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

If you are reading this guide during or in the few months after the Science Demonstration phase of Herschel then please bear in mind that it is not complete; in particular the links are not active and the Appendix and some of the later chapters not written or are still being updated. In addition, many issues to do with the pipeline and the data structure are still under consideration and will change throughout this period. The general documentation on HIPE is also undergoing changes; depending on when you are reading this, the names of other documents referred to may be different to what is given here: we refer to the Quick Start Guide (QSG) and the HIPE Owner's Guide (HOG) but under the older organisation these are both in the HowTo guide (HowTo); we refer to the Data Analysis Guide (DAG) and the Scripting and Data Mining (SaDM) guide but in the older organisation these are in the Advanced User's Manual (AUM).

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Welcome to the PACS data reduction guide #. 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 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, (v) explain more fully what the pipeline steps are doing, why they are doing it, and what their parameters are, and (vi) discuss issues that are of concern for particular AOTs (such as rastering) or targets (such as moving targets) or are still under development.

This guide is aimed at those who are new to HIPE and new to PACS. 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. If the data reduction seems difficult to you it is not because we have made it so, but because it is so. 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. This guide is designed to be read from *beginning to end*, so read the whole thing before you claim something is not working or not understandable.

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. Scattered throughout this guide are "seed" scripts, which were written primarily to accompany the pipeline to allow easy plotting and inspection of the data, but you can also use them to start to learn the scripting language yourself. There is also much help on DP scripting available from the help page, however, unless you are a good programmer, it is probably a good idea to first work your way through the pipeline and this PACS data reduction guide, before starting to script. Doing it the other way around will guarantee much frustration.

There are a number of documents you could read before and along with this one. This may sound boring, but unless you want to use the pipeline just as a black box you really should read-while-you-try. While this PACS data reduction guide is meant to be complete, it is not stand-alone: we link you to other documents rather than repeat here what they explain.

1) A guide to HIPE itself is provided on the HIPE help page (Help#Contents, from the HIPE menu) in the *HIPE Owners Guide* (*HOG*) and the *Quick Start Guide* (*QSG*) (under the older Help organisation these documents are contained in the HowTo guide). These tells you how to start up and work in HIPE, how to extract data from the Herschel Science Archive (HSA), and some basics about working with spectra, cubes and images.

2) The *Data Analysis Guide (DAG)* 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). (Under the older organisation this is called the Advanced User's Manual: *AUM*.)

3) The *Scripting and Data Mining* guide *(SaDM*) (or the *AUM* under the older organisation), also available from the HIPE help page, contains a lot of information about working in HIPE with arrays, the DP syntax and working therein, doing mathematics, plotting and displaying. 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.

5) At least one other document for PACS will be provided (which may not yet be available) on the HIPE help: the PACS Detailed Pipeline Document (*PDPD*). This discusses the glorious details of the pipeline tasks and may include a product description section (i.e. explaining what is what in PACS products). We *strongly* suggest you do not read the *PDPD* until you have read this PACS data reduction guide first.

6) The HCSS or PACS User's Reference Manual (the PACS URM is the HCSS URM + extra PACS bits): these contain information about many of the tasks you will use, but be warned that these have been written by and for internal PACS users and hence may be rather difficult to understand.

7) Another very advanced document is the Developer Reference Manual, 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 help you to understand what you read in the API.

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. The pipeline tasks and inspection recipes are expanded on in Chapter 4 and issues of concern for particular AOTs or types of targets are discussed. Chapters 5 and 6 are the same as 3 and 4 but for the photometer. Finally, in the Appendix we may include some seed data inspection scripts.

Note that chapters 4,5 and 6 are incomplete (or lacking) and the Appendix has not yet been written.

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, because in this data reduction guide we explain only how to work with PACS cubes, not all about integral field spectroscopy. 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. We recommend that you run HIPE with at least 2GB of memory, more if you can. 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*. (You can also use the Edit#Preferences menu to change various HIPE properties.) 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 "Work Bench" icon on the HIPE welcome page; clicking on the small blue (Work Bench) or green (Full Work Bench) clapperboard icon at the top right of the HIPE GUI; selecting from the menu at the top left, Window#Show Perspectives. It is in the Console section of your work bench that you type commands.

1.3.1. First: get your data and populate your pool

First you need to get hold of your entire dataset and then you need to extract from that the "ObservationContext". There are a number of ways of doing each of these separately and at least two ways of doing them both together. (Read this section and the next before you try to do anything yourself. And note that while you may not understand why you are being asked to do all you have to do, it should become more clear as you go through the later chapters of this guide.)

The instructions for retrieving your data from the HSA and reading them into HIPE or transferring them to disk are in the *QSG*, and these instructions we do not repeat here. Essentially you can either request data as a tarball which you ftp to your own disk and then load into HIPE when you need it, or you can call on the HSA directly to fetch the data and place it in memory in HIPE. For both methods you will need to save the data to disk, as a "pool", otherwise next time you run HIPE you will have to retrieve those in the same way data again. (The ftp method is best if you have many observations you want to get hold of, direct retrieval best if you are only looking at a few datasets.) Note that there is usually more than one way to do the same thing in HIPE, so don't worry if you get what appear to be conflicting instructions when reading different documentation: simply try them out and see which method you prefer.

A "pool" is simply a collection of data that belong together—your HSA-obtained data, maybe all your observations of the same object, or all your Level 1 processed products, or everything you worked on in a single day. The commonality between the products in a pool is yours to decide upon. Inside a pool will be many FITS files organised in a particular directory structure that allows the links between related data products to be made. It is the need for these links that is the reason why Herschel data are held in pools, and is also the reason why Herschel products can sometimes take a while to be extracted from or into a pool. 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.

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.

Note that HIPE expects pools to be located at [/Users/me/].hcss/lstore (i.e. off of your home directory). lstore is the default supradirectory in which you place all your pools. In Chap. 3/5 we will explain how to change the default location of /lstore.

1.3.2. Next: get the ObservationContext

What you want to look for in your pool/HSA untared directory is the "ObservationContext" (the capitalisation and concating is a jython thing). An ObservationContext is a container of data products that belong to a specific observation (and *ObservationContext* is the HIPE class of this container#more on classes later). It provides the associations between all the products you need to process that single observation and also includes the results of the automatic pipeline reductions done by the HSA. The products contained in an ObservationContext include not just the actual astronomical observation (raw and reduced), but also the data products that were used to process the data in 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.

Read the *QSG* (really...do) for instructions on the most straightforward way to get data from the HSA, or the <LINK> for a listing of all the methods you can use. Summarising all, and introducing 2 tasks that are (currently) unique to PACS:

- *If you loaded your HSA-requested data directly into the HIPE memory* via "Send to External Application" in the HSA view, then you have already the ObservationContext#you have the file that we call "myobs" below (although its name will not be myobs#look for it in the Variables panel after you have imported the data and you will see it there listed; if you wish you can change the name with a right-click on it in the Variables panel).

- *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 *QSG*). This will extract the ObservationContext from the directory that you untared the data into and put it directly into a user-chosen pool, let's say a pool called "swimming" (by default it will expect "swimming" to be a directory already in [HOME]/.hcss/lstore/swimming, so if it does not exist you will first need to use the PAL to set up "swimming" as a pool). You will then need to get the ObservationContext from that pool into HIPE in the following way:

  ```
  myobs=getObservation(1342182002L ,poolName="swimming" ,od=231)
  ```

  The number specified as the first parameter is the "obsid": this is the observation identifier and is 1342182002 here (this number you should know already, but if not you can hunt for your observation in the HSA and the obsid will be there listed); don't forget the "L" at the end of the number. The parameter `poolName` is the name of the pool into which you had placed the ObservationContext (here that would be "swimming"). The task run with these two parameters will find the ObservationContext with that obsid and in that pool (it is important to specify the obsid, in particular because more than one obsid can be held in a single pool). You may find that you need to specify also the `od` (observing day=231 here—information that should also be listed in the HSA listing of your observation). When you have executed this command, "myobs" will appear in the Variables panel listing.

- *If your ObservationContext is in a pool already* (e.g. someone sent you an entire pool that they had already looked at) you get the ObservationContext using the same command getObservation.

- *If you got your data via the "Retrieve" button*: You use the same method for importing data into HIPE for 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). *Another Note*: when I tried this "retrieve" method on an ObservationContext, it was much slower than the "send to external application" method.

- *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 /.hcss/user.props file with the following lines:

```
hcss.ia.pal.pool.hsa.haio.login_usr = your username
hcss.ia.pal.pool.hsa.haio.login_pwd = your password
```

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")
```

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

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

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

- You save myobs to a pool in the following way

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

where "swimming" is located by default at [HOME]/.hcss/lstore/swimming.

These methods work for an ObservationContext, not for any other type of product. For importing and exporting other products, see the instructions in Chap. 3/5. The full range of parameters for getObservation and saveObservation are given in Chap 3/5, where we also tell you how to save to a location on disc other than the default. Right now we want to keep things short and sweet.

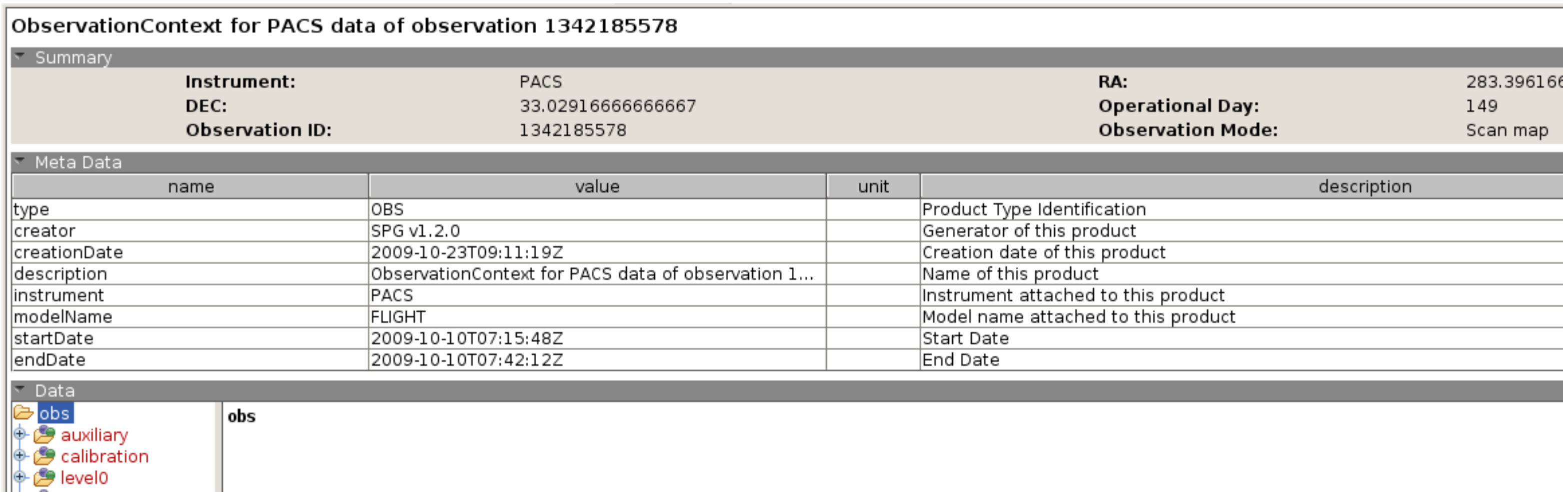
Note

You can give you variables#the things on the left of the = sign#any name you like. So instead of "myobs" 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!

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

One thing that will help you work out what your observation is of and what instrument configuration you had is to have a copy of the AOR (the Astronomer's Observation Request), 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 will have meta data, although they will not always be complete. For your ObservationContext, if you click on the ObservationContext itself you will see the meta data for it. This is shown in the following screenshot: what you will see if you view your ObservationContext with the "Observation Viewer". Look for "myobs" in the Variables panel (HIPE main menu Window#View#Variables). Double clicking on myobs will open a viewer (double click for the default viewer, right click to get a menu of viewer and other options). The viewer opens in the Editor panel.



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

Listed in red are the various individual products that are associated with myobs (more on those in the next section). The top listing are listed meta data. You can scroll down this list to see everything listed in there, which includes the parameters commanded in the AOR of your observation: pointing; repetition factors; observing mode; raster movements; band/wavelength.

If you click now on one of the products listed at the bottom-left ("Data") of the window (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 (myobs, though in the screenshot it is called"obs"). To see the myobs meta data again, simply click on "myobs" (which will be at the top of that bottom-left window, with a folder symbol next to it).

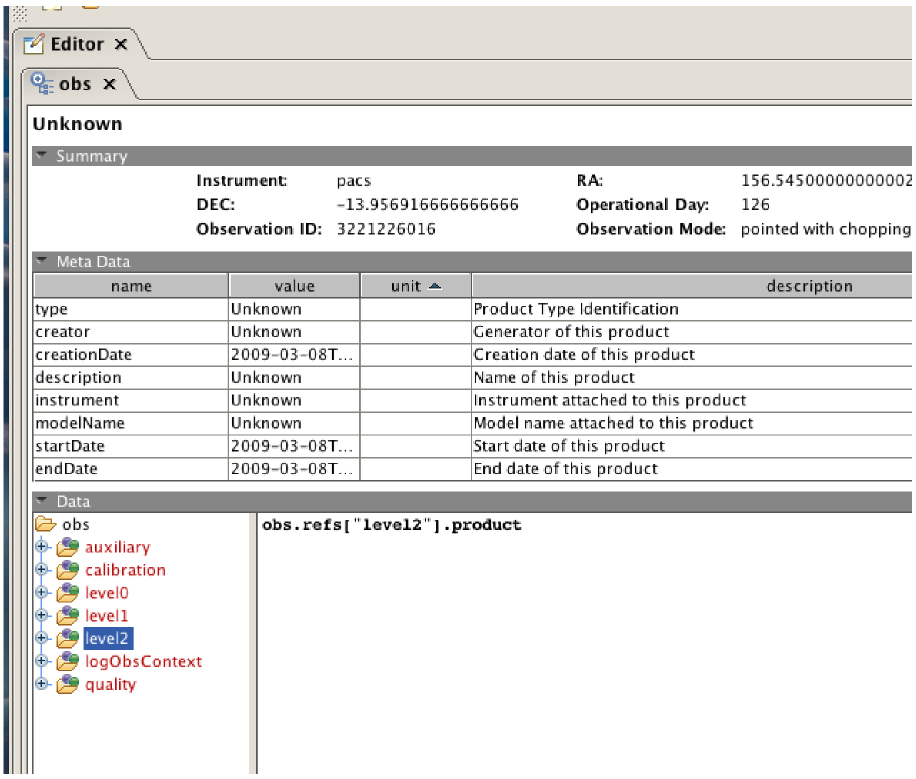
If you have multiple settings in your observation, for example rastering or dithering or cross scans, then unfortunately at present it is not easy to immediately work out what product is what part of your observation. This is something we are working hard to improve.

1.3.4. Then: look the Level 2 products

(This section should also be read by people interested only in photometry.)

1.3.4.1. Spectroscopy

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



Unknown

Summary

Instrument:	pacs	RA:	156.54500000000002
DEC:	-13.956916666666666	Operational Day:	126
Observation ID:	3221226016	Observation Mode:	pointed with chopping

Meta Data

name	value	unit	description
type	Unknown		Product Type Identification
creator	Unknown		Generator of this product
creationDate	2009-03-08T...		Creation date of this product
description	Unknown		Name of this product
instrument	Unknown		Instrument attached to this product
modelName	Unknown		Model name attached to this product
startDate	2009-03-08T...		Start date of this product
endDate	2009-03-08T...		End date of this product

Data

```
obs
  auxiliary
  calibration
  level0
  level1
  level2
  logObsContext
  quality
```

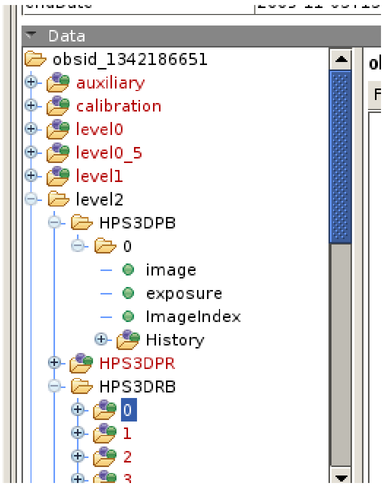
```
obs.refs["level2"].product
```

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

(A listing in red means that has not yet been loaded into memory, black means it has been loaded into memory.)

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 through the automatic pipeline to that level, and hence there are no cubes or maps 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:



Data

