

Basic Beamline Operations

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0. Introduction

This manual describes how to perform the most common tasks on the beamline. These include steering the beam, setting the spot size, navigating on the sample, mapping, and taking EXAFS spectra. This manual does not go into beamline tuneup, maintenance or data analysis. Diffraction is covered in its own manual.

If you are not familiar with LabVIEW controls and, especially, graphs, read the document on Common LabVIEW Conventions before proceeding. The beamline programs are all written in LabVIEW and make extensive use of graphs, cursors, array indicators and the like.

There are cheat-sheets for the mapping and EXAFS programs. You may want to print these out for quick reference. If you have problems, refer to the Troubleshooting guide, a shortcut to which is on the Desktop of the data analysis computer (probably where you're reading this). A copy is appended to this writeup, however the one on the Desktop may be more current.

There is also a note describing the beamline optics. Read this to understand the role of the various mirrors and the roll slits. There is also a full-length paper in *J. Synchrotron Radiation* describing the beamline.

Tricky points which are not obvious and which can be confusing and troublesome are written in *italics*. Names of controls and indicators in the programs are in Arial, as they are on the actual screens on which they appear.

I. Getting beam

You should have been taught how to get in and out of the hutch and how to get beam, but here's a quick review: To lock the hutch and get beam, start by pushing the small black search button on the upstream wall of the hutch next to the optics box. An annoying noise will start. Exit, and while holding the hutch door shut, Push the Lock button on the right side of the box that's next to the door. There is a light labeled READY on the upper left of the RSS box (the big electrical box with lots of lights on it, attached to the hutch). This light will come on after 20 seconds or so. Press the HUTCH SECURE button below the READY light. The noise will stop and the shutter will be enabled. The shutter switch is on the panel to your left, over the label 'BR1032-06'. If you flip the shutter switch before the noise stops, beam will not come on, and you will need to toggle it to the closed position, then to open.

To get back into the hutch, close the shutter and wait for the red SAFETY SHUTTER CLOSED light to come on. Push the DOOR UNLOCK button on the box where the red light is or the equivalent button on the small box near the door. The shutter is open when the green light over the shutter switch is on. The buttons on the RSS box and the small box by the door are exactly equivalent.

The next step is to steer the beam onto the roll slits. This may need to be done at the top of a fill, or when trying to get a small probe spot. Once done, the beam seems to hold for most of a fill, and sometimes for days.

The relevant controls are on the beamline-control computer. The right-hand keyboard, monitor and mouse is connected to two different computers through a 2-port KVM switch. The desktop for the data-taking computer (UXASES) has many icons on a light-blue background. That for the control computer (BL1032BCS) has fewer icons on

a dark-blue background. Steering the beam, setting the spot size, and changing the I_0 and I_t gains are done with the control computer. To switch between computers, hit the `Control` key twice.

To steer the beam, start by moving the roll-slit sizes to $20 \times 10 \mu\text{m}$. This is done using the `Motor Monitor` program, which shows as a window about 85mm high by 95mm long. First, set the horizontal size. Click on the `Motor` control (bottom left) and select `Horizontal Slit Size`. Type '20' into the `Goal` window (top center) and hit the `Move` button (top left). The slit will close through zero and come back to $20 \mu\text{m}$. Similarly, set the `Vertical Slit Size` to $10 \mu\text{m}$.

Next, find the diagnostic monitor. There is a plexiglas cage which holds the roll-slit assembly (big cross with gears and motors). Downstream of this is a 2-3/4" cross with a black linear-motion feedthrough on top. This feedthrough has an indicator showing the position of the monitor. The monitor now consists of a YAG phosphor in the cross with a PIN diode looking at it to detect the fluorescence. In normal operation, this should be all the way up. Use the crank-handle and locking screw to move the actuator so that its indicator lines up with a black line on yellow paper on the right. The monitor now intercepts the beam.

The output of the monitor may be read on the middle one of the row of three DVMs above the shutter switch. Now, go back to `Motor Monitor` and select `M1 roll`. Make sure the `Jog Size` (just above the `Motor` control) is set to 0.01; type this in if it isn't. Now, use the `Jog` buttons (left side) to maximize the reading from the PIN diode. This reading is echoed as `Channel 2` in the set of readouts on the right side of the large `Beamline 10.3.2 Beamline Control System` window, so you don't need to crane your

neck reading the DVM. There is a backlash move when you hit the upper jog button, so wait for the motion to stop before doing anything else. Next, maximize the reading using the M1 Tilt motor with a jog size of 0.0005.

You have now steered the beam through the roll-slits. Lift the PIN diode out of the way (as high as it goes) and set the slit sizes to what you want. Here are some rough guidelines for slit sizes:

Slit size HxV, μm	Spot size HxV, μm	
300x50	15x6	full size, max flux
100x50	6x6	
50x20	3x3	
20x10	~2x2	smallest beam

In some cases, slitting down a little, say to 200x30 μm on the roll slits, can improve stability and normalization by cutting off the fringes of the beam.

The gain on the I_0 and maybe I_t detectors should be set at this point. On the beamline 10.3.2 window, click the Amplifiers tab and select Monitor. The gains for the two current amps can be selected there using the Sensitivities control to the right. To turn offset on or off or change the rise time, pull up Set Up Parameters from the Amplifiers menu. The transmission and I_0 amplifiers are both SRS570s with a maximum output voltage of 7V (5V spec). To be safe from saturation during noise or other spikes, limit the voltage to 5V. Offset (no-beam output) should be such as to make the output ~0.1-0.2V. If doing QuickXAS, the I_0 amp should be set to High Bandwidth mode in the Set Up Current Amp Parameters panel (the one used for offsets). If mapping transmission, the transmission amplifier should be set to High Bandwidth mode. Otherwise, the amplifiers should be set to Low Noise mode. For the transmission

amplifier, if running a foil or other sample with a big edge jump, check for saturation above and below the edge.

This concludes the list of things you have to do on the BL1032BCS computer. Hit `Control` twice to switch back to `UXASES`, where the data-taking programs live.

It may occasionally be necessary to check the monochromator 'tweak', that is the parallelism of the crystals. This is adjusted as follows: There is a gray Ipico hand-paddle sitting atop the half-rack where the YAG current amp is. In the top row of buttons are two labeled `-JOG` and `+JOG`. If you want to detune, use these buttons to get whatever degree of detuning you want. You can use the MCA utility (*v.i.*) to see when the harmonics go away. This operation needs to be done delicately because the tweak is sensitive to very small adjustments. Usually, detuning isn't necessary, but it is when doing TEY mode on lighter elements or transmission on thick spots.

II. Sample mounting and positioning

The standard sample mount is a trapezoid with one 'bent' side. A drawing of this, with dimensions, may be found on the beamline website at <http://xraysweb.lbl.gov/uxas/Beamline/Hardware/Hardware.htm>. The shortest side is the bottom. If you hold it with the short side down and the 'bent' side to the left, you are looking at the front, or upstream face. Something like a microscope slide may be attached to the back side so that the surface of interest shows through the hole in the front. The sample may stick out from the front surface as the stage can be moved backwards from the focus, but the point of interest (POI) should not be any farther back than flush with the back surface of the holder. We want the POI to be at the focus, which is rather close to the end of the I_0 chamber, and if the POI is too far back, the sample

stage and holder may bump into the I_0 chamber. It is more common for samples to be attached to the front of the holder. For small samples or bits of material such as loose soil or plant matter, you can stretch kapton tape over the hole in the holder and stick the sample there. Try to avoid wrinkles in the tape as that causes parallax offsets in the beam position and also lets the sample creep. For more-solid samples, I find that aluminum tape holds with less sample motion than kapton. However, this tape is full of Fe, Mn, and Cu, so you need to keep it well away from your sample if you're looking for these elements. We also have an insert for TEM grids.

The standard sample holder is held by three slotted pins on the sample arm. Two of these pins engage the long straight side, while one engages the bent side. This geometry is a magnified version of the one on STXM. The block with the three pins is on a rotation stage calibrated so that a 0° reading corresponds to a 45° incidence angle. There is a setscrew which locks this axis. If you have rotated the sample, tighten this before attempting to move the sample around. This assembly can be replaced with a Peltier stage on the same rotation stage, for cooling to -27°C .

The whole sample-stage assembly rides on a manually-controlled leadscrew translator which moves the sample towards or away from the optics box. This motion is provided so that the POI on the sample may be brought to the plane of the focus. Getting this positioning right is important for two reasons: the depth of focus is only about 1mm, and the sample microscope does not look straight along the beam, thus leading to a parallax offset between where you think the beam is hitting and where it really is.

