PACS Data Reduction Guide

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PACS Data Reduction Guide

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Chapter 1. A First Quick Look at your Data

1.1. Introduction

Changes from version 3, May 2010: updated Chap. 5, minor changes Chap. 3.

Welcome to the PACS data reduction guide (*PDRG*) #. We hope you have got some good data from PACS and want to get stuck in to working with them. In this guide we will (i) show you how to have a first quick look at your HSA pipeline-reduced data, (ii) explain how data are gathered by PACS and hence how they are structured, and summarise the pipeline steps, (iii) show you how to go through the pipeline yourself, (iv) show you how to inspect the products you produce as you proceed through the pipeline, and (v) discuss issues that are of concern for particular AOTs (such as rastering, moving targets, point-vs-extended sources), or which are still under development, or which require longer explanations.

This guide is aimed at those who are new to HIPE and new to PACS, and it is the first PACS data reduction document you should read. A companion to this guide is the *PACS Advanced Pipeline Topics* (or something similar), available from the HIPE help pages. It will take a while to get used to HIPE and to reducing PACS data, so allow yourself a lot of patience. Satellite sub-mm data are complex because the detectors and the observing requirements are, and the pipeline has to deal with this. Our aim with this guide is to teach by doing: we will take you through the pipeline as a tutorial, so you can learn what to do and how to inspect what you have done. Along the way we will explain the what and the why of the data reduction. We recommend you run though the pipeline once following this guide, and then if you want to change some things you can run through it again on your own.

Once you are comfortable with working with the pipeline you may want to reduce your data following only the "ipipe" scripts—the interactive pipeline scripts that you can access via the "pipeline" menu of HIPE. Basic explanations are incorporated in these scripts, but they are not as detailed as in this data reduction guide.

HIPE is the Herschel Interactive data Processing Environment. HIPE is not just for running the pipeline, it provides an environment in which you can also analyse data using tools provided or by writing your own scripts. In HIPE you can write scripts to do any type of manipulation, mathematics, reformatting, analysis, or fitting on your data. Because it uses jython (python, java) it may be unfamiliar to many astronomers, but python and java both are languages that are well worth learning. Note that while python and java can be used within HIPE, the actual language is (H)DP, that is the (Herschel) Data Processing language. So some jython-ese will not work and there are additional capabilities that have been programmed into HIPE that are unique.

There are a number of other documents you should read before and along with this one. This may sound boring, but it is necessary. While the *PDRG* is meant to be complete, it is *not* stand-alone: we do not describe the elements of HIPE, the GUIs, and scripting, rather we direct you to the relevant documents.

The guides that introduce you to HIPE and to the post-pipeline capabilities of HIPE, and which are available from the Help page, are:

1) A guide to HIPE itself is the *HIPE Owners Guide* (*HOG*), and you should also see the *Quick Start Guide* (*QSG*) <LINK>. These tell you how to start up and work in HIPE and the easiest way to extract data from the Herschel Science Archive (HSA) and take a preliminary look at them.

2) The *Data Analysis Guide (DAG)* <LINK> tells you about the tools that are provided in HIPE for you to do your data analysis (everything you do after your pipeline data reduction) and inspection of your spectra, cubes or images.

3) The *Scripting and Data Mining* guide *(SaDM*) <LINK> contains a lot of information about working in HIPE with arrays, the DP syntax and working therein, doing mathematics, fitting, photometry and so on. This is recommended to be read after you have worked your way through the first chapters of this PACS guide: here we give specific examples of working in HIPE with your data and using the DP language, and there you can go for the more general instructions.

4) The HIPE help page also has a search capability, in which you can type in the names of tasks or acronyms that are unfamiliar to you.

More advanced documents are:

1) *PACS Advanced Pipeline Topics* (*PAPT*) <LINK> (or something similar). This discusses the details of the pipeline tasks (all the parameters and the algorithms) and includes more advanced topics that are too long to fit in the *PDRG*. It is still under construction.

2) The *Product Description Document* (*PDD*) <LINK>, a Herschel reference document, which describes the layout and terminology of the instrument-specific products. It is somewhat, but not overly, technical, and it describes the layers of the PACS products that we will refer to in the *PDRG*.

3) The HCSS and the PACS *User's Reference Manual*: these contain information about the tasks and classes provided in HIPE, and while written in a technical way the aim is that they can also be read by non-experts. The PACS *URM* contains most of the tasks written by the PACS team, the HCSS *URM* contains all the general tasks.

4) The *Developer Reference Manual* (a.k.a. API), which gives you information about the java classes that underlie the DP system. This will be very difficult to understand at first if you are not a (java or python) programmer, but hopefully some of the examples provided in this guide will also help you.

1.2. Structure of this guide

In this first chapter we explain how to get your observations from the HSA and look at your Level 2 product, that is data which has already been pipeline-processed. In Chapter 2 we summarise the data reduction steps from Level 0 (minimally processed) to Level 2 (science quality), and explain a little about how the data are structured. Chapter 3 takes you through the pipelines for the various spectrometer AOTs, with some detail about what you are doing at each stage and presenting you with inspection recipes. In Chapter 4 issues of concern for particular spectral AOTs or types of targets are discussed, and longer explanations are given for some pipeline-relevant information. Chapters 5 and 6 are the same as 3 and 4 but for the photometer.

Note that chapters 4 and 6 are not yet ready.

1.3. A quick-look at your data

Your observations have been performed, now you probably want to know what they look like. This section will show you how to grab the fully pipeline-processed data and look at them. If you then want to run the pipeline yourself you will read Chap. 3 and onwards; but it is a good idea to first have a quick look at your data, to at least see what it is you have be given!

For spectroscopy these fully processed products are cubes, that is data with two spatial axes and one spectral axis (the PACS spectrometer is an integral field spectrograph). If you are not familiar with looking at cubes we suggest you read up a little on integral field spectroscopy before you start working on your PACS data. For photometry the fully-processed data are a stack of frames (images/maps).

Start up HIPE. If you followed the installation instructions this should be a matter of simply typing "hipe" on your command line or clicking on an icon. To simply inspect PACS data you should be able to work with 2GB of memory assigned to HIPE, but for pipeline-processing or if you want to manipulate the data you almost certainly will need more, up to a few 10sGB if you have very large observations to reduce. To increase the memory allocation you can either change it on the HIPE command line—but the allocation will go back to default next time you start HIPE—or you can edit one of the "hcss properties files" before starting HIPE. For instructions, see the *HOG <LINK>*. If HIPE

runs low on memory (it has a tracking bar to show memory use) it will freeze and you may have to kill your session, so don't stint on allocating memory.

When you start up HIPE first go into the Work Bench or the Full Work Bench perspective, by clicking on the green or blue clapperboard icons on the top right of the HIPE GUI. The *HOG* tells you what the various tabs in the Work Bench are for and how to customise your view <LINK>. It is in the Console section of your work bench that you type commands.

1.3.1. First: the ObservationContext (a.k.a. your observation)

1.3.1.1. Definitions: ObservationContext and pool

To start working you of course need to get hold of your data. You will either have been given it by someone, possibly in the form of a tarball, or you will extract it from the HSA. After you have the entire dataset you need to read it into HIPE and at the same time extract from it the "ObservationContext". This ObservationContext contains your observation. It can be thought of as a container of data products that belong to a specific observation; and *ObservationContext* is the HIPE class of this container. This container provides the associations between all the products that you need to process that single observation. Within are the actual astronomical observation—raw and automatically pipeline-reduced—and the intermediate data products that were used to process the observation by the automatic pipeline, such as: spacecraft pointing, time synchronisation data, the satellite orbit, the parameters you entered in HSPOT when you submitted the proposal, and the pipeline calibration tables. The reduced data contained in the ObservationContext are spectra and spectral cubes, or images (spectrometer and photometer respectively); also provided should be a quality assessment of the observation/reductions.

When working with your observation in HIPE you can either hold it in memory the whole time, or you can periodically save the data to disc. The latter is recommended, because if HIPE crashes you will lose everything that was held in memory. To save small dataset to disc you can save them as single FITS files, but for larger datasets, including *ObservationContext*s, you need to save them to a "pool".

On disc a pool is simply a directory of data organised in a Herschel-unique way, and in HIPE a pool is a pointer to this directory. HIPE needs to have data organised in a very specific way so that it can work with them, for example so the associations between the individual products of an *ObservationContext* can be made. Hence the need for pools. By default HIPE expects the pool directories to be located off of [HOME]/.hcss/lstore. The data are held in these directories individually as FITS files, but, as already said, organised in a very specific way. Because the data in a pool are linked to each other, it is necessary to use the tasks we provide to inspect, query, and access them. You cannot simply read a single FITS file from a pool into HIPE and necessarily expect that you can do something with it. Note that you can have more than one observation and more than on type of Herschel product contained in a pool, but it is wise not to put too many different things in a single pool.

Note

A pool can hold any type of Herschel data product, not only the ObservationContext that you will start with in your data reduction experience. You can export products that you produce in the course of your data reduction into pools (more of that later). If you wish to share pools, to send someone processed data for example, tar up the whole directory and send them that. The pool's directory name must *not* be changed or HIPE will not be able to find the data therein (this will be changed in later versions of HIPE). So if your pool is on disc in /Users/me/.hcss/lstore/myFirstHerschelObs, and in there you have a directory (among many others) called "herschel.ia.obs.ObservationContext", then you need to tar up the entire "myFirstHerschelObs", not just "herschel.ia.obs.ObservationContext".

1.3.1.2. Get the ObservationContext (and save it to pool)

So, you first get hold of your data and then you extract the ObservationContext from it. How you do this depends on how you have gotten your observation. We will explain the most common methods here, but you can also see the *QSG* and the first chapter of the *DAG*.

These are the most common methods; read them all as general explanations are scattered throughout.

- *From the HSA load your observation directly into the HIPE memory* via "Send to External Application" in the HSA view. Doing this, what you get is already the ObservationContext. To avoid having to extract the data from the HSA again the next time you work on it, you can save it to a pool:

  ```
  saveObservation(myobs,poolName="swimming")
  ```

  where "myobs" is here the name of the ObservationContext (which can be anything, and with the HSA import method the product will in fact have a standard name, which you will see appear in your Variables panel); and here "swimming" is the directory on disc in which you wish to place these data. As said above, by default the host of this directory is [HOME]/.hcss/lstore/. If the directory ("swimming") does not already exist, it will be created.

  If you want to place the data in some disc location other than [HOME]/.hcss/lstore, you can use saveObservation parameters to do this:

  ```
  saveObservation(myobs [,verbose=<boolean>] [,poolLocation=<string>]
     [,poolName=<string>] [,saveCalTree=<boolean>]
  ```

  where the optional parameters (those in []) are: `poolName`, a single string and is the name of the pool; `poolLocation`, a string and is the directory path, the default path is similar to "/Users/me/.hcss/lstore"; `verbose` (True or False, default is False) for a full reporting; and `saveCalTree`, which allows you to save the calibration tree you have been using along with your ObservationContext (something you are unlikely to want to do at this point in time, but may be useful later). So, if your pool is located at /Users/me/pools/obsid1342111 then you need to specify "/Users/me/pools" as the `poolLocation` and "obsid1342111" as the `poolName`, but if your data are in /Users/me/.hcss/lstore/obsid1342111 then you only need to specify "obsid1342111" as the `poolName`. Note that saveObservation can take a while to run, especially if you ask to save the calibration tree with it. (Note: the wrap-around in the task example above is just to allow the text to fit on one line of the PDF document. You don't wrap around.)

- *If you got your data via ftp from the HSA* then you need to import them into HIPE using the "import Herschel data into HIPE" view (accessed from the HIPE Window menu: see the *DAG* chap. 1 for instructions). This will extract the ObservationContext from the directory that you untared the data into and put it directly into a user-chosen, but must be pre-existing, pool. The reason you have to do this is because the directory into which the HSA data were untarred is not in the correct format for the pipeline tasks to be able to deal with. The data first have to be extract out of the HSA directory and put into a new directory/pool, which will have a different structure.

  Once you have done that you can get the ObservationContext from that pool into HIPE in the following way:

  ```
  myobs=getObservation(obsid [,od=<number>] [,poolName=<string>]
      [,poolLocation=<string>] [,verbose=<boolean>] -)
  ```

  where the optional parameters are the same as for saveObservation, with the addition of "obsid". This is the observation identifier which you should know already, but if not you can hunt for your observation in the HSA and the obsid will be there listed. (You may need to spectify the number as "1342182002L", that is, with an "L" at the end.) The task run only with the obsid should find your ObservationContext if it is located in a standard poolLocation, although you may find you need to specify also the `od` (observing day) and `poolName`. When you have executed this command, "myobs" will appear in the Variables panel listing, this now being name of your ObservationContext. Note that getObservation can take a while to run.

- *If your ObservationContext is in a pool already* (e.g. someone sent you an entire pool that they had been working on) you get the ObservationContext using the command getObservation, explained above.

- *If you got your data from the HSA via the "Retrieve" button*: You use the same method for importing data into HIPE as that when getting data via ftp. *Note*: if you used the "Retrieve" button but only on the Level 2 product, you may not at present be able to use the this interface to get the data (this is being fixed).

- *If you have not already gotten your data from the HSA* and put them in to a pool, and if you know the obsid and don't want to use the GUIs to access the HSA, then with the following command you can get your data and import them into HIPE:

  ```
  myobs=getObservation(1342182002L, useHsa=True)
  ```

  For this to work you must have your HSA username and password written in your [HOME]/.hcss/user.props file with the following lines:

  ```
  hcss.ia.pal.pool.hsa.haio.login_usr = your username # (not in quotes)
  hcss.ia.pal.pool.hsa.haio.login_pwd = your password # (not in quotes)
  ```

  If you are only now writing these in that file, then you should restart HIPE for it to take effect. Alternatively you can type directly into your current session the commands:

  ```
  login_usr = -"hcss.ia.pal.pool.hsa.haio.login_usr"
  login_pwd = -"hcss.ia.pal.pool.hsa.haio.login_pwd"
  Configuration.setProperty(login_usr,"xxxxxx")
  Configuration.setProperty(login_pwd,"xxxxxx")
  ```

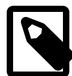
  (Where xxx are your username and password.) We recommend you immediately then save myobs to a pool, because with getObservation you only load the ObservationContext into HIPE memory, not onto disc.

If you want to look at what observations are in a pool, use

```
allObs = LocalPool("swimming", -"/Users/me/.hcss/lstore").allObservations
```

and then double click on allObs in the Variables panel for a human-understandable listing.

These save/getObservation tasks work for an ObservationContext, not for any other type of product. Importing and exporting other products will be explained later.



Note

You can give you variables—the things on the left of the = sign—any name you like. So instead of "myobs" used here, you could write "anobs" or "elmioobs".....

Be aware that when you enter od=number, that number must have no leading 0s. 0045 is not the same number as 45.

1.3.1.3. How can I work out what is in the ObservationContext?

One thing that will help you work out what your observation is of and what instrument configuration you had during the observing, is to have a copy of the AOR, which is where the commanding of the pointing and the instrument configuration would have been taken from. You can also look at the "meta data" of the ObservationContext. These are like FITS headers, a listing of various information about a product. Most products have meta data that are relevant to that specfic product. To see the meta data of your ObservationContext you can look at myobs with the Observation Viewer, getting this via a right-click menu on "myobs" in the Variables panel. This viewer opens in the Editor panel, and at the top are the meta data, as shown in the following screenshot:

ObservationContext for PACS data of observation 1342185578

Summary

Instrument:	PACS	**RA:**	283.39616
DEC:	33.02916666666667	**Operational Day:**	149
Observation ID:	1342185578	**Observation Mode:**	Scan map

Meta Data

name	value	unit	description
type	OBS		Product Type Identification
creator	SPG v1.2.0		Generator of this product
creationDate	2009-10-23T09:11:19Z		Creation date of this product
description	ObservationContext for PACS data of observation 1...		Name of this product
instrument	PACS		Instrument attached to this product
modelName	FLIGHT		Model name attached to this product
startDate	2009-10-10T07:15:48Z		Start Date
endDate	2009-10-10T07:42:12Z		End Date

Data

obs
auxiliary
calibration
level0

obs

Figure 1.1. Meta data

You can scroll down this list to see everything in there, such as the parameters commanded in the AOR of your observation: pointing; repetition factors; observing mode; raster movements; band/wavelength....

There are other panels in the Observation viewer (see the *HOG* or the *DAG* chap. 2.3). The Data panel lists the products and datasets held in the ObservationContext (black means the product has been loaded into memory, red means it has not). To the right of that is an area into which the default viewer of the currently selected product in the Data panel will open. If you click on one of the products listed in the Data panel (e.g. "+level2") the meta data now listed at the top are those associated with that particular product. There will be less meta data here than for the ObservationContext, although this will improve during HIPE track 5. To see the myobs meta data again, simply click on "myobs" at the top of the Data panel (which in the screenshot above however is called "obs").

From later versions of HIPE 3.x onwards the automatic pipeline switched to being the so-called "slicing" pipeline. Where you have multiple settings in your observation, for example rastering or multiple spectral lines, then as the pipeline progresses these "slices" are put as separate products into lists (according to a level-specific and astronomical logic—see Chap. 3). During the middle stage of HIPE 4.x appropriate meta data were added to allow you to understand what the slices are of. More information about spectroscopy Meta data is given in Chap. 4, you can see also <LINK>.

1.3.2. Then: look the Level 2 products

1.3.2.1. Spectroscopy

To look at what is in myobs, in your ObservationContext, open the Observation Viewer on myobs:

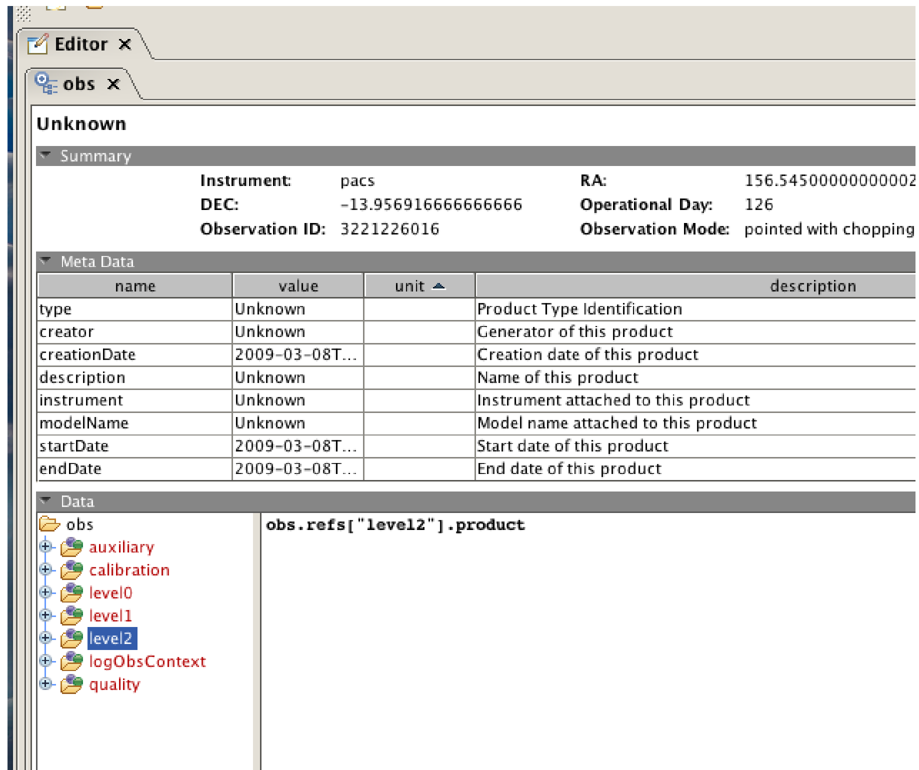


Figure 1.2. Your second glance at an ObservationContext with the Observation Viewer

The entries with + next to them can be thought of as directories of data. In each are products that correspond to the directory name, e.g. quality information are held in "quality". As here we are showing you how to look at a Level 2 (fully processed) product, you need to look at the "level2" entry. If there is no "level2" entry there, it means that your observation has not been processed to that level, and hence there are no cubes for you to look at. In that case you will need to reduce the data yourself through the pipeline. However, you should still read the rest of this chapter because it contains useful information that is not repeated in Chap. 3.

Click on the + next to it "level2" see what lies therein. You will see something like this:

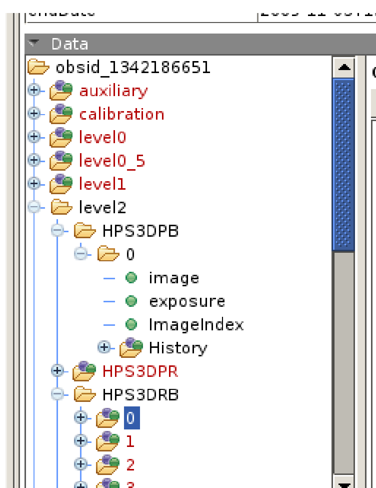


Figure 1.3. A further inspection of your ObservationContext

The screenshot shows you a listing of what is in the Level 2 of your ObservationContext. Listed there should be HPS3D[PB|PR|RB|RR]. The final "B" or "R" means "blue" or "red", and the "3D" indicates that it is a 3D (cube) product. The difference between HPS3DPB and HPS3DRB is that they are Level

2 products produced by different pipeline tasks (more of that in Chap. 3). *Note*: if the product is listed in red and you click on it to view it, you are at the same time loading it into memory. This can sometimes take a long time, *especially* if at the same time the default viewer for that product tries to open (the default viewer will load in the central panel of the Observation viewer).

If you move your mouse over the e.g. +HPS3DPB a banner will pop up indicating what type of product (what "class" of product) it is. It should say "ListContext", which means that this is a list of products (cubes), not a single product on its own. There could be anything from 1 to [a number > 1] products therein contained. If you click on the +HPS3DPB you will get a listing of all the products (the cubes) contained in this list, numbered 0..1..2 etc. In our screenshot the HPS3DPB has only one cube in it, the HPS3DRB has many. Hover over one of the numbers of the HPS3DPB and the banner should tell you that this is a *SpectralSimpleCube*; if you hover over the HPS3DRB you will be told that it is a *PacsRebinnedCube*. The HPS3DR product is the second (of three) cubes that are produced in the course of pipeline processing, HPS3DP is the final one, and the one you will be looking at here.

Exactly what is in your Level 2 depends on what type of observation you requested. You will have multiple HPS3DR cubes if your AOR included dithering/rastering/more than one spectral line, and you will have multiple HPS3DP cubes if you have more than one spectral line in your observation (dithered/rastered pointings have been combined). For each spectral line you will have one cube of the *PacsRebinnedCube* class for each raster poiniting; in the final stage of the pipeline combined these rasters are combined, per line, into the one cube of *SpectralSimpleCube* class.

You should be aware these the cubes have been processed through a standard pipeline and untill you reduce the data yourself, you should consider them to be of browse quality only.

In the screenshot above, showing you the datasets of the HPS3DP cube, you can see that within the +0 "directory" are datasets called "image" etc. These are the datasets that make up the cube, these including the "image" (which contains the cube's flux values), "exposure" and "ImageIndex" (which contains the cube's wavelengths). You can also look at these (right-click on them to see what viewers will work), but that is not particularly useful at this point in time.

1.3.2.2. Photometry

For photometry the same layout and similar syntax is found as for spectroscopy, and you should see something similar to the next screenshot. For ScanMap data this includes products with the names HPP[N|M]MAP[B|R], where again a "B" or "R" as the final letter in the name stands for blue or red, and the difference between the "M" and "N" products is that a different mapping scheme was used ("M" means mad map and "N" means naive map). For PointSource AOT this includes products with the names HPP[D|P]MAP[B|R]

The HPPxxxx are, as before, *ListContext*s and the products therein are *SimpleImage*s. These HPPxxxx products contain multiple dataset within: the actual image, a noise map and a history reporting on what pipeline tasks and parameters were used during the processing.

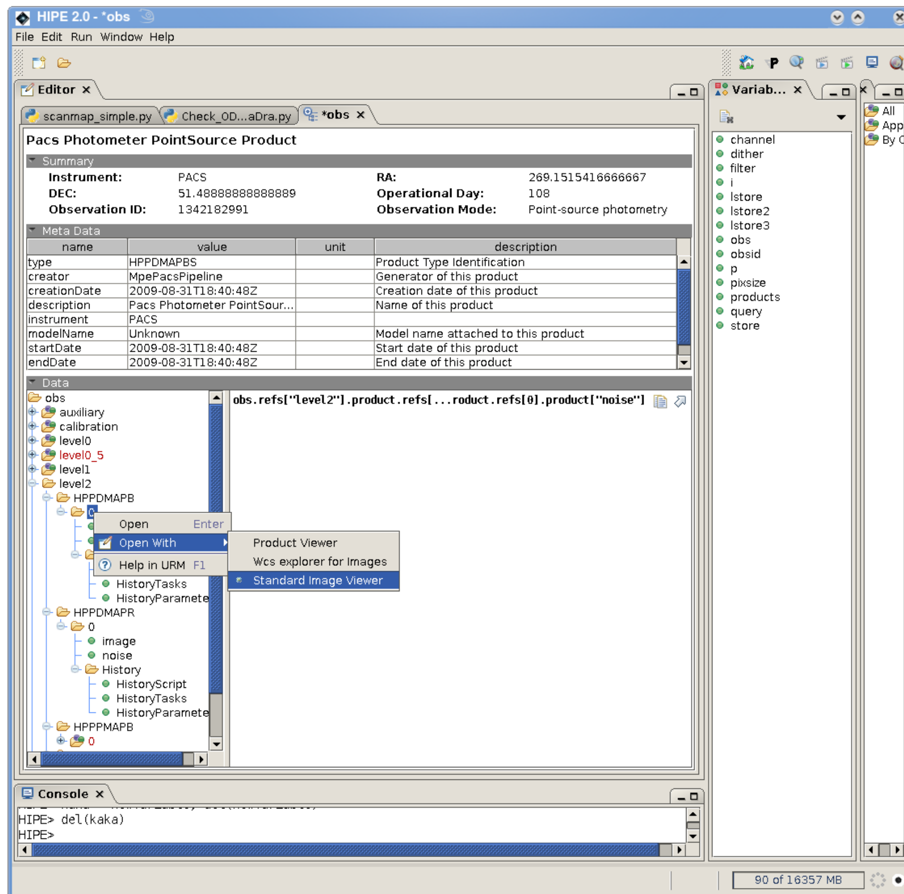


Figure 1.4. ObservationContext layout for photometry

In fact, whatever is (are) listed there in the Level 2 box is (are) what you want to look at, the differences between products there listed being the band and the type of map/cube that was made. More than one product will be listed, because more than one band and more than one type of map will be provided, and repetitions may be held separately and/or combined into one. In Chap. 2 and onwards we explain more about what these various products are.

