

# NHSC/PACS Web Tutorials

## Running the PACS Spectrometer pipeline for CHOP/NOD Mode

### **PACS-301**

### *Level 0 to 1 processing*

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September 2012

# 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*

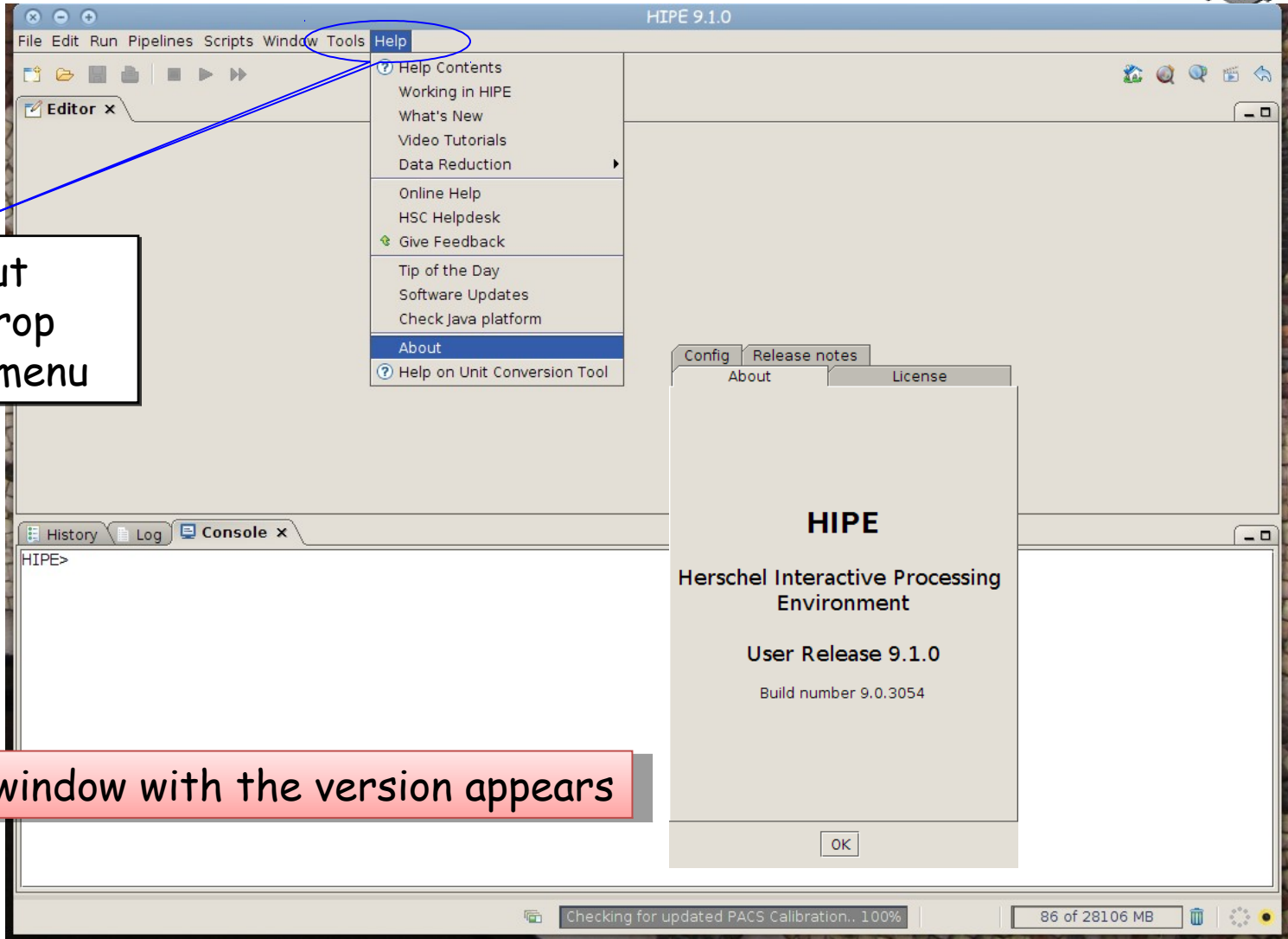
# Overview

- Step 1** Check HIPE version and memory
- Step 2** Setup
- Step 3** Run the 0 → 0.5 pipeline
- Step 4** Run the 0.5 → 1 pipeline

# Step 1

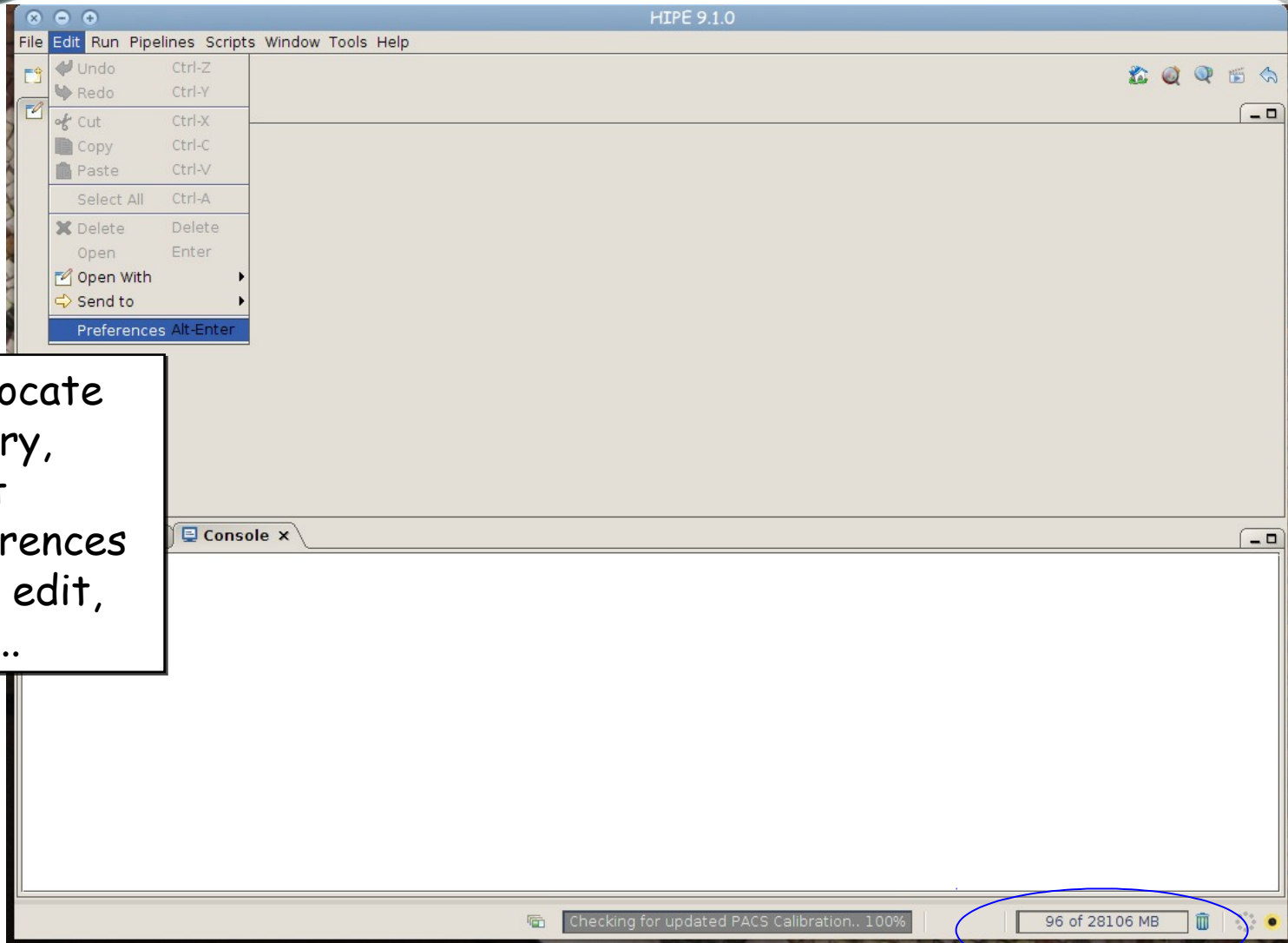
Check HIPE version and memory  
allocation

