



NHSC/PACS Web Tutorials

Running the PACS Spectrometer pipeline for CHOP/NOD Mode

PACS-301

Pipeline Level 0 to 1 processing

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Introduction

This tutorial will guide you through the interactive spectrometer pipeline from loading raw data into HIPE to obtain calibrated data with astrometry in the case of chop/nod mode.

Pre-requisites

The following tutorials should be read before this one:

- ***PACS-101: How to use these tutorials.***
- ***PACS-102: Accessing and storing data from the Herschel Science Archive***
- ***PACS-103: Loading scripts***

Sequel: PACS-302 – Level 1-2 processing



Overview



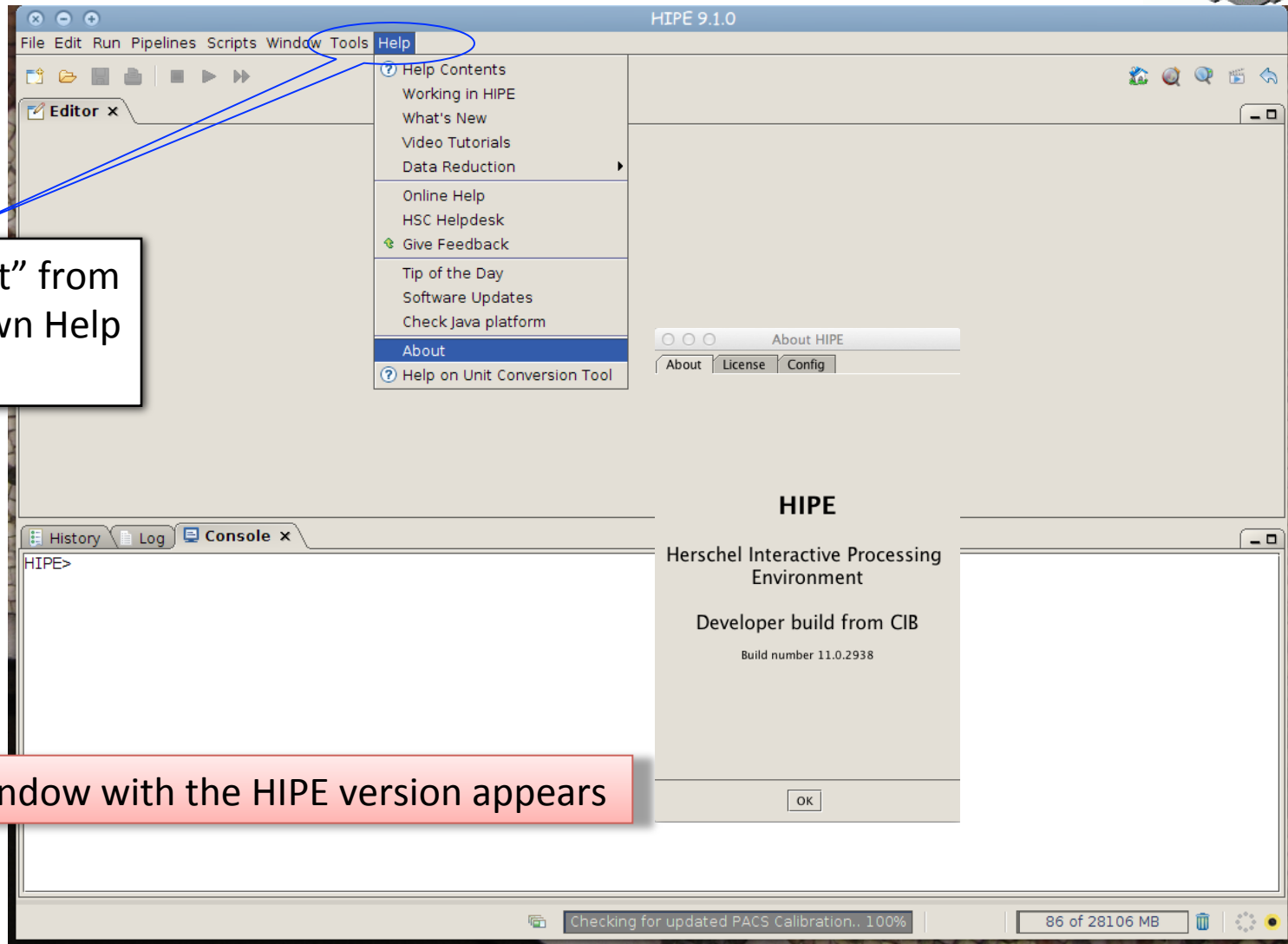
- Step 1** Check HIPE version and your local memory
- Step 2** Set up script for the particular Obs ID
- Step 3** Run the 0 → 0.5 pipeline
- Step 4** Run the 0.5 → 1 pipeline



Step 1

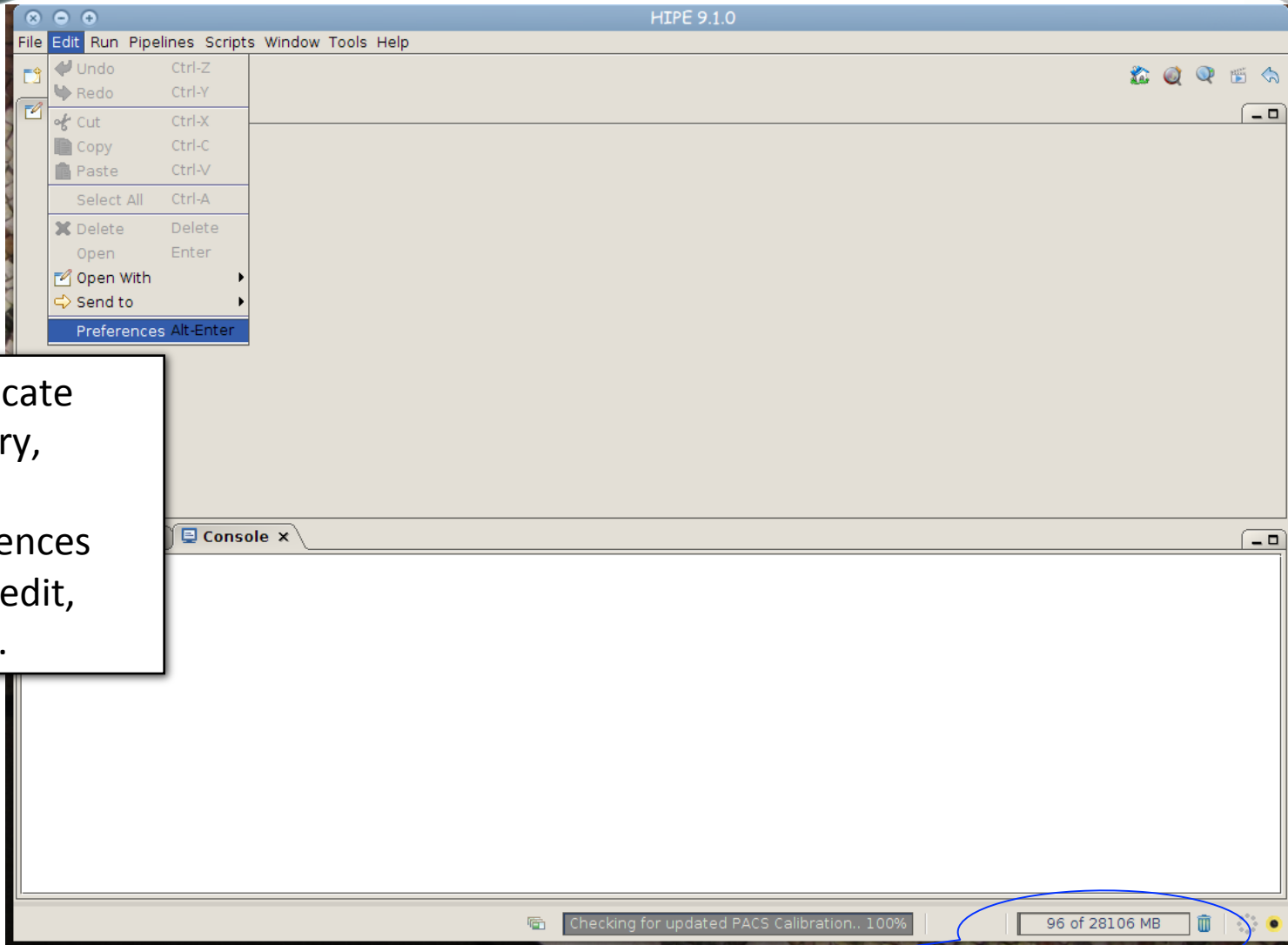
Check HIPE version and memory allocation

The version used for the tutorial is 11.0 build 2938



Select "about" from the drop down Help menu

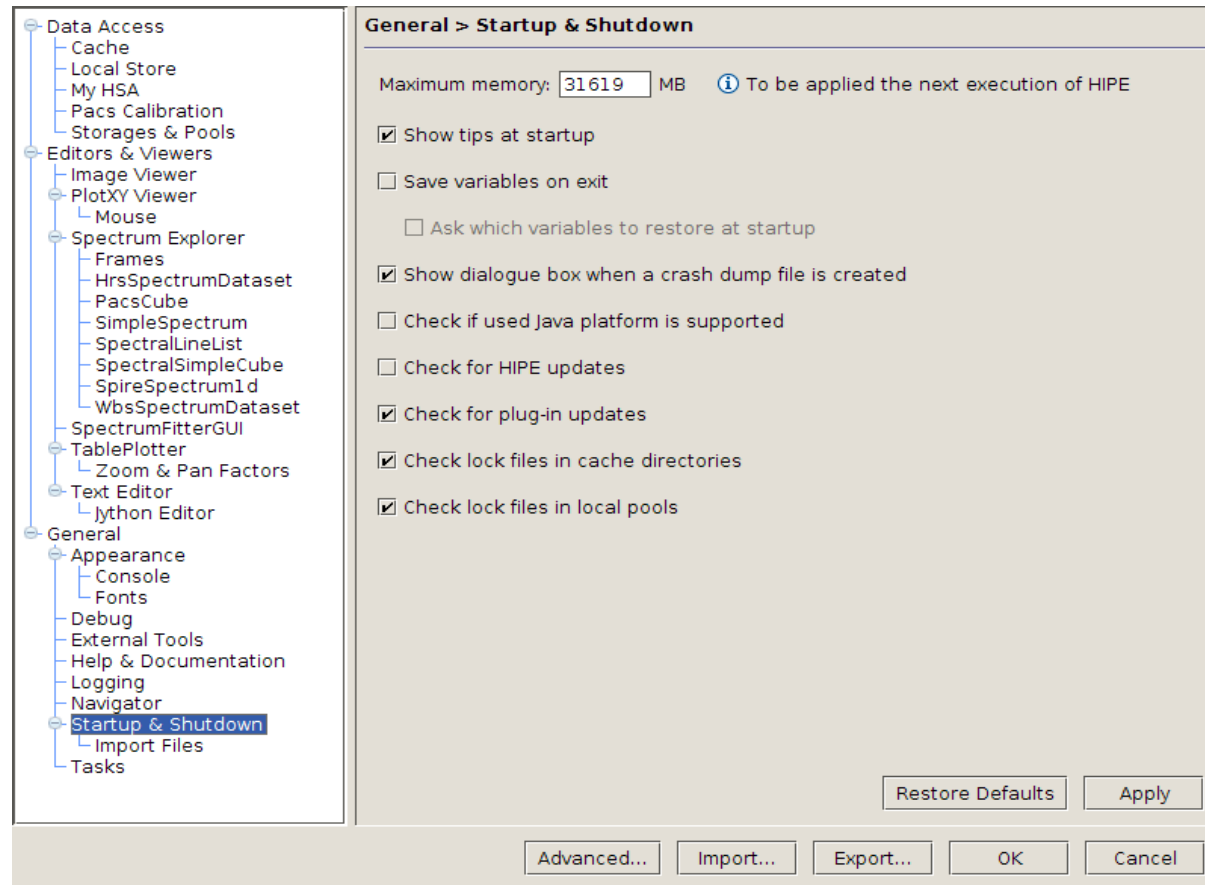
A pop-up window with the HIPE version appears



To allocate memory, select preferences under edit, then ...

