TkT

e	**expand**
fx	**full x range**
fy	**full y range**
ff	**full x y range**
ci	**calculate the integral**
cg	**Gaussian fit**
a	**fit highest peak**
ka	**calibrate with 2 highest peak**
ctrl k	**calibration panel**
ctrl a	
ctrl AF	**remove auto format**
1 or 2	**superimpose previous/next histogram**
ctrl 1 or ctrl2	**pass to previous/next histogram**
sr n	**select spectra number n**
sv n	**display spectra number n**
sza	**spectra zero all**
sva	**spectra view all (I display all spectra saved)**
ctrl open	**reload spectrum (if more are selected (with the button under AF), all are reloaded)**

colors → the white spectrum is the one on which I operate, I can store it assigning to it a color (clicking on a color) or I can recal a stored spectrum with ctr + click on the color (and it will get it white)

Prep_..._100_44_100_traces → Split screen h 6

100 traces x 44 spectra (36 segments, 4 core, 4 empty ?)

mezzdata_00... .dat → Split screen h 7 to have one over the other, or without to have them on a line. format UA

Prod_...3_38_32..._ampli → set: 3 x 38 x 114 → to see only one spectrum
32 kchannel x 38 spectra (36 segments, 2 core) x 3 modality (0: ..., 1: only one segment has a signal, 2: only central core)

Prep_...2_40_16..._ener → Split screen H 6
16 kchannel x 40 spectra (36 segments, 2 core, 2 empty) x 2 modality (0: with corrections, ex. Cross talk, Doppl. Corr., 1: without corrections)

Prod...100_42_100..._trace → Define User Grid 0 600 6
100 sample x 40 detectors (36 segments, 4 core) x 100 traces (signals)
if x max:599 → only one trace

Psa... traces → 2 set of Data : 0 = real data, 1 = PSA fit

trace_capture → traces out of the digitizer (?). set plots like: 1000 x 6 x 664, format: UT
(0 → high gain, 1 → low gain, 3 → noise)
ex: 1000 6 664
155 UT

Traces on one line → **Define User Grid : 0 600 6**
(6 is the thin line inside, 600 - the big line - is because of 6 segments x 10 sample)

60 → 360

To put it invisible → **Toggle User Grid**

Shift > → to go to the right in the spectrum (in case of traces on a line)

[14][ABC] → it displays all the combinations of 14 qitha ABC
10[BC] → it displays the combinations of B and C
10[BC]{5} → it displays the combinations of B and C from the 5th and then sequentially

DM1 = define macro 1 (I can do DM2, DM3, etc.)

to define a sum of the spectra of all the detectors:

sr10 s+20 s+01 s+11 s+21

s = spectra, sr = load the spectra

or, more complete:

fx n sr10 s+20 s+01 s+11 s+21 ci e

→ reload, expand and calculate the integral

0	1								9
10									

Matrix of PSA:

- full depth
- side
- 2nd side
- r – z cut
- slices
- ...

To force to write spectra:
touch /Conf/1B/CrystalProducer.live (?)
ll /Conf/1B/CrystalProducer.live → to check if it still there (until is there I don't have new spectra)
To erase the spectra (while the acquisition is running):
echo a> /Conf/1B/CrystalProducer.live

to run Narval

To kill Narval running: **force_clean_narval name**

to kill Narval + the rest **: ./M51**

- narval_launch

- in **prototype@narval**_base: **screen -r narval**

- browser: **running configuration** → select the second one → **attach** → **destroy**

- Krak → **initialize** → **configure** → file. Xml

First **start** in Krak, then in the run control (after about 20 s).

To save and copy the data and copy them in another folder:
.../zCurrentNarval.../**Save... .sh name_of_the_run**

(old script: /agata/prototype/mv_data_RN.sh name_of_the_run → it has not to exist already!)

From the Narval scheme in Krak I can click on a process → details → I can change parameters

Detector calibration

In: /agatadisks/installation_tests/12.../run.../

To do only one spectrum, in TkT (look at the second set of spectra):

- **ctrl** k → calibration panel
- select **last 2 peaks** so that it consider only the 2 last peaks
- select Co peaks
- a0 → fix
- **calculate** → i get the coefficients

