW \times Z \times 1.66}{V}$$

- Linear Absorption Coefficient:  
Given the cell volume  $V_C$ , and the total photon interaction cross-section  $\sigma_i$  in barns/atom for each atom in the unit cell, the linear absorption coefficient  $\mu$  is calculated by:

$$\mu = \frac{1}{V_C} \sum_{i=1}^n \sigma_i$$

- Mass Absorption Coefficient:  
This is calculated by dividing the linear absorption coefficient  $\mu$  by the density,  $\rho$ :

$$\mu^* = \mu / \rho$$

- The database of atomic information is contained in the file *SNAPdb.dat*, which should be located inside the folder containing the *SNAP.exe* program itself. The format is discussed below:

### 3.3.13 Atom Info Database Format

There are 11 lines per entry:

*Line 1:* Format(a3,i4,2x,a12)

Element symbol, charge or oxidation state, full element name

*Line 2,3:* Format(6f12.6/6f12.6)

X-ray atomic scattering factors in parameterised form:

```

a1  a2    a3  a4  a5  c
b1  b2    b3  b4  b5  0

```

Sources:

- Fit parameters of all atoms/ions (with the exception of O1-) from publication "New Analytical Scattering Factor Functions for Free Atoms and Ions", D. Waasmaier & A. Kirfel, *Acta Cryst.* 1995, A51, 416-431)

- Fit for O1- based on the tabulated values of Table 2 (D.Rez, P. Rez & I. Grant, *Acta Cryst.* (1994), A50, 481-497).

- Fits for all other atoms/ions based on the tabulated values of Table 6.1.1.1 (atoms) and Table 6.1.1.3 (ions) (*International Tables for Crystallography, Vol. C*, 1992)]

$$f(\text{atom}) = a(1)\exp[b(1)] + a(2)\exp[b(2)] + a(3)\exp[b(3)] + a(4)\exp[b(4)] + a(5)\exp[b(5)] + c$$

*Line 4:* Format(f12.6)

Neutron scattering cross section.

*Line 5:* Format(i6)

Flag for the source of the electron scattering factor.

[In some cases, values for atoms have been 'filled in' for ions. In this case the key is the same except the flag is negative (e.g. flag is -1 if have used scattering factors for a neutral atom from Smith & Burge for an ion).]

*Line 6,7:* Format(5f12.6/4f12.6)

Electron scattering factors in parameterised form:

```

a1 b1 a2 b2 a3 b3 a4 b4 c

```

$$f(\text{atom}) = a(1)\exp[b(1)] + a(2)\exp[b(2)] + a(3)\exp[b(3)] + a(4)\exp[b(4)] + c$$

*Line 8:* Format(7e12.4)

$\mu$  ( for the following radiations:

Ti,Cr,Fe,Co,Cu,Mo,Ag

All ions have the same  $\mu$  value as the neutral element.  $\mu$  values are taken from *International Tables Volume C* 193-199

*Line 9:* Format(7f12.6)

df' for the following radiations:

Ti,Cr,Fe,Co,Cu,Mo,Ag

*Line 10:* Format(7f12.6)

df'' for the following radiations:

Ti,Cr,Fe,Co,Cu,Mo,Ag

All ions have the same df' and df'' as the neutral element. df' and df'' are taken from *International Tables Volume C* 219-221.

*Line 11:* Format(2f12.6)

Covalent radius, van der Waals radius.

*Note:* Many Covalent radii and most van der Waals radii are approximate. The ions are given the same van der Waals radii as the neutral atoms. For heavy atoms there is very little knowledge of these parameters

In addition to the items specified above, information is taken from the following sources:

1. "New Analytical Scattering Factor Functions for Free Atoms and Ions", D. Waasmaier & A. Kirfel, (1995) *Acta Cryst.* A51, 416-431.
2. Rez, D, Rez, P. & Grant, I, (1994) *Acta Cryst.* A50, 481-497.
3. Smith, G.H. & Burge, R.E. (1962) *Acta Cryst.* 15, 182-186.
4. Doyle, P.A. & Turner, P.S. (1968) *Acta Cryst.* A24, 390-397.
5. Jiang, J.S. & Fang-Hua, L. (1984) *Acta Physica Sinica* 33, 845-849
6. A Bondi, (1963) *J. Phys. Chem.*, 68, 441-51.

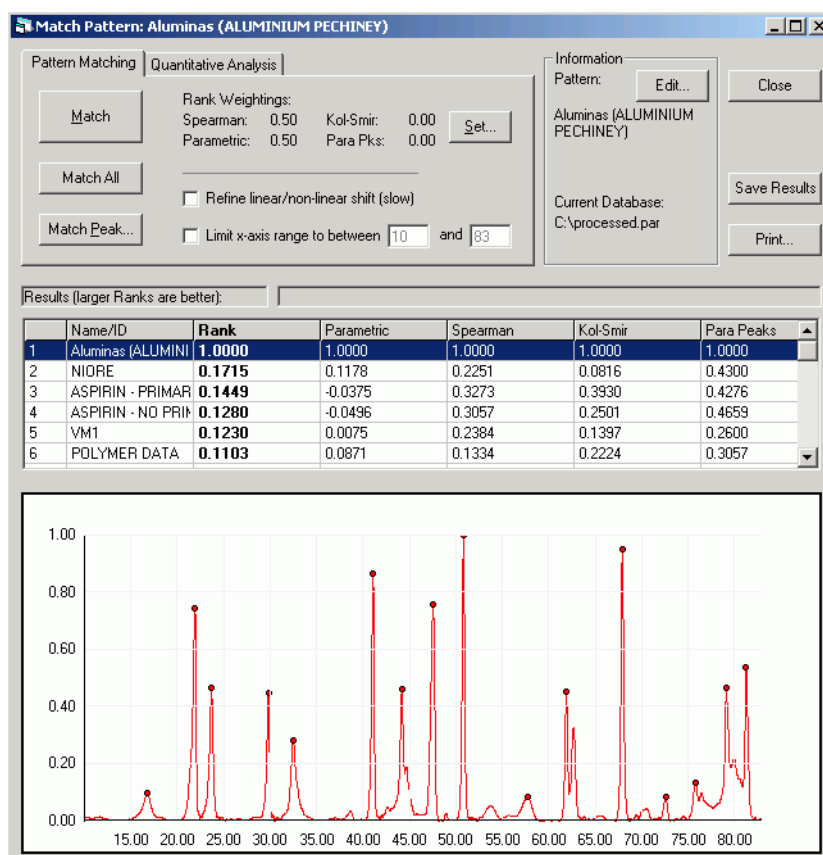
*Note:* The 'Format' described above refers to Fortran-style fixed format numbers. For example if the format is (3I4,2F8.2), the program expects to find 3 integers, each of 4 characters, followed by 2 floating point numbers, each of which total width 8 characters (including the decimal point, with 2 places after it).

---

## 3.4 Pattern Matching and Analysis

### 3.4.1 The Match Window

After selecting a pattern, and clicking the *Match* option, the Pattern Matching window appears:

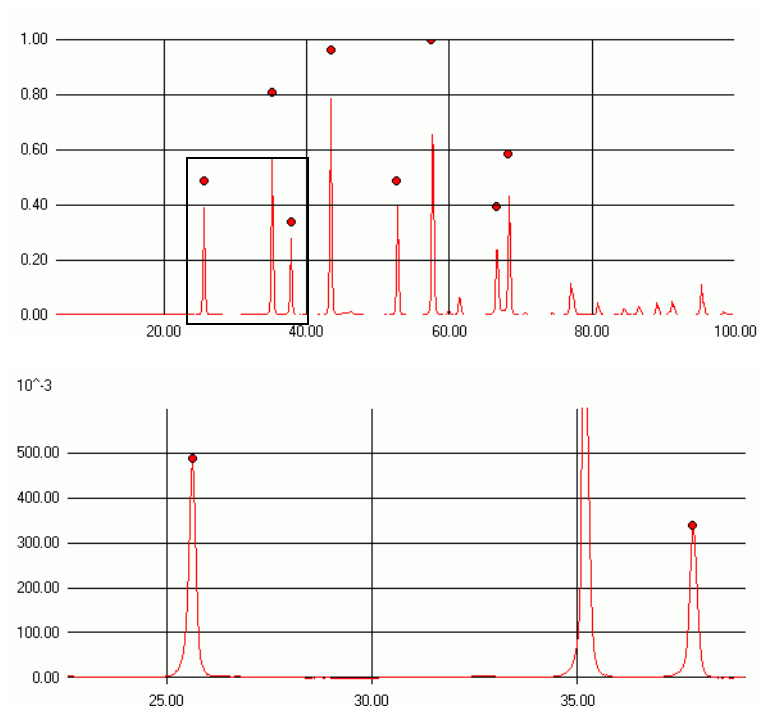


The two main active modes of the program are accessed from this central window.

### 3.4.2 Graph Pane

The pattern being matched appears in red the graph pane in the lower part of the window. It can be zoomed in and out in the same manner

as in the Pattern Editor, by using the mouse to drag a rectangle over the relevant area:



### 3.4.3 Results Pane

The central part of the window is a scrolling list where any matching results are displayed. This results pane contains, from left to right, the following fields:

	Name/ID	Rank	Parametric	Spearman	Kol-Smir	Para Peaks
1	ASPIRIN - NO PRII	2.0000	1.0000	1.0000	1.0000	1.0000
2	ASPIRIN - PRIMAF	1.8248	0.9217	0.9030	0.3012	0.9258
3	SAMPLE H	0.3602	0.0822	0.2780	0.2615	0.2506
4	ALREFHT	0.3449	0.2667	0.0783	0.0060	0.4468
5	Aluminas (ALUMINI	0.2890	-0.0267	0.3157	0.1729	0.3824
6	SAMPLE EB	0.2068	-0.0137	0.2205	0.0733	0.4255

The first field contains the number of the pattern, where No. 1 is at the top of the list. Clicking once in this leftmost column for a particular pattern entry results in a coloured dot appearing, and the corresponding pattern being shown in the graph pane, superimposed upon the matched pattern. The spot is the colour the pattern is displayed on the graph pane.

Clicking the same column again removes the pattern from the graph pane.

The next field is the *Name/ID* field. This normally shows the chemical name, but if this is "(Unknown)", it shows the short-filename of the pattern instead.

---

Next is the *Rank* value calculated for each pattern. This is obtained by summing the results from the four different matching tests, in a user-defined manner. By default the two are combined in a one to one ratio - see Section 3.4.8.2, Rank Weightings.

The *Parametric* field displays the result of the parametric correlation coefficient.

The *Spearman* field displays the result of the Spearman non-parametric correlation coefficient.

The *Kol-Smir* field displays the result of the Kolmogorov-Smirnov non-parametric statistics test.

The *Para Peaks* field displays the result of the parametric correlation coefficient, applied to marked peak regions only.

These individual tests are described in detail later.

The first two tests are applied to the entire full profile (*i.e.* every single datapoint) of each entry in the database. Consequently, they do not require any peak markers to have been located in the individual patterns. The last two tests are performed only upon individual marked peaks that coincide between the sample and database patterns.

### 3.4.4 Status Bar

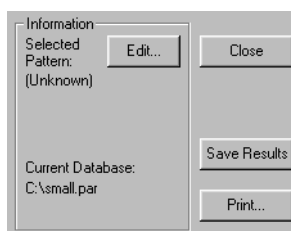
Above the results field is the Status Bar display:



The left side of this displays any status messages or errors. The right hand side consists of a progress bar. This indicates how far through the matching process the program is at any one time.

### 3.4.5 Mode-independent Controls

The upper-right portion of the window contains the matching controls. These are common to all of the operational modes:



*Information* display:



The top section contains the chemical name for the selected pattern (if known). The *Edit* button allows direct access to the Pattern Editor for the current pattern. This means that, for example, peaks could be added or removed at this stage.

The bottom section shows the name and location of the database the user is matching the unknown pattern against.

If either of these are too long to be displayed in the space, then the details are truncated, but the full information can be accessed by resting the mouse cursor over the appropriate region for a few seconds to reveal a 'tool tip' containing the full details.

On the far right hand side are the window controls:

*Close* - closes the window and returns to the database display. If any matching has been done, and results from it have not been saved, then the program will check if the user wishes to save them to a file.

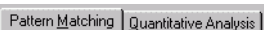
*Save Results* - once a matching calculation has taken place, this option allows the tabled results to be exported to either an ASCII text or Microsoft Excel compatible file. Enter the filename and select the filetype from the list in the standard File Save dialog box. This option is also available from the *File* menu. (*N.B.* only the results from the most recent matching run will be saved by this method, hence separate saves would be required to keep results from multiple runs.)

*Print* - brings up a standard Windows Print dialog, and causes the current contents of the graph pane to be sent to your selected printer. This option is also available under the *Graph* menu.

Note that printing to a postscript printer may be very slow as every single datapoint (usually several thousand) is sent to the printer. Much faster results can be obtained with a non-postscript printer, for example an inkjet.

The remaining controls in the window are the mode-dependant controls.

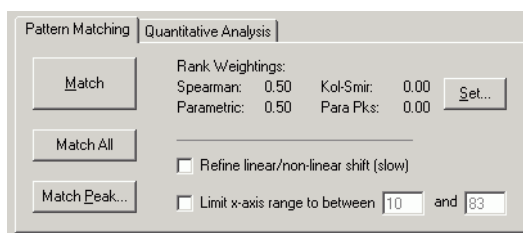
The user can switch between the two matching modes by means of the tabs in the top left of the window:



---

### 3.4.6 Pattern Matching

The first tab represents the Pattern matching program mode:



This process involves the repeated comparison of pairs of datasets, the *sample* and the *database* patterns.

The sample pattern is the pattern that is being compared to the rest of the patterns in the database. For each pattern, a comparison is made as follows:

1. The full profiles of the patterns are compared on a point by point basis using the non-parametric Spearman rank-order coefficient test. The result from this appears in the results column headed '*Spearman*'. A score of 1.0 represents a perfect match, 0.0 the worst possible match, and -1.0 a negative correlation (see Section 3.6, References).
2. A parametric Pearson equivalent of the Spearman test is then applied, both to the full intersecting profile (results shown in column *Parametric*), and to individual corresponding peaks (results shown in column *Para Peaks*).
3. If any peaks have been marked in the sample and database patterns, the probability of correlation between the two is also calculated using the Kolmogorov-Smirnov test (see Section 3.6, References).
4. The range of each peak to be tested is taken to be the intersection of the two peaks ranges, calculated by tracing their shoulders until either the intensity falls below a set threshold, or the intensity starts to increase again.
5. The pattern with the greater number of peaks is taken as a reference, (its number of peaks =  $m$ ).

The Kolmogorov-Smirnov test is then performed on each of these peaks, and a probability value  $p$  returned for each one. This is 1.0 where peaks are identical and zero when a peak is matched against no peak.

Then K-S value for the overall pattern is:

$$(p_1+p_2+p_3+\dots+p_m)/m$$

which returns a value between 0 and 1.0. Note that the test results for each individual peak can also be examined in the Single Peak Viewer - see Section 3.4.8.6, Match Peak.

6. Results are reported in the *Kol-Smir* column, where a result of 1.0 corresponds to a perfect match. This is also true of the *Para Peaks* result, which is calculated in a similar manner.

7. Finally, a *Rank* value is calculated for each database sample after comparison, comprised of a weighted mean of each of the available statistics. These weights are user-definable - see Section 3.4.8.2, Rank Weightings.

### 3.4.7 Non-quantitative Peak Matching:

Click the *Match* button (or press F1). Matching will commence. Progress is indicated by the progress bar and status bar:



Once matching has completed, the results will be displayed in the results pane:

Results (larger Ranks are better):						
	Name/ID	Rank	Parametric	Spearman	Kol-Smir	Para Peaks
1	ASPIRIN - PRIMAF	<b>2.0000</b>	1.0000	1.0000	1.0000	1.0000
2	ASPIRIN - NO PRII	<b>1.8248</b>	0.9217	0.9030	0.1485	0.9247
3	ALREFHT	<b>0.4619</b>	0.4137	0.0482	0.0063	0.4843
4	SAMPLE H	<b>0.3401</b>	0.1171	0.2230	0.1766	0.3885
5	Boldenone undecyl	<b>0.3182</b>	0.1953	0.1229	0.0115	0.3295
6	SAMPLE EB	<b>0.1502</b>	-0.0095	0.1597	0.1984	0.4731

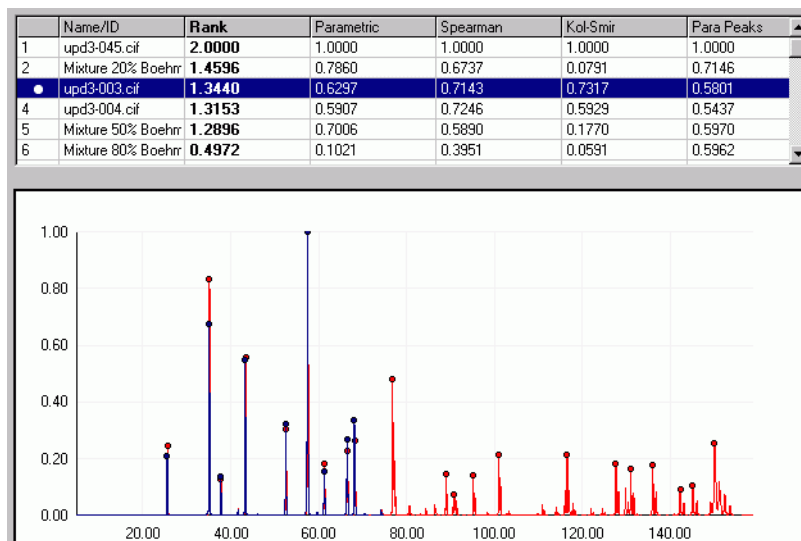
The best overall match is shown at the top of the list, which is sorted by default in descending order of Rank. The best match is always the pattern you are matching against. This provides a useful check that everything is operating correctly, since the unknown pattern matched against itself should give a perfect match in all four tests.

*i.e.* it should have a

- Spearman of 1.0
- Parametric of 1.0
- Kol-Smir of 1.0
- Para Peaks of 1.0

and a rank (calculated from  $0.5 \times \text{Spearman} + 0.5 \times \text{Parametric}$ ) of 1.0 (assuming default weightings).

To view a pattern overlaid on the matched pattern, click once in the leftmost column of that pattern (the third row in the example below):



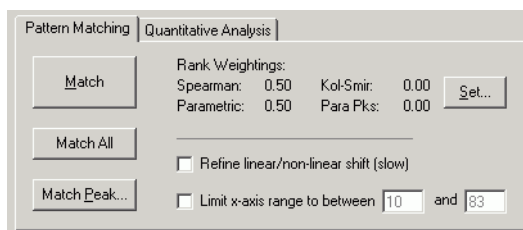
Clicking once in this column for a particular pattern results in a coloured dot appearing, and the corresponding pattern being shown in the graph pane, superimposed upon the matched pattern using the colour of the spot.

