

Probe for EPMA Frequently Asked Questions

FAQ Introduction

This manual will attempt to provide a quick reference for specific solutions to various questions commonly asked by users (and even experts) when using Probe for EPMA. It is divided into several main sections: Acquisition, Analysis, Automation, and Plot (or Output) just as is the main program, each with several sub-sections based on topic specific areas to enable the user to quickly find the answer to their questions.



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General Questions

Installation

How can I install Probe for EPMA off-line on another computer for re-processing my data?

Yes, our software license allows you to install Probe for EPMA on as many computers as you like for data re-processing. In fact every user of your instrument is allowed to have a copy of Probe for EPMA to re-process their data off-line. However, each instrument requires a version of Probe for EPMA with a valid software registration to connect to the EPMA hardware for data acquisition and automation.

To install Probe for EPMA on another computer for off-line reprocessing of EPMA data check that you have a adequate computer system for running the software. Although Probe for EPMA will run on almost any PC computer (or Mac with Windows emulation or disk partition), the following is a recommended minimum configuration:

1. A PC running Windows NT4, 2000, XP, Vista (32 bit only) or Win7 (32 and 64 bit).
2. Enough hard disk space and memory (160 GB hard drive and 2 GB memory).
3. A large monitor, 21" to 24" minimum is suggested
4. The Probe for EPMA Distribution CD or downloaded distribution and update ZIP files.

Instructions:

Step 1. If you have the Probe for EPMA distribution CD, locate the Setup.exe file in the Distribution\Probe for EPMA\Installation folder. You may also download the distribution ZIP file, either the PFW-32_Dist-E.ZIP, or PFW-32_Dist-E_Vista.ZIP files but you will need to contact Probe Software for the ZIP password to extract the files. The Vista ZIP distribution will work on any operating system, NT/2000/XP or Vista.

Step 2. Run the Setup.exe file and follow the instructions to install Probe for EPMA on your computer. You might get two errors during the installation under 32 bit Vista. Just click Ignore and Yes to disregard them.

Step 3. Copy the update files from the CD update folder (Distribution\Probe for EPMA\Update) on the Distribution CD or from the downloaded update ZIP file (PFW-32_Update-E.ZIP) to the application folder (usually C:\Program Files\Probe Software\Probe for EPMA or C:\Probe Software\Probe for EPMA for Vista).

Or

Use the Help | Update Probe for EPMA menu in the Probewin.exe application to automatically update Probe for EPMA if you have an Internet connection.

You only need to run the Setup.exe program once for each computer. Updates can be applied at any time and are frequently available as new features are added.

Note that off-line re-processing of data requires that that STANDARD.MDB file containing the standard compositions be copied from the probe instrument computer to the off-line computer. The STANDARD.MDB file should be re-copied from the probe instrument computer whenever a standard composition is added to the standard database or the composition is modified.

After this has been done, the only files that need to be copied from the probe instrument computer are the user's probe database files. These file have the extension .MDB and are found in the UserData directory usually in a folder under the user's name. Also if it is present you should copy the raw image data file which has the same name as the probe database file, but with the .BIM extension.

The probe database file (*.MDB) is a Microsoft Access relational database file and contains all raw data and instrument parameters. However, for data re-processing you will want to open and read it using the Probe for EPMA or Evaluate applications.

The raw image data file (*.BIM) is a flat binary file consisting only of 4 byte integer long values. This file will be opened and read automatically by Probe for EPMA for displaying image data, but for those interested, the file format is very simple: the first two integers specify the X and Y pixel sizes of the image data for the first image. So you read the first two integers, say 512 for X and 512 for Y. Then you read 512 x 512 integers (262144 integers) worth of data values in normal row-column format. After the image data for the first image has been read, the next two integers specify the image pixel sizes for X and Y for the second image, etc, etc.

How can I install Probe for EPMA on another computer for off-line training so that it uses my current instrument configuration?

Probe for EPMA has a very realistic “demonstration” mode that will simulate standard, unknown and wavecan sample acquisition. Simulated data can be analyzed, plotted and output to any device. Therefore this Probe for EPMA demonstration mode can be used for many purposes including off-line training of new users to avoid wasting valuable instrument beam time in learning to use the software.

To install Probe for EPMA for off-line training follow the instructions in the above section for installing the software to an off-line computer. Then as above copy the STANDARD.MDB standard composition database so the trainee will have the same standard compositions as the actual instrument computer.