N.b.:, Memory used and available

...click on
“Startup &
Shutdown”
and change
the amount of
memory



The allocated memory should be a bit smaller than the total RAM of your computer.
(e.g. 7.5 out of 8.0 Gbytes)
You must exit and restart HIPE to obtain the new amount of memory.



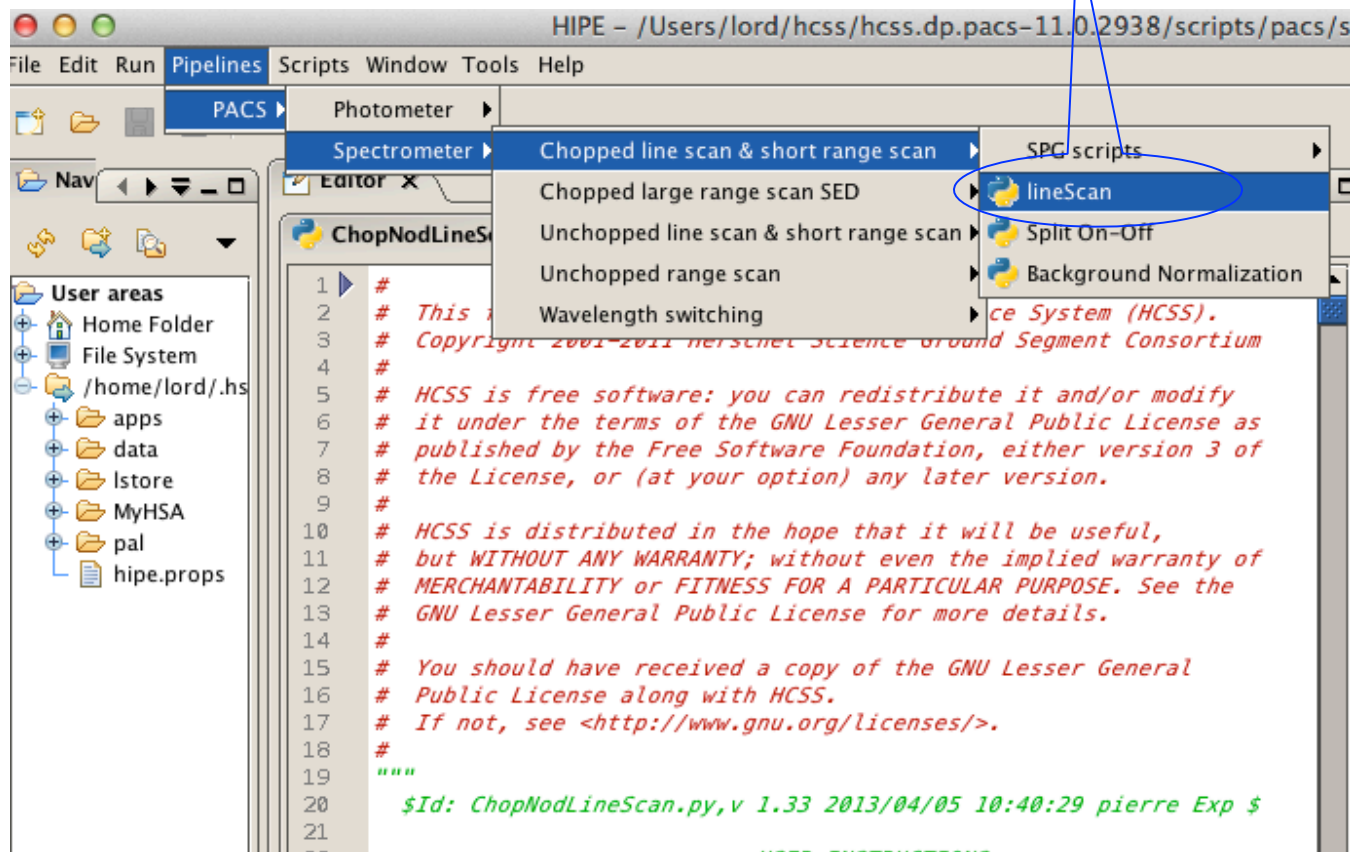
Step 2

Setup

Load pipeline script; load observation; check your data; and select the camera

Loading the script

The “linescan” script used in this tutorial corresponds to the script available directly from the distribution.



Loading the observation

Once the script is loaded, one simply steps through the lines to execute it. But first modify it for OBSID of the observation desired. In the case of this tutorial, the observation was already saved into a pool in the user's local `~/hcss/lstore` directory (created when first installing HIPE). So one modifies the obsid in the script and clicks through using the green arrow....

Hit the green arrow to step through the entire script

```
102
103
104 # -----
105 # GET THE DATA: load the Observation Context with the data of your obsid
106 #
107 # First, set the OBSID of the observation to process. CHANGE THE OBSID
108 # your own.
109 #
110 # As this script is also run as part of the ChopNod multiObs script(s),
111 # following "if" tests for the existence of a variable called multiObs,
112 # will be present if you are running the multiObs script. If multiObs
113 # present, the obsid will have been set already, and if not then the obsid
114 # here. (If you get a NameError, then the obsid had not been set.)
115 if ((not locals().has_key('multiObs')) or (not multiObs)):
116     obsid = 1342188943
117
118 # Next, get the data of that obsid
119 #
120 # If you already have the data stored locally in a pool with saveObserved
121 # the data is read from that pool.
122 #
123 # If you do not have the data stored locally, change useHsa to 1.
124 # You will in this case retrieve the data from the HSA and then make a
```

Modify this line. Here we set obsid to 1342186799.

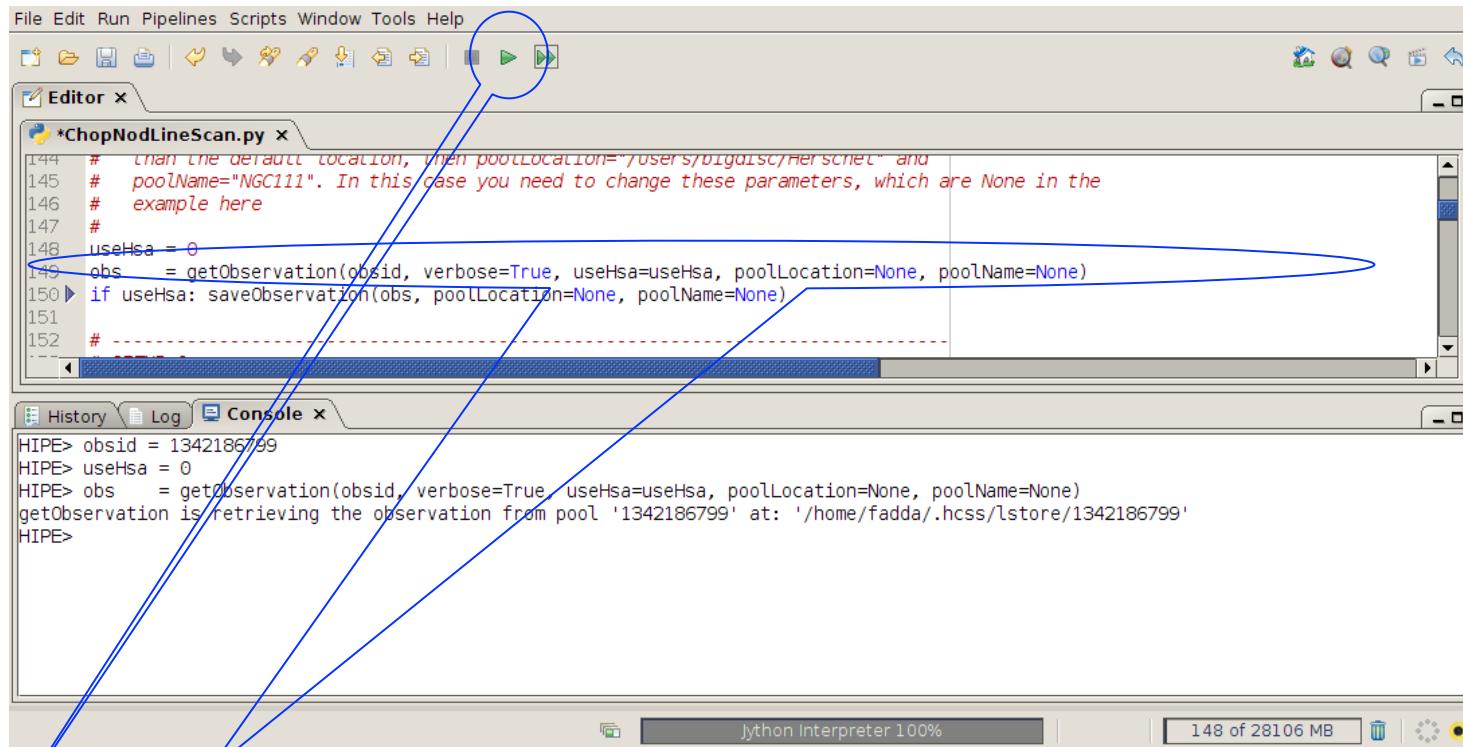
Loading the observation

If the data is not stored as a local pool, you want to tell the script to acquire the data from HSA. In this case edit the line to useHsa=1

```
141 # poolname: this is an optional parameter and is the immediate directory containing
142 # your data. By default the poolName is the obsid.
143 #
144 # If your data are instead in /Users/bigdisc/Herschel/NGC111, or you wish to store
145 # them than the default location, then poolLocation="/Users/bigdisc/Herschel" and
146 # poolName="NGC111". In this case you need to change these parameters, which are
147 # example here
148 #
149 useHsa = 1
150 obs = getObservation(obsid, verbose=True, useHsa=useHsa, poolLocation=None, poolName=None)
151 if useHsa: saveObservation(obs, poolLocation=None, poolName=None)
152
153 # -----
154 # SETUP 0
155 # verbose: 0 - silent, execute the pipeline only
156 #          1 - will trigger diagnostic output on the screen, plots, and displays
157 verbose = 1
158
159 # -----
160 # SCRIPT 0 5
```

Loading the observation

Next step, we load the observational context (a structure containing all the observational data, information about them and calibration data).