An overhead view of the sample area is shown in Figure 1a, with the sample stage shown with the front of the sample at the focus (solid lines) and behind focus (dotted

lines). The difference between these positions lies in the adjustment of the longitudinal stage. What you want to do is to get the place where the beam hits the sample to lie on the focal plane. Since this plane is invisible, it's not obvious how to do that. The fact that the sample microscope doesn't look straight along the beam can be used to advantage. The crosshairs on the video monitor (right screen in hutch; big one outside) are set up so that they line up on the beam when the sample is in focus. Thus, if the sample is out of focus, the beam will hit to the left or right of where the crosshair shows. This situation is shown in Figure 1b, in which the monitor is shown as it would appear with the sample in the same planes as shown in Figure 1a. In both cases, the beam is hitting the center of the black circular grain.

To adjust the focus correctly, we first make a rough adjustment of the longitudinal position to get the image in the sample microscope to be in sharp focus on the monitor, then find a feature with X-rays and move the longitudinal slide so that this feature is on the crosshairs. *Move the longitudinal stage only, not the crosshairs*, which are your reference to where the sample plane is.

III. Moving, mapping and MCA

Now we need to be able to move the sample around and see what's being hit by the X-rays. The programs you will need for all operations other than what was described in Section I reside on the data-taking (UXASES) computer. Switch to it, if you're not already there, by hitting `Scroll-lock` twice then `Enter`.

We first need to move the sample. The **Manual Stage** program (**Set Stage Position**, according to its window) may be accessed two ways: You can get it from its shortcut on the desktop, or by pushing the **Manual Stage** button in the **XY Mapping**

program. Let us use the latter method, as we will need to do some mapping. First, invoke the mapping program, if it's not already running, by using the desktop shortcut. The program will come up, but in a state in which it's not really running. There will be a small arrow in the upper left corner of the window which is white in this state and black if the program is actually running. If the arrow is white, click on it, and the program should start up. At this point, you can push the Manual Stage Control button which should bring up the manual stage program, running. There are four buttons in a diamond pattern at the upper left of this program, and a control labeled **StepSize(um)**. These are the jog controls. When you use these, remember that they move the sample, not the crosshair. You can use these controls to move around on the sample, looking for your POIs.

To understand what and where the X-rays are actually hitting, use the MCA utility. There is a separate manual for this, so I'll just go over the basics. The program is invoked from a desktop shortcut and needs to be started with the little arrow in the upper left. After a few seconds, it starts collecting spectra. Use the graph tools to scale it as you wish. By default, the abscissa is in channels, for which the conversion to energy is 10eV/channel. Thus, the Fe K_{α} line is at 640 channels. The highest-energy large peak is usually the elastic, at whatever energy you've set for the monochromator. You can use the MCA display to find a feature on the sample which corresponds to some feature in the X-ray yield. Typically, you can find the edge of a grain visually and with the MCA. Use a vertical edge to get the best accuracy in finding the right point. You can also use the edge of Al tape, but that tape is thick enough to cause significant parallax error. In some cases, you can't be sure of how the signals you see with the MCA correspond with the

features you see visually. In that case, you may have to do a coarse map to know what's what.

The first ROI displayed in the MCA program is the total counts. This should not exceed about $6-7 \times 10^5$ counts/second at the brightest point for mapping and 3×10^5 counts/second for EXAFS. Count rates that are extremely high can result in contrast reversals in maps, so that the cores of very bright areas appear dark.

A screen shot of the mapping program is shown in Figure 2. Use this Figure to follow along with the description of the steps in mapping. The basic steps are:

1. If needed, do an I_0 offset. This is to make normalization work and isn't really required for navigation. This step is only needed if you have changed the I_0 gain or have not done an offset since the mapping program was started. The offset must be done correctly for automatic beam-dump detection to work. To do this, close the shutter and push the **Measure I_0 offset** button. *This offset is separate from the one in the EXAFS program. Doing one does not keep you from having to do the other.*
2. Set the incident energy where you want it. Some suggested energies:

Purpose	Energy
General	10keV
Lighter elements	5-6keV
As	12900
Pb	13085
Br (trace)	14500

To set the energy:

- a) If the EXAFS program is running (*v.i.*) click on the **Operations** tab, enter the desired energy in the **Target energy** window, then click **Move**.
 - b) Otherwise, switch back to `1032_BL_CONTROLS` and use **Motor Monitor** to move **Mono eV** to the desired value in the same way as you would set a slit size.
3. Define your MCA bins (same as Regions of Interest). This is done by entering the appropriate data into the **Regions of Interest Settings** controls (called out in Figure 2 as MCA Bins). Unlike 10.3.1, this system only collects ROIs, not

complete spectra at each pixel, so if you didn't ask for it, you can't get it from the data. For each ROI, you can enter a name, which gets entered into the file header, and the upper and lower limits for the bin, in eV. These numbers are 10 times the channel numbers you'd pick out of the MCA Utility. For most users, most of the time, the default ROIs are good enough. If you want to add a bin, simply fill in one of the grayed-out ones at the end, *then stop the program (red STOP button) and restart it*. The change won't 'take' unless you start and stop. You don't lose any information by doing that. You can change the data for an existing bin without stopping and starting.

4. Define the starting and stopping points in your map. The map is always a rectangle whose upper left corner is the Start point and whose lower right is Stop. To define a new Start, move to where you want the map to start, then hit the **Get Start Position** button in the middle of the manual stage window. Defining a Stop position works similarly. If you want to center a map about a point, you can go there, then use the jog controls to move by some amount to the upper left, get the start position, then move twice that much to the lower right and get stop. *The program ignores the first and last three points in each line of data as these are taken during acceleration and deceleration, so the map will be narrower than you expect.*
5. Hit the **RETURN** button on the manual stage program, then push the **Scan Params** button in the mapping program. There are three tabs, **Stage**, **File** and **I₀**. Start with the **Stage** tab. The numbers on white backgrounds are the ones you can set; the ones on gray are derived or fixed. The top row includes the pixel size in the X and Y directions and the dwell time. A typical fast map will have 20x20 μ m pixels and a 50ms dwell time. The estimated time for the complete map is shown at the bottom of the window. It's easy to miss the **Hours** indicator, so look for that. Leave the **Settling time** and **# of pts to clip from each end** alone. The next tab is the **File** tab. It lets you set the title of the map (written into the file header), the name and the directory. Make sure you've set it to your current data directory. It's best to use the browse button (the thing that looks like a little folder) to select the directory. When the dialog box comes up and you've navigated to the correct directory, choose the **Select Cur Dir** button. If you type or Copy-Paste into the directory name box, you risk entering an invalid name, which causes the program silently to fail to write the data file. The **Scan number** auto-increments on each scan unless you set it back, thus helping prevent overwriting. Leave the **Extension** at `xrf`. The final tab is **I₀**. This sets the value of I₀ below which a beam dump is declared. You can leave it at 0.01. *You have to push the **Scan Params** button after changing the start and stop positions in the manual stage program, otherwise it will use the old values when you start a map.*
5. Pull up the manual stage program and hit the **Move to Start** button. Return from the manual stage program, then push the **Run** button on the mapping program. A map should start. If it gets to the end and a **Bad Data** indicator lights up, and that

keeps happening, then something is mechanically wrong. The stage may be hitting something, something may be loose, or you may have to slow down the acquisition by increasing the dwell time or decreasing the X pixel size.

The Abort button stops a scan, but not until the stage has reached the end of a line. If you do that, remember to move to the start position before trying again.

There are several ways to move to a specific point on the sample. The simplest is to use the jog buttons. However, if the mapping program is up, you can use the **Move to position** button on the bottom of the manual stage screen to move to where the cursor is on the map. This is useful for zeroing in on a feature of interest. Equivalently, you can use the **Move to cursor** button below the map display (rightmost of 3 green buttons), which does the same thing but doesn't require that the stage control be active. There are also position registers. These are like 'bookmarks' for positions. You can load them, name them and move to any one of them. They don't actually do anything except hold positions for later reference. You can load one either by using the **Load position** button or by filling in the coordinates by hand. Of course, you can also **Move to start** and **Move to stop**.

IV. EXAFS

The point of all this mapping is often to acquire EXAFS or XANES spectra of interesting spots. We therefore turn to the EXAFS program. The first thing that needs to be done is to find the spot of interest. This is often a small area rich in the element of interest. If the area is small, then the EXAFS data will be better if you sit exactly on the spot where the count rate is maximized, even if there are plenty of counts. The reason is that if you're a little off and there's any beam or sample motion, this motion will be

reflected in the signal, causing noise or strange backgrounds. By sitting on a maximum of yield, you cancel out, to first order, the effects of motions.