To ensure the most realistic demonstration mode you should also copy the probe configuration files from the probe instrument computer and copy them to the off-line computer. These files are:

PROBEWIN.INI
DETECTORS.DAT
MOTORS.DAT
SCALERS.DAT

These files are found in the Probe for EPMA application folder (usually C:\Program Files\Probe Software\Probe for EPMA or C:\Probe Software\Probe for EPMA) and should be copied to the newly installed Probe for EPMA folder on the the off-line computer usually found in the same folder name and overwrite the default configuration files these.

These configuration files only need to be copied once to the off-line computer, but should be re-copied if the configuration files on the probe instrument computer are modified by the user (but remember to re-edit the PROBEWIN.INI file “InterfaceType” back to zero if you re-copy modified configuration files to the off-line computer as described below).

Once these files are copied to the off-line computer, you can create probe database files that are exactly the same as would be created on the actual probe instrument computer but there is more more small edit that is necessary for “demonstration” mode.

Open the PROBEWIN.INI file on the off-line computer using any text editor, for example NotePad or TextPad. Scroll down to the [hardware] section and edit the value of the InterfaceType keyword. It will have a non-zero value for interfacing to the actual instrument hardware, but for “demonstration” mode you should change the value to a zero.

Save the changes to the PROBEWIN.INI file and re-start the Probe for EPMA software (Probewin.exe) and say “Yes” to the question: “Do you want to interface to the microprobe hardware?”

The program will now enter the “demonstration” mode and allow you to create realistic simulation runs for training purposes.

I tried to add more physical memory to my computer but it will not recognize the additional memory- what is going on?

If you are using the Matrox drivers for capturing video frames from a Meteor-II or compatible frame grabber board for input into Probe for EPMA, you will need to uninstall the Matrox drivers, re-boot the computer so it will recognize the additional physical memory and then re-install the Matrox frame grabber video drivers.

This is because the Matrox Meteor-II driver allocates some (usually 4-16 MB) of the memory at the top of the memory limit and prevents the operating system from gaining control over that memory and any memory above that. Therefore by uninstalling the Matrox drivers and rebooting, the system will see the additional physical memory. Then, after re-installing the Matrox drivers you can re-allocate some memory at the top of the new memory limit for the frame grabber board.

I am getting “Overflow” errors whenever I try to display a graph in Probe for EPMA- how can I fix this?

This can be caused by two problems. The most common problem is that your computer hard drive is extremely low on free hard disk space. You should immediately delete some files and empty your Recycle Bin. This may allow you to continue to acquire EPMA data but it is strongly suggested that you replace your hard drive with a larger hard drive.

The easiest way to do this without having to re-install all your applications is using Norton Ghost to clone your hard drive to an external drive, replace the hard drive with a larger drive and then re-boot using the Norton Ghost CD-ROM, restore your operating system and applications to the new drive. Norton Ghost will prompt you to allow it to utilize all the hard drive space on the new larger hard drive.

The second problem is less common but is seen when an Epson or InFocus video projector is connected to the computer with a USB cable. This then causes the Epson or DisplayLite USB display software to be installed on your hard drive which interferes with the Probe for EPMA graphics library.

The Epson or InFocus video projector must be disconnected from your computer and the Epson or InFocus DisplayLite USB display software must be uninstalled from the Control Panel Add/Remove Programs applet.

If the Probe for EPMA graphics are still not restored after removing the USB video projector link software you must re-install your computer video graphics driver. Note that on some ATI graphics cards there is a bug in the uninstaller which gives the error “ISLAYER.DLL not loaded into memory, error 0x80040707” when you attempt to uninstall the ATI video driver. This can be fixed by adding a folder named “Desktop” to your C:\Documents and Settings\All Users” folder. I am not kidding- it works.

I am trying to save a PictureSnap image to the clipboard or a BMP file with the stage or analysis coordinates shown and I am getting an “Out of Memory” error. I have 4 GB of memory so how can I be out of memory?

When Windows allocates memory for a device compatible bitmap it does NOT use the system memory but instead uses the video memory on your video display board. This and related memory errors is seen because your video card does not have sufficient memory for both the monitor and the device compatible bitmap.