The screenshot shows a Python IDE with two panes. The top pane is an editor window titled '*ChopNodLineScan.py x' containing Python code. The bottom pane is a console window showing the execution of the code. A green play button in the top toolbar is circled in blue, and a blue oval highlights the line `obs = getObservation(obsid, verbose=True, useHsa=useHsa, poolLocation=None, poolName=None)` in the editor. Blue lines connect the play button to the console and the highlighted line to the console.

```
File Edit Run Pipelines Scripts Window Tools Help
*ChopNodLineScan.py x
144 # than the default location, then poolLocation="/users/pigauisc/Herschel" and
145 # poolName="NGC111". In this case you need to change these parameters, which are None in the
146 # example here
147 #
148 useHsa = 0
149 obs = getObservation(obsid, verbose=True, useHsa=useHsa, poolLocation=None, poolName=None)
150 if useHsa: saveObservation(obs, poolLocation=None, poolName=None)
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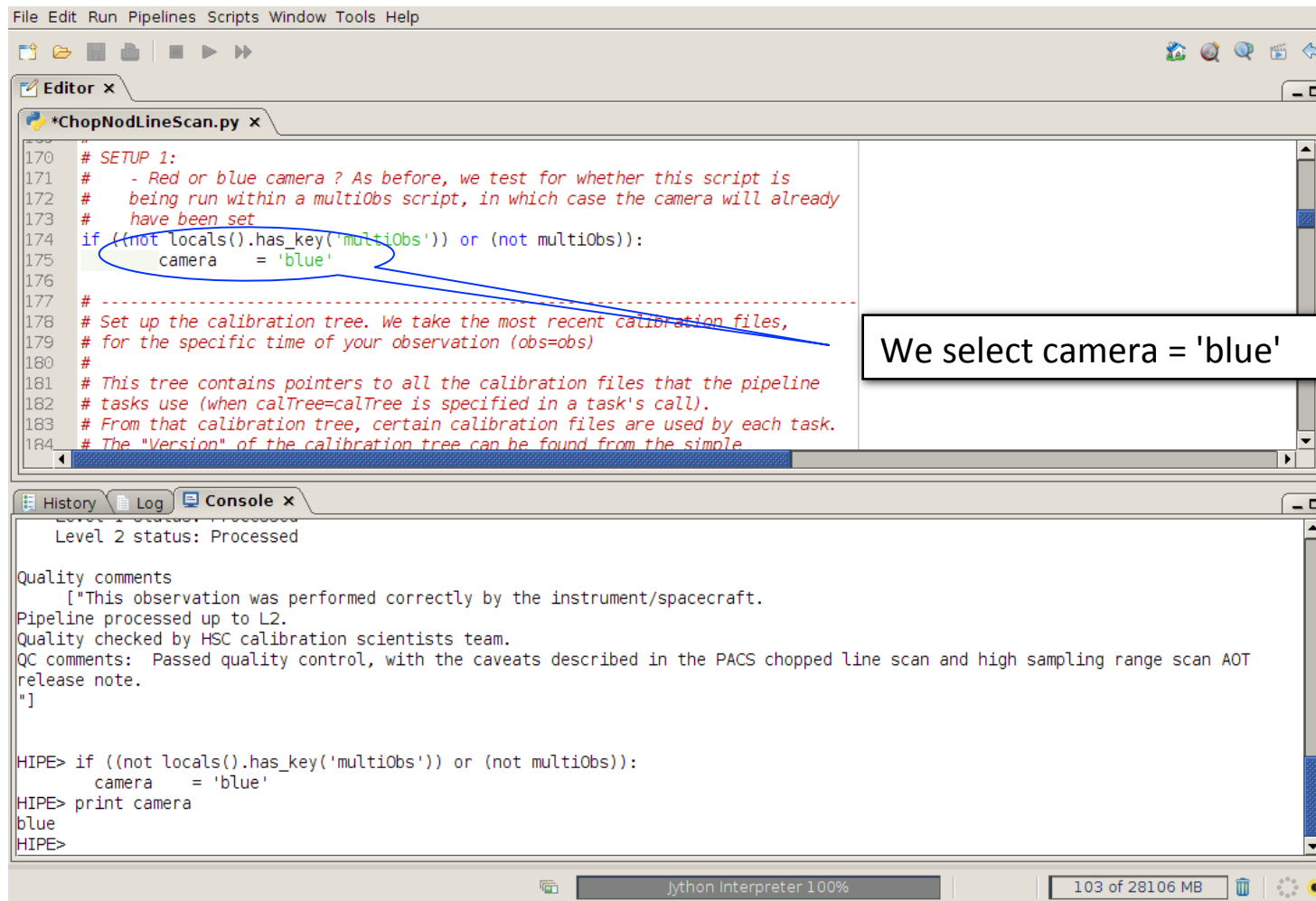
Observation Selection

For this data set, we will concern ourselves with the line observed in the PACS blue channel.

Click through (using the green arrow) the remaining lines, choosing your preferences as described in the comments until you get to the channel section.

```
*ChopNodLineScan.py x
152
153 # -----
154 # SETUP 0
155 # verbose: 0 - silent, execute the pipeline only
156 #           1 - will trigger diagnostic output on the screen, plots, and displays
157 verbose = 1
158
159 # -----
160 # SETUP 0.5
161 # updateObservationContext
162 # At the end of each level, do you want to update the ObservationContext?
163 # choice:
164 #       0 - do not update the observation context
165 #       1 - update the observation context
166 # See further down the script for simple ways to save your reductions on disk
167 # at various steps in the data processing
168 updateObservationContext = 0
169
170 # -----
```

Setting the camera



```
File Edit Run Pipelines Scripts Window Tools Help
*ChopNodLineScan.py x
170 # SETUP 1:
171 # - Red or blue camera ? As before, we test for whether this script is
172 # being run within a multiObs script, in which case the camera will already
173 # have been set
174 if ((not locals().has_key('multiObs')) or (not multiObs)):
175     camera = 'blue'
176
177 # -----
178 # Set up the calibration tree. We take the most recent calibration files,
179 # for the specific time of your observation (obs=obs)
180 #
181 # This tree contains pointers to all the calibration files that the pipeline
182 # tasks use (when calTree=calTree is specified in a task's call).
183 # From that calibration tree, certain calibration files are used by each task.
184 # The "Version" of the calibration tree can be found from the simple

Level 2 status: Processed

Quality comments
["This observation was performed correctly by the instrument/spacecraft.
Pipeline processed up to L2.
Quality checked by HSC calibration scientists team.
QC comments: Passed quality control, with the caveats described in the PACS chopped line scan and high sampling range scan AOT
release note.
"]

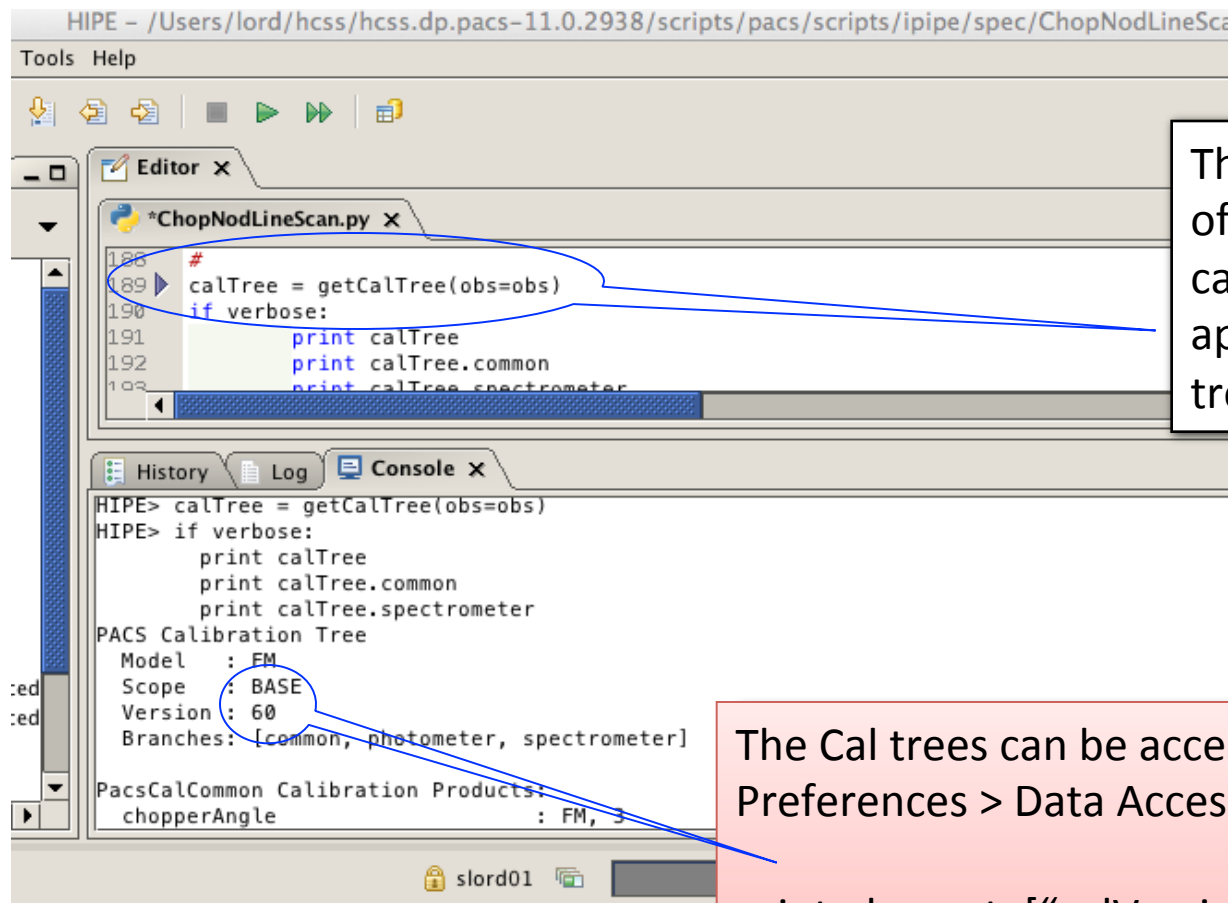
HIPE> if ((not locals().has_key('multiObs')) or (not multiObs)):
        camera = 'blue'
HIPE> print camera
blue
HIPE>
```

We select camera = 'blue'

After selecting the camera, we can check what camera we selected by simply printing:
“print camera”

Setting the calibration tree

Finally, we set the calibration tree.