Clicking the same column again removes the pattern from the graph pane. Up to seven different patterns can be displayed at once in this manner. To remove multiple displayed graphs in one step, a *Remove Overlaid Graphs* option is available from the *Graph* menu, or the pop-up menu obtained by right-clicking on the graph region.

The sort-order in which the results are displayed can be changed by clicking the header of the column on which you wish the results sorted. Clicking the same header again causes the results to be sorted in that same column, but in the opposite order *i.e.* repeatedly clicking on one header causes the sort order to switch between ascending and descending.

If the top few patterns appear to be a really bad match, the chances are that the list has been sorted in descending order. Click again to re-sort.

### 3.4.8 Advanced Options



#### 3.4.8.1 Refine linear/non-linear offset

Selecting the *Refine linear/non-linear offset* checkbox causes an  $2\theta$ -axis offset to be computed when comparing patterns.

For example, if two patterns are very similar, except that one is offset by +0.3 degrees along the  $2\theta$ -axis from the other, selecting this option should reveal this.

The maximum amount by which patterns are allowed to be offset can be changed from the default of 0.4 degrees by changing the values in the *Advanced* pane of the program *Options* dialog box. The program attempts to maximise the correlation between patterns by varying the values  $a_0$  and  $a_1$  in the equation  $\Delta 2\theta = a_0 + a_1 \sin \theta$ , although  $\cos \theta$  or  $\sin 2\theta$  may optionally be used instead.

After turning the option on, click *Match* to begin the matching. This process will be much slower than the default matching, as many more calculations are being performed for each pattern.

Once complete, the results are displayed as before, with one difference. There is now an additional column on the far right - *Offset used*:

	Name	Rank	Parametric	Spearman	Kol-Smir	Para Peaks	Offset used
1	Aluminas (ALUM)	<b>1.0000</b>	1.0000	1.0000	1.0000	1.0000	0, 0
2	ASPIRIN - PRIM	<b>0.2191</b>	0.0149	0.4233	0.3930	0.4276	-0.4, 0.38
3	ASPIRIN - NO P	<b>0.2109</b>	0.0101	0.4117	0.2501	0.4659	-0.4, 0.23
4	NIORE	<b>0.1867</b>	0.1792	0.1942	0.0816	0.4300	-0.25, 0
5	FRANK	<b>0.1399</b>	0.1709	0.1089	0.1455	0.2872	-0.4, 0.4
6	VM1	<b>0.1383</b>	0.0193	0.2574	0.1397	0.2600	-0.4, 0.38

This corresponds to the amount of offset ( $a_0$ ,  $a_1$ ) required to maximise the correlation coefficients for each pattern.

As a shift of up to about one degree can be possible when dealing with patterns of the same substance recorded with different experimental conditions, and this option may be useful to reveal matches between patterns that at first appear to be different.

Note that at present the shift only applies to the profile based tests and that this option can slow down the operation of the program substantially.

### 3.4.8.2 Rank Weightings

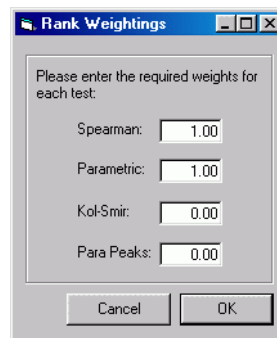
For patterns of a particular type, it may be the case that one particular correlation coefficient proves to be more useful than others.

In order to relate this fact to the overall ranking of pattern matches, it is possible to change the way the overall rank is calculated.

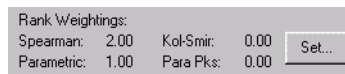
Normally, this is of the form:

$$\begin{aligned} Rank = w_1 \times (Parametric\ score) + w_2 \times (Spearman\ score) \\ + w_3 \times (Kol-Smir\ score) + w_4 \times (Para\ Pks\ score) \end{aligned}$$

where  $w_1$  and  $w_2$  are the rank weightings, normally both 1.0. By varying these weightings.



It is possible to alter the overall rank order of the matched patterns, for example:

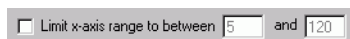


Once the weighting have been altered, the *Apply* button is activated. Clicking it applies the new rank weightings to the current list of matched results:

	Name/ID	Rank	Parametric	Spearman	Kol-Smir	Para Peaks
1	Corundum.txt	<b>3.0000</b>	1.0000	1.0000	1.0000	1.0000
2	upd3-003.cif	<b>2.3966</b>	0.7482	0.8242	0.1534	0.9124
3	upd3-004.cif	<b>2.3810</b>	0.7426	0.8192	0.1700	0.9047
4	upd3-045.cif	<b>2.2111</b>	0.5541	0.8285	0.0758	0.7421

If rank weightings are changed from the default values before a match has taken place, the new values are used automatically when the results are displayed.

### 3.4.8.3 Limit x-axis range...



Turning on the *Limit x-axis range* checkbox has the effect of limiting the analysis calculation to a subset of the entire x-axis range of the unknown pattern. This can be useful if a particular feature of the pattern is causing problems for the calculation.

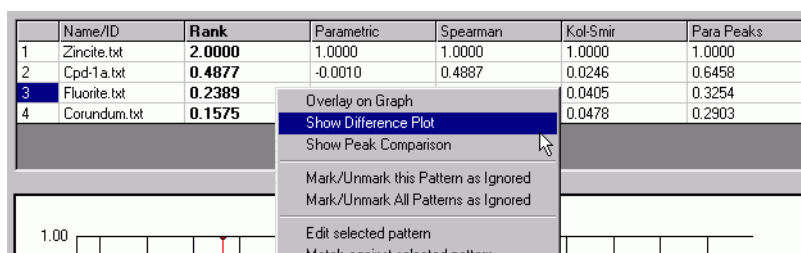
The default values in the textboxes are the full range of the unknown pattern, although these can be changed by either:

1. Typing in the desired start and end angles of the required range into the textboxes, or:
2. Zooming in to the desired range by clicking and dragging a zoom-rectangle on the graph pane. The start and end ranges of the  $2\theta$ -range of the zoomed region of the pattern will be automatically placed in the textboxes.

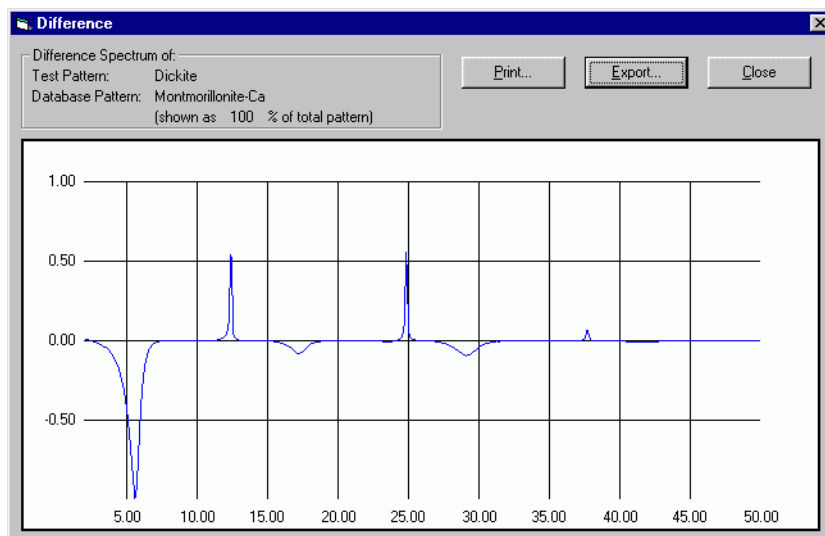
To use this feature, turn the checkbox on, enter the desired start- and end- details, and click the *Calculate* button.

### 3.4.8.4 Difference Plots

When comparing two very similar patterns it can be useful to get a different kind of visual feedback as to their similarity. One such feedback method is the difference plot, which subtracts the selected database pattern from the unknown pattern and displays the remainder. This feature is accessed by first clicking once to select a database pattern from the list of match results, and then either selecting *Show Difference Plot* from the *Pattern* menu, or clicking once with the right-hand mouse button to access the results pane pop-up menu:



Selecting the *Show Difference Plot* option brings up the following window:



The *Print* button outputs the graph pane to the local Windows printer.

The *Close* button returns to the main Match window.

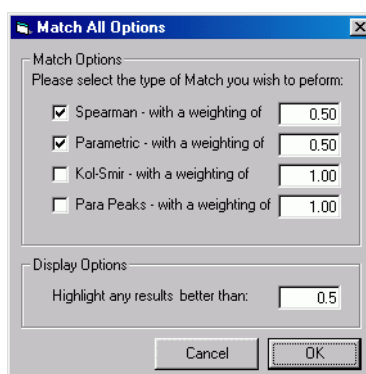
The *Export* button saves the difference profile to an ASCII text file.

#### 3.4.8.5 Match All

This option is only available for a maximum of 1000 patterns in a database. It matches every pattern in the database against every other pattern in one step, and displays a matrix of results.

Please note that with this large number of patterns the matching process will take some time to complete, and this will be exacerbated if the allow x-offset option is enabled.

Clicking the *Match All* button produces a dialog in which to select the individual tests to be used:





Select the tests of choice, their required weightings and enter the highlight cut-off value (any results greater than this value will be highlighted in the results table).

Clicking *OK* initiates the matching process. This may take some time, as  $n^2/2-n$  matching tests are being performed (where  $n$  is the number of patterns in the database). When over 50 patterns are being matched, a window with a progress bar is displayed. When complete, the results are displayed as follows:

	upd3-004.c	upd3-005.c	upd3-006.c	upd3-007.c	upd3-008.c	upd3-010.c	upd3-014.c	upd3-015.c	upd3-016.c	upd3-017.c
upd3-	<b>1</b>	-1.958017E	-1.340543E	-1.788726E	-1.675198E	-6.313147E	-1.085791E	-1.579619E	5.26832E-1	6.930218E
upd3-	-1.958017E	<b>1</b>	<b>0.856992</b>	-2.006913E	<b>0.925139</b>	-0.0159797	-2.706579E	-5.597485E	7.042118E	0.0161234
upd3-	-1.340543E	<b>0.856992</b>	<b>1</b>	-1.078085E	<b>0.940968</b>	-1.085994E	-1.904628E	-7.160438E	-6.845203E	-5.209728E
upd3-	-1.788726E	-2.006913E	-1.078085E	<b>1</b>	6.384566E	-1.180575E	-2.069083E	-9.256598E	-6.849316E	-6.128258E
upd3-	-1.675198E	<b>0.925139</b>	<b>0.940968</b>	6.384566E	<b>1</b>	-1.396583E	-2.449129E	-8.501349E	-8.519993E	-6.499929E
upd3-	-6.313147E	-0.0159797	-1.085994E	-1.180575E	-1.396583E	<b>1</b>	<b>0.733269</b>	3.687835E	3.371778E	0.2762358
upd3-	-1.085791E	-2.706579E	-1.904628E	-2.069083E	-2.449129E	<b>0.733269</b>	<b>1</b>	0.1159216	8.542597E	<b>0.548274</b>
upd3-	-1.579619E	-5.597485E	-7.160438E	-9.256598E	-8.501349E	3.687835E	0.1159216	<b>1</b>	0.1743946	0.2046806
upd3-	5.26832E-1	7.042118E	-6.845203E	-6.849316E	-8.519993E	3.371778E	8.542597E	0.1743946	<b>1</b>	<b>0.548263</b>
upd3-	6.930218E	0.0161234	-5.209728E	-6.128258E	-6.499929E	0.2762358	<b>0.548274</b>	0.2046806	<b>0.548263</b>	<b>1</b>

The results pane is automatically vertically enlarged to show more of the results. To toggle between this enlarged size, and the standard size, click on the grey region between the results table and the graph pane.

Any test scores that are above the cut-off level selected in the preceding dialog box are highlighted in bold. This procedure may reveal hitherto unnoticed correlations between different patterns in a database.

All the matching results obtained against *upd3-004* are shown in the first column, *upd3-005* in the second, and so on. By looking at the intersections between patterns, an idea of the similarities between any two database patterns may be obtained.

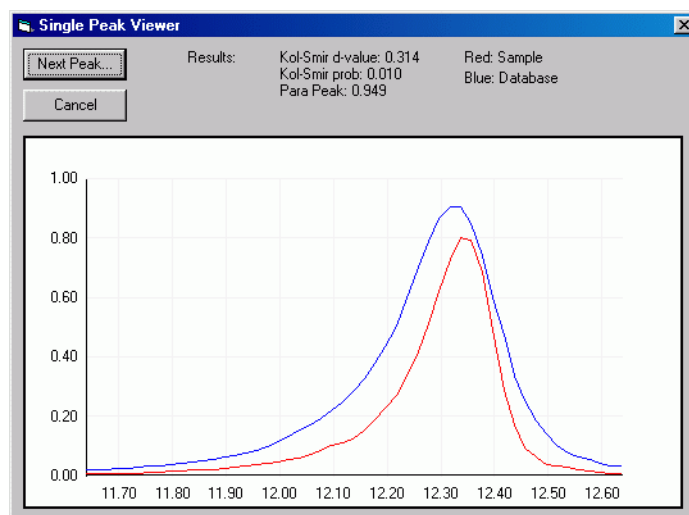
To view a particular correlation of interest graphically, click once on the grid square containing the result. For example, the patterns *upd3-005* and *upd3-008* have a match score of 0.9251 in the above result. Clicking on the square containing the 0.9251 results in the two patterns of interest being superimposed on the graph pane below to allow visual comparison.

If the option to refine pattern shifts was selected, after clicking on a given correlation, holding the mouse steady for a second brings up a tooltip containing the calculated best offset for the two patterns, in the form  $(a_0, a_1)$  as discussed above.

### 3.4.8.6 Match Peak

Individual corresponding peaks can be easily compared in this mode. This can be particularly useful to spot very small differences between otherwise almost identical patterns: click once in the results list to select the pattern you wish to compare the unknown pattern with.

Then click the *Match Peak...* button (or select *Show Peak Comparison* from the *Pattern* menu). The window will appear for the first of the matched peaks:

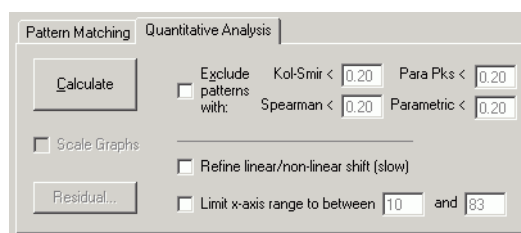


Clicking *Next Peak* closes this window and opens another for the next peak common to both patterns. *Cancel* returns to the match window.

Detailed results of the Kol-Smir and Parametric Peaks test results are shown on an individual peak basis in this window (these individual values are combined to give the result for the whole pattern displayed in the main match window results pane).

## 3.5 Quantitative Analysis

The second tab represents the second of the main program modes: Quantitative Analysis:



This is used with patterns of mixtures to estimate their percentage composition from pure component patterns contained in the

matching database. **Note that for the method to work successfully, patterns corresponding to all pure phases in the mixture must be present in the current working database.**

### 3.5.1 Standard Quantitative Analysis:

Click the *Calculate* button (or press F3). Analysis of the selected unknown pattern will commence. Prior to analysing, a pattern matching calculation is performed.

The progress and status bars indicate this:



Before showing that analysis is taking place:



Note that this process may take some time, depending on the number of patterns included in the calculation. The progress bar is **not updated** during the calculation of relative proportions, so patience is required as the calculations are very processor intensive, and may take several minutes. The screen is not updated or redrawn while this is happening.

Once analysis has completed, the results will be displayed in the results pane:

Analysis Results:								
	Name	Rank	Parametric	Spearman	Kol-Smir	Offset used	Scale %	Std Dev.
1	Anatase	1.8144	0.9995	0.8149	0.0000	0.0000	74.7	4.5
2	Gibbsite	0.1672	0.0219	0.1454	9.2103	0.0000	15.0	8.0
3	Fluorite	0.5043	0.0122	0.4922	20.6356	0.0000	10.3	5.1

Note that the headers have changed. Although the first 6 columns are the same as before, there are 3 new columns:

#### 1. Offset used:

The offset given to a particular pattern that gave the best match; see section 4.4.2.1

#### 2. Scale % or Weight %:

Displays what proportion of the mixture is accounted for by an individual database pattern. This is normally displayed as a scale percentage *i.e.* what percentage of the mixture *pattern* does each individual phase constitute?

If all the required advanced pattern information has been entered (see Section 3.3.11, Additional Pattern Information), the program converts this scale percentage to an actual percentage of the mixture by weight. In this case, the column heading is changed to Weight %.

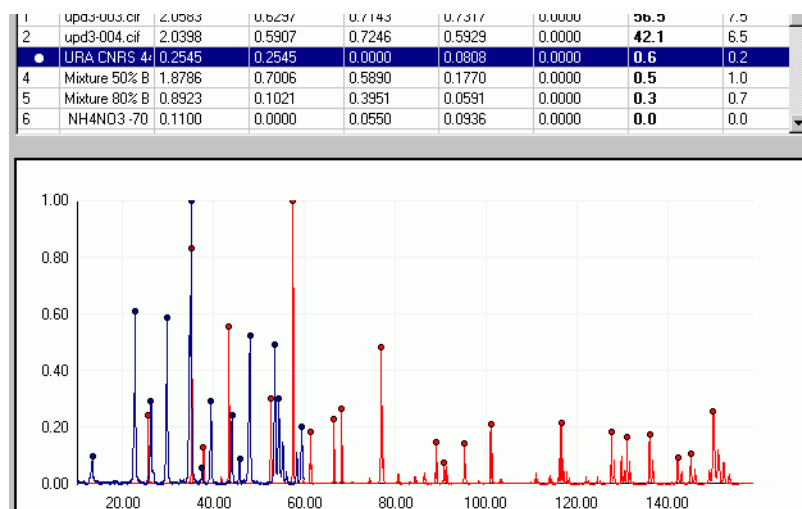
Note that this information must have been entered for ALL phases in the mixture to be able to calculate a weight fraction.

### 3. Std Dev.

The standard deviation of the percentage composition calculation reported for each pattern.

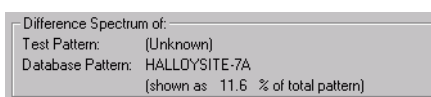
By default, the maximum number of patterns that will be reported as included in a mixture is 6, although this is easily changed. (see section 4.6, Matching Options)

As before, patterns can be displayed over the unknown pattern by clicking once in the leftmost column:



This can provide valuable visual feedback for the user to check if the suggested constituents of the unknown mixture are indeed correct.