You can purchase a video card with additional video memory for best results or for a temporary fix you can right click the desktop and select the Properties menu and then the Settings tab and select either a lower display resolution and/or less color depth. For example, selecting 16 bit color depth instead of 32 bit color depth usually fixes the problem though the desktop icons may suffer slightly in appearance.

After I moved my configuration files from my desktop with a large monitor (or two monitors) onto my laptop, how come I cannot see some of the application windows?

Probe for EPMA automatically saves the application window and dialog positions and sizes for each user and re-uses those positions each time. This information is contained in the WINDOW.INI file.

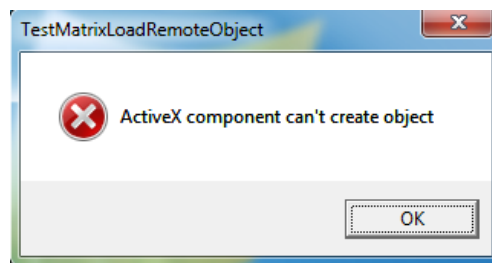
To reset all window positions back to their default positions go to the Probe for EPMA application, and click the Window | Reset Current Window Positions To Default menu and the program will clear the saved window positions for the current user only.

Why do I get the error “InitFilesUserData : Path/File access error” after installing Probe for EPMA on Server 2008 or Windows 7?

Probe for EPMA needs to update some files the first time it runs. Therefore (for at least the first time you launch Probe for EPMA or another Probe Software application), be sure to right click the application icon or shortcut and click the “Run As Administrator” menu.

If you would like to make this permanent to avoid possible problems with updates in the future, you should right click the application icon or shortcut, click the Properties tab, then select the Compatibility tab, then check the “Always Run As Administrator” checkbox. Then click OK.

After I upgraded my operating system to from XP to Win 7 64 bit, I get the following error.



Likewise, when I start Probe Image, none of the crystal names are loaded properly in the Setup | Acquisition dialog.

The reason for this is that the copy protection feature is stored in different places for 64 bit operating systems. To fix this error, search for and delete the xline.dll file from your hard drive. Then reinstall the latest CalcZAF.msi, ProbeforEPMA.msi, ProbeImage.msi and Matrix.msi installers.

When you now run Probe for EPMA, the system will prompt you for a new serial number. Simply click the Copy button and send Probe Software the registration number and we will send you a new serial number to unlock the software.

Acquisition Questions

Setting Up a Run

I tuned some new elements up using the Move window, now how do I get them into the current sample?

Generally it is perfectly acceptable to use the Move window to move spectrometers to specified element positions and one can even peak the spectrometers and run PHA distributions using the Move window but the peaking and PHA scan intensity data is not automatically saved to the current run from the Move window.

Therefore, it is preferable to use the peaking and PHA options from the Acquire! or Automate! windows to tune the element positions and PHAs because then all spectrometer peaking data and PHA parameters are automatically saved to the run and can be inspected later using the “Run | Display, Fit and Export Spectrometer Peaking and PHA Scans” menu.

However, if one has either just moved the spectrometer to the nominal position using the Move window, as indicated by the original question, those elements can be easily imported into the run by clicking the “Elements/Cations” button in the Acquire! window and selecting each element spectrometer position using the colored buttons in the “Elements/Cations” dialog.

I added some elements to a sample, but when I make a new sample why aren't the newly added elements present in the new sample?

New samples in Probe for EPMA are created by default based on the last unknown sample. Therefore when you make a new sample, the program will generally create the new sample based on the conditions, elements and parameters as defined in the last unknown sample.

Exception: if no unknown samples are defined in the run, the program will base the new sample on the last standard sample, and if no standard samples are present, the program will base the new sample on the last wavescan.

Standard samples are also created based on the last unknown as well. New standard samples are based on the last unknown sample because if the standard sample was automatically acquired using one of the “Use Quick Standards” options as defined in the Acquisition Options dialog, then some of the analyzed elements might be missing if those elements were not assigned for use as a primary, interference or background standard.

There is an exception for wavescan samples: how new wavescan samples are created depend on the default new wavescan sample behavior as defined in the PROBEWIN.INI file [software] section by the value of :

UseLastUnknownAsWavescanSetup=0

The program will create a new wavescan sample based on the last (previous) wavescan sample (the default behavior) or based on the last unknown sample. This default behavior can be toggled back and forth in the Acquisition Options dialog by checking or unchecking the “Use Last Unknown As Wavescan Setup” checkbox.