The version used for the tutorial is 9.0.3054



Select about from the drop down Help menu

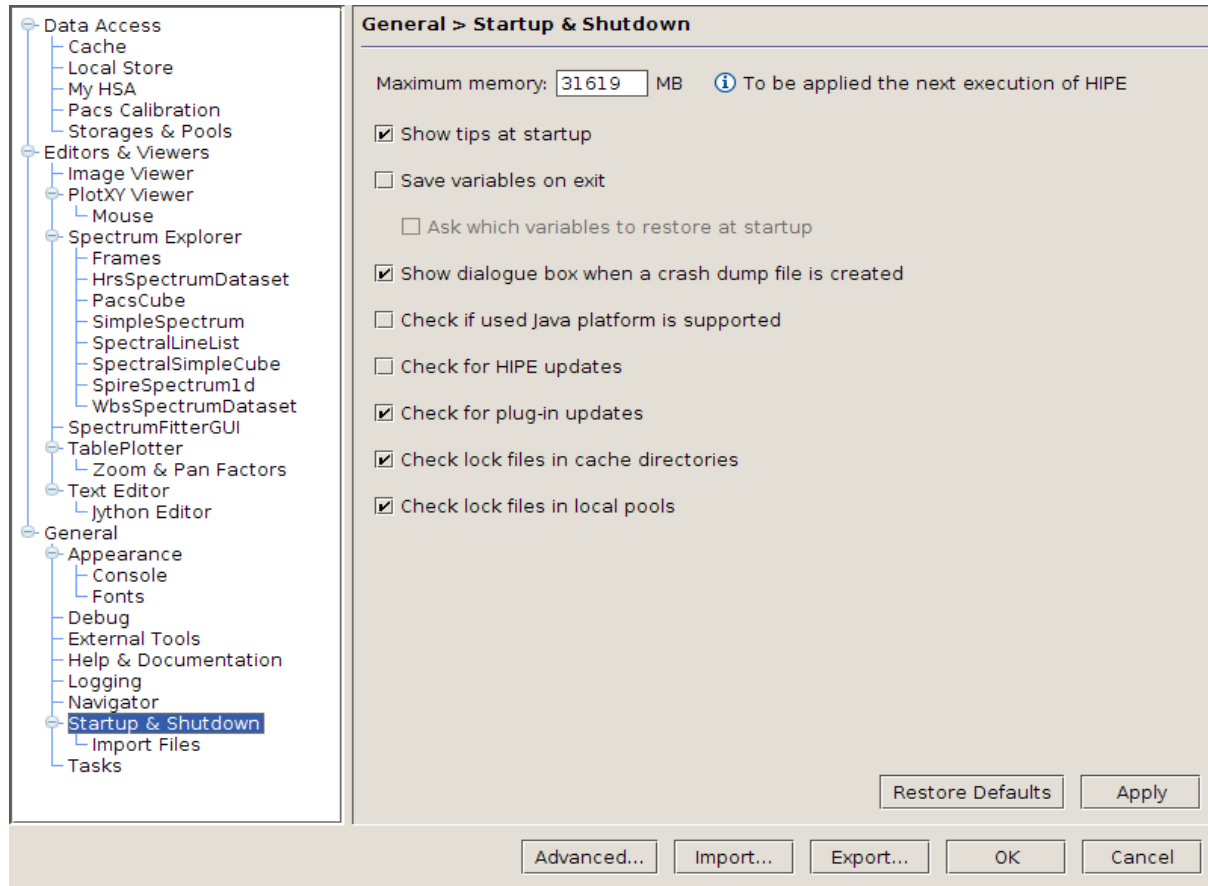
A pop-out window with the version appears



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

Memory used and available

Then click on Startup & Shutdown and change the amount of memory



**General > Startup & Shutdown**

Maximum memory:  MB ⓘ To be applied the next execution of HIPE

- Show tips at startup
- Save variables on exit
  - Ask which variables to restore at startup
- Show dialogue box when a crash dump file is created
- Check if used Java platform is supported
- Check for HIPE updates
- Check for plug-in updates
- Check lock files in cache directories
- Check lock files in local pools

Restore Defaults Apply

Advanced... Import... Export... OK Cancel

The allocated memory should be smaller than the total RAM of your computer. You have to exit and start a new session to use the new amount of memory.

# Step 2

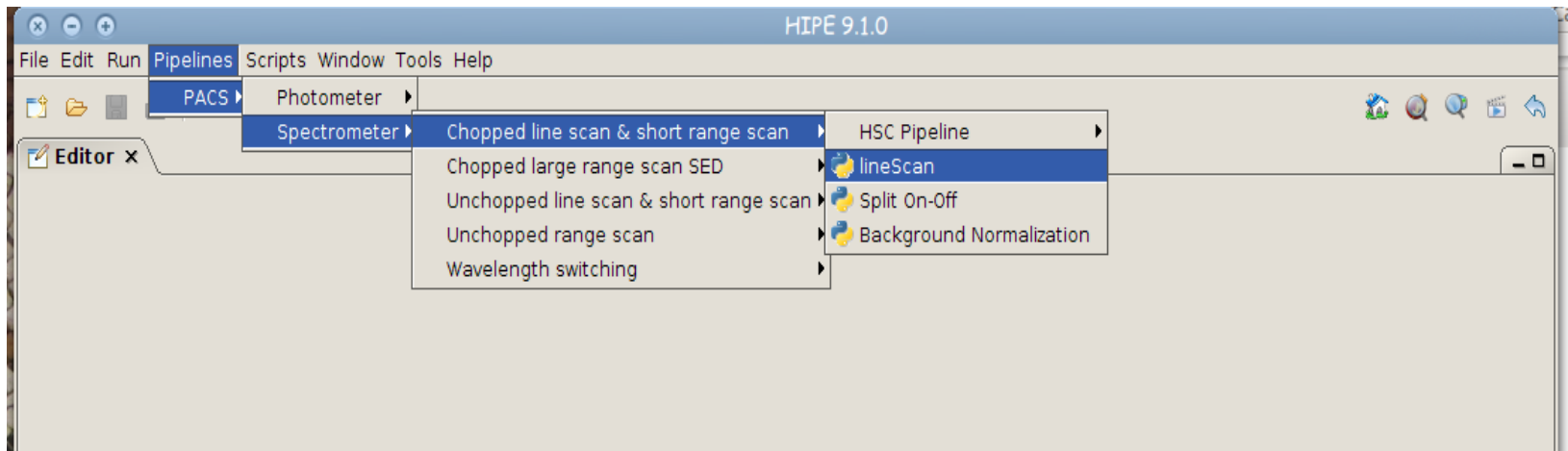
## Setup

Load pipeline script, load observation,  
check data, and select the camera



# Loading the script

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



There are two other interactive scripts available:

- a) Split on-off: allows one to have separate reductions of the on-source and off-source signals;
- b) Background Normalization: uses the emission of the telescope as reference signal to calibrate the signal

# Loading the script

In the case you saved a modified version and you want to load it for analysis of other data, you can access it directly from HIPE clicking on the yellow "folder" icon.

File Edit Run Pipeline Window Tools Help

Look In: 2011A

allocate_memory.png	help.dp
allocate_memory0.png	helphipe.png
<b>ChopNodExtendedSource_WORKSHOPVERSION.py</b>	helpwindow.png
details.aspx	ipipe.png
getData.py	PACS-103.pdf
getObservationHSAINT.py	pacs-202.pdf

File Name: ChopNodExtendedSource\_WORKSHOPVERSION.py

Files of Type: All Files

Open Cancel

Click the icon

Select the file.

Open it.

# Loading the observation

Once the script is loaded, one can simply step through the lines to execute it one by one. The first thing to do is loading the OBSID relative to the observation chosen.

In the case of this tutorial, the observations has been already saved into a pool which has to be put into your `~/.hcss/lstore` directory which is created once installing HIPE. The only thing to do is to write the correct obsid number and then start clicking the green arrow ....

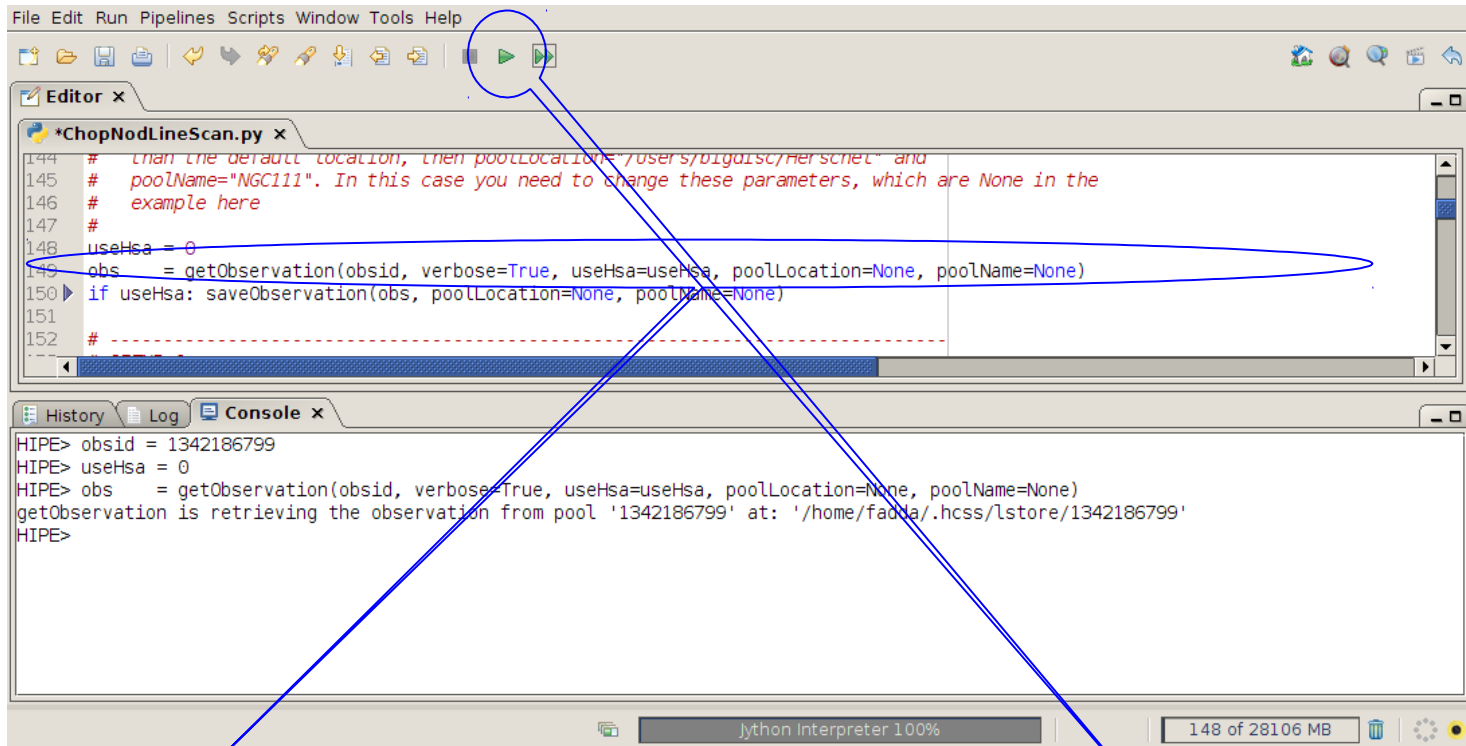
```
File Edit Run Pipelines Scripts Window Tools Help
*ChopNodLineScan.py x
102
103 # -----
104 # GET THE DATA: load the Observation Context with the data of your observation
105 #
106 # First, set the OBSID of the observation to process. CHANGE THE OBSID here to
107 # your own.
108 #
109 # As this script is also run as part of the ChopNod multiObs script(s), the
110 # following "if" tests for the existence of a variable called multiObs, which
111 # will be present if you are running the multiObs script. If multiObs is
112 # present, the obsid will have been set already, and if not then the obsid is set
113 # here. (If you get a NameError, then the obsid had not been set.)
114 if ((not locals().has_key('multiObs')) or (not multiObs)):
115     obsid = 1342188943
116
117     obsid = 1342186799
118
```

Add this line and click on it.

