



NHSC/PACS Web Tutorials Running the PACS Spectrometer pipeline for CHOP/NOD Mode

PACS-301 Level 0 to 1 processing

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page 1

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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







Step 1Check HIPE version and memoryStep 2SetupStep 3Run the $0 \rightarrow 0.5$ pipelineStep 4Run the $0.5 \rightarrow 1$ pipeline

page 3

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Step 1

Check HIPE version and memory allocation The version used for the tutorial is 6.0.1932

page 4

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page 5

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



page 6

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		Concerls Status & Shutdawa
	 Data Access Local Store My HSA Pacs Calibration Storages & Pools 	Maximum memory: 7168 MB (1) To be applied the next execution of HIPE
	 ➡ Editors & Viewers ‒ Image Viewer ‒ Jython Editor 	Show tips at startup
Then click on	 ● PlotXY Viewer └ Mouse ● Spectrum Explorer 	Save variables on exit
Startup &	 HrsSpectrumDataset SpectralSimpleCube 	Ask which variables to restore
Shutdown and	- SpireSpectrum1d - WbsSpectrumDataset	🗹 Inform about dump files
change the	- TablePlotter Zoom & Pan Factors	Check Java platform
amount of	General	Check for updates
memory	- Console - Fonts - Window - Help & Documentation - Navigator	
		Restore Defaults Apply
	,J	Advanced Import Export OK Cancel

The allocated memory should be smaller than the total RAM of yourcomputer

PACS 301





Step 2

Setup

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

page 8

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Loading the script



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



We added a few lines to load the correct set of data and make a few further checks before starting the reduction.

page 9

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Loading the script



The modified script can be found at the IPAC website: ADD WEBSITE HERE

To load the script into your hipe session, just click on the loading icon as shown in the figure. The search the location where you put the file using the pop-up window and finally load it into the session.

File Edit Run Pipeline Window Tools Help		
	Look <u>I</u> n: 2011A	-
	allocate_memory.png	help.dp
	allocate_memory0.png	helphipe.png
	ChopNodExtendedSource_WORKSHOPVERSION.py	🗅 helpwindow.png
	detail s.aspx	🗋 ipipe.png
	🗋 getData py	PACS-103.pdf
	getObservationHSAINT.py	🗋 pacs-202.pdf
Click the icon.	1	
	File <u>Name:</u> ChopNodExtendedSource_WORKSH0	DPVERSION.py
Select the file.	Files of Type: All Files	~
Open it.		Open Cancel
page 10	hsc.ipac.caltech.edu/help	odesk PACS 301



Loading the observation



Once the file is loaded, one can simply step through the lines to execute it one by one. In this tutorial, we will explain how to modify some lines to explore different observations and lines and to check the results of the main operations on the data. 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.





Loading the observation



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







page 13

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Setting the camera



Once we decide the line to explore, we can set the camera to blue or red.

File Edit Run Pipeline Window Tools Help				
	2	Q	Q	۵ 🗟
Editor × Find/replace				
ChopNodERSION.py ×				
<pre>if verbose: obsSummary(obs) if verbose: obsSummary(ob</pre>				
149 #				
We select camera = 'blue'				

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Setting the calibration tree



File Edit Run Pipeline Window Tools Help







Step 3

Run the $0 \rightarrow 0.5$ pipeline

Basic calibration (pointing, wavelength calibration, slicing)

page 16

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Level $0 \rightarrow 0.5$





page 17

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Extracting level-0 data



🥏 Cho	ppNodExRSION.py ×		
164			
165	#		
166	# Extract the level-0 products from the ObservationContext		
167	# Get and prepare the level0 product that you will pipeline on.		
168	# First we copy the metadata from the ObservationContext to the level0 pro	duct	
169	# Then we extract the level0 product from the ObservationContext		
170	pacsPropagateMetaKeywords(obs,'0', obs.level0)		202
171	level0 = PacsContext(obs.level0)		
172			
173	# For your camera, extract the Frames (scientific data), the rawramps (raw data		
174	# for one pixel), and the DMC header (the mechanisms' status information,		
175	# sampled at a high frequency)		
176	<pre>slicedFrames = SlicedFrames(level0.fitted.getCamera(camera).product)</pre>		
177	slicedRawRamp = level0.raw.getCamera(camera).product		
178	<pre>slicedDmcHead = level0.dmc.getCamera(camera).product</pre>		
179			
180	if verbose:		
181	# Get an overview of the basic structure of the data, prior to any proce	ssing	
182	slicedSummary(slicedFrames)		
183	# Plot the grating position & raw signal of central pixel		
184	p0 = slicedSummaryPlot(slicedFrames,signal=1)		
185			- -
			-