1.3.2.3. Both

To now view your product(s) (the maps or cubes) you need to click on the +0 (or +1...) (*not* the individual datasets) next to the HPxxxx entry you are first interested in. This will give you access to the various viewers for your product. A double-click gives you the default viewer, a right-click gives you a viewer menu. Useful viewers for spectroscopy are the CubeAnalysisToolBox and the SpectrumExplorer. The toolbox will open in the window to the right of the Data listing or in a new tab. For photometry the default viewer is the Standard Image Viewer (as shown in the previous screenshot).

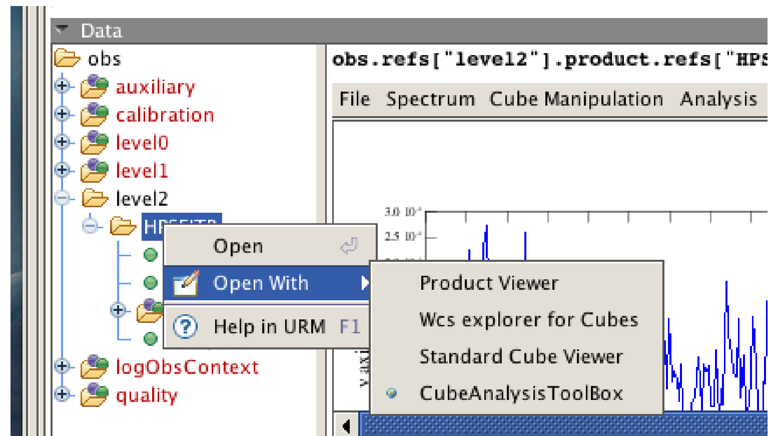
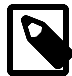


Figure 1.5. Viewing your Level 2 product

Note: as we are still working on the pipeline it is possible that the here-mentioned GUIs will not work on the data you have. Whatever viewers are offered for your product are the only viewers you can use.

For spectroscopy and photometry both you could also export the Level 2 product to FITS files and use a FITS viewer to look at them. To do this you need to extract the maps or cubes out of the ObservationContext first. Briefly: you can click-drag a +0 to the Variables panel, and that will selected out that particular cube/map product. When it appears in the Variable panel it will have a name like "newVariable". If you right-click on it there, you will be offered the opportunity to "Send to" FITS (remember to add the ".fits" to the name, and it is by default saved to the directory you started HIPE from). As you click-drag the product to the Variable panel you will see echoed to the Console the command that does this self-same thing (so you can do this yourself on the command line next time).

If you want to inspect separately the individual datasets, e.g. "image" of a cube, then double click on them for their default viewer which will also open in a new tab (and which will not be the CubeAnalysisToolBox because these datasets are not cubes, they are the information that are held in the cube), or right click for a viewer listing.



Note

Data products are of different classes. The class types are indicated in this guide with *italics*, for example the Level 2 cube "mycube" should be a *SpectrumSimpleCube*. You can tell what class a product has either by hovering the mouse over it in the Variables panel to see the information banner; clicking on it in the Variables panel to see an information listing in the Outline panel, or typing >print mycube.class in the Console panel. The class of a product defines what information are held in it and their organisation, and depends on what level of the pipeline the product has been taken to. Tasks, functions and GUIs are all written to work on specific classes of products, so if you cannot use a particular viewer, for example, it means the class of the product you are trying to use it on is wrong.

1.3.3. And finally: inspect the data with GUIs

In this section we introduce you to the viewers that HIPE provides for you to look at your data. The help page of HIPE—in particular the *DAG*—contains the documentation for these data analysis tools.

For spectral cubes, what you will probably want to look at is the spatial distribution of your spectra, to find where your point source is or to make an emission line map. You will want to look at the spectra from individual spaxels, to access the quality of your data, and maybe add together spaxels to get a spectrum of everything in your field of view (be it a point or an extended source). For photometry you will probably want to look at the maps of different scans, to see how well the map construction has been done, what the background looks like and whether the maps from different scans look the same.

1.3.3.1. Spectroscopy

There are a number of GUIs that can be used to inspect your PACS Level 2 cubes, and one can also use the command line. For a first quick-look (and even spectral manipulation) we recommend these GUIs; working on the command line is introduced in later chapters. The GUIs are called up with a right-click on the cube, be it within the Observation viewer in the Editor panel or listed in the Variables panel.

- To see scroll through wavelength slices of your cubes you can use the Standard Cube Viewer.
- # The SpectrumExplorer (SE). This is a spectral visualisation tool for sets of 1d spectra and the *SpectralSimpleCube* and the *PacsRebinnedCube*. It allows for an inspection and comparison of spectra from individual spaxels. It is a very useful quick-look and quick-compare for the spectra from your cube, and highly recommended as a first look tool. The *DAG* provides a guide to the use of the SpectrumExplorer; you use it on the individual HPS3Dxxx products.
- # The CubeAnalysisToolBox (CAT). This allows you to inspect your cube spatially and spectrally at the same time. It also has analyses tasks#you can make line flux maps, position—velocity diagrams and maps, extract out spectral or spatial regions, and do some line fitting. The *DAG* includes a guide to this GUI. It works on the *SpectralSimpleCube*s and the *PacsRebinnedCube.*
- # The SFTool and other mathematics tasks. The SpectrumFitterTool will allow you to fit and do mathematics on your spectra, and can be accessed via the right-click menu item "Tasks". To access the SFTool, click-highlight the *SpectrumSimpleCube* (the numbered entry, e.g. +0, not the "HPS3Dxxx" entry, see Fig. 1.3); go to the Task panel; and double click on Applicable. All applicable tasks will be listed, this will include various mathematical tasks and the SFTool. The *DAG* explains the use of these tasks.

If you have a version of HIPE for which the GUIs do not work with the *PacsRebinnedCube* you will have to use a command line method (more of which is in Chap. 3). You will first need to extract the cube it out of the ObservationContext, the easiest way being to drag the cube from the Data panel of the Observation viewer to drop it in the Variables panel. You need to drag the "+0" entry of your cube (see Fig. 1.3), not the "HPS3Dxxx" entry. When in the Variables panel you can (right-click) rename it. Here we call it "mycube". Then you can plot out spectra from the (5x5) spaxels with the command

```
#for PacsRebinnedCube, to plot spaxel 2,2
PlotXY(mycube.wavegrid,mycube.flux[:,2,2])
#for SpectrumSimpleCube (included for completeness) to plot spaxel 12,11
PlotXY(mycube.getWave(),mycube.getFlux(12,11))
```

In Chap. 3 we say more about using PlotXY with your PACS data.

1.3.3.2. Photometry

There are fewer separate GUIs for image viewing and analysis than there are for spectra, so there is less for you to learn about! There is one GUI which provides a first look and quick quality assessment of the data: the Standard Image Viewer (SIV). You call this either with a right-click on mymap in the Variables panel or the +0 entry of the ObservationContext, as explained before. If you want to do image analysis then HIPE provides many separate tasks you can run, to do contouring, overlaying, photometry, mathematics, etc. You access these tasks by click-highlighting mymap in the Variables panel, and then looking to see what "Applicable tasks" are listed in the Tasks panel of HIPE (one of the "viewers" you can access from the main HIPE window menu). The instructions for using these tasks are in the *DAG*.

Chapter 2. Introduction to PACS Data

2.1. A PACS observation

If you are not familiar with how PACS works we recommend you read the Observer's Manual (<LINK>). PACS observations involve the synchronised movements of many parts of the instrument for the purpose of exploring the spatial and spectral space your AOR specified. During a PACS observation you can have: chopper movements between two mirror positions; nodding of the telescope between two fields; moving over many fields/scanning directions to make a bigger map; grating movements to sample the wavelength domain; looking at the calibration block (for flux calibration and stability monitoring). All of these movements are tightly synchronised, so that at each field-of-view of each nod, the right (same) number of chops and right (same) wavelength range and sampling are included, and the nods are positioned and timed to fit in correctly with movements between consecutive (mapping/scanning) fields-of-view. The grating moves in discrete steps, usually down the wavelength range and back up again (and maybe more than once), during which the chopper will be chopping. Thus, moving along the time axis you are not just gathering more and more photons, but you will be looking at different sky positions, different wavelengths, and different focal plane positions. It is this instrument dance that the pipeline has to account for.

Spectroscopy:

The PACS spectrometer detectors are photo-conductors. When far-infrared photons fall onto the detector crystal, charge carriers are released that enable an electric current to flow through the detector. These currents are integrated over a capacitance. The more flux that falls onto the detector, the faster the voltage over this capacitance increases, and the larger the signal value will be. It is this voltage increase that is measured in the PACS detector electronics. The voltage over the capacitance is read out at 256Hz. Typically, the detector capacitance is discharged every 0.125 or 0.25 seconds and the voltage reset to a reference value, meanwhile the detector is read out non-destructively (usually 32 or 64 times) before this discharge is performed. The non-destructive reading out is accumulative, that is, the signal you read for readout at time T(2) is the value of the signal of readout at time T(1) plus the extra that is due to the light that fell on the detector since time T(1).

The raw PACS detector signals are ramps ("ramp"="incline") of 32 or 64 increasing voltages. This information cannot be downlinked in its raw volume (which is huge), except for 1 pixel which is fully read out for data-checking purposes (by the PACS instrument team); therefore the instrument reduces the data on-board. For short ramps (32 samples) a slope fitting is done, and per pixel one number (the value of the slope) per integration ramp is downlinked and visible at Level 0. For long ramps (64 samples) the on-board software averages the voltages per 16 samples. In that case the Level 0 data consists of averaged ramps with four numbers per integration ramp.

The easiest way to check which of the two on-board reductions has been applied to your data is to check the Level 0 data (in the same way as explained in Chap. 1 for looking at what is in Level 2). If you see in the Level 0 listing product branches with the name HPSFITB or HPSFITR (Herschel-Pacs-Spectroscopy-FITted-Blue or Red) then on-board slope fitting was done, and you start the pipeline processing from these *Frames* "class" products. If you see products with the name HPSAVGB or HPSAVGR (Herschel-PacS-AVeraGed-Blue or Red detector) then the integration ramps were averaged on-board and you start the pipeline processing from these averaged *Ramps* class products. The dimensions of a HPSFITR product will be something like 18,25,980 (18x25 pixels, each with 980 readouts along the time dimension; later this time dimension is turned into the wavelength dimension). The dimensions of the equivalent HPSAVGR product will be 18,25,980,4 (each of the 980 individual ramps contain 4 averaged readout values).

The Level 2 products HPS3DRR and HPS3DPR stand for Herschel-Pacs-Spectroscopy-3Dimensional-Rebinned_cube-Red (which is of class *PacsRebinnedCube*), and Herschel-Pacs-Spectroscopy-3Dimensional-Simple_cube-Red (which is of class *SpectralSimpleCube*). At Level 1 we also have the HPS3D[B|R], these being of class *PacsCube*.

Your observation will contain data from your astronomical source, auxiliary data to allow the telescope pointing and timings to be calibrated, calibration data so the detector response and dark can be corrected, and more. In your astronomical dataset(s) there will be data not just from your target but also, probably in the beginning, a "calibration block", where the internal calibration sources are observed. Gradual changes to the response of instrument and degradations of the calibrators will be followed by the PACS team over the lifetime of Herschel, and will be included in the calibration files.

There is also a Status table, and later there will be a BlockTable, attached to your *Ramps* and *Frames* products, these contain information about the instrument status of the data and its organisation (in time). These are added to (and changed) as the pipeline proceeds. In Chap. 4 we explain the most useful entries of the Status and Block tables.

The PACS spectrometer detectors (one red and one blue) are of dimensions 18 along the Y and 25 along the X. Each of the 25 columns are a single spaxel (spatial pixel), and collectively these have an on-sky arrangement of 5x5. These columns are referred to as modules: a module is the physical entity which the column corresponds to in the instrument. Each column contains 18 pixels (hence 18 rows), although the first and last hold no astronomical data (the first is an open channel, which has no associated detector unit, and the last is a dummy channel, being a resistor instead of a detector unit). The 16 active pixels between collect the spectral information for their spaxel, where each of the 16 pixels sees a wavelength range that is slightly shifted along compared to the previous. These 16 pixels are also known as "detectors"—confusing, yes, but the name comes from the fact that they are each little detectors of light.

Photometry:

The PACS photometer detectors are bolometer arrays. Each pixel of the array can be considered as a little cavity in which sits an absorbing grid. The incident infrared radiation is registered by each bolometer pixel by causing a tiny temperature difference, which is measured by a thermometer implanted on the grid. What we call "signal" is the voltage measured at this thermometer. The blue channel offers two filters, 60–85 µm and 85–130 µm and has a 32x64 pixel array. The red channel has a 130–210 µm filter has a 16x32 pixel array. Both channels cover a field-of-view of ~1.75'x3.5', with full beam-sampling in each band. The two short wavelength bands are selected by two filters via a filter wheel. The field-of-view is nearly filled by the square pixels, however the arrays are made of sub-arrays which have a gap of ~1 pixel in between. For the long wavelength end 2 matrices of 16x16 pixels are tiled together. For science observations the multiplexing readout samples each pixel at a rate of 40 Hz. Because of the large number of pixels, data compression is required and hence we do not see the raw data; they are binned to an effective 10 Hz sampling rate. The product class at Level 0 is always *Frames*.

As with spectroscopy, the observations contain auxiliary data such as telescope pointing, time, and calibration information beside the target signal. Photometry observations also include nodding and chopping and calibration blocks.

2.2. The data structure (simple version)

The structure of PACS data are given in better detail in the *PAPT* and the *PDD*, but here we give a overview of everything you need to know for now.

Although the screenshots and the emphasis here is on spectroscopic data, the data structure is more or less the same for photometric data.

In Chap. 1 we included some screenshots showing listings of what is held in a PACS Observation-Context. A screenshot of the structure of your ObservationContext will look something like this:

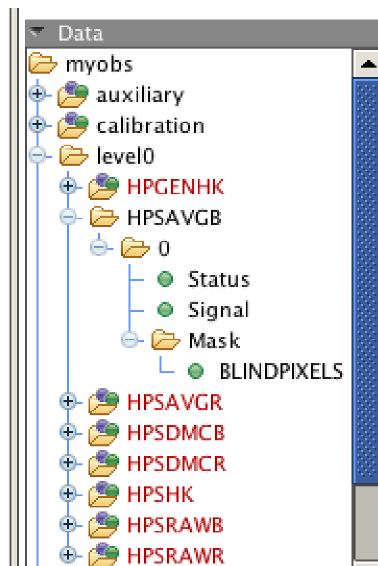


Figure 2.1. The contents of an ObservationContext for spectroscopy

This screenshot (and you could also look again at those of Chap. 1) shows that within an ObservationContext (called "myobs" here) you find layers of products with names such as level0, auxiliary, calibration...Within the level0/1/2 "directories" you can see products called HPSxxx (spectrometer) or HPPxxx (photometer): among these are the products that you will work on, as they contain the actual astronomical observations. The other directories (e.g. auxiliary and calibration) are extra information which are necessary for the data reduction but which you do not need to look at yourself. (The same click methods as previously mentioned can be used to inspect these products: double-click to view, right-click for viewing menu listing.)

On the Console command line you can print-list these products, e.g.,

```
print myobs.calibration.spectrometer
print myobs
print myobs.level0
```

where *the first line* will produce a listing similar to the next screenshot, *the second line* produces a listing of what meta data are there plus the "directories" you can see in the screenshot above, and *the third line* shows what Level 0 products there are in your ObservationContext. Note that this type of syntax will only take you so far: for example to "print" further something in Level 0 (e.g. HPSAVGB) you cannot type "print myobs.level0.HPSAVGB.

In the HPSAVGB "directory" (for photometry this would be called HPPAVGB) in the screenshot above there is only 1 product (0), and in there are the datasets of Status, Signal, and a listing of Masks (in the beginning there will only be one mask listed). It may be that there is more than one HPSAVGB product present (referred to then as 0 1 2 3...). These are all dealt with appropriately in the pipeline. What has just been said applies equally to an HPSFITB/R "directory", which you will have if your Level 0 data are the fit ramps instead of the averaged ramps products.

There may also HPSRAWB/R "directories", these products being the raw ramps that are downlinked for 1 pixel and used for calibration purposes (i.e. not by you). The organisation therein is different than the HPSFIT/AVG products.

All the other HPSxxxx entries in the screenshot above are additional products that contain data necessary for data reduction or data checking. Important for the pipeline are the products called HPSDMCR/B (or HPPDMCR/B), which are the DecMec data (more on this later). Less important for you are the HPS[HK|GENHK|ENG], which are "housekeeping" and engineering data, information about the temperatures, instrument settings, status etc. of the satellite and of PACS. These information are for instrument scientists to interpret.

A calibration tree, containing all the information necessary to calibrate your observation, comes with your data and also with your HIPE installation (more on that later). If you click on "calibration" from the screenshot above you will see:

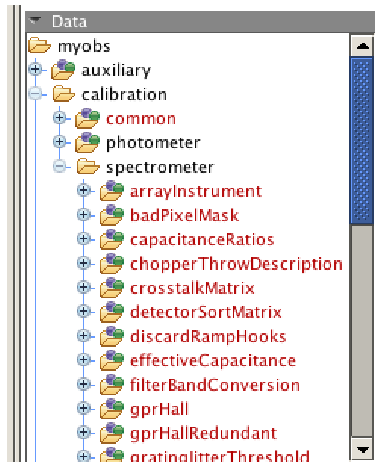


Figure 2.2. The contents of the calibration tree

These all are the calibration products that were used to produce the Level 0.5, 1 and 2 products that are all part of your ObservationContext.

The auxiliary tree, shown below, also contains products that are necessary for the reduction of your data, for example the obit ephemeris and pointing products. These are information that are mainly about the satellite.

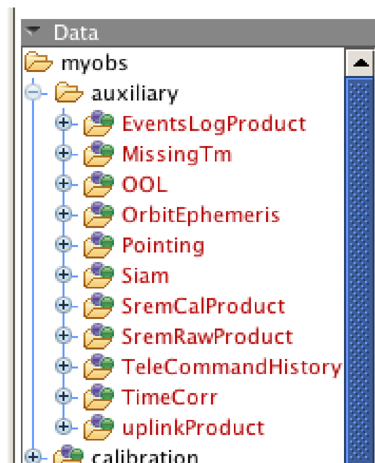


Figure 2.3. The contents of the auxiliary tree

The log and quality listings are: a log of the processing that produced that level's data (even for Level 0 there has been processing to convert the data from raw satellite format to an ObservationContext); and quality information.

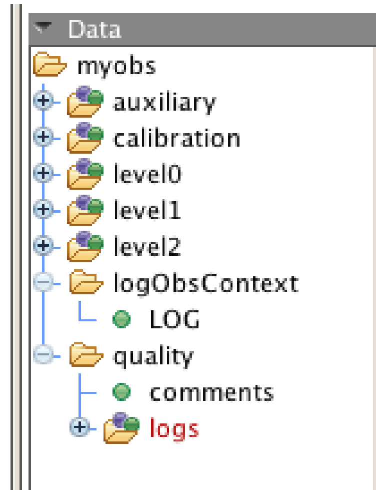


Figure 2.4. The contents of the log and quality trees

2.3. The spectrometer pipeline steps

Level 0 to 0.5 processing is the same for all AOTs (points 1 to 8) and many of the subsequent tasks are also performed for most AOTs.

1. If working on *Ramps* data, flag for saturation. Then fit the slopes to convert the data to a *Frames* product. If working on a *Frames* product skip to 2
2. Signal is converted from digits/readout_interval to Volts/s
3. Status entry for calibration blocks is added to; Status table is updated
4. Spacecraft time is converted to UTC
5. Spacecraft pointing is added to the Status table for the central pixel of the detector; chopper units are converted to sky angle; pointing is added to all pixels
6. Wavelengths for each pixel are calculated; Herschel's velocity is corrected for
7. Data "blocks" are recognised and the information organised in a table
8. Masking. Bad pixels will have already been masked. Masking for readouts taken during grating and chopper movements is performed, and for saturation if the data reduction began on a *Frames* product
9. Masking for glitches is performed
10. Signal non-linearities are corrected for.
11. Signal is converted to a level that would be if the instrument had been set to the minimum capacitance (no change made if that was already the case)
12. The dark current and pixel responses (their individual sensitivities) are calculated using differential (internal) calibration source measurements to populate the absolute response arrays; a response drift is then calculated
13. Chop-nod AOT: the up- and down-chops are combined (i.e. a background+dark subtraction); the signal is divided by the relative spectral response function and then pixel responses (and their drift) are corrected for; calibrated 5x5xlambda data cubes are generated; the cube's wavelength grid is created; outliers are flagged (another glitch detection); The data cube is spectrally resampled; the nod A and B cubes are combined

14.Wavelength-switching AOT: *TBD*

15.Off-map AOT: *TBD*

16.The data cube is spatially rebinned, different pointings combined and resampled (mosaicked) or 3D drizzled (*not yet ready*)

The steps described here follow those in the "ipipe" pipeline scripts. These can be accessed from the HIPE toolbar. The name of the ipipe script corresponds to the AOT type. The reduction for all AOTs will begin with the scripts with L05 in the name (indicating an ending at Level 0.5) and "frames" if your Level 0 product is a *Frames* or "ramps" if the Level 0 product is a *Ramps*, and then will proceed to the AOT-dependent L1 and L2 scripts. Some comments are embedded in these scripts.

During the HIPE 3.x release track the automatic pipeline switched to the so-called "slicing pipeline": the products are sliced, that is organised in distinct and separate, but linked parts using an "astronomical" logic (e.g. separate the different rasters of a single observation; keep together all data of the same spectral line).

2.4. The photometer pipeline steps

We summarise here the basic steps of the PACS photometry data reduction. Level 0 to 0.5 is the same for all AOTs (steps 1 to 10).

1. Identify the structure of the observation and identify the main blocks (calibration and science blocks)
2. Perform data cosmetics: flag bad/saturated pixels and flag/correct cross talk and glitches
3. Convert signal from digits to volts
4. Correct for crosstalk *Currently on hold*
5. Deglitching
6. Spacecraft time is converted to UTC *Not yet ready*
7. Covert chopper position from engineering units into angle
8. Satellite pointing information are added to frames (sky coordinates of reference pixel for each readout)
9. The dark current and pixel responses (their individual sensitivities) are calculated using differential (internal) calibration source measurements to populate the absolute response arrays
10. Flag data taken while the chopper was moving
11. Point Source AOT: check what dithering pattern was implemented and update Status table; average signals taken at each and every chopper position, if more than one in each; add the pointing information; subtract the nod positions (per nod cycle and dither position); average the differential nod A and B images; do the flatfielding and response correction; combine dithers; make a map
12. Scan Map AOT: add the pointing information; remove data taken during slews; run the highpass filter; make a map
13. Small Extended source AOT: check what dithering pattern was implemented and update Status table; average signals taken at each and every chopper position, if more than one in each; add the pointing information; subtract the nod positions (per nod cycle and dither position); average the differential nod A and B images; do the flatfielding and response correction; another adding of pointing information; remove data taken during slews; make a map

The steps described here follow those in the "ipipe" pipeline scripts. These can be accessed from the HIPE toolbar. The name of the ipipe script corresponds to the AOT type. Some comments are embedded in these scripts.

For very large datasets the data will probably have been sliced, that is organised in distinct and separate, but linked parts using an "astronomical" logic.

2.5. The Levels

There is a Herschel-wide convention on the processing levels of its instruments. The different levels reflect how much of the pipeline has been run to create the data and the amount of additional information that has been attached to them.

- *Level 0 data:*

  Level 0 is a complete set of minimally processed data. After Level 0 data generation (done by the HSC) there is no connection to the database from which the raw data were extracted (this database is not available to the general user). Therefore the Level 0 data contain all the information required.

  - Science Data

    Science data are organised in user-friendly classes. The *Ramps* class contain (i) raw channel data (but usually only for a certain number of detector pixels, as these data are huge) (ii) averaged channel data, for all pixels; and the *Frames* class, for which on-board fitting of the slopes of the raw ramps has already been done.

  - Auxiliary data

    Auxiliary data for the time-span covered by the Level 0 data, such as the spacecraft pointing (attitude history, which however is only available after Level 0.5), the time correlation, selected spacecraft housekeeping, etc. The information are partly held as status entries attached to the basic science classes (*Ramp* and *Frame*) and the rest are available as separate products (e.g. the "pointing product") which you can access.

  - Calibration data

    This is the data that is used to calibrate the observations. A calibration dataset is included at Level 0, however calibration data is also provided with your HIPE installation, and generally it is the HIPE calibration dataset you should use when you process your data through the pipeline.

  - Quality data

    Quality control information, including (or maybe only) messages produced by the processes that produced the Level 0 data, or messages from the pipeline processing that produces later levels.

- *Level 0.5 data:*

  Processing until Level 0.5 is AOT independent. These data are also present with what you got from the HSA. At this level additional information has been added to the *Frames* science products (masks for saturation and bad pixels, RA and Dec, the BlockTable,...) and basic unit conversions have been applied (digital values to volts, chopper position to sky angle). For the spectrometer, during Level 0.5 production the *Ramps* are turned in to *Frames*.