```
obsid_1342186651
  auxiliary
  calibration
  level0
  level0_5
  level1
  level2
    HPS3DPB
      0
        image
        exposure
        ImageIndex
        History
    HPS3DPR
    HPS3DRB
      0
      1
      2
      3
```

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] (or something similar: it changes faster than I can keep up!). 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).

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*.

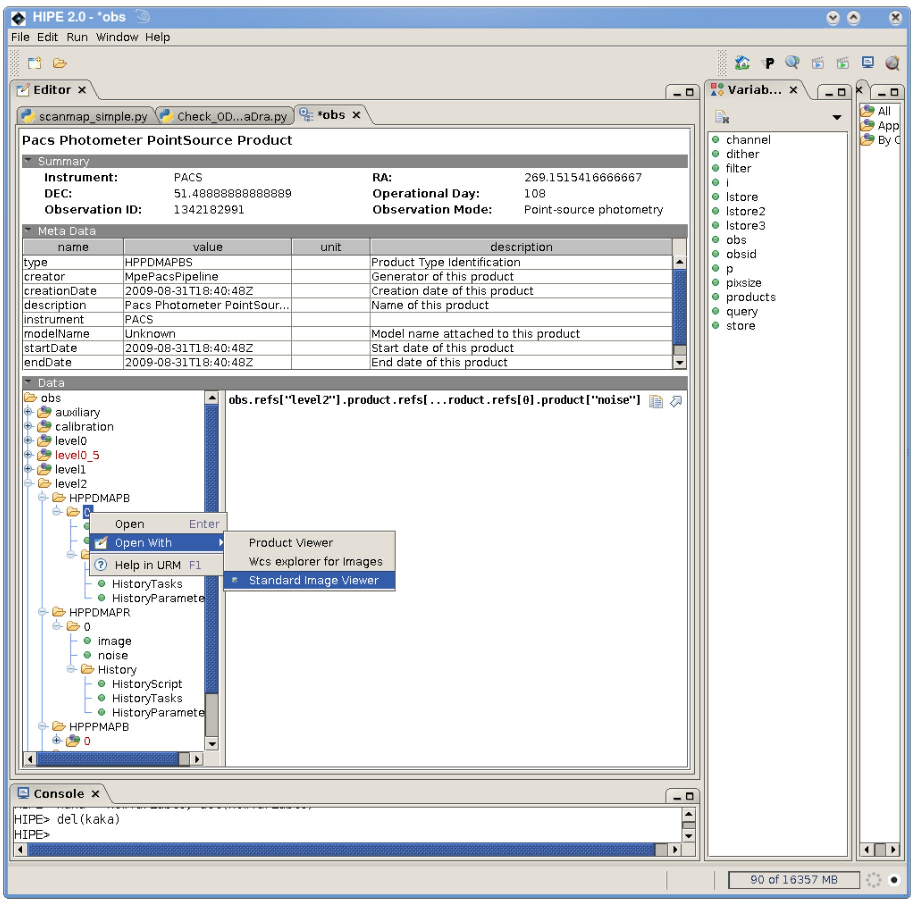
Exactly what is in your Level 2 depends on what type of observation you requested. It is likely that you will have multiple cubes if your AOR included dithering/rastering/more than one spectral line.

You will need to read Chap. 3 to find out what the difference between the *SpectralSimpleCube* and *PacsRebinnedCube* is, but for now, suffice it to say that the rebinned cube is the final output of the pipeline, which takes the 5x5 simple cube as input and "projects" it into a cube of smaller sized but more abundant spaxels. You can chose to look at either or both of these cubes right now.

In the screenshot above 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).

1.3.4.2. Photometry

For photometry the same layout and similar syntax is found as for spectroscopy, and you should see something similar to the next screenshot. 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. 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.



Pacs Photometer PointSource Product

Summary

Instrument:	PACS	**RA:**	269.1515416666667
DEC:	51.48888888888889	**Operational Day:**	108
Observation ID:	1342182991	**Observation Mode:**	Point-source photometry

Meta Data

name	value	unit	description
type	HPPDMAPBS		Product Type Identification
creator	MpePacsPipeline		Generator of this product
creationDate	2009-08-31T18:40:48Z		Creation date of this product
description	Pacs Photometer PointSour...		Name of this product
instrument	PACS		
modelName	Unknown		Model name attached to this product
startDate	2009-08-31T18:40:48Z		Start date of this product
endDate	2009-08-31T18:40:48Z		End date of this product

Data

```
obs.refs["level2"].product.refs[...roduct.refs[0].product["noise"]
```

```
HIPE> del(kaka)
HIPE>
```

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.

1.3.4.3. Both

To now view your product(s) (the maps or cubes) you need to click on the +0 (or +1...) (*not* the 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. The default viewer for spectroscopy should be the CubeAnalysisToolBox (because the Level 2 product is a cube). The toolbox will open in the window to the right of the listing (where the spectrum you can just about see in the screenshot is), and/or in a new tab. For photometry the default viewer is the Standard Image Viewer (as shown in the previous screenshot).

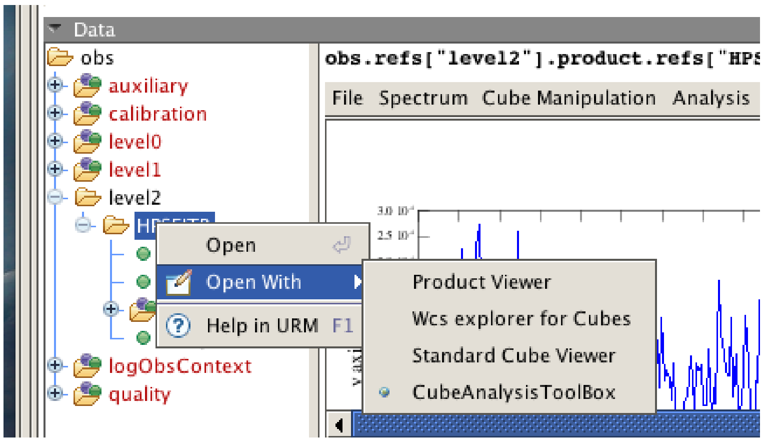


Figure 1.5. Viewing your Level 2 product

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. However, in Chap. 4 and 5 we offer some workarounds.

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 cube out of the ObservationContext first. We postpone a full explanation of how to do this to Chap. 3/5 but in case you want to know right now: 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), and also to rename it. 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", 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. But at present viewing these datasets rather than the entire product will be less than useful for you.

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 incorrect.

1.3.5. 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. We assume that you want to only look at the data, and maybe have a play around with what is in them; the main emphasis of this Data Reduction Guide is the pipeline data reduction, which is the subject of all subsequent chapters.

The help page of HIPE—in particular the *DAG*—is the reference for 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.

For some of the GUIs you need to extract out of the ObservationContext the cube or map. You do this with the click-drag we explained above, for the cube we assume that you have called that new product "mycube" and for the map, "mymap".

1.3.5.1. Spectroscopy

Before beginning we would like to point out that currently, while we are still in the first year of Herschel, the tools for doing spectral manipulation are still under development, and at the time of writing they do not all work directly on PACS cubes. Hence I warn you now that this part of working with PACS spectroscopy data will be rather frustrating. Some workarounds are provided in Chap. 4.

Here we will introduce you to the various GUIs that can be used to inspect your PACS cube of class *SpectrumSimpleCube*. There are other ways you can inspect (and later manipulate) the data, but for a first quick-look we recommend you use the GUIs.

- # The SpectrumExplorer. This is a spectral visualisation tool for sets of 1d spectra and at some point also for your Level 2 *SpectralSimpleCube*. It allows for an inspection and comparison of spectra from individual spaxels. It is probably easier to use than the CubeAnalysisToolBox if you are interested in only looking at individual spectra. The *DAG* provides a guide to the use of the SpectrumExplorer, and it is called up with a right-mouse selection on mycube in the Variables panel. It may at present not work on cubes.
- # The CubeAnalysisToolBox. This allows you to inspect your cube spatially and spectrally at the same time. It will allow for some analyses#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, and it is called up with a right-mouse selection on mycube in the Variables panel. It currently works on the *SpectralSimpleCube*s and the *PacsRebinnedCube*s if the WCS is valid.
- # The SFTool. The SpectrumFitterTool will allow you to fit and do mathematics on your spectra. To access the SFTool, click-highlight mycube in the Variables panel; go to the Task panel at the top-right of the Full Workbench; and double click on Applicable. All applicable tasks will be listed, this will include certain mathematical functions and the SFTool. The *DAG* explains the use of this tool, which unfortunately at the time of writing does not work directly on PACS cubes.
- # The ExplFitter. The line fitting tool (similar to the SFTool). This is also to be found in the Tasks panel and details of use are in the *DAG*. It also allows for spectral line and continuum fitting. It may also at present not work directly on PACS cubes.
- You can image single or multiple wavelength slices of your cube with Display.

  ```
  Display(mycube.flux(1000:1100,:,:],depthAxis=0)
  ```

  will display as a 2D image 100 wavelength bins (1000:1100, and you can scroll through the layers in the display) for all spaxels of your cube (the :,: part of the command). Don't try to display all the wavelength layers: you may use up all your memory and HIPE will freeze! Unfortunately you need to specify the array position (1000 to 1100 here), not the actual wavelengths. To figure out what array positions corresponds to which wavelengths you need to inspect your cube, and for now the most straightforward way to do this is to plot the wavelengths against array position:

  ```
  PlotXY(mycube.getWave())
  ```

  plots the wavelengths on the Y-axis and array position on the X-axis. We explain the syntax of this command in Chap. 3.
- You can plot single spaxels with the command

```
PlotXY(mycube.getWave(),mycube.getFlux(12,11))
```

where 12,11 is the spaxel you are plotting (the dimensions can be found with > print mycube.dimensions, where the final 2 are the spatial dimensions and the first is the spectral dimension).

1.3.5.2. 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 observations work 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 (to account for the rapidly varying telescope background); nodding of the telescope between two fields (to remove the astronomical "sky" background); moving over many fields to make a bigger map; grating movements to sample the wavelength domain (for spectroscopy). 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) 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#the detector is read out non-destructively (usually 32 or 64 times) before a destructive readout is performed, i.e. the voltage across it is reset to a reference value every 0.125 or 0.25 seconds. 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, Herschel-Pacs-Spectroscopy-FITted-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 detector, Herschel-Pacs-Spectroscopy-AVeraGed-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 data.

There is also a Status table, and later there will be a BlockTable, attached to your ramp and frame 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. If you double click on e.g. a Level 1 frame in the Variables panel to view its contents, you will see the Status table there. Right click to select the Dataset Viewer (or the Table plotter, although this cannot plot all the entries of the Status), and you will see a tabular listing. 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, and collectively these have an on-sky arrangement of 5x5. These columns are referred to as modules: a module is the physical entity to 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 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.

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, a calibration block, ...

2.2. The data structure (simple version)

The structure of PACS data are given in better detail in the *PDPD*, 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:

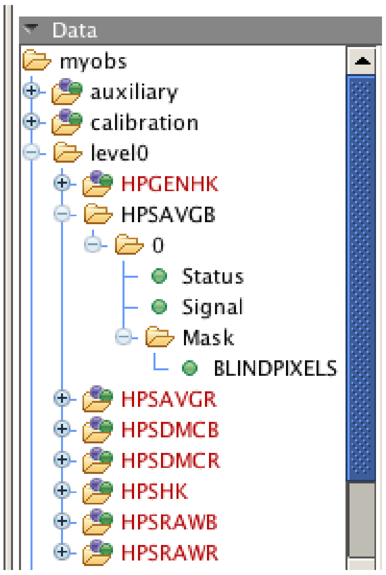


Figure 2.1. The contents of an ObservationContext for spectroscopy

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 access directly yourself. The same click methods as previously mentioned can be used to inspect these products (i.e. 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
```

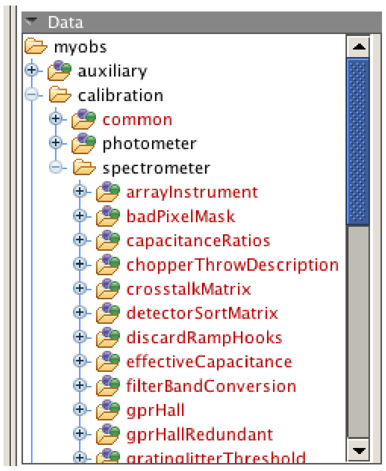
where *the first line* will produce a listing similar to the next screenshot, *the second line* produces a listing of the entries in the meta data (a sort of FITS header) and the "directories" you can see in the screenshot above, and *the third line* shows what Level 0 products there are in your ObservationContext. Be warned, however, 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. We recommend, in any case, that you stick to the GUI listings rather than the command line.

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...), and if so you will later need to extract these out separately to run through the pipeline. What has just been said applies equally to an HPSFITB/R "directory", which you will have if your 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). Not 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:

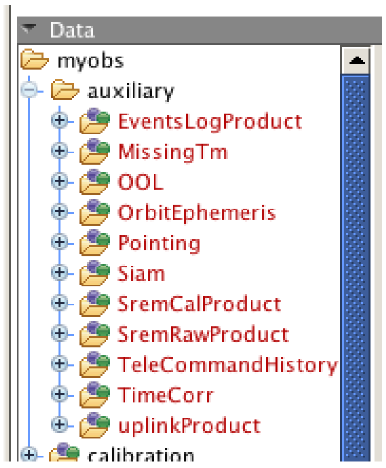


Data
myobs
auxiliary
calibration
common
photometer
spectrometer
arrayInstrument
badPixelMask
capacitanceRatios
chopperThrowDescription
crosstalkMatrix
detectorSortMatrix
discardRampHooks
effectiveCapacitance
filterBandConversion
gprHall
gprHallRedundant
gratingJitterThreshold

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.



Data
myobs
auxiliary
EventsLogProduct
MissingTm
OOL
OrbitEphemeris
Pointing
Siam
SremCalProduct
SremRawProduct
TeleCommandHistory
TimeCorr
uplinkProduct
calibration

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.

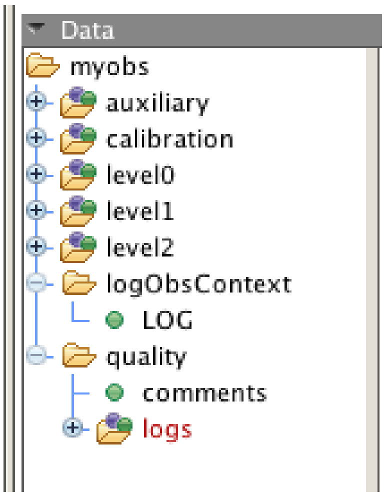


Figure 2.4. The contents of the log and quality trees

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; the nods are averaged, such that each nod-cycle (not each nod) becomes one
14. Wavelength-switching AOT: *TBD*

15. Off-map AOT: *TBD*
16. Calibrated 5x5xlambda data cubes are generated
17. The cube's wavelength grid is created
18. Outliers are flagged (another glitch detection)
19. The data cube is spectrally resampled
20. 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. Within the directory with the HIPE software, these are hopefully located in /scripts/pacs/toolboxes/spg/ipipe. The name of the ipipe script corresponds to the AOT type. *Bear in mind that this data reduction guide is updated less frequently that the pipeline tasks, so if there are differences in the order of running tasks, use the order in the ipipe directory.*

For large datasets the data will probably have been 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). *Once this logic has been worked out and incorporated in the pipeline scripts, that information will be included here.*

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). *This information is out of date.*

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. Within the directory with the HIPE software, these are hopefully located in /scripts/pacs/toolboxes/spg/ipipe. The name of the ipipe script corresponds to the AOT type. *Bear in mind that this data reduction guide is updated less frequently that the pipeline tasks, so if there are differences in the order of running tasks, use the order in the ipipe directory.*

For large datasets the data will probably have been 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). *Once this logic has been worked out and incorporated in the pipeline scripts, that information will be included here.*

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 main purpose of this chapter is to tutor users in running the PACS spectroscopy 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. To this end the sections here are divided into (i) a listing of the task steps with brief explanations and (ii) demonstrations for viewing the data just processed: plotting, displaying etc. More information on inspecting data, on the pipeline, and on particular issues with PACS data are in Chap. 4. However, we recommend you read through this chapter first, to learn at least how to run the pipeline and what sort of things you need to do to check the output.

The PACS pipeline can be run in one of two ways: the scripts in the ipipe directory (hopefully in your installation these are in /scripts/pacs/toolboxes/spg/ipipe and the one you want corresponds to the AOT name of your AOR, e.g. pacschopnodstarframesIA.py for a pipeline starting from a Level 0 *Frames* product, or pacschopnodstarrampsIA.py if starting with a *Ramps* product) can be run in one go, for example you can load it into the Editor panel and run it (see the note below). Or, you can run the pipeline as a long series of individual tasks, one by one. If you want to inspect intermediate products we recommend this method, and it is what is followed here.

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*.

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 loops and note down 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 jython 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).

> **Note**
>
> *How to create and run a script 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 (eventually) 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.

Spacing is very important in jython scripts, both missing and present spaces. Indentation is necessary in loops. Spaces after the end of a line of >if (something):< can mess things up.

Note

Syntax: *Ramps* and *Frames* are the "class" of a data product. "Ramp" or "frame" are what we use in this guide to refer to any particular *Ramps* or *Frames* product. A Frame is an image, for the photometer it is an image corresponding to 1/40s of integration time, for the spectrometer it is and 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. In Chap. 4 we explain more about the tasks, including all their parameters, here we run with the defaults.

3.2. Retrieving your ObservationContext and setting up

How to retrieve the Observation Context from your pool was explained in Chap. 1. Continuing from there: since you are re-reducing the data you will want to this time start from Level 0 (if you want to start instead from Level 0.5 or 1, you follow these same instructions but you will start your pipeline reductions from this later level). You can selected either (i) *Ramps* or (ii) *Frames* products to work on, depending on which you have; these will be called (i) HPSAVGR, HPSAVGB or (ii) HPSFITR, HPSFITB. To do this, on the command line type:

```
myramp = myobs.level["level0"].refs["HPSAVGB"].product.refs[0].product
# or
myframe = myobs.level["level0"].refs["HPSFITB"].product.refs[0].product
```

where myobs is the ObservationContext from Chap. 1. This extracts out from Level 0 the first of the averaged blue ramps or the blue fit ramps. If you want to start with the red ramps, you replace the final B with an R. If there is only one product of HPSXXXX then you still need to specify the ".refs[0]", and if there is more than one you can select out the subsequent with ".refs[1]", ".refs[2]",...... To find out how many HPSAVGBs are present at Level 0, have a look again at Fig. 3 from Chap. 1; if you click on the + next to HPSAVGB it will list all (starting from 0) that are present.

An alternative way to get your HPSAVGB..ref[x] product is to click on myobs in the Variables panel to send it to the Editor panel, click on +level0, then on +HPSAVGB to see the entries 0, 1, 2... You should be able to drag and drop whichever entry you want to the Variables panel (i.e. the 0 or 1 or... is what you drag and drop; although I found that in order to drag out the product rather than the entire observation context, I had to first click on the +0, to turn it into a -0, and then drag and drop the -0). 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 "newProduct" (which name you can change via a right click on it in the Variables panel).