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.

```
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```



Check: level 0



Let's check first the basic structure of the data. It is important to verify if the observation has been performed correctly.



In our case, after the calibration block, we can identify two different lines observed 3 times in the two nod positions. <u>nhsc.ipac.caltech.edu/helpdesk</u> PACS 301

page 19



Some flagging



🟓 Ch	opNodExRSION.py ×	
186	#	•
187	# Processing Level 0 -> Level 0.5	
188	#	
189		
190		
191	# flag the saturated data in a mask "SATURATION" (and "RAWSATURATION": this	
192	# uses the raw data we get for some pixels)	1
193	# used cal files: RampSatLimits and SignalSatLimits	
194	slicedFrames = specFlagSaturationFrames(slicedFrames, rawRamp = slicedRawRamp, calTree=calTree)	
195		
196	# Convert digital units to Volts, used cal file: Readouts2Volts	
197	<pre>slicedFrames = specConvDigit2VoltsPerSecFrames(slicedFrames, calTree=calTree)</pre>	
198		
199	# Identify the calibration blocks and fill the CALSOURCE Status entry	
200	<pre>slicedFrames = detectCalibrationBlock(slicedFrames)</pre>	
201		
202	# Add the time information in UTC to the Status	
203	<pre>slicedFrames = addUtc(slicedFrames, obs.auxiliary.timeCorrelation)</pre>	
204		-
▲		

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Adding pointing products



🟓 Cho	pNodExRSION.py ×	
204		
205	# Add the pointing information to the Status	
206	# Uses the pointing, horizons product (solar system object ephemeries),	
207	# orbitEphemeris products, and the SIAM cal file.	
208	# NOTE for SSOs: you should contact the HSC helpdesk to check whether the	
209	# pointing is currently correctly handled for moving objects.	
210	<pre>slicedFrames = specAddInstantPointing(slicedFrames, obs.auxiliary.pointing, calT</pre>	ree = calTree, orbit
211		
212	# Extend the Status of Frames with the parameters GRATSCAN, CHOPPER, CHOPPOS	1991
213	# used cal file: ChopperThrowDescription	
214	slicedFrames = specExtendStatus(slicedFrames, calTree=calTree)	
215		
216	# Convert the chopper readouts to an angle wrt. focal plane unit and the sky	
217	# and add this to the Status, used cal files: ChopperAngle and ChopperSkyAngle	
218	slicedFrames = convertChopper2Angle(slicedFrames, calTree=calTree)	
219		
220	# Add the positions for each pixel (Ra and Dec datasets)	
221	# used cal files: ArrayInstrument and ModuleArray	
222	slicedFrames = specAssignRaDec(slicedFrames, calTree=calTree)	
223		
224	if verbose:	
225	# show footprint of your observation	
226	slicedPlotPointing(slicedFrames)	-

At this point, astrometry is added to the data. At each pixel a coordinate is assigned and we can check if the pointing was performed correctly.



Check: footprint





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PACS 301

page 22



Masks and wav. calibration



🟓 Cho	opNodExRSION.py ×	
228 229 230	<pre># Add the wavelength for each pixel (Wave dataset), used cal file: WavePolynomes slicedFrames = waveCalc(slicedFrames, calTree=calTree)</pre>	<u>^</u>
231 232 233	<pre># Correct the wavelength for the spacecraft velocity. # Uses the pointing, orbitEphemeris and timeCorrelation product. slicedFrames = specCorrectHerschelVelocity(slicedFrames, obs.auxiliary.orbitEphememerie)</pre>	eris, obs.auxiliary
234 235 236 237	<pre># Find the major logical blocks of this observation and organise them in the # BlockTable attached to the Frames; used cal file: ObcpDescription slicedFrames = findBlocks(slicedFrames, calTree = calTree)</pre>	
238 239 240 241 242	<pre># Flag the known bad or noisy pixels in the masks "BADPIXELS" and "NOISYPIXELS" # used cal files: BadPixelMask and NoisyPixelMask # -> by default the bad pixels will be excluded later when final cubes are buil slicedFrames = specFlagBadPixelsFrames(slicedFrames, calTree=calTree)</pre>	t, the noisy pixels
243 244 245 246 247	<pre># Flag the data affected by the chopper movement in the mask "UNCLEANCHOP" # Uses the high resolution Dec/Mec header and the cal files ChopperAngle and Chop slicedFrames = flagChopMoveFrames(slicedFrames, dmcHead=slicedDmcHead, calTree=cail</pre>	<i>perJitterThreshold</i> lTree)
248 249 250 251	<pre># Flag the data effected by the grating movement in the mask "GRATMOVE" # Uses the high resolution Dec/Mec header and the cal file GratingJitterThreshold slicedFrames = flagGratMoveFrames(slicedFrames, dmcHead=slicedDmcHead, calTree=cal</pre>	lTree)
252	if verbose:	
253	# Summary of the slices boxr6745454te slicedSummary(slicedErames)	
255 256	# Summary of the active (1) and inactive (0) status of every Mask maskSummary(slicedFrames)	
257 258	<pre># Plot the instrument movements without the signal included p1 = slicedSummaryPlot(slicedFrames,signal=0)</pre>	-
		•

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Check: before slicing



]	📮 Console 🗙						
Only 1		HIPE> if verbose:						
