EXAFS GDA survival kit:

1) In the GDA application main window, there are **XAS parameters, Detector parameters** and **Sample Parameters** tabs. In the **XAS parameters** you can change the K region of EXAFS scan by changing the **final energy** value. Whatever changes you make, you will have to do **Ctrl s** to save it. A little asterix (*) sign will appear next to the **XAS parameters** when you change something. When you do **Ctrl s**, this asterix (*) sign will disappear.

2) In the **Detector parameters** tab you can chose between **transmission** or **fluorescence** scan. You don't have to specify it for every scan, only if you want to switch from one to another. If you change from transmission to fluorescence or vice versa, do **Ctrl s** to save it.

3) In the **Sample Parameter** tab, you have to enter a file name for your sample and do **Ctrl s** to save. If you forget to enter a filename an error message will pop up when you try to start the first scan. If you forget to change the filename for a new sample, it will take the last entered file name. However, this is not a problem, since it always saves each scan with a **scan number** before the file name, so just keep track of the scan numbers for each sample. For the **Stage** tab select **none**. You don't have to specify the Stage every time, just change the file name for your samples. Do **Ctrl s** to save.

4) There is a little monitoring window displayed on each desktop. This window monitors the ion chamber counts (**I0, It and lnItI0**). **Press the little stop button on top right corner of this window before starting a scan**. If you forget, the monitoring will stop anyway. **So do not click the little start button on the top right corner of this window**. It is not possible to monitor counts during a scan.

5) To start a scan, select the scan by **left click** of the mouse in the left panel of the window. This will load all the scan parameters and it takes a few seconds, so please be patient. Then **right click on the scan** to open a drop-down menu and then click on **Queue single scan and start queue**. If you want to do several scans on the same sample, then first **right click on scan** and then select **edit repetitions** from the drop-down menu. A table will open where you can enter the number of scans you want. Type the number of scans you want and press enter. Now to start the scans, **right click on scan** and then **Queue single scan and start queue**.

6) In the bottom half of the main GDA GUI window, there is **Command Queue** where you can visualize the progress of a scan. If you want to stop a scan, press the red stop button. However, **Do not press the STOP button to stop a scan just when it is about to finish and the monochromator will move to the start position of the next scan. Wait until the next scan has started and then press STOP.**

7) **For expert users only (non-expert users should call local contact/beamline scientist on call):**

a) In case of crash of the acquisition program, close the main window of **GDA Client**, then close the **GDA server** window (black background). Now restart the **GDA servers** by double-clicking the icon on the desktop. Once it says **server initialization complete**, start the **GDA client**. In case of a more severe crash, close the GDA client and GDA servers and restart in the following sequence: **TangoServers**, **GDA server** and then finally the **GDA client**.

b) In the **Jython console** you can type commands to move the monochromator to certain energy. **This is only meant for beamline scientists and in very exceptional cases, for extremely experienced**

users. The command is **pos bragg1** followed by the value in **eV**. To see the current energy value just type **pos bragg1** and enter.

DO NOT MOVE THE ENERGY BY MORE THAN 1000 eV IN A SINGLE MOVE !!!!

Setting fluorescence channels (To be done by the beamline scientists):

Click on **Detector Parameters**, chose **Fluorescence** and then click **Configure**.

Make a note of the XspressParameters file name that appears in the field next to the Configure button. This should be different for every new element, usually with a different number at the end (e.g., XspressParameters1, XspressParameters2, etc.). You can also change this last number in the file name if you want.

A new tab called **XspressParameters** will open. Put 0 and 4000 in the channel values, select "Apply to all channels", put acquisition time 1000 ms and then press Aquire.

Unclick the little box "Apply to all channels".

After the acquisition is finished, click on channel 0 and select the peak of interest. In order to see the whole fluorescence spectrum, you have to zoom in. The peak of interest, then, can be chosen by dragging the left and right edges of the blue region. Do the same for all the other channels and then press **Ctrl s**.

(In order to select the right peak, you may want to move the mono to below and above the edge energy to see the disappearance and appearance of the peak. This is done by the **pos bragg1** command in the **Jython Console**. For example, for Fe K-edge (7112 eV), do **pos bragg1 7300** and then press **Aquire** to see the total fluorescence spectrum at that energy. Then you could do **pos bragg1 7000** to move below the edge energy and press **Aquire** again to see which peak disappears. Then go back to 7300 eV and repeat the procedure and then select the peak of interest.)

How to change beam size:

To see the beam size type **slitshow** in the SOFT window. Then look at the values of horizontal gap and vertical gap in the first slits. Usually they are 4.0-5.0 and 0.5-1.0 respectively.

To change the vertical gap (for example, if you want to change the vertical gap from 0.5 to 1.0):

mvr s1verg 0.5

To change the horizontal gap (for example, if you want to change the horizontal gap from 4.0 to 5.0):

mvr s1horg 1

Do not increase the vertical gap beyond 1.5 mm and horizontal gap beyond 8.0 mm

To set up a macro for multiple samples:

1. Make sure your scans (EXAFS/XANES, in Transmission or Fluorescence) are ready and all parameters are correct.

2. Put the number of repetitions for each scan by **right click** on the scan, then **Edit Repetition** and then **type the number** in the selected field and **press enter**.

3. Now **right click** on the scan that you want to start and select **Queue single scan**.

4. Now press the **small green (+) button** in the Command Queue which will open a new window. In this window type the motor position of the next sample by either **pos cryoz 4.5** or **inc cryoz 3.0**, for example. In the first case you are specifying the exact motor position and in the second case you are specifying the relative move of the motor, assuming that you know the current motor position and the amount of move required to move to the next sample.

5. Now queue the scan for the second sample in the same way as in step 3.

7. Continue steps 5 and 6 for each sample that you want to measure.

8. When the macro is ready, press the **little start button** in Command console.

9. If you want to delete any part of the macro, just **select** the command (either a scan or a motor move), **right click** and select **Delete**.

In case of problems with SOFT session and GDA
Restart SOFT
Open a new console
>su – blissadm
Password: spec92
>bliss_dserver status

Here you should see
TangoSpecMotor: d26s_bragg d26s_cryox etc
TangoSpec : soft

If TangoSpec : None
then
>bliss_dserver start TangoSpec

If TangoSpecMotor : none
then
>bliss_dserver restart TangoSpecMotor

To start DA server

Log on to VME crate

ssh -X root@bm26-exafs-vme

password: root4esrf

da.server -port -log &

To start Xspress server

Log on to VME crate

ssh -X root@bm26-exafs-vme

password: root4esrf

export TANGO_HOST=dubble27:20000

export LD_LIBRARY_PATH=/usr/local/lib

/usr/local/bin/Xspress1 d26s_xspress1