Hit the arrow

# Loading the observation

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



Click on this line.

Hit the arrow

# Observation summary

```
History | Log | Console x
HIPE> obsSummary(obs)

Observation summary
OBSID: 1342186799
Instrument: PACS
AOR label: NearGalPACS-SB-01-blue
Proposal: SDP_esturm_3
Target: M82
Redshift: 0.000677 (z)
Concat.: Undef.
OD: 178
Start: Sun Nov 08 07:31:26 PST 2009
Duration: 582.0 seconds (incl. spacecraft on-target slew time)

AOT and instrument configuration
AOT: PacsLineSpec
Mode: Pointed, Chop/Nod
Bands: B3A + R1 (prime diffraction orders selected)
Is bright: YES (shortened spectral range mode)
Chopper: large throw
Nod cycles: 1

Observation request summary (HSpot Line/Range Editor Table)
Number of requested primary lines/ranges: 2
List of requested primary line centres [microns]:
Line/range 1 : 63.223 microns, 3 repetitions, ID OI 63
Line/range 2 : 57.359 microns, 3 repetitions, ID NIII 57
```

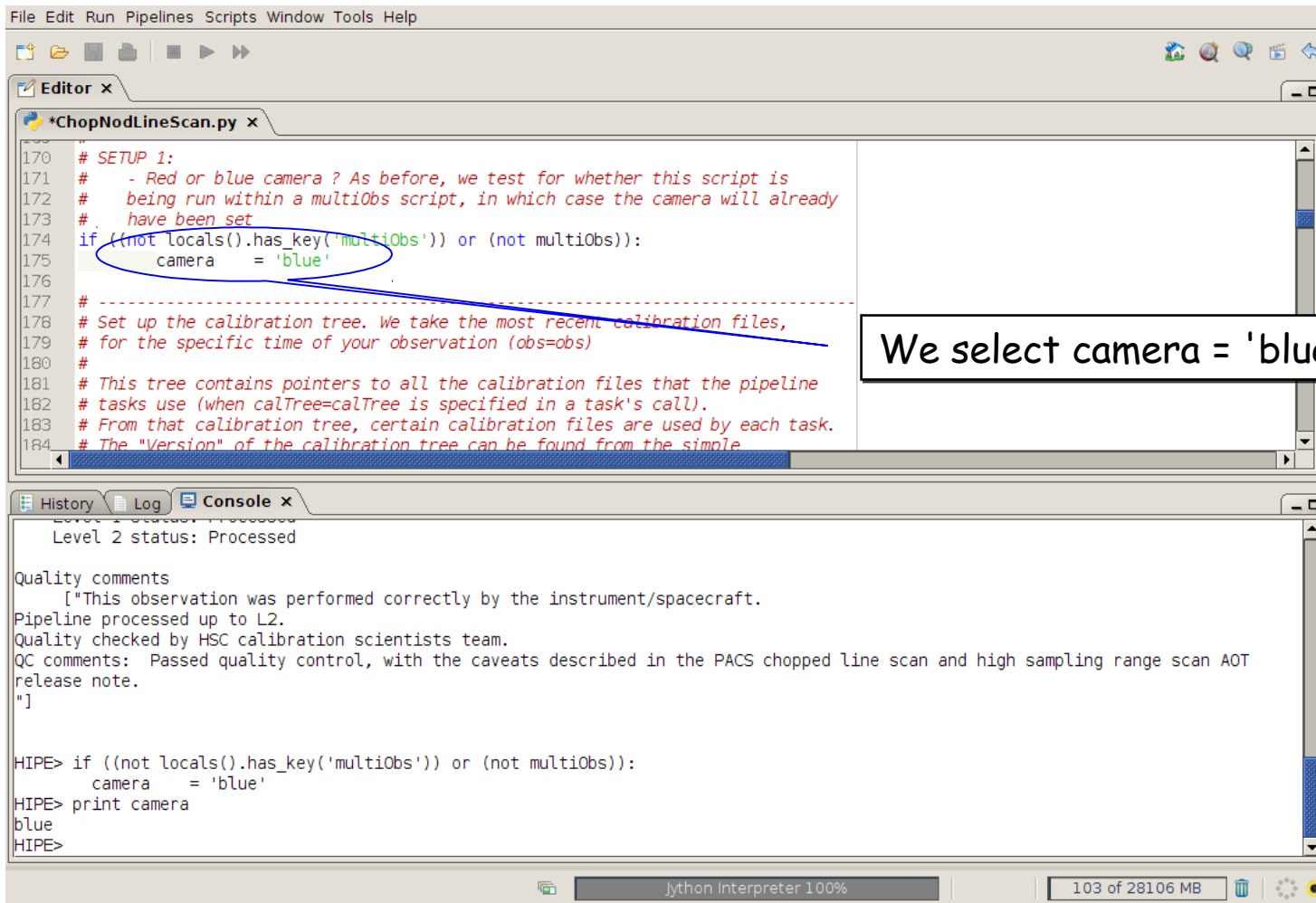
We will select: camera = 'blue'

Unless you know exactly what is in your data, after loading them it is advisable to inspect them. You can do this from the console by writing:

`obsSummary(obs)`

In this case, we discover that two lines have been observed in the blue range of the PACS spectrometer. So, we will have to select the "blue" camera otherwise we will just reduce the parallel "red" data.

# 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"

Finally, we set the calibration tree.

```
File Edit Run Pipelines Scripts Window Tools Help
UnchoppedRangeScan.py x
192 # corresponds to.
193
194 calTree = getCalTree(obs=obs)
195 if verbose:
196     print calTree
197     print calTree.common
198     print calTree.spectrometer
...
History Log Console x
HIPE> print obs.meta["calVersion"]
{description="Version of Calibration Tree", string="PACS_CAL_32_0"}
HIPE> if verbose:
    print calTree
    print calTree.common
    print calTree.spectrometer
PACS Calibration Tree
Model  : FM
Scope  : BASE
Version: 41
Branches: [common, photometer, spectrometer]
PacsCalCommon Calibration Products:
chopperAngle          : FM, 3
chopperAngleRedundant : FM, 3
chopperJitterThreshold : FM, 2
chopperSkyAngle       : FM, 2
csResistanceTemperature : FM, 1
filterWheel2Band      : FM, 2
Python Interpreter 100% 56 of 28106 MB
```

Read the time stamp of our obs and apply the calibration from the used distribution.

Version 41 and later ones incorporate several improvements wrt version 32 (archive reduction)

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

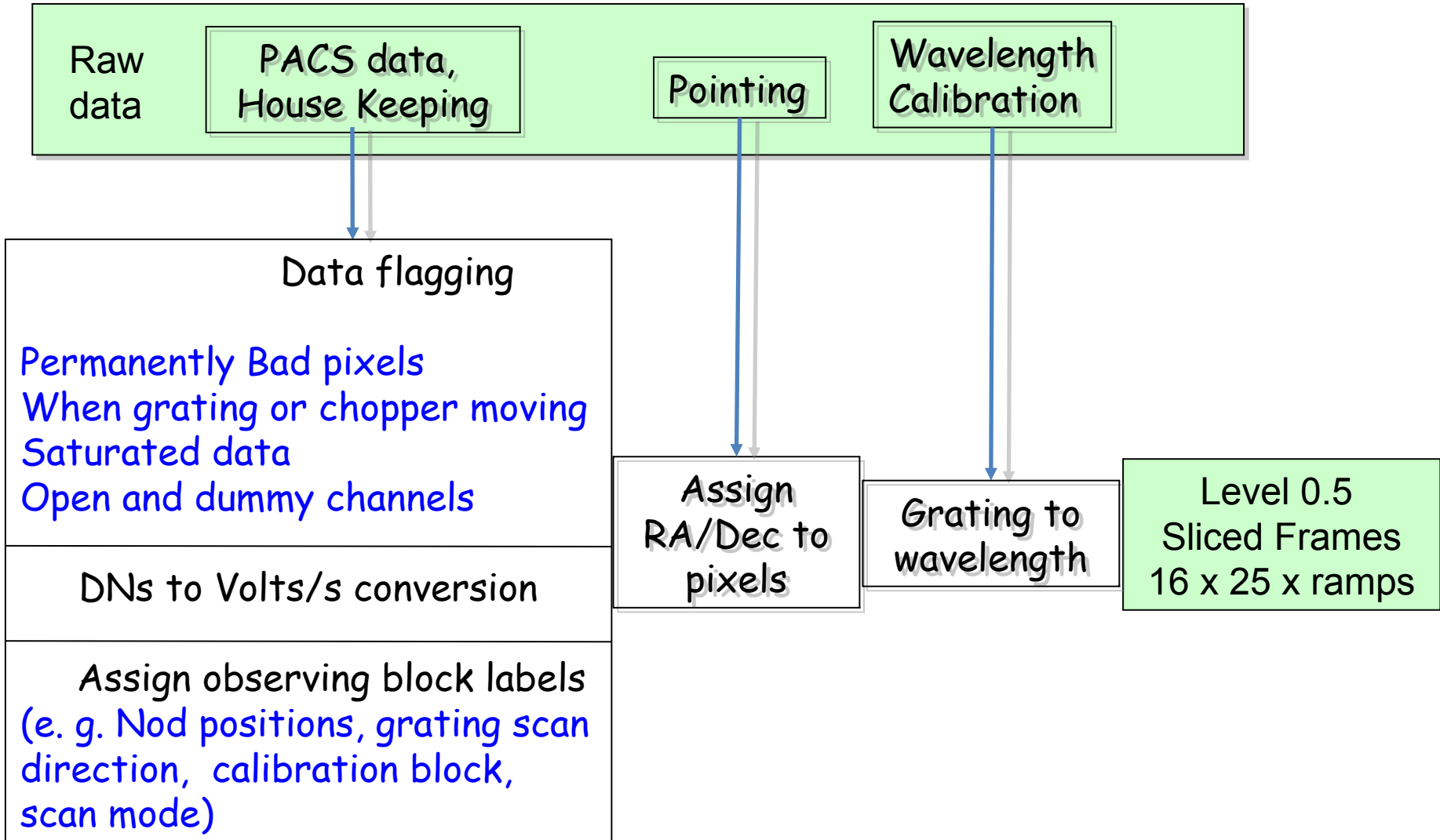
# Step 3

Run the 0 → 0.5 pipeline

Basic calibration (pointing,  
wavelength calibration, slicing)