- *Level 1 data:*

  Level 1 data generation is AOT dependent (although there will be much overlap between the AOTs). Level 1 data are also available for selection from your pool, having been processed automatically at the HSA. Data processing at this level is concerned with cleaning and calibrating, and as the end the data are converted to a basic spectrometer cube (the 16x25 useful pixels have been converted to 5x5 spaxels, each holding 16 individual spectra).

- *Level 2 data:*

  Going from Level 1 to Level 2 the spectrometer cube is spectrally and spatially rebinned. At this level scientific analysis can be performed. Level 2 work is highly AOT dependent.

- *Level 3 data:*

  This is simply a level where the scientific analysis has been done by the data users (e.g. spectral cubes converted to velocity maps, source catalogues), and it is hoped that users will import these products back into the HSA.

Chapter 3. In the Beginning is the Pipeline. *Spectroscopy*

3.1. Introduction

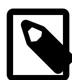
The purpose of this chapter is to tutor users in running the PACS spectroscopy pipeline. Previously we showed you how to extract and look at Level 2 automatically pipeline-processed data; if you are now reading this chapter we assume you wish to reprocess the data and check the intermediate stages. To this end the sections here are divided into (i) a listing of the task steps with brief explanations, followed by (ii) demonstrations for viewing the data just processed: plotting, displaying etc. The sections are separated by Level. Further information on the reduction of PACS data are given in Chap. 4, and the fullest details of the pipeline tasks are given in *PAPT*. This includes a listing of all the parameters of each pipeline task. Here we show you how to run with the default parameters, but if you think you will want to change these you need to read the *PAPT*.

Throughout this chapter are included short scripts to inspect and select on the data as you go through the pipeline, although as various product-inspection GUIs are completed it will become unnecessary to do much of this scripting yourself. Nonetheless, by following the scripts you can learn not only how to handle PACS data but also a little about the scripting that can be done in HIPE.

As well as this *PDRG* you should look at the ipipe scripts—the interactive pipeline scripts. These are updated more frequently than this guide, and hence should be given greater weight where differences are fround. They also form a guide to your memory if you already know how to run the pipeline and don't want to follow this more detailed *PDRG*. They can be acessed via the "pipeline" menu of the HIPE tool bar. The reduction for all AOTs will begin with the scripts with L05 in the name (indicating an ending at Level 0.5) and "frames" if your Level 0 product is a *Frames* or "ramps" if the Level 0 product is a *Ramps*, and then will proceed to the AOT-dependent L1 and L2 scripts.

When you load an ipipe script (it goes into the Editor panel of HIPE), copy it ("save to"), otherwise any edits you make to it will overwrite your reference version of that script! You can run the pipeline via these scripts, rather than entirely on the Console command line, in this way you will have an instant record of what you have done. You can then run it either in one go (double green arrow in the Editor tool bar: <LINK>) or line by line (single green arrow). This latter is recommended if you want to inspect the intermediate products.

We will first take you through the pipeline for a chop-nod observation, then other AOTs will the be discussed; so if you are working with data from one of these other AOTs we recommend you still read this entire chapter. *At present only chop-nod is discussed.*



Note

Spacing/tabbing is very important in jython scripts, both present and missing spaces. Indentation is necessary in loops, and avoid having any spaces at the end of lines in loops, especially after the start of the loop (the if or for statement). You can put comments in the script using # at the start of the line.

Note

Syntax: *Ramps* and *Frames* are how the *PDRG* indicates the "class" of a data product. "Ramp" or "frame" are what we use to refer to any particular *Ramps* or *Frames* product. A frame is also an image (a 2D array), for the photometer it is an image corresponding to 1/40s of integration time, for the spectrometer it is an image made up of the slopes of all detectors over one "ramp" (over one reset interval—see Chap. 2).

Please read this whole chapter before doing your reductions. Explanations for what you are doing are included in the sections that detail the pipeline tasks *and* the sections that detail how to inspect your data.

3.2. The sliced pipeline

As of HIPE continuous integration build 3.0.1307 (User track 3.x) the recommended pipeline is the so-called "sliced pipeline". This was designed to make it easier to reduce datasets in which more than one raster or spectral line was observed. It is also more friendly in its memory use than the previous pipeline. It uses the same "non-sliced pipeline" tasks, and they have the same name with a "sliced" concated to the beginning. The data are sliced according to Level logic, which is to say by raster at Level 0.5 and by line id (spectral line id, not spectral band) and nod at Level 1. To improve the memory use still further, the tasks are run such that within each, the products are read in and out of a temporary pool, rather than holding everything, always, in HIPE memory (but because of this the running time is longer than the old style pipeline). The individual "slices" are kept together at all times—the products (the frames, ramps and cubes) are held in *ListContexts* (lists of products). You can still inspect the individual slices by first extracting them out of the list and then using your favorite Viewer on them. It is the sliced pipeline that we describe here.

(The ObservationContext may itself be sliced, this follows a logic to do with filesize rather than anything astronomical.)

The first time you use a sliced pipeline task a pop-up will give you some information about the use of temporary pools. What this means is: in order for the pipeline to run more efficiently on memory, you can run it so that products are not held in memory the whole time but rather are read into and out of a temporary pool (in .hcss/lstore/temppool). However, to do this you need to set some [HOME]/.hcss/user.props parameters before starting HIPE. These parameters are

```
hcss.pacs.spg.usesink=true
hcss.ia.pal.store.tempstore= {temppool}
hcss.ia.pg.tmpstore=tempstore
```

The downside of this is that the pipeline processing is slower, which can be a problem when reducing large SEDs, for example. If you are working on a machine with several 10sGB free memory, you probably do not need to set these parameters. The temporary pool is not used by default by the sliced pipeline, it is only used if you set these parameters in your user.props file.

3.3. Setting up to run the pipeline

The ipipe script that this section and the next follow is either L05_frames or L05_ramps, depending on whether your Level 0 product is *Frames* or *Ramps* (see below). This part of the pipeline is AOT independent, so everyone will want to read Secs 3.3 and 3.4.

To set up the running of the pipeline you will: first decide if you wish to reduce the red or blue data and set a variable, here called "camera", accordingly; then you need to propagate the Meta data (kind of a FITS header) of the ObservationContext to the Level 0 product (more below) and extract the Level 0 product from the ObservationContext; next you need to gather some necessary auxiliary products. To do all of this you need to have in HIPE your ObservationContext already loaded into HIPE—this was explained in Chap. 1—and here we call this product "myobs". The steps are:

```
camera = -"blue"
pacsPropagateMetaKeywords(myobs,'0', myobs.level0)
level0 = PacsContext(myobs.level0)
timeCorr = myobs.auxiliary.timeCorrelation
pp = myobs.auxiliary.pointing
orbitEphem = myobs.auxiliary.orbitEphemeris
```

The propagating of the Meta data is mainly for your own convenience, although later in the pipeline this propagation becomes necessary for certain tasks to work. The full Meta data of the ObservationContext is not repeated at each level: if you use the Product viewer on a Level 0/0.5/1/2 product you will not necessarily see all the information about your observation listed because by default only the information relevant to that direct level is included. Since it is useful for you to be able to see, for

example, the AOR parameters you programmed into the observation no matter which level product you are looking at, we recommend you run this pacsPropagateMetaKeywords task.

Continuing with the script explanation: "level0" is the Level 0 product containing your astronomical and calibration-block data; the "pp" is the pointing product, is used to calculate the pointing of PACS during your observation; the orbit ephemeris is used to correct for the movements of Herschel during your observation; and the time correlation product is used by the time conversion task.

Next you should select from "level0" the *Ramps* or *Frames* product and the DecMec header. Whether you begin with *Frames* or *Ramps* depends on your data—when you look at myobs (for example with the Observation viewer accessed via a right-click on "myobs" in the Variables panel) you will only have the HPSFIT (*Frames*) or HPSAVG (*Ramps*) products, not both. The DecMec product contains the position and status of the PACS mechanisms and detectors sampled at high frequency. You will also select out a raw *Ramps* product, this containing only the fully-raw data for a single pixel of the PACS detector and used in the saturation detection task of the pipeline.

These steps are:

```
# EITHER
slicedRamp = level0.averaged.getCamera(camera).product
# OR
slicedFrames = SlicedFrames(level0.fitted.getCamera(camera).product)
# AND THEN
slicedRawRamp = level0.raw.getCamera(camera).product
slicedDmcHead = level0.dmc.getCamera(camera).product
```

(You can, of course, give these extracted-out products any name you please.)

Finally, you should define the calibration tree to use with your reductions. The calibration tree contains the information HIPE needs to calibrate your data, e.g. to translate grating position into wavelength, to correct for the spectral response of the pixels, to determine the limits above which flags for instrument movements are set. You have the choice of (i) the calibration tree that comes with the Observation-Context or (ii) that from your installation of HIPE. If your ObservationContext came from the HSA, the "caltree" is that which was used by the automatic pipeline, whereas if someone else reduced the data, the caltree will be that which they used *if* they added their caltree to the ObservationContext themselves (we show you how below). As long as your HIPE is recent then the caltree that comes with it will be the most recent, and thus most correct, calibration tree, and is the one we recommend you use.

The steps are:

```
# EITHER (recommended)
#  get the calTree from HIPE and add it to the ObservationContext
myobs.calibration = getCalTree(obs=myobs)
calTree = myobs.calibration
# OR
#  get the calTree directly from the ObservationContext
calTree=myobs.calibration
```

You are not actually putting the caltree physically (so to speak) into myobs, rather you are placing in there the pointers to the calibration files that you will use in your subsequent pipeline processing. The old versions of these calibration files are never thrown away—you will get all versions with your installation of HIPE. Hence the pointers will be valid no matter how old they are, but if the pointers are newer than your HIPE installation, you will need to update HIPE to access them. The specification of "obs=myobs" in getCalTree is there so that as you process your data, any calibration information taken from calibration files that are *time-specific* will take the information that is valid for the time of your observation.

3.4. Level 0 to 0.5

First we list the pipeline steps, then we tell you how to inspect the products just created.

Tip

As you run tasks in HIPE you will see a small rotating circle at the bottom right of the HIPE GUI indicating that "processing is occurring". While this is running you cannot execute other commands. You can usually stop a task runing with the red STOP button, although it does not have an immediate effect.

HIPE task names, and most other things you will type in HIPE while reducing your data, are case sensitive.

Names of variables, such as "slicedFrames" or "myframe", are not objects themselves, rather they are pointers to the objects which are held in memory. Hence, if you copy >myframe_save=myframe, and then change something in "myframe" (e.g. run it through a pipeline task), the same change will be made to "myframe_save". So if you want to save a copy of a product before you run a task on it, the safest way to do this is with the syntax >myframe_save=myframe.copy(). The ".copy()" part of the syntax copies the data which the variable name (myframe) is pointing to, i.e. the actual data that is the product "myframe". This same .copy() method will work on slicedFrames/Cube/Ramps products, athough not on any other type of *ListContext* product (slicedFrames/etc are special *ListContexts*).

This stage of the pipeline corresponds to the ipipe script L05_frames or L05_ramps. You can open it in your Editor panel (from the Pipeline menu), and if you want to write in it then first save it to another name.

3.4.1. Pipeline steps

You may need to import before beginning your processing:

```
from herschel.pacs.spg.pipeline import *
from herschel.pacs.signal.context import *
from herschel.pacs.cal import GetPacsCalDataTask
```

If you are working on a *slicedRamps* you will begin with:

```
slicedRamps = slicedSpecFlagSaturationRamps(slicedRamps, rawRamp = slicedRawRamp,
   calTree=calTree)
slicedRamps = slicedActivateMasks(slicedRamps, String1d([" -"]), exclusive = True)
slicedFrames = slicedFitRamps(slicedRamps)
```

(Note: the wrap-around in the task example above is just to allow the text to fit on one line of the PDF document. You don't wrap around.)

If you start with a *slicedFrames* you begin instead with:

```
slicedFrames = slicedSpecFlagSaturationFrames(slicedFrames,
   rawRamp = slicedRawRamp, calTree=calTree)
```

The task slicedActivateMasks we explain at the end of this section. The task slicedSpecFlagSaturationRamps/Frames flags the data for saturation, creating a mask called SATURATION which subsequent tasks can take into account. Later we show you how to inspect this mask. The task uses a calibration file held in the caltree to work out where saturation has occurred, this all being based on ground-based and Performance Verification observations. In this task you can include the "rawRamp" product if you have extracted that out of your ObservationContext (as explained above), but if you don't have this product you can just leave it out. slicedFitRamps is a task that fits the individual ramps (the slopes, as explained at the top of Chap. 2) with a 1st order polynomial and returns a *Frames* product with data values that are the slope values in units of digits/readout_interval. slicedFitRamps does not take into account any masks, rather it propagates them. So if in pixel 0,0, for the 545th ramp the 4th readout is saturated, the whole ramp, including the saturated readout, will be fit but for pixel 0,0 the 545th slope value in myframe will carry the saturation flag=True.

The ramp fitting task changes the dimensions of the data, which you can check in the following way,

```
print slicedRamps.refs[0].product.dimensions
print slicedFrames.refs[0].product.dimensions
```

which will return something like: 18,25,980,4 and 18,25,980, respectively: 980 individual ramps, each of which has 4 readout values, have been converted to 980 new readouts, the value of each being that of the slope of the polynomial fit to the 4 original readouts. The ".refs[0]" refers to the first slice in the list.

At this point in the pipeline there will be only one slice in your slicedFrames, but later there will be more.

You now continue with the following:

```
slicedFrames = slicedSpecConvDigit2VoltsPerSecFrames(slicedFrames, calTree=calTree)
slicedFrames = slicedDetectCalibrationBlock(slicedFrames)
slicedFrames = slicedSpecExtendStatus(slicedFrames, calTree=calTree)
slicedFrames = slicedAddUtc(slicedFrames, timeCorr)
slicedFrames = slicedSpecAddInstantPointing(slicedFrames, pp, calTree = calTree,
   orbitEphem = orbitEphem, horizons = None)
slicedFrames = slicedConvertChopper2Angle(slicedFrames, calTree=calTree)
slicedFrames = slicedSpecAssignRaDec(slicedFrames, calTree=calTree)
slicedFrames = slicedWaveCalc(slicedFrames, calTree=calTree)
slicedFrames = slicedSpecCorrectHerschelVelocity(slicedFrames, orbitEphem, pp)
slicedFrames = findBlocks(slicedFrames, calTree = calTree)
slicedFrames = slicedSpecFlagBadPixelsFrames(slicedFrames, calTree=calTree)
```

And to explain this all:

- In the order listed these tasks do the following: Convert the units to V/s; Add to the Status table information about the calibration sources; Update the Status table with chopper and scanning position information; If timeCorr is present, then convert from spacecraft time to UTC; Add the pointing and position angle of the central detector pixel; Convert the chopper positions to sky positions; Calculate the pointing for every pixel (which is not just a set offset from the central pixel, but depends on the chopper position seen by each pixel); Calculate the wavelengths; If the orbit ephemeris and pointing products are present, correct the wavelengths for Herschel's velocity; Organise the data into blocks (per line observed, per raster position, per nod....); Flag for bad pixels.

- If a parameter is specified as "calTree=mycalTree" then it can be anywhere in the call, but if you specify only the parameter value (i.e. just "calTree") then it has to be in the right place in the call.

- The task slicedSpecFlagBadPixelsFrames creates the masks BADPIXELS and NOISYPIXELS, the former being truely bad pixels and the latter are pixels for which elevated noise was found from instrument tests done in-orbit. If you ran slicedFitRamps you will also then have a BADFITPIX mask, which is a quality indicator for pixels for which the averaged ramps are suspected to have not been well fitted during fitRamps. The SATURATION mask is created where your AVG (*Ramps*) or FIT (*Frames*) ramps exceed a certain signal limit. We should point out that because the AVG or FIT products that you are reducing are not the raw data, it is not 100% certain that the readouts that exceed the pre-determined saturation limit are saturated, it is only very likely. If this task is called with as input the "rawramp" product, then it will also create a mask called RAWSATURATION, where this mask is based on saturation having been detected in raw data and thus it is certain they really are saturated. However, because the raw data are huge, we can only downlink from Herschel these raw data for a single pixel, and for that we have chosen the most responsive pixel of the detector (5,12 for the blue 10,12 for the red). When saturation is detected in this pixel then for all pixels of the detector for those same readouts (those same time-line datapoints), the mask is filled with 1, i.e. True. At the same time a Status column called RAWSAT will be filled. However, just because the most responsive pixel is saturated doesn't necessarily mean that all are (since the other pixels are less responsive and hence their signal level will be lower). Thus this mask should be considered a warning mask. Finally, the raw data may have a BLINDPIXEL mask from the beginning, this simply being a bad pixel that is masked already at Level 0.

- The Status table contains information about the status PACS during the observation, and is added to as the data processing proceeds (e.g. here by the task slicedSpecExtendStatus). You can look at these information as a dataset or plot <LINK>, which you can access in the following way:

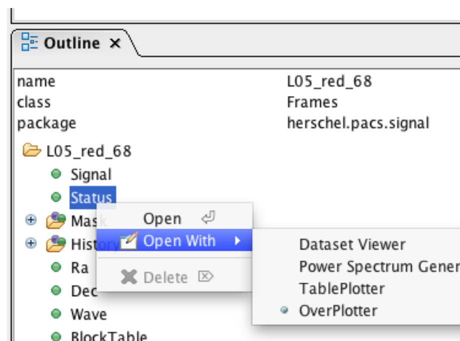


Figure 3.1. Viewing the Status or BlockTable

The BlockTable (the task findBlocks) is an organisation table showing the data "blocks", that is the observation organised by instrument status (raster, nod, grating scan direction...). You can look at this also via the Dataset viewer, in the same way as for the Status

The next step is to slice the data according to the Level 0.5 logic, which is by raster. If there is only one raster pointing in your observation, there will be only one science slice created. In addition, the calibration block(s) (usually taken at the beginning of the observation) is extracted out as a separate slice(s) in the *ListContext*. After slicing the astronomical data you will do the same to the dmcHead product, telling the task to take the same slicing organisation as slicedFrames has. Finally you run two masking tasks.

```
slicedFrames = pacsSliceContext(slicedFrames, level='0.5')
slicedDmcHead = pacsSliceContextByReference(slicedDmcHead, slicedFrames)
slicedFrames = slicedFlagChopMoveFrames(slicedFrames,
  dmcHead = slicedDmcHead, calTree=calTree)
slicedFrames = slicedFlagGratMoveFrames(slicedFrames,
  dmcHead = slicedDmcHead, calTree=calTree)
```

The tasks slicedFlagChopMove and slicedFlagGratMove flag data taken while the chopper and grating were moving, creating the Masks UNCLEANCHOP and GRATMOVE. As data is taken continuously—it does not stop for chopping, grating movements, nodding, or even rastering—those taken during movements should be masked out. These masking tasks use automatic criteria, mostly taken from the calibration tree, to determine if a readout needs to be flagged as potentially bad. See Chap. 4 for how to modify and add to these masks, and later here for how to inspect the masks, although we do recommend that you accept the default masking.

Now, what is this slicedActivateMasks task? Some pipeline tasks produce masks others may propagate masks. Tasks that create masks also by default activate them. Once activated, either by being created or via the activateMasks task, a mask remains so until deactivated. You deactivate a mask either with the task activateMasks or deactivateMasks, and these tasks and their parameters are explained in the PACS *URM* (<LINK>). Because some tasks run better if only certain masks of the input frame are "active" and others are "inactive", we recommend that you specify which masks should be active and which should be inactive before running these sensitive tasks; that is what slicedActivateMasks does.

This marks the end of Level 0.5, up to which the data reduction is AOT independent. Before continuing with the rest of the pipeline you may wish to save the slicedFrames back to the *ObservationContext* you started from (myobs here), and save that to a pool (to disc). This you would do so that when you work on myobs later, you can see the full product—the Meta data, each Level, all the auxiliary data, etc. When saving the new Level 0.5 product you have just created back to myobs, you will be overwriting the Level 0.5 product that was there before, i.e. that which the HSA produced via the automatic pipeline. If you wish to later compare the HSA result with yours, you can always copy myobs first:

```
myobs_hsa = myobs.copy()
```

and then save that to a new pool. Note: if you save two ObservationContexts of the same obsid to the same pool, when you use getObservation later to load one back into HIPE, you will get only the last saved ObservationContext. To avoid this you can save the myobs_hsa to a pool with a different `poolName`.

First, to copy your new Level 0.5 product (your blue or your red reduced data) to the ObservationContext, you first grab the whole of Level 0.5, then you copy into in your red or blue reduced ListContext, and then you place that back into the ObservationContext. So, first:

```
if myobs.level0_5 == None:
   pc0_5 = PacsContext()
else:
   pc0_5 = PacsContext(obs.level0_5)
```

This if-loop will do the following: if there is already a Level 0.5 in myobs then extract out the whole level—here we call it pc0_5, and it is of class *PacsContext*—but if there is nothing presently in Level 0.5 then a new, empty variable, of class *PacsContext* and (here) called pc0_5 is created.

Within pc0_5 can be the red *and* the blue data reduced to Level 0.5. If your data were already pipeline-processed then of course a Level 0.5 will already exist and will be filled with the red and blue camera products. The level will also exist if this is the second time you are running this part of the pipeline, first you ran it on the blue camera and now you are running it on the red. When you next add your new blue and red camera Level 0.5 products then you will overwrite what was there before (hence we suggested that you copy the whole ObservationContext if you want to compare to the automatic pipeline-produced data). If you want to be sure to clear the level before copying into it you can use the command,

```
obs.level0_5 = None
```

Next you put your newly-created red or blue slicedFrames product into pc0_5:

```
# add the pipeline processed result to the PacsContext; this is camera-specific
pc0_5.spectrometer.fitted.getCamera(camera).product = slicedFrames
pc0_5.spectrometer.dmc.getCamera(camera).product = slicedDmcHead
```

where the variable "camera" was defined in the beginning of this chapter ("red" or "blue").

Finally you can copy some of the Meta data and slicing logic information to the Level 0.5 (so it is there for you if you later extract out that level to look at), and then place pc0_5 back in to myobs:

```
pacsPropagateMetaKeywords(myobs,'0.5', pc0_5)
addSliceMetaData(pc0_5, -'0.5')
myobs.level0_5 = pc0_5
```

New Meta data are added to the bottom of the Meta data listing you will see in the Observation viewer. To save myobs to pool you can use the task saveObservation, explained in Chp. 1, and again note that if you save the *ObservationContext* to the same pool you took it from, when you get it from pool next time you will get this new version, not the old one.

You can also save just the slicedFrames or the PacsContext pc0_5 to pool: this is explained in Chap. 4 and *DAG* <LINK>.

Next we will tell you how to save and inspect the products you have just created.

3.4.2. Inspecting the results

What are you likely to what to check of your frame as you work through the pipeline to the end of Level 0.5? One obvious thing is to check the effect the reduction tasks have had on your spectra by looking at befores and afters. You could also look at the pointing, the masking, and the relationship

between the movements of the chopper, grating, and nodding and how they modulate your signal. These latter would be mainly to find out what happens during an observation, they are not a diagnostic of the pipeline processing. We will introduce you to the Status; tell you how to look at the chopper and grating; show you how to (over)plot the spectral signal; the pointing; and show you how to inspect masks. In this part of the pipeline there is not that much to check; looking at the spectra in more detail is discussed in Sec. 3.5.

To inspect your reduced product you need to extract them out of the *ListContext*, out of "slicedFrames". To work out what a particular slice in a slicedFrames (or slicedRamps, although there is little to check of the *Ramps* products) corresponds to you need to look at the BlockTable—each individual *Frames* product in slicedFrames has a BlockTable and there is also a MasterBlockTable for slicedFrames. This is explained in Chap. 4. There will also soon be a "method" or task that will list what each slice in your slicedFrames is (meanwhile we provide in Sec. 3.5.3.1 a very basic selection script). As the slicing proceeds, more *Frames* slices are added to slicedFrames. The first slice will usually be the calibration block and as, in our current AOT implimentation, only one calibration block is done at the beginning of each observation, probably only one calibration slice will be created. You can check on this with the command

```
print slicedFrames.getNumberOfCalFrames()
print slicedFrames.getNumberOfFrames()
print slicedFrames.getNumberOfScienceFrames()
```

to see the number of calibration, all, and science frames in slicedFrames. At this point in the pipeline the slices correspond only to different raster positions, so each individual slice can contain data from different instrument configurations: nod, chop, wavelength range, grating scan number. To extract out a particular slice you can use

```
myframe=slicedFrames.getScience(i)
```

where i is the ith science frame (not, note, the ith of all frames) you want to extract out (remembering that 0, not 1, is the 1st). This method is an alternative to the

```
myframe=slicedFrames.refs[i].product
```

which has been introduced before and which simply extracts sliced number i from slicedFrames. You can also get a list of the slice numbers from the MasterBlockTable in the column "FramesNo".

The instructions here expect you to be working on a single frame/slice of a slicedFrames.

To know the dimensions of your frame (or ramps), use:

```
print myframe.dimensions
# giving us something like: array([18, 25, 672], int)
print myramp.dimensions
# giving us something like: array([18, 25, 672, 4], int)
```

The first 3 dimensions of myframe will be the same as those of myramp (the 1st and 2nd are spatial axes, the 3rd is the time-line and later spectral axis): the "4" in the 4th dimension of myramp are the 4 averaged readouts per ramp, and as these are fit when creating myframe, that dimension has disappeared.

Another thing you can check are the Meta data of your individual slices, your individual *Frames* (e.g. using the Observation Viewer). This works after you have run the tasks pacsPropagateMetaKeywords and addSliceMetaData, as these add Meta data to the *Frames* in slicedFrames. New data are added to the end of the listing, and some of these information indicate what your slices contain. (Unfortunately, at present these new Meta data are a little brief.) See Chap. 4 for more information on the Meta data keywords relevant to your observation.

There are two approaches to looking at what is in your ramps and frames: use one of the viewer applications, or plot out bits of the data.

Tip

Note that when you look at images of the PACS detector you will see that the Y length is 18 and the X length is 25. However, C, python and java expect references to (row, column) which here is (Y,X), and this is why the lengths are actually always listed or referred to as 18,25.