To find the spot, set the beam size as appropriate and move the mono to an appropriate energy, say mid-scan or 200eV above the edge. Use the MCA program to look at the signal in the peak corresponding to the element you want. Set an MCA ROI (see MCA utility manual) so you can see the count rate in counts/second. Now use the jog controls in the manual stage program to move around and maximize yield. With the spot size set large, you should finish up with steps of no more than 2 μ m for a localized spot. Diffuse spots can be examined with bigger step sizes. For a small beam, you should get down to 0.5-1 μ m motions. Now you're sitting on the spot. To 'polish' the position, you can use the **Measurement** panel (*v.i.*) which shows you the signal as a function of time so you can see the trends as you work,

When you need the best energy resolution, for instance for XANES or chemical mapping, set the vertical slit size to 20 μ m, or if really hurting for counts, 30 μ m. Ideally, unknowns should be done with the same slit size as references.

The detector has limits on how fast it can count. The total counts in all channels (0-2047, usually the 1st bin set in the MCA utility) should not exceed 300,000/second. If it does, you can do one of the following:

1. Filter using Al foil. There are usually some pre-made sheets which go in a little slot at the snout of the detector. This is good when most of the counts are due to an interfering element whose fluorescence occurs at a lower energy than that you're interested in. The canonical example here is Zn EXAFS in soils, which are full of Fe and Mn. The Be window detector protector may be used as a template for cutting foil into filters.
2. Pull the detector back. The detector is on a slide. Clockwise on the shiny wheel pulls it back.

3. Slit down. This is preferred where the sample is vulnerable to radiation damage as you then want to use your incident flux in the most efficient way.

There is also a means of setting up the detector so that it runs faster, but at the cost of decreased energy resolution. Ask about that for use with such systems as Ni in Fe.

The EXAFS program has several complicated and non-intuitive aspects. One of these is that for historical reasons it's called mainscreen1. Another is the scaler map file. The program is designed to count any of a wide variety of inputs, including analog inputs, a counter board, and the Ge detector. The scaler map file tells it what physical devices to associate with a logical scaler. For basic EXAFS, in which you count all 7 elements together in one channel, we have a number of pre-made scaler map files. There is a shortcut on the desktop for the scaler map file in use, and a number of shortcuts for scaler map files for different elements to be counted. These files are all alike except for the specification of which MCA channels to count. Thus, the files for Fe and Zn look like this:

Fe	Zn
[Gate] board=1 counter=0	[Gate] board=1 counter=0
[Scaler 0] type=660x counter=1 board=1	[Scaler 0] type=660x counter=1 board=1
[Scaler 1] type=660x counter=3 board=1	[Scaler 1] type=660x counter=3 board=1
[Scaler 2] type=XIA detector=-1 roilow=605 roihigh=671	[Scaler 2] type=XIA detector=-1 roilow=835 roihigh=893
[Scaler 3] type=XIA detector=-1 roilow=0 roihigh=2047	[Scaler 3] type=XIA detector=-1 roilow=0 roihigh=2047
[Scaler 4] type=end	[Scaler 4] type=end

The entries in bold are the ones which differ from element to element. These files specify that the first and second scalers (Scalers 0,1) are counters. In practice, these are always connected to I_0 and I_t , respectively. The third scaler is the fluorescence channel. The `detector=-1` entry shows that all 7 elements are summed. The `roilow` and `roihigh` entries show the limits of the MCA bin used. The entry for Scaler 3 looks like the one for Scaler 2 except that it encompasses all channels. This is used for deadtime correction. The final entry isn't actually a scaler; it just indicates the end of the list.

Scaler maps are described in more detail in another writeup in the 10.3.2 Docs folder.

To set the scaler map, you have to stop the EXAFS program using the big red STOP button, edit the scaler map, then start mainscreen1 again. You are offered the opportunity to save the scan parameters when you exit the program.

The scan parameters are what tell the program what energies to work at, how many points to take, how long to count, how many regions, where to write the data, etc. The easiest way to generate one of these is to copy it from a previous file (often somebody else's) and edit it. The file is a text file, so you can edit it off-line, but it's easier to use the scan editor built into the EXAFS program to do it. In that spirit, Figures 3a-3e show screen shots of the tabs available when editing a typical scan file. This file shows a scan on the Zn edge with 6 regions of energy defined. The first is a pre-edge region and is tabulated at a coarse 5eV/step. The next is the XANES region, at 1eV per step. After that follow EXAFS regions in which the step is constant at 2eV but the count time goes up linearly with energy. The settling time is the time allotted for the mono to settle down after each point and is always 0.5sec. There is enough overhead per point that it's not worth going below 2sec/point. There is a program (icon on the desktop) which generates scan files having energy steps which increase with increasing energy, simulating a constant step in k . Scans defined that way typically run a little faster than equivalent scans done with constant energy steps because k -mode scans have fewer data points than constant E-step scans.

Figure 3b shows the file-related stuff. The final path name, shown on a blue background, is the concatenation of the directory name, the base file name, the scan

number (in 3-digit format) and the extension, which should always be `.dat` so that the analysis programs can read it. The scan number is auto-incremented in each scan.

Figure 3c shows the dump-detection criterion. The criterion is that the counts in the selected scaler, with no offset removed, must be greater than a user-defined factor times the offset of that scaler. Otherwise, a beam dump is declared. Thus, the dump factor should be set slightly greater than 1. This offset may be read from an indicator on the right side of the Operations page. This 'factor' approach was done so that the user almost never has to change this setting. In the example shown in Figure 3c, the factor is 1.2, and the offset is 6228, so the minimum counts in I0 below which a beam dump is called is $1.2 \times 6228 = 7474$. Normally, you don't have to do anything to it, but if you read in an old scan file, then check it and change it to 1.2 or whatever your favorite number is.

The **Set** tab of the scan edit screen tells the program how many scans to take. There is a fairly complex option for automatically moving the stage between scans which is discussed below. but for now, let's assume that we're not using it. Thus, the switch at the bottom of this screen is left in the **No - stage stays put** position. The estimated time for the set to complete is shown on a blue background.

Finally, the **Plot** tab indicates what should be plotted by default. The plotting may be changed on the fly at any time during or after a scan, but this tab affects what default plotting specification is written into the file. In the example shown, we are plotting the third scaler (Scaler 2 - fluorescence) divided by the first (Scaler 0 - I₀) without taking the log of the ratio. See the manual for the EXAFS Data Editor for more detail on plotting specifications.

Anywhere an energy is required, you can enter it in a number of ways. Here are some examples of each of the different modes:

8976.73	8976.73eV
cuk	Cu K-edge energy
cukf	Cu $K_{\alpha 1,2}$ fluorescence energy
cuk+200	200eV above Cu K edge
cuk+200/3	(Cu K-edge energy+200)/3
present	Where it is now
start	Start of scan
mid	Middle of scan
end	End of scan

Thus, it is never necessary to look up the edge energies and do arithmetic. This notation is also useful for such things as moving to mid-scan.

Some useful things to know about scan definitions:

1. You can change the time-per-point in mid-scan. This may be useful for speeding up a scan to get it in before the fill.
2. If you want the current scan to finish, but don't want to do more, you can go into the **Set** tab and change the number of scans to 1.
3. If a beam dump occurs, the program will terminate and save the present scan, then, when beam comes back, start a new scan with the scan number incremented by 2 (a bug). It will attempt to take the full quota of good scans you programmed in the **Set** tab.

If you're following along with this manual while running the program, you will probably have noticed that there's an extra switch in the **Set** tab of the scan editor which is not shown in the Figures. This switch was put in after the screenshots were taken. This switch sets whether to freeze the mono crystal translation during EXAFS scanning and should be set to **Yes** (default) unless running at very low energies such as S. The reason is that the second crystal moves in order to keep the exit height of the mono fixed, but that motion is quantized in steps of about 5 μ m. This can cause subtle steps and noise

in the data. Thus, we need to freeze that motion during EXAFS scanning, unless running at low energies, in which this motion is large enough to swamp the steps. The color of the Move Mono button changes when Freeze mode is active. The mono translation motion is automatically unfrozen when not actually scanning.

Another 'gotcha' is the counter offset. *Redo this if you change gains or are starting the EXAFS program after having quit out of LabVIEW. Note that all the programs (MCA, mapping, etc) have their own, separate offsets.* Close the shutter and hit the Measure offset button on the Operation page. Look at the four numbers in the pink-backgrounded indicator on the right. The third and fourth should be small (<100). If they are large, hit the green Reinitialize XIA Detector button, wait a few seconds and do it again - the detector electronics had a hiccup.