clico		# Summa	ry of the slice	s				
Silce		slicedSum	mary(slicedFram	es)				
		# Summary	of the active	(1) and in	active (0)	status of e	every Mask	
		maskSumma	ry(sliced⊢rames)			- d = -d	
		# Plot th	e instrument mo	vements wi licedEreme	thout the	signal inclu `	laea	
		$ \dots $ br = sric	easummaryPlot(s	liced⊢rame	s,signat=⊍)		
		noSlicos 1						
		noCalSlices. 1)					
		noScienceSlices	0					
		slice# isScience	nodPosition	nodCvcle	rasterId	lineId	band	
		dimensions w	avelengths			11.1010		
		0 false	["","A","B"]	0	0 0	[0,1,2,3]	["B2B","B3A","UNDEF"]	
		[18,25,5536] 5	7.213 - 88.119					
		Nb of slices: 1						
		Slice 0						
		BLINDPIXELS	1					
		SATURATION	1					
		RAWSATURATION	Θ					
		NOISYPIXELS	0					
		BADPIXELS	1					
			1					
		GRAIMOVE	1					333
		SLICE edges: [0,	[9530					
		HINE>						

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

page 25

PACS 301









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.

page 26

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Check: after slicing



	E Console ×				
5 slices !	HIPE> rules = [SlicingRule("LineId",1),Slicing ngRule("NoddingPosition",1),Slic Rule("Band",1)] HIPE> slicedFrames = pacsSliceCo	Rule("Rasto ingRule("No ntext(slico	erLineNum" odCycleNum edFrames,	,1),SlicingR ",1),Slicing slicingRules	ule("RasterColumnNum",1),Slici Rule("IsOutOfField",1),Slicing = rules)
	HIPE> if verbose: slicedSummary(slicedFram p2 = slicedSummaryPlot(s noSlices: 5	es) licedFrame:	s,signal=0)	
Line 1 – B & A	noCalSlices; 1 noScienceStices: 4 slice# isScience nodPosition	nodCycle	rasterId	lineId	band
nodes	dimensions wavelengths 0 false ["","B"] [18 25 1460] 57 213 - 88 119	0	0 0	[0,1]	["B2B","B3A","UNDEF"]
	I true ["B"] [18,25,1019] 63.093 - 63.379	1	0 0	[2]	["B3A"]
Line 2 – B & A	2 true ["A"] [18,25,1019] 63.093 63.379	1	0 0	[2]	["B3A"]
nodes	3 true ["B"] [18,25,1019] 57.213 - 57.548	1	0 0	[3]	["B3A"]
	4 true ["A"] [18,25,1019] 57.213 - 57.548	1	0 0	[3]	["B3A"]
	Slice edges: [0,1460,2479,3498, HIPE>	4517,5536]			<u>></u>

page 27

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

page 28

PACS 301





Step 4

Run the 0.5 → 1 pipeline Glitch detection, chop differentiation, RSRF, flat

page 29

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Level 0.5 \rightarrow 1





page 30

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Deglitching



- cin			
297 298 299	<pre># De-activate all masks before running the glitch flagging slicedErames = activateMasks(slicedErames String1d([" "]) exclusive = True)</pre>		
300			
301 302	lf verbose: maskSummary(sliced⊢rames,slice=0)		
803	# Detect and flag glitches ("GLITCH" mask)		
304 305	<pre>slicedFrames = specFlagGlitchFramesQTest(slicedFrames)</pre>		
306			
307	if verbose:		
308	slicedSummary(slicedFrames)		-999-
309	# Summary plot, including the signal		
310	p3 = slicedSummaryPlot(slicedFrames,signal=1)		
311	# Plot of signal vs wavelength for the central pixel for a single slice (you can c	hose any s	5
812	# Detector signal: you will see the on and off chop spectral data together		
813	# on this plot, as they have not been subtracted from each other yet		
814	# (compare this plot to p6 below)		
B15	slice = 1		
816	<pre>p4 = plotSignalBasic(slicedFrames, slice=slice)</pre>		
817	# Inspect timeline of signals and masked signals via a viewer		
318	MaskViewer(slicedFrames.get(slice))		
R10_			┦┻┤

At this point, a deglitching code creates a glitch mask. Sometimes, this deglitching can be too aggressive. It is therefore possible to ignore this mask and detect outliers using data redundancy (see tutorial level $1 \rightarrow$ level 2)

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Glitch detection





page 32

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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.

page 33

PACS 301



Chop differentiation



🥏 Cho	pNodExRSION.py ×
348	
349	# Compute the differential signal of each on-off pair of datapoints, for each chopper cycle
350	# The calibration block is cut out of the slicedFrames, so only the scientific slices remain.
351	<pre>slicedFrames = specDiffChop(slicedFrames, scical = "sci", keepall = False, normalize=False)</pre>
352	
353	if verbose:
354	# Data Structure. Only science blocks are left
355	slicedSummary(slicedFrames)
356	p5 = slicedSummaryPlot(slicedFrames,signal=0)
357	# Detector signal: signal is now differential, with the offs having been
358	# subtracted from the ons (compare to p4 above)
359	p6 = plotSignalBasic(slicedFrames, slice=0)
360	
361	

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

page 34

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Chop differentiation





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page 35



Chop differentiation



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



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page 36



RSRF, response, flat field



PACS 301

nopNodEx...RSION.py 🗙