```
HIPE - /Users/lord/hcss/hcss.dp.pacs-11.0.2938/scripts/pacs/scripts/ipipe/spec/ChopNodLineScan
Tools Help
Editor x
*ChopNodLineScan.py x
188 #
189 calTree = getCalTree(obs=obs)
190 if verbose:
191     print calTree
192     print calTree.common
193     print calTree.spectrometer
194
History Log Console x
HIPE> calTree = getCalTree(obs=obs)
HIPE> if verbose:
    print calTree
    print calTree.common
    print calTree.spectrometer
PACS Calibration Tree
Model : FM
Scope : BASE
Version : 60
Branches: [common, photometer, spectrometer]
PacsCalCommon Calibration Products:
chopperAngle : FM, J
```

This reads the time stamp of our obs and applies the calibration from the appropriate calibration tree.

The Cal trees can be accessed and updated from Preferences > Data Access > Pacs Calibration.

`print obs.meta["calVersion"]` shows the calibration used in current observation.

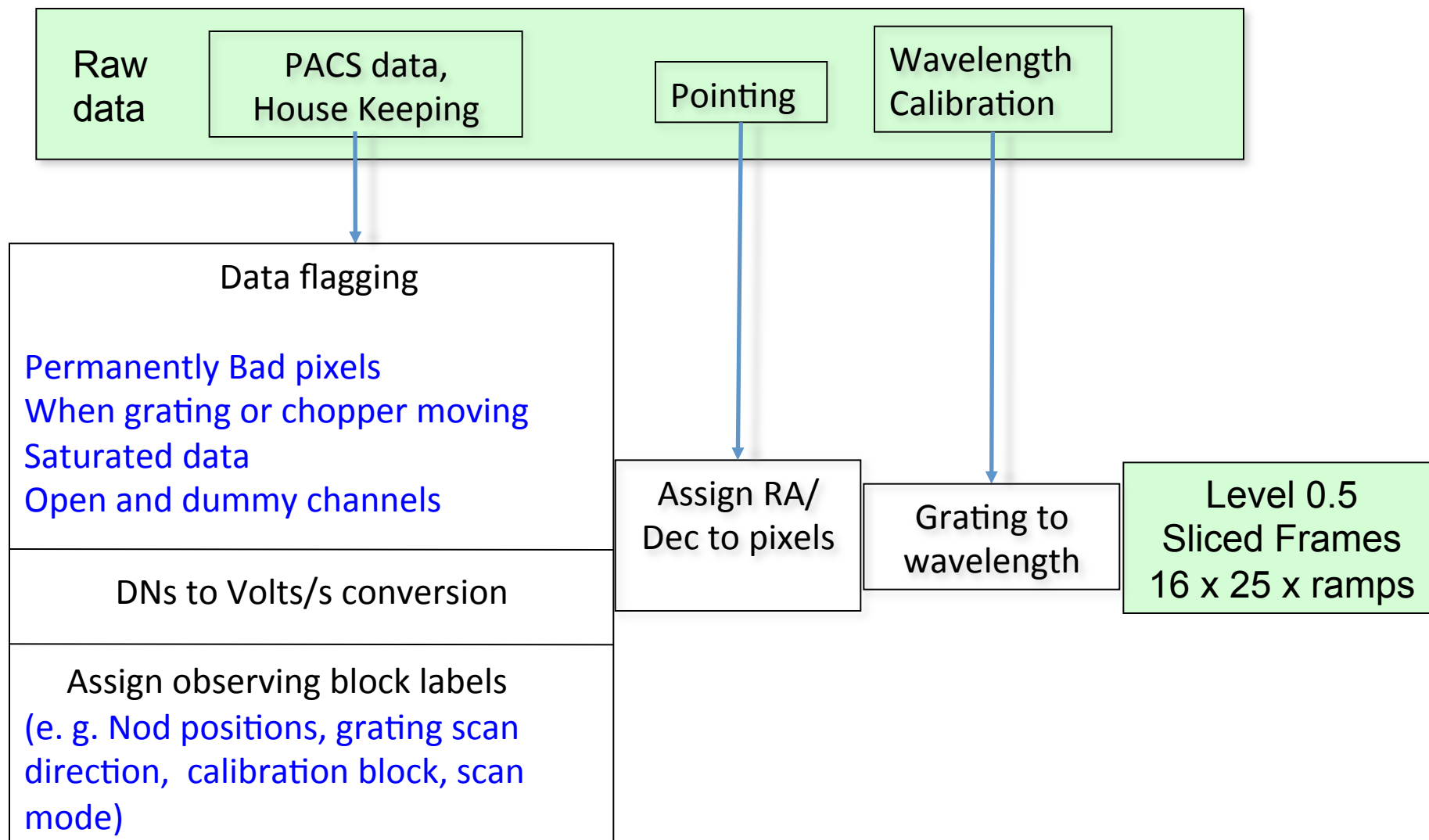


Step 3

Run the 0 → 0.5 pipeline

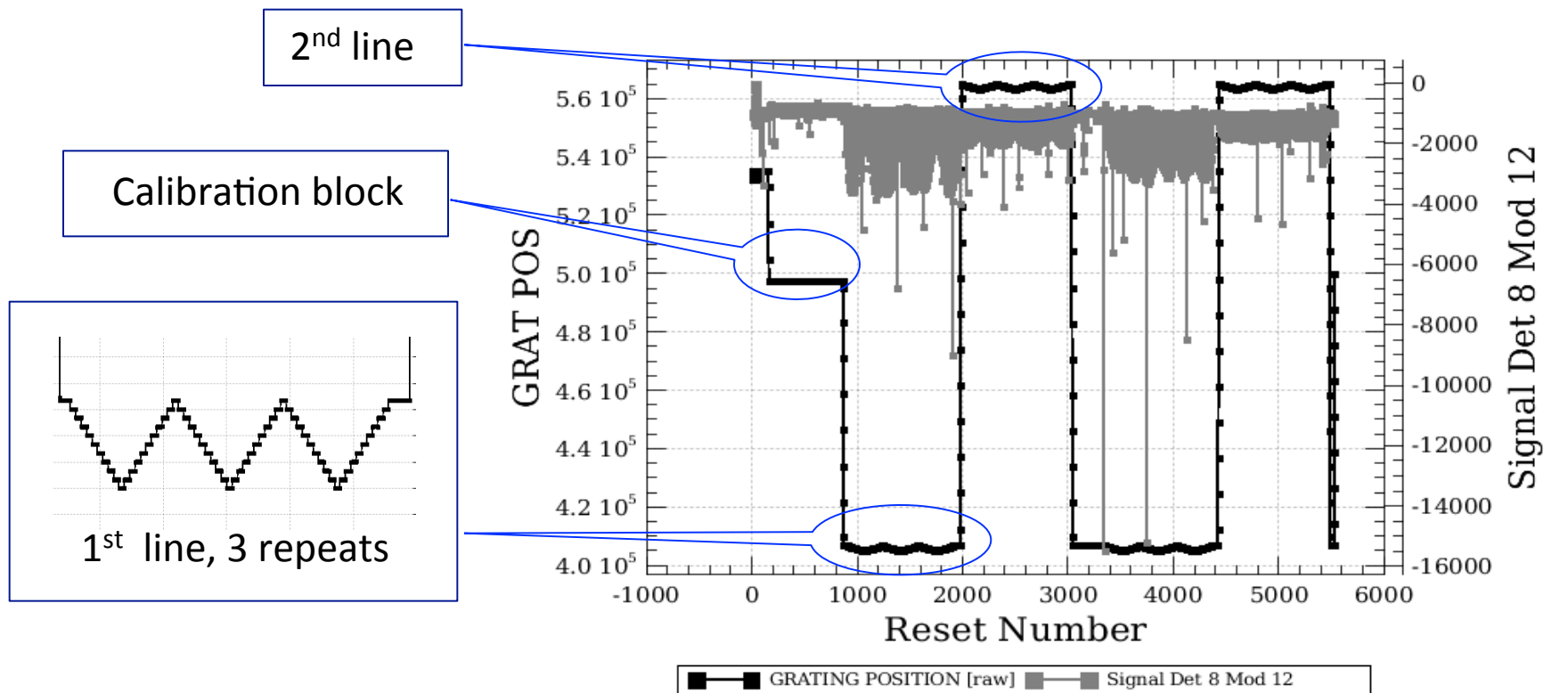
Basic calibration (pointing,
wavelength calibration, slicing)

Level 0 → 0.5



Check: level 0

From now on, we will step through the script line by line using the green arrow on the menu bar. The first step consists in extracting the 0-level products from the observation context.



The plot appears after: `'p0 = slicedSummaryPlot(slicedFrames,signal=1)'`
 In our case, after the calibration block, we can identify two different lines

Continue ...

With remaining Level 0 to 0.5 processing steps as outlined in slide 17. Step through with the green arrow.

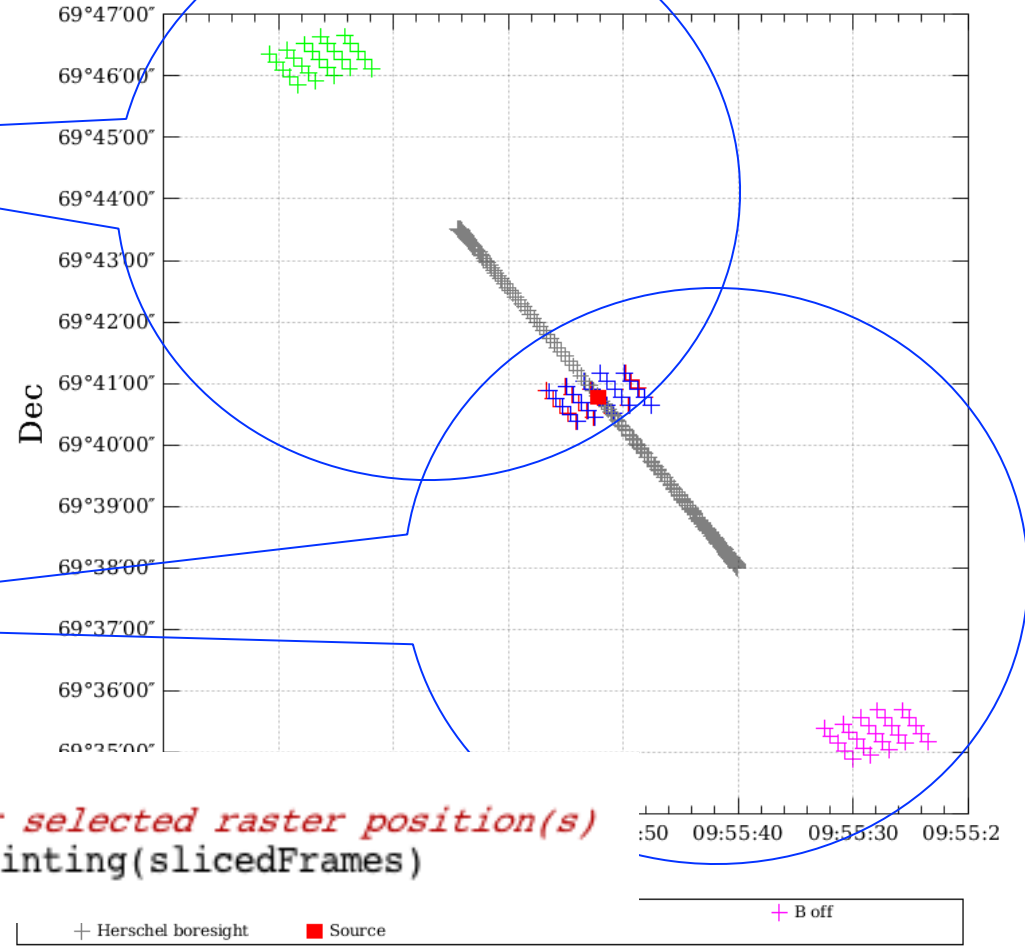
```
237 # this before you start pipelineing.
238 ▶ slicedFrames = specFlagSaturationFrames(slicedFrames, rawRamp = slicedRawRamp, calTree=calTree, c
239
240 # Convert digital units to Volts, used cal file: Readouts2Volts
241 slicedFrames = specConvDigit2VoltsPerSecFrames(slicedFrames, calTree=calTree)
242
243 # Identify the calibration blocks and fill the CALSOURCE Status entry
244 slicedFrames = detectCalibrationBlock(slicedFrames)
245
246 # Add the time information in UTC to the Status
247 slicedFrames = addUtc(slicedFrames, obs.auxiliary.timeCorrelation)
248
249 # Add the pointing information of the central spaxel to the Status
250 # Uses the pointing, horizons product (solar system object ephemeris),
251 # orbitEphemeris products, and the SIAM cal file.
252 slicedFrames = specAddInstantPointing(slicedFrames, obs.auxiliary.pointing, calTree = calTree, o
253
254 # If SSO, move SSO target to a fixed position in sky. This is needed for mapping SSOs.
255 if (isSolarSystemObject(obs)):
256     slicedFrames = correctRaDec4Sso (slicedFrames, timeOffset=0, orbitEphem=obs.auxiliary.orbitEph
257
258 # Extend the Status of Frames with the parameters GRATSCAN, CHOPPER, CHOPPOS, ONSOURCE, OFFSOURC.
259 # used cal file: ChopperThrowDescription
260 slicedFrames = specExtendStatus(slicedFrames, calTree=calTree)
261
262 # Convert the chopper readouts to an angle wrt. focal plane unit and the sky
263 # and add this to the Status, used cal files: ChopperAngle and ChopperSkyAngle
264 slicedFrames = convertChopper2Angle(slicedFrames, calTree=calTree)
265
266 # Add the positions for each pixel (ra and dec datasets)
267 # used cal files: ArrayInstrument and ModuleArray
268 slicedFrames = specAssignRaDec(slicedFrames, calTree=calTree)
```

Check: footprint

Nod A

Nod B

PACS footprint and S/C boresight positions



```

270 if verbose:
271     # show footprints for selected raster position(s)
272     ppoint = slicedPlotPointing(slicedFrames)
273