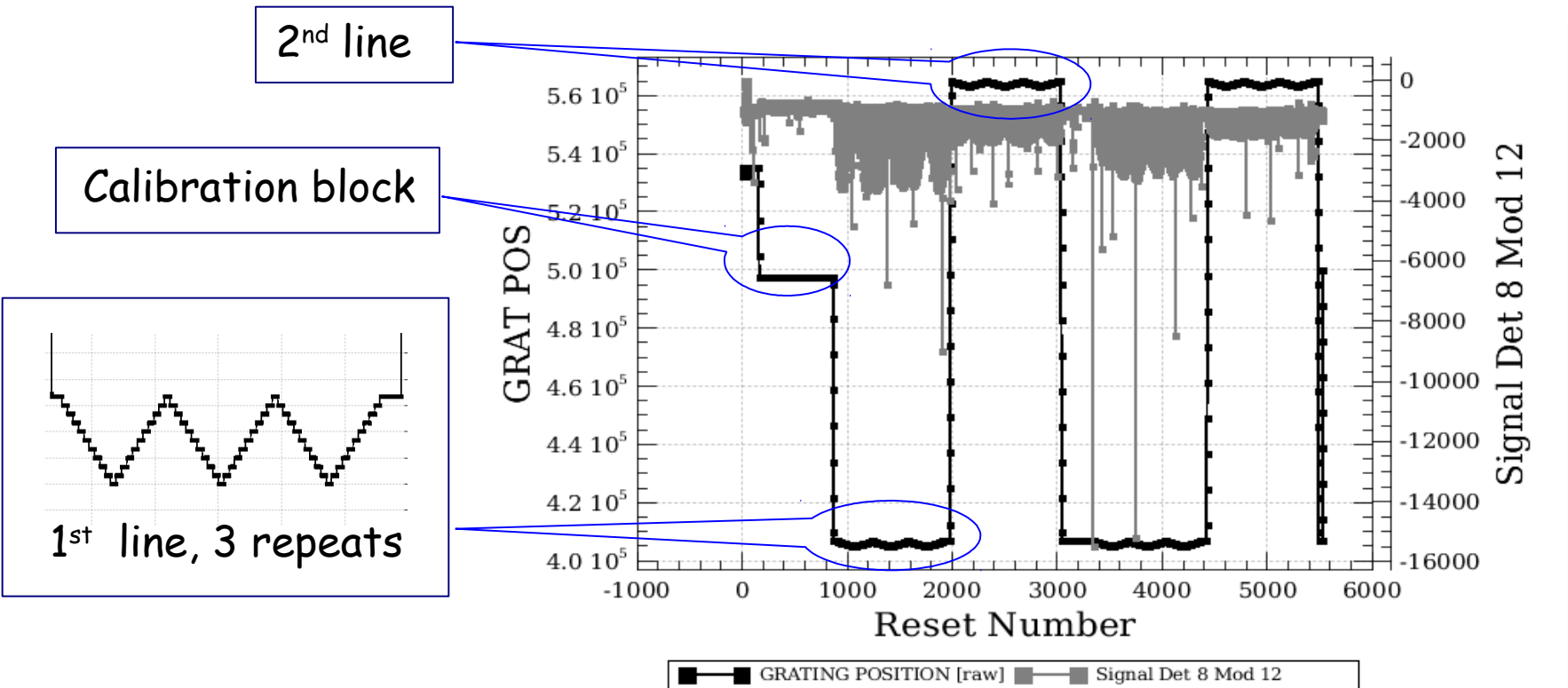


# Level 0 → 0.5



# 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.

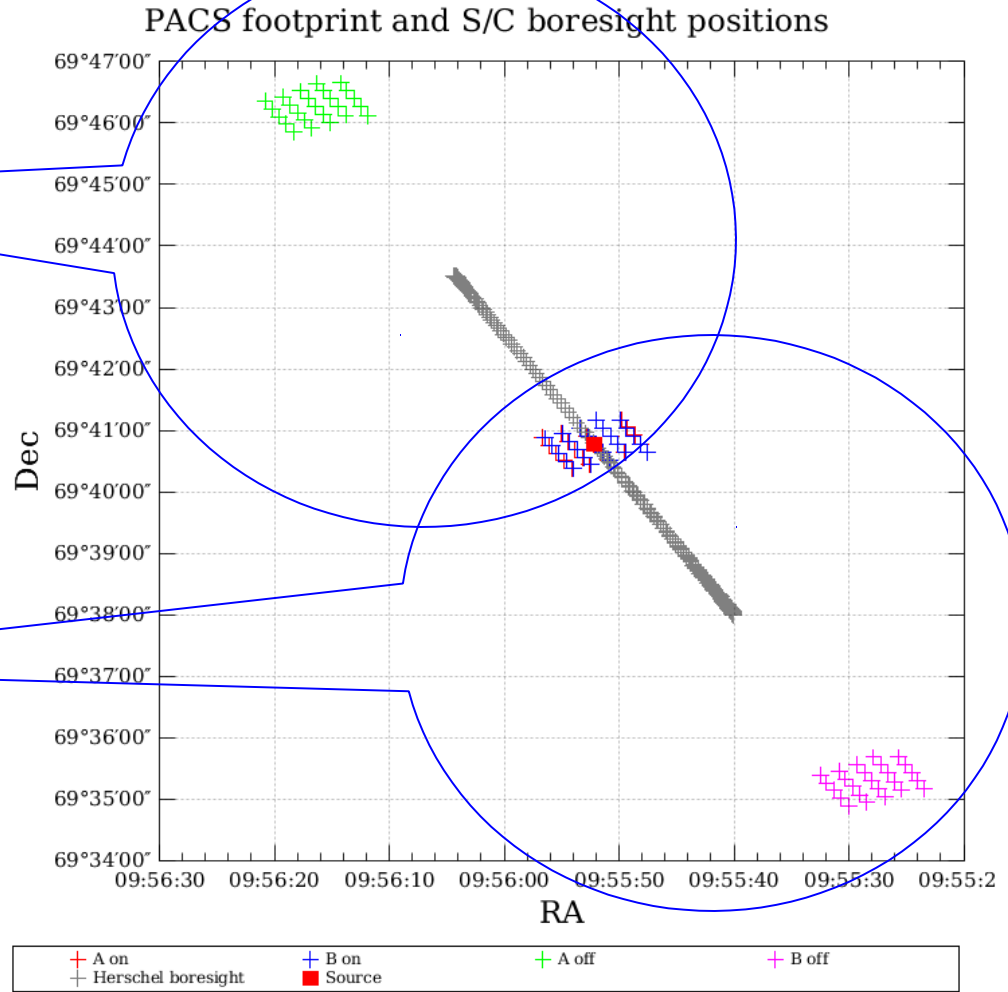


In our case, after the calibration block, we can identify two different lines observed 3 times in the two nod positions.