How do I change the acquisition order for the elements on a spectrometer?

Click the Acquisition Options button in the Acquire! window and select either

Channel Order
Descending Angstroms
Ascending Angstroms
User Defined Order

If “User Defined Order” is selected then you can click on each element row in the grid and individually specify the numerical order manually by editing the value of the “Spectrometer Order Number”.

How do I change the channel (or printout) order of the elements in a sample?

Once a sample has intensity data acquired, the channel order cannot be changed except by using the “Geological Order” output buttons in the Analyze! window or the J.J.D.-2 or H.W. menus in the Output menu. See the “Elemental Output Sort Order” in the “Analytical | Analysis Options” menu for more output options.

However, one can change the output order any time for subsequently acquired samples by making a new sample with no intensity data and then clicking the “Combined Conditions” button in the Acquire! window. From this dialog the analytical conditions (kilovolts, beam current and beam size) can be changed individually for each element. But to answer the original question, in the lower section of the dialog the channel order of an element can be moved up or down in the element list by selecting the element and using the large “spin” button to move it.

Subsequent samples created will utilize the new channel order, however the acquisition order will not be changed for a given spectrometer.

Why is the software sometimes not able to set the beam current to the specified nano-amps?

Usually this is a sign of a dirty beam current regulating aperture. Sometimes the column is not properly aligned or needs cleaning.

On JEOL instruments this is sometimes caused when the aperture is dirty and the condenser lens calibration needs to be performed again.

This is easily done from the Window | Analytical Conditions menu button by clicking the Calibrate Set Beam Current button. Be sure that the proper aperture is selected for the calibration to be saved properly. In addition it should be noted that JEOL 8500 instrument columns can be run in SEM or EPMA mode. Be sure the instrument is in the EPMA mode for setting the beam current.

Acquiring X-ray Intensities

How do I move a spectrometer to a specified element position?

If the element in question is one of the elements already tuned up in a run, then the easiest method is to click the “Peaking Options” button in the Acquire! window and double-click one of the elements listed in the element list. The program will not only move the element to the specified (hopefully already peak centered) position, but also set the PHA parameters automatically.

This is useful for using the “audio” x-ray feature of some instruments for listening to a specific element intensity for fine stage adjustments on very small inclusions and also for setting elements up for use with Probe Image for x-ray mapping runs.

One can also force all elements to their starting analysis positions using the “Return To On Peak (start analysis) Positions”, however the program will do that automatically when the acquisition is started. However, if the spectrometers are not already at their starting positions for an acquisition, the faraday cup may be withdrawn before the spectrometers move to their start positions depending on whether synchronous or a synchronous motion has been selected in the “Acquisition Options” dialog.

To move the spectrometers to any arbitrary element, simply use the Move window and click the small periodic table button for each spectrometer, then simply click “Go Spectros” to move all spectrometers to the specified positions.

Analysis Questions

Analyzing Standards

How can I tell if the standard sample is the primary standard for a specific element?

One could simply click the “Standard Assignments” button in the Analyze! window and check which standard is assigned to what element (this will also indicate what the assigned interferences are also), but the easiest method is to look at the analytical output to the log window.

For each analyzed element in a sample simply check the printed line labeled “STDS:”. The integer number is the standard number of the primary assigned standard. If the number displayed is the same as the standard number of the standard sample being analyzed, then the standard is merely analyzing itself as the primary standard.

Analyzing Unknowns

How do I specify a fixed or “specified” concentration of an element in my analyses?

Make sure the element is present in the sample as a “specified” element using the “Elements/Cations” button from the Analyze! window. That is an element with a blank x-ray line (the last item in the x-ray line drop down list). Note that more than one sample can be selected at a time for all operations.

Then click the “Specified Concentrations” button in the Analyze! window and click on each specified element to enter its concentration in elemental or oxide percent. One can also specify elemental concentrations using formula entry. Any elements in the formula already being analyzed for will be skipped.

Note that if the sample is actually a standard being run as an unknown, then the user can simply select the standard from the list of standards and click the “Specify By Standard” button. Only those elements not analyzed will be loaded. Also any elements not already present as specified elements will automatically be added to the sample.