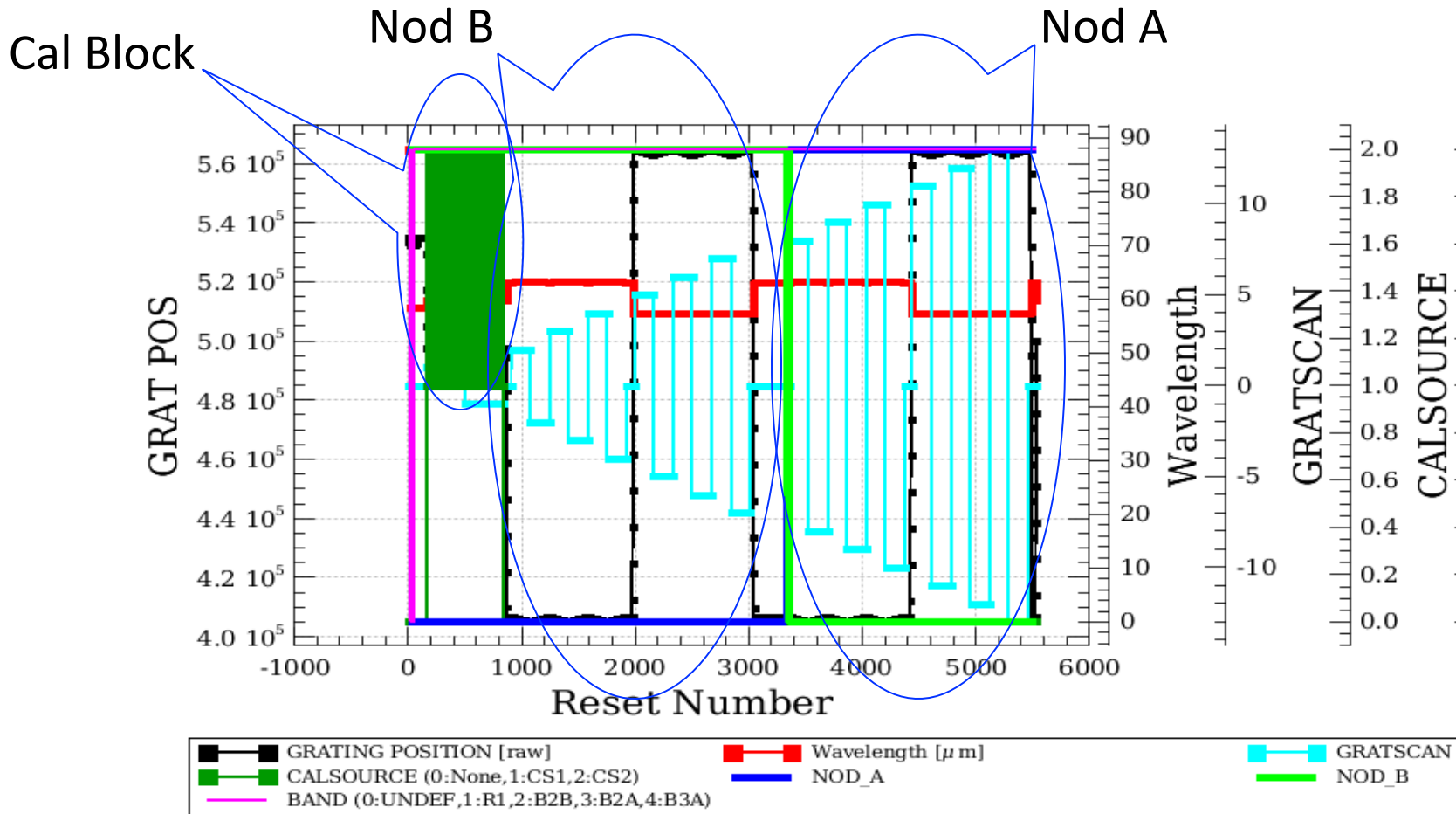
```

Continue ...

With remaining Level 0 to 0.5 processing steps as outlined in slide 17. Step through with the green arrow.

```
ChopNodLineScan.py x
272     ppoint = slicedPlotPointing(slicedFrames)
273
274     # Add the wavelength for each pixel (wave dataset), used cal file: WavePolynomes
275     slicedFrames = waveCalc(slicedFrames, calTree=calTree)
276
277     # Correct the wavelength for the spacecraft velocity.
278     # Uses the pointing, orbitEphemeris and timeCorrelation product.
279     slicedFrames = specCorrectHerschelVelocity(slicedFrames, obs.auxiliary.orbitEphemeris, obs.aux
280
281     # Find the major logical blocks of this observation and organise them in the
282     # BlockTable attached to the Frames; used cal file: ObcpDescription
283     slicedFrames = findBlocks(slicedFrames, calTree = calTree)
284
285     # Flag the known bad or noisy pixels in the masks "BADPIXELS" and "NOISYPIXELS"
286     # used cal files: BadPixelMask and NoisyPixelMask
287     # -> by default the bad pixels will be excluded later when final cubes are built, the noisy
288     slicedFrames = specFlagBadPixelsFrames(slicedFrames, calTree=calTree)
289
290     if verbose:
291         # Summary of the slices
292         slicedSummary(slicedFrames)
293         # Summary of the active (1) and inactive (0) status of every Mask
294         maskSummary(slicedFrames)
295         # Plot the instrument movements, without the signal
296         pl = slicedSummaryPlot([slicedFrames,signal=0])
297
```

Check: after slicedSummaryPlot(slicedFrames...)



There are two lines (two wavelengths in red). Grating scans are numbered positive if upscans and negative if downscans.

Check: `slicedSummary(slicedFrames)`

The slicing of the data is performed according to rules made explicit in the pipeline. In our example, two lines are observed in two nodding positions. So, we expect 4 slices plus an initial slice containing the calibration block.

```
History Log Console x
HIPE> if verbose:
# an overview of the slicedFrames contents
slicedSummary(slicedFrames)
p2 = slicedSummaryPlot(slicedFrames,signal=0)
noSlices: 5
noCalSlices: 1
noScienceSlices: 4
slice#  isScience  nodPosition  nodCycle  rasterId  lineId  band
onSource  offSource
0      false      ["B"]      0         0 0      [1]      ["B3A"]
no      no
1      true        ["B"]      1         0 0      [2]      ["B3A"]
both    both
2      true        ["A"]      1         0 0      [2]      ["B3A"]
both    both
```

Check: after slicing

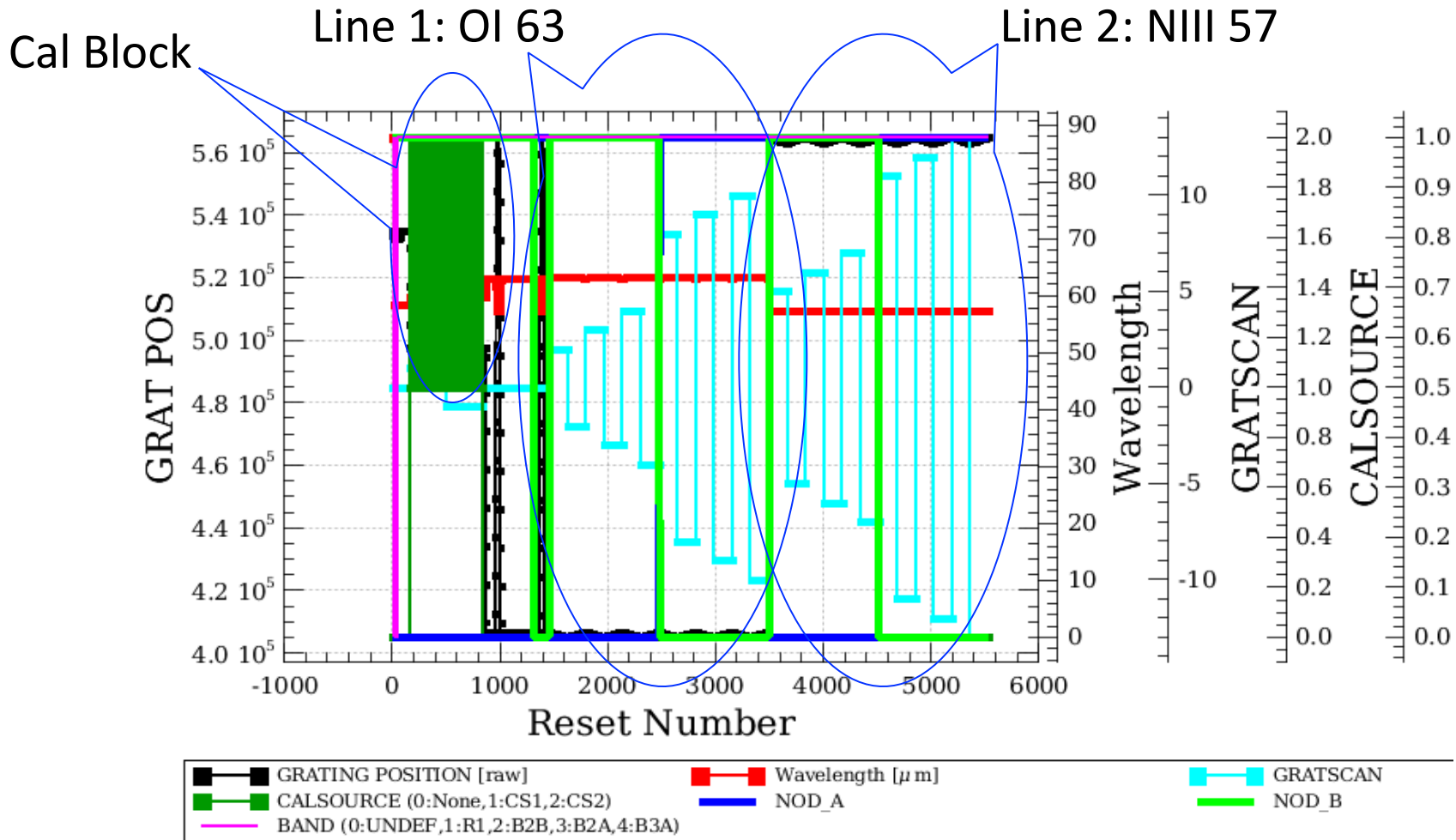
5 slices !

Line 1 – B & A nodes

Line 2 – B & A nodes

```
History Log Console x
# get/saveObservation are also accepted by saveSlicedCopy and readSliced.
# See their description given above (for getObservation).
noSlices: 5
noCalSlices: 1
noScienceSlices: 4
slice# isScience nodPosition nodCycle rasterId lineId band dimensions wavelengths
onSource offSource
0 false ["B"] 0 0 0 [1] ["B3A"] [18,25,679] 59.816 - 60.067 no
no
1 true ["B"] 1 0 0 [2] ["B3A"] [18,25,1019] 63.093 - 63.379 both
both
2 true ["A"] 1 0 0 [2] ["B3A"] [18,25,1019] 63.093 - 63.379 both
both
3 true ["B"] 1 0 0 [3] ["B3A"] [18,25,1019] 57.213 - 57.548 both
both
4 true ["A"] 1 0 0 [3] ["B3A"] [18,25,1019] 57.213 - 57.548 both
both
Slice edges: [0,679,1698,2717,3736,4755]
HIPE>
```


Check: after slicing



There are four slices (calibration, nod A and B for the 1st line, nod A and B for the 2nd line).



Continue ...



With remaining Level 0 to 0.5 processing steps as outlined in slide 17. Step through with the green arrow.

```
# -----  
#           Processing           Level 0.5 -> Level 1  
# -----
```

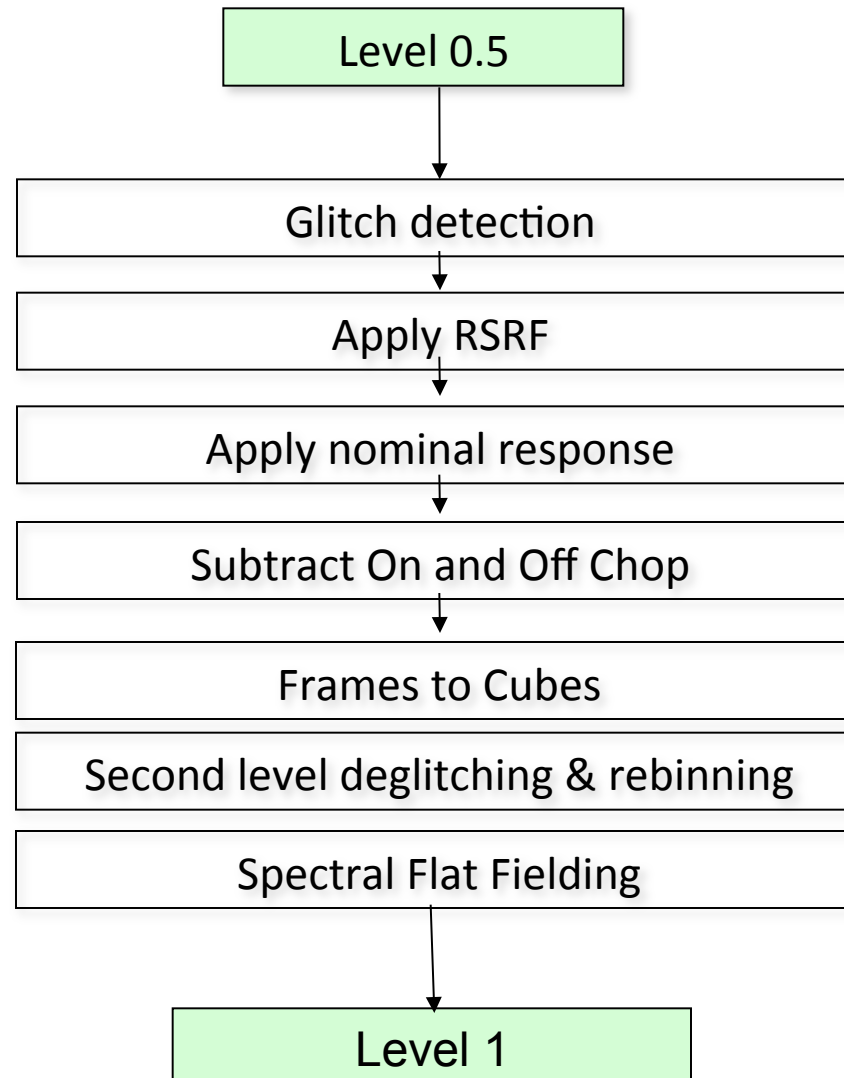


Step 4

Run the 0.5 → 1 pipeline

Glitch detection, chop differentiation, RSRF, flat

Level 0.5 → 1



Step through glitch detection