# Check: footprint

Nod A

Nod B



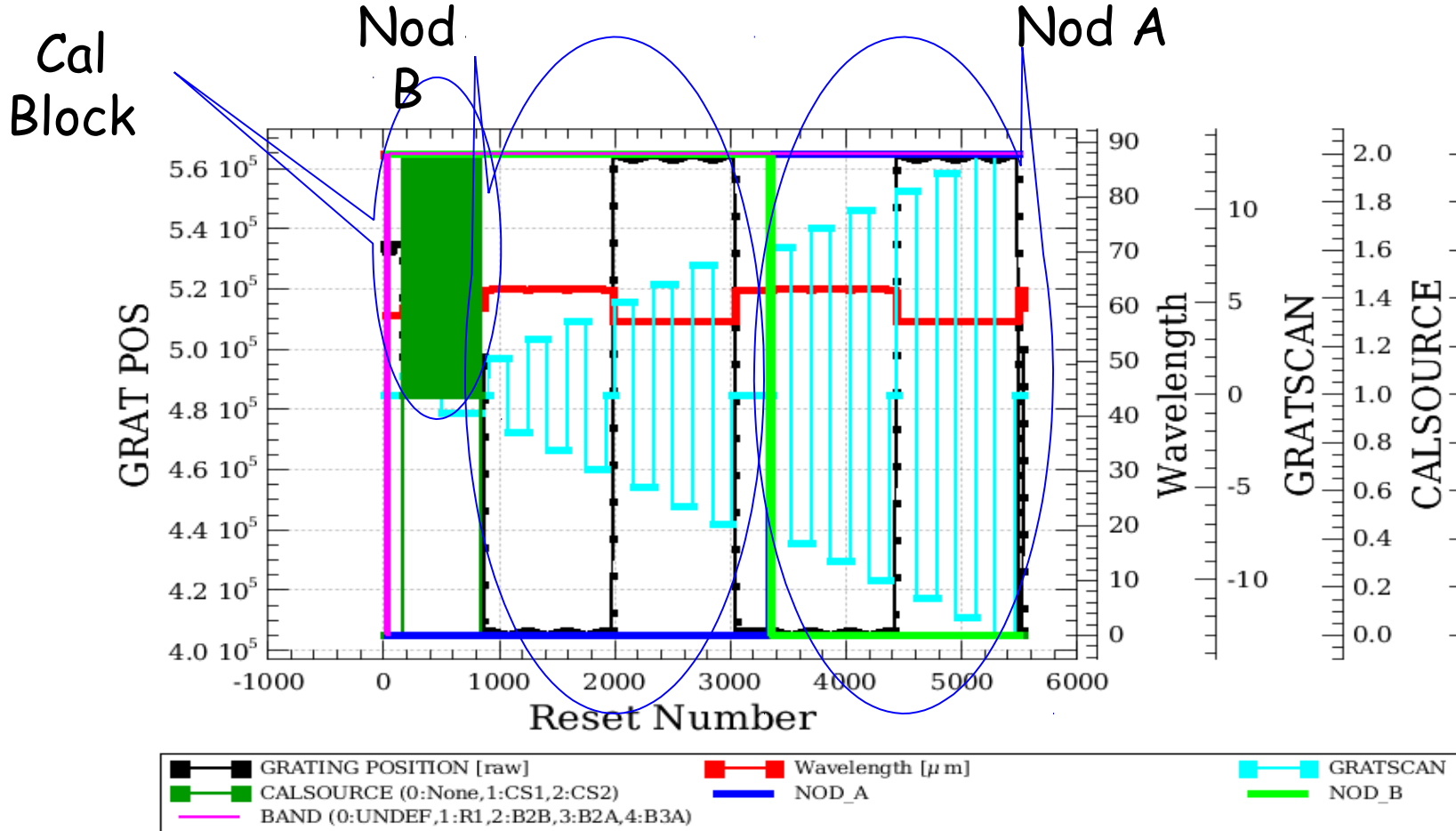
# Check: before slicing

Only 1 slice

```

History Log Console x
HIPE> slicedFrames = flagChopMoveFrames(slicedFrames, dmcHead=slicedDmcHead, calTree=calTree)
HIPE> slicedFrames = flagGratMoveFrames(slicedFrames, dmcHead=slicedDmcHead, calTree=calTree)
HIPE> if verbose:
    # Summary of the slices
    slicedSummary(slicedFrames)
    # Summary of the active (1) and inactive (0) status of every Mask
    maskSummary(slicedFrames)
    # Plot the instrument movements, without the signal
    p1 = slicedSummaryPlot(slicedFrames,signal=0)
noSlices: 1
noCalSlices: 1
noScienceSlices: 0
slice# isScience nodPosition nodCycle rasterId lineId band dimensions wavelengths
onSource offSource
0 false ["","A","B"] 0 0 0 [0,1,2,3] ["B2B","B3A","UNDEF"] [18,25,5536] 57.213 - 88.133 both
both
Nb of slices: 1
Slice 0
BLINDPIXELS 1
SATURATION 1
RAWSATURATION 0
NOISYPIXELS 0
BADPIXELS 1
UNCLEANCHOP 1
GRATMOVE 1
Slice edges: [0,5536]
HIPE>
    
```

# Check: before slicing



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

# Slicing

```
*ChopNodLineScan.py x
299
300 # Slice the data by Line/Range, Raster Point, nod position, nod cycle,
301 # on/off position and per band.
302 # The parameter removeUndefined is for cleaning purposes
303 # Virtually any column in the "BlockTable" can be used as a SlicingRule, but do
304 # not modify the SlicingRules if you are not 100% aware of what you are doing!
305 ► rules = [SlicingRule("LineId",1),SlicingRule("RasterLineNum",1),SlicingRule("RasterColumnNum",1),\
306           SlicingRule("NoddingPosition",1),SlicingRule("NodCycleNum",1),SlicingRule("IsOutOfField",1),SlicingRule("Band",1)]
307 slicedFrames = pacsSliceContext(slicedFrames, slicingRules = rules, removeUndefined=1)
308
```

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.

# Check: after slicing

5 slices !

```

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>
  
```

Line 1 - B & A nodes

Line 2 - B & A nodes

# Check: after slicing

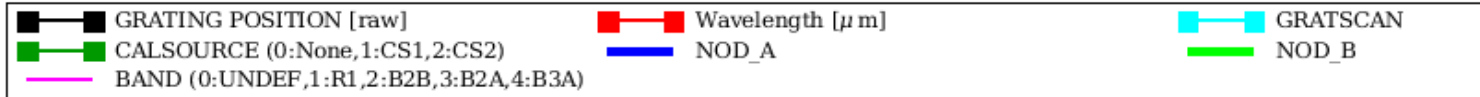
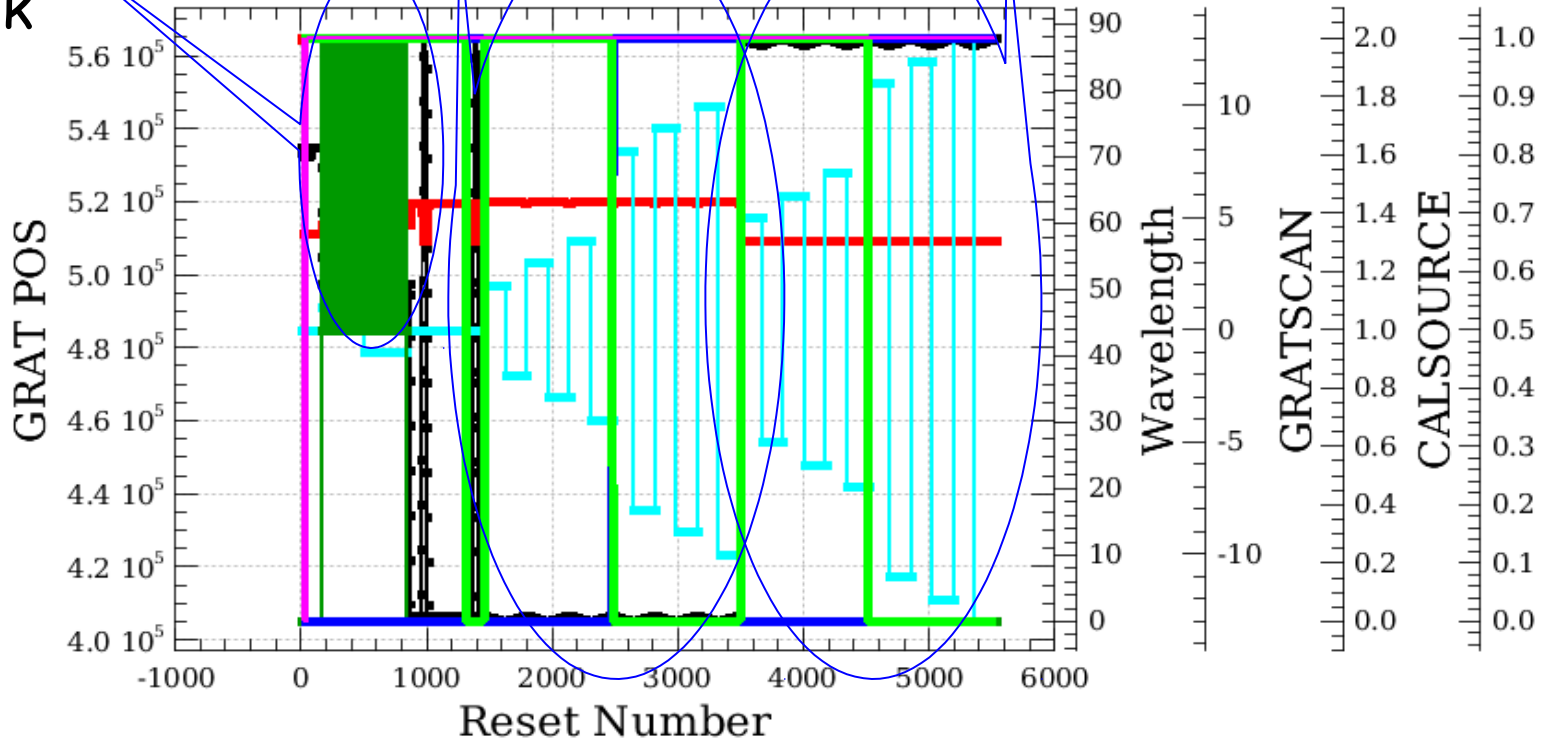
Cal  
Block