To view a phase pattern on top of the mixture pattern scaled to the percentage result suggested, check the *Scale Graphs* checkbox, and then click on the pattern to display it in the usual way. If the *Scale Graphs* option is checked, and the *Show Difference Graph* option is selected, the individual phase pattern will be subtracted from the mixture pattern scaled to the relevant %. The amount of scaling performed is shown in the difference graph window:

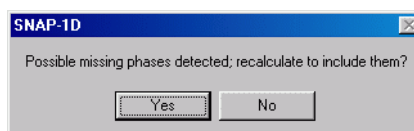


Additional feedback on the results is given by the calculated error on the suggested percentage, and by how good the matching results of the Spearman, Parametric and Kol-Smir tests were for each phase.

Occasionally if an incorrect pattern has been suggested by the program, this may be shown by extremely low values of the Spearman, Parametric and Kol-Smir tests, and such patterns can be marked to be ignored during subsequent runs - see 3.5.2.2, Exclude patterns...).

### 3.5.1.1 Automatic Missing Phase Detection

The program examines the results from the analysis, and based on the calculated error and residual trace can suggest if the result does not account sufficiently for all of the unknown pattern intensity:



This would occur in a case where not all of the phases present in a mixture pattern were in the database being used.

Selecting *Yes* in the above dialog causes the program to simulate a pattern corresponding to the intensity unaccounted for by the current results. (This simulated pattern is equivalent to the pattern obtained by saving the positive intensity trace from the Residual window; see Section 3.5.2.6, Residual Window for more details.)

The calculation is then re-run to include this simulated missing phase, and results re-calculated:

	Name	Rank	Parametric	Spearman	Kol-Smir	Offset used	Scale %	Std Dev.
1	Mixture.TXT	<b>2.0000</b>	1.0000	1.0000	1.0000	0.0000	0.0	0.0
2	Phase 2.TXT	<b>1.1987</b>	0.9619	0.2368	0.6668	0.0000	44.9	0.8
3	Simulated Mis:	<b>0.8548</b>	0.2642	0.5905	0.2242	0.0000	53.8	3.0
4	Phase 1.TXT	<b>0.0000</b>	0.0000	0.0000	0.0866	0.0000	1.3	0.5

Note that results cannot be calculated in terms of weight fraction when simulated missing phases are included.

After doing an analysis, and choosing to include a missing phase, when the user closes the match window, the program checks to see if the simulated phase should be retained in the current database or discarded.

If the pattern is retained, it shows up in the database window with a name of 'Simulated Missing Phase', although this can of course be altered in the Edit window later.

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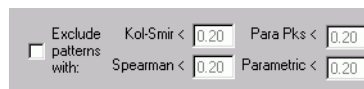
The settings used by the program to determine if a missing phase may be present can be controlled by the user; see section 4.3.10 on page 118.

### 3.5.2 Advanced Analysis

#### 3.5.2.1 Refine linear/non-linear shift

This option works as described in Section 3.4.8.1, Refine linear/non-linear offset.

#### 3.5.2.2 Exclude patterns...



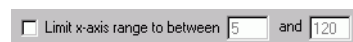
Selecting the *Exclude Patterns* checkbox can be extremely useful to narrow down the number of patterns to be considered as components of the unknown pattern. It does this by excluding patterns that are below user-set thresholds on any of the matching tests to be included in the quantitative calculation.

The default values may be easily altered by changing the relevant values in the text boxes. The best values to use can change depending on the type of data being considered.

Generally, the best approach is to perform a standard analysis with defaults to begin with, and see if any poorly matching patterns have been included. The results from this will then give a feel for what values the cut-offs should be set at. This option also has the side benefit of speeding up the process as less patterns are used.

To use this option, turn on the checkbox, enter the desired values, and click the *Calculate* button as normal.

#### 3.5.2.3 Limit x-axis range...



Turning on the *Limit x-axis range* checkbox has the effect of limiting the analysis calculation to a subset of the entire x-axis range of the unknown pattern. This can be useful if a particular feature of the pattern is causing problems for the calculation.

The default values in the textboxes are the full range of the unknown pattern, although these can be changed by either:

1. Typing in the desired start and end angles of the required range into the textboxes, or:

2. Zooming in to the desired range by clicking and dragging a zoom-rectangle on the graph pane. The start and end ranges of the x-range of the zoomed pattern will automatically be placed in the textboxes.

To use this feature, turn the checkbox on, enter the desired start- and end- details, and click the *Calculate* button.

### 3.5.2.4 Ignore selected pattern

	Name/ID	Rank	Parametric	Spearman	Kol-Smir	Para Peaks
1	Zincite.txt	<b>2.0000</b>	1.0000	1.0000	1.0000	1.0000
2	Cpd-1a.txt	<b>0.4877</b>	-0.0010	0.4887	0.0246	0.6458
3	Fluorite.txt	<b>0.2389</b>	-0.0034	0.2423	0.0405	0.3254
X	Corundum.txt	<b>0.1575</b>	-0.0042	0.1617	0.0478	0.2903

If a particular pattern included in the list of suggested results is known to be incorrect, it can be excluded from the calculation, by clicking once on it in the results pane to select it, and then by either right-clicking to bring up the results-pane pop-up menu, using the *Mark/Unmark Pattern as Ignored* option in the *Pattern* menu.

Select *Mark/Unmark this Pattern as Ignored*. A large, bold **X** will appear next to the pattern name in the first column, to indicate it is being ignored for the purposes of the calculation.

Once a pattern has been selected as ignored, click the *Calculate* button again to re-run the calculation, which will be performed without any the 'Ignored' patterns.

If the pattern was incorrectly marked as ignored, it may be unmarked, by simply repeating the above procedure, and selecting *Mark/Unmark this Pattern as Ignored* once more. The large **X** will disappear.

It is possible to mark multiple patterns to be ignored by repeating this process with different selected patterns.

### 3.5.2.5 Ignore All patterns except.

	Name/ID	Rank	Parametric	Spearman	Kol-Smir	Para Peaks
X	Zincite.txt	<b>2.0000</b>	1.0000	1.0000	1.0000	1.0000
X	Cpd-1a.txt	<b>0.4877</b>	-0.0010	0.4887	0.0246	0.6458
X	Fluorite.txt	<b>0.2389</b>	-0.0034	0.2423	0.0405	0.3254
X	Corundum.txt	<b>0.1575</b>	-0.0042	0.1617	0.0470	0.2000

In situations where the particular constituent patterns of an unknown mixture are known, but only the relative percentages of each are unknown, it is useful to be able to only include the correct components in the calculation. This not only speeds up the process but can generally improve the accuracy of the results.

The simplest way to achieve this is to first mark all of the patterns in the database to be ignored, and then un-mark the individual patterns that are known to be present in the mixture.

To achieve this, right-click on the results pane to bring up the pop-up menu, or use the *Pattern* menu: select *Mark/Unmark all Patterns as Ignored* from the options presented. A black bold **X** will appear in the first column of the results pane next to every pattern shown. (*N.B.* if any patterns have previously been marked as ignored, these will be un-marked by this process).

Next, individually unmark the patterns that are to be included by selecting them singly, and selecting *Mark/Unmark this Pattern as Ignored* from the pop-up menu. Then select *Calculate* as normal.

To unmark all of the marked patterns simultaneously, select *Mark/Unmark all Patterns as Ignored* again from the pop-up menu. All patterns that were marked as ignored will become unmarked, and *vice-versa*.

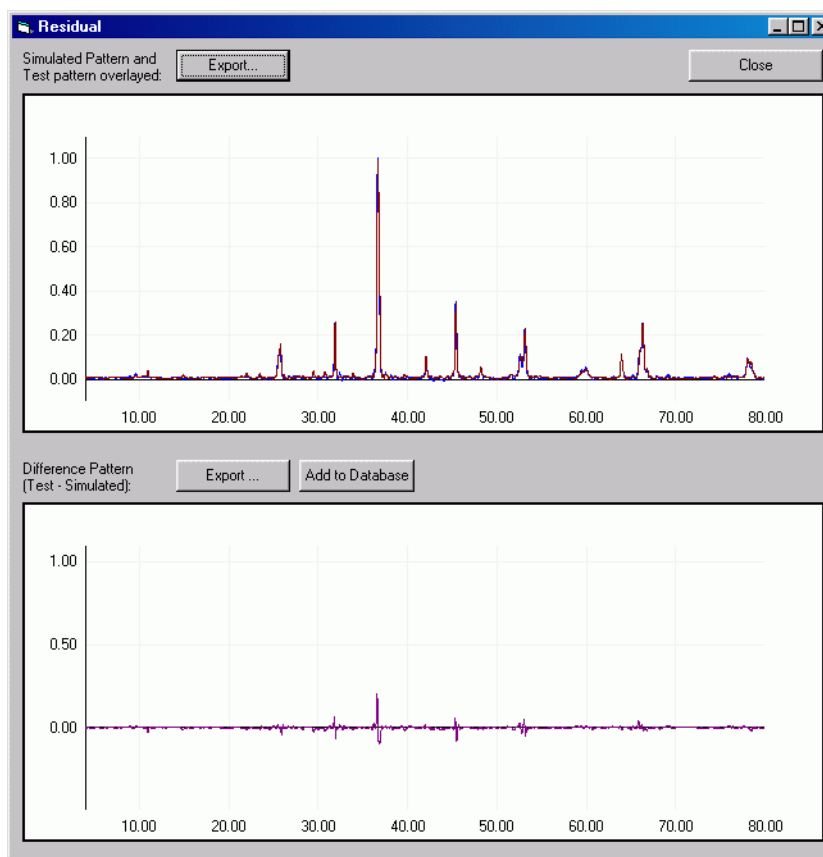
*N.B.* If the patterns that have been marked and unmarked become confused, it is possible to reset all of the patterns in the database to the default state of all being included in a calculation, by closing the match window and then re-opening it.

### 3.5.2.6 Residual Window

To see if the suggested results are correct, or if they include a pattern not present in the mixture, or if they miss out a pattern that should be there, the residual window constructs a calculated pattern made up from the various individual patterns suggested as mixture components, in the proportions calculated.



Clicking the *Residual* button brings up the following window:



The upper window overlays the original mixture pattern (in blue) with the calculated one using the suggested results (in red/brown).

The difference between the two profiles is shown in the bottom window. Large negative peaks in this correspond to incorrect peaks, and would suggest one or more of the suggested constituent phases are incorrect. Positive peaks here would represent peaks in the original pattern not accounted for in the suggested results.

The simulated mixture pattern can be saved to an ASCII text file using the *Export Simulated* button. The difference plot can be saved to an ASCII file using the *Export Difference* button.

In the latter option, two different formats are available from the pop-up list at the bottom of the Windows Save dialog. The first (*Full residual*) saves the difference profile as it is shown in the window, with some peaks negative and some positive. The second (*Positive residual*) ignores any negative peaks and saves only positive ones in order to make a pattern comprising only intensity not accounted for by the current pure phases.

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Exported difference profiles can be re-imported and treated as new patterns, and further quantitative analysis can be performed using them if required. This can be done manually or by using the *Add to Database* option.

### 3.5.3 Other Options

#### *Edit this pattern*

Having performed a match or analysis procedure, it may be that one pattern listed in the results table is of particular interest. It is possible to view the Pattern Editor window for such a pattern directly, by first clicking once on the pattern of interest in the list, and either selecting *Edit* from the *Pattern* menu, or *Edit this Pattern* from the pop-up menu.

Either option brings up the editor dialog allowing detailed information about a pattern to be viewed or edited.

#### *Match against this pattern*

Having performed a match or analysis procedure, it may be that one pattern listed in the results table is of particular interest, and the user may wish to perform an additional match or analysis with that pattern.

It is possible to open another Match window for such a pattern directly, by first clicking once on the pattern of interest in the list, and either selecting *Match* from the *Pattern* menu, or *Match against this Pattern* from the pop-up menu.

Either option brings up a new Match window. The original Match window is still open and may be viewed as desired. As many Match windows as required may be open at the same time.

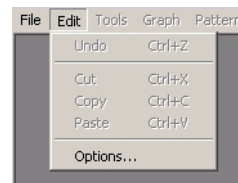
## 3.6 References

1. Spearman, C. (1904). 'The proof and measurement of association between two things'. *American Journal of Psychology*, 15, 72-101.
2. Smirnov, N.V. (1939). 'Estimate of deviation between empirical distribution functions in two independent samples.' *Bulletin Moscow University*, 2(2) 3-16.
3. Press, W.H., Teukolsky, S.A., Vetterling, W.T., Flannery, B.P. *Numerical Recipes in C: The Art of Scientific Computing*, Second Edition, Cambridge University Press, 1992.

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## 4.1 Accessing Options

The options menu can be accessed at any point from the *Edit* menu.



The *Options* window is comprised of three tab sections which can be selected from the top of the window.



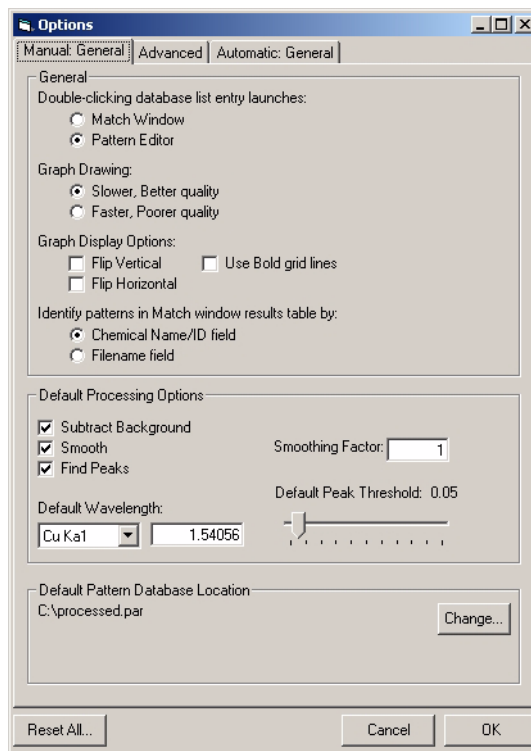
These are each described in turn below.

Note that that 'Manual' settings do not affect Automatic Analysis runs and vice versa.

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## 4.2 Manual Analysis: General Options

When the *Options* window first opens it displays the *Manual Analysis* section first by default.



This first tab is split a general section and a processing section.

### 4.2.1 General Section

#### *Double-clicking Database Lists*

The first option controls whether double-clicking a pattern entry in an open database window brings up the match window or the pattern editor window. By default this is set to being the *Pattern Editor*:

#### *Graph Drawing*

Decides whether the patterns are displayed in a high-quality, but slow to draw mode, or a faster but lesser quality mode. The slower option is the default.

*Use Bold Grid Lines* checkbox controls if a black grid shown behind patterns on the graph, or if light-grey lines are used. The latter is the default.

The two *Data Display* checkboxes control whether the patterns are displayed as read in from their original data files, or flipped in either

the x or y axes. These options may be useful when examining different types of non-powder diffraction x-y data.

#### 4.2.1.1 Results Display

This section contains a toggle to switch between displaying the Chemical name/ID or the Filename of patterns in the Match window and other results lists.

#### 5.1.1.3 Processing Options

The next section controls which of the three main processing options are turned on by default in the window which appears when patterns are being imported. A default wavelength can be selected - either one of the standard ones from the pop-up list, or a custom value entered into the text box. The default value is CuK $\alpha$ .

#### 5.1.1.4 Smoothing Factor

Varying the number in this box controls the amount of noise removal performed by the wavelet smoothing. The larger the number, the smoother the resulting pattern. Be careful of oversmoothing and losing valuable information. 1 is a good default value in most cases.

#### 5.1.1.5 Default Peak Threshold

The next control changes the default peak threshold. Only peaks whose maximum intensity are above this cut-off value will be marked as such. The default value of 0.05 can be changed by dragging the slider left or right. The corresponding numerical value for the threshold is shown to the right of the slider.

#### 4.2.1.2 Default Pattern Database Location

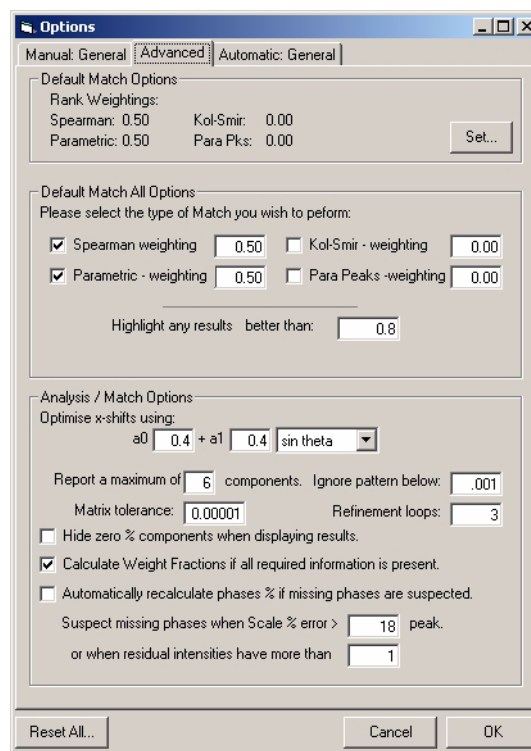
The final region lets the default database be located and selected. This is the database that is opened when the *Open Default* option is selected from the *File* menu.

To change, click the *Change...* button. A Windows file selection dialog box will appear. Locate and select the database required, and click *Open*.

The file and location selected should be displayed in the window. In the example shown above, the default is *processed.par* which is located at C:\.

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## 4.3 Manual Analysis: Advanced Options



The second tab, *Advanced*, contains the more in depth matching and quantitative analysis controls.

### 4.3.1 Default Match Options

This section controls the default values for the Rank Weightings in the Match Window.

The default values are: Spearman 0.5, Parametric 0.5, Kol-Smir 0.0, Para Pks 0.0.

### 4.3.2 Default Match All Options

This section controls which matching tests and what corresponding weightings come up by default in the Match All settings window. Initial values are to use the Spearman and Parametric tests, each with a weighting of 0.5.

Note that it is recommended that the sum of any weights used is 1.0.

### 4.3.3 Optimise x-shifts

This section controls how patterns will be shifted in an attempt to maximise the correlations between them. By default the program attempts to maximise the correlation between patterns by varying the

values  $a_0$  and  $a_1$  in the equation  $\Delta 2\theta = a_0 + a_1 \sin \theta$ , although  $\cos \theta$  or  $\sin 2\theta$  may optionally be used instead by selecting the relevant item from the drop-down menu.

The values of  $a_0$  and  $a_1$  that may be entered here represent the maximum values that will be allowed by the program during the refinement.

#### 4.3.4 Report a maximum of $n$ components

Report a maximum of  components.

The maximum number of patterns that PolySNAP M suggests as being constituents of an unknown mixture can be easily changed by the user. By default, it reports a maximum of 6 components. This default can be changed to any integer between 1 and 15. Note that this must be done before a match window is opened in order for any changes to take effect.