PACS data processing proceeds through various stages: Level 0 data have had almost nothing done to them and is where we begin here. Level 0.5 data processing is AOT-independent, the ramps are fit to turn a *Ramps* product in to a *Frames* one, and information is added to the data (telescope pointing is translated into RA, Dec and added in, bad data masks are set, etc.). The AOT-dependent part then continues to Level 1, from which level scientific-grade data is found. At Level 1 the wavelengths will have been calibrated, response of the detector corrected, chopping and nodding accounted for, etc. At Level 2 the data are turned in to a 5x5 cube, spatially and spectrally rebinned, and that marks the end of the pipeline.

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 HSC 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
mycaltree=myobs.calibration
# or from HIPE recommended
mycaltree=getCalTree("FM")
# 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 dmcHead, the pointing product, and the orbit ephemeris. You can get these with

```
pp=myobs.auxiliary.pointing
dmcB=myobs.level["level0"].refs["HPSDMCB"].product.refs[0].product
dmcR=myobs.level["level0"].refs["HPSDMCR"].product.refs[0].product
orbitephem = myobs.auxiliary.orbitEphemeris
timeCorr=myobs.auxiliary.timeCorrelation
```

The pointing product is used to calculate the pointing of PACS during your observation, the dmcB/R, or the products called HPSDMCB and HPSDMCR, contain the position and status of the PACS mechanisms and detectors sampled at high frequency. 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 tasks. If the time correlation and orbit ephemeris products are not present, don't worry, you can run the pipeline for now without them.

Note: It is possible that there will be more than one HPSDMCR/B layer (to check double-click on myobs in the Variables to send to the Editor; click on Level 0 and then on HPSDMCR/B; if only 0 is there, there is only 1 layer). This is unlikely, but (especially during SD phase) it is possible. At present the only way to know which one you want to extract is to look at the "FINETIME" status column, this being the time stamp (in microseconds). If you print and compare the first and last timestamp for your frame or ramp and for the dmcHead you should be able to figure out which dmcHead you need. You can do this with the following commands:

```
# print the first and last time stamp of your frame/ramp
# (the syntax is the same for both)
print myframe.getStatus("FINETIME").data[0],myframe.getStatus("FINETIME").data[-1]
# then print the same for the layers of the DMCheader
# for the first layer, for the blue one
dmcB=myobs.level["level0"].refs["HPSDMCB"].product.refs[0].product
print dmcB["DmcHeader"]["FINETIME"].data[0],dmcB["DmcHeader"]["FINETIME"].data[-1]
# then do the same for the next layer,
dmcB=myobs.level["level0"].refs["HPSDMCB"].product.refs[1].product
print dmcB["DmcHeader"]["FINETIME"].data[0],dmcB["DmcHeader"]["FINETIME"].data[-1]
# etc
```

Then compare the results and see which dmcHead covers the time range of your data (they don't have to match exactly, they just need to cover the same time range).

3.3. Level 0 to 0.5

First we list the pipeline steps, then we tell you how to inspect the products just created. More information about the tasks will be provided in Chap. 4.

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.

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

If you want to stop a task running with the red stop button, you can only do that if you ran the task from a script in the Editor panel, not if you ran it from the Console command line.

3.3.1. Pipeline steps

Let's say we have elected to start with the blue product called HPSAVGB. As this is a *Ramps* product we begin with

```
myramp = specFlagSaturationRamps(myramp, calTree=mycaltree)
myramp=activateMasks(myramp,String1d([" "]), exclusive=True)
myframe = fitRamps(myramp)
```

The task activateMasks we explain at the end of this section. The task specFlagSaturationRamps flags the data for saturation, creating a mask called SATURATION which subsequent tasks can take into account (or not). Later we show you how to inspect this mask. The task uses data in the caltree to determine where saturation has occurred. "myramp" and "myframe" are the names of the products you are creating and working on (you can, of course, give them any name you like). fitRamps is a task that fits the ramps with a 1st order polynomial (the details of which have been determined by the PACS team) and returns the slopes values in units of digits/readout_interval. It changes the dimensions of the data, so

```
print myramp.dimensions
print myframe.dimensions
```

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.

fitRamps 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 also carry the saturation flag.

You now continue with the following, this also being the starting point if you extracted a Level 0 *Frames* product (i.e. HPSFITB instead of HPSAVGB)

```
myframe = specConvDigit2VoltsPerSecFrames(myframe, calTree=mycaltree)
myframe = detectCalibrationBlock(myframe)
myframe = specExtendStatus(myframe, calTree=mycaltree)
if timeCorr != None: myframe = addUtc(myframe, timeCorr)
myframe = specAddInstantPointing(myframe, pp, calTree=mycaltree)
myframe = convertChopper2Angle(myframe, calTree=mycaltree)
myframe = specAssignRaDec(myframe, calTree=mycaltree)
myframe = waveCalc(myframe, calTree=mycaltree)
# pay attention to the syntax here
# if you are typing this next command in the Console a return will allow
# you to wrap to the next line(s). If typing in a script then make sure
# there is no space after the : at the end of the next line
# and make sure there is a tab before the "myframe="
# line (2 down)
if ((orbitephem != None)&(pp != None)):
   myframe = specCorrectHerschelVelocity(myframe, orbitephem, pp)
myframe = findBlocks(myframe, calTree=mycaltree)
myframe = specFlagBadPixelsFrames(myframe, calTree=mycaltree)
myframe = flagChopMoveFrames(myframe, dmcHead=dmcB, calTree=mycaltree)
myframe = flagGratMoveFrames(myframe, dmcHead=dmcB, calTree=mycaltree)
# and, if you began from a Frames product
myframe = specFlagSaturationFrames(myframe,calTree=mycaltree)
```

And to explain this all:

- For now, keep the order of the parameters in the tasks as we have give here. If a parameter is specified as "calTree=mycalTree" then it can be anywhere in the call, but if you specify only the parameter value (e.g. "pp" above) then it has to be in the right place in the call. In Chap. 4 we list all the parameters the tasks have.

- 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; 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, for a moving chopper, and for a moving grating (and for saturation).

- The reason for flagging data taken while parts of the instrument were moving is that data is taken continuously, it does not stop for chopping, grating movements, nodding, or even rastering. To do so would be time-inefficient. These masking tasks (the final 3 or 4 tasks) use automatic criteria, mostly taken from the calibration tree. For example, detector readouts taken while the grating is moving are flagged in flagGratMoveFrames. In Chap. 4 we discuss how to modify and add to these masks, but we do recommend that you accept the default masking. The masks that were created here are SATURATION, UNCLEANCHOP, GRATMOVE.

- The masks that are present in your raw data should be NOISYPIXELS and BADPIXELS. If you run fitRamps you will also then have a BADFITPIX mask. The NOISYPIXELS mask is an information mask only, it is simply an indication that these pixels are noisier than the others; the BADPIXELS mask indicates that the data from these pixels will be bad; the BADFITPIX mask is a quality indicator for pixels for which the averaged ramps are suspected to have not been well fitted during fitRamps. If you began work on fit ramps, however (i.e. HPSFIT[B|R}), this mask will not be present.

- You may also have the information masks DEVIATINGOPENDUMMY, which masks an entire pixel column if the dummy or open channel of that column shows deviating ramps or `weird' signals; OBSWERR, which masks if randomly checked deviations of the onboard to onground reductions are larger than the expected noise. These masks are not interesting for users, they are for project scientists.

- The pipelines tasks that will be described in the next section will take into account the masks you have created here, each task having its own set of default masks it considers (those believed necessary).

- Note that the tasks that use the dmcHead as a parameter may well run without specifying the dmcHead, *but* the results will be wrong. Here, as we have elected to reduce the blue data, the dmcHead we are using in dmcB[lue], as was extracted earlier in this chapter. When working with the red data, naturally you should use the dmcR extracted product. Make sure you use the right one, as the task does not necessarily know if you give it the wrong one.

- The Status table contains information about the status of Herschel and PACS during the observation, and is added to as the data processing proceeds. You can look at these information (as a dataset or plot) by double clicking on myframe from the Variables panel, then in the Editor tab this appears in select the "Status" dataset. Selecting with a right click presents a menu for viewing, including as: a plot, which however does not show all the parameters; and a dataset, i.e. a table.

- Ideally the tasks do not change the input frame unless you give the output frame the same name as the input frame; if you gave the output a different name to the input, the input should be preserved in the pre-task state. I.e., the syntax myframe=waveCalc(myframe) should add to myframe, whereas myframe_wave=waveCalc(myframe) should create a new product called myframe_wave and not change myframe. However, some tasks unfortunately do not do that. Therefore we recommend, for now, that if you want to preserve the pre-task state of a frame, you first copy it and then run the task. So,

```
# you want to do this:
myframe_prewave=myframe.copy()
# then
myframe = waveCalc(myframe, calTree=mycaltree)
# and now myframe_prewave and myframe are distinct products
```

It is really not necessary to make a new product for every pipeline task you run (certainly not for waveCalc), only perhaps for the tasks that actually alter the state of the data. Of the steps so far described, none really qualify as that. PS do not forget the .copy() part of the syntax!

Now, what is this activateMasks task? Pipeline tasks can produce masks and/or they can propagate masks. Tasks that create masks also by default activate them. Once activated, a mask remains so until deactivated. It turns out that some tasks run better if only certain masks of the input frame are "active" and others are "inactive". This is particularly true for the pipeline reductions from Level 0.5 onwards; so far we have only activated masks once, before fitRamps. Hence it is necessary to specify which masks should be active and which should be inactive before running one of these sensitive tasks; that is what activateMasks does.

The full syntax of activateMasks is

```
# for myramp, deactivate all masks (by activating none)
myramp = activateMasks(ramp, String1d([" "]), exclusive = True)
# or activate certain masks and deactivate all others
myramp = activateMasks(myramp, String1d(["UNCLEANCHOP","GLITCH"]),
 exclusive = True)
# or activate certain masks and leave all others untouched
myramp = activateMasks(myramp, String1d(["UNCLEANCHOP","GLITCH"]),
 exclusive = False)
```

The parameter `exclusive` set to True lets tells the task to make all the *unspecified* masks inactive while making the *specified* ones active. This is the default behaviour of the task. Setting `exclusive` to False means that the unspecified masks will be *untouched* while the specified one will be activated. By declaring an empty string in the first example you are effectively telling the task to deactivate all masks. It is safest to always active with `exclusive`=True all the masks you want to be active before running a task for which masks are used. activateMasks works on *Ramps*, *Frames*, and all cubes that have masks.

This marks the end of Level 0.5, up to which the data reduction is AOT independent. Next we will tell you how to save and inspect the products you have just created.

3.3.2. 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 should 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 checks will not all be for quality control, it is recommended you look at these things so you understand what builds up to create your final cube.

First we will introduce you to the Status, tell you how to look at the chopper and grating, then masks and then how to (over)plot the spectral signal. Finally we will explain how to plot the pointing.

First, to know the dimensions of your data, use:

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

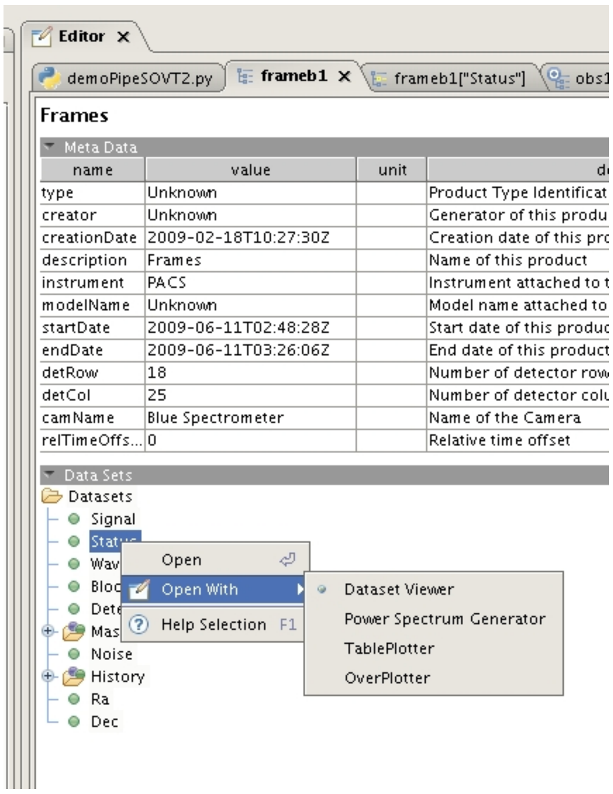
There are two approaches to looking at what is in your ramps and frames: use one of the viewer applications, or plot out bits of the data.

> **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.

3.3.2.1. The Status - what was PACS doing during your observation?

The Status is a attached to your *Frames* or *Ramps* product 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. To view Status information for your observation you can click-to-view your frame or a ramp in the Editor panel, locate the Status therein, and right-click on it to view using the Dataset Viewer, Table-Plotter, or OverPlotter (screenshot below). 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. You cannot currently overplot easily entries that have very different ranges. In Chap. 4 we explain more about the Status and what parts of the Status table you are likely to want to look at and how you can plot the entries that are not numbers.

For a *Frames* product the column entries are single values per time (per reset index) and for a *Ramps* product some entries will be an array of values. The Status is added to as the pipeline processing proceeds. The Status table of myframe contains the same as, and more columns than, myramp and is more useful to look at (the frame has had more tasks run on it). Of particular interest to you at this point in time will be the chopper movements (CPR) and the grating movements (GPR), and maybe also how the signal modulates with these. 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 rapidly varying telescope background and also remove the dark current. This chopping happens with a very high frequency. You may want to check that the signal really is lower in the blank-sky position than the on-target position (although bear in mind that with the short integration times that PACS operates at, the difference in signal between the chopper positions will not be huge). (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). You may also want to look at how the signal changes with grating position.



name	value	unit	d
type	Unknown		Product Type Identificat
creator	Unknown		Generator of this produ
creationDate	2009-02-18T10:27:30Z		Creation date of this pro
description	Frames		Name of this product
instrument	PACS		Instrument attached to t
modelName	Unknown		Model name attached to
startDate	2009-06-11T02:48:28Z		Start date of this produc
endDate	2009-06-11T03:26:06Z		End date of this product
detRow	18		Number of detector row
detCol	25		Number of detector colu
camName	Blue Spectrometer		Name of the Camera
relTimeOffs...	0		Relative time offset

Figure 3.1. Viewers for the Status

You cannot inspect the "Signal" product of frame/ramp with Table/OverPlotter, nor can you overplot to see two Status entries whose axes ranges do not overlap. For these cases we can recommend PlotXY, an in the next section we show you how to use PlotXY and in particular how to use it to overplot the CPR, GPR and signal.

3.3.2.2. Plotting the spectrum to understand what you have: 1

We cannot predict everything you will want to look at for your data so we provide examples of the most likely possibilities, and you can bootstrap from those to plot other things. Here we show you how to plot the signal (v.s. time or wavelength), the chopper and the grating.

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")
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)))
```

Why?: 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.

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

To plot a spectrum, that is signal versus wavelength, after you have run the waveCalc 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 [Jy]"
```

Now, depending on what type of observation you are looking at (e.g. SED vs. line scan) and at what 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 (take at the key wavelengths only); multiple spectra/spectral lines if your observation includes more than one field-of-view (for rastered/ dithered observations); 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 the next stage of the pipeline). In addition, if you have several grating runs (if you sampled the wavelength domain more than once), then each spectrum will be multiple and it is possible that the spectra from multiple grating runs will not be exactly at the same "counts" levels. So, if you have a line scan and you see this:

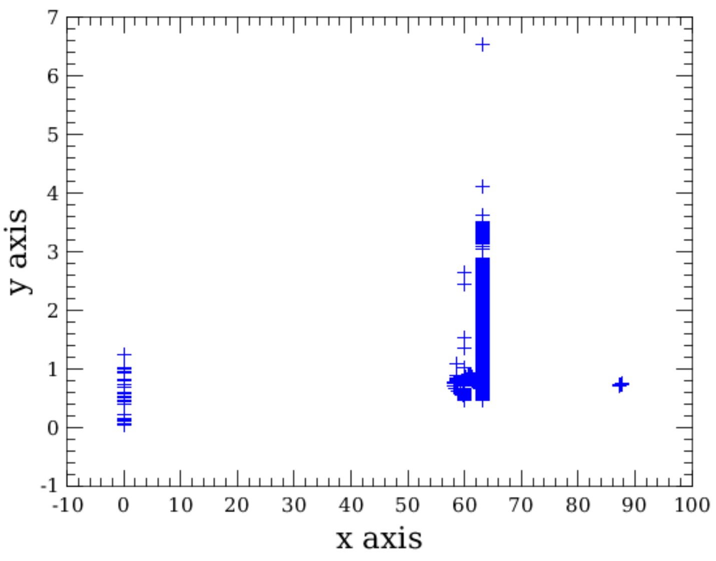


Figure 3.2. Level 0.5 line scan spectrum: entire dataset

try to zoom in on the wavelength you requested in your AOR, when you should see this:

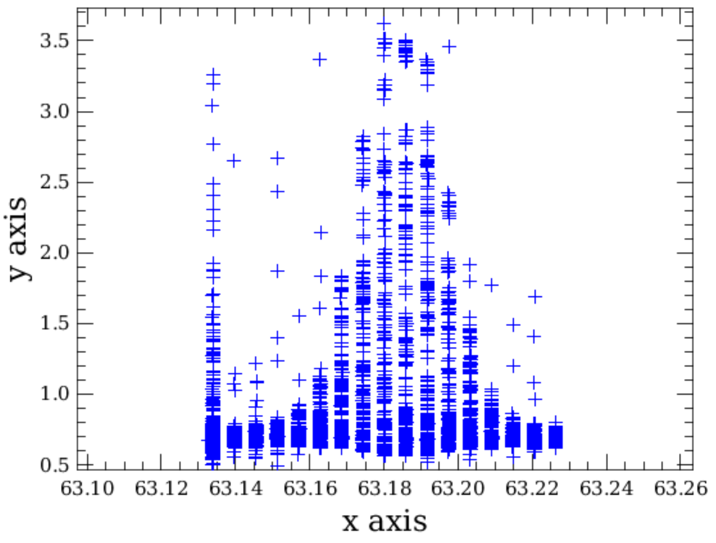


Figure 3.3. Level 0.5 line scan spectrum: zoom

In this spectrum (of a single pixel) 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. For this observation there were also several rasters (several fields-of-view), and these have not yet been separated out. Hence this spectrum is that of at least 5 different pointings. In the next section we will show you what this spectrum becomes when further corrected.