Line 1: OIII

Line 2: NIII

63

57



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

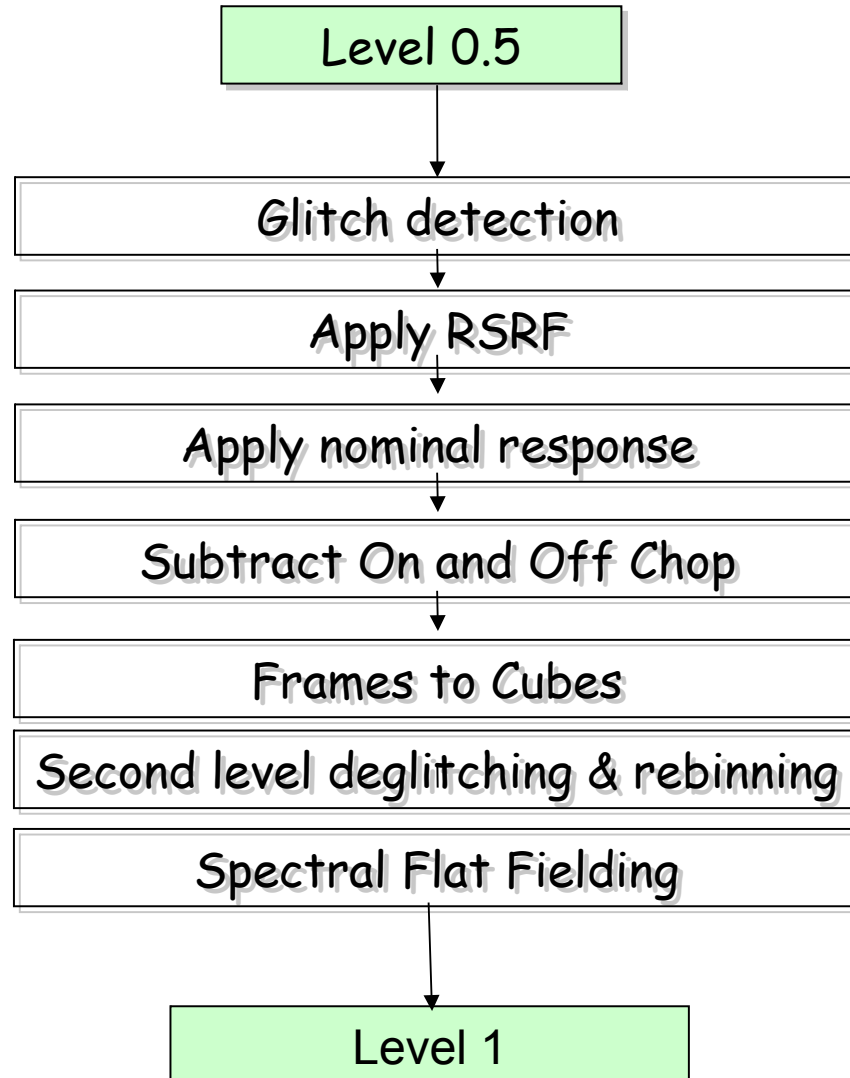


# Step 4

Run the 0.5 → 1 pipeline

Glitch detection, chop differentiation, RSRF, flat

# Level 0.5 → 1



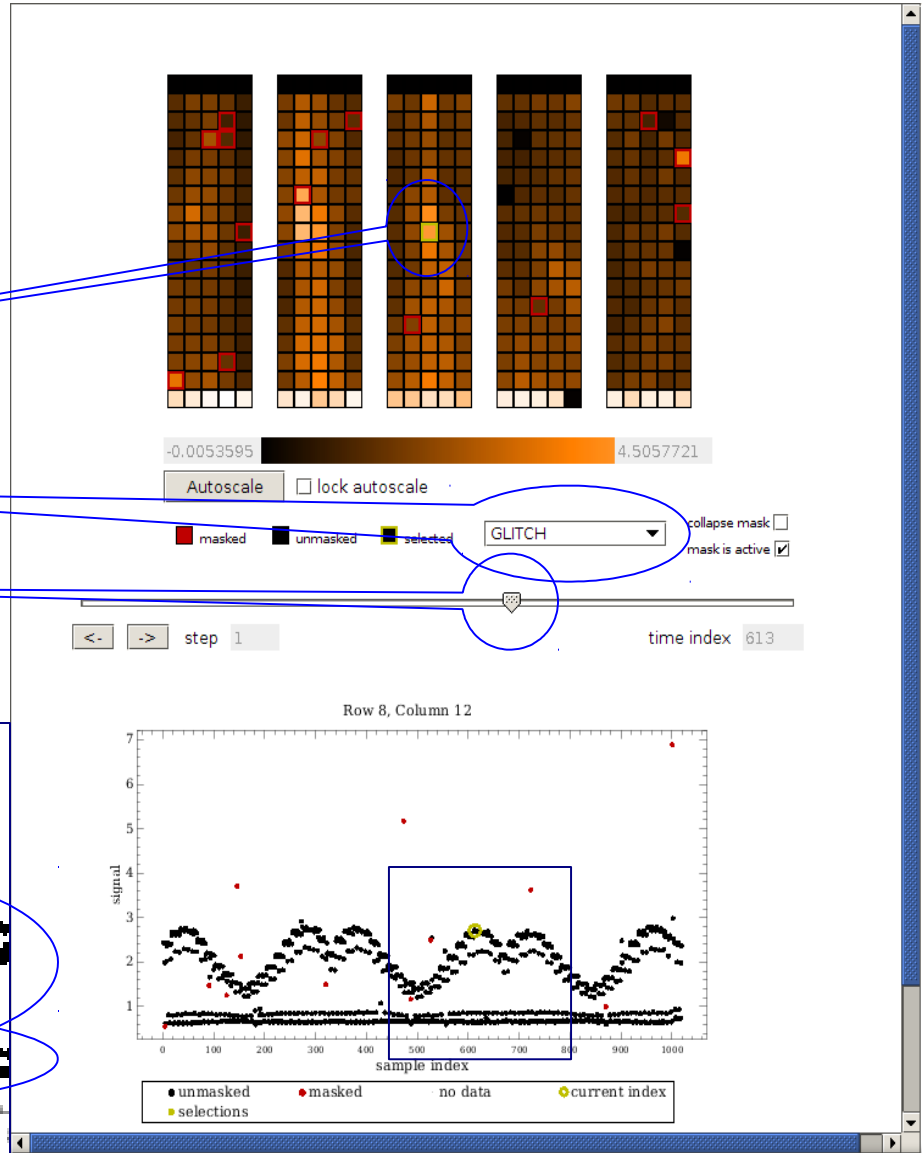
# Glitch detection

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

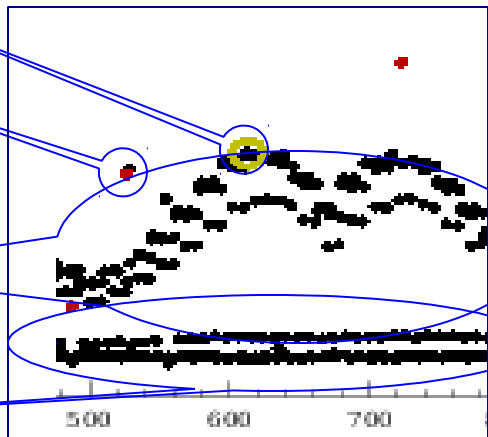


Current frame

Masked glitch

ON signal

OFF signal



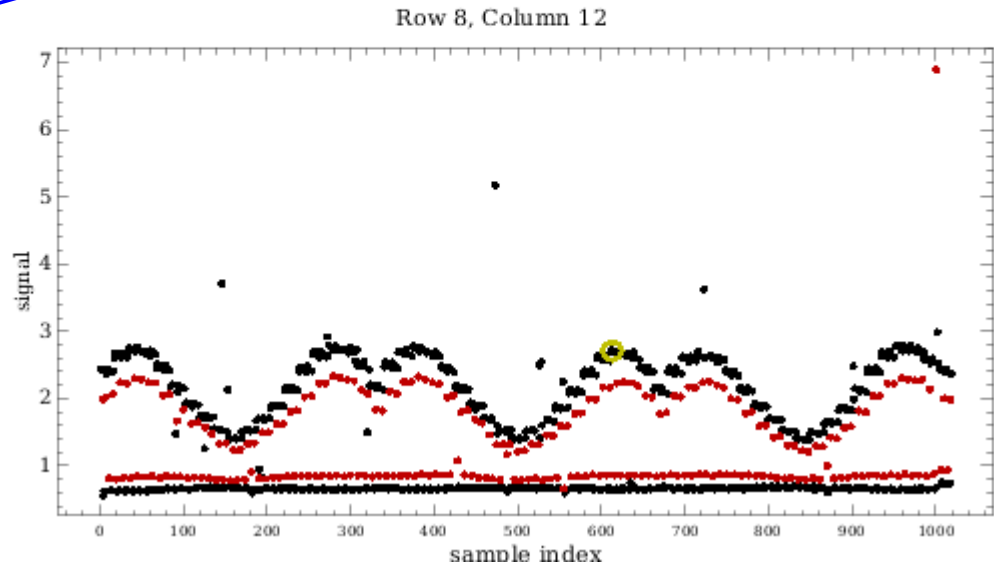
# More masks

It is possible to explore other masks

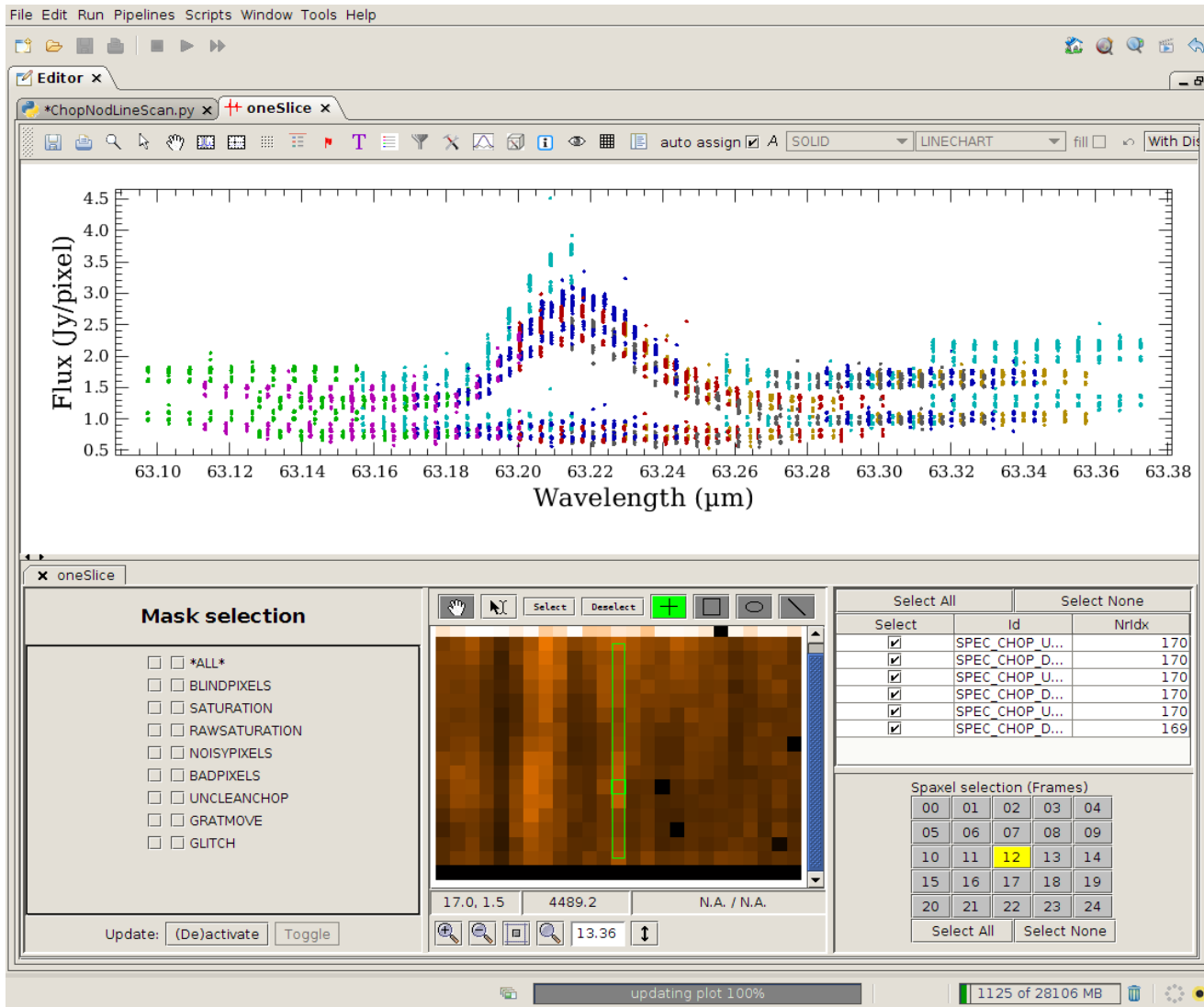
masked unmasked selected **UNCLEANCHOP** collapse m mask is ac