Tip

You should use the .copy() method (first introduced in towards the end of Sec. 3.4.1) to make a secure copy of a product, and that you can do this for single *Frames* products and *slicedFrames* products. You do this because >slicedFrames_save=slicedFrames does not actually copy slicedFrames, it just creates a new pointer to it, and so anything you change in slicedFrames will also change in slicedFrames_save. We add here that the same holds to the product placed in slicedFrames, i.e. the individual *Frames* slices. For example, doing the following on a single frame slice:

```
signal=frameSlice1.getSignal(8,12)
signal=2*signal
frameSlice1.setSignal(8,12,signal)
```

will not only change frameSlice1, but you will find that the first slice in slicedFrames has also been changed. So you need to do the follow to the product (a single *Frames* or a *slicedFrames*) before working on it:

```
frameSlice1=framesSlice.copy()
slicedFrames1=slicedFrames.copy()
```

Tip

There are many "methods" you can use on your *slicedFrames*, or *Frames,* or any product to interact with it—add to, remove from, inspect, list etc. "Methods" are described in the *DRM* entry of slicedFrames, or Frames, or whatever.

3.4.2.1. GUIs

There is a nice PACS product viewer (right click on a single *Frames* product to access it) which shows the detector layout and the spectra in the pixels. In this way you can look at the spectra, in the form of signal vs readout (#time), for each pixel, one by one. It allows you to plot flagged data and overplot Status values on the signal datapoints. This was called the MaskViewer before, and using it as a mask viewer is explained here in 3.4.3.1. A screenshot of the PACS product viewer:

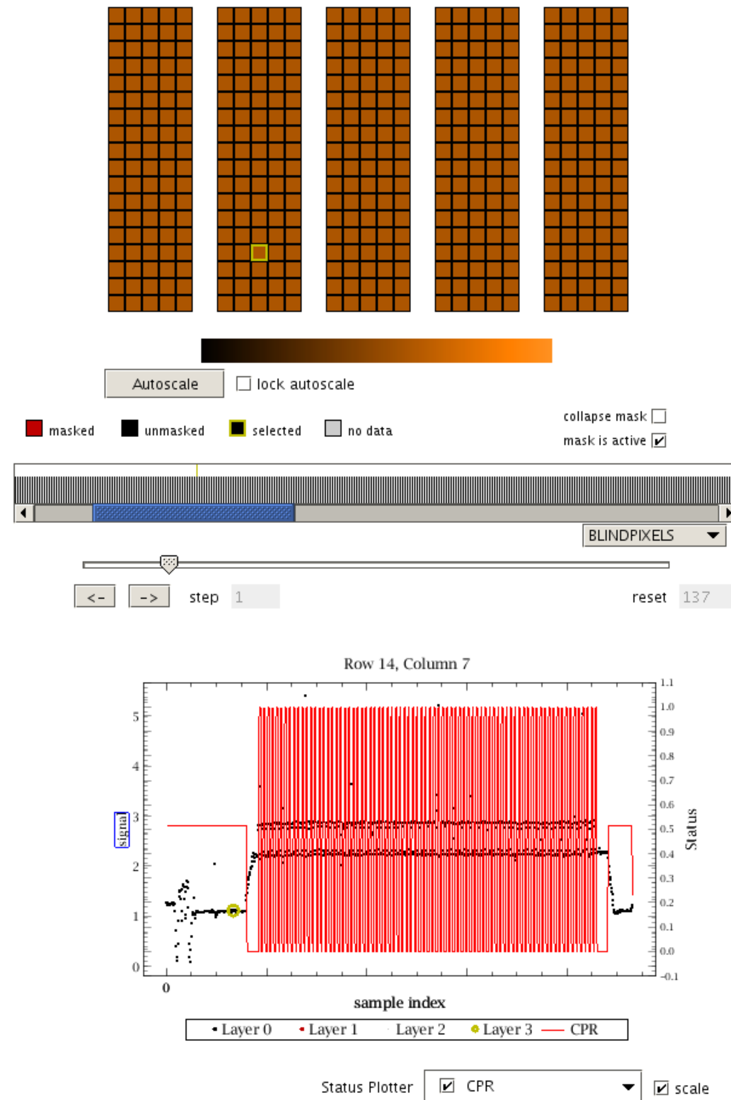


Figure 3.2. The PACS Product Viewer

The top part shows the PACS detector, from which pixels are selectable for viewing. The 25 columns are the 25 spaxels, and in each are 18 pixels containing the spectral data, although pixel row 0 and 17 contain no astronomical data. The bottom is the plot of the data from the selected pixel, and in the middle (black stripy block) is an X-axis scroll bar. In the plot, masked data are plotted as red dots, otherwise the data points are black dots. You can select which masks to plots via the drop-down box on the right of the central scroll bar ("BLINDPIXELS" in the screenshot), and you can see which array layer is displayed on the top by the small yellow circle on the plot.

You can also chose various Status values to overplot on datapoints, via a drop-down menu be the bottom of the plot (here we have plotted CPR in red over the datapoints in black. You can zoom in on the plot by selecting a window within the plot panel, and you can obtain a menu of actions via a right-click inside the plot. The Status table is introduced in 3.4.2.2 and detailed further in Chap. 4, so read there to know more about what Status values you may want to look at.

Note that the PACS product viewer will not plot wavelength on the X-axis.

As of HIPE continuous build version 4.0.461 (User track 4.x) the SpectrumExplorer GUI (first mentioned in Chap. 1) can be used to inspect *Frames* products in a friendly way. This will allow you to overplot spectra (flux vs wavelength) from different pixels and different time-frames of your data (although note that it is slow when un/plotting many spectra at once). To see if the SE will work on your data you need to extract individual *Frames* slices out of slicedFrames and run it on those. Use

of the SE is described in <LINK>. If it is not offered for your frames then you will need to inspect your spectra in a more manual way; how do to this is described below. In these next sections we will also explain a little about what you will be looking for when you inspect your frames, and we will also explain how to plot the pointing; hence it is worth reading the next sections even if you use the SE.

3.4.2.2. What to look at in the Status: chopper and grating

The Status is a attached to your *Frames* or *Ramps* product (not the *slicedFrames* product, but the individual *Frames* slices therein) and holds information about the instrument status, where the different parts of PACS were pointing and what it was doing, all listed in time order. We explained in Sec. 3.4.1 how to view the Status: use the Dataset Viewer, TablePlotter, or OverPlotter <LINK>. The entries in the Status table are of mixed type—integer, double, boolean, and string. The ones that are plain numbers can be viewed with the Table/OverPlotter, the others you need to look at with the Dataset Viewer. (Overplotting to see clearly entries that have very different Y-ranges can be a bit difficult.) In Chap. 4 is explained more about the Status and how you can plot the entries that are not numbers.

For a *Frames* product the Status column entries are single values per time stamp (per reset index) and for a *Ramps* product some entries will be an array of values instead. The Status is added to as the pipeline processing proceeds. The Status table of a *Frames* contains the same as, and more columns than, a *Ramps* and is more useful to look at (the *Frames* has had more tasks run on it). What you can check at point in time are the chopper movements and the grating movements, and if you like also also how the signal modulates with these (for your interest, as this is not very useful as a diagnostic of the pipeline). To remind you what the chopper and grating do: (i) The chopper moves between a position that is pointing at your target and a position that is pointing at blank sky. The blank-sky data will be subtracted from the on-target data in order to remove effect of the telescope background and also remove the dark current. This chopping happens with a very high frequency (as it samples at each grating step). The chopping necessitates a nodding, and our arrangements is that chop+ nod A is on-target and chop- nod A is off-target, while chop- nod B is on target and chop+ nod B is off-target. In the next pipeline stage we show you how to compare the spectra from these different combinations, for now we only explain how to plot the Status parameter "CPR", which is the chopper position in instrumental units. (ii) The grating moves with a certain speed and step size in order to sample the wavelength range at the dispersion you have requested, and does this usually at least twice (once down in wavelength and once up in wavelength). We will show you how to plot the Status parameter "GPR", which is the grating position in instrumental units.

You can also look at the pointing, which uses information contained in the Status. More on this later.

You can look at these Status parameters with one of the viewers that work on the Status, or you can plot them manually. The viewers are explained in <LINK>, here we introduce the manual method (and also explain what you should see).

Manual method

The following is an example of how to plot, with full annotation, the Status parameter CPR (chopper position), GPR (grating position) and signal together for a *Frames* product:

```
# first create the plot as a variable (p), so it can next be added to
p = PlotXY(titleText="a title")
# (you will see p appear in the Variables panel)
# add the first layer, that of the status CPR
l1 = LayerXY(myframe.getStatus("CPR"), line=1)
l1.setName("Chopper position")
l1.setYrange([MIN(myframe.getStatus("CPR")), MAX(myframe.getStatus("CPR"))])
l1.setYtitle("Chopper position")
p.addLayer(l1)
# now add a new layer
l2 = LayerXY(myframe.getStatus("GPR"), line=0)
l2.setName("Grating position")
l2.setYrange([MIN(myframe.getStatus("GPR")), MAX(myframe.getStatus("GPR"))])
l2.setYtitle("Grating position")
p.addLayer(l2)
# and now the signal for pixel 8,12 and all (:) time-line points
```

```
l3 = LayerXY(myframe.getSignal(8,12), line=2)
l3.setName("Signal")
l3.setYrange([MIN(myframe.getSignal(8,12)), MAX(myframe.getSignal(8,12))])
l3.setYtitle("Signal")
p.addLayer(l3)
# x-title and legend
p.xaxis.title.text="Readouts"
p.getLegend().setVisible(True)
```

The Y-range is by default the max to the min, so you would not need to specify those if you wanted to plot from max to min. The "l1." commands create new layers which are then added to the plot with p.addLayer(). Each new layer is plotted in a different colour.

If you want to plot for myramp rather than myframe, then around every myramp.getStatus() or myramp.getSignal() command you will need to write RESHAPE(), for example:

```
sey = RESHAPE(myramp.getSignal(8,12))
l3 = LayerXY(sey, line=2)
l3.setYrange([MIN(sey), MAX(sey)])
```

Why the RESHAPE? The dimensions of a *Frames* product is 18,25,z where z is the number of slopes present. When you plot pixel 8,12,[all z] you are plotting a 1D array. For our averaged *Ramps* product, however, the dimensions are 18,25,z,4, and selecting out pixel 8,12 will give you a 2D array to plot; PlotXY does not like this, so you need to reshape the data.

If you fiddle with the plot Properties and/or zoom in tightly the plot you just made should look something like this:

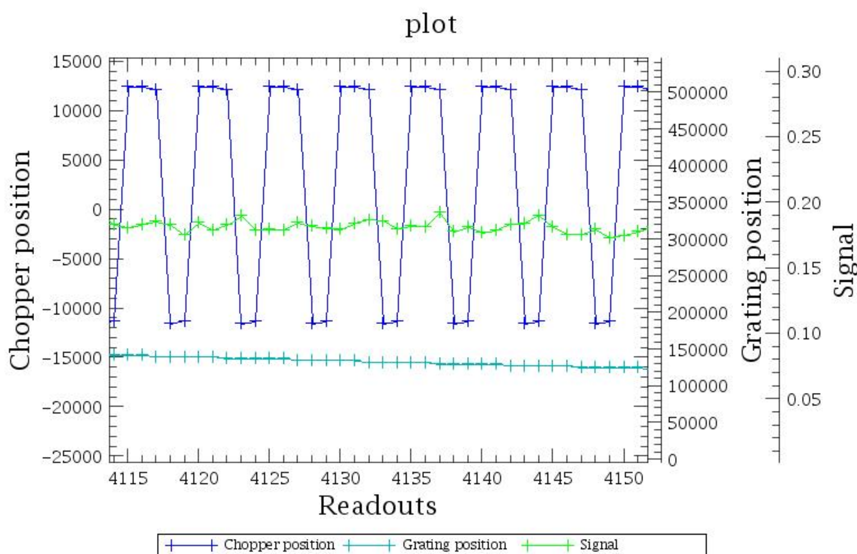


Figure 3.3. A zoom in on PlotXY of the grating and chopper movements for frame

What the figure above shows is that the chopper (dark blue) is moving up and down, with 2 readings taken at chopper minus and 3 readings taken at chopper plus. The grating (light blue) is moving gradually, and its moves take place so that 2 minus and 3 plus chopper readings are all made at each grating position (there are 5 grating points for 5 chopper points). The signal (green) can be seen modulating with chopper position, as it should be because one chopper position is on target and the other on blank sky. Your data should show a similar arrangement of movements (but with different samplings).

3.4.2.3. Plotting the spectrum

If you are not using the Spectrum Explorer to look at the spectra, you can use the manual methods discussed here. Here is also discussed a little of what you will be looking at when viewing your spectra.

If you just want to plot the signal of frame, in the (time=array) order it is held:

```
p=PlotXY(myframe.getSignal(8,12), titleText="your title", line=0)
p.xaxis.title.text="Readouts"
p.yaxis.title.text="Signal [Volt/s]"
```

(The titles are not necessary.) To do the same for myramp you need to add RESHAPE() to the command:

```
PlotXY(RESHAPE(myramp.getSignal(8,12)))
```

It is not necessary to specify >p=PlotXY(), you could just type >PlotXY(), but with the first you can add more things to the plot afterwards (more data, annotations...).

To plot a full spectrum, that is signal versus wavelength after you have run the slicedWaveCalc task,

```
p = PlotXY(myframe.getWave(8,12),myframe.getSignal(8,12),
   titleText="title",line=0)
p.xaxis.title.text="Wavelength [$\mu$m]"
p.yaxis.title.text="Signal [Volt/s]"
```

The "methods" .getWave(8,12) and .getSignal(8,12) allow you to extract out the wavelength and signal arrays for pixel 8,12 (over a range of 18,25, where 0,: and 17,: do not contain useful data). You can find more information about the methods for the *Frames* (or *Ramps*) product by looking in the *DRM* <LINK>.

A method is a set of commands that you can call upon for an object (myframe) of a class (*Frames*), these commands will do something to the object you specify—in this case it extracts out the signal or wavelengths from the frame. Methods can have any number of parameters you need to specify, in this case it is just the pixel number—8,12.

Depending on what type of observation you are looking at (e.g. SED vs line scan) and at what pipeline stage you are looking at your plotted spectrum, it is possible that you will see something that does not look quite like right. When you plot using the command above, you are plotting everything that is in your dataset. This can include: data from the calibration sources (taken at the key wavelengths only); multiple spectra, if your observation includes more than one field-of-view (for rastered/dithered observations) and grating scan; data taken while the telescope was slewing; data from the two chop positions and from the two nod positions (chops and nods are not combined until a later stage of the pipeline). So, if you have a line scan AOT and your plot looks like this:

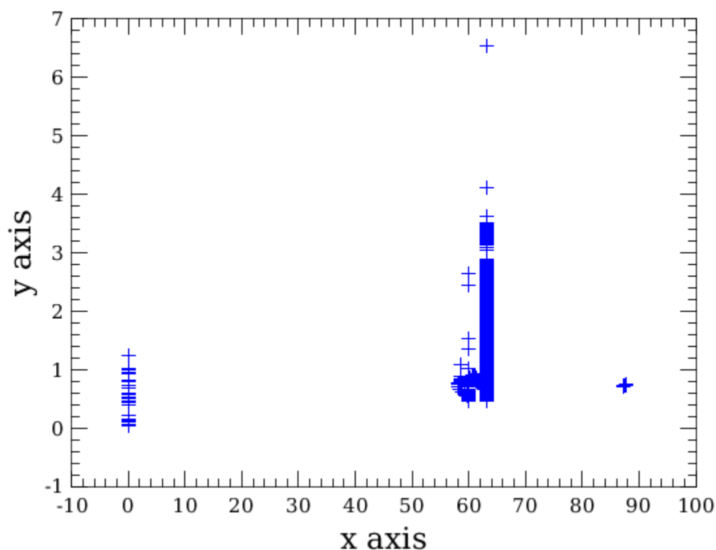


Figure 3.4. Level 0.5 line scan spectrum: entire dataset

then you probably still have in your frame the calibration block. Zoom in on the wavelength you requested in your AOR, and you should see this:

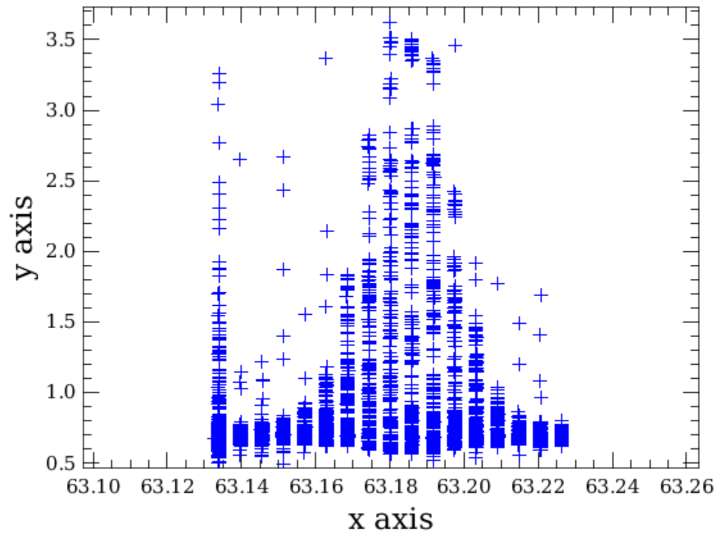


Figure 3.5. Level 0.5 line scan spectrum: zoom

In the spectrum shown above the spectral line is "filled in", which is not what one would expect. However, bear in mind that these data have not yet been corrected for the nodding and chopping, and may include multiple rasters. This spectrum shown is that of 5 different pointings. In the next section we will show you what this spectrum becomes when further pipeline-processed.

Each of the 16 active pixels that feed into each spaxel (spatial pixel, a.k.a. module) sample a wavelength range that is slightly shifted with respect to the next pixel. Hence if you overplot several pixels of a single module (e.g. 1 8 and 16 of module 12) in different colours you will see this:

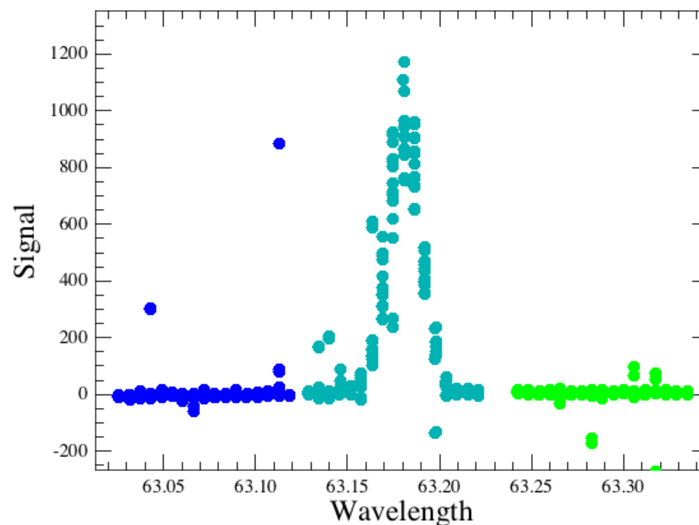


Figure 3.6. 3 pixels of a single module

where the dark blue is pixel 1,12; light blue is 8,12; green is 16;12. Hence, if you just plotted pixel (16,12) and the spectral line looks partial, this may be the reason why (noting though that with more recent AOTs the wavelength range sampled is wider than shown here). If you want to plot the spectra from all pixels of a module at once (in one colour), then in the PlotXY command you will need to

use the RESHAPE command (because otherwise you are asking PlotXY to plot out a 2D product). The following script is to plot all the active pixels (1 to 16 inclusive) of module 12 (the central spaxel of the field of view):

```
p = PlotXY(RESHAPE(myframe.wave[1:17,12.:]),RESHAPE(myframe.signal[1:17,12,:]),
   titleText="title",line=0)
p.xaxis.title.text="Wavelength [$\mu$m]"
p.yaxis.title.text="Signal [Volt/s]"
```

Here we have changed the way to extract the wavelength and signal arrays because the method used before does not allow you to specify a range of pixels to plot. The .wave and .signal syntax calls upon the "wave" and "signal" datasets of myframe.

Consider also that the dispersion is also important in determining what you see when you plot a single pixel. If your dispersion is low then it is possible that a spectral line as viewed in a single pixel will "fall" a bit between the gaps in the dispersion. You will need to plot all the pixels of the module to see the fully sampled spectrum.

3.4.2.4. Plotting the pointing

Since you have run the tasks to calculate the pointing, you can plot the RA Dec movements of the central pixel (i.e. where was PACS pointing?). Positions are held in three places in your observations: the programmed pointing from your AOR is given in the Meta data (see Chap. 4), the Status contains the RA and Dec for the central pixel, and the RA and Dec for each pixel is held in separate datasets attached to the *Frames*. To plot the central spaxel's position (the "boresight"):

```
p = PlotXY(myframe.getStatus("RaArray"),myframe.getStatus("DecArray"),
           line=0,titleText="text")
p.xaxis.title.text="RA [degrees]"
p.yaxis.title.text="Dec [degrees]"
```

where you will get something that shows the entire track of PACS while your calibration and astronomical data were being taken:

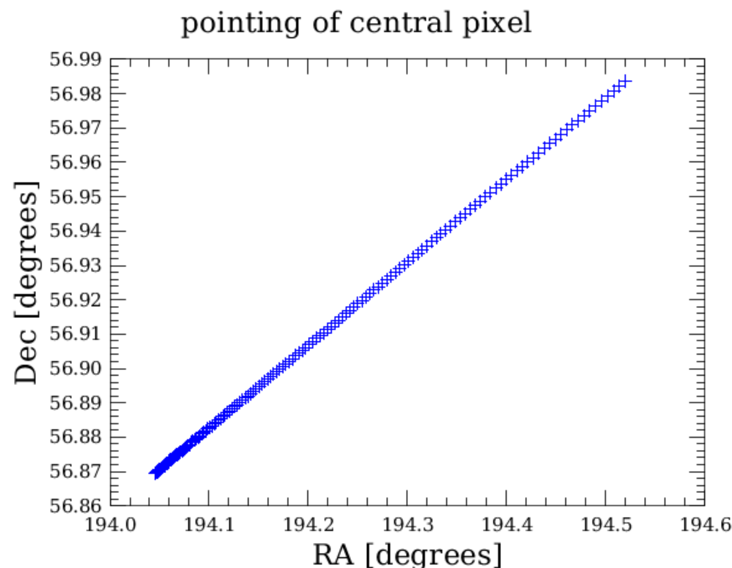


Figure 3.7. Movement of PACS during an observation

To plot all the spaxels' sky positions together with the source position for the last datapoint of myframe:

```
pixRa=RESHAPE(myframe.ra[:,:,-1])
pixDec=RESHAPE(myframe.dec[:,:,-1])
```

```
plotsky=PlotXY(pixRa, pixDec, line=0)
plotsky[0].setName("spaxels")
srcRa=slicedFrames.meta["ra"].value
srcDec=slicedFrames.meta["dec"].value
# note, -"ra" is in -"myobs" as well as -"slicedFrames"
plotsky.addLayer(LayerXY(Double1d([srcRa]),Double1d([srcDec]), line=0,
  symbol=Style.FSQUARE))
plotsky[1].setName("Source")
plotsky.xaxis.title.text="RA"
plotsky.yaxis.title.text="Dec"
plotsky.getLegend().setVisible(True)
```

giving you something like this:

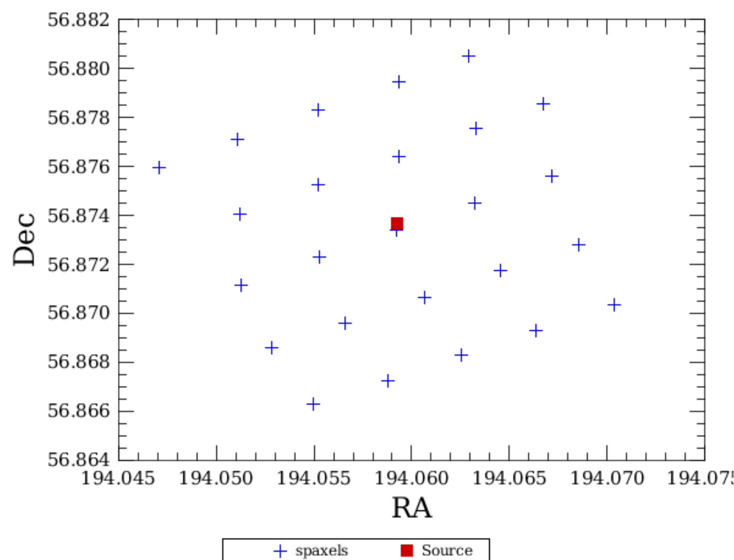


Figure 3.8. Pointing of the PACS IFU and the source position. This also shows you what the on-sky layout of the IFU

Explanation:

- RESHAPE() is necessary for ra and dec because they have dimensions X,Y and Z, and so extracting out only the last entry of the third dimension (-1) gives you a 2D array.
- myframe.ra/dec are the ra/dec datasets, which is not the same as the Ra/DecArray in the Status. "ra" and "dec" have dimensions X,Y,Z and were produced by the task specAssignRaDec, whereas Ra/DecArray are 1D (they are just for the central pixel), and were produced by the task specAddInstantPointing.
- The "-1" is how you ask to plot the ra for the last element of the array; you can of course ask to plot all but that will make a very busy, and *very* slow, plot.
- srcRa and secDec are taken from the Meta data of the ObservationContext or the slicedFrames (if it is in there), these being the source positions that were programmed in the observation. Here we plot them as Double1d arrays, because PlotXY cannot a single value (which is what they are), so we "fake" them each into an array (in fact we are converting them from *Double* to *Double1d*).
- The different syntax here to previous examples shows you how flexible (or annoying) scripting in our DP environment can be. p[0].setName("spaxels") does the same as the l1.setName("signal") in a previous example. The first layer (layer 0) is always the one created with the "PlotXY=" command, subsequent layers can be added with the "plotsky.addLayer(LayerXY())" command.

