Amor

Apparatus for Multi Option Reflectometry

short users' guide

alignment:

for alignment a laser following the neutron path can be activated as an a overlap filter:

conf laserlfilter

for the real measurements it is **essential** to return to the configuration *fili* there are 3 priciple set-ups: horizontal, deflected unpolarised, or deflecte accessible via:

conf horizontallpolariserldeflector

you can switch between single and area detector with:



importand commands:

check position of *device*: <device>

drive device to value dr <device> <value>

redifine the value for device: sp <device> <value>

to drive the vertical slit number to opening: slit <number> <opening>

or, if all 4 slits should be changed: slit <opening1> <2> <3> <4> <5>

the present openings can be obtained by the command

slit

scan commands:

center-scan for *device* around *value* with *number* setps to either side of *i* pre-set:

cscan <device> <value> <width> <number> <pre-set>

step-scan for device from value1 to value2 with number points and monit sscan <device> <value1> <value2> <number> <pre-set>

after a scan it is possible (please check the value reported back!) to get a peak

and then to drive there with center

magnets:

switch the polariser [analyser] to spin up or down neutrons, or off: spin +I0I- [+I0I-]

drive the magnetic field at the sample: dr hsy <field in Oe>

(re)mount polariser / analyser magnets: conf pbylaby

mount / unmount 1 T electro magnet: fmaset onloff

TOF data acqusition:

start a TOF measurement for a monitor *pre-set*: count monitor <pre-set>

the data file is created after finishing the data acquisition (a *pre-set* of 4e approx. 1 h)

a (simple) batch-job is a line-by-line list of the commands to be executed define a *directory* where the *batch-files* are located:

batchroot /home/amorInsg/ execute the *batch-job*:

batchrun <batch-file>