To recap, here's the checklist for starting EXAFS:

1. I_0 gain. Is the gain set right to keep from saturating or having too little signal? If you're at very low or very high energy, is the gas appropriate? N_2 is OK for most energies.
2. Scaler map. This only needs to be changed if you change edges.
3. Scan definition. Check the scan range, dump level, and filenames.
4. Offsets. Need to redo them?
5. Spot size. Appropriate for the size of the feature? Beam motions and other mechanical noise seems to be worse when the spot size is comparable to the feature size, so you may either want to flood or put a pinpoint beam on the feature, depending on its size. You have to try it to see what will work best for your particular sample.
6. Vertical slit size. For XANES, keep it down to $20\mu\text{m}$, or $30\mu\text{m}$ if really hurting for flux.
7. Sample position. Did it drift since you started doing all this other stuff?
8. Count rate. Is the detector at the right distance, with the right filtering to

keep the total count rate below 300,000 while preserving as many good counts as possible?

If you're truly ready, hit the **Start** button, sit back and watch. It is probably easier to find out by experiment what the controls on the **Plot** page do than to read about it. However, I will note that the plot only updates on each data point when a scan is in progress.

The smaller plot below the main one is used for inspecting I_0 . It consists of I_0 , but with a smooth (cubic) background divided out and the log taken, so you can better see glitches and other such features. For instance, if a glitch represents a 1% drop, it will show up as a dip of 0.01 depth. The cursor tracking control allows you to link the cursors on the main and I_0 plots so that you can better see if a feature in one matches one in the other.

If you want to do XANES, there's another important step - calibration. The EXAFS program's plot screen offers a **Differentiate** switch, which is useful for locating the edge of your standard. The standard is often a foil run in transmission. To use the foil, you can tape it onto a sample holder, mount it in the usual way, then turn the holder using the knob on top until the foil is flat on to the beam. There is an Allen-head setscrew which is used to unlock this degree of freedom. Alternatively, you can swing the sample holder out of the way and use some Newport bits to hold the sample in place. Run a XANES scan in one region around the edge and use the **Differentiate** function to see where the edge is. For a better read on it, transfer the data file over to the analysis machine, read it in EXAFS Editor, and use **Regularize Energies** and the **Differentiate?** button (see manual on EXAFS Editor). You can use the cursor to get a number. Once the scan is done, move to that energy, then type in the nominal value for

that edge energy (e.g. CuK for Cu), then hit the tiny green **Reset Mono** button under the **Target energy** field. You should now be calibrated. The calibration holds for days at a time. An alternative way to calibrate is to use the glitches in I_0 . The energies of these features are relatively stable and have been tabulated. The glitches are useful as internal calibrants, allowing the energy to be adjusted without the need for redoing the foil.

If you have a number of points on which you want to do EXAFS and you want to get some sleep, it's possible to program the system to take EXAFS spectra at each of a set of programmed positions. This is done using the options exposed when you flip the **Use Positioning?** switch in the **Set** tab of the scan editor, as shown in Figure 4. The current position appears on the left. An array holding positions and repeat counts appears towards the right. For each position which appears in the array, the program will take a number of scans specified by the **Repeat count** on the right. Thus, in this example, the first, third and fourth positions are to be done once, and the second twice. To clear this array, right-click on the index spinner and select **Reinitialize to default value**.

To set up a position, first go to it using the **Manual Stage VI**. Usually, this is done with reference to a map, tweaked up by looking for a local maximum in fluorescence yield. Use the index spinner on the upper left of the **Positions** indicator to scroll to the entry you want to modify or add. Push the round green button labeled **Load current pos'n**. Repeat for all positions you want to run. The cycle runs like this:

1. Pick a spot on the map
2. Go to that spot by putting the cursor there and using the **Cursor Position -> Move to position** button in the manual stage control.
3. Optimize using the jog buttons on the manual stage control to move the sample

around, and the MCA Utility and, optionally, the Measurement panel to see what you're doing.

4. Load the position into the next slot in the array.

To go to any of these positions, use the index spinner to make the one you want to go to appear at the top of the list, then hit the square green button **Go to this pos'n**. The stage will move to that spot.

The number of scans which will be done is still controlled by the **# scans in set** control at the top right. Thus, you have to make sure to tell it to do as many scans as you want. You usually want a full round of all the specified positions. The number of scans in such a set is given by the **Length of cycle** indicator, which has a blue background and is under the arrow to the right of the **Load current pos'n** button.

There is an important bit of logic which must be mentioned. The program decides what position to go to by looking at the scan number of the file it's about to take. Thus, scan 0 will be done at the first position, etc., with appropriate correction for positions for which there is a repeat count other than 1. Let's take the example shown in Figure 4, and refer to the four distinct positions shown as A,B,C,D. Also, assume that there isn't any fifth position which would be revealed by spinning the index spinner. Now, since B has a repeat count of 2, the list of positions is really A,B,B,C,D. The scans will be taken in the following order:

Scan #	Position
0	A
1	B
2	B
3	C
4	D
5	A
6	B
...	
32	B ($32 \bmod 5 = 2$)
40	A ($32 \bmod 5 = 0$)

As you can see from this example, the positioning is based on the scan number modulo the cycle length, with repeated positions counted separately.

One side effect of this way of specifying positions is that if there's a beam dump, the current scan will be written in its incomplete state, then the scan number will increment by one, so the program will go onto the next position, and you will have missed one. If you are doing a long series with the cycle repeating two or three times, then it's probable that you will get the missing point on the next cycle. The program automatically adds one to the number of scans to do if one is lost to a beam dump.

This is perhaps a good place to discuss the Measurement panel. When you push the round green button **Open Measurement Panel**, a screen pops up showing a trend graph of the signal vs. time. You can clear the graph by pushing the appropriately-labeled button. To use this panel for maximizing signal, watch the graph, do a jog in the manual stage control, and keep watching. You'll find that it may take seconds for the stage to respond fully. Return from this panel to do anything else.

The Measurement panel has another important use. It's used to assess the noise level on the signal. It does this by dividing a count into 10 (default) sub-samples and

computing the variance of the set of counts. This is then expressed as an 'effective count rate' which is the number of counts/second an ideal Poissonian counter would need to equal that signal to noise. For example, suppose we set it up for a 10-second count, broken up into 1-second samples. Now imagine that the average signal level (for instance, F/I_0) is 100 and the standard deviation among the 10 sub-samples is 1, in whatever units are being used. Thus, it's as if you were getting 10^4 counts worth of Poisson statistics in each of the 1-second sub-counts, since the standard deviation is 1% of the mean, so $s = 0.01N = N / \sqrt{10^4}$, with N the number of counts. Therefore, the effective count rate is 10^4 counts/second. If you're really counting at 100kHz, then you have a problem. Perhaps something is vibrating. This panel is useful for assessing the signal quality in analog counters, where it's hard to define counts/second.

It's common to find that the effective counts are OK when the sampling time is 1 second, but drop off dramatically when sampling for 30 seconds. Since a typical, short count in an EXAFS scan might be 3 seconds, it's useful to have the sub-counts be 3 seconds each when judging the expected signal quality in EXAFS. Therefore, set the count time to 30 seconds (3×10) and watch what happens. Set it back to 1 second before returning from the Measurement panel or else you'll have to wait for a 30 second count before doing anything next time you enter this panel.

V. Uh-Oh!

The above procedures seem rather complex and counterintuitive when written down in a manual, but you will find as you use the beamline that there is a logic to it and it does make sense. There are a number of writeups available in the 10.3.2 Docs directory (shortcut on the Desktop) which should be of assistance.

There is a troubleshooting guide on the desktop which gets updated every time a user manages to elicit a new symptom from the beamline. Read it if something is strange as your problem may have been seen before. There is a Trouble Call procedure which tells you whom to call and when, in case you get really stuck