If your observation includes several raster pointings you may want to plot the pointings for each. To to this you need to select out the relevant slices from slicedFrames that corresponds to each pointing

(each slice is in fact a unique pointing), and then you can use the same commands as written above to plot the pointings of each subframe.

More about the numbering of the modules of the frames and spaxels of the cubes is given in Sec. 3.6.2.3.

3.4.2.5. Display

It is also possible to look at your frame in 2D using a display tool <LINK>. This is launched with:

```
Display(myframe.signal[:,:,100:150])
```

and when you zoom in you will see a 2D image: we are looking at the signal part of frame. In the example call all Y and X ranges but only 50 wavelength/time-line layers are displayed (to plot all uses a lot of memory). Plotting "spectra" is not possible with Display; you can, however, scroll through the signal time-line using the scroll bar at the bottom right of the image. RA and Dec will be given by Display.

The 100:150 specified above are the array positions, not the wavelength positions. If you want to Display specific wavelengths of your frame you need to figure out what array positions are what wavelengths. To do this you can extract out the wavelength array, and by printing or plotting it, you can identify what array positions correspond to which wavelengths. So,

```
wave=myframe.getWave(8,12)
PlotXY(wave)
```

will plot a line of points, array position on the X axis and wavelengths on the Y axis.

3.4.3. Masks

First we introduce the PACS Product Viewer GUI—see Sec. 3.4.2.1—and then explain how to plot single spectra with and without masked data. The masks that you may want to check in a quantitative way are the RAWSATURATION, SATURATION and NOISYPIXELS: how noisy are the spectra from the pixels with the latter mask (will you want to exclude them when creating your final cubes?), and do the spectra masked as saturated really look saturated (see Sec. 3.4.1), e.g. does saturation occur at the peak flux and does the signal level flatten off (see chap. 4)?. UNCLEANCHOP, BADPIXELS and GRATMOVE can of course also be inspected, but only under rare circumstances are they likely to be incorrect. If you are curious you may want to compare the former and latter masked data to the movements of the CPR and GRP, to see if the masks have been set at times when the chopper or grating were moving.

3.4.3.1. PACS Product Viewer (PPV) GUI

With the PPV you can see the time-line spectra of each pixel, the masks, and you can overplot some Status parameters. You can also see which masks are active, although this can also be done on the command line:

```
print myframes.mask.activeMaskTypes
```

The PPV works on a frame and a ramp but not a cube. Using the PPV you can also create and modify masks yourself, although if you wanted to do a mass-flagging of data it is easier to do that with a python script (see Chap. 4 for some help). To use the PPV on a PACS product simply right-click on it in the Variables panel and it will be offered.

A screenshot of the PPV was shown in Sec. 3.4.2.1, and a zoom on the plot part is shown below. In the PPV the plots you see, when you look at any pixel, are the actual detector signal time-line for the selected pixel—"signal" vs "sample index" (never wavelength). If you use it on a *Ramps* product, as in the example here, then you will see in the plot 4 lines of datapoints following a zig-zag pattern. In the beginning the detector was looking at the internal calibration sources (the narrow messy block of data at

the very left). Then it moved to observe an astronomical source, moving back and forth in wavelength leading to an up-down pattern in the data-line (as the signal varies strongly with wavelength, if only due to the spectral response of PACS): 3 repeats of wavelength switching performed in nod position A (the first 3 "triangles"), B (second 3), B (third 3), and then again A (final 3). (Bear in mind that if your observations are in a flat part of the relative spectral response function and of a flat-spectrum, or very faint line, source, then you may not see well-defined triangle shapes because the flux from your source does not vary much with wavelength.)

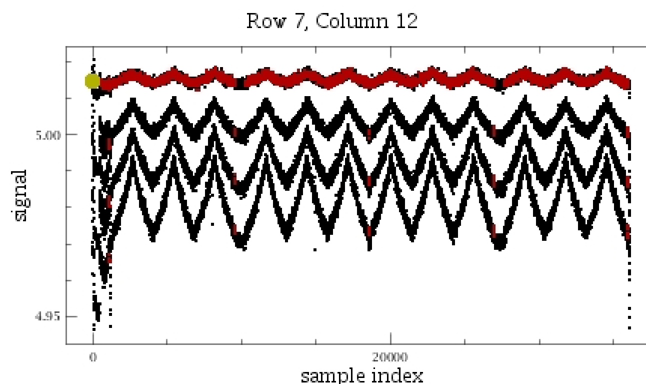


Figure 3.9. The MaskViewer plot

The plot is based on PlotXY, and so the functionalities of PlotXY are available to you <LINK> (e.g. use the properties to change the size of the data point dots). If you zoom in very tightly (right click inside the plot), and change the properties so that lines are joining the datapoints, you will see that the data of these 4 lines are joined, from the top to bottom. Each line of 4 descending dots is a single ramp of your *Ramps* product.

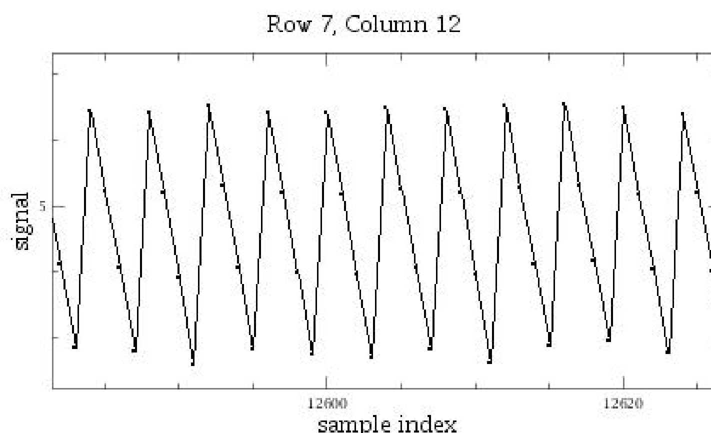


Figure 3.10. Zoom on a "spectrum" of a pixel of ramp in the MaskViewer

The slope of the line joining each 4 is similar to what is fit by the task fitRamps; this slope is a measure of the photocurrent in the detector and related to the infalling FIR flux. If you look at your *Frames* data in this same way you will only see 1 line of data, the values thereof being the fit slopes.

If you zoom in tightly on the left of your timeline you should see the data of the calibration block (taken at the key wavelengths only). The two calibration sources have a different temperature and we chop between them, so you should see either 2 lines of datapoints of different signal level (for myframe) or 2 lines of sets_of_4 datapoints of different mean level (for myramp).

(Data that have been flagged are plotted in a different "layer" to the rest and by default as small red dots. Thus if you change the plot properties to have a line+points, the flagged data will be joined to themselves and not to the rest, leading to a plot that looks a little different to this. But this is just a facet of the plotting, not of the data themselves.)

3.4.3.2. Plotting masked data manually

You can plot and overplot masked and unmasked data-points for single pixels using PlotXY. It is a more cumbersome way of looking at your data, but it is necessary at present if you want to overplot different datasets of your frame (in this case, the signal and the masks). Here is an example of plotting all datapoints for pixel 8,12 and then overplotting only the ones not masked for UNCLEANCHOP:

```
flx=myframe.getSignal(8,12)
wve=myframe.getWave(8,12)
p=PlotXY(wve,flx,line=0)
index_cln=myframe.getUnmaskedIndices(String1d(["UNCLEANCHOP"]),8,12)
p.addLayer(LayerXY
   (wve[Selection(index_cln)],flx[Selection(index_cln)],line=0))
```

What does this do?

- The first two lines are how you extract out of your frame the fluxes and wavelengths and put in each them a new variable (which is of class *Double1d*, as you will see if you type > print flx.class).
- The third command opens up a PlotXY and puts it in the variable "p", which you need to do if next want to add new layers to the plot. Line=0 tells it to plot as dots rather than a line (the default).
- The next command places into a (*Int1d*) variable called index_cln the X-axis (wavelength) array indices of the frame where the data have not been flagged for the specified mask. The parameters are the mask name/names (listed in a *String1d*) and the pixel coordinates (8,12). (You can use getMaskedIndices to select out the indices of the masked data points.)
- Finally you add a new layer to "p", in which you plot the unmasked data points, and these appear in a new colour. The syntax wve[Selection(index_cln)] will select out of wve those array indices that correspond to the index numbers in index_cln. You need to use the "Selection()" syntax because you are doing a selection on an array.

(In the DP scripting language there is more than one way to do anything, and you may well be shown scripts that do the same thing but using different syntax. Don't panic, that is OK.)

To now look at your masked—unmasked signal vs the mask—you mix-and-match the instruction here with those given previously for plotting masks (and noting that it is easier to do if you plot the signal against readout- or time-array position rather than wavelength). To look at, for example, the signals masked as UNCLEACHOP and the chopper movements for the same datapoints, you will plot the masked and unmasked signal and the Status CPR together. This would product a plot such as this:

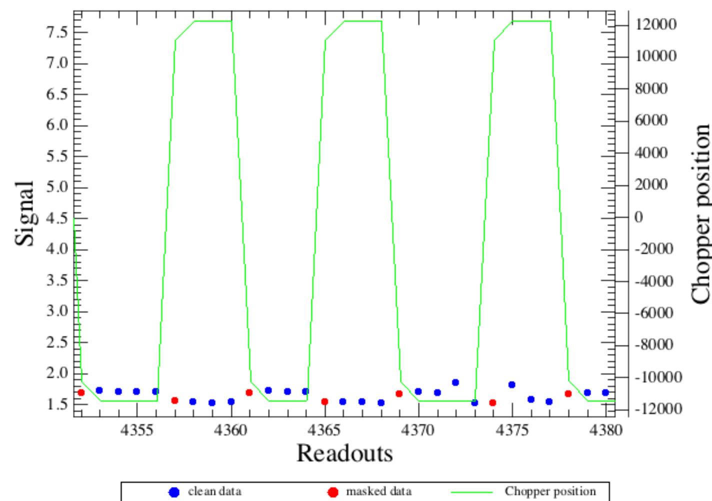


Figure 3.11. Masked/unmasked data v.s. Status

which was produced with the following script:

```
signal=myframe.getSignal(8,12)
x=myframe.getStatus("RESETINDEX")
# need to plot vs x so that the selected data ("Selection" below) are
# of the same dimensions as the unselected data
p=PlotXY()
l1=LayerXY(x,signal,line=0,symbol=Style.FCIRCLE,symbolSize=5)
l1.setName("clean data")
index_ncln=myframe.getMaskedIndices(String1d(["UNCLEANCHOP"]),8,12)
l2=LayerXY(x[Selection(index_ncln)],signal[Selection(index_ncln)],
   line=0,color=java.awt.Color.red,symbol=Style.FCIRCLE,symbolSize=5)
l2.setName("masked data")
l3 = LayerXY(myframe.getStatus("CPR"), line=1)
l3.setName("Chopper position")
l3.setYrange([MIN(myframe.getStatus("CPR")), MAX(myframe.getStatus("CPR"))])
l3.setYtitle("Chopper position")
p.addLayer(l1)
p.addLayer(l2)
p.addLayer(l3)
p.xaxis.title.text="Readouts"
p.yaxis.title.text="Signal"
p.getLegend().setVisible(True)
```

You can see that the red datapoints (masked) were taken at the same time that the chopper was not yet stable in position, i.e. it was still moving in to a stable value. For the data shown here there are 4 readouts taken at a negative chopper position (-12000), then 4 at the positive (+12000), then back to the negative and so on. The first readout at each chopper + or - setting is still moving into position, which you can tell because the absolute value of the chopper position here is lower than those of the following 3 readouts. Changes in chopper or grating at the beginning of a "plateau" (i.e. where the values of the positions for these Status entries are stable) will be very slight.

This plot is not something you need to do when reducing your data, as the flagging of these datapoints is a well-established procedure. We have included this as an example so you can learn a little more about how PACS observations work.

In Chap. 4 we explain a little about creating your own masks.

3.5. Level 0.5 to 1

In this part of the pipeline you will do a further slicing and do the flux calibration, ending with the first of the three cubes created by the pipeline. One issue that you need to consider after you have run this pipeline is to do with the nodding part of the chop-nod AOT. As discussed in the *Observer's Manual* and here in Chap. 2, the chop-nod AOT sees PACS nodding between an A and a B pointing, and off- and on-chop positions within each nod pointing. In this part of the pipeline the chop-off and chop-on positions are subtracted, and you may want to check the before and the after products.

3.5.1. Pipeline steps

This stage of the pipeline corresponds to the ipipe script L1_ChopNod.py. If you are beginning from this level then follow the next 3 script boxes. Otherwise skip to the "You need to import...".

Extract out of the ObservationContext, myobs, the level0_5 product:

```
level0_5 = PacsContext(myobs.level0_5)
```

and, as before, you should also define the variables camera and calTree. You can either use the calTree that is in myobs, for example if you reduced the Level 0.5 yourself and wish to continue from there, or you can get it from HIPE:

```
# get the calTree from myobs
```

```
calTree=myobs.calibration
# get the calTree from HIPE
calTree=getCalTree(obs=myobs) # see Sec. 3 for what obs=myobs is for
# put that HIPE calTree into myobs, if you have not already done so
myobs.calibration=getCalTree()
```

Next you extract the slicedFrames from level0_5:

```
slicedFrames = level0_5.fitted.getCamera(camera).product
```

You need to import before running this part of the pipeline:

```
from herschel.pacs.spg.pipeline import *
from herschel.pacs.signal.context import *
from herschel.pacs.cal import GetPacsCalDataTask
from herschel.pacs.spg import SlicingRule
```

If you are continuing from the Level 0 to 0.5 reductions from before then you begin from these imports.

The next task is where you slice slicedFrames further, this time according to line id logic. If you have more than one spectral line defined in your AOT, extra slices are here created. Spectral ranges (for range or SED AOTs) do not get sliced. It is also necessary to slice by nod. These two slicings are done in one command: you end up with a slice per line and nod, plus the (usually) first slice being the calibration block. Remember that any repeats on the grating scan will be contained within each single slice.

```
rules = [SlicingRule("NoddingPosition",1)]
slicedFrames = pacsSliceContext(slicedFrames, slicingRules = rules, level='1')
```

The slicing by line id is done in pacsSliceContext because you have specified that the "level" to slice is 1, where the slicing logic is line id. The extra slicing by nod is commanded via the slicingRules parameter. The "rules" have been set by specifying the column name of the MasterBlockTable that you want to slice on (see Chap. 4 for more on BlockTables) and the "1" means you want to have 1 nod value to enter each new slice. This is what you want to do when reducing spectroscopy (for photometry a value of 2 is sometimes wanted). You can tell what sequence you have after slicing by looking at the MasterBlockTable, either via the Product viewer, or on the command line this would be:

```
print slicedFrames["MasterBlockTable"]["NoddingPosition"]
# in the output, 1 = A and 2 = B
```

Now you can run the pipeline:

```
slicedFrames = slicedActivateMasks(slicedFrames, String1d([" -"]), exclusive = True)
slicedFrames = slicedSpecFlagGlitchFramesQTest(slicedFrames)
# optional...
slicedFrames = slicedActivateMasks(slicedFrames, String1d(["UNCLEANCHOP",
   -"GRATMOVE", -"GLITCH"]), exclusive = True)
slicedFrames = slicedSpecEstimateNoise(slicedFrames)
# -...back to required
slicedFrames = slicedSpecCorrectSignalNonLinearities(slicedFrames, calTree=calTree)
slicedFrames = slicedConvertSignal2StandardCap(slicedFrames, calTree=calTree)
slicedFrames = slicedSpecDiffChop(slicedFrames, scical = -"sci", keepall = False)
slicedFrames = slicedRsrfCal(slicedFrames, calTree=calTree)
slicedFrames = slicedSpecRespCal(slicedFrames, calTree = calTree)
slicedCubes = slicedSpecFrames2PacsCube(slicedFrames)
```

- These tasks do the following: Flag the data for glitches (cosmic rays) using the Q statistical test, creating a mask called GLITCH. Prior to this task you need to run activateMasks to dectivate all masks (i.e. it is as if there were no masks at all); the statistical test runs a lot better this way); Optional task to estimate noise based on the signal level; Correct the signal slope (V/s) for non-linearities (based on ground-based and PV phase measurements); Convert the signal to a value that would be if the observation had been done at the lowest detector capacitance setting (if this was the case anyway, no change is made. This task is necessary because the subsequent calibration tasks have

been designed to be used on data taken at the lowest capacitance); Subtract the off chops from the on chops to remove the sky background. This will change the number of readouts and also subtracts the dark current; Apply the relative spectral response function; Correct for the pixels' response; Turn the sliced frame into a sliced cube with dimensions of 5x5 spaxels (created from the 25 modules) and Z wavelength points, with 16*x individual spectra held in each spaxel. These 16*x spectra are from the 16 pixels that feed into each spaxel (pixels 1—16) each being of a slightly shifted wavelength range than the previous, and the x runs on the grating (ups and downs).

- The task to estimate the noise is an information task only, and hence not necessary for the pipeline. Its workings are given in the *PAPT*: basically it determines the signal error at Level 1, and these errors will be propagated to the end of the pipeline (as are any errors that are included in the calibration files).
- The ipipe scripts may have an extra set of tasks listed, including "specDiffCs". At present the product of this task is not used (slicedSpecFitSignalDrift), hence it is not included here.
- The task slicedSpecFrames2PacsCube simply rearranges the data of the input frame, from 18x25 pixels to a cube of 5x5 spaxels. It does nothing else. In particular it does not exclude any masked data (that is done when creating the final cube). If you want to look at spectra from spaxels free of masked redouts you will need to select and plot in the same way as has been described previously, that is select only unmasked indices to plot. The individual slices of slicedCubes are *PacsCubes*.
- The task slicedSpecRespCal corrects for the differential pixel responses (flatfielding), their the response drift (that occurs during your observation) and subtracts the dark current for staring AOTs —for chop-nod AOTs that is done when the chops are subtracted from each other. To do this it uses the calibration blocks observed with your observation. However, at this point in time (June 2010) the dark current and nominal response used are the nominal values, rather than those from the observation itself, and we are still in the process of improving on this. See the "WorkArounds" section below.
- The task slicedRsrfCal does the flux calibration. This is based on observations of calibration stars that have been taken during the mission.
- The tasks here that change the state of the data are slicedSpecCorrectSignalNonLinearities (except for the blue dataset if you began the pipeline on a *Frames*), slicedSpecDiffChop (see Sec. 3.5.3.1.4), slicedRsrfCal, and slicedSpecRespCal (see Sec. 3.5.2.1). SlicedSpecDiffChop will subtract the on- from the off-chops, so before this task you will have for nod A and B data from chop- and chop+, now for nod A data you have only chop+ and for nod B you have chop- (as these positions are on-source). You can look in the Status columns IsAPosition, IsBPosition, and CHOPPPOS to see what nod A, nod B, and chops are in your *Frames*. (IsA/BPosition will be filled with True and False, and CHOPPOS with "+/-small/median/large".)

The glitch detection task by default it works on chopped data, and as this section is for a chop-nod AOT then you want the default case. (If you observed with a staring AOT then you need to add the parameter "splitChopPos=False".) It has been tested on chopped and non-chopped data. Glitches stand out as bright and narrow spikes in the signal timeline (more information is in Chap. 4). It is possible that some readouts which are GITCH masked will not look deviant. Extensive testing has shown that many of these readouts would have been taken just after a cosmic ray (glitch) hit the detector, but that it hit between readouts being taken and hence is not obvious in the readout before. (A later "outliers" pipeline masking task is also peformed.)

Finally you can save your slicedCubes back into the *ObservationContext* you began with, as first explained in 3.4.1:

```
if myobs.level1 == None:
   pc1 = PacsContext()
else:
   pc1 = PacsContext(myobs.level1)

pc1.spectrometer.fitted.getCamera(camera).product = slicedFrames
```

```
pc1.spectrometer.cube.getCamera(camera).product = slicedCubes

pacsPropagateMetaKeywords(myobs,'1', pc1)
addSliceMetaData(pc1, -'1')
myobs.level1 = pc1
```

3.5.2. WorkArounds

There are some particular considerations that will require to you step out of the pipeline, issues we are still dealing with. These are (i) flatfielding.

3.5.2.1. Flatfielding

Flatfielding in the context of PACS spectroscopy means making it so that the gain of each pixel has been corrected for. To tell if your spectra have been flatfielded properly, you can overplot the spectra of the 16 individual data-containing pixels of each module (i.e. pixels 1:17 of each of the 25 modules) for the same nod, raster pointing, and grating scan direction: the continua of the spectra within a single module should sit on top of each other. You can do this overplotting with the Spectrum Explorer, or the manual PlotXY method using selection syntax discussed in Sec. 3.5.3. If the spectra are offset from each other then the flatfielding, and specifically the task specRespCal, has not done a perfect job. This task is still being worked on, and in the version of HIPE you are working with it may still not be perfect.

To correct for this for line scan AOTs a function/tool has been written and placed in <LINK>. Contact the Herschel help desk to know how to import it (the location in the build had not been decided on by the time of writing this guide), or if you have an SED or Range scan AOT and need to redo the flatfielding for these data. This file contains a number of functions which were written for the Dec. 2009 Madrid data reduction workshop.

3.5.3. Inspecting the results

In the Level 1 pipeline the *Frames* contained in the *slicedFrames* are turned into *PacsCube*s contained in the *slicedCube*. The *PacsCube* contains, in each spaxel, all the spectra lined up in time order; they have not yet been mathematically combined. This is done in the next stage of the pipeline, and before that a further glitch flagging task is run.

To inspect a *PacsCube* or *Frames* slice you need to first extract it out of slicedFrames/Cubes:

```
# frame
myframe=slicedFrames.getScience(i)
# cube
mycube=slicedCubes.getSlice(i)
```

The difference in the syntax is because slicedFrames will contain at least one calibration frame along with the science frames, so you specify to select out a science slice, but the slicedCube does not, so you can simply select any slice. To get a listing of what each slice is you need to inspect the MasterBlockTable for slicedFrames. (A task of method to do this will be provided, a temporary work-around is given below.) For the *slicedCubes* there is currently no MasterBlockTable but the order of the cubes in the *slicedCubes* is the same as the order of the frames in the *slicedFrames*.

It is likely that for each frame or cube you will want to look at these individual spectra in each spaxel. As explained before, a right-click on the frame or cube in the Variables panel will tell you which viewers (GUIs) you can use to inspect the product (Spectrum Explorer and PPV), or you can use PlotXY in a manual way. For the cube created in this part of the pipeline, which has class *PacsCube*, the SpectrumExplorer will work, the PPV may not. Use of the SE is described in <LINK>. If it is not offered for your frames or cubes then you will need to inspect your spectra in the manual way.

For the Level 0.5 frame, before you send it to a cube, you may want to check the spectra after the task slicedSpecFlagGlitchFrames and those that change the state of the data (see Sec. 3.5.1; mainly the slicedSpecDiffChop, slicedRsrfCal, and slicedSpecRespCal). How to do this (GUI or manual) was

discussed in the previous pipeline's section. Here we will show you how to select out spectra manually from different nods and grating scans so you can compare them. Again, this is done most easily with the Spectrum Explorer, but the manual methods are explained here, as well as what it is you are looking at. Since the final task of this level of the pipeline only rearranges the spectra of the input *slicedFrames* to turn them into a cube, inspecting the *slicedFrames* or the *slicedCube*s will show much the same thing.

3.5.3.1. Listing and combining slices from slicedFrames and slicedCubes

To work out what slice in your slicedFrames in what, currently you need to look at the MasterBlock-Table, the individual *Frames* Status tables or the Meta data. These are all explained in a little more detail in Chap. 4, and you can access them all via the Observation Viewer on your ObservationContex or your slicedFrames. The Meta data for the slicedFrames as a whole and the individual *Frames* slices therein are uppated at the end of each pipeline, after you have run the tasks pacsPropagateMetaKey-words and addSliceMetaData. New data are added to the end of the listing, and some of these information indicate what your slices contain. (Unfortunately, at present these new Meta data are a little brief.)

Until we have written convenient methods to identify and select out slices from your ListContexts of frames or cubes, the following information will help you identify what slices correspond to what part of your observation if you want to do this on the command line.

Frames:

The frames at this point in the pipeline, before the slicedFrames is turned into a slicedCubes, have been sliced on line id, raster and nod, and each frame will contain in it data from different grating scans, but only one chop position if you are looking at slicedFrames after having run slicedSpecDiffChop. On the command line you can type this:

```
nod=slicedFrames.getMasterBlockTable()["NoddingPosition"]
line=slicedFrames.getMasterBlockTable()["LineId"]
rasterc=slicedFrames.getMasterBlockTable()["RasterColumnNum"]
rasterl=slicedFrames.getMasterBlockTable()["RasterLineNum"]
print nod, line, rasterc, rasterl
```

to get a set of *Int1d* arrays ("nod", "line", etc) containing the nod, line and raster column/line values from the MasterBlockTable. The numbers in this arrays are the slice index counters.

A conceptually easy way to look (e.g. plot) at data from a particular combination of nod, line and raster is to create a new frame containing only these parts of the observation. You will first create a Selection; say you want to select the rasterc/l value 0, the line value 1 and nod value 2 (A):

```
select=nod.where((nod == 2) & (line == 1) & (rasterc == 0) & (rasterl == 0))
```

where select now contains the index values in the MasterBlockTable that corresponds to this particular instrument configuration. You then select those frames out of slicedFrames and put them into a new, single *Frames* product using:

```
newframe=slicedFrames.select(select)
```

You can now either use PlotXY to plot the spectra of any particular pixels of the new *Frames* product, or use the Spectrum Explorer on it, or plot the pointing, and so on. Note that you can use the .select() method to select any blocks, instead of "select" in the () you can write: Selection([4,5]) to select out blocks 4 and 5.

PacsCubes:

For PacsCubes there is no MasterBlockTable but the organisation of the slices is the same as for the slicedFrames that was fed into the task slicedSpecFrames2PacsCube. Since there is no MasterBlock-Table, the syntax given for slicedFrames above will not work here. Neither will the select method.