#### 4.3.5 Matrix tolerance

The second controls what proportion of the patterns that do not contribute significantly to the overall pattern are ignored. This should be a number between 1 and 0. The default is  $1 \times 10^{-5}$ .

#### 4.3.6 No. of refinement loops

The Refinement loops field controls how many loops of refinement the program performs. This should be an integer between 1 and 3. If it is 1, all patterns are included. If it is 2, all patterns are used, then only the top 15 are included the second time around. If it is 3, then all patterns, then the top 15, then the top  $N$ , where  $N$  is the number of components selected above, are included.

#### 4.3.7 Ignore pattern below...

This (default is 0.001) controls how much of each database pattern is treated as background upon inclusion in the calculation. This is done to simplify the problem and reduce the effect of background noise.

#### 4.3.8 Hide zero % components in results

Hide zero % components when displaying results.

With a database containing a large number of patterns, performing an analysis usually results in a few patterns contributing towards a

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mixture, with the rest being ranked at 0.0%. This option hides any patterns that are not considered contributors to the mixture.

#### 4.3.9 Calculate Weight Fractions if possible

Calculate Weight Fractions if all required information is present.

This checkbox allows the program to automatically display analysis results as a weight fraction rather than proportional to scattering power, if all the necessary pattern information is available.

With it turned off, a scale percent is reported even if all pattern information is present. (See section 3.3.11 on page 87 for information on what details are required to calculate a weight fraction).

#### 4.3.10 Suspect Missing Phases...

Automatically recalculate phases % if missing phases are suspected.  
Suspect missing phases when Scale % error >  %  
or when residual intensities have more than  peak.

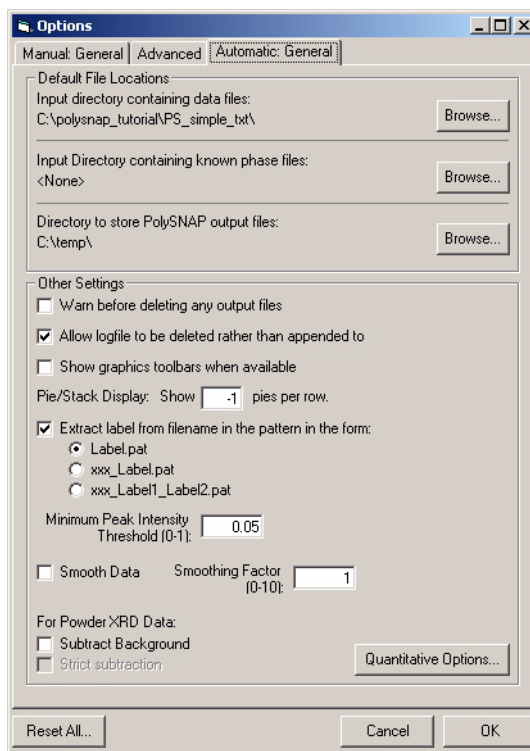
These controls set the values beyond which the program considers that missing phases may be present in a mixture (see section 3.5.1.1 on page 107 for more information).

The two criteria used are the size of the largest calculated error on the quantitative results, and if the residual intensity trace has any peaks above the default minimum peak height.

In addition, if the *Automatically Recalculate for Missing Phases* option is checked, the program will recalculate to include missing phases automatically, without consulting the user first. The default value for this is to consult the user.



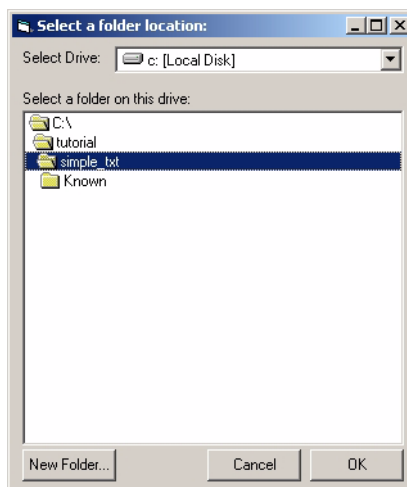
## 4.4 Automatic Analysis: General Options



### 4.4.1 Default File Locations

#### 4.4.1.1 Default Directories

If no working input directory has been specified *via* a command-line argument or other input method, the program uses the directories specified here as its default. To alter any of them, click on the *Browse* button to bring up a directory selection window:



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Selection of a new working directory is carried out by first selecting the correct drive letter from the pop-up menu at the top, and then navigating to the desired folder *via* the lower navigation box. To open a folder to see what other sub-directories it contains, double-click on it. When the desired folder has been located, double click on it to ensure it is selected, and click *OK*.

Ensure these settings are correct, as problems here may prevent the program from running correctly in automatic mode. Note that setting the input and output directories to the same location is not permitted, and will generate an error.

#### 4.4.2 Other settings

##### 4.4.2.1 Warn before deleting any output files

With this option selected, the user is always warned when selecting an output folder that already contains files from a previous program run. The older files will be deleted if the user continues. If the related option, *Allow logfile to be deleted*, is off then logfiles and errorlogs are merely appended to on subsequent runs, rather than started afresh.

##### 4.4.2.2 Show graphics toolbars when available

In the results display window, several of the graphics panes have toolbars to allow quick access to commonly used functions. This option sets if they are displayed by default or not.

##### 4.4.2.3 Cell/Stack display: Show [ ] pies per row

For a display puposes the number of pies in a row can be altered to suit the users needs. *e.g.* for a run of 12 samples the number entered may be 6, which would create 2 rows of 6. The minimum value is 2 and the maximum value is 199. If the value is set to -1, the program makes its own judgement as to the best number to display for a given run to fit in the display window, and this behaviour is the default.

##### 4.4.2.4 Extract label from filename in the pattern in the form

With this option on, sample ID information contained be parsed and used to identify the pattern on the Cell Display and Dendrogram Display. With the first option, *Label.pat*, the entire unique part of the filename is used (though only the final 7 characters are displayed; the full label can be seen in a tooltip by hovering the mouse over a sample). With the second option, *xxx\_Label.pat*, only that portion of the filename after the final underscore character is used as a sample label. The third option, *xxx\_Label1\_Label2.pat* uses the information

after the final two underscores as the label, and ignores any previous part of the filename.

#### 4.4.2.5 Minimum Peak Intensity Threshold

This control changes the default peak threshold. Only peaks whose maximum intensity are above this cut-off value will be marked as peaks, and therefore included for comparison in the peak-based tests. The number of peaks marked can also be used as an indicator of crystallinity of a sample. The default value is 0.05; the acceptable range is from 0 to 1.0.

#### 4.4.2.6 Smooth Data and Smoothing Factor

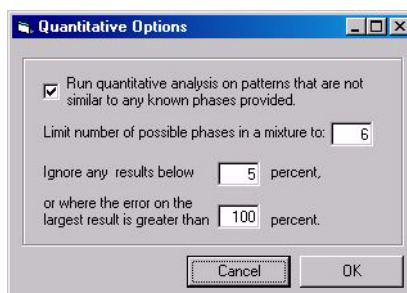
Varying the number in this box controls the amount of noise removal performed by the wavelet smoothing routines. The larger the number, the smoother the resulting pattern. Be careful of oversmoothing and either losing valuable information, or introducing artifacts into the signal. The default value is 1.

#### 4.4.2.7 Powder Data: Background Subtraction

Selecting the first checkbox performs the standard powder background subtraction as used in Manual Analysis. The second checkbox, *Strict subtraction*, applies an additional pass that is intended for use when there is a large amorphous contribution to the patterns that is required to be removed. It should be used with caution as the possibility of removing more pattern than is required is more likely.

#### 4.4.2.8 Quantitative Options

Clicking on the *Quantitative* button opens the *Quantitative Options* window.



*Run quantitative analysis on patterns that are not similar to any known phases provided* - This option can be activated or deactivated by clicking on the check box, and controls whether or not the

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program performs quantitative analysis on samples it considers to be possible mixtures.

It is possible to limit the maximum number of phases the program will suggest as possible components in a mixture with the option:

*Limit number of possible phases in a mixture to [ ]*

This can have any integer value between 1 and 15. The default value is 6; if the initial number of results returned is greater than the value set here, only the top x results are reported (where x is the value entered here). The results which are reported can be further filtered by means of the following two options:

*Ignore any results below [ ] percent* - can have any value between 0 and 100. The default value is 5%. This sets the smallest percentage value which will be returned as significant; anything below this cutoff level will be ignored.

*or where the error on the largest result is greater than [ ] percent* - can have any value between 0 and 1000. The default value is 100. This sets the level for the error value calculated for each phase. If the error on a particular phase exceeds the amount entered here, it is not considered as a possible phase in the mixture pattern.

## 4.5 Reset All



There is a *Reset All...* button located at the bottom of the options window. Clicking this button resets all of the program options to their default settings. This option cannot be undone.

## 5.1 Introduction

This tutorial has been designed to guide the user through a few examples using PolySNAP M with typical data that might be encountered in general use. It is not intended as a replacement for the full program manual, but as a basic introduction to actually using the program. It should therefore be read in conjunction with the manual itself for a more detailed explanation where necessary.

The tutorial requires the user to have already installed PolySNAP M, and be familiar with Windows-based interfaces. The data files used in the tutorial are installed along with the software, and can usually be found in the *tutorial* folder in *C:\Program Files\PolySNAP M*.

### 5.1.1 Simple Automatic Pattern Matching

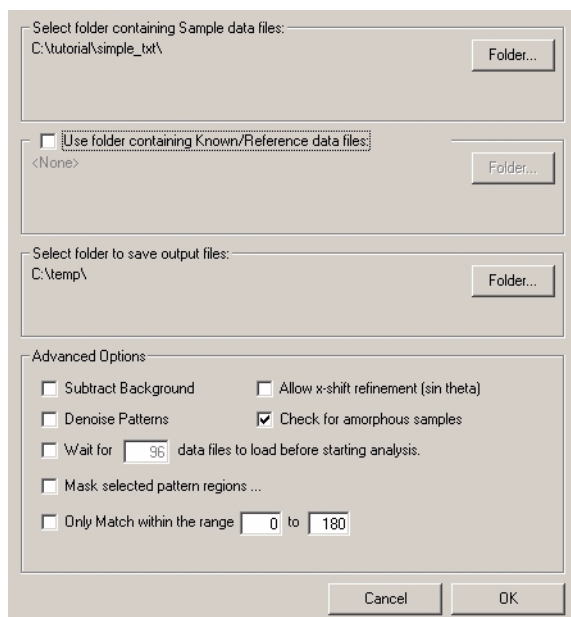
To gain experience with PolySNAP M, a simple run using 21 X-ray powder diffraction patterns is performed. The example assumes the program defaults are used, and any more advanced options are unnecessary.

To begin, launch the PolySNAP M program from either the icon on Windows desktop or *via* the shortcut in the Windows *Start* menu.

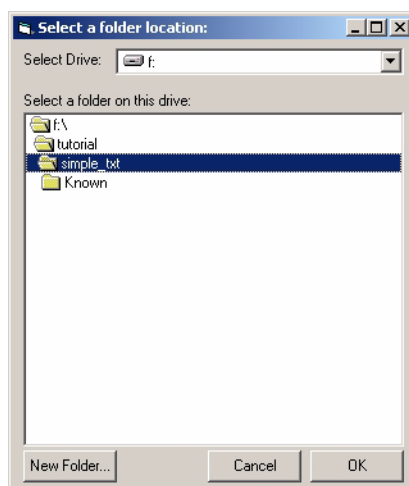
### 5.1.2 Selecting Input and Output Folders

Once PolySNAP M has been launched the user is presented with an empty window that contains only a menu bar. From this, the first step is to define the input folder containing the necessary patterns and the output folder where the results are to be placed.

From the *File* menu, select *Automatic Analysis* and the *Run on...* option. The following dialog box should appear.



1. To define the input folder containing the sample data files, click the *Folder* button in the top section of the dialog box. A folder-selection dialog box will appear.



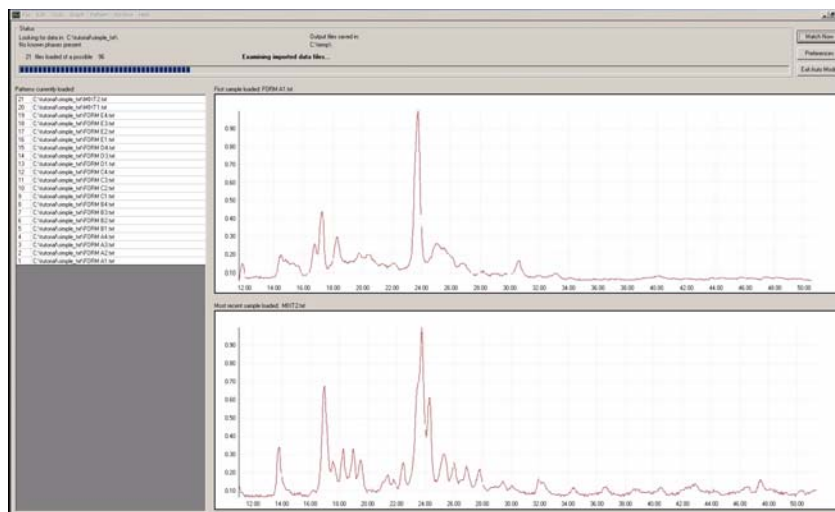
2. Select the drive containing the tutorial data from the pop-up menu at the top. In this case, select *D:*.
3. Navigate to the folder *C:\Program Files\PolySNAP M\tutorial\simple\_txt\*. Ensure that the last folder of the desired path (*i.e.* *simple\_txt*) is selected by double clicking it (the folder icon should appear 'open').
4. Click *OK*. The selected path should be displayed in the upper portion of the dialog box. Check it is correct; if it is not, repeat the previous step.
5. In the *Run PolySNAP M on...* dialog box again, ensure that the central section of the dialog box has no defined folder, indicated

- by the word '<None>'. If this is not the case, uncheck the checkbox labelled *Use Folder containing Known/Reference data files*. The use of this setting will be explained later.
- The output folder where the result files are to be placed must be defined. Click the third *Folder* button in the next section of the dialog box. A folder selection dialog box will appear as before.
  - Select the local hard disk on your machine, which in this case is C:. (Alternatively any other drive you wish to use for the output data may be selected.)
  - Navigate to the folder you wish to place the output files. e.g. C:\output\. If required use the *New Folder* button to create a new folder. Ensure that the last folder of the path is selected by double clicking it (the folder icon should appear 'open'). Note that you **cannot** use the same directory for both input and output.
  - Click *OK*, and check that the desired path is displayed correctly.
  - Leave the Advanced Options settings to their default values (all should be off except for *Check for amorphous samples*).
  - Finally, in the *Run PolySNAP M on...* dialog box click *OK*.

The pattern files from the specified input folder will now be loaded into PolySNAP M.

### 5.1.3 Pattern Matching the Different Powder Patterns

PolySNAP M is now in automatic mode, and proceeds by reading the sample files from the specified input folder, and loading these into a database located in the output folder.

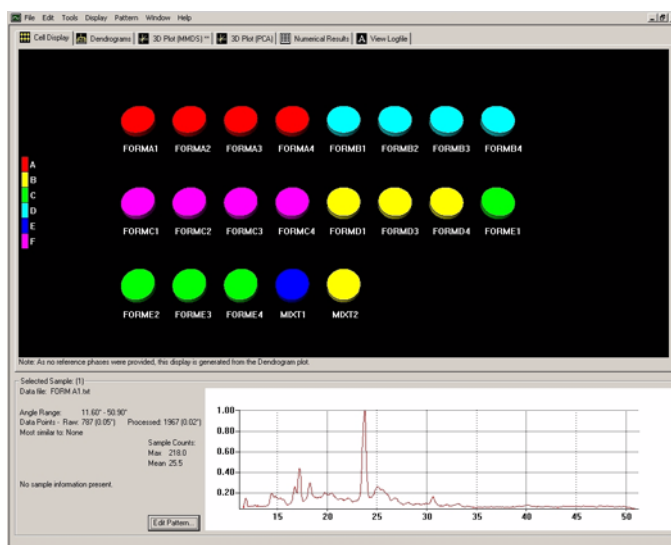


Each pattern is loaded in turn, with the first pattern profile shown on the top right and the most recently loaded profile below it. When all 21 patterns have been loaded the process will stop.

The program now examines the input files, checking for amorphous samples, matches the data files against one another, and then performs cluster analysis. When complete the results window will appear.

### 5.1.4 Viewing the Results in the Cell Display

There are now a number of ways to view and examine the PolySNAP M results. The first of these, and default view displayed is the *Cell Display*, which visually represents the contents of each sample cell.

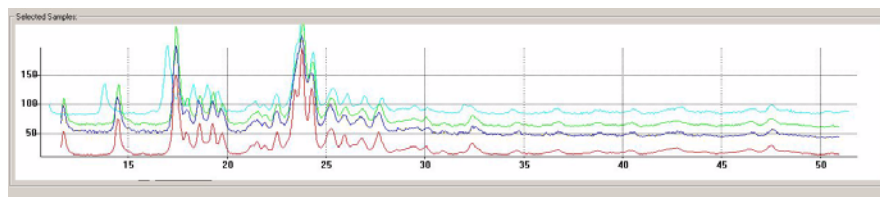


Each cell (shown as a disc) represents a different pattern from the input folder, with colour being used to denote the suggested grouping of compounds. In other words, similar samples are given the same colour. In the lower part of the window the sample information and pattern display of the selected cell is available. The first sample cell is selected automatically when the window is first opened.

1. In the *Cell Display* click on cell *FORMD1*. The associated full pattern profile of pattern D1 is now displayed in the lower region of the window beside the sample information. In this particular case the information available is limited, so many of the fields are blank.
2. Hold down the *shift* key and click on cell *FORMD4*. The cells from D1 to D4 are now selected, and the sample information pane now disappears, leaving only an extended view of the profiles of patterns D1, D3 and D4 overlaid to allow a visual comparison. From this view they are all obviously the same compound.
3. From the *Display* menu select *Offset Overlaid Pattern Profiles* and click *on y-axis*. This will now display the multiple patterns with an offset along the y-axis of the plot, when any further cells are selected.

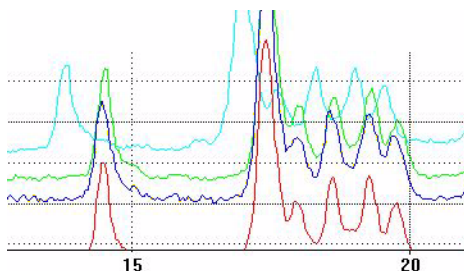


4. Hold down the *control* key and click on cell *MIXT\_2*. The display now includes this new fourth pattern, and to allow an easy comparison are displayed overlaid with an offset along the y-axis.