```
361 # -----
362 #           Processing           Level 0.5 -> Level 1
363 # -----
364
365 if verbose:
366     # Display the active (1) and inactive (0) status of every Mask
367     maskSummary(slicedFrames)
368
369 # De-activate all masks before running the glitch flagging
370 slicedFrames = activateMasks(slicedFrames, StringId([" "]), exclusive = True)
371
372 if verbose: maskSummary(slicedFrames,slice=0)
373
374 # Detect and flag glitches ("GLITCH" mask)
375 # copy=1 makes slicedFrames a fully independent product; it is recommended you do
376 # this before you start pipelineing at this level, i.e. here.
377 slicedFrames = specFlagGlitchFramesQTest(slicedFrames,copy=1)
378
379 if verbose:
```

Diagnostics

With verbose=1 (earlier in the script) several diagnostic plots and print out (watch your console) will appear after these lines ...

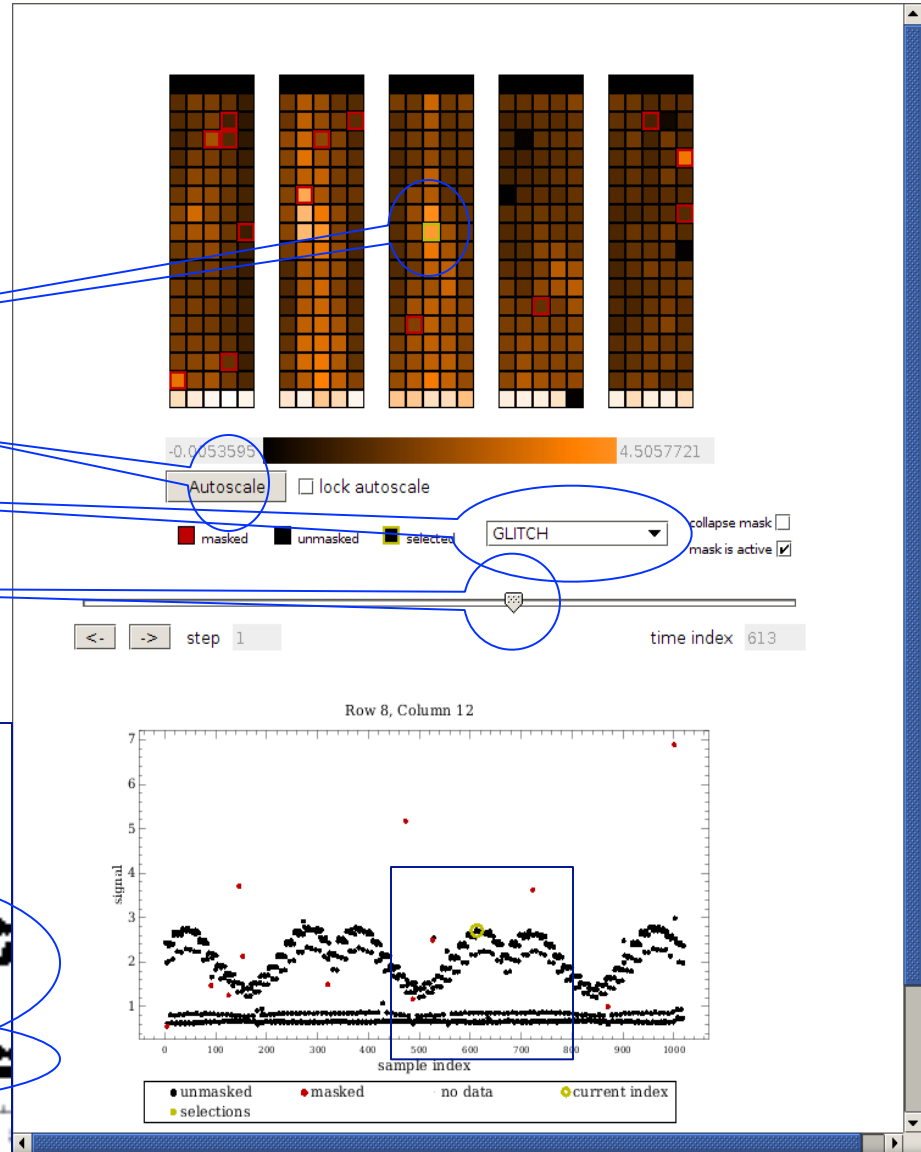
```
379 if verbose:
380     slicedSummary(slicedFrames)
381     # Summary plot, including the signal
382     p3 = slicedSummaryPlot(slicedFrames, signal=1)
383     # Plot of signal vs wavelength for the central pixel for a single slice
384     # Only unmasked datapoints are plotted
385     # Detector signal: you will see the on and off chop spectral data together
386     # on this plot, as they have not been subtracted from each other yet
387     slice = 1
388     p4 = plotSignalBasic(slicedFrames, slice=slice, detector=8, module=12)
389     # Inspect timeline of signals and masked signals (e.g. GLITCH) via a viewer
390     MaskViewer(slicedFrames.get(slice))
391     # later you will be shown how to inspect the GLITCHed datapoints on a spectrum
392     #
393     # Interactive inspection in the wavelength domain: Spectrum Explorer (PDRG Chap. 6)
394     oneFrame = slicedFrames.get(slice)
395     openVariable("oneFrame", "Spectrum Explorer")
396
```

Check: Glitch detection

You can check manually the points flagged as glitches or masked for other reasons using the *maskviewer*

- Select a pixel by clicking on it
- Select a mask
- Select a frame

Do first



Current frame

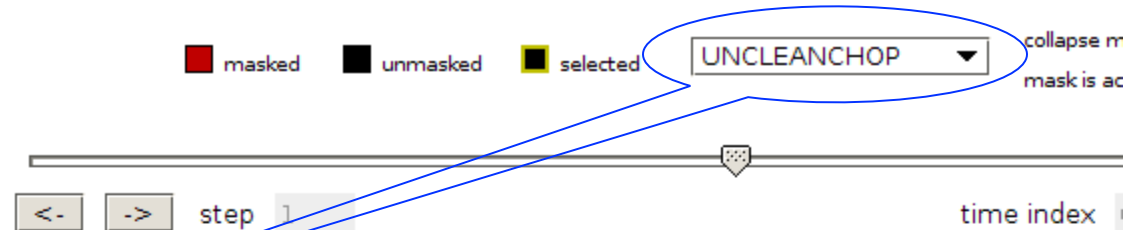
Masked glitch

ON signal

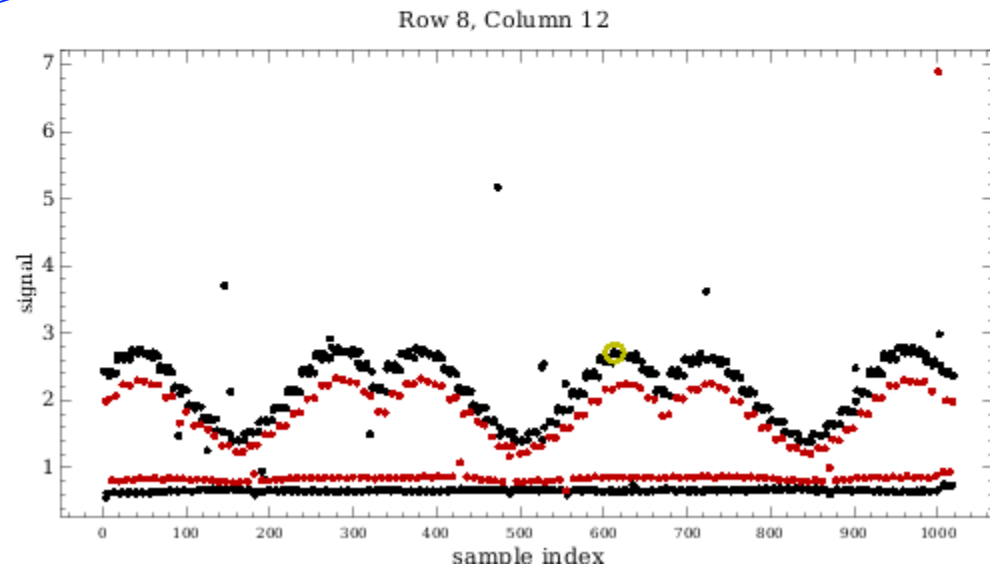
OFF signal

More masks

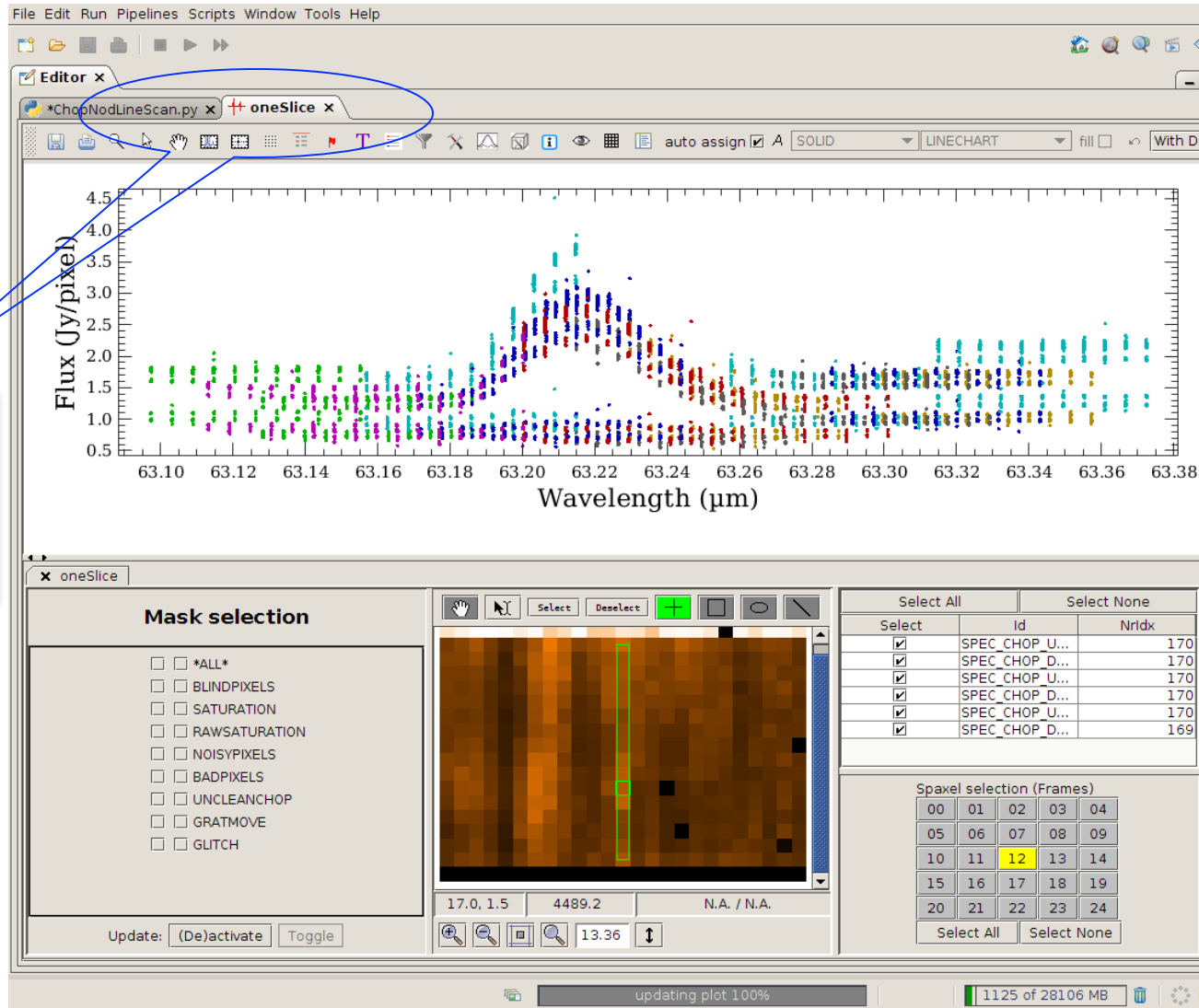
It is possible to explore other masks



Select unclean chop



In this case, it is clear why there is a second group of points for the ON and OFF positions. These corresponds to signals obtained when the chopper was not yet in the correct position.



Look for this new tab in your editor window.

Adjust screen to match this view.

A further inspection of your data is now possible using the Spectrum Explorer. Several options are available such as selection of pixels and different masks for the first slice.

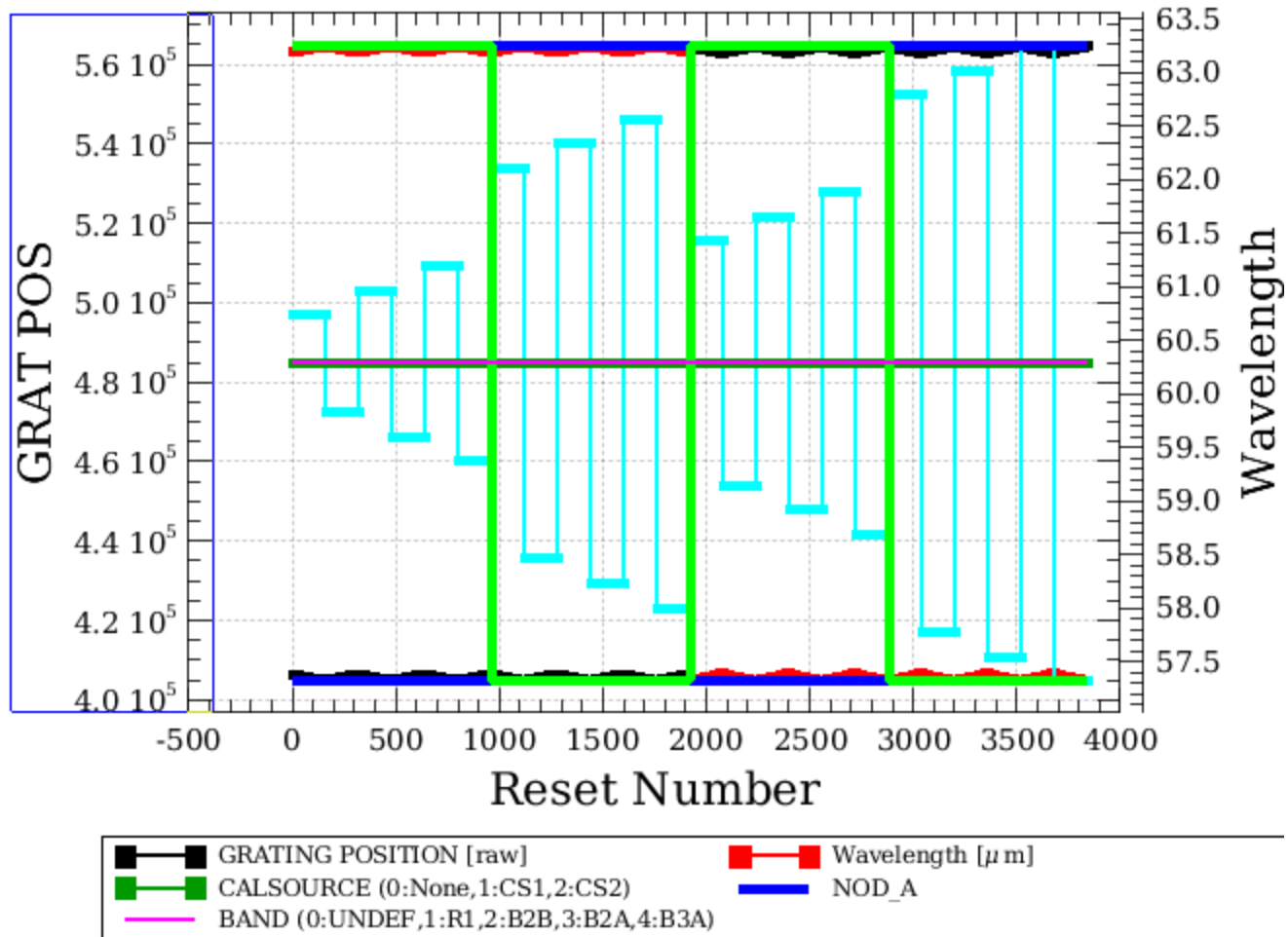
Continue ...

With remaining Level 0.5 to 1.0 processing steps as outlined in slide 28.
Step through with the green arrow.