3.5.3.2. For the *Frames*

Looking at single *Frames* can be done with the Spectrum Explorer; the more manual methods are described here in case you have a version of HIPE for which the SE does not yet work on PACS products. Bear in mind that when looking at your spectra, unless you specify—i.e select for—to show only the unmasked data, your spectra will look noisy. We do not include here how to select unmasked datapoints only, as that is described in Sec. 3.4.3.2. The Spectrum Explorer allows you select masks to plot.

Before and after tasks

To compare the spectra before and after a task has been run, e.g. the slicedRsrfCal and slicedSpecRespCal tasks, is simple and uses variations on the same recipies we have already given for the previous level's data reduction. Remember to copy the data before you run it through tasks if you want to compare a before and after result. You can either copy the whole slicedFrames, or an individual element thereof:

```
# copy a slicedFrames
slicedFrames_b4 = slicedFrames.copy()
# copy a single slice
slice1_b4 = slicedFrames.refs[1].product.copy()
# or also copy a single slice
slice1 = slicedFrames.getScience(0).copy
```

As before, to plot the spectrum from a pixel of a slice you need to extract the slice from the *slicedFrames*, and then you follow the same plotting commands that were introduced in 3.4. So if you extracted "slice1_b4" before you ran slicedRsrfCal and "slice1_aft" after running the task, then:

```
sig=slice1_b4.getSignal(8,12)
wve=slice1_b4.getWave(8,12)
p = PlotXY(wve,sig,titleText="your title",line=0)
p[0].setName("before rsrf")
p[0].setYrange([MIN(sig), MAX(sig)])
p[0].setYtitle("V/s")
sig=slice1_aft.getSignal(8,12)
wve=slice1_aft.getWave(8,12)
p.addLayer(LayerXY(wve,sig),line=0)
p[1].setName("after rsrf")
p[1].setYrange([MIN(sig), MAX(sig)])
p[1].setYtitle("Jy")
p.xaxis.title.text="Wavelength [$\mu$m]"
p.getLegend().setVisible(True)
```

where the labelling of the Y axis and its range will here be different for the two spectra, allowing you to compare them.

Since the first task of this part of the pipeline was to slice on nod and line id (slicedFrames = pacsSliceContext(slicedFrames, slicingRules = rules, level='1')), each frame slice will be of a single nod, a single line and a single raster pointing only. Hence, in a single myframe there should be repeats of spectra only for grating scan (number). Bit if you follow this script before having done this first pipeline task of Level 0.5 to 1, each myframe will contain nod A and B both, and may also contain multiple line ids.

Bear in mind that when you look at the spectrum if a single pixel, signal versus wavelength, before slicedSpecDiffChop has been run, you will see what looks like several spectra plotted on top of each other, one for each chop position and one for each grating scan, and these will all be slightly different. If you plot the spectra versus array position (i.e. simply do not specify the X axis), this is the same as plotting versus time, and there you will see the spectra changing with time because with time the instrument configuration (grating, chopper) also changes. The chops are merged in the pipeline task slicedSpecDiffChop; the grating scans and nods will be combined in the next part of the pipeline. So, if you plot a pixel, signal versus wavelength, before having subtracted the chops, the plot will contain

several spectra all sitting on top of each other, but if you plot the spectra as signal versus time, they will be separated in time. An example of this is shown in the next two plots:

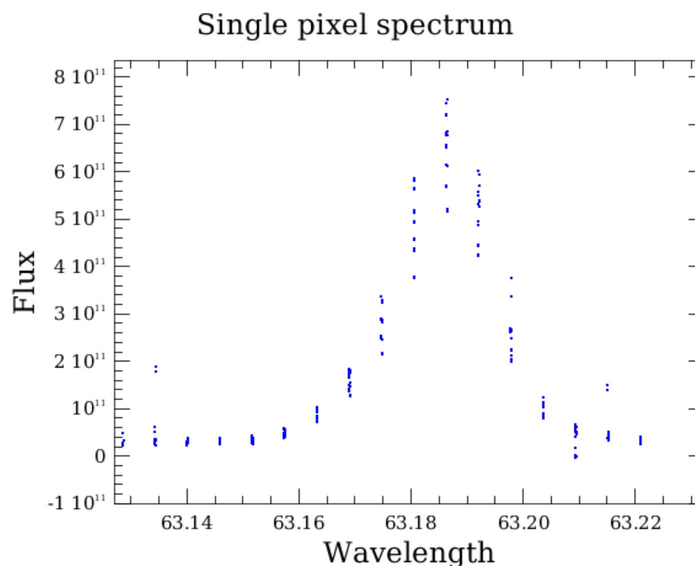


Figure 3.12. Spectrum of a single pixel. The spectrum is plotted versus wavelength and there are in fact two spectra plotted here, one for each grating scan

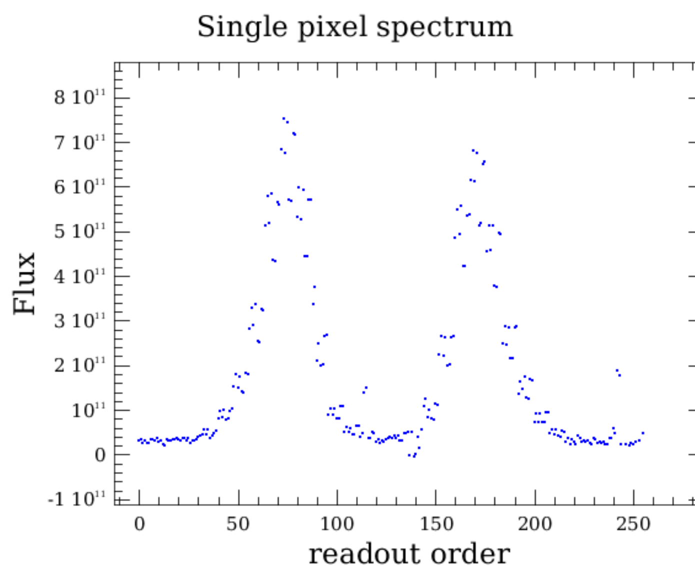


Figure 3.13. Spectrum of a single pixel. The spectrum is plotted versus readout and the separate spectra that in the figure above lie on top of each other are now distinguishable

In these plots there are two separate spectra because there were two grating scans in this observation. When this this frame is turned into a cube by the pipeline task specFrames2PacsCube, 16 pixels, each (in this case) with 2 spectra, are put into each spaxel. Later pipeline tasks will take these 16*2 spectra and merge them into one.

If you ran the task slicedSpecExtimateNoise, to inspect the noise spectrum is the same as inspecting the astronomical spectrum; the dataset you want to look at in your frame slice is "noise", and you can use the method .getNoise() in the same way as .getSignal().

Plotting grating scans

Note: this is much easier to do using the Spectrum Explorer!

If you wish to compare the spectra of different scan directions for *all* the slices in a *slicedFrames* in one go, then you should select on the MasterBlockTable, from the column called "ScanDir" (which you will see if you use the Dataset inspector on the MasterBlockTable). If you wish to look at only one *Frames* slices at a time, you should select on the individual BlockTables, and it is this method that is shown here. You can also select on the Status of the *Frames* slices, on the column called SCANDIR, but selecting on Status has been shown before and is not repeated here.

Again, to follow the script snippets here you need to have first selected your slice—"myframe"—out of your slicedFrames.

The BlockTable is a dataset of your frame, in which block identifications have been given to the readouts that correspond to distinct instrument settings (see Chap. 4 for a longer explanation). You will select on the data from the BlockTable entry "ScanDir", which separates all the 0 and 1 scan direction readouts. (0 is for moving along the grating in one direction, 1 for moving back again, and there will only be entries 0 or 1, no matter how many times the grating went back and forth.) Selecting on the BlockTable, however, will get you all the data of scan direction 0 or 1; if you wish to select particular 0s or 1s only you will need to select on at the start and end index that corresponds to the particular 0s and 1s you wish to look at. This script is not short, but does not require much manual inspection and so can be applied quite generally.

First, take out the slice from slicedFrames; here we call that slice "myframe". Then:

```
# to make an array of BlockTable ScanDir entries:
scanIds = myframe["BlockTable"]["ScanDir"].data
print scanIds

# let's say this gives a listing: 0 1 0 1 0 1
# and you want to plot all 0 vs all 1
# find the starting and ending indices for the 0 and 1
scanIdsSel = scanIds.where(scanIds == 0)
startIdx0 = myframe["BlockTable"]["StartIdx"].data[scandsSel]
endIdx0 = myframe["BlockTable"]["EndIdx"].data[scanIdsSel]
scanIdsSel = scanIds.where(scanIds == 1)
startIdx1 = myframe["BlockTable"]["StartIdx"].data[scanIdsSel]
endIdx1 = myframe["BlockTable"]["EndIdx"].data[scanIdsSel]
# create smaller frames containing only these data
selectionFrames=Bool1d(myframe.getSignal().dimensions[2])
selectionFrames[:] = False
for j in range(len(startIdx)): selectionFrames[startIdx0[j]:endIdx0[j]] = True
frame0=myframe.select(selectionFrames)
selectionFrames[:] = False
for j in range(len(startIdx)): selectionFrames[startIdx1[j]:endIdx1[j]] = True
frame1=myframe.select(selectionFrames)
# now plot
p=PlotXY(frame0.getWave(8,12),frame0.getSignal(8,12),line=0,
   color=java.awt.Color.blue)
p.addLayer(LayerXY(frame0.getWave(8,12),frame0.getSignal(8,12),line=0,
   color=java.awt.Color.red)
```

Since the first task of this part of the pipeline was to slice on nod and line id (slicedFrames = pacsSliceContext(slicedFrames, slicingRules = rules, level='1')), each frame slice will be of a single nod, a single line and a single raster pointing only. Hence any repeats of 0 and 1 scandir in myframe will be due to repeated scannning directions, not due to different pointings or wavelength ranges. But if you follow this script before having done this first pipeline task of Level 0.5 to 1, each myframe will contain nod A and B both, and may also contain multiple line ids.

To read the entire BlockTable for a *Frames* you can use the Dataset viewer on the BlockTable dataset of your myframe. You can also inspect the MasterBlockTable of slicedFrames using the same viewer. The MasterBlockTable is all the individual BlockTables of the slices in slicedFrames. There is no MasterBlockTable for slicedCubes, but the individual cube slices should have BlockTables.

Note that it is not unexpected that the spectra from different grating scan directions differ somewhat in their flux levels.

Plotting different bands

This may be informative for Range or SED AOTs, it will not tell you much for Line scan AOTs. First, take out the slice from slicedFrames; here we call that slice "myframe".

If you want to compare the bands in your observation (and this makes sense after you have run slicedRsrfCal and slicedSpecRespCal) then you need to extract on the Status. Bands are not separated in the BlockTable or MasterBlockTable. The Status entry to look for is BANDS, and your script could look something like this:

```
print UNIQ(myframe.getStatus("BAND"))
# giving a reply such as ["B2A", -"B2B"]
# BAND has only the timeline dimension
band1 = (myframe.getStatus("BAND") == -"B2B")
if (ANY(band1)):
    w = band1.where(band1)
    signal=myframe.getSignal(pix,mod)[w])
    wave=myframe.getWave(pix,mod)[w])
```

Explanation: first you locate all the readouts (the timeline datapoints) that correspond to observations at band "B2B", then you create a *Selection* product called w which is True for the readouts where the band was so set and False otherwise. Then you create the spectrum for those selected readouts only.

Since the first task of this part of the pipeline was to slice on nod and line id (slicedFrames = pacsSliceContext(slicedFrames, slicingRules = rules, level='1')), each frame slice will be of a single nod, a single line and a single raster pointing only. For SED or Range scan AOTs, there will be only one line id (i.e. all bands will have the same line id), hence you have effectively sliced on raster pointing and nod only. But if you follow this script before having done this first pipeline task of Level 0.5 to 1, each myframe will contain nod A and B both.

Plotting chop-nod combinations

As discussed in the Observer's Manual and in Chap. 2, the chop-nod AOT sees PACS nodding between an A and a B pointing, and a chopping between blank sky and the source. The pipeline task slicedSpecDiffChop subtracts the off-chops (blank sky) from on-chops. There are 4 chop-nod combinations possible (chop- nodA, chop+ nodB, chop+ nodA, chop- nodB), the former two are off-source and the latter two are on-source. After slicedSpecDiffchop you are left with nod A (chop+) and nod B (chop-). Before running the task slicedSpecDiffChop you may want to look at the off-chop spectra, to see if they are clear of any spectral signature (any non-blank sky signal) and to compare them to the on-chop spectra.

To compare the spectra from chop+ and chop- for a single frame from your slicedFrames before running slicedSpecDiffChop you could do something like this:

```
myframe = slicedFrames.getScience(1)
stat = myframe.getStatus("CHOPPOS")
on = (stat == -"+large") # a boolean, true where +large
on = on.where(on) # a Selection array
off = (stat == -"-large")
off = off.where(off)
p=PlotXY(myframe.getWave(8,12)[on],frame.getSignal(8,12)[on])
p.addLayer(LayerXY(myframe.getWave(8,12)[off],frame.getSignal(8,12)[off])
```

To run this script you only need to know whether your chopper throw was "large", "medium" or "small", and this you can get by looking at the CHOPPOS entries of the Status; then change the 3rd line of the script appropriately.

Since the first task of this part of the pipeline was to slice on nod and line id (slicedFrames = pacsSliceContext(slicedFrames, slicingRules = rules, level='1')), each frame slice will be of a single nod, a single line and a single raster pointing only. However, if you requested repeats of the grating scan, then for each chopper position you select to plot here, you will get repeated spectra.

This script will work for any single myframe slice from slicedFrames before you run the pipeline task slicedSpecDiffchop, since you have chop+ and chop- in all slices. After runnning that task, for the nod A frames you will have only chop+ and for the nod B slices only chop-, as these are the respective on-source positions. We explain how to compare the nod A and B spectra in the next part of the pipeline, as this is easier to do then.

Plotting the pointing of raster slices

To compare the pointing for different rasters you can follow the script snippets of above to select out the *Frames* products you want to look at, and then plot the RA and Dec using the instructions provided in Sec. 3.4.2.5.

See Sec. 3.6.2.2 for more information on the placement of the spaxels of PACS.

3.5.3.3. For the *PacsCube*

By far the easiest way to inspect your *PacsCubes*, which is the class of product that are contained within your slicedCubes at this point in the pipeline, is to use the Spectrum Explorer on them. However, if that is not available in your version of HIPE, here are some more manual methods.

The description here is for the *PacsCube* product, that is a single slice of a *slicedCubes* product. Here we describe how to inspect such a cube, called "mycube". You can search for the organisation of the slices, and extract them out of the *ListContext* in a similar way as has already been explained for the *slicedFrames*, although without a MasterBlockTable (at this point in time) for the cube you will need to use that of your slicedFrames (which is organised in the same order) to work out what slice in your slicedCubes is what. Extracting a cube slice:

```
mycube=slicedCubes.getSlice(0)
```

The *PacsCube* product is undergoing a change, after which it should contain a Status table in the same way that a *Frames* product does. When this has been implemented, selecting out parts of a *PacsCube* will follow the same logic as selecting out parts of a *Frames* product, and most of what was said above will apply here also. An addition to the Status will be pixel, so you will be able to select for each spaxel the individual pixels (of which there are 16), to inspect or manipulate as you wish. At present the *PacsCube* holds the relevant information in separate datasets, as you can see in the screenshot below. It also has a BlockTable.

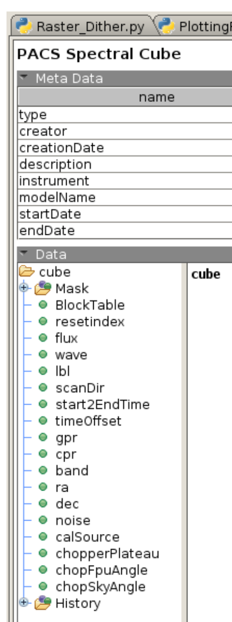


Figure 3.14. PacsCube listing

Certain methods previously introduced for *Frames* work on *PacsCube* also. For example, to plot the spectrum of a single spaxel and overplot the spectrum of the unmasked data points:

```
flx=mycube.flux[:,2,2]
wve=mycube.wave[:,2,2]
p=PlotXY(wve,flx,line=0)
index_cln=mycube.getUnmaskedIndices(String1d(["GLITCH"]),2,2)
p.addLayer(LayerXY(wve[Selection(index_cln)],flx[Selection(index_cln)],line=0))
```

Note that the wavelength dimension is the first, not the last as with a frame, and the spatial dimensions are 5,5.

As mycube contains in each of its 5x5 spaxels simply all of the spectra that belong to that point of the sky, if you plot versus wavelength you will see a mess of a spectrum, at least 16 spectra overlayed, and probably more (one spectrum per pixel and one also per grating run). If you plot versus array order (which is the same as time) then you will see these separated out. This is clear from the next two figures.

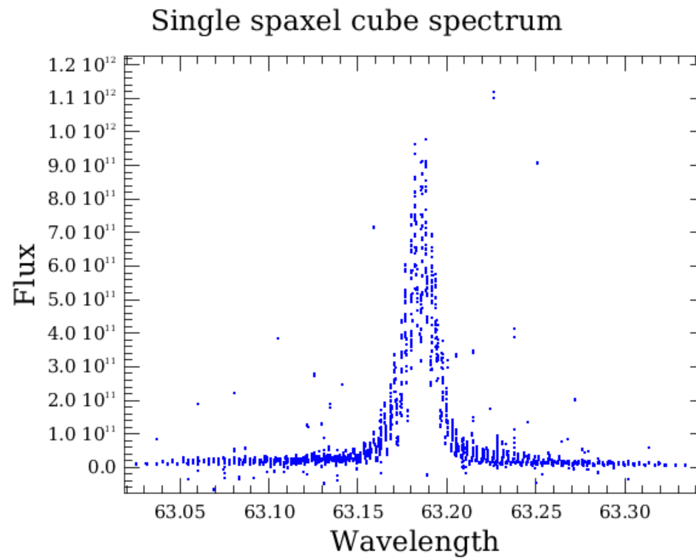


Figure 3.15. Spectrum of a single spaxel in the PacsCube. The spectrum is plotted versus wavelength and the separate spectra all lie on top of each other: 32 in total: 2 grating runs from each of the 16 pixels that each spaxel is fed by

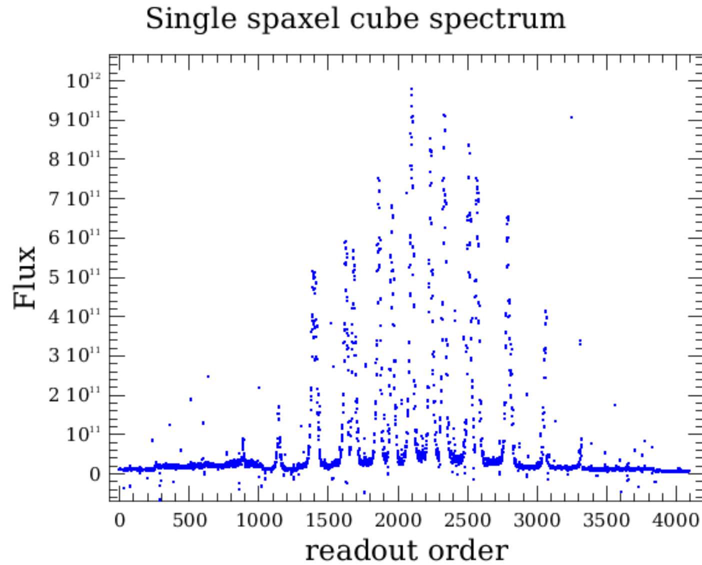


Figure 3.16. Spectrum of a single spaxel in the PacsCube. The spectrum is plotted versus readout order and the separate spectra that in the figure above lie on top of each other are now distinguishable

If you want to see where in the cube your source is located, so you know which spaxel to plot, you will need to use Display to plot the 2D image:

```
Display(mycube.flux[1000:1010,:,:])
```

Which will display a 2d image that is 10 (wavelengths) thick, and the brightest spaxel will be your source. Note that the 1000:1010 specifies the array positions of flux, you do not type in the wavelengths here.

Plotting the spectra of the different pixels in each spaxel

How do you go about selecting out the various pixels in each spaxel of a *PacsCube* to plot and compare? In fact, the only thing that will be separatable in the cubes' spaxels via the BlockTable will be the grating scan direction, because the chops have already been combined and the nods sliced out, and pixels are not offered as a BlockTable or Status parameter. To compare the spectra of different pixels in a spaxel it is far easier for you to inspect the equivalent *Frames* product rather than the cube.

3.6. Level 1 to 2

In this part of the pipeline you will rebin the cubes along the wavelength array, combine the nods, and then project the cube spatially and at the same time combine raster pointings. This follows the ipipe script L2_ChopNod.py.

A word about the nods: the nods, A and B, have by now have their corresponding off-source pointings subtracted, and the A and B now need to be added. After launch we discovered that the nod A and B do not align perfectly for all spaxels. The offset is smallest for the smallest chop throw (<LINK>), and you can check this offset by plotting the pointing of a A cube with that of a B cube (discussed below). This offset will have an effect on the final cubes, because you are combing A and B pointings that are from very slightly different sky positions. However, nod A and B *must* be added before the final cubes are created. For the reasons why, see Chap. 4.

3.6.1. Pipeline steps

3.6.1.1. Basic procedure

The final tasks take the cube from Level 1 to Level 2. As explained before, if you are not simply continuing from Level 1 (when the *slicedFrames* are converted to a *slicedCubes*) there are a few steps you do first:

```
level1 = PacsContext(myobs.level1)
slicedFrames = level1.fitted.getCamera(camera).product
slicedCubes = level1.cube.getCamera(camera).product
# get the calTree from myobs...
calTree=myobs.calibration
# -...or get the calTree from HIPE
calTree=getCalTree(obs=myobs) # see Sec. 3 for what obs=myobs means
# put that HIPE calTree into myobs, if you have not already done so
myobs.calibration=getCalTree()
camera="blue" # or -"red"
```

(You need the slicedFrames as well as the slicedCubes because the first is used to do a selection on slices, which currently you cannot do on the second.) Next, or to begin with if you didn't need to do the above:

```
from herschel.pacs.spg.pipeline import *
from herschel.pacs.signal.context import *
from herschel.pacs.cal import GetPacsCalDataTask
```

And then get a list of the (spectral) line identification, as this stage of the pipeline does a slicing on this:

```
lineIdCol = slicedFrames.getMasterBlockTable().getLineId()
print lineIdCol
```

This will give a list of numbers, a unique one for each line (but the numbers will be repeated if there are multiple pointings per line and for the nod As and Bs). To know what spectral line each line number refers to you can look at the LineDescription column (together with the lineId column) of the MasterBlockTable. Note that the calibration block, if in the beginning of the observation, will be the first lineId number(s), as the lineIds are assigned according to grating range and in the order the grating ranges are encountered in the BlockTable. However, the calibration block should have been sliced out of your slicedFrames by now.

As you will not want to create the final cubes of the pipeline with mixed spectral lines therein, the next stages of the pipeline will be iterated over the line ids present in your dataset. If there is only one line, you will run these tasks only once. You also have the choice of combining the nods when creating the projected cube, combining them before, or not at all.

Now you run part of the pipeline. The script here will iterate over each lineId to create rebinned cubes, which are the penultimate cubes created by the pipeline. In each slicedRebinnedCubes (one per spectral line) there will be one rebinned cube per nod and per raster pointing:

```
rebinnedCubesList=ListContext()
# iterating over all lineIds
for lineId in UNIQ(lineIdCol):
   print -"Doing lineId",lineId
   # 1
   blocksel = lineIdCol.where(lineIdCol==lineId)
   rasterslices=slicedFrames.getMatchingFrames(blocksel)
   # 2
   cube = slicedCubestemp.refs[rasterslices[0]].product
   waveGrid=wavelengthGrid(cube, oversample=2, upsample = 1, calTree = calTree)
   # 3
   slicedCubes_select = slicedActivateMasks(slicedCubes,
      String1d(["GLITCH","UNCLEANCHOP","SATURATION","GRATMOVE", -"BADFITPIX"]),
      exclusive = True, sliceSelection = rasterslices, keepall=False)
```

```
slicedCubes_select = slicedSpecFlagOutliers(slicedCubes_select, waveGrid
                     nIter = 1, nSigma = 5)
# 4
slicedCubes_select = slicedActivateMasks(slicedCubes_select,
   String1d(["GLITCH","UNCLEANCHOP","SATURATION","GRATMOVE", -"BADFITPIX",
   -"OUTLIERS"]), exclusive = True)
slicedRebinnedCubes = slicedSpecWaveRebin(slicedCubes_select, waveGrid)
rebinnedCubesList.refs.add(ProductRef(slicedRebinnedCubes))
```

The for-loop runs over UNIQ(lineIdCol) rather than lineIdCol because the lineIdCol is a list of all the lineIds you have and the entries in here will be repeated (repeated for raster, nod and repetition factor); you want to include in each slicedRebinnedCubes *all* the individual cubes (all nods and rasters) that belong to each lineId. You could of course chose to run these tasks lineId by lineId, rather than in a loop. The "rebinnedCubesList=ListContext()" in the beginning and "rebinnedCubesList.refs.add(ProductRef(slicedRebinnedCube))" at the end allow you to put each slicedRebinnedCubes—one per lineId—in a *ListContext*, storing them for use in the final part of the pipeline. If you only have one lineId you don't need to do this, and another alternative to storing the slicedRebinnedCubes in a list is to give each one a separate name. That is up to you, but in the next script we assume you have followed what is written here.

An now an explanation of each step:

1. For the lineId, identify the parts of the BlockTable corresponding to that value. Then feed that into an array (rasterslices) that contains the selection numbers of the raster slices with that lineId.

2. Select the first cube, for that set of raster slices, of the slicedCubes and create a wavelength grid from it. This wavelength grid will be applied to all the other rasters and nod with that lineId so they can later be combined (the wavelength range will be the same if the lineId is the same). If you have an SED or Range scan AOT then all the slices will have the same wavelength range anyway. The task creates a single and uniform wavelength grid according to the wavelengths that are in the input cube. The parameters listed here are all optional, the values given are our recommendation. `oversample` is by how much you want to oversample the wavelength bins from what they are at present and `upsample` is by how much you move forward along the original wavelength array as you calculate the new resampled wavelength array. It is possible that waveGrid you create will depend on the type of observation you have, so try various grids and compare the resulting spectra. Bins too large will smooth the data, bins too small will make the spectra too "bitty".

