
Chapter 1. PACS Launch Pads

1.1. Introduction

May 2012. The PDRG has been split into a Spectroscopy and Photometry part. The pipeline chapters have been updated. This has been written for track 9 of HIPE, but much will also be valid for track 10.

Welcome to the PACS data reduction guide (PDRG) #. We hope you have gotten some good data from PACS and want to get stuck in to working with them. This guide begins with a series of "launch pads" that from Chap. 1; essentially quick-start guides to working with PACS data. These will show you the fastest ways to get your data into HIPE, to inspect the HSA-pipeline reduced cubes (spectroscopy) or images (photometry), and will outline what you need to consider before you start to reduce the data yourself through the pipeline. For PACS observations we recommend you always re-reduce your data: to include the latest calibrations, so that you can check the intermediate results (deglitching, map-making and masking, flat-fielding, etc), and because some pipeline tasks are not carried out by the automatic pipeline that the HSA-retrieved data were processed through.

Contents: Chap. 2 takes you through what you need to do and know before you start pipeline processing your data, Chap. 3 is dealing with the different PACS photometry pipelines and Chaps 4 and 5 contain more detailed information about photometry data processing (e.g. deglitching and MADmap). In the appendix are issues that are common to photometry and spectroscopy such as explained the organisation and contents of PACS data products.

Additional reading can be found on the HIPE help page, which you can access from the HIPE "Help>Help Contents" menu. This covers the topics of: HIPE itself, I/O, scripting in HIPE, and using the various data inspection and analysis tools provided in HIPE. We will link you to the most useful bits of this documentation—we do not repeat the information given there, only material that is PACS-specific is in this *PDRG*. You can also consult the PACS public wiki for the Observer's Manual and calibration information and documentation (herschel.esac.esa.int/twiki/bin/view/Public/PacsCalibrationWed?template=viewprint). This is also linked from the PACS section of the HIPE help page. Information on the calibration of PACS data is **not** covered in this *PDRG*, you have to look at the wiki for these.

1.2. PACS Data Launch Pad

1.2.1. A quick on terminology

The following Help documentation acronyms are used here (the names are links): **DAG**: the Data Analysis Guide; **SaDM**, the Scripting and Data Mining Guide.

Level 0 products are raw and come straight from the satellite. **Level 0.5** products have been partially reduced, corrected for instrument effects generally by tasks for which no interaction is required by the user. **Level 1** products have been more fully reduced, some pipeline tasks requiring inspection and maybe interaction on the part of the user. **Level 2** products are fully reduced, including tasks that require the highest level of inspection and interaction on the part of the user. **Level 2.5** products, which are found for some of the pipelines, are generally those where observations have been combined or where simple manipulations have been done on the data.

Text written *like this* usually means we are referring to the class of a product (or referring to any product of that class). Different classes have different (java) methods that can be applied to them and different tasks will run (or not) on them, which it why it is useful to know the class of a product. See the SaDM to learn more about classes. Text written *like this* is used to refer to the parameter of a task.

1.2.2. Getting your data from the archive into HIPE

There are a number of ways to get Herschel data into HIPE, and those data can come in more than one format. The PACS pipelines use one method, which is documented in the pipeline script, but here

we give an overview of the simplest ways to get Herschel data into HIPE. This topic is covered in detail chap. 1 of the DAG.

Herschel data are stored in ESA's Herschel Science Archive (HSA),

- They are identified with a unique number known as the Observation ID (obsid)
- HIPE expects the data to be in the form of a **pool**, so HSA data must be *imported* into HIPE
- A **pool** is like a database, with observations organised as an **Observation Context**, containing links to all the data, calibration, and supplementary files, and including the raw, partially-, and fully-reduced data products

There are several ways to get observations imported from the HSA, or disk, into HIPE:

- Directly from the HIPE command line, using

```
obsid = 134..... # enter your own obsid
# to load into HIPE:
myobs = getObservation(obsid, useHsa=True)
# to load into HIPE and at the same time to save to disk:
myobs = getObservation(obsid, useHsa=True, save=True)

# You must be logged on to the HSA for this to work:
# See the DAG sec. 1.4.5.
```

See the *DAG* sec. 1.4.5 for more information on `getObservation` (for example, how to log-on to the HSA before you can get the data). If you use the parameter `save=True` in `getObservation` then the data are at the same time saved to disk to your MyHSA: note that saving can take a while. Information and links about accessing MyHSA are also provided in sec. 1.4.5.