We have already pointed out that each of the 16 active pixels that feed into each spaxel 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) you will see this:

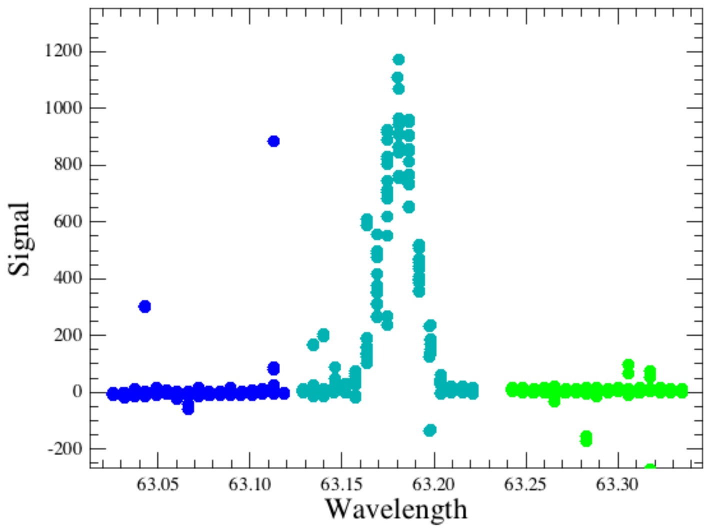


Figure 3.4. 3 pixels of a single module

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 saw no spectral line, this may be the reason why.

Consider also that the dispersion is also important in determining what you see when you plot a single pixel. If your dispersion is low, e.g. you have a fast SED AOT, 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.

Plotting the spectrum to understand what you have: 2

You can next check the movement of the instrument during your observation, and maybe look to see how the signal varies with these movements. This is not so much for checking the quality of the pipeline reductions, because at this point in your PACS experience you do not know enough to tell what is good and what is bad, but you should be a little curious.

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. However, we have included these so you know the syntax.

As before, 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)])
```

(This also shows you an alternative way of specifying things to plot.)

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

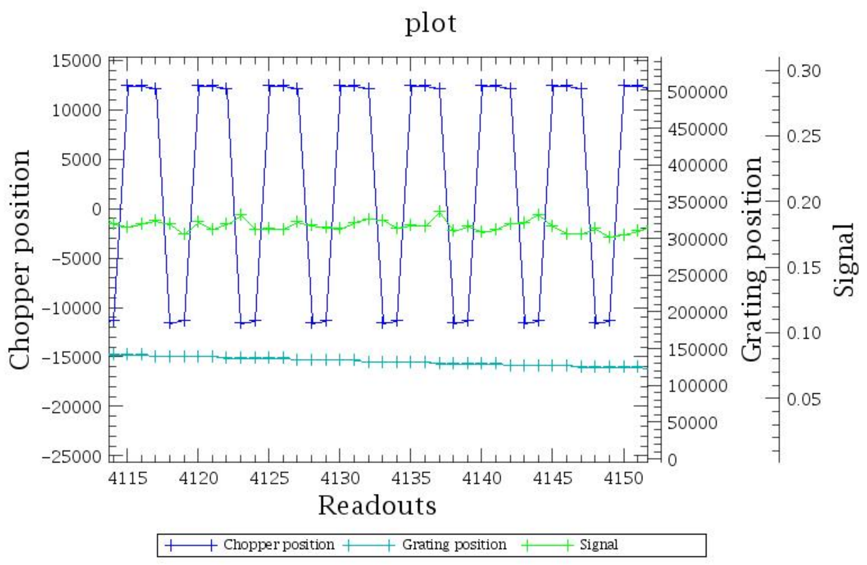


Figure 3.5. A zoom in on PlotXY of the grating and chopper movements for frame

Later we will explain how to interpret this plot, but for now note: the chopper is moving up and down, with (in this case) 2 readings taken at chopper minus and 3 readings taken at chopper plus. The grating 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 can be seen modulating with chopper position, as it should be because one chopper position is on target and the other on blank sky.

Since you now know how to plot out the chopper movements, you could overplot this on the spectrum for a random pixel, where the datapoints that have been masked for chopper movement (UNCLEAN-CHOP) are plotted in a different colour. Similarly, you could do the same for the other masked data (GRATMOVE mainly). Next we show you how to plot masked/unmasked data, and we leave it up to you to figure out how to combine the masked/unmasked and Status plotting instructions.

3.3.2.3. Masks

First we explain the MaskViewer GUI, and then how to plot single spectra with and without masked data.

MaskViewer GUI

With the MaskViewer you can see which data were flagged in the masking tasks *and* at the same time you also get to see the data themselves. You can also see which masks are active, although this can also be done on the command line:

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

The MaskViewer works on a frame and a ramp but not a cube. Using the MaskViewer 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.

The capabilities of the MaskViewer are explained in <LINK>. To call it up type

```
MaskViewer(myramp)
```

At the top of the mask viewer (see the screenshot below) you see the PACS detector displayed in 5 bits, in which the individual pixels are selectable for viewing as a plot shown at the bottom of the GUI. In between these is a menu in which you can select which mask to look at—pixels (in the image) and data-points (in the plot) subject to this mask are plotted in red, all others in black. What you see in the plot below is the actual detector signal time-line for the selected pixel#"signal" vs. "sample index"##and for the example averaged ramps data shown here there are 4 lines of datapoints following a zig-zag pattern. (Note that the x-axis is never wavelengths.) To explain the data pattern: in the beginning the detector was looking at the internal calibration sources (this is the short messy block of data at the very left). Then it moved to observe a spectral source, moving back and forth in wavelength leading to an up-down pattern in the dataline: 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). If your Level 0 products is averaged ramps (HPSAVGB/R) it will look similar.

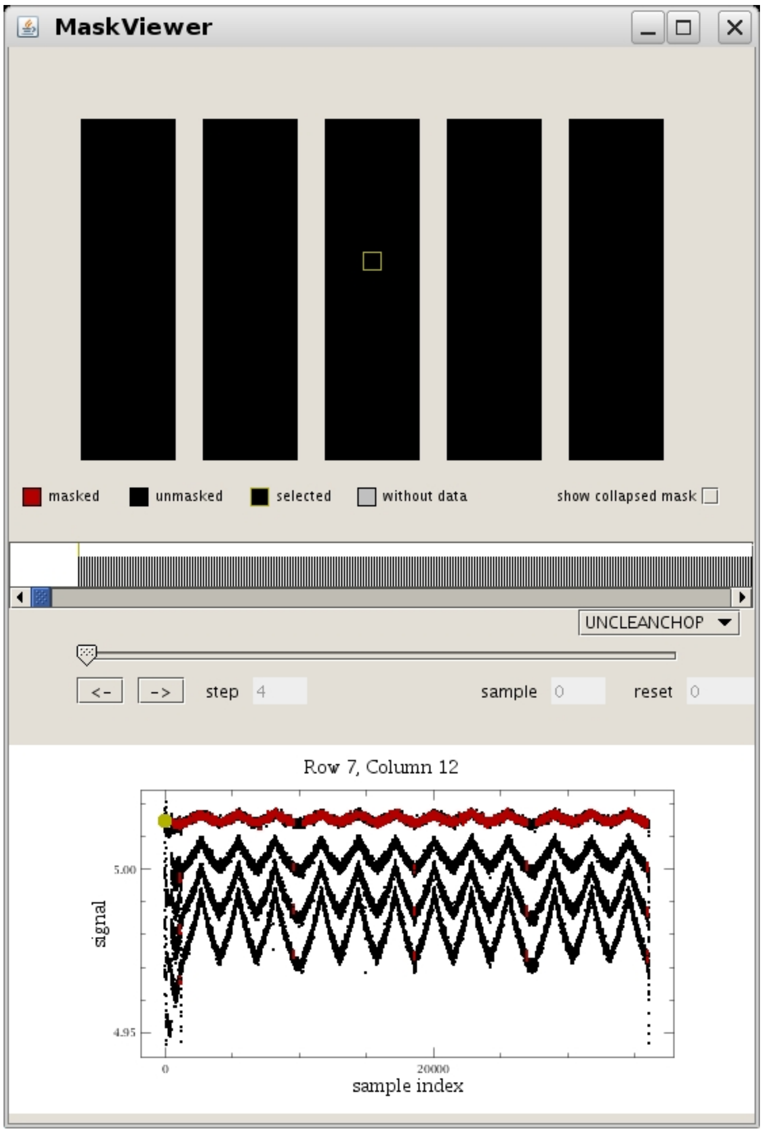


Figure 3.6. The MaskViewer window

The plot is based on PlotXY, and so the functionalities of PlotXY are available to you <LINK>. 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.

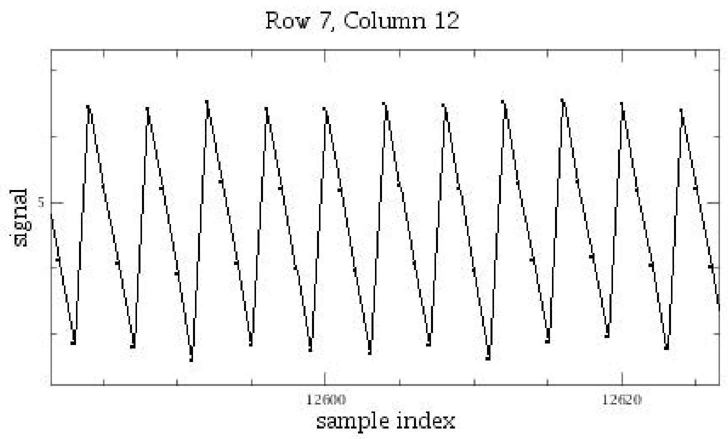


Figure 3.7. Zoom on a "spectrum" of a pixel of ramp in the MaskViewer

The slope of the line joining each 4 is essentially what is produced 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. 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 plotting with 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.)

Plotting masked data

You can plot and overplot masked and unmasked data-points for single pixels using PlotXY. This is a more cumbersome way of looking at your data, but it is also something you will have to get used to so you may as well start now :-). Here is an example of plotting all datapoints for pixel 8,12 and then overplotting the unmasked ones:

```
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))
```

Now to explain this. Have a little patience please, because this involves telling you something about the DP scripting language.

- 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 syntax "myframe.getSignal()" means you are calling on a "method" that is available for a *Frames* class object. 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.
- 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 indicated mask (GLITCH). The

parameters are the mask name/names (listed in a *String1d*) and the pixel coordinates (8,12). You could also 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 (your *Double1d* from above) 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. But, do pay attention to the syntax—using a (instead of a [can cause a command to fail (or do the wrong thing).

See <LINK> to learn more about using PlotXY, and see the *SaDM* to learn more about scripting.

3.3.2.4. 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 Herschel/PACS pointing?):

```
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:

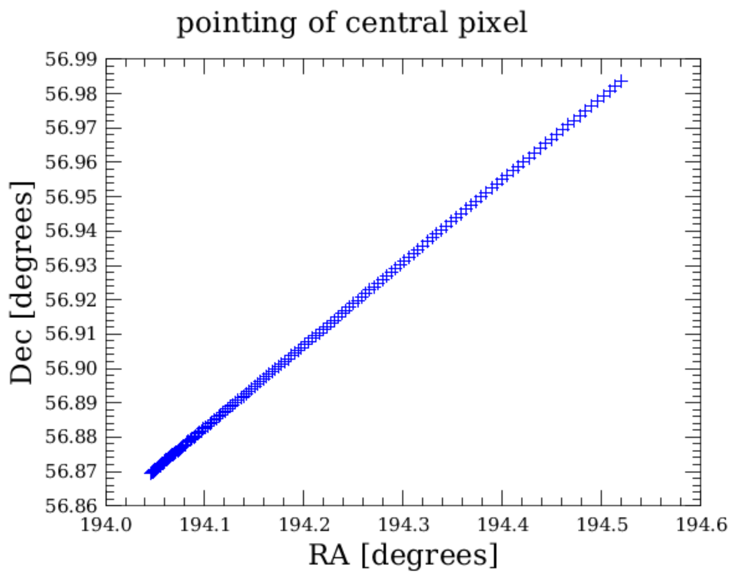


Figure 3.8. Movement of PACS during an observation

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=myobs.meta["ra"].value
srcDec=myobs.meta["dec"].value
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:

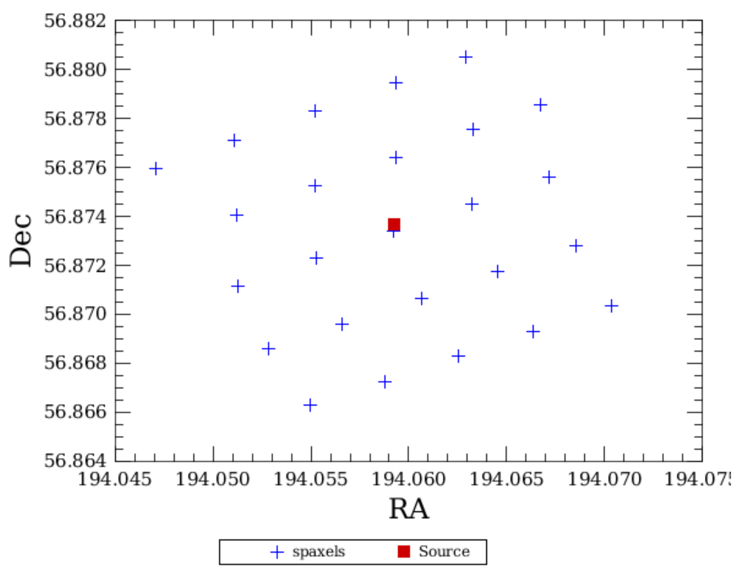


Figure 3.9. Pointing of the IFU and the source position

Some explanation is necessary here:

- 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, which is what the -1 syntax does, gives you a 2D array.
- myframe.ra/dec are the ra/dec datasets, which is not the same as the RaArray 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" means you are asking to plot the ra for the final readout of the timeline (the last element in an array is specified with a -1); 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, 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.

PS a spaxel is a spatial pixel. PACS has 5x5 spaxels.

It is likely that you will also want to plot the pointing for the two nods (A and B) and the chops, and if you have rastered or dithered observations, for the unique pointings also. That we leave to the next pipeline stage.

3.3.2.5. 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],depthAxis=2)
```

and when you zoom in you will see a 2D image: we are looking at the signal part of frame. Here we plot all X and Y ranges but only 50 wavelength/time-line layers (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. depthAxis=2 tells Display to show the whole detector on the (2D) image and scroll along the time-line axis. depthAxis=0 and 1 are not useful to view with Display, showing you 1D "spectra" that are a single slice looking down successively along each of the detector axes. Hopefully later it will not be necessary to specify the depthAxis.

Unfortunately, the 100:150 you specify above are the array positions, not the wavelength positions. If you want to Display (or otherwise look at) 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. Level 0.5 to 2

3.4.1. Pipeline steps: 0.5 to 1

The next set of tasks to take you to Level 1 are

```
myframe = activateMasks(myframe, String1d([" "]), exclusive=True)
myframe = specFlagGlitchFramesQTest(myframe)
myframe = activateMasks(myframe, String1d(["UNCLEANCHOP","GRATMOVE",
  "GLITCH"]), exclusive = 1)
myframe = specEstimateNoise(myframe)
myframe = specCorrectSignalNonLinearities(myframe, calTree=mycaltree)
myframe = convertSignal2StandardCap(myframe, calTree=mycaltree)
myframe = activateMasks(myframe, String1d(["UNCLEANCHOP", "GLITCH",
  "BADFITPIX"]), exclusive=True)
csRespAndDark = specDiffCs(myframe, calTree=mycaltree)  RESULT IS CURRENTLY NOT USED
myframe = activateMasks(myframe, String1d(["BADPIXELS",
   "GLITCH", "BADFITPIX", "SATURATION"]), exclusive=True)
#respDrift = specFitSignalDrift(myframe, csRespAndDark)   DO NOT RUN
myframe = specDiffChop(myframe)
myframe = rsrfCal(myframe, calTree=mycalTree)
myframe = specRespCal(myframe, calTree=mycaltree)
#myframe = specAddNod(myframe) DO NOT RUN
```

- 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); estimate the noise for each pixel and fill the Noise dataset (prior to this task you need to run activateMasks); correct the signals for the intrinsic non-linear shape of the ramps; 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); calculate the dark current and pixel responses (prior to this task you need to run activateMasks), *although note that at present we do not use the result of this task so there is not much point you running it*; take the output from that and calculate the drift in response of the detector during your observation (prior to this task you need to run activateMasks) *at present this task is not run*; subtract the off chops from the on chops to remove the rapidly varying telescope 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; add the nods (the As and the Bs), reducing the number of readouts again (*but see below because currently we do not recommend you run this task*); turn the frame into a 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). In Chap. 4 we show you how to locate the 16*x separate spectra to inspect them.

- The glitch detection task works well in identifying glitches. By default it works on chopped data, and as this section is for a chop-nod AOT then you want the default case. (If not then you need to add the parameter "splitChopPos=False".) It has been tested on chopped and non-chopped data. After running this task if you look at your GLITCH mask it may seem to you that rather a lot of non-glitched datapoints have been masked, but in fact our tests show that a significant fraction of these are actually also glitch-affected. You could of course also write your own glitch detection algorithm, if you wanted. In Chap. 4 we tell you more about glitches.

- specRespCal corrects for the pixel responses, their the response drift (that occurs during your observation) and subtracts the dark current. **Warning**: at present (Nov. 2009) the flatfielding—that is correcting for the pixel responses—is being improved upon; you may notice, when you plot the spectra for all pixels in a module that there is still an offset in the continuum levels. We are working on this, but if it is a problem for you right now, contact the Herschel helpdesk.

- The tasks here that change the state of the data (and for which you may want to make a copy of myframe before running, as recommended in Sec. 3.3.1) are specCorrectSignalNonLinearities, specDiffChop, specAddNod, rsrfCal, and specRespCal.

- A very quick explanation of why specDiffChop and specAddNod are necessary; much more on this is in Chap. 4:

  Remember that while observing your target the chopper has been moving between an on- and off-field position. One is subtracted from the other and in this way the rapidly varying telescope background, as well as the detector's dark current, are subtracted. The instrument however also nods, at a lower frequency, between two fields. The chop positions and nod positions are arranged so that chop+, nodA and chop-, nodB are the same point in the sky and are on the target, while chop-, nodA and chop+, nodB are either side of the target and are in blank field positions. The task specDiffChop subtracts the chop off-target from the chop on-target for nodA and nodB separately, creating two spectral images. These are then added together in specAddNod. In Chap. 4 we show how to extract out parts of the data belonging to different chops and nods, so you can compare spectra and pointings.

- **specAddNod**: at present (end of 2009) we are still working on the details of combining nods. While it is important that these nods are combined, because that removes the telescope background, at present they are not the same where they should be, and hence not combinable. We recommend you do not run this task. Instead you should "slice" the frame into 2, proceed with the final task of this Level, and store your cubes in a *ListContext* (a list of products, in this case *PacsCube*s).