5. Zoom into the area between around 15° and 20° by holding down the left mouse button and dragging a box over the desired area. When the mouse button is released, the graph region is redrawn to show just the selected area. Zooming in and out smoothly can also be accomplished by clicking in the display and then holding down the *control* key while moving the scroll wheel of the mouse (if available).
6. To move around the area and position the view more accurately, hold down the *Alt* key and *left mouse button* simultaneously while dragging with the mouse - the display updates in real time.

These zoom and movement functions are the same for all graphical displays within the PolySNAP M program.



To check which of the plotted profiles correspond to which sample, 'hover' the mouse over part of the plotted line; a tooltip appears with the sample filename in it.

This closer view of the overlaid patterns makes it easier to see that the top pattern (*MIXT\_2*) is noticeably different from the other patterns - note the extra peak around 14° for example - and may not actually belong to this group of compounds.

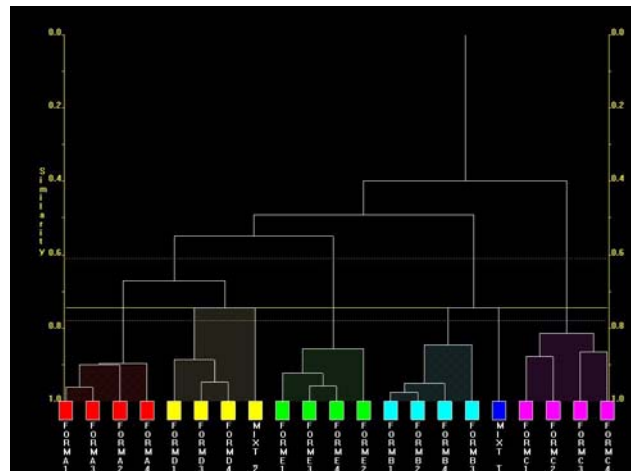
7. Reset the view with a *right click* of the mouse in the graph pane and selecting *Reset View* from the pop-up menu.

### 5.1.5 Viewing the Results by Dendrogram

In the PolySNAP M window there are a series of tabs just below the menu bar, each of which display a different view of the data. Select the tab labelled *Dendrogram*.

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The partitioning of the data into groups that were displayed in the coloured cells is carried out by the cluster analysis of the sample data. In PolySNAP M there are five different methods of clustering available, each of which tend to give slightly different results. The program computes the best, in the sense of the most internally consistent, dendrogram method and displays the results from that (although the user can choose to view the results from the other methods and overrule the selected one if required).



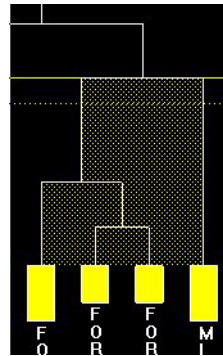
A dendrogram provides a visual display of the results from the hierarchical method of data classification using cluster analysis. The dendrogram itself takes the form of a tree-diagram in which each terminal branch (coloured box) is representative of a single pattern sample.

The higher up the similarity scale two samples are connected by a horizontal line, the less similar they are. Hence samples FORMA1 and A3, with a similarity value of around 0.9 are very similar, whereas samples FORMA1 and FORMC1, which are only joined much further up the tree by a horizontal line with a similarity value of around 0.4, are quite different.

In this dendrogram there are 6 separate clusters, each distinguished by its own colour. These are the same colours displayed earlier in the cell display and throughout most of the other PolySNAP M displays. The number of clusters are defined by the yellow cut-line which in this case was initially set to 0.744. The calculation of this level is *via* a number of statistics. The confidence levels on this choice of cut position are shown by the yellow dotted lines either side. Selecting a cut-line for a dendrogram is a difficult procedure, and the results must be treated with caution. The program-calculated level therefore should always be carefully examined by the user to see if looks sensible.

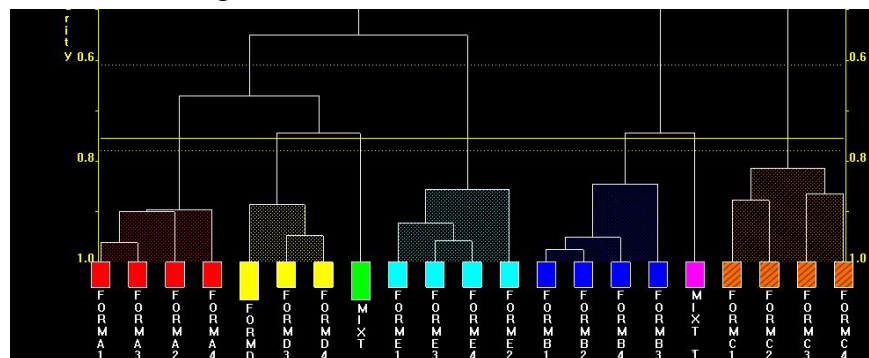
Adjusting the cut level upwards creates fewer separate clusters, and effectively reduces the discrimination between differences; adjusting the cut-level downwards creates more separate clusters.

1. In the *dendrogram* click on the yellow square cell *FORMDI*. The pattern profile of the sample is displayed.
2. Using the *control* key, also select cell *MIXT\_2*. These are the two patterns that appeared different from one another when they were overlaid in the cell display.



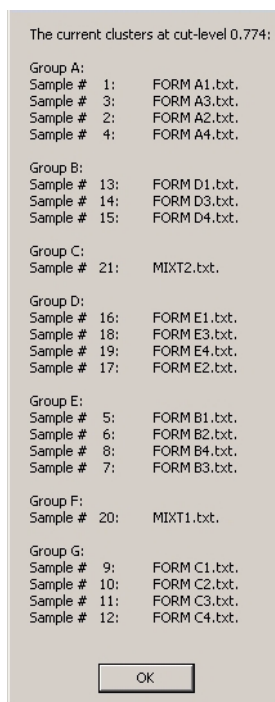
Looking at the position of the cut-line it is seen to be only very slightly above the similarity line between cell *MIXT\_2* and the other yellow cells. It can also be seen that another group (the dark blue and light blue samples) has only just been split by it. With the confidence levels indicated by the yellow lines being between 4 and 7 clusters, it is possible that the present level is not ideal.

3. To manually adjust the cut-line, either click in the Dendrogram area and use the *scroll wheel* or hold down *control* and the *left mouse button* while dragging up or down. Move the cut-line down slightly so that it is still above the lower confidence line but so there are now 7 different clusters. Notice that the assigned colours change, and that cell 20 is now in a cluster of its own.



4. In the dendrogram area click the *right mouse button* and select *Save Modified Trees....*, to ensure that the changes are retained.

- 
5. From the *Tools* menu select *List Pattern Cluster Members...* A dialog box will appear containing a list of the clusters.

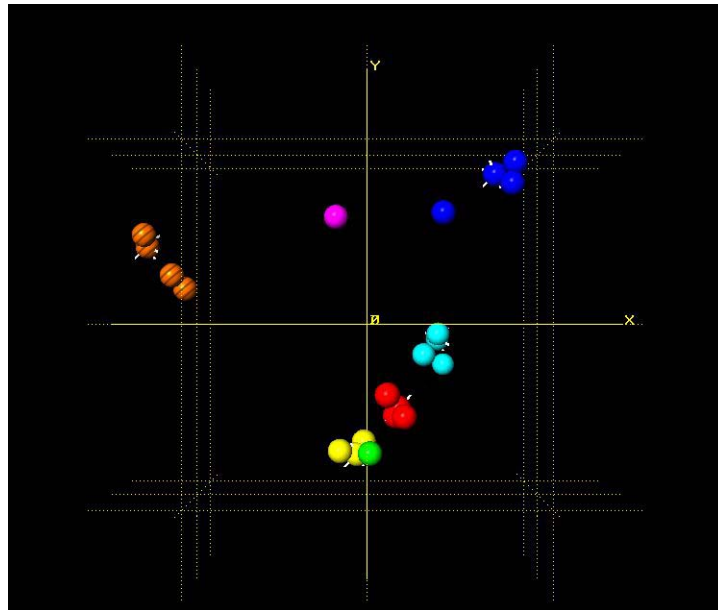


This dialog box displays the different clusters with their sample numbers and actual file names. From the file names used in this demonstration example it can be seen that the samples are now all properly grouped, with the two mixtures separate from the rest. Notice in the dendrogram display that these two mixture patterns are quite dissimilar to anything else, having a low similarity connection value to their neighbours.

### 5.1.6 Viewing the Results by 3-D Plot

The samples can also be viewed by making use of the distances between objects derived from the correlation matrix to give a representation of the data in three dimensions. There are two methods used for calculating the resulting 3-D plots: these are *Metric Multi-Dimensional Scaling* (MMDS) and *Principle Component Analysis* (PCA). They both give different views of the samples because of the differences in calculation and will therefore give slightly different results. The control of each plot is the same so only the MMDS will be described here in detail.

Select the tab *3D Plot (MMDS)* (or PCA if you wish).



The initial view shows only the x and y axis, while the z axis lies in projection. Each point represents a sample. The position on the plot is taken from the MMDS calculation. The colour of each sample is taken from the dendrogram display to allow easy comparison of the results from these different methods. Allowing the mouse to hover over a sample displays the sample label in a tooltip popup.

Samples that are similar are plotted close to one another, so are seen to clump together in groups. Note that different coloured samples can also be close, this shows that they also have similarities. This can be seen by the yellow group being very close to the green sample, which is pattern MIXT\_2 and, when comparing to the dendrogram display, is only separated from the yellow group by the current level of the cut-line.

Also notice the number plotted at the top-left of the display, in this case, 0.96. This is a correlation coefficient measuring the quality of the 3D representation to the original data. The closer to 1.0 it is, the greater the reliability of the results. This value tends to decrease when larger data sets are used.

Use the following methods for exploring the 3-D plot.

Action	Control
Rotate the 3-D plot	Drag while holding shift key and left mouse button
Move plot laterally	Drag while holding alt key and left mouse button

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Alter size of spheres	Drag up or down while holding control key and left mouse button
Zoom on centre	Click in area, hold shift key and use mouse scroll wheel
Zoom on area	Hold left mouse button and draw box over area
Select a sample	Click on sphere
Select multiple cells	Hold control key and select additional cell
Alter rendering quality	Press F2 and adjust scale (lower values are better for slower graphics cards)
Centre view	Right click mouse and select <i>Centre Selection</i>
Reset view	Right click mouse and select <i>Reset View</i>

The 3D plot is useful to spot patterns that are quite different from the others, as they tend to stand out on their own and are not easily grouped. Also, cases where the colours (from the dendrogram) and the positions (from the MMDS) of the samples appear to contradict each other are the samples that should be looked at manually in more detail.

To end this session select *Close Window* from the *File* menu.

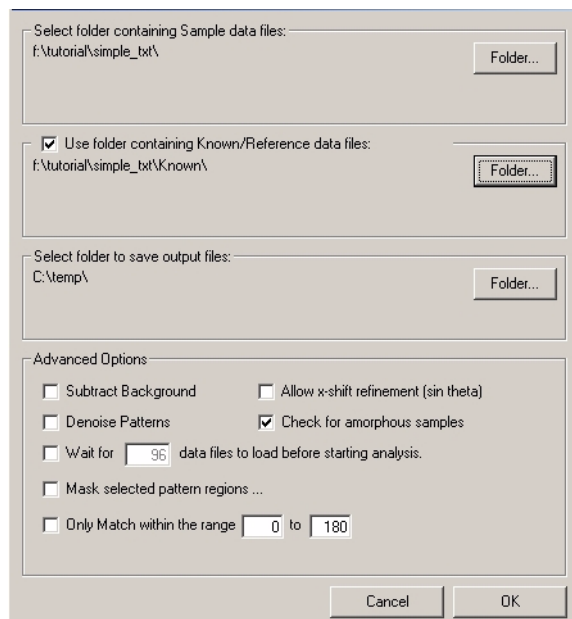
#### Automatic Quantitative Pattern Matching using Known Phases

A more sophisticated pattern match might include a database of known phases for comparison purposes. These are patterns that have been previously identified and can be used to decide whether the sample is a previously known substance, a mixture of known materials, or something completely different.

#### 5.1.7 Selecting the Input, Output and Known Phase Folders

To begin, the user should start with the empty PolySNAP M window containing the menu bar, as in the previous example.

From the *File* menu, select *Automatic Analysis* and the *Run on...* option. The following dialog box will appear.



Set the input, output and known phase folders as before, except this time we will additionally select a folder containing some known phases prepared earlier.

1. To define the input folder containing the sample data files, click the *Folder* button in the top section of the dialog box. A folder-selection dialog box will appear.
2. Select the drive containing the tutorial data from the pop-up menu at the top. In this case, select *D:*.
3. Navigate to the folder *C:\Program Files\PolySNAP M\tutorial\simple\_txt\*. Ensure that the last folder of the path (*simple\_txt*) is selected by double clicking it (the folder icon should appear 'open').
4. Click *OK*. The selected path should be displayed in the upper portion of the dialog box. Check it is correct; if it is not, repeat the previous step.
5. The known phase folder containing the known sample data files must be defined. Turn **on** the checkbox labelled *Use Folder or Database containing Known/Reference data files*. Click the *Folder* button in the that section of the dialog box.
6. Select the drive containing the tutorial data, in this case *D:*.
7. Navigate to the folder *C:\Program Files\PolySNAP M\tutorial\simple\_txt\known\*. Ensure that the last folder of the path (*i.e. known*) is selected by double clicking it (the folder icon should appear 'open'), and click *OK*. This folder contains an example pattern of each of Form A, B, C *etc.*

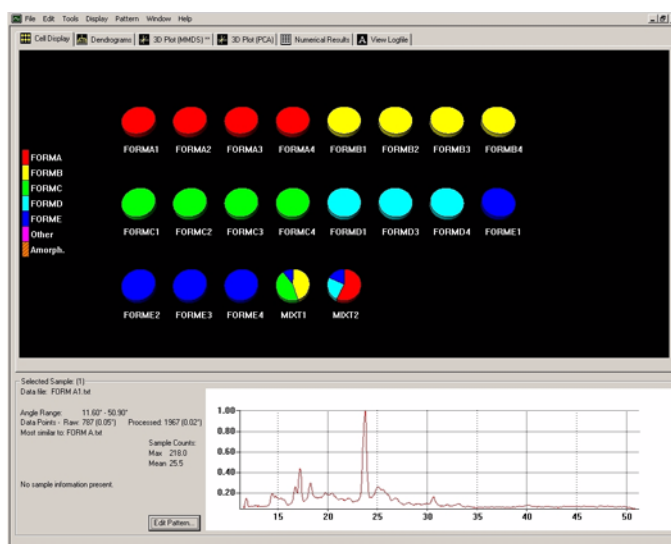
8. The output folder where the result files are to be placed must be defined. Click the third *Folder* button in the bottom section of the dialog box. A folder selection dialog box will appear as before.
9. Select the local hard disk on your machine, which in this case is *C:*. (Alternatively any other drive you wish to place the output data may be selected.)
10. Navigate to the folder you wish to place the output files. e.g. *C:\output\*. If required use the *New Folder* button to create new folders. Ensure that the last folder of the path is selected by double clicking it (the folder icon should appear 'open').
11. Click *OK*, and check that the desired path is displayed correctly.
12. Finally, in the *Run PolySNAP Mon...* dialog box click *OK*.

The pattern files in the specified input folder are now loaded into PolySNAP M, which proceeds to the matching and analysis phase automatically after loading the 21 datafiles.

When complete the results window will appear, with an initial view of the *Cell Display* as before.

### 5.1.8 Viewing the Results

The input files are now displayed in the *Cell Display* as in the first tutorial example. However, it now looks a little different with cells MIXT\_1 and MIXT\_2 being shown as pie charts.



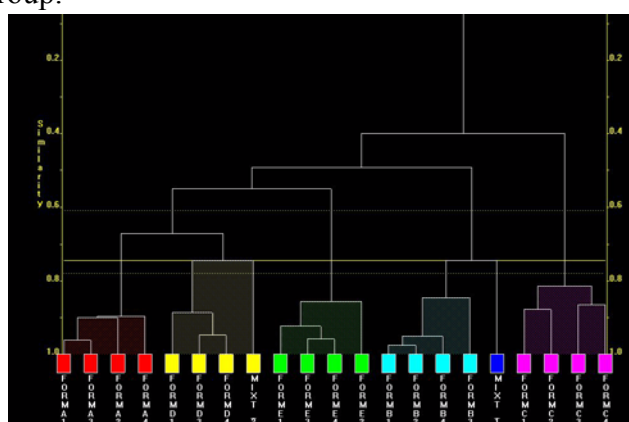
Unlike the previous run, the colours here are **not** taken from the dendrogram plot, but from comparing each sample in turn to the provided known phases. Samples such as MIXT\_1 and 2 that do not give high matching correlation coefficients to any of the known reference patterns are tested to see if they are mixtures, and if so, quantitative analysis is performed. The results from this are



displayed in pie-chart form, the colours of each slice corresponding to the pure phases listed in the key on the left hand side.

Another change to the view is the sample key - it now shows the known phases FORM A to FORM E. By clicking on the colours of the key all the samples matching the designated phase are selected. For example, clicking on the red box labelled FORM A, cells A1 to A4, as well as MIXT\_2 are selected, as they are all of the samples thought to either be, or contain, Form A. The key titles are taken from the reference phase filenames.

Select the tab labelled *Dendrogram*. This view is exactly the same as in the first example, including cell 20 being contained within the yellow group.



The reason for this difference between views is that the cluster analysis does not take the known phases into account. Only the results shown in the *Cell Display* are directly affected by them. Because of the way they work, the dendrograms and other methods merely show the similarity between samples without taking account of the known phase information.

With the quality of data available for this sample the predicted mixture composition is not very good, and the quantitative results should therefore be taken as a very approximate measure, certainly not accurate to any more than around 10% at best. This approximate value could however be useful as a starting point for a more rigorous analysis later.

## 5.2 Identification of Amorphous Samples

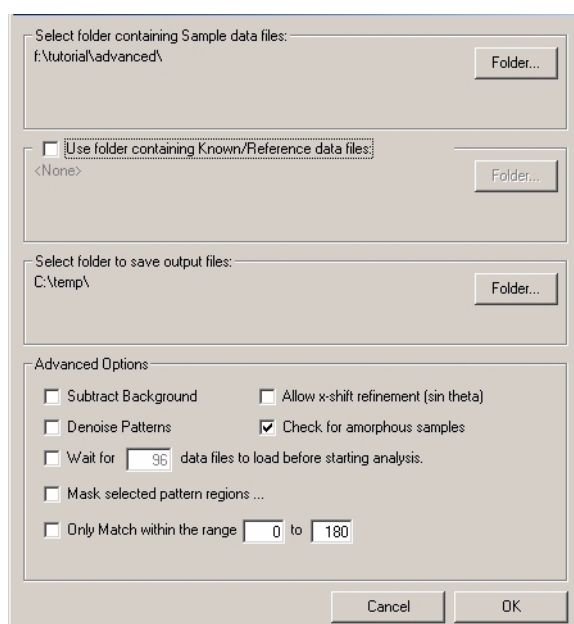
The first two tutorial examples of this tutorial have covered simple PolySNAP M procedures. This part will cover some of the more advanced options available that include pattern matching while

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allowing for a  $2\theta$ -shift, and automatic identification of non-crystalline samples.