This method is useful for single observations and brings the data directly into HIPE in the format that the PACS pipeline requires.

- Download a tar file (which is not a pool) from the HSA. See the *DAG* sec. 1.4.7 for more information on this. This is the method to use if you have several observations, or a very large one.

If you are getting a tarfile, then you will have gone into the HSA, identified your observations, and asked for them to be send via ftp. From the tar file you get, you will need to import the data into HIPE. This is explained in the *DAG* sec. 1.5; to summarise, after having untarred the file you do the following in HIPE:

```
# Get the data from the HSA as a tarball
# On disk, untar the tarball, e.g.
cd /Users/me/fromHSA
tar xvf memel342.tar

# in HIPE, then
myobsid=1342..... # enter your obsid
mypath="/Users/me/fromHSA/mel342"
myobs=getObservation(obsid=myobsid,path=mypath)

# obsid is necessary only if more than one observation
# is in that directory, i.e. if your tarfile has several
# obsids in it
```

- Import directly into HIPE from the HSA via its GUI, which is useful for single observations and brings the data directly into HIPE in the format that the PACS pipeline requires. This is covered in the *DAG* sec. 1.4.5 ("using the GUI: HUI"). Briefly, you need to find your observation (e.g. by obsid), then in the query results tab of the HUI, click the download icon to access a "Retrieve Products" menu, from which select to download "All".

Tip

To get to the HSA from HIPE use the viewer from the HIPE menu *Window>Show View>Data Access>Herschel Science Archive*. Anything you download directly into HIPE from there will appear in the *Variables* pane of HIPE, and often the command will also be echoed to the *Console*.

After you have done this you can:

- If you loaded your data into HIPE using the first or third method above, then you must save the observation to disk.

If using `getObservation` you can chose two ways to save the data to disk: either to your MyHSA, using the parameter `save=True` in `getObservation` as explained above; or to a pool on disk, using the command `saveObservation`.

To use `saveObservation`:

```
# "myobs" is the name of the ObservationContext
pooln = "NGC3333"
saveObservation(myobs, poolName=pooln)
```

where the observation goes to your **local store** (`HOME/.hcss/lstore`) to a directory (pool) with the name that is either the `obsid` or as it given in `poolName`. The *DAG* does not explain `saveObservation` but it does explain the same parameters of `getObservation`: see sec. 1.7.

Note: if using `saveObservation`, the *ObservationContext* is not saved by default with the calibration tree (calibration files) it was reduced with. If you wish to do that, see Sec. 2.6: you need to set the parameter `saveCalTree=True`, which will save whatever calibration tree is in your *ObservationContext*.

f you used the second method you do not need to save your observation as a pool, you could keep them as they are. If you do want to convert your observation data on disk from the "HSA-format" to the pool format, you can simply use `saveObservation` as in the example above.

- Once the data are saved to this pool with `saveObservation`, on your disk, then any other time you want to access them you should use `getObservation`,

```
obsid = 134..... # enter your obsid here
pooln = "NGC3333"
myobs=getObservation(obsid, poolName=pooln)
```

The *DAG* explains these parameters of `getObservation`: see sec. 1.7 to know how to access the data if they were saved elsewhere than your local store. The command will get the data as located in the local store (`HOME/.hcss/lstore`) and with a directory (pool) name that is either the `obsid` (e.g. "342221212") or the value set by `poolName`. You can also use a GUI to get data, e.g. from your MyHSA: see sec. 1.7 of the *DAG*.

So, to summarise the command-line methods:

```
obsid = 134..... # enter your obsid here

# Direct I
# Get the data from the HSA and then save to
# /Users/me/.hcss/lstore/MyPoolName
myobs=getObservation(obsid, useHsa=True)
saveObservation(myobs, poolName="MyPoolName")
# Then, to later get those data
myobs=getObservation(obsid, poolName="MyPoolName")
#
# Get the data from the HSA and then save to
# /Users/me/.hcss/lstore/[obsid as a string]
myobs=getObservation(obsid, useHsa=True)
saveObservation(myobs)
# Then, to later get those data
```

```

myobs=getObservation(obsid)

# You must be logged on to the HSA for this to work:
# See the DAG sec. 1.4.5.
# See Sec. ??? to learn about saving and then
# restoring the caltree

# Direct II
# Get the data from the HSA and immediately save
# to /Users/me/.hcss/lstore/MyPoolName
myobs=getObservation(obsid, useHsa=True, save=True, poolName="MyPoolName")
# Then to later get those data
myobs=getObservation(obsid, poolName="MyPoolName")

# DIRECT III
# Get the data from the HSA as a tarball
# On disk the data are in directories off of /Users/me/fromHSA
# In HIPE, then
myobsid=1342..... # enter your obsid
mypath="/Users/me/fromHSA/me1342
myobs=getObservation(obsid=myobsid,path=mypath)
obsid = 134..... # enter your obsid here
mypath="/Users/me/fromHSA/me1342
myobs=getObservation(obsid=myobsid,path=mypath)