```
399 # used cal file: CapacitationCal
400 slicedFrames = convertSignal2StandardCap(slicedFrames, calTree=calTree)
401
402 # Derive detectors' response from calibration block
403 # used cal files: observedResponse, calSourceFlux
404 calBlock = selectSlices(slicedFrames, scical="cal").get(0)
405 ▶ csResponseAndDark = specDiffCs(calBlock, calTree = calTree)
406
407 # OPTIONAL: Save complete slicedProduct to a pool before the next task so you
408 # can then compare the results before and after. You can compare by running the plotSignalBasic
409 # helper task (see above) on the saved copy and the copy created after the next pipeline task
410 # To save:
411 #   name="OBSID_"+str(observid)+"_"+camera+"_slicedFrames_1_BeforeSpecDiffChop"
412 #   saveSlicedCopy(slicedFrames, name)
413 #
414 # To read back:
415 #   slicedFrames_1 = readSliced(name)
416 #
417 # Alternatively, you might save a copy inside your session, simply like this:
418 # slicedFrames_1 = slicedFrames.copy()
419
420 # Compute the differential signal of each on-off pair of datapoints, for each chopper cycle
421 # The calibration block is cut out of the slicedFrames, so only the scientific slices remain.
422 # It is advised to check the on-source and off-source spectra independently (chopper positions)
423 # as it will reveal at least the most obvious cases of off-pointing contamination.
424 # See also the "split on-off" script from the pipeline menu
425 slicedFrames = specDiffChop(slicedFrames, scical = "sci", keepall = False, normalize=False)
426
```

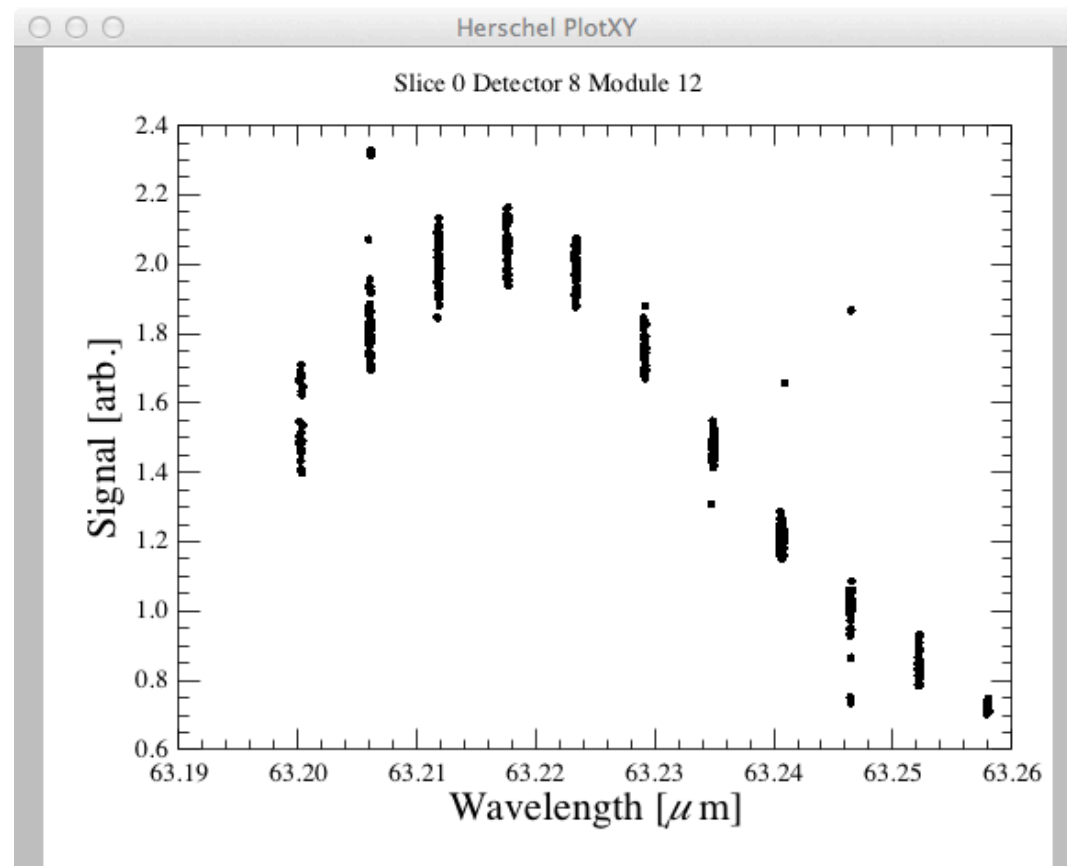
Chop differentiation

Verbose=1, shows
 After chop differentiation, the calibration block is excluded from the data



Chop differentiation

Verbose=1 shows
The data are only on the ON position (OFF being subtracted)



Continue ...

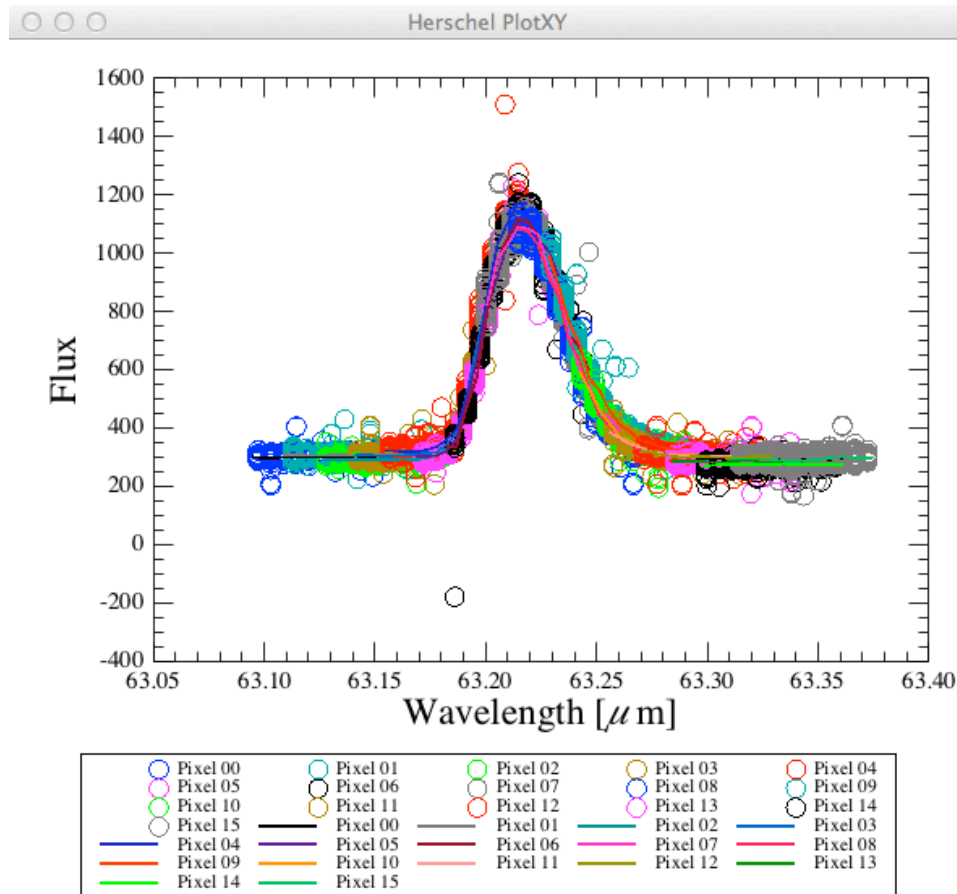
With remaining Level 0.5 to 1.0 processing steps as outlined in slide 28.
Step through with the green arrow.