To begin, the user should start as before with only the empty PolySNAP M window containing only the menu bar as before.

From the *File* menu, select *Automatic Analysis* and the *Run on...* option. The following dialog box will appear.



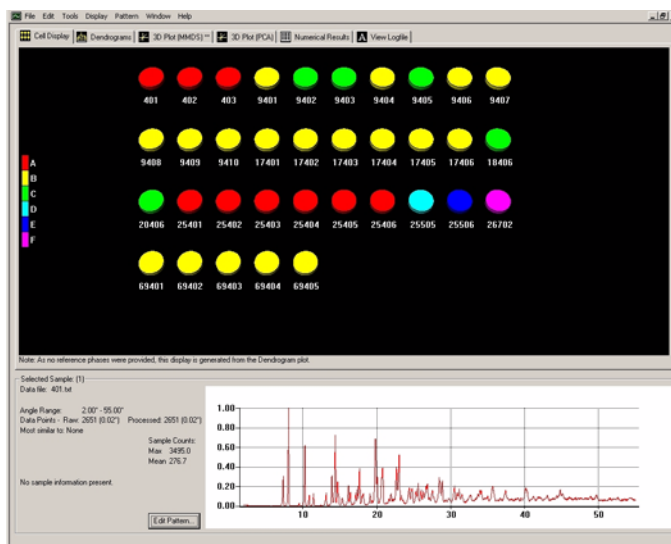
1. To define the input database containing the sample data, click the *Folder* button.
2. Select the drive containing the tutorial data, in this case *D:*.
3. Navigate to the folder *C:\Program Files\PolySNAP M\tutorial\advanced\*
4. Ensure that no known phases are used by making sure the relevant checkbox is turned off.
5. Define the output folder where the result files are to be placed. Click the third *Folder* button in the bottom section of the dialog box. A dialog box will appear.
6. Navigate to the folder you wish to place the output files. e.g. *C:\output\*. If required, use the *New Folder* button to create new folders, ensuring that the last folder of the path is selected by double-clicking on it (indicated by the folder icon being in an open position). Click *OK*.
7. Leave the *Advanced Options* settings at their default values.
8. In the *Run PolySNAP M on...* dialog box click *OK*.

The pattern files in the specified database are now loaded into PolySNAP M, where it checks for amorphous samples, matches the patterns with one another, and performs a cluster analysis. This may

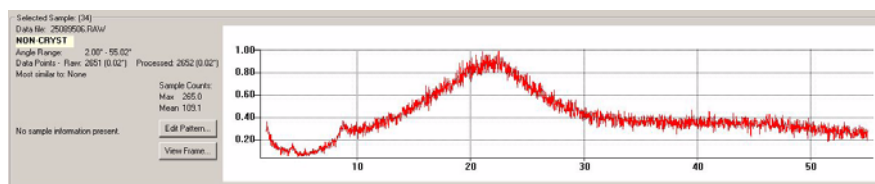
take a little time to complete, but once finished the results window will appear with an initial view of the *Cell Display*.

### 5.2.1 Analysis of the Results

The 35 samples contained within the database are now presented in the *Cell Display*.



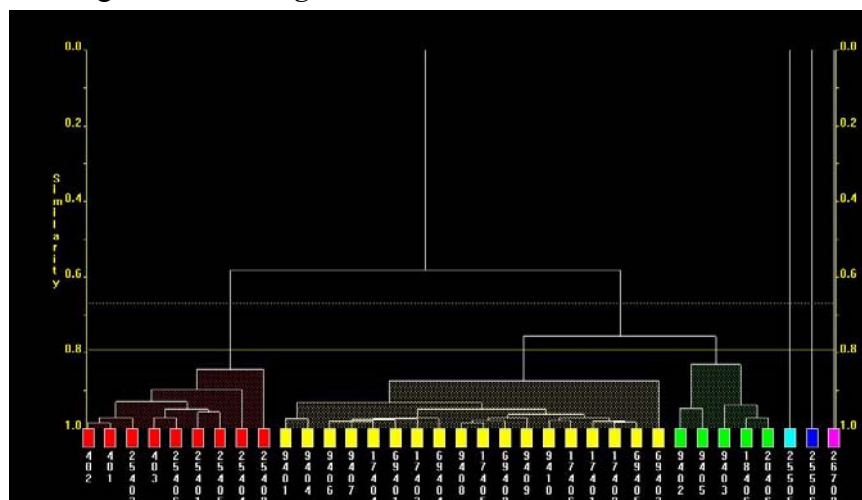
The program is using the last few digits of the filename of each sample to label them. Selecting pattern number 25505, the pattern information display shows that it has been labelled as a non-crystalline sample, which seems reasonable given its profile.



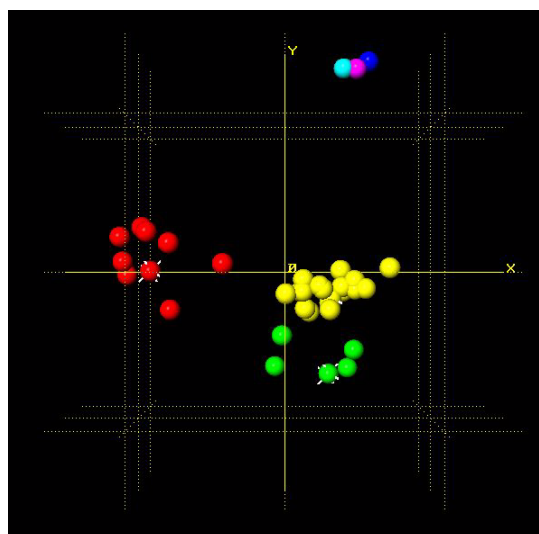
The other two patterns, 25506 and 26702 are similarly labelled for the same reason. Identification of such amorphous samples is done on the basis of checking to see if any signal (corresponding to peaks) would be left after subtraction of the entire amorphous hump. The method tends to err on the side of caution.

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Looking at the *Dendrogram* tab:



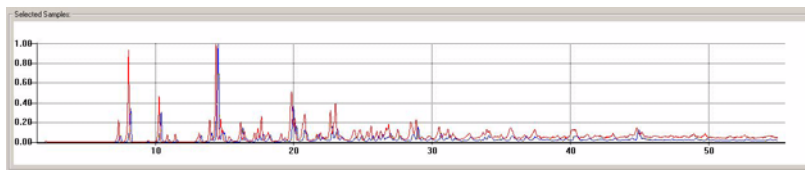
It is seen that three non-crystalline labelled patterns are placed on the far right of the diagram with a zero similarity to the rest. This is deliberate, in order to remove them from the main clusters. There also appears to be one main grouping of the data - within which some patterns seem much more closely grouped than others. Compare this to the 3D (MMDS) plot:



Again, the three non-crystalline samples are quite separate from the rest of the patterns. Both the dendrogram and 3D plots suggest a loose grouping of the rest of the patterns, suggesting there may be some differences between them.

Using the *control* key, click two patterns which are on opposite sides of the main (yellow) group from each other, for example patterns 9401 and 69403. Examining their profiles, it appears that in addition

to some preferred orientation issues, there seems to be a noticeable  $2\theta$ -shift between the otherwise relatively similar profiles:



This completes the initial analysis of the data, but the  $2\theta$ -shift in some of the samples could be examined in more detail. From the *File* menu select *Close Window*.

### 5.2.2 Reprocessing the Data allowing for an x-shift

When collecting powder diffraction data from a diffractometer the sample or instrument alignment can result in linear or non-linear shifts along the x-axis of the resulting pattern. This can especially be a problem with the Bruker GADDS systems if the sample height varies from sample to sample. This can give rise to systematic errors in the pattern matching unless it is accounted for. However, to allow for this is a time consuming process and should therefore not be used unless such a shift is suspected - it is switched off by default.

A general expression for the shift is:

$$\Delta(2\theta) = a_0 + a_1 \sin \theta \quad (5.1)$$

where the  $a_0$  coefficient corresponds to a linear (zero-point) shift described earlier, and the  $a_1$  coefficient a non-linear component [Zevin & Kimmel, 1995]. The requirement then is to find values of  $a_0$  and  $a_1$  that results in a maximum matching correlation result between two patterns. The default maximal allowed values for  $a_0$  and  $a_1$  are 0.4.

The same data as in the previous run will now be examined again. Unlike the last time, the program will vary the x-offset parameters to attempt to maximise the match result.

Define the input database, known phases and output folder as before:

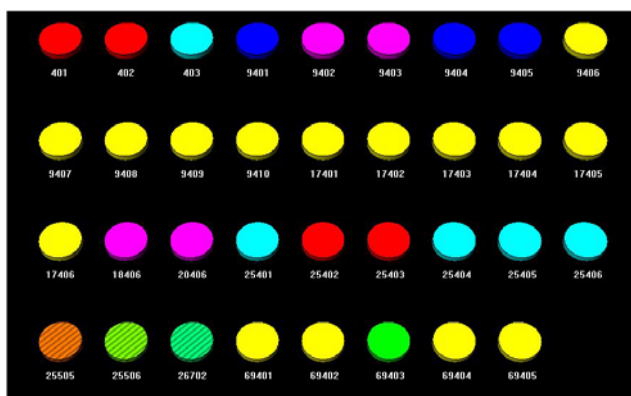
1. From the *File* menu, select *Automatic Analysis* and the *Run on...* option. Define the same input folder as used before in the previous run of PolySNAP M. *D:\tutorial\advanced\*
2. Select *None* for the known phases directory.
3. Ensure that an appropriate output folder is selected. e.g. *C:\output\*.
4. In the Advanced Options area, turn on the *Allow x-shift calculation (sin theta)* checkbox.

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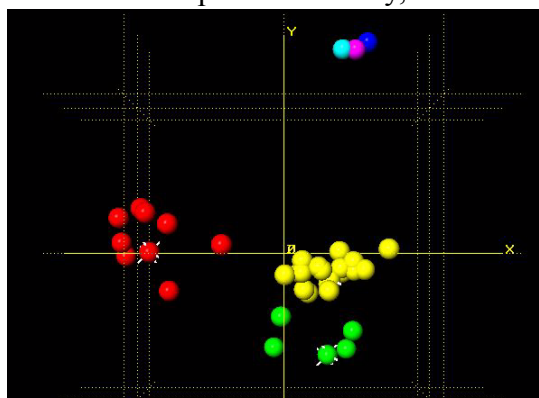
5. In the *Run PolySNAP M on...* dialog box click *OK*.

The same data as before is now run allowing x-shifts on the patterns. The time required to process this will take much longer than a normal run of PolySNAP M. For this data the calculation will take approximately ten times longer than before - so prepare to be patient!

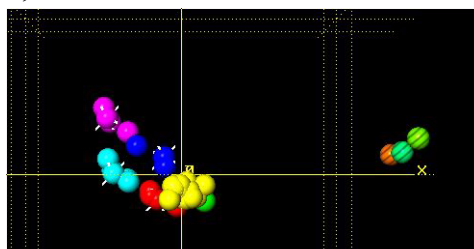
When finished, the initial output should look similar to the previous run:



Now look at the 3D MMDS plot. Previously, it looked like this:

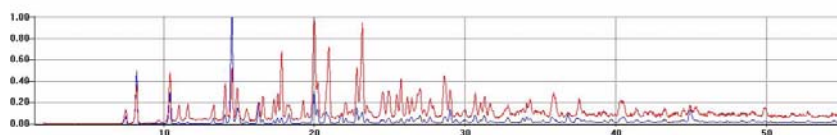


Now, with the option to calculate the best-offset value for each pattern turned on, it looks like this:



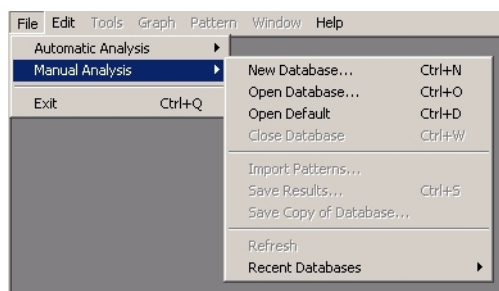
The three non-crystalline patterns are still quite separate, but the rest of the patterns have condensed together as a result of allowing for the  $2\theta$ -shift, showing that a large part of the differences between the pattern profiles was due to variation in sample heights during data collection. The program still separates them out within this grouping due to the preferred orientation problems.

Similarly with the dendrogram display, the similarity values between the patterns are much improved. The remaining differences appear to arise from preferred orientation effects, which are quite noticeable in some cases. For example, overlay the profiles of samples 401 and 69403:



### 5.3 Manual Matching: Working with Databases

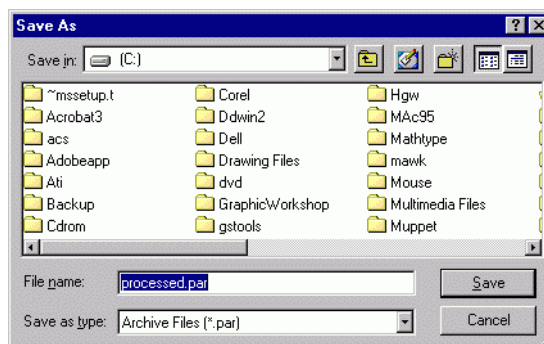
The rest of the examples in this tutorial demonstrate the manual analysis section of PolySNAP M. This mode can be accessed from the *Manual Analysis* section of the *File* menu.



The first thing to do is to create a new database of patterns with which to work.

We first need to create a new database, which will initially be empty. We will then load some powder patterns into it, and work with them.

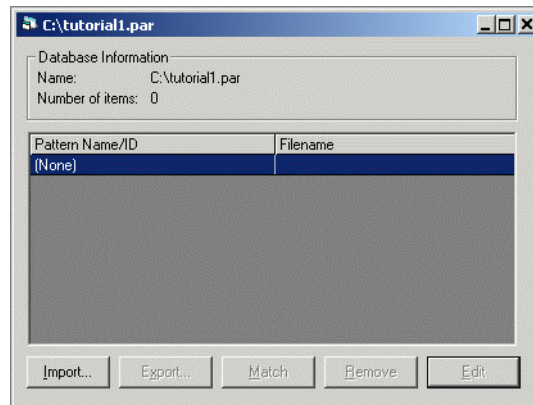
Choose *New Database* from the *Manual Analysis* section of the *File* menu. A standard Windows file dialog box appears, and you are invited to choose a name and location for the new database.



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Enter *tutorial1* as the database name, select a location (*C:/* for example), and click *Save*. The dialog box disappears, and a new window opens inside the PolySNAP M workspace.

This is our new empty database; its filename is displayed in the window title bar. Like any other window, it can be moved around the screen by clicking and dragging on the title bar, and can be re-sized by dragging at the edges of the window.



The filename and your selected location appear in the Database Information section of this new window.

The number of patterns in this database is also displayed - as expected, it is currently zero.

Several buttons are arranged along the bottom of this window. Most of these are unavailable as there are no data files in the database. The only one that is available for use is the *Import* button.

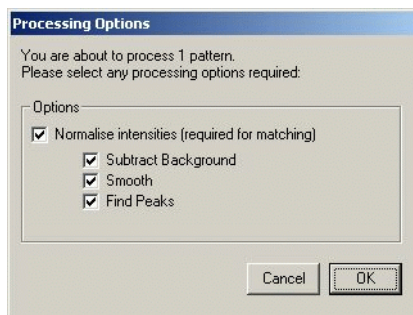
We now need to bring some pattern data files into the database.

Click the *Import* button. We need to navigate to where the data is stored - *C:\Program Files\PolySNAP M\*. The folder *manual* should be found within the '*tutorial*' folder.

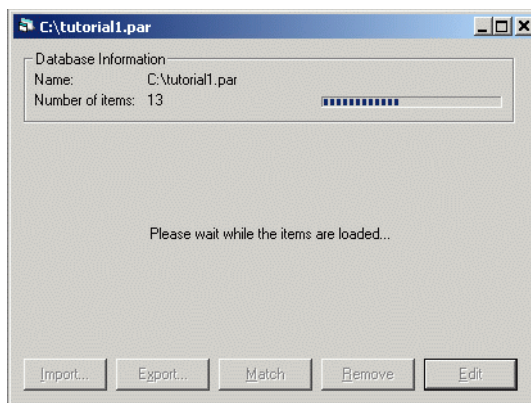
Once in the correct location, a list of different files in the folder that the program recognises is listed.



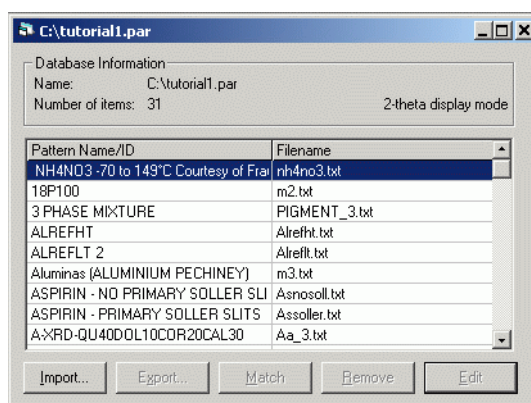
We want to open all of the files in this particular folder, so hit *control-A* on the keyboard to select them all, and then click *Open*. A new window appears with the pattern processing options.



These will be discussed in more detail later, so leave them with their default values for the moment and click OK. A progress bar appears at the top of the database window to allow progress to be monitored. As there are only a few patterns in the folder, this process should only take a couple of seconds.



Once importing has finished, the patterns will be listed in the main part of the database window:



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If the window is too small to see all of the patterns, the scroll bar on the right hand side can be used to view the rest, or you can drag the window border to enlarge the window.

Each entry in the list represents one pattern file that has been imported.

Initially, the patterns are listed in the order they were imported. The list can be sorted by either *Pattern Name/ID*, or *Filename*, by clicking on the headers at the top of the list.

If some of the chemical names here look very similar to filenames this is because the ASCII files we have imported do not contain any chemical name information, so the filename is used instead. The actual chemical name, if known, can be added manually later.

You can select a particular pattern in the list by clicking once on it. When you do so, the other buttons along the bottom of the window become activated.

The *Import* button has already been used. The *Export* button lets you make a copy of a particular database entry to a separate file, in either ASCII text or PolySNAP M pattern format.

*Remove* deletes the selected pattern or patterns from the database.