```

For the GUI-based methods, read chap. 1 of the DAG. For full parameters of `getObservation`, see its URM entry: [here](#). (Note: there are two "getObservation"s in the URM. The one I link you to is the correct one, it is also the first in the URM list.)

1.2.3. Looking at your fully-reduced data

Once the data are in HIPE, the *ObservationContext* will appear in the HIPE Variables panel. To look at the fully-reduced, final Level 2 product (cubes for the spectrometer and images for the photometer) do the following,

- Double-click on your observation (or right-click and select the **Observation Viewer**)
- In the directory-like listing on the left of the Observation viewer (titled "Data"), click on the + next to the "level2"
- *For photometry*: go to HPPMAPB to get the blue map or the HPPMAPR to get the red Naive map. The map will open to the right of the directory-like listing, but if you want to view it in a new window then instead double-click on the "HPPMAPB" (or right-click to select the **Standard Image Viewer**)
- *For spectroscopy*: go to the + next to the HPS3DPR (red *projected* cube) or HPS3DPB (blue *projected* cube) or to the + next to the HPS3DRR (red *rebinned* cube) or HPS3DRB (blue *rebinned* cube)—see e.g. Sec. ??? to know what the difference between these two cubes are (basically, the projected cubes are the result of a mosaicking of the rebinned cubes, and the projected cubes have smaller, but more, spaxels). The list of numbers (+0, +1...) are the individual cubes, one per wavelength range specified in your AOR (observation request) and also one per pointing for the rebinned cubes. The tooltip that appears when you hover over a cube in the listing will help you work out what the contents of that cube is. Click on the number to see the cube open to the right of the directory-like listing, or to see it in a new window, right-click and chose the **Spectrum Explorer** (SE: see the DAG chap. 6). From the SE you can look at the spectra of your spaxels, perform mathematical operations, extract spectra or subcubes, make velocity and flux maps and fit your spectra. (Note, however, that you cannot perform all the mathematical operations if you open the SE from the Observation viewer in this way; you need to drag and drop the cube to the *Variables* pane and open it from there.)

To learn more about the layers of the *ObservationContext* and what the products therein are, see Sec. ???.

1.3. PACS Photometry Launch Pad

The following Help documentation acronyms are used here: **DAG**: the Data Analysis Guide; **PDRG**: PACS Data Reduction Guide.

1.3.1. Does the observation data need re-processing?

The PACS ICC recommend that you always reprocess your data,

- The pipeline tasks and the calibrations are still undergoing improvement and the pipeline that the reduced data you got from the HSA may not have been the most recent
- There are some pipeline stages that for all but the most simple data you ought to inspect the results of the pipeline task yourself, to decide if you wish to change the default parameters

Information about calibration files held in the **calibration tree**:

- When you start HIPE, HIPE will begin by looking for a calibration file update: Sec. 2.5.1.
- To check what version of calibration files and the pipeline your HSA-gotten data were reduced with, and to compare that to the current version and to see what has changed, see Sec. 2.5.4.
- You can also look at the Meta data called calTreeVersion, see Sec. 2.5.4.
- To load the calibration tree into HIPE when you pipeline process, see Sec. 2.5.3.

1.3.2. Re-processing with the pipeline scripts

The subsequent chapter of the *PDRG*, linked to below, cover different pipelines each.