<- -> step 1 time index

Select unclean chop



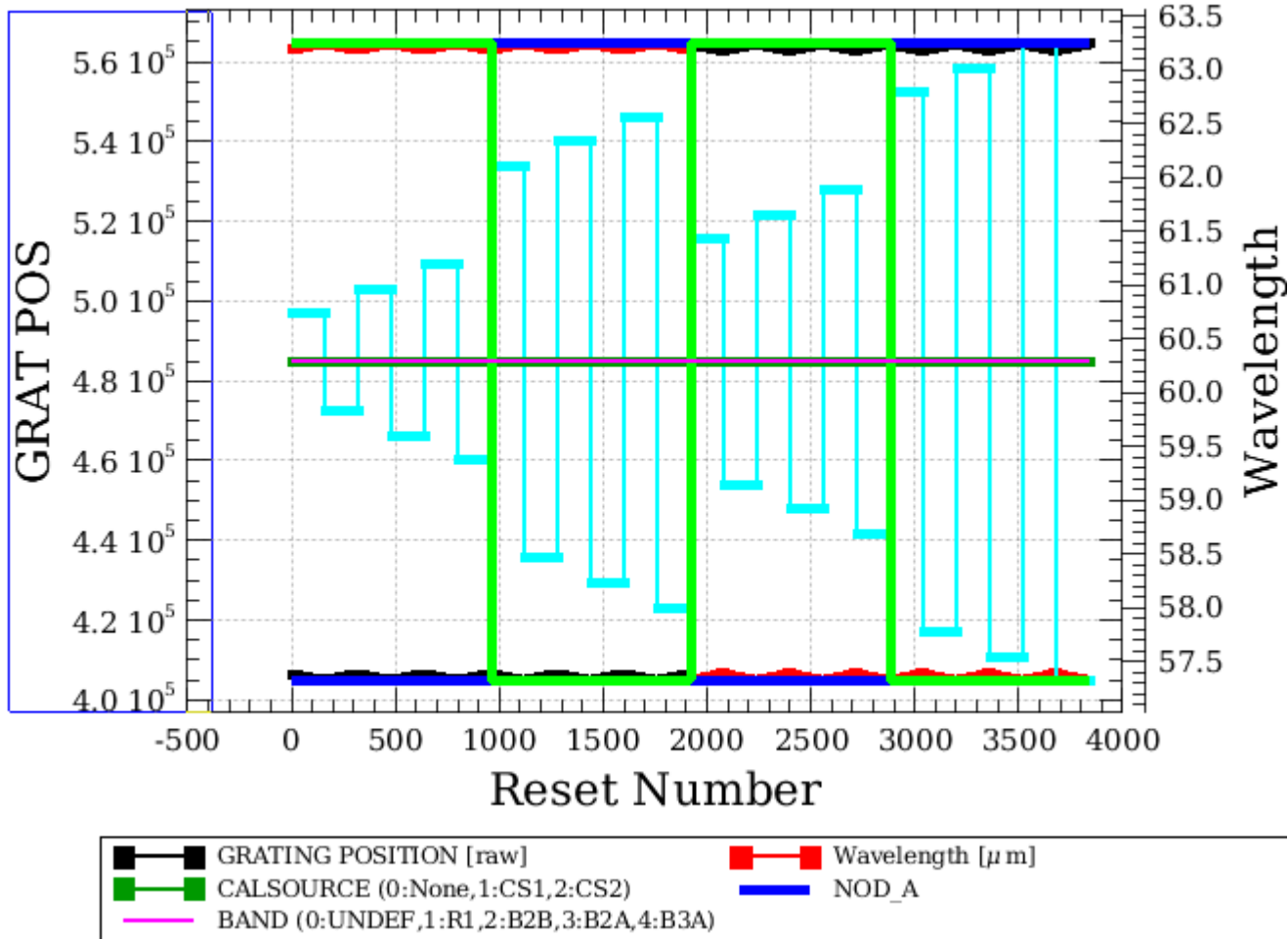
In this case, it is clear why there is a second group of points for the ON and OFF positions. These corresponds to signals obtained when the chopper was not yet in the correct position.



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.

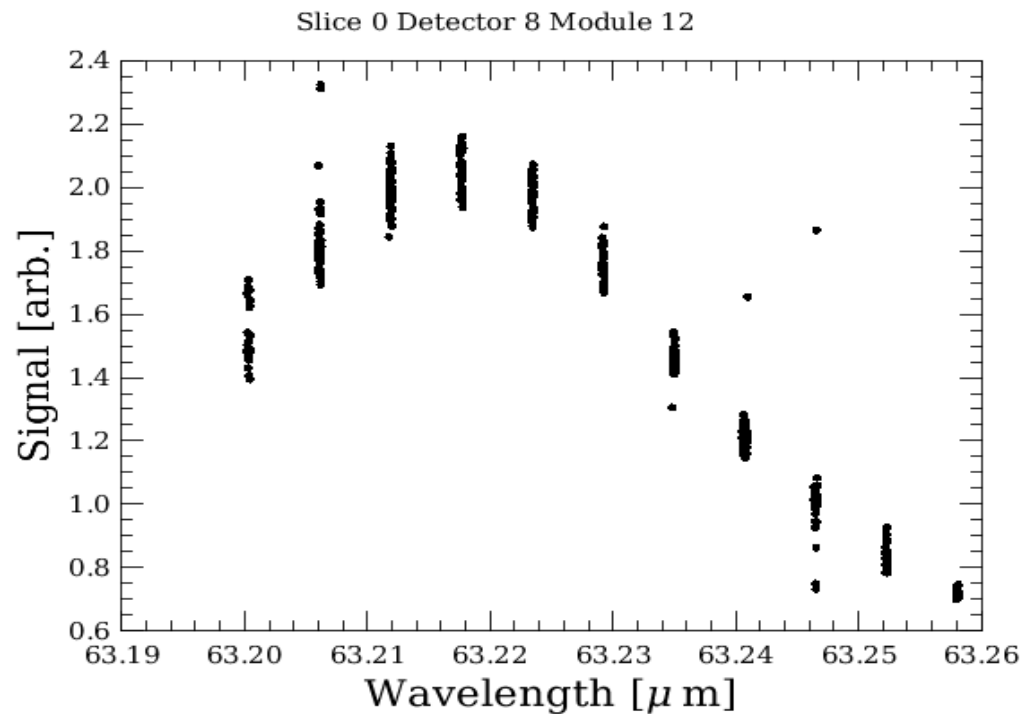
# Chop differentiation

After chop differentiation, the calibration block is excluded from the data



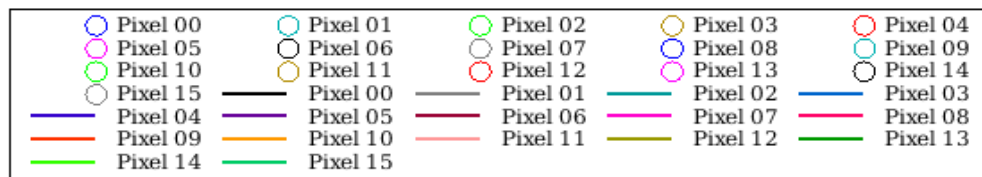
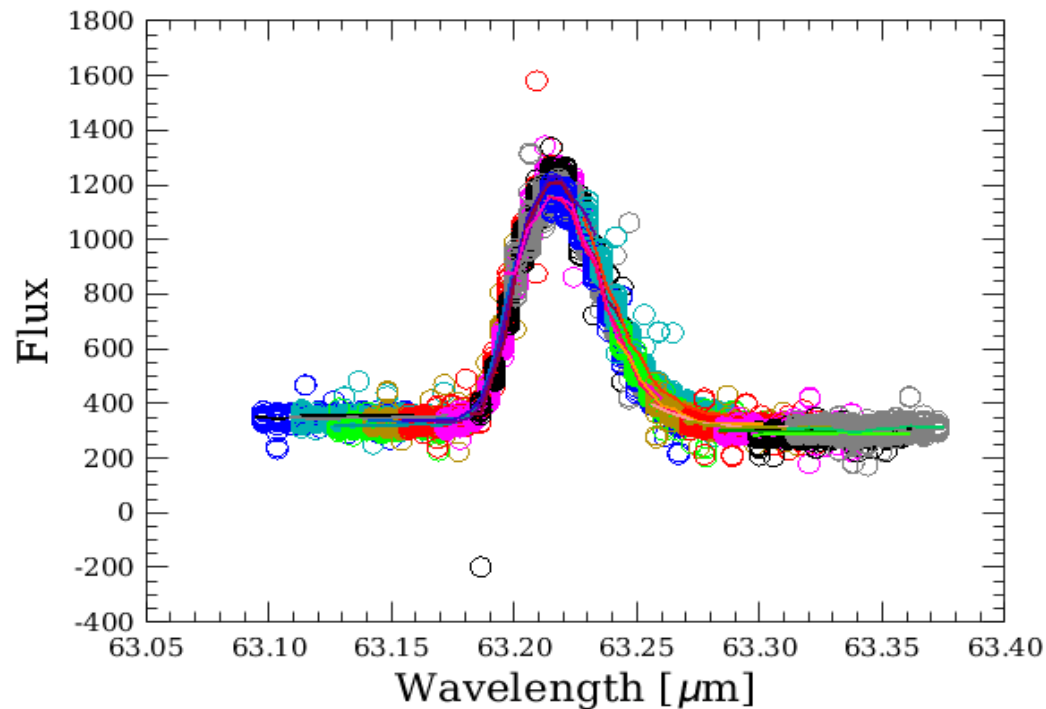
# Chop differentiation