Experiment with these options by exporting a pattern to a separate ASCII text file under the name *exporttest.txt*. Make sure to note where you saved it! Then try importing the file you have just saved. Finally, select the *exporttest.txt* pattern in the list and delete it from the database using the *Remove* option.

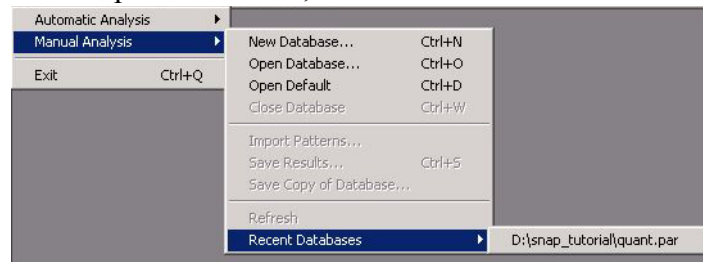
Removing patterns from the database does not in any way affect the original data files which are left intact and unchanged throughout all operations performed using PolySNAP M - the program works on a copy of the data only.

The *Match* and *Edit* options will be dealt with in following sections, so leave them be for the moment.

Now quit the program by choosing *Exit* from the *File* menu. All windows will close. Note that any changes made to a database are automatically saved, so there is no need to manually save any changes before closing.

Relaunch the program again in the same manner as before. We want to return to the database we have just been working with. You could select *Open Database* from the *Manual Analysis* section of the *File* menu, navigate to where the database was saved, select it and click *Open*, but there is a much easier way.

The program keeps a record of the last four databases used in the *Recent Databases* submenu of the *Manual Analysis* section of the *File* menu. Open this now; one of the entries should be the

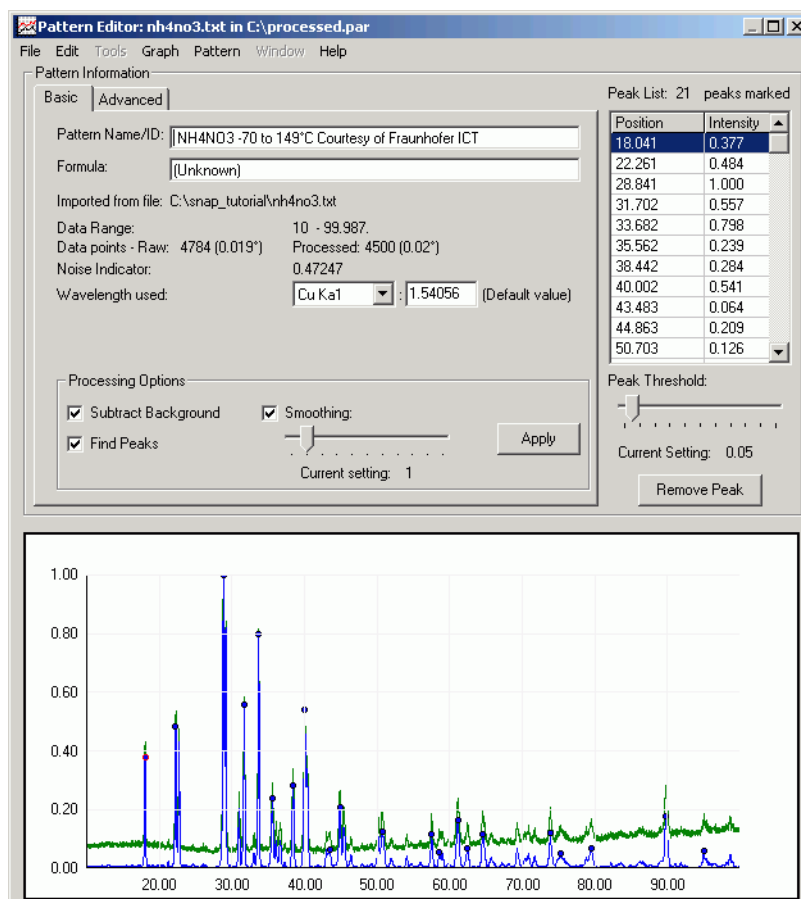


*tutorial1.par* database we were using earlier. Select it from the menu, and it should start to open automatically.

Next, we want to examine some of the patterns we have just imported in more detail.

## 5.4 Editing Patterns

Select the pattern *nh4no3.txt* from the list in the database by clicking once on it. Click the *Edit* button, and the Pattern Editor window appears.

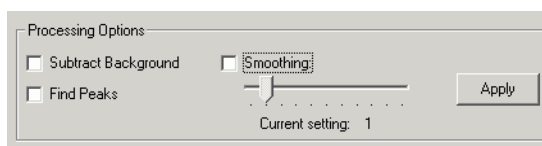


Several useful pieces of information about the pattern you have selected are displayed in this window, and a plot of the pattern itself is shown at the bottom.

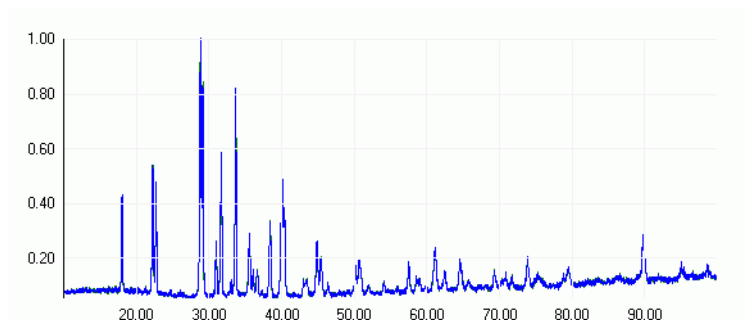
The chemical name or pattern ID can be changed here by editing the current name ("*NH4NO3 -70 to 149°C Courtesy of Fraunhofer ICT*") in the white text box.

Details such as the pattern filename, its start and end angles, and the number of data points are also displayed.

There are three check boxes labelled Processing Options just above the region where the pattern is displayed. To begin with, click once in each of the checkboxes, so that they are all turned off:



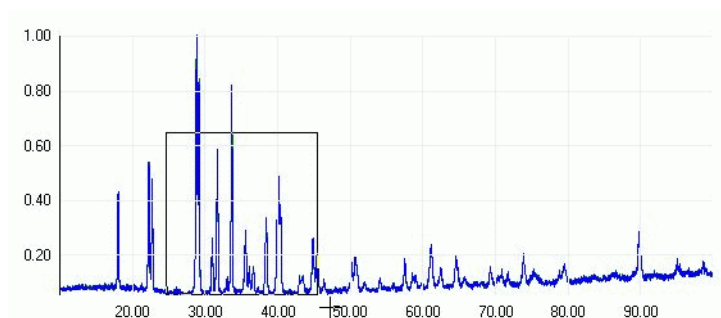
Then click *Apply*. The graphing region should now look like this:



As you can see, the data has been scaled along the y-axis to run from 0.0 to 1.0. This operation is performed for all data being imported into PolySNAP M in order to allow for suitable scaling between different data sets.

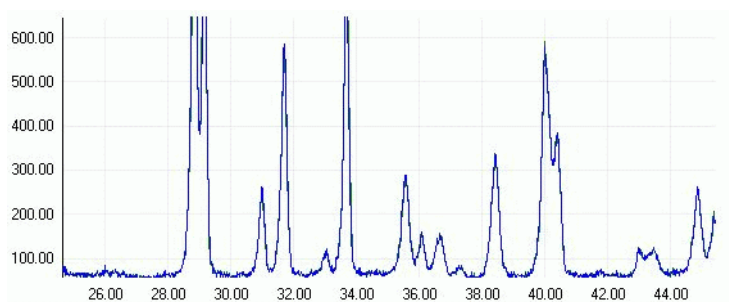
The raw data has also been interpolated from its original resolution, to the PolySNAP M standard 0.02 degrees. Again, this is for consistency between patterns.

You can zoom into the pattern display, by clicking and dragging a rectangle on the region you wish to see more closely:



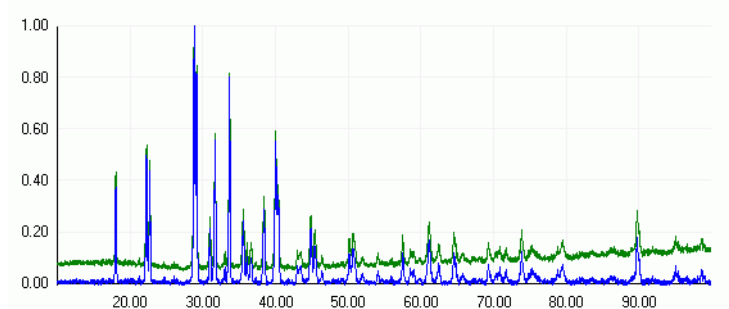
---

The view will then change to just the selected region:



To return to original view, right-click anywhere on the pattern display, and select *Reset View* from the resulting pop-up menu. Multiple zooms are possible by repeating the process.

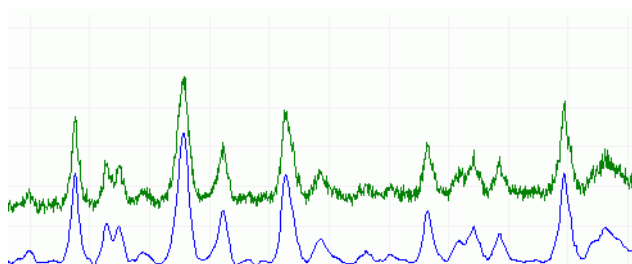
Now click the *Subtract Background* checkbox, and then click *Apply*. The pattern display should change:



The green line represents the raw pattern data. The blue line shows the same pattern after the background level has been subtracted. To see what the program considered to be background before subtractions, select *Show Background Curve* from the *Pattern* menu. A new window will open showing the subtracted background curve where the blue line now represents what is subtracted as background. Once you are finished looking, click *Close* to close this window and return to the standard view.

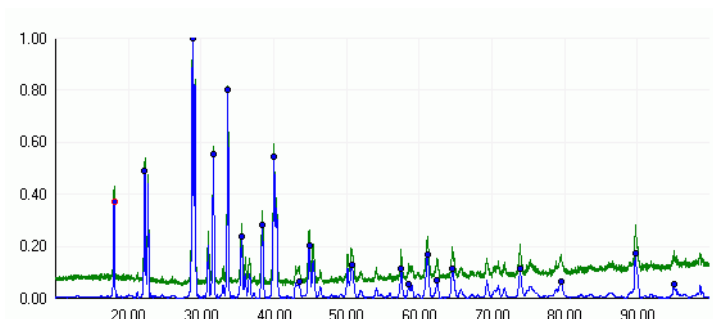
Now click the *Smoothing* checkbox, so both it and the *Background Subtraction* boxes are checked, and click *Apply* again.

The graph pane will be updated, and any noise in the pattern will be smoothed out (shown here zoomed in).



Finally, check the *Find Peaks* option, and click *Apply*.

The pattern display will update, and several small blue circles should appear on the top of the larger peaks:



These mark the location of what the program considers peaks. There is a minimum peak height below which any peaks are ignored. This is set as a default to 0.05, which is why the smallest peaks are unmarked.

A list of the peaks the program has found is shown in the upper right corner of the pattern editor:

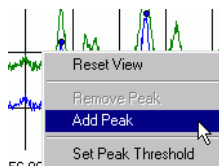
Angle	Intensity
18.041	0.372
22.261	0.479
28.841	1.000
31.702	0.554
33.682	0.794
35.562	0.237
38.422	0.284
40.022	0.536
43.463	0.064
44.863	0.205
50.703	0.123

This lists the peaks found in order of increasing Bragg angle, and displays the corresponding intensity for each.

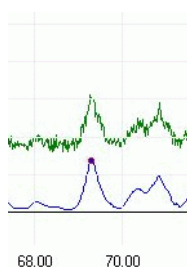
If the program has missed a peak you believe should be included, it is easy to add manually. Note that peak locations are added to the blue, processed pattern line, not the green, raw data line on the graph profile.

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For example, if we wish to add the small peak that is located at around 54°, just right-click once at the point on the graph where you judge the peak maximum to be:

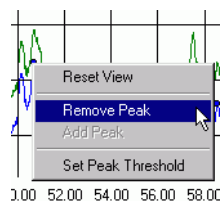


Then select *Add Peak* from the resulting pop-up menu. A round blue peak marker should appear at the top of the peak, and an entry for it should be added to the peak list:

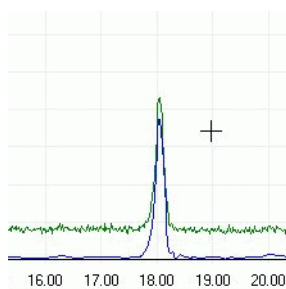


If this does not appear, try clicking as close as possible to the top of the peak. It may help to zoom in to the area of interest.

It is also possible to remove peaks you believe to be incorrect. For example, say we wish to delete the marker from the peak around 18°:



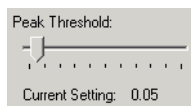
Right click as close to the peak marker as possible, and select *Remove Peak* from the pop-up menu that should appear. The peak marker, and its corresponding entry in the peak list, should vanish.





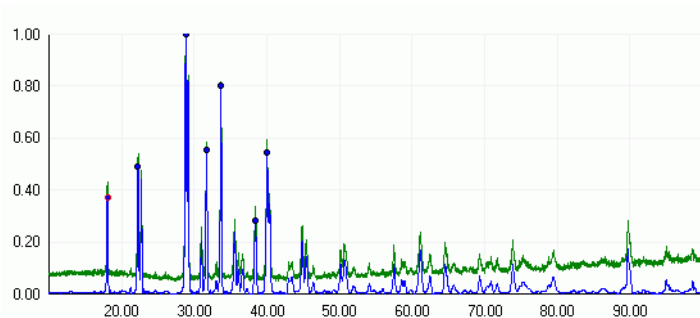
If the *Remove Peak* option is unavailable from the pop-up menu, you have not clicked close enough to the marker. Zoom in to make this easier, and try again.

Finally, it is possible to adjust the minimum peak height threshold to include less of the smaller peaks. Look at the slider just below the peak list - it should be set to 0.05.



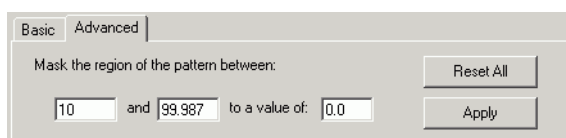
Drag the handle on the slider until it is set to about 0.25.

Several additional peaks that were marked before should now show up without peak markers, as they are now below the new minimum threshold of intensity.



Finally, return the slider to 0.05. The peaks that previously became unmarked should show up again.

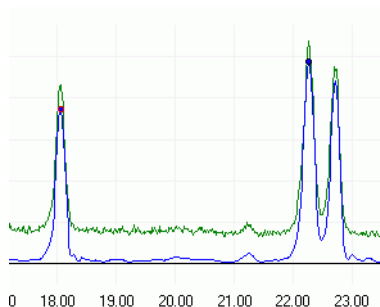
Now click on the *Advanced* tab in the top-left of the window.



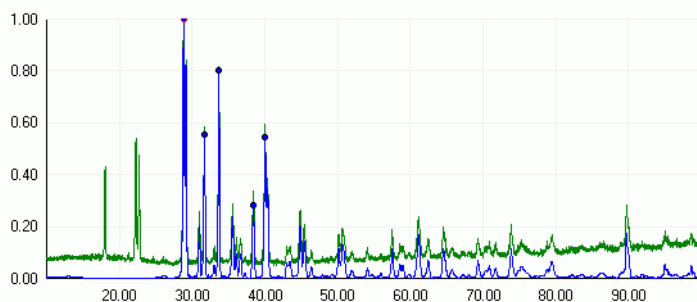
The top section revealed allows us to mask selected regions of the pattern to be ignored during matching or analysis processes. This may be useful where a particular peak is negatively affecting results. Say we wish to mask the peaks in the region of the pattern between 15° and 25°. Enter the start and end angles of the region to be masked in the relevant text boxes.

---

Examine the blue processed pattern in this region to determine its average background level – in this case, a value of zero should suffice, so enter 0.0 in the level text box, and click *Apply*.



The change in the pattern should be quite noticeable – while the green line of the raw data is untouched, the blue processed data line no longer has any peaks or features between the ranges we have entered:



Now repeat the process and mask the peak at approximately 90° using the same method.

Once finished, return the pattern to its initial state by clicking *Reset All*.

The rest of the *Advanced* tab options will be discussed in the *Analysing Mixtures* section later in this tutorial.

Choose *Close Window* from the *File* menu to dismiss the editor window. The program will check if you wish to retain any of the changes made in the editor. At present you do not want to keep any changes, so click *No*. You are returned to the main database window.

Feel free to look at some of the other patterns in the database in the editor window, and investigate the various processing options.

## 5.5 Matching Patterns

Assume that you have just obtained a new, unknown, powder pattern.

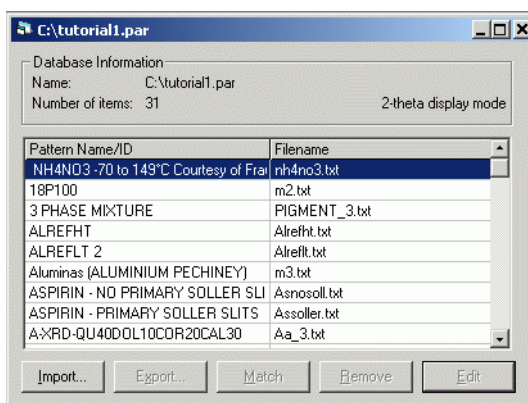
You want to find out what pattern in your existing database it is most similar to - and hence possibly identify what substance it may represent.

First, close any currently open database or editor windows.