Note that standard samples cannot have unanalyzed element specified concentrations entered by the user because these elements are automatically loaded by the program at analysis time. However, if an element is present in the standard database, but is NOT present as an analyzed or unanalyzed element in the sample and the element concentration is also below the minimum value (internally set by the program to 0.05 wt.%), then the user can force the specified element concentration to be loaded automatically to the analysis by manually adding the element as a specified (not analyzed) element from the “Elements/Cations” dialog.

How do I add water by difference to my glass analyses?

Make sure that hydrogen is present in the sample as a “specified” element using the “Elements/Cations” button from the Analyze! window. That is an element with a blank x-ray line. Note that more than one sample can be selected at a time for all operations.

Then click the “Calculation Options” button in the Analyze! window and check the “Element By Difference” checkbox and select “h” in the drop down element list.

If the sample has the “Calculate Using Stoichiometric Oxygen” option clicked, the hydrogen will automatically get calculated as H₂O and properly incorporated into the matrix correction. Note that the

ZCOR correction factors for the other elements will generally increase slightly because, for example, Si K α is more absorbed by oxygen than by itself, so adding H₂O by difference will decrease the amount of H₂O compared to a simple subtraction from 100%.

If the sample has oxygen present as an analyzed element then other options for specifying H₂O are available. See specifically the “Hydrogen Stoichiometry To Excess Oxygen” option in the “Calculation Options” dialog. In this instance the software will calculate the excess oxygen by subtracting the calculated stoichiometric oxygen from the measured oxygen and add then hydrogen by the specified stoichiometry to the excess oxygen.

How do I calculate my carbonate analyses without measuring carbon?

Simply add carbon as a “specified” element (no x-ray line) from the “Elements/Cations” dialog in the Analyze! window.

Then click the “Calculation Options” button in the Analyze! window and making sure that the “Calculate With Stoichiometric Oxygen” option is selected, check the “Stoichiometry To Calculated Oxygen” checkbox and enter 0.333 atoms of “c” (for carbon) to each calculated oxygen atom have the program calculate “CO₃” automatically.

The program will then automatically calculate stoichiometric oxygen for each analyzed cation and also automatically add the proper stoichiometric amount of carbon to the analyses to give a proper formula of the form “(Ca,Mg,Fe,etc.)CO₃”.

Analysis Output Options

How do I get the analyzed and specified elements to print out on one line in the log window?

Click the “Analytical | Analysis Options” menu and check the “Print Analyzed and Specified On The Same Line” checkbox.

Note also that one can toggle between 8 elements per line and all elements on a line for the log window output by using the “Output | Extended Format” menu.

How can I display analysis coordinates on analog signal (SE, BSE, etc.) images?

From the Run | Display, Annotate, Export Analog Signal Images menu click the Plot Stage Positions checkbox to display either the specified sample analysis coordinates (double-click the image list to change the selected sample) or all analysis positions within the image area within the currently open probe run.

Specify any additional image display options such as palette color, scale bar, etc. and use the Copy To Clipboard or one of the Save As image file formats to save the image and drawing objects if desired.

Alternatively one can export all images (and any drawing objects such as analysis positions and scale bar) using the Output | Save Images To BMP Files menu.

How can I display acquired analysis coordinates on PictureSnap images?

There are two menus for displaying position coordinates on a calibrated PictureSnap image. For the display of currently **digitized** position samples displayed in the Automate! window, use the Display menu from the PictureSnap window to specify standard, unknown or wavescan sample positions and also sample and line numbers if desired. Note that the sample numbers will be the position sample number and the line numbers

will be the grid row number. These numbers will be different once the data is acquired and these menus are not available when re-processing data off-line.

Once the sample positions have been acquired, the user can display the **acquired** analysis coordinates for standards, unknowns or wavescans from the Run menu along with sample numbers and line numbers. These numbers will reflect the sample and line numbers displayed in the Analyze! window sample list. This menu is available for on-line or off-line data re-processing.

Use one of the File | Copy or Save As menus to save the image along with any drawing objects such as sample coordinates and line numbers.

Automation Questions

Digitizing Sample Positions

How can I quickly and automatically create position samples and digitize a single point or random cluster of points?

The trick here is to save mouse clicks and key strokes. So from the Digitize window check the “Auto Increment” and “Auto Digitize” checkboxes. Then enter a sample prefix name in the “Unknown or Wavescan Position Samples” text field.