  ```
  frameA=myframe.select(myframe.getStatus("IsAPosition") == True)
  frameB=myframe.select(myframe.getStatus("IsBPosition") == True)
  ```

  to run the next task you do this:

  ```
  Listcubes = ListContext()
  cubeA = specFrames2PacsCube(frameA)
  cubeB = specFrames2PacsCube(frameB)
  Listcubes.refs.add(ProductRef(cubeA))
  Listcubes.refs.add(ProductRef(cubeB))
  ```

  In the ipipe scripts this task is not commented out. This is one occasion where you should believe the PACS data reduction guide, not the ipipe scripts, as long as the version of the guide you are reading is up-to-date.

  Now read the next bullet point.

- **Dithered/Rastered AOTs**: if you have multiple pointings in your dataset you need to do another slicing, because at present the later cube rebinning task does not honour these pointings but combined them as if all the same. To check you could look at the Status entries

  ```
  print UNIQ(myframe.getStatus("RasterColumnNum"))
  print UNIQ(myframe.getStatus("RasterLineNum"))
  ```

Where the first tells you how many column pointings were made (UNIQ will print out all the uniq values in the frame.getStats()) and the second, the line pointings. If you are dithering, that is observing with small (2" or so) jumps between successive pointings, you will probably have a small number of differe column pointings, and if you have a full raster, you could have several line and column pointings.

With multiple pointings in your data you need to make a longer *ListContext*, or 2 of them. We chose the second route as it is easier to follow. So, including the commands from above you could now write the following script and run it (green arrow in Editor panel):

```
ListcubesA=ListContext()
ListcubesB=ListContext()
# first slice on nod
frameA=frame.select(frame.getStatus("IsAPosition") == True)
frameB=frame.select(frame.getStatus("IsBPosition") == True)
# now for each of these, slice on raster. You will do this twice, one
# for each nod (frameA and frameB)
for rasterLine in UNIQ(frameA.getStatus("RasterLineNum")):
   for rasterColumn in UNIQ(frameA.getStatus("RasterColumnNum")):
      print "doing pointing",rasterLine,rasterColumn
      frame_temp=frameA.select((frameA.getStatus("RasterLineNum")
       == rasterLine ) & (frameA.getStatus("RasterColumnNum") == rasterColumn))
      cube = specFrames2PacsCube(frame_temp)
      ListcubesA.refs.add(ProductRef(cube)) # add the cube to the list

# note that you won't wrap around the line where I have above. I've just
# done this so the text fits in the page. if you do want a carriage return
# where I have wrapped around, use \ after the & to indicate continuation
# on the next line
```

This is quite complex scripting, and so we need a good explanation (but read also the *SaDM* guide for more scripting advice). First you make a frame for nod A and one for nod B. Then you look at the Status for the entry that indicates raster/dither position, which are RasterLineNum (a counter, 1 2 3 ...) and RasterColumnNum (also a counter). Changing column means PACS was moving along the PACS slit direction, changing line means PACS was moving perpendicular to the slit (this will probably make more sense to you later). Look at the Status table and at these columns, you will see the column entries move from 1 to 2 to 3 ... as you scroll down the time direction (assuming you have multiple rasters in your dataset, that is). You now need to isolate the unique line and column values, and then slice iteratively on these. For each slice you turn it into a *PacsCube* and place that cube in a *ListContext* called ListcubesA|B. In here now are as many cubes as there were unique line/column raster pointings

```
print len(ListcubesA.refs)
```

Now you are finally ready to run the next stage pipeline.

3.4.2. Pipeline steps: 1 to 2

The final tasks take the cube from Level 1 to Level 2. First we need work out the rebinning details for the cube to give it a uniform wavelength grid, based on what wavelengths are currently in the cube. We then do another glitch detection, creating a mask called OUTLIERS. The 16*x spectra held in each cube are then resampled and merged according to the wavelength grid. Finally, the cube is spatially resampled. The cube is projected onto a regular RA and Dec grid on the sky and rasters can be combined. *At some point soon we will release a tool that will allow you to inspect your cubes, before converting from the first to the second to the third, to let you easily check and edit the individual spectra before they are combined. At present you will have to accept the pipeline has done a good job.*

We are now dealing with not a single cube but rather a *ListContext* of cubes, either ListcubesA|B or Listcubes. Here we show you how to deal with Listcubes where Listcubes is a list of cubes of the *same* nod and the whole range of raster/dither pointings (do *not* combine nods).

```
Listrcubes=ListContext()
```

```
num=len(Listcube.refs) # how many cubes are there?
for i in range(num):
   mycube=Listcube.refs[i].product # extract the cube from the list
   waveGrid = wavelengthGrid(mycube, calTree=mycaltree, oversample=2,
      upsample=3)
   mycube = activateMasks(mycube, String1d(["GLITCH","UNCLEANCHOP",
     "SATURATION","GRATMOVE", "BADFITPIX"]), exclusive=True)
   mycube = specFlagOutliers(mycube, waveGrid, nIter=2, nSigma=5)
   mycube = activateMasks(mycube, String1d(["GLITCH","UNCLEANCHOP",
     "SATURATION","GRATMOVE", "BADFITPIX", "OUTLIERS"]), exclusive=True)
   rebinnedCube = specWaveRebin(mycube, waveGrid)
   Listrcubes.refs.add(ProductRef(rebinnedCube))

projectedCube = specProject(Listrcubes)
```

We are iterating over all the cubes held in the ListcubesA, extracting out the cubes, running the pipeline tasks on them, and then putting the final cube into a new *ListContext*, in the same order that you originally sliced on. This last step is not necessary but in this way, at least, you can track the relationship between the final cubes and the originally slices frames.

If your Listcubes is a combination of nod A and B (cubeA and cubeB from above) then rather than doing this part of the pipeline in a for loop, just do it first for Listcubes.refs[0].product (nod A) and then Listcubes.refs[1].product (nod B), creating a projectedCubeA and projectedCubeB.

Now for a description of the tasks. In wavelengthGrid, `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. These are both optional parameters. The values given here are our recommendations, but you are welcome to play around: it is likely that the way you should do the spectral resampling will depend on the type of observation you have, so try various grids and compare the resulting spectra. Bins too large with smooth the data, bins too small will make the spectra too "bitty". specWaveRebin resamples the flux domain based on this wavelength grid. specFlagOutliers 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 parameters we specify are our recommendations, and they are optional (there are good default values hardwired into the task). `nIter` is the number of iterations and `nSigma` the sigma value to flag at. Again, feel free to play around with the values yourself, or even write you own clipping task. specProject is a task that projects the cube onto an irregular grid and also reduced the size of the spaxels (but increases their number). You see, the PACS integral field unit is not completely evenly spaced out. Although when you look at images of the cubes (as we explain below) you will see a 5x5 square of spaxels, in fact they are a bit higgledy-piggledy. specProject corrects for this. This task also combines the multiple pointings, which is why were here are sending it as input not a single rebinnedCube (which is possible) but the *ListContext* Listrcubes.

So the end of the pipeline will be 2 *projectedCubes*, one for nod A and one for nod B. As we said before, this is a temporary solution to overcome an issue we still have with the calibration of PACS spectroscopy. You can compare the spectra from the same spaxels for the two cubes and see if they look the same (the CubeAnalysisToolBox allows you to do this). If you have gotten to this stage in your data reduction then you need to contact the Herschel Help Desk to ask what to do next. Oh, and....CONGRATULATIONS!

The mycube is a final Level 0.5 product, rebinnedCube is Level 1 and projectedCube is a Level 2 product. The mycube is a *PacsCube* class product, the rebinnedCube is a *PacsRebinnedCube*, and the projectedCube is a *SpectrumSimpleCube*.

Spatial coordinates: at present (Nov. 2009) the calibration of the pointing for all the pixels/spaxels of PACS is not 100% correct. This is being worked on, but at present consider the positions in the cube to be of "browse" quality rather than full science quality. It can be off in absolute terms by a few arcsec, less in relative terms within a cube.

Skewed lines: if your target is a point source (or close to one) and has spectral lines, then if it was not placed in the centre of the a spaxel (normally 2,2) the lines may display a skew (google "skewed

Gaussian/Normal profiles" if you don't know what this means). If you think you have this, you need to contact the Herschel helpdesk.

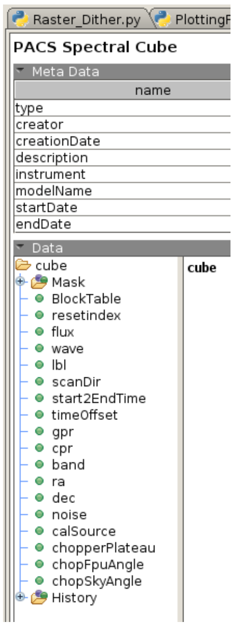
3.4.3. Inspecting the results

To inspect a cube you need to take it out of the *ListContext* we have had you place them in. The syntax for doing this is:

```
mycube=ListcubesA.refs[0].product
```

and etc. So you need to do this before following any of the advice next given.

The cubes do not have Status tables, rather the relevant information is held in separate datasets, as you can see in the screenshot below (which is for a *PacsCube*; this listing will be shorter for the other cubes). We are not going to show you how to inspect all of these entries (the idea is that you would have done most of your checking on the frame product, before getting to the cube stage), but we will explain how to plot the spectra.



PACS Spectral Cube

Meta Data

name
type
creator
creationDate
description
instrument
modelName
startDate
endDate

Data

cube
- Mask
- BlockTable
- resetindex
- flux
- wave
- lbl
- scanDir
- start2EndTime
- timeOffset
- gpr
- cpr
- band
- ra
- dec
- noise
- calSource
- chopperPlateau
- chopFpuAngle
- chopSkyAngle
- History

cube

Figure 3.10. PacsCube listing

For the Level 0.5 frame you are likely to want to check the spectra, masked data, and see how the spectra vary with chop and nod, that is the spectra after the tasks specFlagGlitchFrames, specDiffChop and specAddNod. You will probably also want to compare the spectra before and after the rsrfCal and specRespCal tasks, since these move the flux units from V/s to Jy.

3.4.3.1. Plotting the spectra of the frame

The same methods as explained in Sec. 3.3.2 for looking at a frame can of course be used also on your pre-cube frame. The main difference is what you will want to plot. We leave the decisions about this up to you (hint: masks; before specDiffChop versus after specDiffChop; likewise for specAddNod).

To compare the spectra before and after the rsrfCal and specRespCal tasks is simple and uses the basic PlotXY recipies given in Sec. 3.3.2. However, to overplot a before and after spectrum you will need to copy the frame before you run it through tasks:

```
frame_b4 = myframe.copy()
```

```
# then run the pipeline tasks
myframe = rsrfCal(myframe, calTree=calTree)
myframe = specRespCal(myframe, csResponseAndDark=RespandDark,
   calTree=mycalTree)
# then plot
sig=myframe.getSignal(8,12)
wve=myframe.getWave(8,12)
p = PlotXY(wve,sig,titleText="your title",line=0)
p[0].setName("after rsrf")
p[0].setYrange([MIN(sig), MAX(sig)])
p[0].setYtitle("Jy")
sig=myframe_b4.getSignal(8,12)
wve=myframe_b4.getWave(8,12)
p.addLayer(LayerXY(wve,sig),line=0)
p[1].setName("before rsrf")
p[0].setYrange([MIN(sig), MAX(sig)])
p[0].setYtitle("V/s")
p.xaxis.title.text="Wavelength [$\mu$m]"
p.getLegend().setVisible(True)
```

where the labelling of the Y axis, as well as its range, will here be different for the two spectra.

With the same set of commands you can overplot the spectra before and after the specDiffChop and specAddNod tasks (i*f specAddNod is to be run, which at present it is not*). Bear in mind that when you look at the spectrum, for a single pixel, plotted versus wavelength before either of these tasks have been run, you will see what looks like many spectra plotted on top of each other: at least one for each chop position and one for each nod position (and probably one for each run on the grating, as there should be at least two runs on the grating per observation). 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 instrument configuration (grating, chopper, nodding), because the instrument configuration changes with time. An example of each case is shown here:

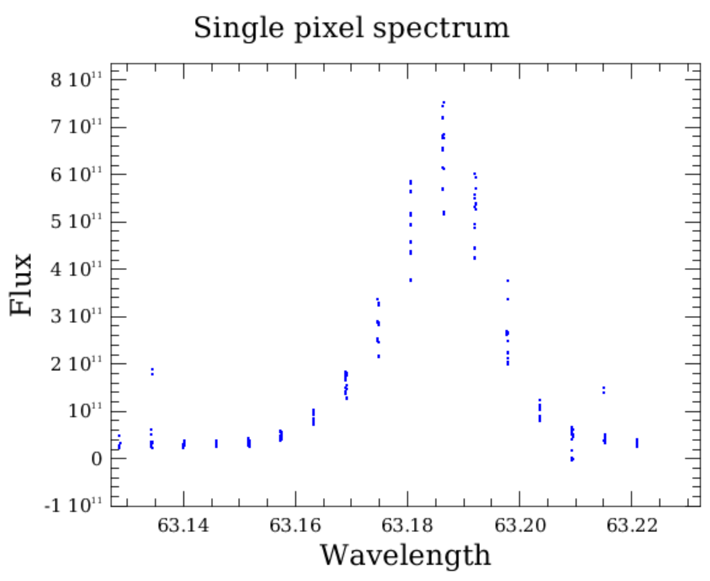


Figure 3.11. Spectrum of a single pixel. The spectrum is plotted versus wavelength and there are in fact 2 spectra plotted here, one for each run on the grating

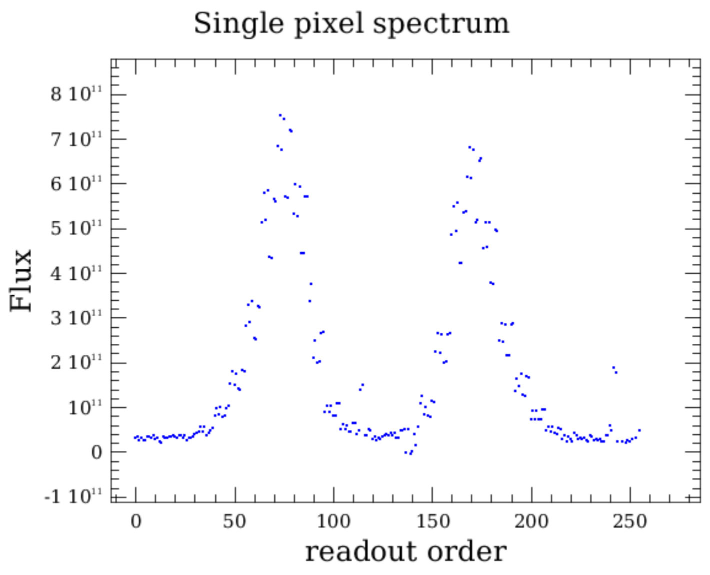


Figure 3.12. Spectrum of a single pixel. The spectrum is plotted versus readout order and the separate spectra that in the figure above lie on top of each other are now distinguishable

This spectrum is also a continuation of the ones shown in the previous section: the chops and nods have been subtracted—combined, and the rasters separated out. Now the spectrum looks much cleaner.

3.4.3.2. Plotting the spectra at different pointings

Here we show you specifically how to overplot, for your frame (not cube), the spectrum of chop+ nod A and chop- nod B, which should be pointing both at the target, and chop- nod A and chop+ nod B which should both be off-target, and how to plot the pointings corresponding to these datapoints.

First you need to select out the parts of the frame that correspond to these different parts of the observation. To select all the timelines that belong to nod A and B you do the following

```
frameA=myframe.select(myframe.getStatus("IsAPosition") == True)
frameB=myframe.select(myframe.getStatus("IsBPosition") == True)
```

You can then use the previously given scriptettes to overplot the spectrum from the same pixel for frameA and frameB (Sec. 3.2.2), and to plot out the pointing for the final datapoint (or the first, or the middle, or any random datapoint) in frameA and frameB (Sec. 3.2.4). If you want to select out the chop throw + and - you do the frame selection thus:

```
frameP=myframe.select(myframe.getStatus("CHOPPOS") == "+large")
frameM=myframe.select(myframe.getStatus("CHOPPOS") == "-large")
```

This works if your programmed chopper throw was large. You will need to look at the CHOPPOS Status entry to see if your throw range is large, medium or small (it will not change during an observation, but can between observations).

To select on nod and chop together you combine the selections like this:

```
framePA=myframe.select( (myframe.getStatus("CHOPPOS") == "+large") &
 (myframe.getStatus("IsAPosition") == True) )
frameMB=myframe.select( (myframe.getStatus("CHOPPOS") == "-large") &
 (myframe.getStatus("IsBPosition") == True) )
```

(where you can use >print UNIQ(myframe.getStatus("CHOPPOS")) to find out what CHOPPOSitions were for your observations.) You should see a spectrum looking something like this:

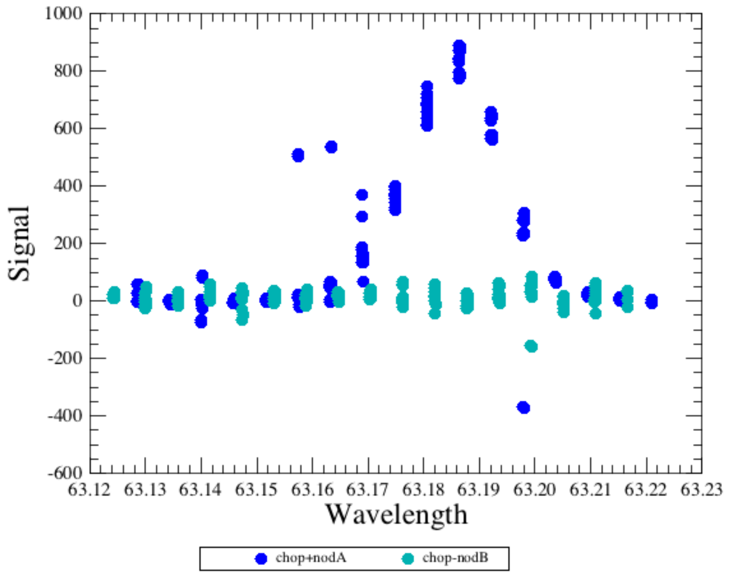


Figure 3.13. Spectrum of chop- nod A and chop+ nod B

And the pointing that corresponds to these positions will look like:

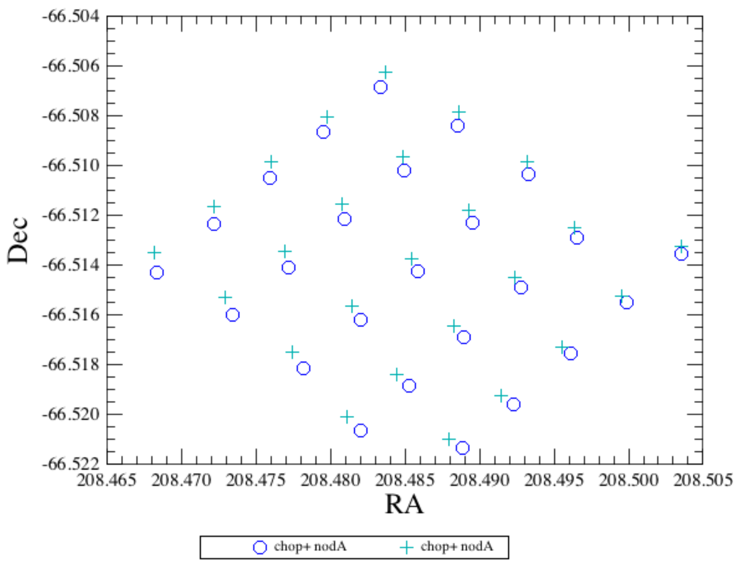


Figure 3.14. Pointing for chop- nod A and chop+ nod B

These data are from PV phase, hence the slight offset in the positions for the spaxels. Your spaxels will overlay much more closely.

You will now be able to add in any other selections you wish to compare, e.g. for raster position (Status entries RasterLineNum and RasterColumnNum, and look at the Status table yourself to see what range of values these take on).

One thing to bear in mind is that depending on when in your data reduction you do this, it is possible that you will be plotting data/pointings that belong to the calibration block or to slewing periods as well. These parts of the data should generally be cleaned away by the time the frame is ready to be turned into a cube, or you can use other Status entries to eliminate them. We refer you to Chap. 4 where the Status is further explained.

Tip

In this section of the guide we have had you plotting out bits of the data by doing a selection on the frame, creating a smaller frame where the Status corresponds to some desired limits. There is (at least one) other way to select out the fluxes and wavelengths from the pixels of your frame that correspond to particular instrument configurations:

```
pix=8
mod=12
notGlitched = (myframe.getMask("GLITCH")[pix,mod,:] == False)
cleanChop = (myframe.getMask("UNCLEANCHOP")[pix,mod,:] == False)
goodPixel =  (myframe.getMask("BADPIXELS")[pix,mod,:] == False)
notBad = notGlitched & cleanChop & goodPixel
if (ANY(notBad)):
    w = notBad.where(notBad)
    signal=myframe.getSignal(pix,mod)[w])
    wave=myframe.getWave(pix,mod)[w])
```

For pixel (8,12), you are first looking for the data that are not glitched, have a clean chop, and are from a pixel that is not one of the bad ones. "notGlitched", "cleanChop" and "goodPixels" are all *Bool1d*, that is arrays of length equal to the timeline-length of myframe, and which are of class *Bool1d* and hence contain the values True or False where the condition (e.g. GLITCH=False) has or has not been met. These are then merged into one *Bool1d* called notBad. Then, if there are any Trues in noBad, (i) move notBad into an array and (ii) extract out of myframe the signal and wave but selecting only those array positions that correspond to the "w" array that was made from notBad. You can then plot these *Double1d* arrays or do anything else you wish to them.

The information checked for in this example are from the Mask dataset, but you can do the same check on Status columns, for example to select out all "IsAPositions" that correspond to "nod A".

3.4.3.3. Plotting and visualising cubes

The syntax for locating the portions of the three cubes you have created by running through the pipeline are all different, although the tasks you can run on them are almost the same.

PacsCubes:

Previously we introduced a method called getMaskedIndices() for selecting out unmasked (or masked) data. The same works also for a *PacsCube*, so 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))
```

Currently none of the visualisation GUIs that were listed in Chap. 1 works on mycube (the first PACS cube you created with the task specFrames2PacsCube), which is a *PacsCube* product. (If a particular viewer is not offered when you right click on a variable in the Variables panel, then that viewer will not work for that product, probably because it is of the wrong class.) Instead, for mycube you can plot the spectrum of a single spaxel in the cube with

```
# first, what are the dimensions?
print mycube.flux.dimensions
# then plot
p=PlotXY(cube.wave[:,2,2],cube.flux[:,2,2],titleText="your title")
p.xaxis.title.text="Wavelength [$\mu$m]"
p.yaxis.title.text="Signal [Jy]"
```

Note that the wavelength dimension is the first, not the last as with a frame.

Now, 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. Below we provide examples of this:

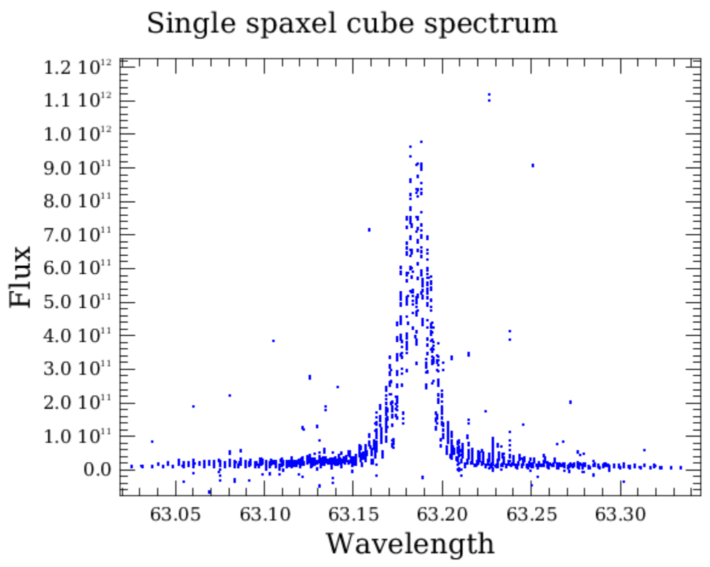


Figure 3.15. Spectrum of a single spaxel in the pacsCube. The spectrum is plotted versus wavelength and the separate spectra all lie on top of each other: 32 in total: 2 grating runs from each of the 16 pixels that each spaxel is fed by

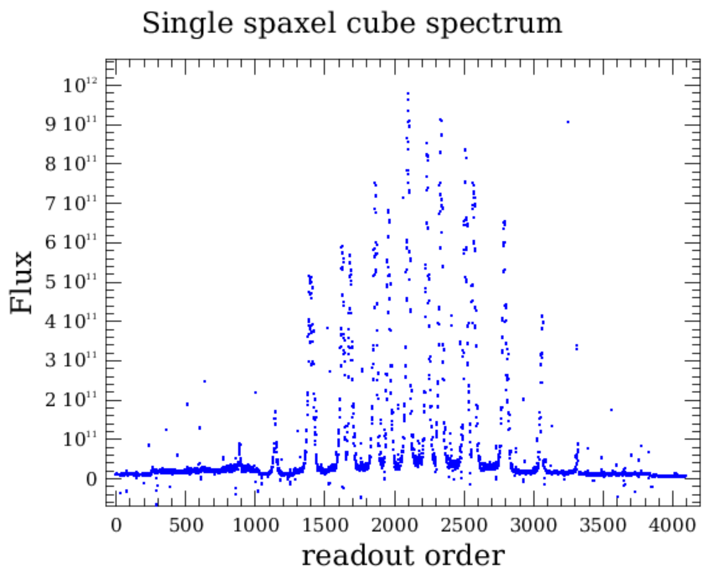


Figure 3.16. Spectrum of a single spaxel in the pacsCube. The spectrum is plotted versus readout order and the separate spectra that in the figure above lie on top of each other are now distinguishable

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 (see Sec 3.2.5):

```
Display(mycube.flux[1000:1100,:,:],depthAxis=0)
```

Where you need to find out which array positions (1000:1100 here) correspond to the wavelengths you want Display (by plotting the cube's wavelengths against nothing, for example (Sec. 3.3.2.5).

depthAxis=0 here because it is being run on a cube, not a frame. Below is a (very boring) screenshot of Display:

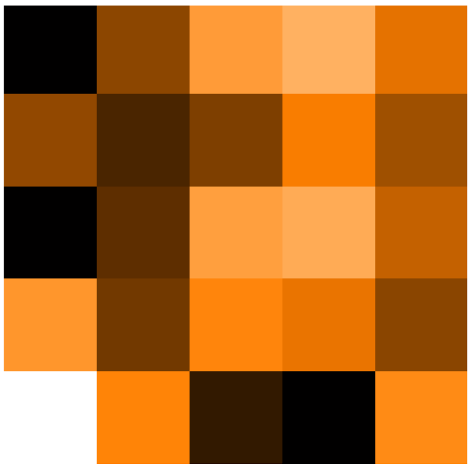


Figure 3.17. Display on a pacsCube

PacsRebinnedCube and SpectrumSimpleCube:

Plotting a single spectrum from rebinnedCube and projectedCube (respectively these are *PacsRebinnedCube* and *SpectrumSimpleCube* products and are the output of the tasks specWaveRebin and specProject) are done differently, an inconsistency that you will have to bear with for now.

```
# 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 (valid for HIPE of Jan, 2009):
PlotXY(rebinnedCube.wavegrid,rebinnedCube.flux[:,2,2])
# PROJECTED/SPECTRUMSIMPLE CUBE
# get the dimensions
print projectedCube.dimensions
PlotXY(projectedCube.getWave(),projectedCube.getFlux(10,10))
```

(Note that to get the dimensions of mycube you must type > print mycube.flux.dimensions, not > print mycube.dimensions.)

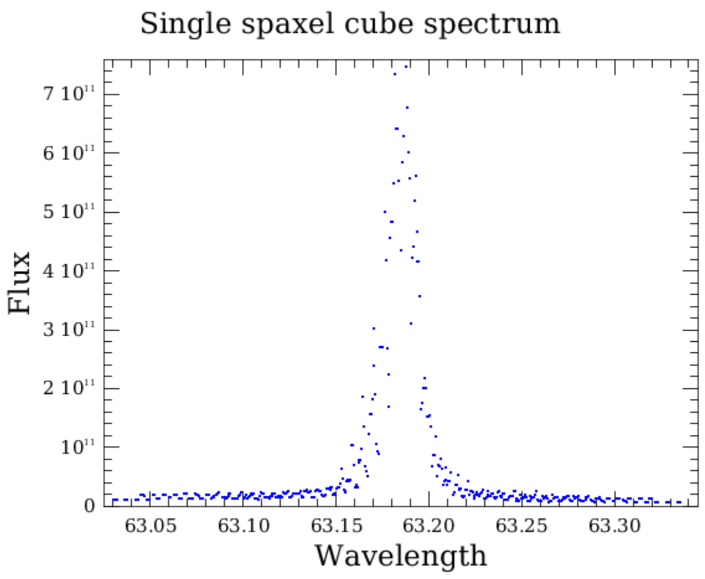


Figure 3.18. Spectrum of a single spaxel in the rebinnedCube. The spectrum is cleaner than the example from the PacsCube because the spectra have been combined and rebinned

For these cubes you can also use Display, with the same syntax as with the pacsCube. Below is a (less boring) screenshot of Display on the projectedCube (data from an observation of more-or-less nothing):

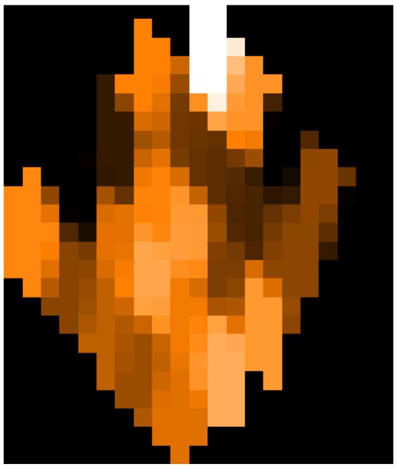


Figure 3.19. Display on a projectedCube

GUIs introduced in Chap. 1: To know which GUIs and tasks can be used to inspect your cubes, go back to Chap. 1.

3.5. Saving and restoring products

What if you want to save your data now? Currently saving and restoring is a bit awkward, but things will improve with time. There are several ways to save and restore products but we are only going to show you one or two ways for each; any others are to be found in the Appendix. There is also much information in the <LINK>.

The easiest way to save a single product, e.g. myframe or myramp, is to right click on it In the Variables panel to get a menu and select Send to#Local store (send to a pool) or #FITS file. This opens up a tab in the Editor panel and you can then need to input (i) for saving to a pool, either select a pre-existing pool from the pull-down menu or type the *entire* path name of a new pool in the box below, or (ii) the entire path and full name (including the .fits) of a FITS file.

3.5.1. FITS

To save to a FITS file from the command line:

```
myfits=FitsArchive()
myfits.save("frame.fits",myframe)
```

where the file is sent to your home directory. To then restore that FITS file, either locate it with the Navigator (HIPE menu Window#View#Navigator) and double click on it (you will see it appear in the Variable panel) or on the command line write

```
myfits = FitsArchive()
myframe_restored = myfits.load("frame.fits")
```

where the file is expected to be in your home directory.

3.5.2. To a pool: ObservationContext and other products

We introduced the tasks get|saveObservation earlier in this guide. The full syntax for getObservation is

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

and for saveObservation is

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

where the optional parameters (those in []) are: `od` (observation day); `poolName`, a string and the name of the pool if you have given it your own, unique name (getObservation by default expects a particular naming convention, so it may always be necessary specify this parameter); `poolLocation`, a string and is given in case the pool directory is not in /.hcss/lstore; `verbose` (True or False, default is False, no "" when specifying) for a full reporting; and `saveCalTree`, which allows you to save the calibration tree you have been using along with your ObservationContext. Note that `poolName` is the name of the directory in which your data are located, *not* the entire path#the entire path is the parameter `poolLocation`. 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/lstar/obsid1342111 then you only need to specify "obsid1342111" as the `poolName`.

> **Note**
>
> Actually, what we sometimes call "pool" is in fact a "storage" into which you want to a "pool". But it is far too confusing to discuss the wonderful world of HIPE syntax, so we don't.

To save a frame, ramp, cube or ListContext to a pool on the command line we do not use the same commands as for saving and restoring ObservationContexts. The PAL Storage Manager view allows you to save to and from pools with a GUI, so here we only explain the command line methods. First, before you save your product give it a comment in its meta header because otherwise you will have no idea of what you are later restoring. This is because there is very little in the saved product that bears a relation to the name it currently has.

```
myframe.meta["mycomment"] = StringParameter("frame processed by me to level 0.5")
```

where the first string is a keyword and the second string is the comment itself. This will work for any of the aforementioned products. Then do the following

```
# define where on disc your data should go
mypool = ProductStorage(LocalPool("stuff","/Users/me/bigdisc"))
ref=mypool.save(myframe)
```

The compound command (the first command) is because this is the easiest way for us to tell you how to save data in a way that allows you to save to anywhere you want on your disc. As before, the first parameter in LocalPool() is the pool directory name and the second the full disc path, which you can leave unspecified if you want to put the data in the default location. The directory you requested is created if it doesn't already exist, and you can save to that pool any number of products with the same commands (you only need to define "mypool" once). Note that this process only saves "myframe", it does not save any other variables at the same time: so if you were to start HIPE again to work on your saved frame having been reduced to only to Level 0.5, you will also need to re-get the calibration tree (mycaltree=getcalTree()), which is necessary for later pipeline stages, and you may need to get from the original ObservationContext also the pp, orbitEphemeris and dmHead if you think you will need those particular products again.