```
437 # OPTIONAL: before these next two tasks you could here also save the slicedFrames to pool, so
438 # you can compare the before and after results. You can compare by running the plotSignalBasic helper
439 # (see above) on the saved copy and the copy created after the next 2 pipeline tasks
440 # To save:
441 #   name="OBSID_"+str(obsid)+"_"+camera+"_slicedFrames_2_BeforeRsRf"
442 #   saveSlicedCopy(slicedFrames,name)
443 #
444 # To read back:
445 #   slicedFrames_2 = readSliced(name)
446 #
447 # For a simple copy, inside your session:
448 # slicedFrames_2 = slicedFrames.copy()
449
450 # Divide by the relative spectral response function
451 # Used cal files: rsrfl, rsrfb2A, rsrfb2B or rsrfb3A
452 ▶ slicedFrames = rsrflCal(slicedFrames, calTree=calTree)
453
454 # Divide by the response
455 # Use intermediate product from specDiffCs : csResponseAndDark
456 slicedFrames = specRespCal(slicedFrames, csResponseAndDark = csResponseAndDark)
457
458 # Convert the Frames to PacsCubes
459 slicedCubes = specFrames2PacsCube(slicedFrames)
460
```

Check: RSRF and response

After `pb4ff = plotPixels(slicedCubes.get(.....`

After applying RSRF and response corrections we have a first look at the spectrum

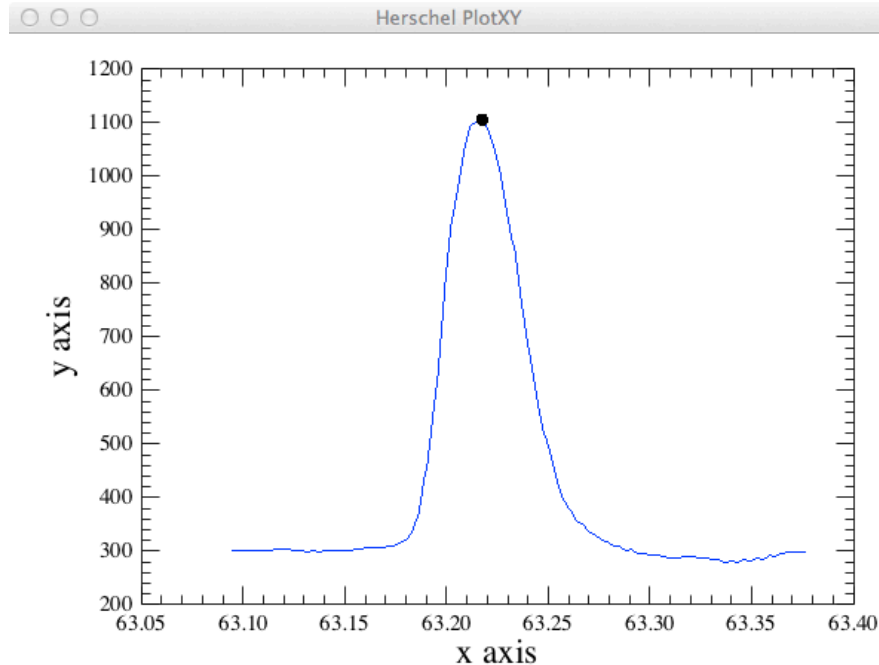


Continue ...

With remaining Level 0.5 to 1.0 processing steps as outlined in slide 28.
Step through with the green arrow.

```
502 # 2. Mask the spectral lines
503 # First the spectral lines are automatically detected, in every slice.
504 # widthDetect, expressed in FWHM, and threshold, expressed in local RMS of the
505 # continuum, are used to detect the spectral lines, in contrast with the local continuum
506 # widthMask, expressed in FWHM, is used to mask the relevant wavelength ranges
507 # For more information, print maskLines.__doc__ or consult the help.
508 # It is recommended to work with verbose=True and carefully inspect the plots
509 # for what is accepted as a spectral line.
510 # If necessary, tune the parameters and relaunch slicedMaskLines
511 # Via the parameter 'lineList', it is possible to skip the automatic detection
512 # of lines, and instead force the list of lines to be masked.
513 # This is necessary e.g. for absorption lines.
514 widthDetect = 2.5
515 threshold = 10.
516 slicedCubesMask = maskLines(slicedCubes,slicedRebinnedCubes, lineList=[], widthDetect=widthDetect, wid
517
```

Check: Spectral FlatField



As a default, the code will search for lines in all the pixels and then mask them before computing the spectral flat field.

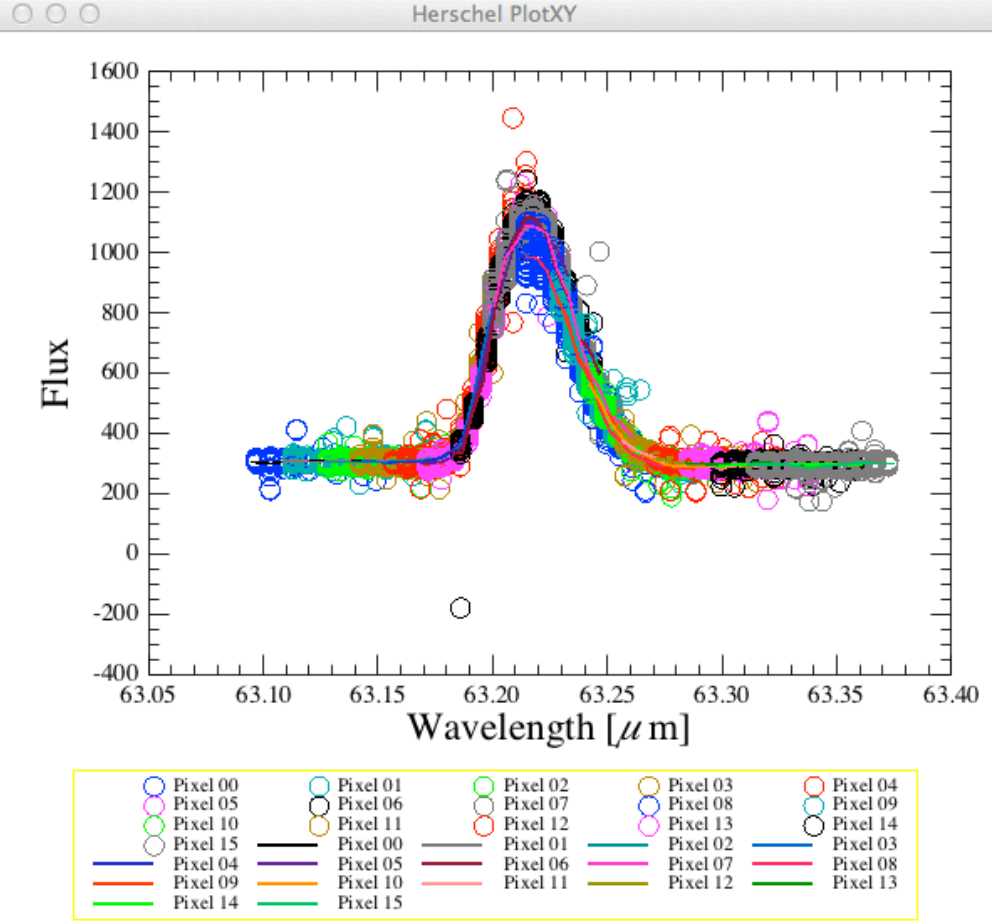
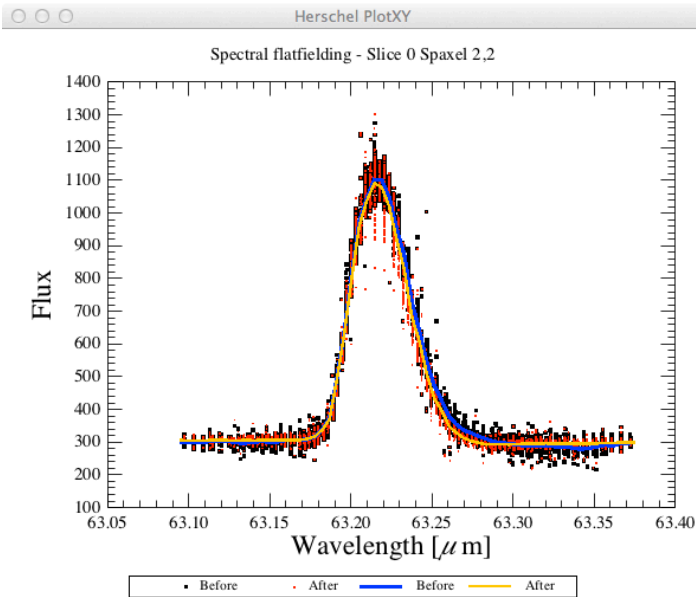
It is possible to give directly the list of lines to be masked via the parameter `lineList = [63.227]`, for instance.

Continue ...

With remaining Level 0.5 to 1.0 processing steps as outlined in slide 28.
Step through with the green arrow.

```
528
529 # 4. Rename mask OUTLIERS to OUTLIERS_B4FF (specFlagOutliers would refuse to overwrite OUTLIERS) & de
530 ▶ slicedCubes.renameMask("OUTLIERS", "OUTLIERS_B4FF")
531 slicedCubes = deactivateMasks(slicedCubes, StringId(["INLINE", "OUTLIERS_B4FF"]))
532 if verbose: maskSummary(slicedCubes, slice=0)
533
534 # 5. Remove intermediate results
535 del waveGrid, slicedRebinnedCubes, slicedCubesMask
536
537 # OPTIONAL. Compare the "cloud" of measurements for one spaxel before and after spectral flatfielding
538 # B. After FF
539 if verbose:
540     slice = 0
541     x,y = 2,2
542     offset = 0.
543     pffed = plotPixel(slicedCubes.get(slice), x=x,y=y,masks=slicedCubes.get(slice).getActiveMaskN
544
545 # --- End of Spectral Flat Fielding
546
```

Check: Spectral FlatField



At this point, the frames are converted in calibrated cubes and we have reached level 1 !



You are ready to continue with PACS-302

```
545 # --- End of Spectral Flat Fielding
546
547 # -----
548 #           Processing Level 1.0
549 # -----
550
551 # OPTIONAL: Save the intermediate results
552
553 # OPTION 1 - simple use of pools
554 # 1. To save, use saveSlicedCopy
555 # name="OBSID_"+str(obsid)+"_"+camera+"_slicedCubes_endL1"
556 # saveSlicedCopy(slicedCubes,name)
557 # 2. To restore, use readSliced
558 # slicedCubes = readSliced(name)
559
560 # OPTION 2 - work with the complete observationContext
561 if updateObservationContext:
562     # 1. Update the observationContext
563     obs = updateObservation(obs, camera, "1", slicedFrames=slicedFrames, slicedCubes=slicedCubes)
564     # 2. Save the final, updated observationContext to a specific pool
565     # name="OBSID_"+str(obsid)+"_"+camera+"_endL1"
566     # saveObservation(obs, poolName=name)
567     # 3. To restore the data
568     # a. use getObservation
569     # obs = getObservation(obsid, poolName=name)
570     # b. Extract your slicedFrames from obs
571     # levell = PacsContext(obs.levell)
572     # slicedCubes = levell.cube.getCamera(camera).product
573
574 # -----
575 #           Processing      Level 1 -> Level 2
576 # -----
```