Now whenever you hit the enter button (whenever the Digitize window has the focus), the program will do two things, first it will automatically add a position sample to the Automate! position sample list with the sample name you entered as a prefix and a numerical string such as “_001”, “_002”, etc appended to it. This will be incremented automatically each time you hit enter. To have the program reset the starting number or start on a different increment number simply edit the number next to the “Auto Digitize” checkbox and uncheck and re-check the “Auto Increment” checkbox.

Second, the program will automatically digitize a number of random stage coordinates based on the values specified in the “Shotgun” digitize option and the current state position. If the number of “Shotgun” points is 1 then the program will add a single point at the current stage position.

Automation Options

What is the “Use Quick Standards” option and how do I use it?

Normally one should acquire all elements on all standards as this may be helpful for performing interference corrections and/or MAN background corrections. It is also useful for evaluating the accuracy of secondary measurements on standards that are not assigned as the primary standard for an element.

However, if one is satisfied with the accuracy of the standard calibrations and/or all interference and/or MAN background calibrations have already been acquired, then one may save considerable time by specifying the use of “Quick” standards.

When the “Use Quick Standards” option is checked in the Automate! window the program will check to see if each element is used as a primary, interference or MAN standard assignment and if not, the program will not acquire that element for that standard.

However, if the standard has no elements that are utilized in the primary, interference or MAN standard assignments the program will treat the standard as a pure secondary standard and acquire all elements in that standard.

There are two options for how the “quick” standards are actually acquired as defined in the “Acquisition Options” dialog from the Acquire! window. The default is to acquire standard intensities along the lines already described. A second option is to acquire all the standard element intensities that are assigned as primary, interference or MAN standard and ALSO any elements in standards whose abundances are greater than the elemental percentage as defined by the user in the “Acquisition Options” dialog.

How do I run both standards and unknowns automatically?

To have Probe for EPMA acquire data for both standards and unknown position samples (and/or wavescan samples), simply click the “All Sample” option in the Automate! window so that all position sample types are displayed in the position sample list.

Then use the “Select Stds” button to select the current standards and then <ctrl> click the unknown samples you wish to run also. Then simply select the Automation Actions such as “Acquire Standard Samples”, “Acquire Unknown Samples” and possibly “Acquire Standard Samples (again)” if you would like the standards acquired both before and after the unknown samples for a drift correction.

Finally just click the “Run Selected Samples” button and confirm the Automation Actions.

When I acquire automated standards from the Automate! window, why is the program ignoring the “Standard Points To Acquire” value and only acquiring standard positions if they are explicitly digitized?

From the Acquire! window, Acquisition Options dialog, simply uncheck the checkbox in the Automated Standard Acquisition frame labeled “Use Only Digitized Standard Positions”.

Plot (and Output) Questions

Output Menus

How do I export my data to Excel?

One can open a live link to Excel using the “Output | Open Link To Excel” menu and then utilizing the “>>>Excel” button in the Analyze! Window to export the specified data types (set in the Acquisition Options” dialog from the Acquire! window) to the “live” Excel spreadsheet.

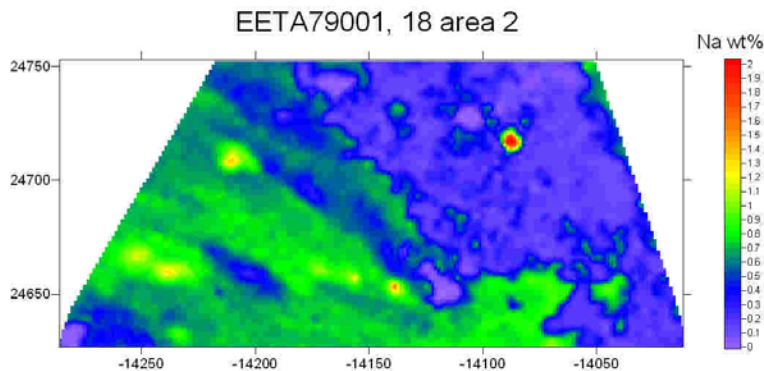
However one can also output all standard or unknown analytical data to Excel by using one of the “custom” output formats from the Output menu that also have an option to export to Excel. The output formats that will also export to Excel as a user option are the J.H. (#3), J.J.D. (#4), J.J.D.-2 (#5), H.W. (#6) and P.C. (#9) custom output formats. The details on these custom formats are available in the “User’s Guide and Reference” manual.