Now, go to the *Manual Analysis* section of the *File* menu, and select *Open...*

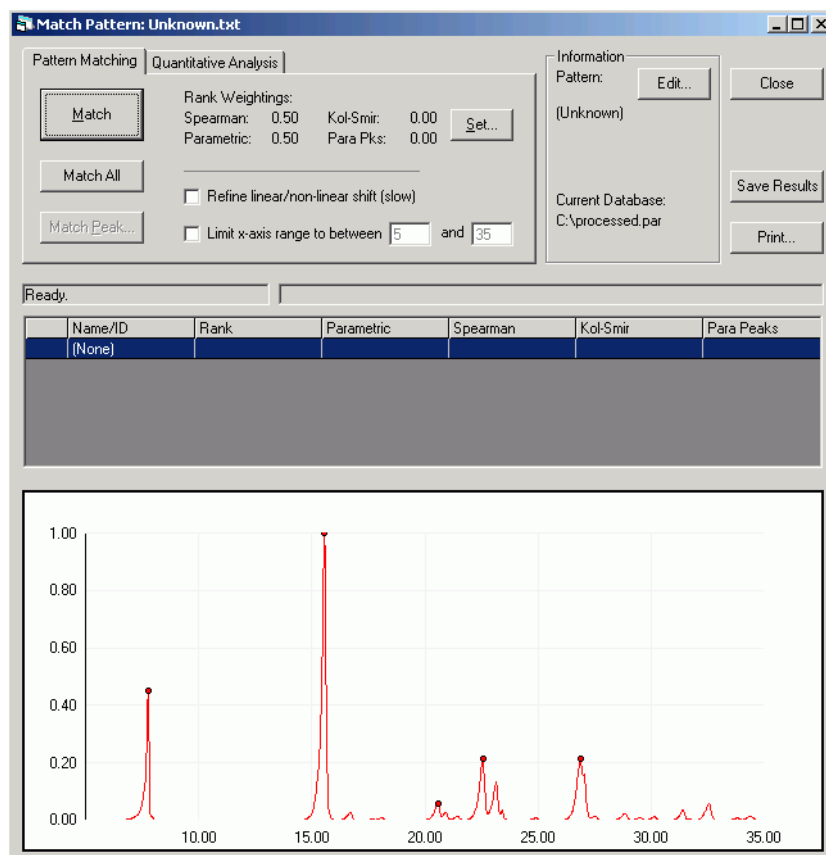
Open the pattern database you created earlier, *c:\tutorial1.par*.

A new database window will open, and the pattern data will be loaded into it.



The first step would normally be to import the unknown pattern into this existing database in order to examine it. In our case however, it is already loaded in the database.

Locate the pattern *Unknown.txt* in the scrolling list of patterns in the database, click once to select it, and then click on the *Match* button. The main program match window will appear.



Our unknown pattern is displayed in the graph pane in the bottom half of the window. Note that the pattern name and the database we are using are listed at the top right. On the top left of the window are the matching and analysis controls contained within two tabs – *Pattern Matching* and *Quantitative Analysis*. The default tab is *Pattern Matching*, which is what we wish to do first.

Click on the *Match* button. A progress bar appears as the program runs through various tests in order to compare our selected pattern to every other pattern in the database. Once matching is complete, the



centre section of the window fills with the numerical results, sorted by the column in bold type, Rank.

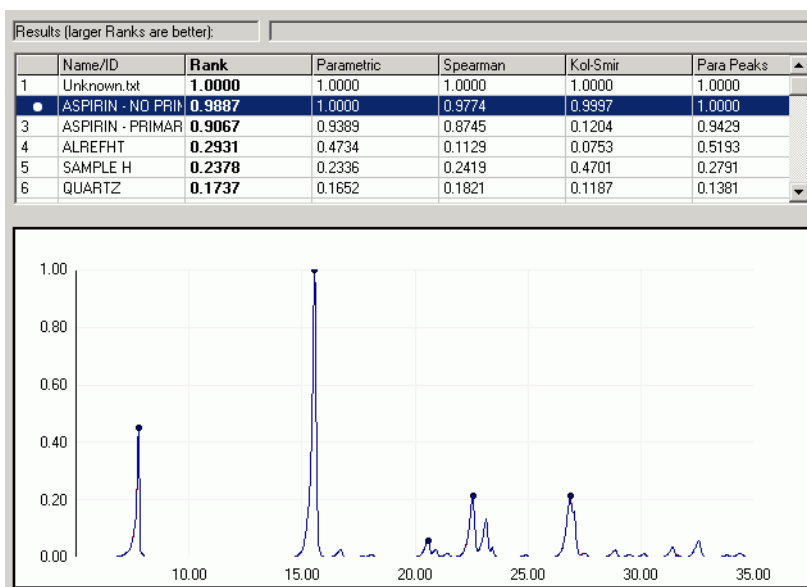
Results (larger Ranks are better):						
	Name/ID	<b>Rank</b>	Parametric	Spearman	Kol-Smir	Para Peaks
1	Unknown.txt	<b>1.0000</b>	1.0000	1.0000	1.0000	1.0000
2	ASPIRIN - NO PRIN	<b>0.9887</b>	1.0000	0.9774	0.9997	1.0000
3	ASPIRIN - PRIMAR	<b>0.9067</b>	0.9389	0.8745	0.1204	0.9429
4	ALREFHT	<b>0.2931</b>	0.4734	0.1129	0.0753	0.5193
5	SAMPLE H	<b>0.2378</b>	0.2336	0.2419	0.4701	0.2791
6	QUARTZ	<b>0.1737</b>	0.1652	0.1821	0.1187	0.1381

To sort the results by a different column, click once on that column's header. To change the sort order, e.g. to sort a column ascending instead of descending, or *vice versa*, click the header again. For the moment, click on the Rank header to re-sort by this column, and ensure the largest value (normally 1.0) is at the top of the list.

Look at the pattern associated with this value. This is what the program considers the 'best match' to our unknown. If it looks familiar, that is because it is – it is the *Unknown.txt* pattern itself. Because it is in the database, it is compared to itself. If this does not result in perfect match scores, there is a problem somewhere, so this is a useful check.

More interesting is the next entry down in the list. The next best match has a rank value of above 0.9, quite close to the perfect score of 1.0. The individual test scores reading along the row reflect this: all close to 1.0. The rank value is calculated by default by summing the Spearman and Parametric test scores and dividing by 2.0.

To see these scores reflected visually, we can overlay the best-match pattern with the unknown pattern. Click once in the left-most column of the pattern you wish to overlay (the one with '2' in it in this case).



The '2' is replaced by a coloured dot, and a pattern in this colour appears in the graph pane. It is obvious the two patterns are very similar. Click on the coloured dot in the left-hand column once again to remove the extra graph.

This suggests our unknown sample is aspirin.

Experiment with overlaying different graphs on the unknown; this helps to get a feel for how the pattern scores correlate to similarity

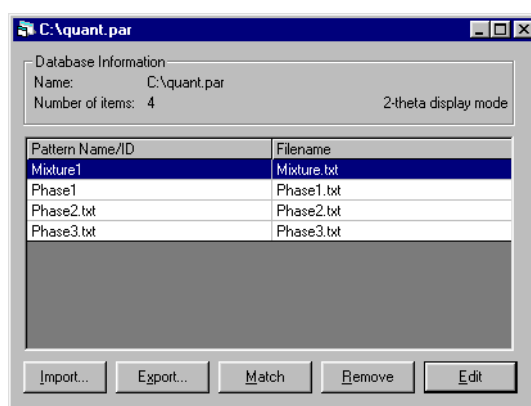
---

between patterns. Several patterns can all be overlaid at once on the graph; to clear them all in one go select *Clear Overlaid Graphs* from the *Graph* menu.

## 5.6 Analysing Mixtures Manually

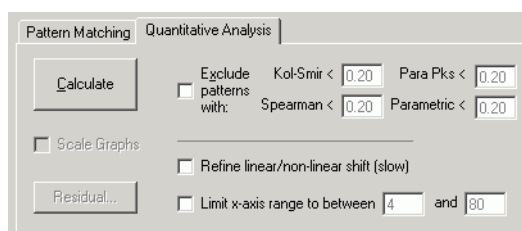
Using PolySNAP M, open the database file *quant.par* in the tutorial data folder. (Normally found on the PolySNAP M CD-ROM in the 'tutorial files', e.g. *tutorial* -> *manual\_data*).

It contains four patterns – one mixture, and the three pure component phases.



We will use the program to quantify the amounts of each phase in the mixture. Select the mixture from the list of patterns, and click *Match* to bring up the match window.

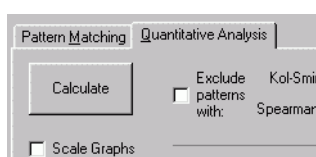
Go to the *Quantitative Analysis* tab, and click calculate. After a few seconds when a progress bar is displayed, the program should display its answers.



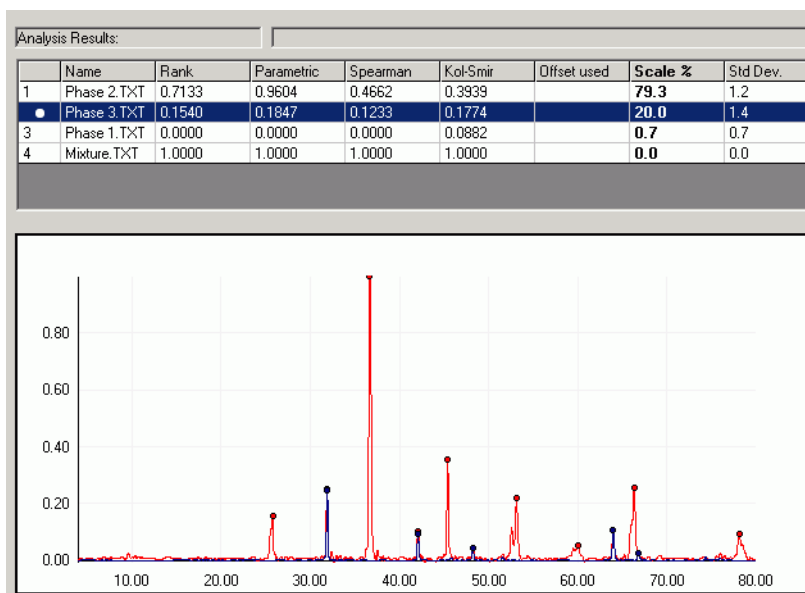
These are in a similar form as before, except that there are two additional columns – Scale % and Std Dev – the amount of each phase in the mixture, and the error on the calculation.

Analysis Results:								
	Name	Rank	Parametric	Spearman	Kol-Smir	Offset used	Scale %	Std Dev.
1	Phase 2.TXT	0.7133	0.9604	0.4662	0.3939		<b>79.3</b>	1.2
2	Phase 3.TXT	0.1540	0.1847	0.1233	0.1774		<b>20.0</b>	1.4
3	Phase 1.TXT	0.0000	0.0000	0.0000	0.0882		<b>0.7</b>	0.7
4	Mixture.TXT	1.0000	1.0000	1.0000	1.0000		<b>0.0</b>	0.0

There are various ways available to see if the programs suggested percentages are sensible. First, check the *Scale Graphs* box on the upper left.



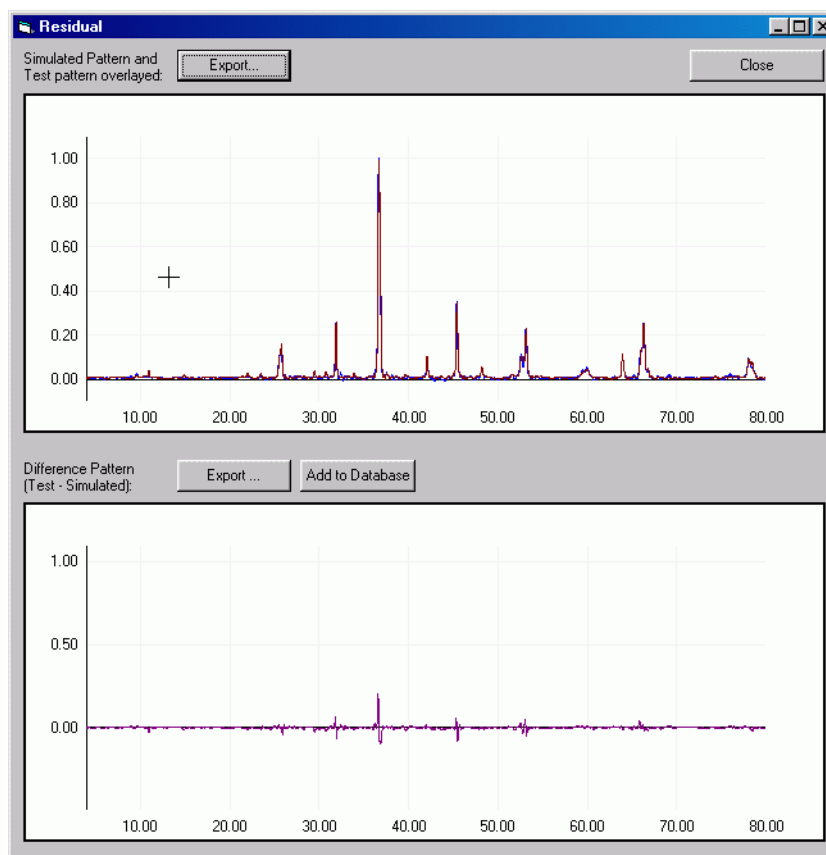
Then click on the left-most column of the results table for one of the phases.



As before, this overlays the selected pattern over the mixture, but is now scaled to the percentage intensity suggested by the programs analysis. The pattern should hopefully look sensible.

---

Another option is to click the *Residual* button, which brings up a window with two graph panes.



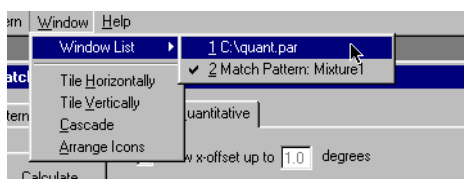
The upper one superimposes a simulated mixture pattern, made up of combining the pure phases in the amounts suggested by the program, on top of the original mixture. The bottom panel is then the difference between the two. This difference plot helps show up either missing phases or extra intensity which is not part of the mixture. If required, it can be output to a file to be imported as a new pattern at a later date. In this case, the small amount of residual intensity suggests the calculated answer is quite good.

Click *Close* to dismiss the window.

So far, we have quantified the mixture in terms of how much of each of the pure phase *patterns* are required to make it up. A more useful number in the real world would be in terms of the weight of each phase used in the mixture.



In order to calculate this, we need to add some additional information to each of the pure phase patterns. To do this, first select the database *quant.par* from the list of open windows in the *Window* menu.



This brings it to the front. Now select the first pure phase pattern: Phase 1. Click *Edit* to bring up the pattern editor window, and click on the *Advanced* tab.

Please enter additional known information:

Unit cell contents: Al<sub>2</sub>O<sub>3</sub>    a: 4.7592    b: 4.27592    c: 12.992  
 Z: 6    alpha: 90    beta: 90    gamma: 120

Using the above information, the following have been calculated:

Unit cell volume: 228.97  
 Formula Mass: 101.96  
 Density (g cm<sup>3</sup>): 4.44  
 Linear Abs. Coeff. (cm<sup>-1</sup>): 23.37  
 Mass Abs. Coeff. (cm<sup>2</sup>/g): 5.26

Update  
 Enter manually

We need to enter information into the lower region of this window, in particular the chemical formula of the phase, its unit cell dimensions, and the number of formula units per unit cell.

Phase	Formula	a	b	c	$\alpha$	$\beta$	$\gamma$	Z
Phase 1	Al <sub>2</sub> O <sub>3</sub>	4.7592	4.7592	12.992	90	90	120	6
Phase 2	Ca F <sub>2</sub>	5.4649	5.4649	5.4649	90	90	90	4
Phase 3	Zn O	3.2501	3.2501	5.2071	90	90	120	2

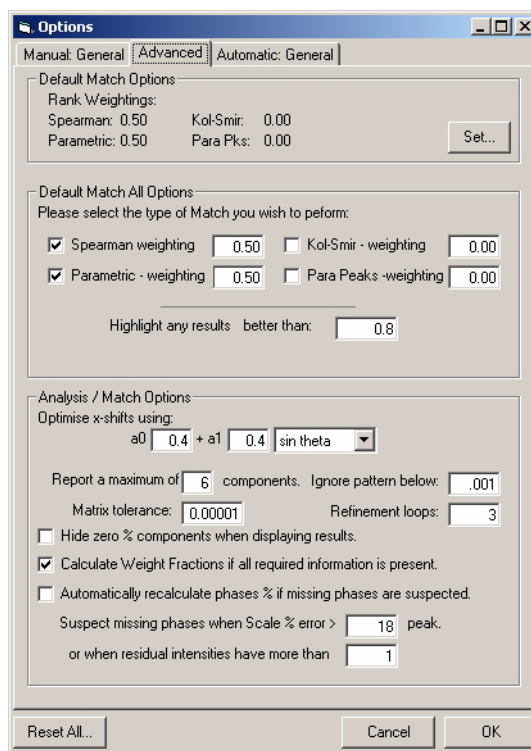
Using the information in the table, enter the relevant details for this phase, and click *Update*. The fields showing molecular weight and absorption coefficients and so on for this phase should update. If not, be sure to enter the formula in the form

<Atomic Symbol><No. of atoms> <AtomicSymbol><No. of atoms> etc.

(The allowed formats for formula entry are discussed in more detail in section 3.3.11, Additional Pattern Information in the main program manual).

Repeat for the other two phases.

Once all sets of information have been entered and updated, go to the program *Options* dialog box in the *Edit* menu.



Go to the *Advanced* tab, and make sure that the *Calculate Weight Fractions when all information is present* option is checked. Then close the *Options* dialog by clicking *OK*.

Click on the mixture pattern database entry to select it, before clicking the *Match* button to bring it up in the main match window.

Return to Match window, and in the *Quantitative Analysis* tab, click *Calculate* again.

This time, the results table should be slightly different – the results should be headed *Weight %* rather than *Scale %*. If not, go back and check that all of the three pure phases has had the extra information added successfully.

Analysis Results:								
	Name	Rank	Parametric	Spearman	Kol-Smir	Offset used	Weight %	Std Dev.
1	Phase 2.TXT	0.7133	0.9604	0.4662	0.3939		77.9	0.29
2	Phase 3.TXT	0.1540	0.1847	0.1233	0.1774		19.0	0.00
3	Phase 1.TXT	0.0000	0.0000	0.0000	0.0882		3.1	73.49
4	Mixture.TXT	1.0000	1.0000	1.0000	1.0000		0.0	0.00

If successful, the weight fractions should be close to:

- Phase 1 – 3%
- Phase 2 – 78%

Phase 3 – 19%

which are the correct answers.

## **5.7 Conclusion**

This completes the basic tutorial. There are many other features and options in the program that should allow much more complex problems to be examined. Each of these are described in the full program manual, which should be consulted for more information.



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### **PolySNAP M Version 2.0.1**

- Fixed an issue in countries using the comma as a decimal point where shifted patterns were not being displayed correctly in the Numerical Results pane.
- A new program splash screen and window background are displayed.
- The program version number is now displayed in program title bar.
- The program, documentation and website now use the new Bruker logo.
- A new option has been added to force quantitative analysis to be attempted on all input samples regardless of how similar they are to the reference phases. This can be selected via the '*Perform analysis on all samples regardless of similarity*' checkbox in the Options: Automatic: Advanced / Quantitative options dialog box.

### **PolySNAP M Version 2.0.0**

- The installer now adds a copy of the tutorial files to a folder named *tutorial* in the SNAP Program Files folder.
- The copy-protection system has been updated, and the *License* menu item removed as it is no longer used.
- PolySNAP M incorporates a limited subset of the PolySNAP style graphical analysis and cluster analysis tools, for datasets of up to 96 patterns.
- The program manual and other documentation has been comprehensively reorganised.

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