You typed "ref=" for the final command, rather than just "mypool.save()" because if you now type > print ref, you will see something like urn:stuff:herschel.ia.pal.ListContext:0. This is a reference to the URN, which is kind of an address for the product you just saved. It is one way you can find your product back out of the pool. The other way to find your product again is to save with the following command

```
mypool = ProductStorage("myfirstpool")
```

```
mypool.saveAs(myframe,"frame_blue_first")
```

Now the "frame_blue_first" is a "tag" with which that particular frame (or cube, or ListContext...) can be located.

To restore your frame/s use the following

```
mypool = ProductStorage("myfirstpool") # if not already defined
# With the URN
myframe_restored=mypool.load(ref.urn).product
# or
myframe_restore=ref.product
# or, if you don't have "ref" as a variable any more but you did
# write down that ref is urn:stuff:herschel.ia.pal.ListContext:0, then
myframe_restore=load("urn:stuff:herschel.ia.pal.ListContext:0").product
# With the tag
mylist = mypool.load("frame_blue_first")
myframe_restored = mylist.product
```

If you have neither tag nor ref you need to inspect mypool to see what is in there and select out your frame. This is where the meta comment becomes useful.

```
mypool = ProductStorage(LocalPool("stuff","/Users/me/bigdisc")) # if not already
 defined
mylist = browseProduct(mypool) # this is a browsing GUI
myframe_restored = mylist[0].product
```

The use of the product browser (browseProduct) GUI is explained in the <LINK> but a quick summary here: go to the "Product Class" pull-down menu in the middle of the GUI and select the option ending in "Frames" (if you had saved a frame), "Ramps" (if you had saved a ramp), "[something]cube" (if you had saved a cube). Click the "submit" tab and a listing of all frames (or ramps or cubes) is shown in the Query result window. To see what it is, click on it (*not* on the small tick box on the left of the row. Not yet!) and information appears in the Product Panel on the right. As you explore that information, in the Meta data listing you should see the "mycomment" keyword and entry that you wrote in there. Lots of other information is also shown, but we will not explain those here. To select the frame you want, now you can click on the tick box to the left of the listing in the Query result window, and that frame is sent to the Download window. When you have all that you want, click "Apply" or "Ok" at the bottom of the GUI. (You can not currently deselect a Download.) What you have gotten out, what "mylist" is, is an (ArraySet) listing of everything you put in the Download window (and in the same order). The final command (myframe_restored=) is how you extract out the product(s) that you put in there; if you put only one product in mylist you can extract it out with mylist[0].product, and if you put more in, the number in [] will be 1 or 2 or 3....

If you accidentally typed in the wrong name of your pool, the product browser won't tell you it is looking in a non-existent place. It will just not find anything.

There is also a Data Access viewer (HIPE menu Window# Show view) that is an alternative to the product browser. The <LINK> explains its use (select a pool to Query and press Search. It produces a listing in a new variable called QUERY_RESULT. Click-send that to the Editor panel to see the listing, and when you find the one you want therein, double click on it to send that product to a new Variable).

..

And that, Ladies and Gentlemen, is the end of Chapter 3. Phew. Pat yourself on the back for having gotten this far :-D

Chapter 4. Further topics. *Spectroscopy*

4.1. Introduction

In this chapter we discuss futher issues to do with the pipeline and with PACS data:

- The pipeline tasks will be more fully explained and their parameters listed
- The Status and Block tables are introduced *To Be Written*
- Converting between PACS format and other formats *Being Updated*
- Particular issues with the data that you should be aware of are discussed, this largely being important for data taken during the beginning of the mission, when the AOT logic, as the instrument configuration and the pipeline are still being work on. As we fix these issues, they will be taken out of this chapter. *To Be Written*

This chapter is currently incomplete

4.2. The pipeline tasks more fully explained

Here we present the parameters of the pipeline tasks and for the more important tasks explain what it is they are doing. Please consider that the deep and dirty details of most of the pipeline tasks, and of all of the calibration files, are too long to explain in this user-level data reduction guide. Many of the tasks will also have entries in the PACS *URM* and they are also explained in much more detail in the PACS Detailed Pipeline Document (*PDPD*), a more advanced-level document than this one you are reading (but which has not yet been written).

Tasks are listed roughly in the order they are called, although see Chap. 3 for the most recent task order (most recent within this guide, at least). The parameters given in [] are optional and where there are default values we have put them in.

You can also get information on a pipeline task by typing, for example

```
print specFlagSaturationRamps
```

which gives information for all the task's parameters—class, default value, etc.—and some other information that probably will not make much sense. For most of the parameters it is not intended that users change them from the default values.

The calibration files used in the tasks are named. One has the choice of specifying the individual calibration files or the entire calibration tree (calTree). If you did want to replace the default calibration with you own (an expert job if ever there was one) you could send the task your new parameter file(s) and you would then not specify the calibration tree. (Strictly speaking the calibration tree is often an optional parameter, however it is so important that here we classify it as mandatory *unless* you specify instead the individual calibration files to use.) Unless you really know what you are doing, it is not considered a good idea to try to change the calibration files.

4.2.1. Level 0 to 0.5

```
ramp = specFlagSaturationRamps(ramp ,pacsCalTree=<mycalTree>
          [,rampSatLimits=<calfile>] [,copy=0])
frame = specFlagSaturationFrames(frame ,pacsCalTree=<mycalTree>
          [,rampSatLimits=<calfile>] [,copy=0])
```

This tasks flags frames pixels which have saturated data points, this being determined by comparing the values of the data points (ADU for ramps and V/s for Frames) to the value at which saturation sets in, as given the calibration file rampSatLimits. (>print calTree.spectrometer.rampSatLimits)

For this and all other tasks, `copy`=0 means that the input frame has the mask added, setting it to 1 means that the mask is not added.

```
frame = fitRamps(ramp [,degree=1] [,firstReject=0] [,lastReject=0])
```

This task fits the raw or averaged ramps with a polynomial to determine the ADU/s count rate. The fit uncertainties are also calculated. Any masks present are propagated, they are not taken into account when the fit is made. A mask BADFITPIX is created, being set to True for readouts for which the fits may have been poorly done. This can be considered a warning mask, it is not actually by default used in any of the pipeline tasks. `lastReject` and `firstReject` allow you to specify the number of first or last readouts to ignore in the fit. This is only really worth doing for raw ramps—for the averaged ramps most users will get hold of the number of readouts is too small for it to make sence to reject readouts.

To be written: how the uncertainties are calculated and the badfitpix mask calculated

```
frame = specConvDigit2VoltsPerSecFrames(frame ,calTree=<mycalTree>
           [,readouts2Volts=<calfile>] [,copy=0])
```

This task converts the units to V/s using conversion factors from the calibration file readouts2Volts.

```
frame=detectCalibrationBlock(frame)
```

This task simply identifies the calibration blocks (i.e. where they lie in the data time-line) and fills the CALSOURCE entry in the status table.

```
outFrame = specExtendStatus(inFrame ,calTree=<mycalTree>
           [,ChopperThrowDescription=<calfile>] [,copy=0])
```

This task simply adds information to the Status table about the grating and the chopper. The calibration files used is chopperThrowDescription. The Status columns GRATSCAN, CHOPPER and CHOPPOS are added.

```
frame = specAddInstantPointing(frame, pp ,calTree=<mycalTree>] [,copy=0])
```

"pp" is the pointing product (see Chap. 3). This task associates the PACS centre-of-field coordinates and the position angle (the RA and Dec of the central detector pixel) to the raster point counter and/or nod counter of the frame. The calibration file used is siam. The Status columns RaArray and DecArray are added.

```
frame = convertChopper2Angle(frame ,calTree=<mycalTree> [,redundant=0]
           [,chopperSkyAngle=<calfile>] [,chopperAngle=<calfile>]
           [,chopperAngleRedundant=<calfile>] [,copy=0])
```

This task converts the chopper position angle from engineering units to an angle (arcmin) on the sky. `redundant` (for this task and all others where it is a parameter) is a switch to tell the task whether the redundant unit (=replacement unit, in case of accidents to the main unit) or the main unit (default, value=0) was used. The calibration files used are chopperSkyAngle and chopperAngle or chopperAngleRedundant.

```
frame = specAssignRaDec(frame ,calTree=<mycalTree> [arrayInstrument=<calfile>]
           [,moduleArray=<calfile>] [,copy=0])
```

This task takes the pointing previously added for the central pixel, of the centre of the field-of-view coordinate, and assigns an RA and Dec to every pixel. It uses in the calibration files arrayInstrument and moduleArray, and it adds the datasets "ra" and "dec" to frame (>print frame.ra). The conversions are sensitive to the chopper throw and pixel position (i.e. it is not adding just an offset for each pixel, as the relationship between pixel position and conversion is non-linear).

```
frame = addUtc(frame, timecor, [,copy=0])
```

The parameters of this task were explained in Chap. 3. It converts from spacecraft on-board time (OBT) to coordinated universal time (UTC) using the time correlation table timecor.

```
frame = waveCalc(frame ,calTree=<mycalTree> [,filter=<string>]
           [,littrowPar=<calfile>] [,copy=0])
```

This is a task that calculates the wavelength corresponding to a grating position, using calibrations measured on ground. `filter` is a string, being "R1", "B2", "B3" for the red array filter, blue array green filter and blue array blue filter. The calibration file used is littrowPolynomes.

```
frame = specCorectHerschelVelocity(frame, orbitEphem, pp)
```

This task corrects the wavelengths for Herschel's velocity. The parameters of this task were explained in Chap. 3. If you were not able to extract out these parameters from your frame, then don't run this task. It wont affect anything except the accuracy, at a low level, of your wavelengths.

```
frame = findBlocks(frame [,copy=0])
```

This tasks sets up the BlockTable, sorting out different "blocks" of data (nod, raster, grating scan, and other detector parameters). How many chop—nod cycles where there, what are the different raster pointings, etc. More on the BlockTable is given later in this chapter.

```
frame = specFlagBadPixelsFrames(frame ,calTree=<mycalTree>
          [,badPixelMask=<calfile>] [,copy=0])
```

This task takes the list of bad pixels from the calibration file badPixelMask and sets a mask called BADPIX that says where these bad pixels are. This information comes from ground-level and PV tests. It also looks at the calibration files flatfield and noiseLimits.

```
frame = flagChopMoveFrames(frame, dmcHead=<dmcHead> ,calTree=<mycalTree>
          [,redundant=0] [,chopperJitterThreshold=<calfile>]
          [,chopperAngle=<calfile>] [,chopperAngleRedundant=<calfile>]
          [,qualityContext=<calfile>] [,copy=0])
```

This task masks unreliable readouts at the chopper transition phases, that is data taken while the chopper is still moving. It works this out by comparing the individual chopper positions to an allowed normal jitter value; anything larger is considered a real movement. It uses the calibration file chopperJitterThreshold to do this, and also looks at the calibration files chopperAngle or chopperAngleRedundant. `redundant` (for this task and all others where it is a parameter) is a switch to tell the task whether the redundant unit (=replacement unit, in case of accidents to the main unit) or the main unit (default, value=0) was used. The mask UNCLEANCHOP is created.

Be warned that this task will run without specifying `dmcHead` but (and it will not tell you this) the results will be wrong.

```
frame = flagGratMoveFrames(frame, dmcHead=<dmcHead> ,calTree=<calTree>
          [,gratingJitterThreshold=<calfile>] [,qualityContext=<calfile>]
          [,copy=0])
```

This task masks readouts take while the grating was moving, creating a mask called GRATMOVE. It uses the calibration file gratingJitterThreshold to do this, comparing the individual grating positions to this allowed jitter (as opposed to real movement) limit. `qualityContext` is a quality control product, but may just be a null file.

Be warned that this task will run without specifying `dmcHead` but (and it will not tell you this) the results will be wrong.

4.2.2. Level 0.5 to 1

```
frame = specFlagGlitchFramesQTest(frame [,copy=0] [,qtestwidth=16]
           [,thresholds=Double1d([2., 1., 1., 0.7]] [,qtestlow=3]
           [,qtesthigh=3] [,splitChopPos=True)
```

This task masks data for glitches, using the Q test to find them. It has been tested extensively and works well. It even masks quite well the data points that are immediately post a glitch event; these data points are probably also affected by the glitch (see later in this chapter for more about glitches). By default it works on chopped data, if there was no chopping during your observation then set the parameter `splitChopPos` to False. The other parameters are the details of the Q test, and are too long to explain here. See the PACS URM entry to learn more.

```
frame = specEsimateNoise(frame [,binWidth=5] [,copy=0])
```

A task that estimates the noise at level1 for each pixel and fills the Noise dataset. First it selects the data according to chopperplateau position 1, 2 or 0. Then it subtracts the median filtered signal (median filtering done using bins with width binWidth); then it calculates the standard deviation, again in bins with width binWidth and with a discarding of the readouts masked by the Master mask (this is because such readout could propagate and fake a very high noise in the neighboring readouts). The noise in the masked readouts is then set to the square root of the signal.

```
frame = specCorrectSignalNonLinearities(frame ,calTree=<mycalTree>
           [,nonLinearity=<calfile>] [,copy=0])
```

This task corrects for intrinsic non-linearities that are the shapes of the raw ramps of each pixel. The correction is a 2nd order polynomial fit using the coefficients from the calfile nonLinearity. (The task does work on a *Frames* product, not a raw or averaged *Ramps* product as you may think.)

```
frame = convertSignal2StandardCap(frame ,calTree=<mycalTree>
           [,capacitanceRatios=<calfile>] [,copy=0])
```

This task reads the capacitance ratios calfile (capacitanceRatios) and scales all the signals in the frame to the lowest available integration capacitance, which is referred to as the standard capacitance. This is done because the subsequent flux calibration and dark subtraction tasks use calibrations based on data taken at the smallest capacitance value. It will also allow one to compare signals (from different observations, for example) that were recorded using different integration capacitances.

```
csResponseAndDark = specDiffCs(frame ,calTree=<mycalTree>
                    [,calSourceFlux=<calfile>])
                    [,relCalSourceFluxProduct=<calfile>])
```

For each pixel and each readout, this task calculates the difference between the signal from the chopper calibration sources. By comparing this to the actual calibration source fluxes in Jy, information contained in the calibration file calSourceFlux, it computes the dark current and the response of the detector at the start of your observation (at the start because that is usually when the calibration block is executed). The responses are produced for each band (3 in the blue, 1 in the red), and uses also the calibration files the keyWavelengths and relCalsourceFlux. specDiffCs also computes the errors on the response and dark.

```
responseDrift = specFitSignalDrift(frame, csResponseAndDark=<product>)
```

This task calculated how the response drifted during your observation, putting that value in the parameter responseDrift. It takes as a starting position the value of the dark and response in the product csResponseAndDark, which was created by specDiffCs. The response drift is worked out by looking at the data taken at chopper positions where PACS was pointing off-source, i.e. at the blank sky.

```
frame = specDiffChop(frame [,removeCalStr=True>]
              [,normalize=False])
```

For chopped AOTs, this task subtracts every off-source signal from every consecutive on-source signal, at the same grating position and within each same grating scan. The resulting frame now is of a shorter length along the time-line dimension, being one data point per chopper cycle (a chopper cycle being most likely ABBA, less likely ABAB). The parameter `normalize` is set to True if you do want to normalise the calculations: False will calculate A-B, True will calculate (A-B)/(2*(A+B)). The ON pointings and wavelengths are propagated, as are any masks and most Status entries. The ON reset indices are stored in the RESETINDEX status column and the OFF reset indices in the OFF_RESETIDX column. In this way you can check which data points the algorithm has subtracted from which. The ON and OFF LBL values of the original Status table are merged into a new column LBL2.

```
frame = rsrfCal(frame ,calTree=<mycalTree> [,rsrfR1=<calfile>]
           [,rsrfB2B=<calfile>] [,rsrfB2A=<calfile>] [,rsrfB3A=<calfile>]
           [,normalise=1] [,copy=<0])
```

This task corrects for the wavelength-dependent response of the system as mapped in the Relative Spectral Response Function. Per band, it reads the RSRF calibration file; normalised the RSRFs over the prime key wavelengths of the band; loops over all pixels and interpolates the normalised RSRF to the wavelengths sampled in those pixels; divides the signal by the interpolated response. copy is as for all other tasks and normalise is an integer, 0 to not normalise to the key wavelength, 1 (the default) to normalise. The calibration files give a value per pixel and are anyway contained in the caltree.

```
frame = specRespCal(frame ,calTree=<mycalTree> [,responseDrift=<product>]
           [,csResponseAndDark=<product>] [nominalResponse=<calfile>]
           [,copy=0])
```

This task divides by the best known and most recent responsivity values. The optional inputs responseDrift and csResponseAndDark are the products that were created by the tasks specFitSignalDrift and specDiffCs. If you did not (or could not) run those tasks, then this will still work but will take standard calfile values for its work, rather than those worked out from the dataset you are working on. The nominal response calfile can be used if the csResponseAndDark is not.

```
frame = specAddNod(frame [,useWeightedMean=0])
```

This task combines the nod positions for a chop-nod observation. It adds every upscan on nod A to the subsequent upscan on nod B. It retains the pointing and chopper positions of nod A. It then does exactly the same for the downscans. By default it combines using a non-weighted mean, i.e. it combines the average of nod A and B of each nod cycle, separately, it does not average the grating up and downscan (i.e. these are retained as separate time-lines). If there is an error array present it is added to as the standard deviation of the mean. If you want to use the error-weighted mean and you have an error array to do that, then specify the parameter useWeightedMean, with value >0 (value=0, the default, corresponds to using the standard mean), at the same time the error array is propagated accordingly.

```
cube = specFrames2PacsCube(frame)
```

This task converts a frame to a fully calibrated, oversampled 5x5xn PacsCube, which is the end of the Level 1 stage. The cube dimensions are 5x5xlambda, where within each spaxel all the spectra of the 16 modules that contribute to that spaxel. It does no manipulation of the spectra.