3. Activate masks and run an outlier flagging task (a second glitch detection task). Note that the name of the output product from the slicedActviateMasks—slicedCubes_select here—must not be the same as that of the input product. The reason is that the output product has to be a subselection on the input product, containing only the slices/cubes that you want to feed into the slicedSpecWaveRebin task. If you give the output the same name as the input then you will lose all the left-over slices of the input slicedCubes; if you have more than one line id, you will have lost the rest of that data (i.e. you need to recreate the slicedCubes). The removing of the unwanted slices is set by the parameter `keepall`=False (if you set it to True and you have multiple line ids in your observation, then your slicedRebinnedCubes will be created from the wrong input slicedCube).

   SlicedSpecFlagOutliers does a type of sigma-clipping, and by activating the masks before running it you are telling it not to mask these data points which have already been masked. The parameter `nIter` is the number of iterations and `nSigma` is the sigma value to flag at. The values listed here are the default, but feel free to try out other values.

4. Rebin the raster slices to the wavelength grid previously defined. This will merge all the individual spectra held in each spaxel, so there will now only be one specrum in each. Before running this task you should select all the masks you wish to exclude the data from (slicedActivateMasks). You may therefore want to check these masked data before (e.g. do you want to also exlclude the NOISYPIXELS masked data?). The task creates a cube of dimensions [wavelength,5,5] where now in each spaxel holds a single spectrum. The individual slices of the slicedRebinnedCubes are of class *PacsRebinnedCube*. There should be one cube per nod and raster pointing held in each slicedRebinnedCubes.

To see how many slicedRebinnedCubes have been placed in the rebinnedCubesList, and to see the number of slices contained in any particular slicedRebinnedCubes:

```
print len(rebinnedCubesList.refs)
print len(rebinnedCubesList.refs[i].product.refs)
```

(At present the convenient methods for looking at the *slicedFrames* product, such as .getnumberOf-Frames, are not available for the sliced cubes products, so this longer syntax is necessary.)

Next you will need to combine the nods:

```
slicedRebinnedCubes = specAddNodCubes(slicedRebinnedCubes)
```

Finally you will create, for each rebinned cube, a projected cube. This is done with a task that takes the RA and Dec coverage of the rebinned cube and "projects" it onto a uniform grid. By default this grid has a spaxel size of 3 arcsec (compared to the 9.4 arcsec that is the original). Remember that the PACS FoV coverage is not a uniform as it looks when you display your cubes (e.g. in the Cube of Spectrum explorer GUIs or with Display): see the plots in 3.4.2.5 and below. To do the "spectral projection":

```
projectedCube=specProject(slicedRebinnedCubes)
```

The task specProject will also run if you omitted to combine the nods first, but this is strongly discouraged. See Chap. 4 for the reasons why. In the *PAPT* the specProject task itself is explained in more detail.

3.6.2. Inspecting the results

For the *PacsProjectedCube* you can use a number of GUIs, outlined in Chap. 1, to inspect it. At some point during the 4.0 track of HIPE these, or other, GUIs will also work on the *PacsCube* and the *PacsRebinnedCube*, that is the output of the pipeline tasks slicedSpecFrames2PacsCube and sliced-SpecWaveRebin. To know which GUIs will work on the respective cubes, you can right-click menu select on the cube in the Variables panel, or highlight it in the variables panel and look to see what Applicable Tasks will work on it (Tasks panel).

To inspect a cube you need to take it out of the *ListContext* in which it is to be found. The syntax for doing this is similar to:

```
mycube=ListCubes.refs[0].product # or
mycube=ListCubes.getScience(i)
```

but bearing in mind that the SpectrumSimpleCube, the last cube of the pipeline ("projectedCube" here), is a single cube, not a ListContext.

3.6.2.1. Selecting out slices from slicedRebinnedCubes

For cubes with no MasterBlockTable it is not so easy to identify what slice is what in an automatic way. We are working on providing a task to do this. The cubes held in slicedRebinnedCubes have been placed there in the order that the for-lineId-loop above was run. At present you will have to look at the Meta data or the BlockTable of the *PacsRebinnedCubes* slices to work out what they are. Bear in mind that there will be one per line id and per raster position.

3.6.2.2. GUIs

The GUIs or viewers that work on the *PacsRebinnedCube* and the *SpectrumSimpleCube* are the Spectrum Explorer and/or the Cube Spectrum Analysis Toolbox, both introduced in Chap. 1. Their use in explained in <LINK>. The *PacsRebinnedCube* will contain one spectrum per each of 25 spaxels, created from the multiple spectra per spaxel of the *PacsCube*, with bad data having been exluded. The *SpectrumSimpleCube* also contains one spectrum per spaxel but, if run with the default parameters (as shown here), there will be more, and smaller, spaxels, and multiple raster pointings will have been combined.

3.6.2.3. With PlotXY: spectrum and pointing

Plotting a single spectrum from "rebinnedcube" (a *PacsRebinnedCube*) and "projectedCube" (a *SpectrumSimpleCube*) are done differently:

```
# REBINNED CUBE
# first check the dimensions to know how many spaxels can be plotted:
print rebinnedCube.dimensions
# plot a single spaxel's spectrum as thus
PlotXY(rebinnedCube.wavegrid,rebinnedCube.flux[:,2,2])
# PROJECTED/SPECTRUMSIMPLE CUBE
# get the dimensions
print projectedCube.dimensions
PlotXY(projectedCube.getWave(),projectedCube.getFlux(6,6))
```

This will give you plots looking similar to this:

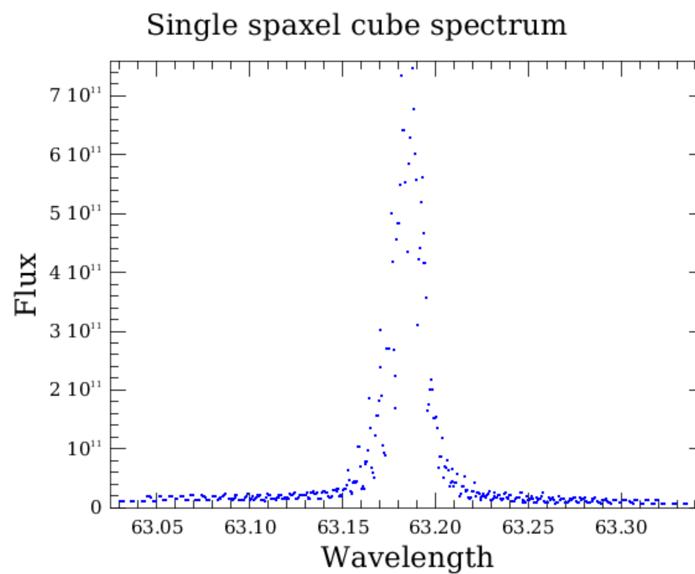


Figure 3.17. Spectrum of a single spaxel in the rebinnedCube. The spectrum is cleaner than the example from the PacsCube because the spectra have been combined and rebinned

Remembering that the rebinnedCube contains only one spectrum per spaxel, created from the throng of spectra that occupied each spaxel of the previous stage *PacsCube*, there is not so much to check here. One thing you could check is the IFU footprint, for a single pointing or for the a whole set of rasters. To plot the pointing you can follow a script like this:

```
#select the final ra and dec of a PacsRebinnedCube
ra=RESHAPE(rebinnedCube1.ra[-1,:,:])
dec=RESHAPE(rebinnedCube1.dec[-1,:,:])
plotsky=PlotXY(ra, dec, line=0)
plotsky[0].setName("cube1")
#select the final ra and dec of a second PacsRebinnedCube
ra=RESHAPE(rebinnedCube2.ra[-1,:,:])
dec=RESHAPE(rebinnedCube2.dec[-1,:,:])
plotsky.addLayer(LayerXY(ra, dec, line=0))
plotsky[1].setName("cube2")
plotsky.xaxis.title.text="RA"
plotsky.yaxis.title.text="Dec"
plotsky.getLegend().setVisible(True)
```

Which will plot the RA and Dec of 2 raster pointings, from 2 *PacsRebinnedCubes* you have taken out of your rebinnedCube list. If you want to know what cube is what part of your observation (which line id, nod, raster), see the advice in Sec. 3.6.2.1.

Below we show you the footprint of the PACS IFU, allowing you to relate module number from a *Frames* to spaxel coordinate from a *PacsCube* or *PacsRebinnedCube*.

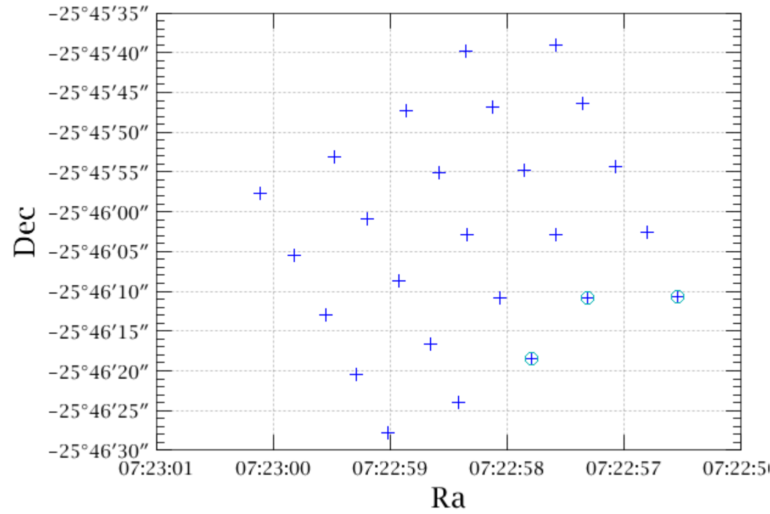


Figure 3.18. The IFU footprint for a cube. Crosses are the spaxel centres and circled ones are spaxels [0:0] (right-most),[1:0],[2:0]

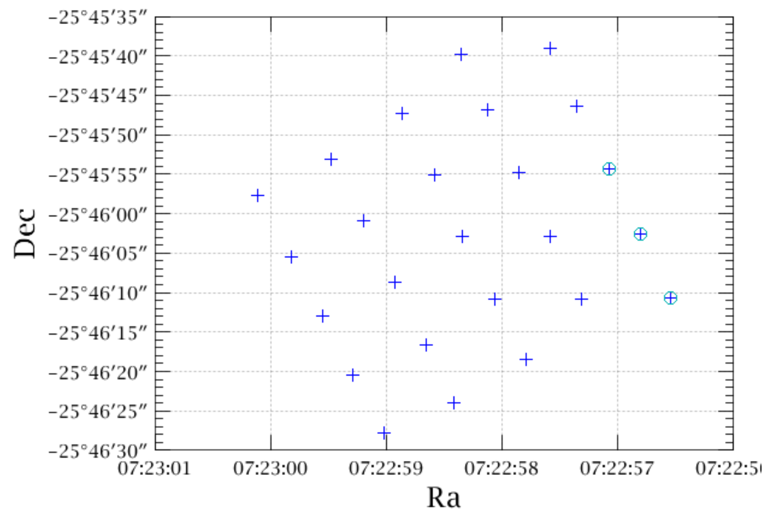


Figure 3.19. The IFU footprint for a frame. Crosses are the module centres and circled ones are modules 0 (bottom-most),1,2. Module 5 would then be to the left of module 0.

For all cubes you can also use Display (and this shows the cube RA and Dec coordinates also). Below is a screenshot of Display on your projectedCube (data from an observation of more-or-less nothing). From it you can see that the spaxels are smaller, but they do cover the same total area:

Figure 3.20. Display on a projectedCube

3.6.2.4. Comparing nod A and B spectra and pointings

After having run the task slicedSpecDiffChop in the previous pipeline stage, you will no longer have the chop+ and chop- datasets for each nod slice, as they have been subtracted from each other. You will only have chop+ for the nod A, and chop- for the nod B. From the *PacsRebinnedCube*s created by the task slicedSpecWaveRebin and before the task specAddNodCubes, you can easily compare the nod A and B spectra and pointings. These rebinnedCubes are held as slices (per raster, line id and nod) in your slicedRebinnedCubes list. Scripts to plot spectra and the pointing have already been provided, all you need to do here is identify which slice of your rebinnedCubes list is what, so you can compare meaningfully (see the advice in Sec. 3.6.2.1). When comparing nod A to B bear in mind that (i) looking at the relative pointings tells you what spatial offset your nods have, and hence by how much you are "blurring" the individual spaxels's field-of-views when you add the nods, and (ii) the spectra of nod A and B will be different even if they were exactly at the same sky position because they are looking through different parts of the mirror and so have a different (mainly continuum) contribution. However, if you have observed a very extended and spatially variable source, you may want to see if the spectral lines themselves differ much. If you are worried about what you see you can always, of course, contact the Herschel Helpdesk.

3.7. The End Of The Pipeline

Congratuations! Now you know how to run the pipeline and how to inspect the intermediate products. The hard work is only just beginning...

In Chap. 4 (not yet complete) are discussed issues that are of importance for certain types of AOTs and also issues that have arisen in the course of your pipeline processing. In the *PAPT* the pipeline tasks are explained in more detail, in particular the parameters and algorithms are presented.

Chapter 4. Further topics. *Spectroscopy*

4.1. Introduction

This chapter is still being written. Chapter 4 will be reinserted in April.

Chapter 5. In the Beginning is the Pipeline. *Photometry*

5.1. Introduction

The main purpose of this chapter is to tutor users in running the PACS photometry pipeline. Previously we showed you how to extract and look at the Level 2 fully pipeline-processed data; if you are now reading this chapter we assume you wish to reprocess the data and check the intermediate stages. Later chapters of this guide will explain in more detail the individual tasks and how you can "intervene" to change the pipeline defaults; but first you need to become comfortable with working with the data reduction tasks.

The PACS pipeline runs as a long series of individual tasks, rather than as a single application. We will take you through the pipeline tasks one by one through all the levels. Up to Level 0.5 the data reduction is level independent.

A suggestion before you begin: the pipeline runs as a series of commands, and as you gain experience you may want to add in extra tasks, construct your own plotting mini-scripts, write *if statements* and *for loops* and remember what it is you did to the data. Rather than running the tasks on the command line of the Console (and having to retype them the next time you reduce your data), we suggest you write your commands in a python text file and run your tasks via this script.

The pipeline steps we outline here are also available in the ipipe scripts (one per AOT). These can be found in the directory where you installed the HIPE software, hopefully in /scripts/pacs/toolboxes/spg/ipipe. We suggest you copy the relevant file and open it in HIPE. You can then follow this manual and that ipipe script at the same time, editing as you go along (and please excuse any differences between the ipipe script and this guide, but they will not always be updated at the same time: generally the ipipe scripts should be updated first).

This chapter has been taken from the more advanced data reduction guide and so it is more complex than you will need. Throughout PV and SD phase it will be improved upon, at present you will just have to accept that it is not quite ready. You will need to read Sec. 1 and 2 of Chap3. before beginning here. Also, what there is called mycalTree, here is called calTree.

How to write in a script text file in HIPE:

From the HIPE menu and while in the Full/Work Bench perspective select File → New → Jython script. This will open a blank page in the Editor. You can write commands in here (remember at some point to save it... if HIPE has to be killed you will lose everything you have not saved). As you are doing so you will see at the top of the HIPE GUI some green arrows (run, run all, line-by-line). Pressing these will cause lines of your script to run. Pressing the big green arrow will execute the current line (indicated with a small dark blue arrow on the left-side frame of the script). If you highlight a block of text the green arrow will cause all the highlighted lines to run. The double green arrow runs the entire file. The red square can be used to (try to) stop commands running. If a command in your script causes an error, the error message is reported in the Console (and probably also spewed out in the xterm, if you started HIPE from an xterm) and the guilty line is highlighted in red in your script. A full history of commands is found in History, available underneath Console for the Full Work Bench perspective.

5.2. Retrieving your ObservationContext and setting up

Before beginning you will need to set up the calibration tree. You can either chose that which came with your data or that which is attached to your version of HIPE. The calibration tree contains the

information HIPE needs to calibrate your data, e.g. to translate grating position into wavelength, to correct for the spectral response of the pixels, to determine the limits above which flags for instrument movements are set. As long as your HIPE is recent then the caltree that comes with it will be the most recent, and thus most correct, calibration tree. If you wish to recreate the pipeline processed products as done at the Herschel Science Centre you will need to use the calibration tree there used, i.e. that which comes with the data (and which is shown in Fig. 2 of Chap. 1). We recommend you use the calibration tree that comes with HIPE. Structurally, the two are the same, but the information may be different (more, or less, up-to-date).

```
# from your data
caltree = myobs.calibration
# or from HIPE recommended
caltree = getCalTree("FM","BASE")
# where FM stands for flight model and is anyway the default
```

It is necessary to extract a few other products in order for the pipeline processing steps to be carried out. These are the pointing product, and the orbit ephemeris, the time correlation product, and the housekeeping data. You can get these, to be used later, with

```
pp = myobs.auxiliary.pointing
oem = myobs.auxiliary,refs["OrbitEphemeris"].product
timeCorr = myobs.auxiliary.timeCorrelation
hkdata = myobs.level0.refs["HPPHK"].product.refs[0].product["HPPHKS"]
```

The pointing product is used to calculate the pointing of PACS during your observation, the orbit ephemeris (oem) is used to correct for the movements of Herschel during your observation. The time correlation product provides a synchronisation of the observatory and instrument clocks. Finally, the houskeeping product provides monitoring data of all crucial instrument components.

Then you need to retrieve the Observation Context from your pool as it was explained in Chap. 1. Continuing from there: since you are re-reducing the data you will want to start from Level 0 in case of scanmap and level_0.5 sliced frames in case of the point source AOT.

5.2.1. Scan map AOT

For scan map mode you access you data in the following way

```
myframe = myobs.level["level0"].refs["HPPAVGB"].product.refs[0].product (in case
of the blue array)
or
myframe = myobs.level["level0"].refs["HPPAVGR"].product.refs[0].product (in case
of the red array)
```

where myobs is the ObservationContext from Chap. 1. This extracts out from Level 0 the first of the averaged blue (or red) ramps. If there is only one you still need to specify refs[0], if there is more than one you select the subsequent with refs[1], refs[2],...... To find out how many HPPAVGBs are present at Level 0, have a look again at Fig. 2 from Chap. 1; if you click on the + next to HPPAVGB it will list all (starting from 0) that are present.

An alternative way to get your HPPAVGB..ref[x] product is to click on myobs in the Variables panel to send it to the Editor panel, click on +level0, then on +HPPAVGB to see the entries 0, 1, 2... You can then drag and drop whichever entry you want to start working on first to the Variables panel. The command that is echoed to the Console when you do this will be very similar to the one you typed above, only now the new product is called "newVariable" (which name you can change via a right click on it in the Variables panel).

In case you want to retrieve a parallel mode observation getObservation does not work, and the following script shall be used:

```
archive = HsaReadPool()
store = ProductStorage()
```

```
store.register(archive)
query=MetaQuery(ObservationContext,"p","p.instrument=='PACS' and
p.meta['obsid'].value==%il" %(obsid))
result=store.select(query)
myobs=result[0].product
```

Since you start with the level0 product you need to identify the blocks in the observations. In the current observation design strategy a calibration block is executed at the beginning of any observation. It is possible that in the future the current design will be changed to include more than one calibration block to be executed at different times during the observation. In order to take into account this possible change, the pipeline includes as a very first step a pre-processing of the calibration block(s) that is planned to work under any possible calibration block(s) configuration. The calibration block pre-processing is done in three steps: a) the calibration block(s) is identified and extracted from the frames class, b) it is reduced by using appropriate and pre-existing pipeline steps, c) the result of the cal block data reduction is attached to the frames class to be used in the further steps of the data reduction.

```
myframe = findBlocks(myframe, calTree=calTree)
```

and remove the calibration block to keep only the science frames:

```
myframe = removeCalBlocks(myframe)
```

Unfortunately removeCalBlocks still leaves a few frames of the calibration block hence the following is recommended until further notice to remove the initial calibration block

```
skip=430
myframe = myframe.select(Int1d.range(frames.signal.dimensions[2]-1-skip)+skip)
```

These are organisational tasks. Their purpose will be discussed in later chapters. You also need to add the pointing information using:

```
myframe = photAddInstantPointing(myframe, pp,calTree=calTree, orbitEphem=oep,
horizons=horizons, isSso=isSso)
```

The purpose of the photAddInstantPointing task is to perform the first step of the astrometric calibration by adding the sky coordinates of the virtual aperture (center of the bolometer) and the position angle to each readout as entry in the status table. In addition the task associates to each readout *raster point counter* and *nod counter* for chopped observations and *sky line scan counter* for scan map observations.

This first part of the astrometric calibration deals with two elements: the satellite pointing product and the SIAM product. Both are auxiliary products of the observation and are contained in the Observation context delivered to the user. The satellite pointing product gives info about the Herschel pointing. The SIAM product contains a matrix which provides the position of the PACS bolometer virtual aperture with respect to the spacecraft pointing. The time is used to merge the pointing information to the individual frames.

5.2.2. Point Source AOT

For point source mode you start with the level0.5 sliced frames so you don't need to worry about the calibration blocks and initial pointing.

```
camera= -'blue'
```

or

```
camera = -'red'
level0_5 = PacsContext(obs.level0_5)
slicedFrames = level0_5.averaged.getCamera(camera).product
pacsPropagateMetaKeywords(myobs,'0',slicedFrames)
```

The last line is needed to make sure that all the keywords which are available for the level 0 products are assigned to the slicedFrames as well. You can also check what is the size of your data cube and the number of slices you have:

```
print -"Data cube dimension: -"+str(slicedFrames.refs[1].product.signal.dimensions)
noofsciframes=  slicedFrames.meta["repFactor"].long/2
```

For the old (pre OD150) L0 processed data the filter information is not correct so you need to execute the following piece of code to make it right. Later it is going to be an independent pipeline task but for the time being we need to live with this temporary solution.

```
if camera == -'blue':
  # calibration block slice
  wpr=slicedFrames.refs[0].product.getStatus("WPR")
  band=slicedFrames.refs[0].product.getStatus("BAND")
  if wpr.where(wpr == 0).length() > 0:
    if band[wpr.where(wpr == 0)][0]=='BS':
      print -'WARNING for blue filter: WPR=0 was erroneously assigned BS, now
reset to BL'
      band[wpr.where(wpr == 0)] = String('BL')
  if wpr.where(wpr == 1).length() > 0:
    if band[wpr.where(wpr == 1)][0]=='BL':
      print -'WARNING for blue filter: WPR=1 was erroneously assigned BL, now
reset to BS'
      band[wpr.where(wpr == 1)] = String('BS')
  slicedFrames.refs[0].product.setStatus("BAND",band)
  # science block slice
  wpr=slicedFrames.refs[1].product.getStatus("WPR")
  band=slicedFrames.refs[1].product.getStatus("BAND")
  if wpr.where(wpr == 0).length() > 0:
    if band[wpr.where(wpr == 0)][0]=='BS':
      print -'WARNING for blue filter: WPR=0 was erroneously assigned BS, now
reset to BL'
      band[wpr.where(wpr == 0)] = String('BL')
  if wpr.where(wpr == 1).length() > 0:
    if band[wpr.where(wpr == 1)][0]=='BL':
      print -'WARNING for blue filter: WPR=1 was erroneously assigned BL, now
reset to BS'
      band[wpr.where(wpr == 1)] = String('BS')
  slicedFrames.refs[1].product.setStatus("BAND",band)
```

You also need to correct one of the keywords in case of a red channel

```
# for red channel only key word missing
if camera == -'red':
   slicedFrames.meta["repFactor"] = LongParameter(noofreps)
```

You can make several check on your data before beginning to process. E.g. check the size of the cube

```
print frames.signal.dimensions
```

which might be interesting to know if you deal with large amount of data. Or the repetition factor

```
print obs.meta["repFactor"].value
```

which helps you determine how many slices you will need (see later).

5.3. Proceeding to Level 0.5

The PACS Photometer pipeline is composed of tasks written in java and jython. In this section we explain the individual steps of the pipeline up to Level 0.5. Up to this product level the data reduction is mostly AOT independent, except for the MMT deglitching that is not applied during the point source AOT pipeline. We have already reached an intermediate level of data processing in previous steps and will continue from there. In this section we explain the individual steps of the pipeline up to Level 1.

Next the pipeline tasks are introduced in the order they should be run. They are explained for the example of the point source AOT mode pipeline, but are basically the same as for the scan map pipeline.

Having the sliced frames, you execute the following for each nod-cycle. For the scanmap mode you have to skip the "Extract one slice" part and start directly with the processing since there are no slicing in scanmap mode.

```
for i in range(noofsciframes):
  # +++++++++++++++++++++++++++++++++++++++++++++++++
  # Extract one slice
  # +++++++++++++++++++++++++++++++++++++++++++++++++
  framesnod = slicedFrames.getCal(0).copy()    # This stands, index is always zero
  framesScience = slicedFrames.getScience(i).copy()  # this goes from 0 to the
number of ABBA nods.
  framesnod.join(framesScience)
  #
  # +++++++++++++++++++++++++++++++++++++++++++++++++
  # Processing
  # +++++++++++++++++++++++++++++++++++++++++++++++++
  framesnod = photFlagBadPixels(framesnod)
    if (camera == -'blue'):
        blue_badpix=calTree.photometer.badPixelMask.blue
        blue_badpix[2,30]=1
        framesnod.setMask("BADPIXELS",blue_badpix)
  framesnod = photFlagSaturation(framesnod)
  framesnod = photConvDigit2Volts(framesnod)
  #framesnod = photCorrectCrosstalk(framesnod)
  # ground-based correction is overcorrecting, hence switched off for the time
being.
  framesnod = addUtc(framesnod, timeCorr)
  framesnod = convertChopper2Angle(framesnod)
  framesnod = photAssignRaDec(framesnod)
```

5.3.1. photFlagBadPixels

The purpose of this task is to flag the damaged pixels in the BADPIXEL mask. The task should do a twofold job: a) reading the existing bad pixel mask provided by a calibration file ("PCalPhotometer_BadPixelMask_FM_v1.fits" in the current release), b) identifying additional bad pixels during the observation. In the current version of the pipeline only the first functionality is activated. The algorithm for the identification of additional bad pixels is not in place. So the task is just reading the bad pixel calibration file and transforming the 2D mask contained in it in the 3D BADPIXEL mask. The task is doing the same for the BLINDPIXEL mask. This is an uplink mask, which currently is completely set to false. The purpose is to use it to indicate the pixels which should not be read at all and for which data should not be downloaded.

```
myframe = photFlagBadPixels(myframe,calTree=calTree)
```

A note on syntax: myframe is the input frame (which in Chap 1. and 3. we have called myframe) and myframe in the output frame. It is up to you whether you give myframe the same name as myframe; it is certainly possible for you to do so, and for tasks that only flag data it is recommended, otherwise you will clutter up the HIPE memory with many products. Also note that we use myframe as frame in the individual task description to be consistent with the previous chapters but the ipipe script uses different variable name (e.g. framesnod as in the above partial script). In this example, the existing BADPIXELS mask is updated to use one additional pixel that recently turned out to be misbehaving, too.