Also any data selected in the Plot! window data columns can also be exported to Excel as tab delimited files using the “Send Data To ASCII File (X, Y, (Z)...)” option. Once exported from Probe for EPMA like this they can be easily imported into Excel and saved as a normal Excel spreadsheet.

How do I create a color flood map of my random or rectangular or polygon grid acquisitions?

For this you will need to create an output file suitable for Golden Software’s SURFER plotting application. SURFER expects X and Y coordinate data in the first two columns, followed by multiple columns of Z data for plotting contours or surfaces. To accomplish this from the Plot! window, select the “3-D (three axes)” graph type and then select the “Send Data To ASCII File (X, Y, (Z)...” option and then the “SURFER .BAS File” option which automatically selects the X coordinate data in the x-axis list box, the Y coordinate data in the y-axis list box and then manually select the appropriate Z data (weight percents, etc.) in the z-axis list box using multiple selection.

When the Output button in the Plot! window is clicked, Probe for EPMA will create a .BAS basic script file containing OLE code for creating contour and surface plots. To run the .BAS script, double click the GS Scripiter icon, select File, Open and double click the newly created .BAS file. Then click the “Run | Start” menu to begin the automatic creation of the surface and contour plots. All plots are automatically saved and can be opened in the SURFER application and modified as necessary afterwards.



Hint: if the output contains duplicate elements, be sure to edit the output filename in the newly created .BAS file from within the GS Scripiter application to differentiate them by, for example, indicating which spectrometer they are, in addition to the element symbol.

Wavescan Plotting and Background Modeling

How can I see what the background fit looks like?

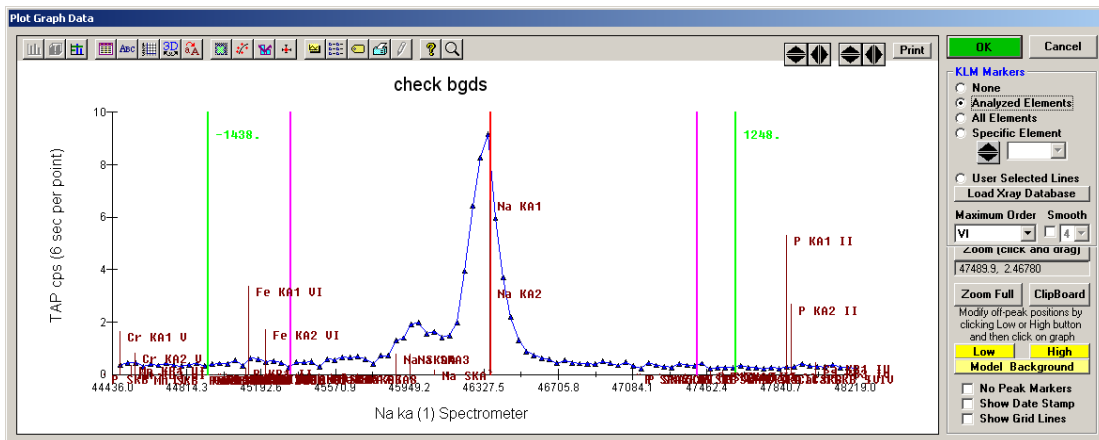
The best way to see how well your off-peak backgrounds are positioned is to acquire a wavescan sample on a material similar to your typical unknown. The point being that one should select off-peak measurement positions that are not interfered with by any other secondary peaks from other elements. This could be an appropriately selected standard but could also be the actual unknown sample.

Note that Probe for EPMA makes this rather easy because the wavescan sample acquisition will automatically acquire all the elements in your sample without you having to make multiple wavescans for each set of elements (if you have more than one element per spectrometer specified) in the unknown sample.

Note that the acquisition time for each element on a spectrometer should be adjusted using the “Count Times” button in the Acquire! window to “load balance” the wavescan acquisition as there is no point in having a spectrometer idle while other spectrometers are still acquiring photons.

Once the wavescan is acquired go to the Plot! Window and select the wavescan just acquired. The program will automatically select all samples associated with that scan and also the spectrometer position and intensity of the first element for the X and Y axes of the plot. Use the “spin” button next to the “Output” button to select the next spectrometer and element automatically and then click the “output” button.