The data are only on the ON position (OFF being subtracted)



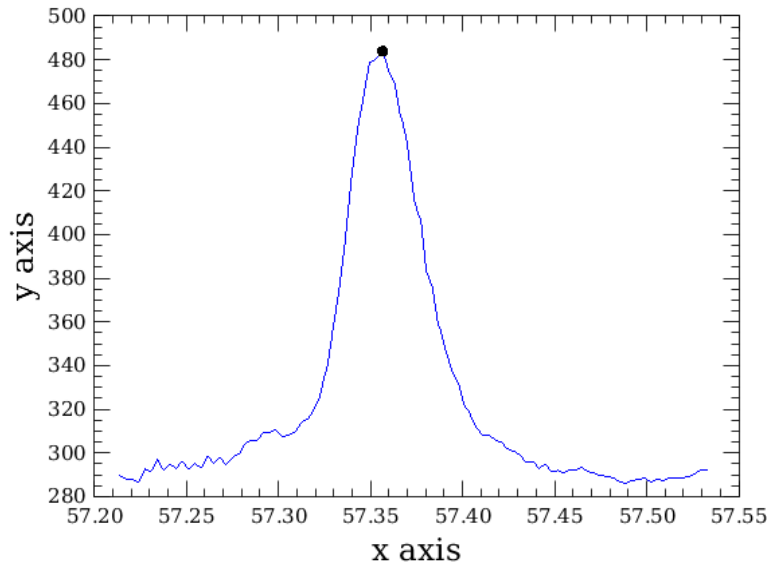
# RSRF and response

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



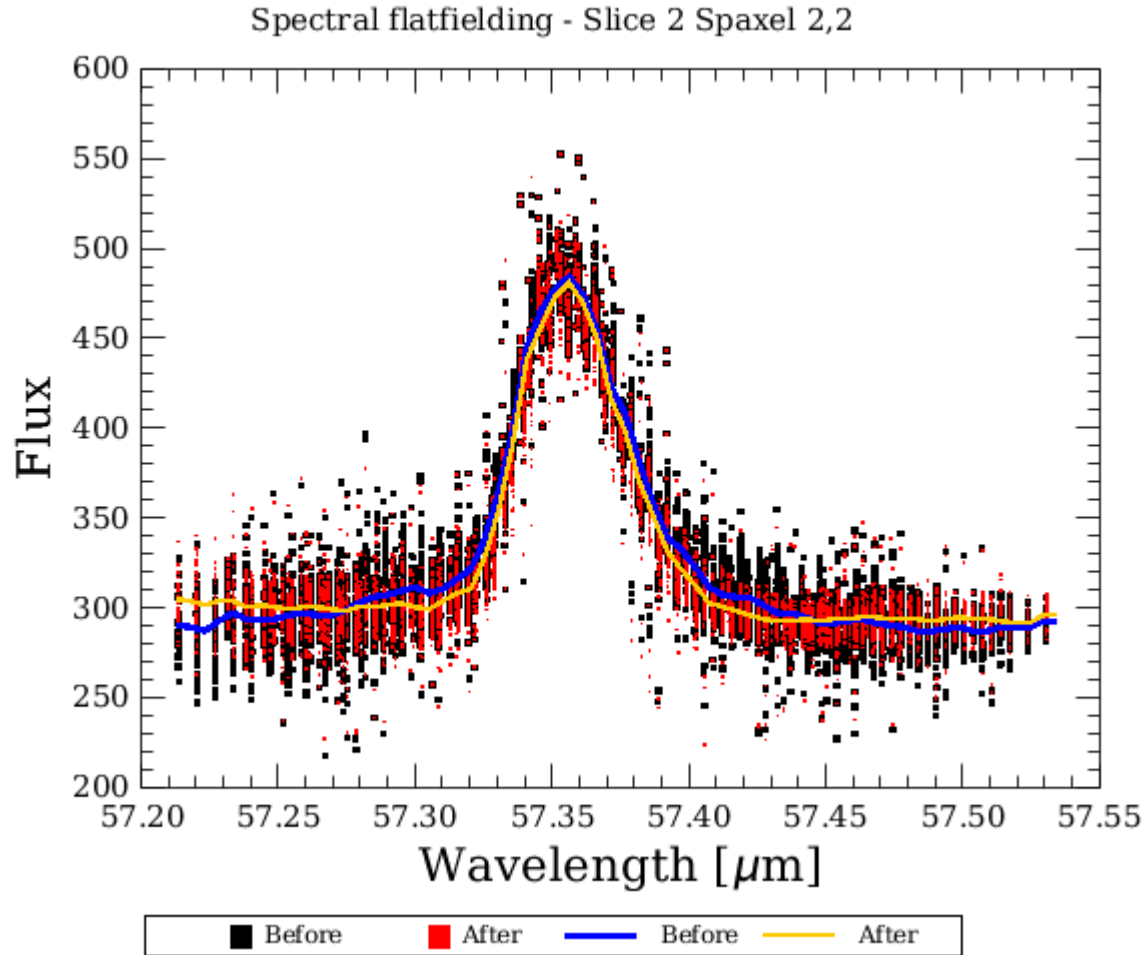


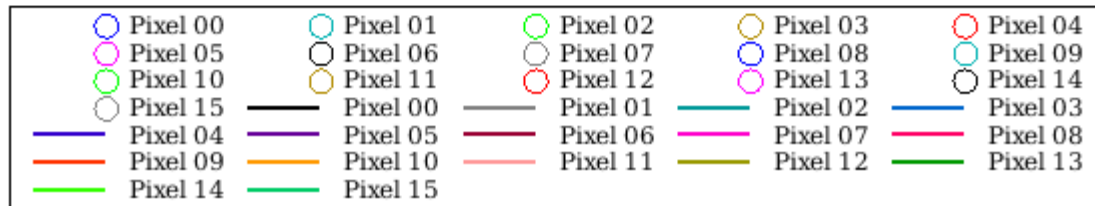
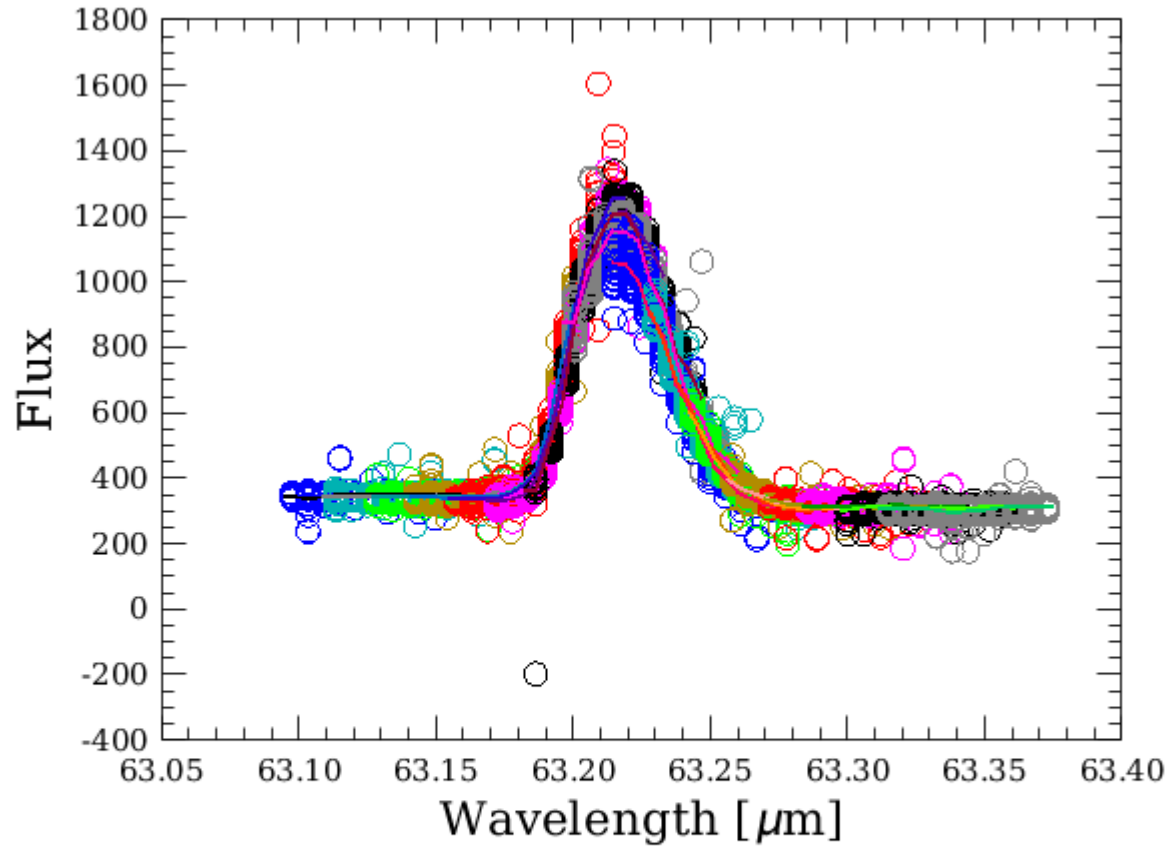
# Spectral FlatField



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 = [57.36]`, for instance.

# Spectral FlatField





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