5.3.2. photFlagSaturation

This tasks identifies the saturated pixels on the basis of saturation limits contained in a calibration file. Before doing that, the task identifies the reading mode led by the warm electronic BOLC (Direct or DDCS mode) and the gain (low or high) used during the observation. These information are provided for each sample of the science frames by the BOLST entry in the status table. The task compares the

pixel signal at any time index to the dynamic range corresponding to the identified combination of reading mode and gain. Readout values above the saturation limit are flagged in the 3D SATURATION mask.

```
myframe = photFlagSaturation(myframe -,calTree=calTree)
```

5.3.3. photConvDigit2Volts

The task converts the digital readouts to Volts. As in the previous task, as a first step the task identifies the reading mode and the gain on the basis of the the BOLST entry in the status table for each sample of the frame. This is redundant and this step will be skipped when mode and gain will be stored in the metadata of the Level 0 Product. The task extracts, then, the appropriate value of the gain (high or low) and the corresponding offset (positive for the direct mode and negative for the DDCS mode) from the calibration file (PCalPhotometer_Gain_FM_v1.fits in the current release). These values are used in the following formula to convert the signal from digital units to volts:

signal(volts) = (signal(ADU) - offset) * gain

```
myframe = photConvDigit2Volts(myframe -,calTree=calTree)
```

5.3.4. addUtc

The task provides correction of time difference between the on board time and ground UTC using the time correlation file. A new status column Utc is added.

```
myframe = addUtc(myframe -,timeCorr)
```

5.3.5. photCorrectCrosstalk

The phenomenon of electronic crosstalk was identified, in particular in the red bolometer, during the testing phase. The working hypothesis of this task is that the amount of signal in the crosstalking pixel is a fixed percentage of the signal of the correlated pixel. A calibration file (PCal_PhotometerCrosstalkMatrix_FM_v2.fits in the current release) reports a table containing the coordinates of crosstalking and correlated pixels and the percentage of signal to be removed, for the red and the blue bolometer. The task reads the calibration file and use the info stored in the appropriate table to apply the following formula:

Signal_correct(crosstalking pixel)) = Signal(crosstalking pixel) - a*Signal(correlated pixel)

where '*a*' is the percentage of signal of the correlated pixel to be removed from the signal of the crosstalking pixel. The task is still under investigation, in the sense that invariability of 'a' is still an assumption to be tested in further tests. Currently it is not used in the pipeline because ground-based correction is over correcting.

5.3.6. photMMTDeglitching and photWTMMLDeglitching

These tasks detect, mask and remove the effects of cosmic rays on the bolometer. Two tasks are implemented for the same purpose: photMMTDeglitching is based on the multi resolution median transforms (MMT) proposed by Starck et al (1996), WTMMLDeglitching is based on the Wavelet Transform Modulus Maxima Lines Analysis (WTMML). The former task is in the testing phase. The tests aim at identifying suitable ranges of parameters for different scientific cases. The latter task is still under investigation and debugging phase. At this stage of the data reduction the astrometric calibration has still to be performed. Thus, the two tasks can not be based on redundancy. Both tasks have to overcome the following problems:

- signal fluctuation of each pixel

- the movement of the telescope
- the hits received by one pixel due to several cosmic rays having different signatures and arrival time
- the non-linear nature of each glitch

A full explanation of what these tasks do, how they work and results of testing them, is left to the Appendix. To run them, use

```
myframe = photMMTDeglitching(myframe, incr_fact=2,mmt_mode='multiply', scales=3,
nsigma=5)
myframe = photWTMMLDeglitching(myframe)
```

However, these task are not part of the standard PS pipeline, so do not use them when reducing PS data. We mention them here because later they might become part of the pipeline. The photMMT-Deglitching is part of the scanmap pipeline.

5.3.7. convertChopper2Angle

This task converts the Chopper position expressed in technical units to angles. This is done by reading the CPR entry in the Status table and express it in two ways:

- as angle with respect to the FPU (CHOPFPUANGLE entry in the Status table)
- as angle in the sky (CHOPSKYANGLE).

Both angles are in arc seconds. In particular, the CHOPFPUANGLE is a mandatory input for the PhotAssignaRaDec task, to be executed after Level 0.5 for the final step of the astrometric calibration. Thus, the convChopper2Angle task must be executed even if the chopper is not used at all as in the scan map (chopper maintained at the optical zero). CHOPFPUANGLE corresponds to the chopper throw in arc seconds in HSpot.

```
myframe = convertChopper2Angle(myframe, calTree=calTree)
```

The calibration between chopper position in technical units (voltages) and angles is give by a 6th order polynomial. The calibration is based on the calibration file containing the Zeiss conversion table.

5.3.8. photAssignRaDec

The purpose of this task is to convert the image into World Coordinate System by assigning RA and DEC coordinates to each pixels.

```
myframe = photAssignRaDec(myframe)
```

5.4. The AOT dependent pipelines

After level 0.5, the pipeline is AOT dependent. In the following sections we will describe separately the different AOT pipelines, point source, small source, chopped raster, scan map AOTs, up to Level 2. There is two observing modes available using the PACS Photometer. The point source mode and the scanmap mode.

5.5. Point Source AOR

5.5.1. Level 0.5 to Level 1

```
framesnod = photMakeDithPos(framesnod)
framesnod = photMakeRasPosCount(framesnod)
framesnod = photAvgPlateau(framesnod,skipFirst=True,copy=1)
```

```
framesnod = photAddPointings4PointSource(framesnod)
framesnod = photDiffChop(framesnod)
framesnod = photAvgDith(framesnod,sigclip=3.)
framesnod = photDiffNod(framesnod)
framesnod = photCombineNod(framesnod)
framesnod = photRespFlatfieldCorrection(framesnod)
#framesnod = photDriftCorrection(framesnod)
```

5.5.1.1. photMakeDithPos

The task just checks if exists a dithering pattern and identifies the dither positions. The task adds a dither position counter, *DithPos*, to the Status table. Frames with the same value of *DithPos* are at the same dither position.

```
myframe = photAvgPlateau(myframe)
```

5.5.1.2. photMakeRasPosCount

The task adds raster position counter to status table.

```
myframe = photMakeRasPosCount(myframe)
```

The task needs the output of the `photAddInstantPointing` task to be executed otherwise an error is raised saying that the pointing information are missing for the observation. The module uses the virtual aperture coordinates and the raster flags in the status table to identify different raster positions. The raster positions are identified in the Status Table by the new entries *OnRasterPosCount* and *OffRasterPosCount*.

5.5.1.3. photAvgPlateau

The task averages all valid signals on chopper plateau and resamples signals, status and mask words for the photometer. It calculate noise map but not the coverage map. The result is a Frames class with one image per every single chopper plateau.

```
myframe = photAvgPlateau(myframe,skipFirst=True,copy=1)
```

The module uses the status entry CHOPPERPLATEAU (CALSOURCE in case of calibration block pre-processing) to identify the chopper plateau in the same way as `CleanPlateau`. Then it computes the average (sigma clipping if *sigclip > 0*, and median if *mean =1*) for each pixel over the chopper plateau .

The signal of the bad pixels, identified by the BADPIXEL mask, is reduced by the task as the unmasked pixel. The pixels flagged in the other available masks (SATURATION, GLITCH, UNCLEANCHOP) are discarded in the average. If the chopper plateau contains no valid data (all pixels masked out) the signal is set to *NaN* (Not a Number). The noise is calculated for each pixel (*x,y*) and each plateau (*p*) as:

noise[x,y,p] = STDDEV(signal[x,y,validSelection[p]]) / SQRT(nn)

where *nn* is the number of valid readouts in the chopper plateau. This number is then stored as addition entry (`NrChopperPlateau`) in the status table. The noise is stored in the `Noisemap`. The skipFirst=True option gets rid of the first frame of each plateau. It is needed since the first group of 4 averaged readout after the chopper motion will have a different value from the one following it as the signal takes a few 40 Hz readouts to adjust to the new level

5.5.1.4. photAddPointing4PointSource

The task extracts pointing information for further photometer PointSource processing. Stores the averaged ra,dec of the virtual aperture for both nod positions, dither positions and chop positions and adds the PhotPointSource Dataset to the Frames class. It contains per nod position, dither position and chopper position the first value of : RaArray, DecArray, PaArray, CPR, DithPos, NodCycleNum,

ChopperPlateau, isAPosition. This information is later used on PhotProjectPointSource to map the Frames.

```
myframe = photAddPointing4PointSource(myframe)
```

5.5.1.5. photDiffChop

Subtract every off-source signal from every consecutive on-source signal. The result is a Frames class with one image per one chopper cycle. Note that in PS mode the 'off-source' image also contains the source but on a different position.

```
myframe = photDiffChop(myframe)
```

To better subtract the telescope background emission and the sky background the 'off-source' image is subtracted from the 'on-source' image (consecutive chopper positions). The module accepts as input the output of `photAvgPlateau` module. It returns as output a Frames class with the differential image of any couple of on-off chopped images. The module resamples the status table and the the masks accordingly.

The on and off images are identified on the basis of the status entries added by the `photAddInstantPointing` task. The noisemap is computed in the following way:

noise [x,y,k] = SQRT(noise[x,y,pON]**2 + noise[x,y,pOFF]**2)

where *k* is the frame number of the differential on-off image, *pOn* is the frame number of the on source image, *pOFF* is the frame number of the off source image, *noise[x,y,pON]* and *noise[x,y,pOFF]* are the error maps at the on and off source images, respectively (output of the previous pipeline step).

5.5.1.6. photAvgDith

The chop cycle is repeated several times per any A and B nod position. This task calculates the mean of the on-off differential chopped images per any A and B position within any Nod cycle. If the dithering is applied in the point-source mode as offered by HSpot, the average is done separately per dithered A and B nod positions.

```
myframe = photAvgDith(myframe, sigclip=3.)
```

This task uses several entries in the status table to identify the on-off differential images (output of `photDiffChop`) belonging to the A and B Nod position of a given Nod cycle and dithered position (*DithPos*, *NodcycleNum*, *IsAPosition*, *IsBPosition*, see output of `photAddIstantPointing`). Since only the average of the identified images is performed, the noise is propagated as follows:

For "c" chopper cycles (c=k), we average the n/2 differences: noise [x,y] = SQRT(MEAN(noise[x,y,:]**2)) / SQRT(n)

The sigclip=3. takes care of the deglitching. Users may want to explore different values as well.

5.5.1.7. photDiffNod

This task is performing the last step of the background (sky+telescope) subtraction. It subtracts the images corresponding to the A and B positions of each nod cycle and per each dither position. The module needs as input the output of `photAvgDith`.

```
myframe = photDiffNod(myframe)
```

The noise is propagated as follows:

noise [x,y,k] = SQRT(noise[x,y,A]**2 + noise[x,y,B]*+2)

where the *A* and *B* indexes refer to the A and B nod position.

5.5.1.8. photCombineNod

The Nod cycles are repeated many times per any dither position. This task is taking the average of the differential *nodA-nodB* images corresponding to any dither position. The results is a frames class containing a completely background subtracted point source image per any dither position.

```
myframe = photCombineNod(myframe)
```

The noise is propagated as follows:

noise[x,y,d] = STDDEV(signal[x,y,nd]) /SQRT(nd)

where *d* is the index of the dither position and *nd* is the number of nod cycles per dither position.

5.5.1.9. photRespFlatFieldCorrection

The task applies flat field corrections and converts signal to a flux density:

```
myframe = photRespFlatFieldCorrection(myframe,calTree=calTree)
```

The formula managing the flat-field, the flux calibration and the photometric adjustment is the following:

$$\mathcal{f}(t) = \mathcal{s}(t) * \frac{(\mathcal{DC}_0)}{(\mathcal{DC})} * \frac{1}{(J\Phi)}$$

Figure 5.1.

where *f(t)* is the flux in Jy, *s(t)* is the signal in Volt, *DC0* is the difference of the calibration sources got during a calibration campaign, *DCs* is the difference of the calibration sources computed by the cal-block pre-processing, *J* is a flux calibration factor which contains the responsivity and the conversion factor to Jansky, *Phi* is the normalized flatfield. The ratio *1/J*Phi* converts the signal *s(t)* in Volt to *f(t)* in Jansky. This task applies the ratio *1/J*Phi* to flat-filed and flux calibrate the data.

The noise is calculate in the following way:

```
noise = SQRT( s_out^2 * [ (sigmas2/s2) + (sigmaC0^2/C0^2) + (sigmaCs^2/Cs^2) -] -)
```

where *s* is the input signal in Volt, *sigmas* is the input noise, *C0* is our reference, *sigmaC0* is the noise of the reference, *DCs* is the differential image of the cal-block and *signaDCs* is the noise associated to that.

Addendum: the first *DC0* has been determined with data collected during ILT test campaign. The following biases have been used: 2.6 V for both the blue and green channel, 2.0 V for the red one.

5.5.1.10. photDriftCorrection

The task applies the drift correction of the flat field and controls the photometric stability:

```
myframe = photDriftCorrection(myframe)
```

The `PhotDriftCorrection` task has the goal to multiply the signal *s(t)* by the ratio *DC0/DCs*, where *DC0* is the differential image of the two internal calibration sources (calculated from the same data of the flat-field), *DCs* is the differential image of *CS1-CS2* obtained from the calibration block of the observation (output of the cal-block pre-processing). This factor corrects possible drift of the flat

field. This drift can be due either to an alteration of the internal calibration sources or to an evolution of the detector pixels. The drift is compared with photometric stability threshold parameters (stored in the calibration files). If the ratio overtakes these thresholds, a *DriftAlert* keyword is added to the metadata. Note, that the task is currently not part of the standard pipeline

5.5.2. Level 1 to Level 2

5.5.2.1. photProject and photProjectPointSource

The `photProject` task provides one of the two methods adopted for the map creation from a given set of images (in the PACS case, a frame class). The task performs a simple coaddition of images, by using a simplified version of the drizzle method (*Fruchter and Hook, 2002, PASP, 114, 144*). It can be applied to raster and scan map observations without particular restrictions. The only requirement is that the input frame class must be astrometric calibrated, which means, in the PACS case, that it must include the cubes of sky coordinates of the pixel centers. Thus, `photAddInstantPointing` and `photAssignRaDec` should be executed before `PhotProject`. There is not any particular treatment of the signal in terms of noise removal. The *1/f* noise is supposed to be removed before the execution of this task, e.g. by the previous steps of the pipeline in the case of chooped-nodded observations and by the `photHighPassFilter` or similar tasks in the scan map case. The tasks projects all images onto a map with a pixel size defined using the "outputPixelsize" option. Note, that the option "calibration=True" must be set in order to properly conserve fluxes of image that are not using native pixel sizes (3.2 in the blue and 6.4 in the red). The photProjectPointSource() is specific version of photProject for the chopped/nodded point source AOT style observations. If the allInOne=1 is set then the task creates a final map by combining both chop and nod positions (4 images altogether) and rotate the image so that North is up and East is left. World Coordinate System data are produced as metadata for a later FITS file generation of the final product.

```
map1 = photProject(framesnod,outputPixelsize=3.2,calTree=calTree,calibration=True)
map2 = photProjectPointSource(myframe,
allInOne=1,outputPixelsize=3.2,calTree=calTree, calibration=True)
# update metadata for FITS header
    for m in(myobs.meta.keySet()):
        map1.meta[m]=myobs.meta[m]
        map2.meta[m]=myobs.meta[m]
    pass
```

The four lines of code after the creation of the final map products adds additional metadata that have not been propagated throughout the data processing and will later be written to the FITS header. They are simply copied from the Observation Context. Displaying both final maps and saving them to FITS files is done by:

```
Display(map1)
Display(map2)
product = simpleFitsWriter(map1,"filename"+str(i)".fits")
product = simpleFitsWriter(map2,"filename"+str(i)".fits")
```

Since there are three additional copies made of the final dithering corrected product, the final map contains additional images of the source, but only the one in the centre is considered to be the relevant result. Besides the final image, the task creates additional products: i) error map: distribution of errors propagated throughout the data reduction; these errors do not reflect the statistical error of the final image, but also includes systematic uncertainties. As a result, the values usually overestimate the photometric error in the final image. ii) coverage map: gives the number of detector pixels that have seen a certain logical, rebinned pixel in the final image iii) exposure map: similar to coverage map, but this time it gives the total observing time spent on each logical, rebinned pixel in the final image

You can check the result of the projection by looking at the data using the 'Display' task. Don't forget that in most cases you will have more than one slice so name your files in a way that you can retrieve them easily. (See in the example)

The difference between the two task can be seen in the two different map created in the above example

map1 = photProject() gives a de-rotated map (equatorial, N up, E left) that contains all individual frames co-added to one, showing the characteristic four point chop nod pattern. Advantage: more homogeneous coverage of the sky background for determining the background noise. Disadvantage: S/N ratio of one individual image of the target is a factor of two lower than the map2 product.

map2 = photProjectPointSource() applies a simple shift-and-add algorithm to combine all images of the target into only one in order to provide to optimised S/N ratio. The relevant results will be in the centre of the final map; the other eight copies are just an artefact of the reconstruction and should not be used. Disadvantage: The area of homogeneous coverage is relatively narrow and closely confined around the source.

5.5.2.2. Combining the final image

If you have more then one slice you need to combine them in order to get the final image.

```
from java.util import ArrayList
from herschel.ia.toolbox.image import MosaicTask

# making an empty list in which we are going to store the images
images1=ArrayList()
images2=ArrayList()

for i in range(slicedFrames.numberOfScienceFrames):
ima1 = simpleFitsReader("filename"+str(i)+'.fits')
ima2 = simpleFitsReader("filename"+str(i)+".fits")
ima1.exposure = ima.coverage   # this swap is peformed because the current
exposure map is incorrect.
ima2.exposure = ima2.coverage
images1.add(ima1)
images2.add(ima2)

# mosaicking
mosaic1=MosaicTask()(images=images1,oversample=0)
mosaic2=MosaicTask()(images=images2,oversample=0)
```

With the simple fits reader you need to read all the fits files created using photProjectPointSource and/ or photProject project and mosaic them using the "MosaicTask" that simply combine all the images in the "images" array

5.6. Scan Map AOR

5.6.1. Level 0.5 to Level 1

See the detailed description of the same steps in the Point-source pipeline section:

- `photMMTDeglitching`
- `photDriftCorrection`
- `photRespFlatFieldCorrection`
- `photAssignRaDec`

5.6.2. Level 1 to Level 2

But first you need to save your frames. you will need them later.

```
save(savefile, -"frame, variables")
```

At this stage of the data reduction (after calibrating for instrumental effects) the scan map pipeline is divided in two branches: a simple projection given by photProject and the inversion given by MadMap.

The two methods are implemented to satisfy the requirements of different scientific cases. See following subsections for more details.

5.6.2.1. High pass filter and simple projection on the sky

photHighPassfilter

The purpose is to remove the 1/f noise. Several methods are still under investigation. At the moment the task is using a Median Filter by removing a running median from each readout. The filter box size can be set by the user (*filterbox* parameter in the scheme below).

```
myframe = photHighPassfilter(myframe,20)
```

The width of the high pass filter, here 20, depends on the scan speed and PSF width, The smaller the better the 1/f is filtered out, but flux of the source and PSF will be affected for too small values. For bright sources a previous photMaskFromImageHighpass has to be applied At medium speed (20 arcsec/s) a width of 20 is a good compromise in the blue and green channel , and 30 in the red channel, which corresponds to 40/60 arcsec on the sky respectively. At high speed (60"/s) a width of 10 can be used, corresponding to a length in the sky of 1 arcmin. For deep fields, the current best values for the widths are 15 readouts in the green and 26 in red channel.

At this stage you may want to remove the turnover loops between scan legs and check the cube before projection, this can be done with the following command

```
myframe=myframe.select(myframe.getStatus("BBID") == 215131301l
Display(myframe.signal.depthAxis=2)
```

photProject

```
map1 = photProject(frames, calTree=calTree,calibration=True,outputPixelsize=1.0)
Display(map1)
```

See the detailed description in the Point-source pipeline section.

Then you need to disable the deglitching on the target in order to preserve the flux in interest. You can do it with the following piece of code which set the mask for deglitching to exclude the target

```
mask=frames.getMask('MMT_Glitchmask')
awaysource=SQRT(((frames.ra-rasource)*cosdec)**2+(frames.dec-decsource)**2) >
7./3600.
frames.setMask('MMT_Glitchmask',mask & awaysource)
```

Then of course you need to re-project the map and save the first pass as a fits file.

```
map1 = photProject(frames, calTree=calTree,calibration=True,outputPixelsize=1.0)
Display(map1)
simpleFitsWriter(map1,filename1'.fits')
```

2nd pass: high pass filter mask

Now you need to restart the whole process from the frames saved before the high pass filtering.

```
from herschel.pacs.spg import PhotReadMaskFromImageTask
photMaskFromImageHighpass = PhotReadMaskFromImageTask()
restore(savfile)
mask        = simpleFitsReader(maskfile)
frames_mask = photMaskFromImageHighpass(frames,si=mask,maskname="HighpassMask")
frames_mask = highpassFilter(frames_mask,hpfwidth,maskname="HighpassMask")
```

Of course you need to disable the deglitching on the target again and remove the turnover loops from the masks, project and write out as a fits file

```
mask=frames.getMask('MMT_Glitchmask')
awaysource=SQRT(((frames.ra-rasource)*cosdec)**2+(frames.dec-decsource)**2) >
7./3600.
frames.setMask('MMT_Glitchmask',mask & awaysource)
frames_mask = frames.select(frames_mask.getStatus("BBID") == 215131301l)
map2  = photProject(frames_mask,
calibration=True,outputPixelsize=outpixsz,calTree=calTree)
Display(map2)
Display(map2.coverage)
simpleFitsWriter(map2, filename2'.fits')
```

Mosaic the two scan maps

Usually the recommended way of doing observations in scanmap mode is to make two scanmaps with different scan angles (they are called scan and cross scan). These observations are executed as standalone maps and both is defined in its own AOR so they have different obsids (in opposite to SPIRE where you define the scan and cross scan in one AOR). You have to repeat the above steps for both obsids then create a single mosaic of the two maps.

Creating the mosaic out of the two scan maps is very similar to that of combining the slices in the case of point source AOT

```
from java.util import ArrayList
from herschel.ia.toolbox.image import MosaicTask
images=ArrayList()

ima = SimpleImage()
importImage(image=ima,filename=filename2_AOR1'.fits')
ima.exposure=ima.coverage
images.add(ima)

ima = SimpleImage()
importImage(image=ima,filename=filename2_AOR2.'.fits')
ima.exposure=ima.coverage
images.add(ima)

# mosaicking
mosaic=MosaicTask()(images=images,oversample=0)
Display(mosaic)
Display(mosaic.exposure)


simpleFitsWriter(mosaic,"Mosaic.fits")
```

5.6.2.2. The MadMap case

MadMap uses a maximum-likelihood technique to build a map from an input Time Order Data (TOD) set by solving a system of linear equations. It is used to remove low-frequency drift ("1/f") noise from bolometer data while preserving the sky signal on large spatial scales. (Reference: http://crd.lbl.gov/~cmc/MADmap/doc/man/MADmap.html). The input TOD data is assumed to be calibrated and flat-fielded and input InvNtt noise calibration file is from calibration tree.

First you need to reset the on-target flag to True, as it is unreliable in the pointing product so far

```
myframe.setStatus("OnTarget",Bool1d(myframe.dimensions[2],True))
```

and correct for the offset differences between matrices.

```
myframe = photOffsetCorr(myframe)
```

makeTodArray

Builds time-ordered data (TOD) stream for input into `MadMap` and derives meta header information of the output skymap. Input data is assumed to be calibrated and flat-fielded. Also prepares the "to's" and

"from's" header information for the `InvNtt` (inverse time-time noise covariance matrix) calibration file.

```
tod = makeTodArray(myframe,1,0.0,optimizeOrientation=True)
```

The TOD binary data file is built with format given above and the tod product includes and the astrometry of output map using meta data keywords.

The weights are set to 0 for bad data as flagged in the mask. Dead/bad detectors (detectors which are always, or usually, bad), are not included in TOD calculations. The skypix indices are derived from the projection of each input pixel onto the output sky grid. The skypix indices are increasing integers representing the location in the sky map with good data. The skypixel indices of the output map must have some data with non-zero weights,must be continuous, must start with 0, and must be sorted with 0 first and the largest index last.

The first argument of the task is the input frames in untis of mJy/pixel, the second is the output pixel scale in relation to the PACS detector pixel size, so for scale=1 the map has square pixels with size of the PACS nominal pixel size. The third argument is the crota2 keyword (default is 0.0).

runMadMap

The module `runMadMap` is the wrapper that runs the JAVA MadMap module.

```
map = runMadMap(tod,calTree=calTree)
Display(madmap)
```