Once the wavescan has been plotted you can click and drag to zoom an area of interest and also use the KLM options to display nominal x-ray lines from the NIST x-ray database. To change the spectrometer position of subsequent off-peak measurements simply click the “Low” or “High” buttons and click the graph where the new off-peak background position should be located.



Now to see the background fit simply click the “Model Background” button and the program will open a dialog that will allow you to try different background fit models for this data. Note that this fit is only a “nominal” fit as the actual off-peak measurements will be utilized in subsequent quantitative analysis of standards and unknowns, but modeling using the wavescan sample will help to see what problems might be present in these compositions under these conditions.

If you find a model that gives a good fit you could simply make a note of it and then go the “Elements/Cations” button in the Acquire! window to select the new background model, but an easier method is to simply select the samples to assign the new background model to in the “Model Background” dialog (be sure to include the last unknown sample so it will take effect for new samples) and click the “Assign Background Model To Selected Samples” button. Once you click “Close” and “OK” the changes will be saved to the selected samples.

Note that the new off-peak positions (if specified by the user) will be changed, without using the “Model Background” dialog, by simply clicking “OK” from the “Plot Graph Data” dialog.

Additional Help

Context Sensitive Help

Software Help

At any time while using the software you can simply hover your mouse over a control and our “Tool Tip Help” will pop up a short English sentence describing the control or button in additional detail.

Additionally you can hit the F1 key in any window or dialog box or on any selected menu and the software will automatically pull up the most relevant section of the User’s Guide and Reference manual as a standard Help file.

Updating Probe for EPMA

Always be sure to stay updated with the most recent version of the software. We are constantly updating documentation, improving existing features and adding new capabilities all the time. Updating Probe for EPMA is easily accomplished using the the Help | Update Probe for EPMA menu in the main Probe for EPMA (Probewin.exe) application. You may select HTTP or FTP methods for downloading the update.

For some sites behind firewalls, this option may not be usable. In these cases we suggest you install a copy of Probe for EPMA for off-line processing on another computer (using the original Probe for EPMA Distribution CD) that is connected to the Internet and not behind a firewall and run the Help | Update Probe for EPMA menu update from that computer. When the update download is complete you will find a file named “PFW-32_Update-E.ZIP” in the Probe for EPMA application folder (usually C:\Probe Software\Probe for EPMA or C:\Program Files\Probe Software\Probe for EPMA).

Simply copy this ZIP file to a thumb drive and bring it to the computer connected to your electron microprobe and copy the file to the Probe for EPMA application folder (usually C:\Probe Software\Probe for EPMA or C:\Program Files\Probe Software\Probe for EPMA). Make sure no Probe for EPMA applications are running and extract all the files in the update ZIP to the Probe for EPMA application folder and overwrite all existing files. All your site specific setup and configuration files will not be changed and you will be updated.

Documentation

There are a number of manuals provided to assist you in getting the most out of your Probe for EPMA experience. For example:

User’s Guide and Reference

This manual provides an exhaustive listing of every window and menu in Probe for EPMA. It is written from the perspective of telling you what everything in Probe for EPMA does or is for, with additional suggestions and advice for certain specialized procedures. It also documents all the Probe for EPMA configuration files and the many defaults that the user can specify for a truly customized software experience.

Quick Start

This manual provides a short overview of the main steps usually utilized in setting up a new Probe for EPMA run. For example, selecting the elements for quantification, peaking the spectrometers, running a wvescan to select off-peak backgrounds and acquiring standards, evaluating accuracy and acquiring unknown samples and outputting results.

Getting Started

The Getting Started manual provides an complete and detailed step by step guide to all the basic procedures in Probe for EPMA. Creating your standard composition database, starting a new run, tuning the spectrometers, digitizing acquisitions, imaging and plotting and output methods are all covered in extensive detail.

Advanced Topics

This manual provides a detailed step by step guide for a large number of specialized and advanced procedures in Probe for EPMA. For example, using Element, Sample and File setups, deadtime calibrations, time dependent intensity (TDI) corrections, Area Peak Factors (APFs) for correcting for peak shift and shapes changes in low energy emission lines, and many other topics.

Contact Us

Don't hesitate to contact us by email or phone. We are happy to assist as best we can in answering your Probe for EPMA or EPMA questions in general. We view ourselves as a community of microprobe users and we are pleased to help you.

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Good luck and have fun!

John Donovan
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