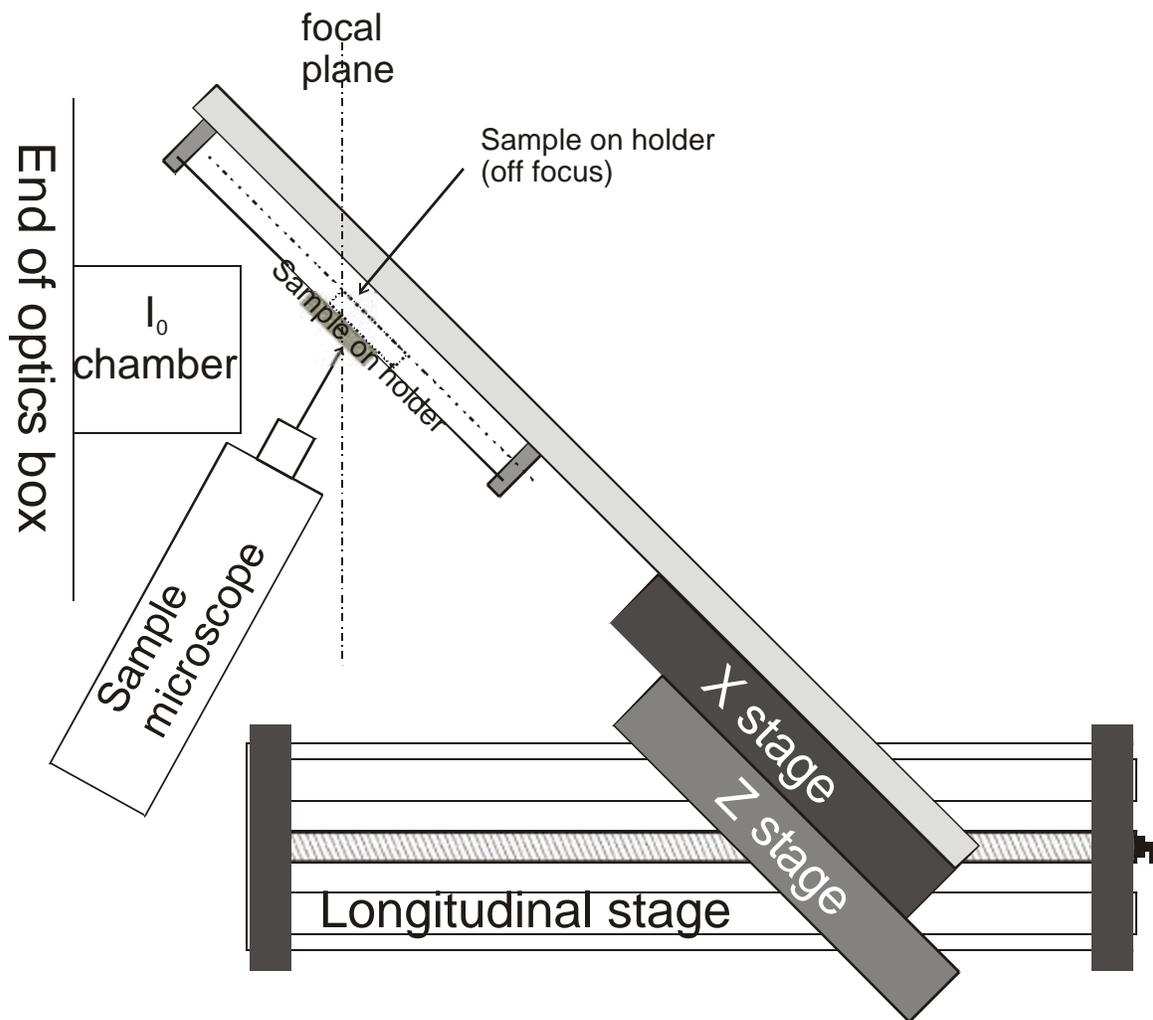
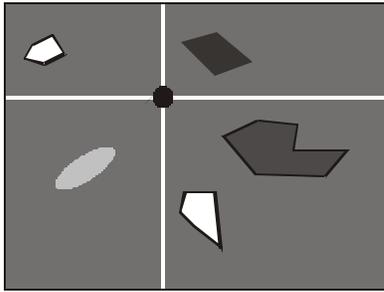
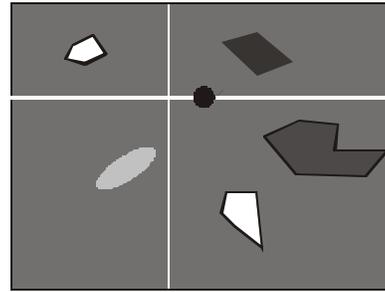


Figure 1. Overhead schematic view of the sample stage area showing the focal plane (dash-dotted line), the position of the sample when it's on focus, an off-focus position (in dotted lines) and the stages. The difference between the two positions lies in the adjustment of the longitudinal stage, which should be set so that the strike point of the beam on the sample is at the crosshair in the sample microscope.



On focus



Off focus

Figure 1b. The sample shown on- and off-focus. In both cases, the X-ray beam is hitting the center of the small, round, black grain. In the off-focus case, the crosshairs indicate a position to the left of where the beam actually hits because the sample is too far back and parallax creates an offset.

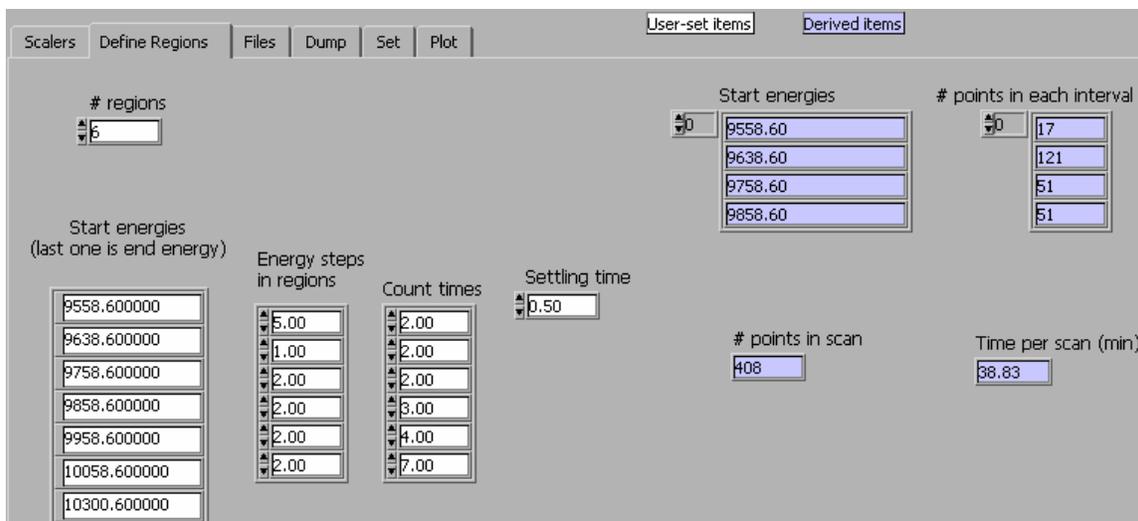


Figure 3a. This is the Define Regions screen of the scan editor. The Scalers tab is not normally used.

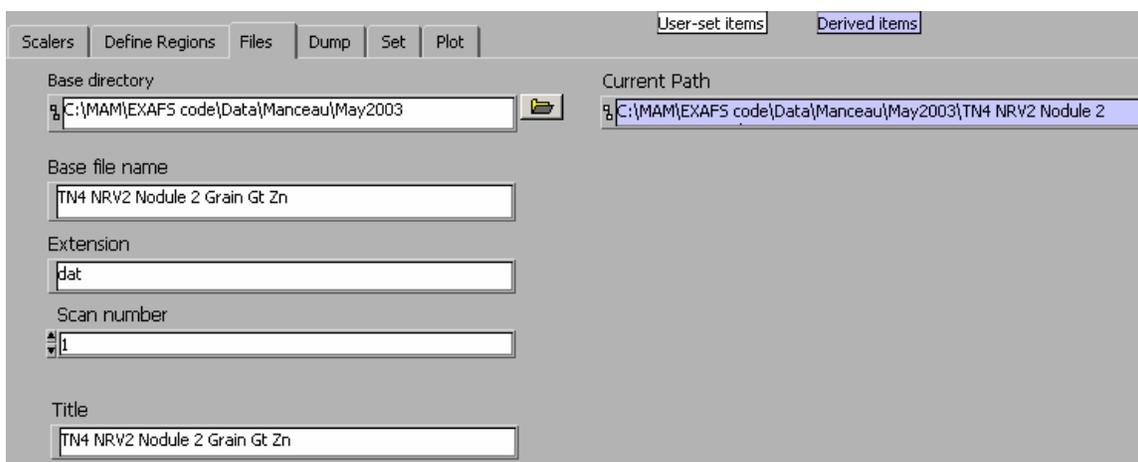


Figure 3b. The Files tab of the scan editor. The blue indicator is a little short to show the full path name: C:\MAM\EXAFS code\Data\Manceau\May2003\TN4...Zn001.dat.

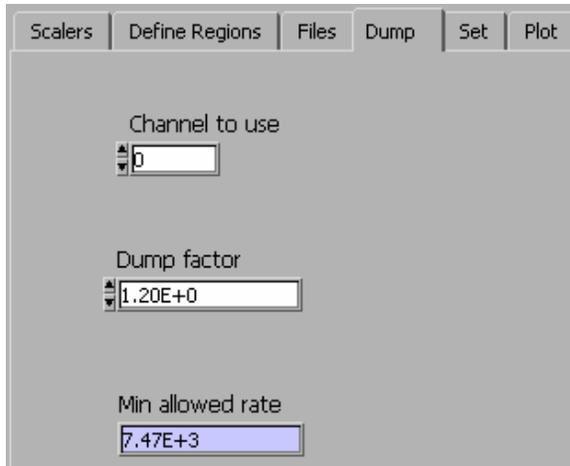


Figure 3c. The Dump screen. If the I_0 counts go below 7474 (0.0747V on the DVM), a beam-dump will be called.