4.2.3. Level 1 to 2

```
grid = wavelengthGrid(cbe [,oversample=<number>]
       [,upsample=<number>] [,calTree=<mycalTree>])
```

This task calculates the wavelength bins for your dataset, which are dependent on the actual wavelengths present and the requested oversampling factor (the default value of which is 2.0; type: double, and can be sub-integer in value). upsample (type: double) is how much you shift forward by when creating the bins; the default value is 3.0 and it can take on values 1.0, 2.0, or 3.0. The grid created by this task is a product.

The oversample factor is used to increase the number of wavelength bins by the formula bins*oversample, where the number of bins is based on the theoretical resolution of your observation. The upsample factor specifies how many shifts per wavelength bin to make while rebinning. Each bin is sampled "upsample" times, shifting forwards by 1/upsample. An upsample value of 2 means sample, shift by binwidth/2, and sample again. In this example, since both samples are the width in wavelength of the original wavelength bin, the second sample will overlap the next bin.

```
cube = specFlagOutliers(cube, grid [,nSigma=<number>] [,nIter=<number>]
       [,ignoreMasks=<string>] [,saveStatus=<boolean>])
```

This task flags outliers in each wavelength bin and introduces the mask OUTLIERS. It should not mask data already masked (hence the activateMasks prior to this task that is recommended in the pipeline). `nSigma` (default value 5.0) is the sigma value to flag at, `nIter` is how many repeats (iterations) of the outlier hunting you want to do (default value 1 but 2 would be a better first try value). `ignoreMasks` is a String1d of mask names that you want the task not to take in to account. The task gets the flux and wavelengths, for each spaxel, sorts the wavelengths, applies the masks, calculates the median and median absolute deviation of the flux in each wavelength bin, and clips outliers (+ and -) using that information. `saveStats` set to True (not the default) will save the median and deviation values calculated as *ArrayDatasets* attached to the cube.

```
rebinnedCube = specWaveRebin(cube, grid)
```

This task constructs 5x5xlambda data cube which is the integral field view of the PACS spectrograph. It rebins the fluxes of the spectra held in each spaxel of the input cube, using the grid constructed by the wavelengthGrid task. The end result of this task is a cube of 5x5xlambda, where lambda now is of dimensions on your input grid, and in the course of the rebinning the 16 spectra that were originally stored in each spaxel have been merged into 1 spectrum per spaxel. By default any masks that are present are considered, except DEVIATINGOPENDUMMY and OBSWERR.

```
projectedCube = specProject(rebinnedCube [,outputPixelSize=<number>]
                    [,use_mindist=<boolean>] [,norm_flux=<boolean>]
                    [,threshold=<number>] [,filter_nans=<boolean>]
                    [,debug=<boolean>] [interactive=<boolean>]
                    [qualityContext=<smthng>])
```

This task projects a rebinned cube (the output of SpecWaveRebin) onto a regular RA/Dec grid on the sky. The grid (the corners and dx,dy) will be determined by the task using the RA and Dec information in rebinnedCube. Input and output both are *SimpleCubes*. The parameters are: `outputPixelSize` is the output spaxel side in arcsec (default 3.0); `use_mindist` tells the task whether it should use the minimum spaxel distance rather than the average (default False); `norm_flux` (default True) tells the task whether it should divide by the exposure map to normalise fluxes; `threshold` (default 2.0) is used only if a *PacsCube* is input, rather than a *PacsRebinnedCube*, and is the minimum jump, in arcsec, which triggers a new raster position; `filter_nans` (default False) if True all frames with one or more NaN values will be discarded; `debug` (default False) set to True will create extra datasets in the output product for debugging purposes; `interactive` (default False) set to true will produce several plots while running; `qualityContext` (default None) is only used in SPG mode.

The task:

1. scans all the RA/Dec values in the input cube and selects (all) the unique scan position(s). Store for each scan position the frame numbers which match these positions, the RA and Dec and rotation matrix of the spaxels (method: selectUniquePositions).

2. computes a regular RA/Dec grid which encompasses all the raster positions from the previous step (method: computeGrid).

3. loops over all raster positions and do for each position the following: i) compute the weights for projecting the input spaxels to the output grid. These weights determine which input spaxel(s) the output spaxel(s) overlap and by how much. The results are stored in two 3D arrays, one containing the overlapping modules for each output RA/Dec, and one with their corresponding weights. ii) compute for each frame at each position in the cube the output fluxes on the new regular grid. This is done by adding up for each spaxel the fluxes of the contributing spaxels multiplied by their overlap weights.

4. Combine the projected images from different raster positions and normalise by dividing with the sum of the weights of all positions.

5. Write the resulting projection to the output cube.

This task is worth running even if you only have one pointing in your observation because it does not just add together, or mosaic, multiple pointings, but also sets the correct spatial grid for each wavelength of your cube. For the PACS spectrograph, each wavelength sees a slightly different spatial position, even for spectra within a single spaxel.

4.3. The Status table

Data that comes from the satellite will have some of the Status columns filled with values. Pipeline tasks then add columns, either because they do a conversion from engineering to astronomical values or calculate a "status". *TBC*

4.4. The Blocktable

To Be Written

4.5. Converting cube and frame spectra to other formats, to do spectral mathematics

Because at present PACS cubes do not read directly into the various GUIs and tasks that allow you to inspect and fit spectra, we provide some workarounds. First we tell you how to convert individual spectra to *Double1/2d* and *Spectrum1d* format so these GUIs and tasks will ingest them, and then we may provide some scripts do to a more complex conversion, one that honours better the different parts of the PACS data which you will want to check and compare with this GUIs and tasks. The GUIs and tasks are particularly useful because they allow you to separate spectra from different "segments" of the observation, which for PACS would be data from different chops, nods, rasters, grating runs and pixels within a module. The simple conversion we discuss first does not allow you to segmentise the data, however reading this section will allow you to get a feeling for what is done when converting from PACS format to these other formats. The more complex scripts will allow you to segmentise the data and thus you will be able to compare the chops and nods etc. more easily.

Spectrum mathematics can be done directly on your cube/frame spectra via tasks offered in the Tasks panel; those applicable to your cube or frame you will see in the Applicable listing of the Tasks panel (add, avg, subtract...) when you click-highlight your cube in the Variables panel. The <LINK> offers a short (and somewhat incomplete) guide on the use of these particular functions. However, at present the tasks do not all work well on PACS cubes (there may well be no applicable tasks listed). You are better off extracting out single spectra and converting to *Spectrum1d* class. Mathematics can also be done on the command line working directly from the cube with the spectral in *Double1/2d* format. The <LINK> contain information about what can be done mathematically and visually with these *Double1/2d* arrays, for example using the numerics package.

One drawback, of course, with extracting out single spaxel/pixel spectra to do spectral mathematics is that you need to first know from which spaxels/pixels you want spectra. Unfortunately, until the SFTool or ExplFitter work on PACS cubes you have no other choice. To identify the spaxels, use Display or the CubeAnalysisToolBox. Both of these print the spaxel coordinates that your mouse is hovering over.

Here we will show you how to extract out spectra from the PACS *Frames* and *Cube* products and convert to *Spectrum1d* or *Double1/2d*. We do not show you how to do mathematics or other types of manipulations, for that you will need to read the other documentation mentioned here.

4.5.1. A projectedCube

There are, in fact, several ways you can extract single spectra from your cube and convert to a different format, but to explain all the methods would be confusing.

First, to convert to *Double1/2d*:

```
# first, define a Double2d array to take your spectrum
Spec=Double2d(2,mycube.getWave().dimensions[0])
# put in there the wavelength and then flux of a single spaxel, here 10,10
Spec[0,:] = mycube.getWave()
Spec[1,:] = mycube.getFlux(10,10)
# now plot to check all is well
PlotXY(Spec[0,:],Spec[1,:])
# using python, add a value from the fluxes
Spec[1,:] += 10.0
# or divide
Spec[1,:] = Spec[1,:] / 10.0
```

The first line: mycube.getWave() is a "method" used to extract the wavelengths from this cube, and the .dimensions part tells you what the dimensions are. The [0] specification allows you to grab the first part of the returned dimension listing (which is, in order: wavelength, Y axis, X axis) and return that number as an integer. *The second and third line*: these are the methods to extract as *Double1d* arrays the wavelengths and the fluxes and place them in a *Double2d* array (Spec). *The final line*: is the way you plot your *Double2d*.

If you do this for a number of spectra, wrapping your commands around in jython for or do loops, then you can extract out any number of spectra and do mathematics on the command line/in a script. This is because the data you have are held in simple (*Double2d*) arrays, rather than as DP product classes (e.g. *Spectrum2d*). Mathematics you can then do on the command line include, +, -, /, *, MEDIAN(), STDDEV(), MEAN()...More on this is explained in the <LINK>.

One way to convert single spectra in your cube to *Spectrum1d* format is to use the CubeAnalysisToolBox: read its documentation to learn how to do this, but basically it involves doing a single/range spaxel selection and clicking "save [as] a Product" (doing this one by one for each spectrum you want to convert to *Spectrum1d*. And yes, this is an awkward thing to have to do).

If you want to convert single spectra of your cube to *Spectrum1* without using the CubeAnalysisToolBox then these are commands you can use:

```
wave = mycube.getWave()
flux = mycube.getFlux(10,10)
segs = Int1d(mycube.getWave().dimensions[0]) + 1
flag = Int1d(mycube.getWave().dimensions[0]) + 1
weight = Double1d(mycube.getWave().dimensions[0]) + 1.0
spec = Spectrum1d(flux, weight, flag, segs)
spec.set("wave",wave)
a.setMeta("name","mycube_spax10_10")
```

The segs array holds segment information (more on this in the Appendix) which for your spectra will all be the same (so here set to 1). Flag at present is not useful, so set to 1. The syntax "Int1d(mycube.getWave().dimensions[0]) + 1" creates a 1-dimensional integer array of the same size as the spectral dimension of your spectrum from mycube, with value everywhere of 1. Adding meta information is optional but generally a good idea (so you can later work out what this Spectrum1d was made from, for example).

All of these instructions have been taken from the <LINK>. Now you know how to convert to *Spectrum1d* you can read there about how to convert to *Spectrum2d*.

4.5.2. A rebinnedCube

The same method as for the projectedCube is used to extract out the data and convert class. The only difference is the method to extract the wavelengths and fluxes, here being:

```
# first, define a Double2d array to take your spectrum
Spec=Double2d(2,rebinnedCube.flux.dimensions[0])
# put in there the wavelength and then flux of a single spaxel, here 2,2
Spec[0,:] = rebinnedCube.waveGrid
```

```
Spec[1,:] = rebinnedCube.flux[:,2,2]
```

and to convert to Spectrum1d format

```
wave = rebinnedCube.waveGrid
flux = rebinnedCube.flux[:,2,2]
len = flux.dimensions[0]
segs = Int1d(len) + 1
flag = Int1d(len) + 1
weight = Double1d(len) + 1.0
spec = Spectrum1d(flux, weight, flag, segs)
spec.set("wave",wave)
a.setMeta("name","rebinnedCube_spax2_2")
```

4.5.3. A pacsCube

Again, the same idea here as for the previous cube types, but with slight differences. To convert to Double2d

```
# first, define a Double2d array to take your spectrum
Spec=Double2d(2,mycube.flux.dimensions[0])
# put in there the wavelength and then flux of a single spaxel, here 2,2
Spec[0,:] = mycube.wave[:,2,2]
Spec[1,:] = mycube.flux[:,2,2]
```

and to convert to Spectrum1d

```
wave = mycube.wave[:,2,2]
flux = mycube.flux[:,2,2]
len = flux.dimensions[0]
segs = Int1d(len) + 1
flag = Int1d(len) + 1
weight = Double1d(len) + 1.0
spec = Spectrum1d(flux, weight, flag, segs)
spec.set("wave",wave)
a.setMeta("name","mycube_spax2_2")
```

4.5.4. A frame

Again, the same idea here as for the cubes, but with slight differences. To convert to Double2d

```
# first, define a Double2d array to take your spectrum
Spec=Double2d(2,mycube.flux.dimensions[0])
# put in the wavelength and flux of a single pixel, here 8,12 (detector centre)
Spec[0,:] = myframe.wave[8,12,:]
Spec[1,:] = myframe.flux[8,12,:]
```

and to convert to Spectrum1d

```
wave = myframe.wave[8,12,:]
flux = myframe.flux[8,12,:]
len = flux.dimensions[0]
segs = Int1d(len) + 1
flag = Int1d(len) + 1
weight = Double1d(len) + 1.0
spec = Spectrum1d(flux, weight, flag, segs)
spec.set("wave",wave)
a.setMeta("name","myframe_pix8_12")
```

4.6. Data/observing/instrument issues

Most of the issues we discuss here are those that arise at particular points during the mission. As the issues are solved and become part of the normal data reduction pipeline, they will be taken out of this chapter. Hence, look at the date of last edit of this data reduction guide to know what is important for you.

4.6.1. Nodding

To Be Written

4.6.2. Dithering/Rastering

To Be Written

4.6.3. The PSF

To Be Written

4.6.4. Flatfielding and flux calibration

To Be Written

4.6.5. Saturation

To Be Written

4.6.6. Glitches

To Be Written

4.6.7. Errors/Noise

To Be Written

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 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
obs.calibration=calTree
```

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

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

The orbit ephemeris (oem) is used to correct for the movements of Herschel during your observation, the pointing product is used to calculate the pointing of PACS during your observation.

You also need to get the time correlation product to correct the time in the meta data

```
timeCorr = obs.auxiliary.timeCorrelation
```

Then you need to retrieves 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)
obs=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.

```
myframes = findBlocks(frames, calTree=calTree)
```

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

```
myframes = removeCalBlocks(frames)
```

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

```
skip=430 (or some other observation dependent number)
frames = frames.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(obs,'0',slicedFrames)
```

The last line is needed to make sure that all the keywords which are available for the level0 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
print noofsciframes
```

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 keyword 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. Level 0 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. The only AOT dependent task executed in this part of the data reduction is the CleanPlateauFrames task, which is executed only for chopped observations.

Next the pipeline tasks are introduced in the order they should be run.

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 that 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)
framesnod = photFlagSaturation(framesnod)
framesnod = photConvDigit2Volts(framesnod)
#framesnod = photCorrectCrosstalk(framesnod)
# ground-based correction is overcorrecting, hence switched off for the time being.
if (timeCorr != None) :
   frames = addUtc(frames, timeCorr)
framesnod = convertChopper2Angle(framesnod)
framesnod = photAssignRaDec(framesnod)
```

5.3.1. photFlagBadPixels

The purpose of this task is to flag the bad or noisy 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).

5.3.2. photFlagSaturation

This tasks identifies the saturated pixels on the basis of saturation limits contained in a calibration file for the two types of saturation possible: readout circuit and the Analogue to Digital Converter (ADC) 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 latter task is still under investigation and debugging phase, so only the multi-resolution median transform is supported. 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 using the Array Instrument calibration file with spatial distortions.

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

5.3.9. cleanPlateauFrames

This task is executed before Level 0.5 only for chopped observations.

```
myframe = cleanPlateauFrames(myframe)
```

The module flags the readouts at the beginning of a chopper plateau, if they correspond to the transition between two chopper positions. In the chopper transition phase, the chopper is still moving towards to proper position and the signal of this readouts does not correspond to the on or off position. Usually the chopper is moving so fast that only one readout needs to be masked out. The module just adds the 3D UNCLEANCHOP mask to the input frame. The task identifies the chopper plateaus on the basis of the CHOPPERPLATEAU (for the science data) and CALSOURCE (for the calibration block) entries in the status table. For each chopper plateau the readouts with a chopper position deviating from the mean position (threshold provided by the calibration file ChopJitterThreshold) are flagged in the UNCLEANCHOP mask. However, this task is superfluous in its current implementation, hence it is not used.

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)
#frames = photDriftCorrection(frames)
```

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(framesnod)
```

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.

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:

$$\mathcal{S}_f(t) = \mathcal{S}_s(t) * \frac{(\delta\mathcal{C}_0)}{(\delta\mathcal{C})} * \frac{1}{(J\Phi)}$$

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-field 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 create 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 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)
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 slices 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` we advise to use :

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

  it gives rather good results on scan maps at medium scan speeds, if the target it not too bright (above a few hundreds of mJy), otherwise the PSF core is also deglitched. Check the exposure map to see if this is not the case. You can reduce the scales to scales=2 to overcome this problem. At high speed (60'/s) deglitching is challenging, even with scales=1, the brightest sources in the galacctic plane can be affected.

- `photRespFlatFieldCorrection`

- `photAssignRaDec`

5.6.2. Level 1 to Level 2

At this stage of the data reduction 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). The high-pass filter is well suited for deep fields with faint point-sources, but not for fields with extended emission as all structes at scales above 2*filterbox+1 will be filtered out in this process.

```
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, this can be done with the following command :

```
myframe=myframe.select(myframe.getStatus("BBID") == 215131301l
```

photProject

```
map = photProject(frames, calTree=calTree,calibration=True,outputPixelsize=2.0)
Display(map)
simpleFitsWriter(map,'filename'.fits')
```

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

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). If the optimizeOrientation-true is set the task will try to compute a rotation for the final map so that both image pixel coordinates (x,y) and the WCS (ra,dec) are intelligently aligned. The idea is to save on the "empty" space in the final map. It only works if the rotation is larger than 15 degrees.

runMadMap

The module `runMadMap` is the wrapper that runs the JAVA MadMap module and creates the final image.

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