The pipeline script you will run will depend on the observing mode,

- *Chopped point source data*: see Sec. ??? for observations taken in chop-nod photometry mode (an old mode).
- *Bright Point sources*: see Sec. ??? for observations containing bright point sources for single observations, and Sec. ??? to combine multiple observations (usually a scan and cross-scan).
- *Deep survey*: see Sec. 3.2.2 for deep survey observations containing many faint sources for a single observation, and Sec. 3.3 to combine multiple observations (usually a scan and cross-scan).
- *Extended source using high pass filtering and photproject*: see Sec. 3.2.3 for single observations, and Sec. 3.3 to combine multiple observations (usually a scan and cross-scan)
- *Extended sources using MADMap*: see Chap. 5 for observations of extended sources (only use when scan and cross scan data are taken).
- *Mini Scan-map*: see the pipelines for bright, deep or extended sources, whichever your source(s) is(are).
- There is no major difference in the pipeline between point-sources and extended sources for the high-pass filtering+photproject pipeline, only the parameters of the masking task will be different. MADMap is good to use for extended sources.
- The pipeline scripts contain all the pipeline tasks and simple descriptions of what the task are doing. But if you want to know all the details you need to consult the pipeline chapters (links above). Individual pipeline tasks are also described in the *PACS User's Reference Manual (PACS URM)*.
- The pipelines take you from Level 0 (raw) to Level 2 (fully-processed), although in some cases you can just begin from Level 0.5. If a Level 2.5 is done, that means maps have been combined.

To access the scripts, go to the HIPE menu *Pipelines>PACS>Photometer*. The scripts assume:

- The data are already on disk or you can get them from the HSA using `getObservation` (so you must know the Observation ID)
- You have the calibration files on disk; normally you will use the latest update, but you can run with any calibration tree version: see Sec. 2.5.3 to know how to change the version of the calibration tree you are using.
- You chose to do the red or the blue camera separately

To run the scripts,

- Read the instructions at the top, and at least skim-read the entire script before running it
- Although you can run most all in one go, it is *highly* recommended you run line by line at least for the first time
- If you are going to comment within the script or change parameters, then first copy the script to a new, personalised location and work on that one (HIPE menu *File>Save As*): otherwise you are changing the script that comes with your HIPE installation

As you run the scripts,

- Plotting and printing tasks are included with which you can inspect the images and masks themselves. The plots will open as separate windows
- The scripts will save the data into FITS files after each Level (this is a difference with the spectroscopy pipeline)

1.3.3. Considerations when running the pipeline

Considerations concerning the technicalities of running the pipeline are:

- If you chose to run the pipeline remotely or as part of bulk processing you might want to disable the plotting tasks by commenting out the lines starting with "Display(...)"
- **Memory vs speed**: the amount memory you assign to HIPE to run the pipeline depends on how much data you have, but $\geq 4\text{Gb}$ for sure is recommended.

If you wish to fiddle with your data (other than using the plotting tasks provided in the pipeline) it would be a good idea to do that in a separate running of HIPE.

- Save your data at least at the end of each Level, because if HIPE crashes you will lose everything that was held only in memory (the scripts, by default save your data after each Level so **DO NOT** modify that part)

Things to look out for in your data as you run the pipeline are:

- Saturated and Glitched data
- Non-smooth coverage map (the coverage map is not uniform but the transitions should be fairly smooth towards the edges)
- Up and down scan offsets (distorted Point Spread Function)
- Dark spots around bright point sources (sign of inappropriate high-pass filtering)

1.3.4. Further processing

There are a number of tasks that can be used to inspect and analyse your PACS Level 2 images. For a first quick-look inspection (and even for some image manipulation) we recommend the tasks' GUIs.

The tasks are listed in the *Tasks* panel under *Applicable* if the image is highlighted in the *Variables* panel. Double-click on the task will call up its GUI, except for the *Standard Image Viewer* which is invoked by a right-click on the image in the *Variables* panel and selecting *Open with>Standard Image Viewer*

- To simply look at the images you can use the **Standard Image Viewer**: see the *DAG*: note that this section is still being written but you can see the *DAG* sec. 2.2.1.
- # The **annularAperturePhotometry** task: see the *DAG*: note that this section is still being written but you can see the *DAG* sec. 4.12. Performs aperture photometry using simple circular aperture and a sky annulus. There are other aperture photometry tasks: *fixedSky*, *pacsAnnularSky*, *rectangular*.
- # The **sourceExtractorDaophot** and **sourceExtractorSussexextractor**: see the *DAG*: note that this section is still being written but you can see the *DAG* sec. 4.13. Extracts sources from a simple image using different algorithms.
- # The **sourceFitter**: see the *DAG*: note that this section is still being written but you can see the *DAG* sec. 4.14. Fits a 2D Gaussian to a source in a specified rectangular region on an image.

See the image analysis chapter of the **Data Analysis Guide** *chap. 4* for more information on image processing in HIPE.