```
373
374
     # Divide by the relative spectral response function
375
     # Used cal files: rsrfR1, rsrfB2A, rsrfB2B or rsrfB3A
376
     slicedFrames = rsrfCal(slicedFrames. calTree=calTree)
377
378
     # Divide by the response
379
     # Used cal file: nominalResponse
380
     slicedFrames = specRespCal(slicedFrames, calTree=calTree)
381
382
     if verbose:
383
             slice = 0
384
             frame = slicedFrames.get(slice)
385
             module = 12
386
             flux = frame.signal[1:17,module,:]
387
             wavelengths = frame.wave[1:17, module,:]
388
             pwave = PlotXY( line=Style.NONE,titleText="Slice "+str(slice),subtitleText=" Module "+str(md
389
              for i in range(16):
390
                     pwave[i] = LayerXY(wavelengths[i,:], flux[i,:],line=Style.NONE,symbol=Style.DOT)
391
             del frame, wavelengths, flux
392
393
394
     # Refine the spectral flatfield.
395
     # Parameters:
          minWaveRangeForPoly (microns). If your spectral ranges are > this value, a poly is fit to the
396
     #
397
             spectra, of order "polyOrder", on a pixel by pixel basis independently for each module/spaxe
398
     #
             This (continuum) fit is then used normalise the individual 16 pixels to the module/spaxel me
399
     #
          minWaveRangeForPoly (microns). If your spectral ranges are < this values, the median of the spe
400
     #
             is calculated, on a pixel by pixel basis independently for each module/spaxel.
401
     #
             This value is then used normalise the individual pixels to the module/spaxel median.
402
     #
          --> the values of polyOrder and minWaveRangeForPoly can be adjusted by the user
403
     #
          In both cases the correction is a division.
404
405
     # See also the specFlatFieldRange URM entry and the PDRG Chap. 3 for more information.
406
     slicedFrames = specFlatFieldRange(slicedFrames,polyOrder=5, minWaveRangeForPoly=4., verbose=1)
   •
```



RSRF, response, flat field



Check of the central module (all spectral pixels)



RSRF & response

Flat field

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



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