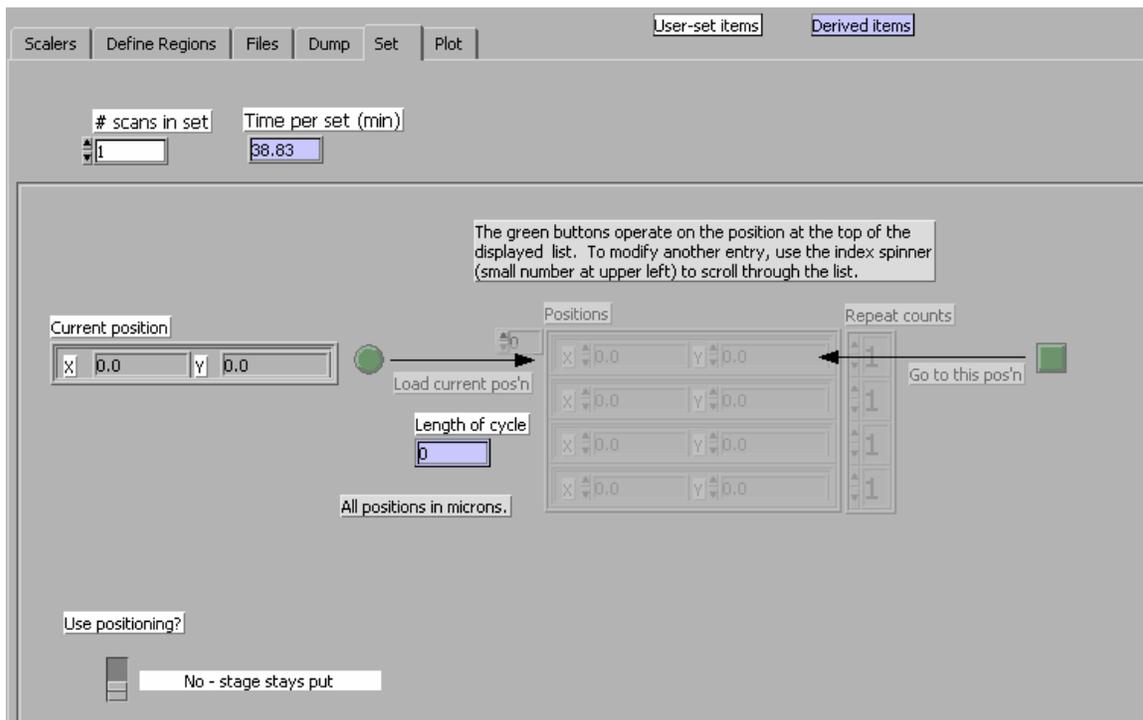


Figure 3d. The Set tab, with the multi-point feature disabled. The only control here is the number of scans.

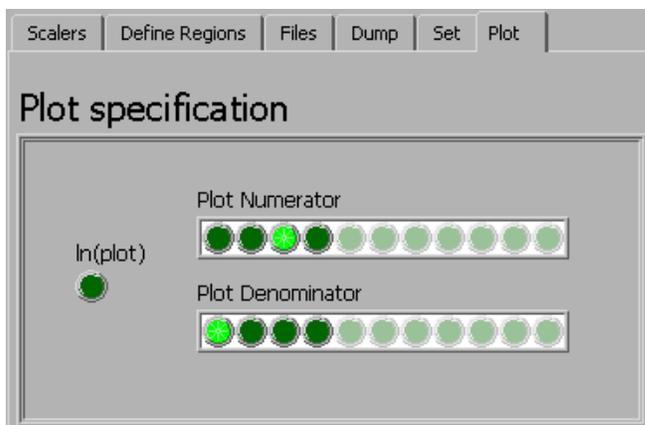


Figure 3e. The Plot tab, specifying that the quantity to plot is fluorescence divided by I_0 (Scaler2/Scaler0).

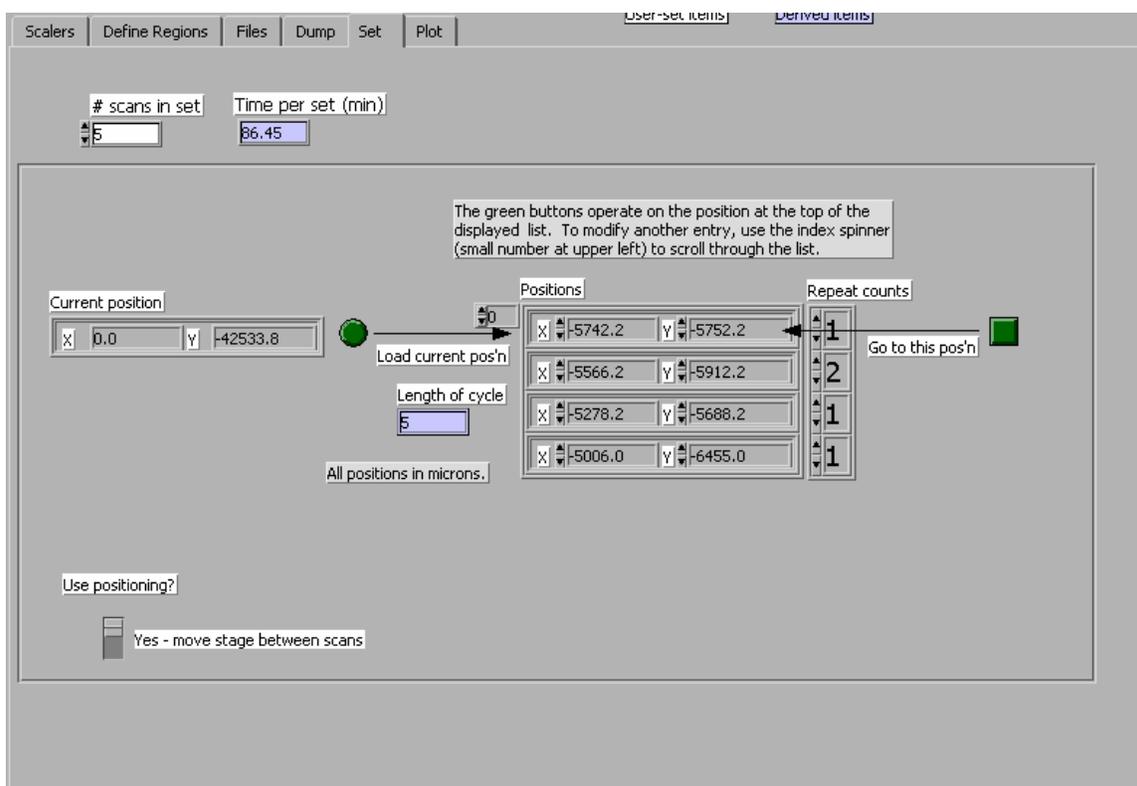


Figure 4. The Set tab showing the multipoint scan feature enabled.

Appendix A: Symptom-based troubleshooting guide

Symptom-based Troubleshooting Guide

This is a partial list of trouble symptoms, some possible causes, and fixes.

Trouble contacts:

Matthew Marcus x7604 510-981-1965 (H)

Please try the fixes listed below before calling.

Detection system:

1. No counts in MCA, mapping or EXAFS:

In EXAFS, it could be a known, intermittent bug in the vendor software. The cure for this is to stop the scan (NOT THE PROGRAM) and hit the "Reinitialize XIA detector" button on the Operations page of the EXAFS program and wait a few seconds. Then start the scan again.

You may be getting no beam. Check I0. If I0 is low or zero (after subtracting offset), see the Optics section.

Detector HV may be off. This power supply is in the hutch. Check LN2 level before turning on.

LN2 may have run dry. The auto-fill system control box is just outside the hutch, sitting on the lucite box which contains the roll-slit assembly just upstream of the hutch.

Its readout shows you how much (0-100) LN2 is left. This should no longer be able to happen because we have an LN2 drop from the house system. If LN2 did run dry, correct the problem and let the detector fill. Turn off the high voltage and wait 12-24hrs before turning it on and trying again.

Note: This should not happen anymore since we have an LN2 drop.

2. Plenty of counts showing in MCA, but no edge jump or very poor signal recorded in fluorescence channel in EXAFS.

When you edit the scaler map to switch to a new edge, you have to stop and restart the EXAFS program to make

the program read in the new scaler map.

