**BMM Command Cheat Sheet**

|  |  |
| --- | --- |
| shb.open() / shb.close() | Open / close the photon shutter |
|  |  |
| RE(mv(dcm.energy, <value>)) | Move **TO** an energy value |
| RE(mvr(dcm.energy, <value>)) | Move **BY** an energy step |
|  |  |
| RE(mv(xafs\_liny, <value>)) | Move motor **TO** a position |
| RE(mvr(xafs\_liny, <value>)) | Move motor **BY** an amount |
|  |  |
| RE(slot(N)) | Move to sample wheel slot #N ( 1 ≤ N ≤ 24 ) |
|  |  |
| %w <thing>  [dcm | slits3 | m2 | m3 | xafs\_table] | where's the mono? slits? mirror 2 (focusing)? mirror 3 (harmonic rejection)? XAFS table? |
|  |  |
| RE(change\_edge('X')) | configure beamline to measure XAS for element ‘X’ |
| RE(change\_xtals('h11')) | set monochromator, Si(111) or Si(311), h=1 or h=3 |
|  |  |
| RE(rocking\_curve()) – or –  RE(rocking\_curve(detector='Bicron')) | optimize pitch of 2nd DCM crystal (moves automagically) |
| RE(slit\_height()) | explore position of slits3 (then pluck to move dm3\_bct) |
|  |  |
| %m / %h / %k | Show motors / show help / show keyboard shortcuts |

To stop a scan or a move

**Ctrl-C twice**

then

RE.stop()

|  |  |  |
| --- | --- | --- |
| **Mode** | **focused** | **energy range** |
| A | yes | 8keV and up |
| B | yes | below 6 keV |
| C | yes | 6keV to 8keV |
| D | no | 8keV and up |
| E | no | 6keV to 8keV |
| F | no | below 6 keV |
| XRD | yes | 8keV and up |

**Slits3 coordinated motions:**

* slits3.hsize (nominally 8 mm) and slits3.hcenter
* slits3.vsize (nominally 1.4 mm) and slits3.vcenter

**Common motors:**

|  |  |  |
| --- | --- | --- |
| **Motor** |  | **description** |
| xafs\_x | x | sample stage, X direction, + is outboard |
| xafs\_y | y | sample stage, Y direction, + is up |
| xafs\_pitch | p | tilt stage, pitch, + lifts downstream edge |
| xafs\_wheel | wh | sample wheel, + clockwise when viewed from upstream |
| xafs\_roll | r | tilt stage, roll |
| xafs\_ref | ref | reference foil wheel, + clockwise when viewed from upstream |

Where is a sample motor? %w xafs\_x

What are the soft limits? xafs\_x.hlm.value / xafs\_x.llm.value

Set a soft limit: xafs\_x.hlm.put(-95) / xafs\_x.llm.put(-157)

**Line scan:**

RE(linescan(<motor>, <detector>, <start>, <stop>, <N>))

where

<motor> is a motor name, e.g. xafs\_x

<detector> is one of: 'it', 'if', 'i0', or ‘ir’

<start>,<stop>,<N> are the boundaries and the number of steps.

The plot will be determined from the values of <motor> and <detector>

This is a **relative** scan.

After prompt, *single click the left button*  after a linescan to move to a position.

Do

RE(pluck())

to repeat that on the current plot. RE(pluck()) only works on *most recent* plot.

**Energy scan:**

RE(xafs('scan.ini'))

Argument to the xafs command is the name of a control file in *your* data folder.

In the INI file, set “mode” to transmission, fluorescence, reference, or both to control the in-scan plotting display (both = show transmission *and* fluorescence)

**Experiment log:**

Log entries are made for each scan. System and beamtime specific logs are maintained. To insert a comment in the log, do:

BMM\_log\_info(“This is my log entry”)

|  |  |
| --- | --- |
| tu() / td() | Tune the mono 2nd crystal |
| TUNE\_STEP=0.004 | Tuning step size – 0.004 ok for Si(111), 0.002 for Si(311) |