To do all the detectors all together (better give a look before one by one):

for a in 1B 1C 4A 4B 4C; do echo; Recal -spe $a/Prod_... -num 38 -sum38 -TR -dwa 20 50; done;
(→ I see the result)
for a in 1B 1C 4A 4B 4C; do echo; Recal -spe $a/Prod_... -num 38 -sum38 -TR -dwa 20 50> cal_$a.txt; done;
(→ I write the result in a file)
for a in 1B 1C 4A 4B 4C; do echo; Recal -spe $a/Prod_... -num 38 -sum38 -TR -dwa 20 50> cal_$a.log; done;
(→ I have also a description)
cat Conf/.../PreprocessingFilterPSa.conf
→ move the column **gain*slope** in Preproc...PSA.conf

calibrations without Narval
→ spec files from mezzanine with Dino's program

- i.e.: Recal - … -sub 6 -22Na
  -sub 6 because the order here is different, in this way I take the segments
  -22Na if I have Sodium source in stead of Co
  I can add condition in minimum wideness and highness of the peak and range
  → i get calibr coefficients, threshold present in Preproc...PSA.conf, offset for time
- I check the valued obtained with manual fit (CP)
- I move the column **gain*slope** in Preproc...PSA.conf

polezero
psa_test@scgw1
/config_crystal/....rc → for the electronics

all risetime → for the segments → parameters trapezoid after preamplifier
polezero

cc risetime → for the cores
polezero

→ check that they are the same as in Preproc...PSA.conf
polezero is ~ shaping time
To set the polezero of the cores (for the segments I leave them like they are!) I have to fit the exponential of the long traces:

- display long traces
- first 2 markers for the background and second 2 for the exponential fit
- → tau is the value of polezero in file … .rc (threshold in file .rc is the one that we set from the carrier)

! To load this values I have to press **Load file** in the browser.

calibrations with **calibDEMON.sh**

from Narval putting in Mask the configurations to have only the energies or running in the emulator the file mezzdata... → file: **energy....bdat**
if they are splitted, do for example: cat energy...0001 > energy....bdat
because the program search energy....bdat.
From a directory above the one of the crystals: **calibDEMON.sh** (this programs is set for 15 detectors)

require **type hgain shaping decay**

type → 2 for energy calibration, 3 for cross talk correction (but it require the 2 done first)
hgain → energy gain set in the electronics
shaping, decay → polezero, etc... values that are present in the file .rc

hgain shaping and decay we can take the default ones (i.e. calibDEMON.sh 2).

→ file **DEMONresol**: resolution of the detectors at the 1.3keV of the Co (→ to check if the detectors are working badly or the calibrations are wrong) → they have to be around 2 keV, below 2.5 keV (th core of course has worst resolution)
I can see DEMONresol in TkT (format A): the detectors are displayed in the sequential order (1A, 1B, 4A, …) and for each I have the 6 sectors with the six peaks for the 6 segment (0,1,2,3,4,5).
KA → calibrates automatically the Co lines → I check manually if the values of the resolution make sense.

Fort.9SG → will become the PreprocessingFilterPSA.conf

XCG....matr → crosstalk matrix

inside the crystal folder: xTalkeMake -f … → as in the description of Dino, without -g ...parameters

→ I copy in fort.9GS the values of polezero (i.e. 4400) of the cores obtained before from the traces. For the segments I leave them like they are in PreprocessingFilterPSA.conf, not in Demon!

→

- i do a backup of the old PreprocessingFilterPSA.conf
- I copy Fort.9SG in PreprocessingFilterPSA.conf
- I delete the old /Data/

redo the link (ln) to the data files

- in genconf.py I enable the crosstalk matrix: in preproducer filter: the inverse, in the PSA filter: the direct (check Dino's explanation)
- reprocess the data and I check the calibrations are good

Replay Data Offline

- in genConf.py:

- Mask → 0
- #Validate rate
- …

- ./genConf.py -o cp .../conf/... ? (-o to copy from the online)
-
- I copy the ADF.conf from the online
- TopologyTotal → define for each crystal and for the Global level the chain of actors

Set Look Up Table:

in Replay → original (?) . in /Conf/Global/**Crystal...LookUpTable**: **n id det angles and conversion coefficients**

I have to know which detectors are mounted to know which put inside the system, but once i know the correct values of angles and conversion coefficients I can change the id det in the topology file so I can have only numbers below 15. (the program is still set for at most 15 crystal, when we will have more the program will be updated with 45).
→ I put the values in the topology file (!no, in genconf.py, in the database!) with their PSA bases.
→ ./genConf.py
→ run: **femul_new TopologyTotal.conf**

Base line alinement

- copy old values (to have a backup)
- load in the Browser the stored values (**Restore**....) and select the proper board for each sector
- look in TKT the traces (); the correct value of the baseline is 4000
- calculate the difference of the baseline and 4000 and multiply it by 4 (gain factor) ->for each segment
- add or subtract it to the value on the browser and press on the „ball“ (it will be set on a value that the system can accept)
  example: _____ 4200
  _____4000

  old value:-15000
  → new value: -15800
- restart the acquisition and check the result of the new values (even if they have not been saved on the script, the acquisition reads the value on the browser)
- redo the procedure until they are all almost aligned (perfectly is not possible because of default offset of the values that can be set)
- **Save...to Database**

I can do this correction also with Recal giving a parameter with 4000