3. You find a hotspot in XRF mapping, but don't get any counts.
Make sure you're above the edge.

Make sure you did a move-to-crosshair in the Manual Stage Control.
4. You try to change the gain on I0 or transmission, but nothing happens.
You have to turn the knob on the Keithley VI and then hit the blue Set button. Nothing happens until you hit that button.
5. When doing CI, you see the same thing everywhere.
CI is ubiquitous. Run a blank. If you're using the air excluder on the detector, try rotating it a little to put the beam off any spot of epoxy. If your sample is a thin section, the problem may be the embedding epoxy, which is usually full of CI.

Software - General

1. Buttons 'push' but nothing happens and they don't 'pop out' again when they should.
When you invoke a program, it's in a dormant state. A small icon in the upper left will hold a white arrow if it's in that state. Push that arrow, and it will turn black, signifying that the program has started.

The EXAFS and XY map programs have 'pop-up' subroutines (e.g. Measure and Scan Editor) which need to be Returned from before the rest of the program will work.
2. Data-taking computer completely locked up
If you exit from all the stage programs, you can tickle a bug in the stage-control drivers (vendorware). This bug locks the computer. Hard-boot it. It's UXASES and it's in the half-rack labeled 'BRUKER AXS'. The login and password are posted at the line. If pushing the button on the front panel doesn't work, then slide the computer out a bit, reach behind it, and feel for and yank the line cord.
3. You stopped one of the programs, but another program thinks it's still running.

If you use the small stop-sign icon to stop a program rather than its stop button, it doesn't have a chance to turn off the flag which says that it's running. Cure: You can start and stop the offending program properly, or you can use the desktop shortcut marked "No, it's NOT running!", which turns off that flag.

4. The data analysis computer shows an unfamiliar screen.

That monitor is connected to three different computers via a KVM (Keyboard-Video-Mouse) switch. To switch to Computer 1, hit the sequence

`<Alt><Ctl><Shift>1<Enter>`.

Computer 1 is UXAS_DATA, the analysis computer. Computer 2 is the diffraction computer. Computer 4 is used for tuning the focusing mirrors. This is a similar situation to what obtains with the right (data-taking) screen, which is connected to two computers. The two-port KVM switch has a simpler sequence for switching - `<Ctl><Ctl>` toggles between the two machines.

5. You rebooted and now face a login/password screen. Logins and passwords for the computers are posted above the left-hand screen. Each computer also has on its desktop a text file 'logins.txt' with this information. You can therefore look on one of the other computers for the 'key' to the one you're trying to open.
6. You try to print and nothing happens. This is a stupidity of our server system. All printing, even to the printer right at the beamline, goes through a server, XRAY-1. If the connection is broken, it won't automatically re-establish itself. Find the xrays-1 shortcut and double-click on it. It will want a login and password. Use esgworker for the login and leave the password blank and click OK. Printer icons should appear. Close the window and try again to print.
7. You try to use the executable analysis programs from home and they don't work right. Check to see that the file lvalys.dll is present in the same directory as the executable. Odd bugs can result from its absence.

If your computer is European, make sure that the Use Localized Decimal Point option is un-selected. In some countries, a comma is used instead of a period. If this option is selected, then the programs will attempt to read and write files this way, which will conflict with the way they're written at the beamline.

8. The mouse or keyboard of one of the computers which go through the left-hand screen doesn't work.

This has occurred once so far. The cause was that the KVM switch (on the upstream desk) had gotten confused and needed to be power-cycled. This required pulling out all the keyboard and mouse cables until the red light went out, since the KVM switch can power itself from any keyboard or mouse. After this, all computers on the KVM switch needed to be rebooted, since disconnecting the mouse from a Windows machine causes the mouse driver to die.

Software - EXAFS program:

1. Scan editor won't let you return
You've entered something it doesn't understand or thinks makes no sense. Example: leaving the edge code off an edge-relative energy ("ge" instead of "gek").
2. Scan keeps aborting and restarting
Dump level may be set incorrectly. If the dump level is too high, it will call a dump even if there isn't one.
If the dump level is OK, then the channel for dump detection may have gotten set incorrectly. This should be set to 0 (default configuration) because that's the channel on which I0 comes in. This control is in the Scan Editor, under Dump.
3. EXAFS curve is very strange, but not due to 4) above.
Make sure Differentiate switch is OFF.

Make sure offsets were done correctly. Offset for detector channels should be 0. If not, then initialize detector and try again.

Make sure your plot specification is correct (usually, 2/0 [third button for numerator, first for

denominator]) for fluorescence. For transmission, the first button for numerator, second button for denominator, and the log button on top should be on.

4. Start button is grayed and disabled.
Make sure MCA isn't running and that a fluorescence map isn't being taken. Indicators should pop up to tell you about these conditions.

5. Start button and mono-control buttons are grayed and disabled.
If you change the mono energy from outside the program (say, using Motor Monitor) or have disabled the mono motor, the program gets confused and thinks there's a motion problem and that the mono is trying to get where it's told. Press the 'Mono really got there!' button on the Operations page to clear this.

If you make a big energy jump from or to low energies, say <5keV, then the mono translation sometimes doesn't catch up properly. This results in the mono getting stuck. Go to the control computer and use Motor monitor to manually move Mono eV to a value close to where it is. Then, go back to the data-taking computer and push the 'Mono really got there' button.

It sometimes happens that the communication with the server program on 1032_BL_CONTROLS is lost. In that case, no monochromator functions work. Stop and restart the EXAFS program to reconnect. Don't forget to save the current scan definition before stopping and reload it on starting.

6. When doing a multi-point scan (automatic move), the stage doesn't go to the point you expected.

The first position on the list is #0, the next #1, etc. The position it moves to when starting a scan is determined by the scan number:

$$\text{index} = (\text{scan \#}) \bmod (\text{cycle length})$$

Example: You have three positions, but have specified that the second one is repeated twice. The cycle is therefore

Scan 000	1st position
Scan 001	2nd position
Scan 002	2nd position
Scan 003	3rd position

the sort of tactic which has been described as 'waving a dead chicken'.

2. Your map doesn't cover the area you think it should.
You have to Return from the Manual Stage Control, then you have to hit Edit Scan to 'set' it.

The map is always a little narrower than you specify because three points on the left and right are thrown out in order not to take points during which the stage was accelerating or decelerating.
3. When you start a map, it doesn't start where you told it to.
When you set the Start and Stop positions, you have to go into the Scan Params editor (green button) to make it 'take'.
4. You point at a position in a map, tell it to go there, and it goes somewhere else.
If you have gone into Scan Params and changed the start and stop position, that affects the scaling of the graph.
Solution: Re-read the map with Read New File.
5. Your map takes hours longer than you thought it would.
Check the 'hours' indicator in the Scan Edit screen.
It's easy to miss.
6. Make sure your spot size and scan pixel size differ by no more than a factor of 2, otherwise you waste either beam intensity or scan steps.
7. You added a channel to the Regions of Interest Settings area but no counts appear there.
You have to stop and restart the program to make additional channels work.
8. Normalization doesn't seem to be working.
Did you do an I0 offset? If not, your data can be salvaged post-hoc with the Offset I0 program.
9. One or two lines on your map are horizontally offset from the others.
This is a known stage problem with no known cure except re-running the map. It's random.
10. The more-uniform areas of your map are speckled with defects

consisting of one light pixel with a dark pixel immediately to its right.

Another known stage problem. The stage 'catches' at random places instead of moving uniformly. You can try changing the dwell time to change the motion speed and see if that helps, but there's no known cure.

11. Your map didn't get written.

It's possible that it did get written, but in the wrong directory. Check to see that the directory specified in the scan-param editor is indeed where you wanted it.

If you type in (or Copy-Paste) a name of a directory which doesn't exist, it will silently fail to write.

If you catch this before starting or reading in another map, you can fix the directory name, then hit Force File Save.

Stage

1. Stage doesn't run.

If stage stopped when you were moving it, you probably hit a limit. First, clear the mechanical problem. Then move the stage way back along the beam direction so that you can home the stage (will make big motions in X and Y) so that the stage can move. The manual Stage program has a button which might clear the error condition. Scroll down on the manual stage control to see it. It's labeled 'Enable' with a red background. Push it, then click on the "home" button (right next to "enable") and see if the stage moves. Otherwise, you'll need to quit the Manual Stage program and restart it. If that doesn't work, quit all the programs including the Stage Wrapper and start them again, with the Manual Stage first.

Whenever the stage has been homed, it's in a position far from where you might want it. Pull up the manual stage control and hit Move to Start. This should move it to someplace reasonable. It sometimes happens that only one axis moves. In that case, hit it again and the other axis should go.

If it still doesn't run, check the circuit breaker on the Aerotech controller on the right side of the electronics rack, under the notation "BR1032-06". This affects the Z axis.

If the X-axis won't run and everything else seems OK, the problem may be the fuse inside the Aerotech controller. The Unidex program will complain about a velocity or position error when you try to move and will then disable the axis. Also, you will be able to move the stage horizontally by hand and there will be no holding torque. This fuse is in the leftmost of the three unpluggable modules in the Aerotech driver box, next to the fan. Pull out the module, inspect the fuse and if need be, replace it. If the Unidex program is still on, it will know where it is and not need to be homed, though it will need to be enabled. This happens only if the stage hit something during a move, so be sure to clear any obstructions before trying the stage again.

**** This is quite rare and only affects the X-axis - don't suspect unless nothing else is possible ****

2. You hit the Jog button in the Manual Stage Control and nothing happened.

The buttons are a little flaky (some subtle timing problem) and don't always give you one and only one step at a time. The green "Moved?" light under the "Y+" jog button will blink if and only if the stage actually moved.

3. The Manual Stage Control screen is not visible, but the corresponding button is grayed out in all programs.

You probably closed it by hitting the x in the upper right corner instead of Return. Don't do that. To fix, find the Set Stage Position Wrapper, which appears as a blank gray panel and close it with the little x. Then hit the Manual Stage Control on the Desktop. This will pop up the Manual Stage Control and the Wrapper. Close the former with Return and that will do the job. Alternatively, stop the mapping program, double-click the "No, it's NOT Running!" icon on the Desktop, close out the resulting panel and restart the mapping program.

Optics and X-rays

1. I_0 jumps up and down 2-6% on a regular basis

This is due to an EPU (probably #4) switching. You can't do much about it except try to get the normalization to work really well. There is now a compensation system which removes this problem, but there are rare occasions in which it doesn't work.

2. Beam is not well focused in the vertical direction at low energies.

This is due to scatter off of M2 and you can't do much about it, either.

3. Normalization isn't good or data noisy

Check offsets (dark counts). If that was wrong, you can salvage the data in EXAFS Editor.

See item 1 under Detection above.

Make sure you're on a local max or min of count rates with respect to position.

Try reducing the slit size if it isn't already somewhat down from full open.

Try steering beam through roll slits with M1.

If $I_0 < 1V$, try raising the I_0 gain, remembering to do offset again.

Check to see that the I_0 gas, if any, is appropriate. If I_0 was set up for Br with a rich Ar/N₂ gas mixture, it will cause strange noise when running at lower energies. Similarly, if He is running and the energy is high, the I_0 will be weak and noisy. The former error is harder to notice just by inspection of the signals.

If you're using a gas mixture, try switching to a single gas. The mixing panel sometimes doesn't produce a stable mixture.

4. Fluorescence data shows strange dips or peaks in the scan
Check the total counts (4th channel) and see if there's a big peak. If so, you may have a Bragg diffraction peak being thrown into the detector. This can cause a deadtime-related dip by swamping one detector element with scattered light, or a peak in Fe or Cu by virtue

of a beam hitting something in the detector. The latter case can be sneaky because the scattered beam causing the problem may not be directly detected.

Kludge: Go to the energy at which this occurs. Use the MCA utility and look at each detector element. There will be one or two which show anomalously high counts in elastic, Fe or Cu bins. Go into the hutch and disconnect the BNC cable from the preamp whose number corresponds to the affected channel. The preamps are in two rows along the snout of the detector and each has a BNC and RJ connector on them. Then, check the MCA to see that the offending channel is truly disabled. When doing deadtime correction, adjust the deadtime from 0.46us to 0.54us (1 detector disabled) or 0.64us(2 disabled).

*** Don't forget to reconnect it afterward! ***

Another fix: You can set up the scaler map so the program records all detectors individually. There's an example on the Desktop on the data-taking computer. Change the ROI numbers to suit. Deadtime on a file taken this way can be corrected detector-by-detector in EXAFS Editor using the Correct Deadtime from File option in the Deadtime tab.

5. Mono energy calibration drifts

Check cooling water level in mono chiller.

Make sure the hutch door doesn't stand open for a long time. Temperature fluctuations may affect calibration.

6. Data shows 0.1%-1% jumps at regularly-spaced energies (60eV interval at Cu edge; 80eV at Zn).

This is a known problem with the monochromator and optics. What's happening is that a picomotor controls the gap between the two crystals to get a constant height offset in the mono. This motion is quantized in units of about 0.5um. For reasons unknown, when one of these steps occurs, the data can be affected, especially when the sample is highly inhomogeneous.

The fix is to disable the motion during the scan. This is done as follows:

1. Under the rack marked 'BR1032-04', between the 10.3.2 and 10.3.1 beampipes is a black box

with switches and connectors. It's fairly well-hidden.

2. On the upper right of the front panel of this box is a row of 4 switches, labeled 'Closed/Open-Loop Select'.
3. Move to mid-scan and flip the leftmost (#1) switch to the up position. This will freeze the motion. The problem should now go away.
4. **IMPORTANT!** Restore the switch position before moving to a different edge.

7. Little or no beam at all.

Several possible causes for this. Check to see if there's been a beam dump (yes, that's obvious). Insert the YAG monitor and see if there's good beam. If not, it's possible the slits are closed down and you don't know it. Open them to 2000um each way and see if beam shows up. If it does, close them gradually until beam starts to be cut off. See if adjusting M1 roll and tweak do anything good. If M1 is centered, then the problem may be that one or both of the slits has an incorrect idea of where it is. Close down one of the slits until the beam just goes away. If the size shown on Motor Monitor isn't nearly zero, reset it to zero. You may have initially hit Reset instead of Move and cause this problem in the first place.

The YAG monitor goes only to the point indicated by the 'YAG' line on the green sticky attached to the motion feedthrough. It should not go all the way to the bottom.

Suppose the monitor shows beam but you still don't get any in I0. The mono may be excessively detuned. If the Picomotor control box (black thing with knob on left and redpilot light on right) is set to channel 2 (mono tweak active), it seems to pick up some disturbance and move the tweak. Retune it and leave it set to an inactive channel (say, 1).

If the flux is good at one energy and dies at others, the problem may be the mono servo switch mentioned in

6) above. If this switch is left in the up (freeze) position and you move to a very different energy, the beam out of the mono will move off the input acceptance of the KB pair and the output flux will drop. The cure is to put the switch down when changing edges or otherwise making a big energy move.

8. I0 pre-amp shows 'OVERLOAD'.
If running He/N₂ mix, you can't use the full 600V on I0 as it breaks down. Go down to 300V (connect to middle connector on battery box instead of end).
9. You're using the PIN diode for transmission and it has glitches
It's made of single-crystal Si and has diffraction peaks. You can move these around by tilting and rotating, but you can't get rid of them altogether.
Workaround: Use an ion chamber (there's a long one in the hutch somewhere) instead.
10. You're using an ion chamber for transmission and the signal is noisy.
If the end windows aren't capped, slap some Kapton tape on them. You don't want the breezes blowing into it.

If you're using Ar at energies below ~8keV, switch to N₂. The absorption length at 7keV is about 3cm. You don't want all the beam absorbed in the first couple of cm because then much of the signal will come from places with nonuniform fields in the ion chamber.
11. All of a sudden, you see a rising or falling background
If you're using a gas in I0 or another ion chamber, check the tank. You may have run dry.

Data and Analysis

1. Individual EXAFS scans look good, but average looks noisy or glitches don't normalize.
The likely cause is that the sensitivity of the detection system, that is how much signal you get for a given I0 and absorbance, isn't the same between files.
This has three common causes:
 1. The I0 gain was changed between scans.
 2. The detector was moved in or out between scans.
 3. The concentration of the element of interest isn't the same from scan to scan. This is

usually due to the spot moving on the sample, either intentionally (taking different spots to avoid radiation damage) or unintentionally.

The EXAFS Editor has an option for changing the gain on a channel, that is, multiplying the counts in a scaler by a constant. If I0 is much quieter than the fluorescence or transmission (usually the case) then you want to do this adjustment on I0. For Cause 1, you obviously want to adjust the gain of the I0 channel so it's the same in all files. Thus, if some files were taken on the 1E-9 scale of the I0 current amp, and others at 1E-10, then use the Change Gain option to increase the I0 counts (scaler 0) in the 1E-9 files by 10x. This should make F/I_0 or I_t/I_0 come to about the same value in all files. For the other causes, if I0 is less noisy than the fluorescence or transmission (whichever you're using), then change the I0 gain so that the files all match in edge jump. It sounds a little odd to adjust I0 when it's the fluorescence channel which changed, but it's statistically sounder to do it this way if I0 is quieter, which it usually is.

A similar thing seems to happen if the time/point was changed for a region in one or more of the scans.

There is a writeup on this in the 10.3.2 Docs folder, called `gain_change.doc`.