

# Chapter 1. PACS Launch Pads

## 1.1. Introduction

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 images, and will outline what you need to consider before you start to reduce the data yourself through the pipeline. A complete archive of PACS documentation, from data reduction and product advice, through calibration reports, to highly technical notes, can be found on the Herschel documentation archive: the [HELL](#) pages.

*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).

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 ([herchel.esac.esa.int/twiki/bin/view/Public/PacsCalibrationWed?template=viewprint](https://herchel.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*.

## 1.2. PACS Data Launch Pad

### 1.2.1. Terminology

The following Help documentation acronyms are used here (the names are links): [DAG](#): the Data Analysis Guide; [SG](#), the Scripting 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 is why it is useful to know the class of a product. See the [SG](#) to learn more about classes. Text written like `this` is used to refer to the parameter of a task.

### 1.2.2. Getting and saving PACS observations

Herschel data are stored in the **HSA**.

- They are identified with a unique number known as the Observation ID (**obsid**). You can find the **obsid** via the HSA.
- They can be downloaded directly into HIPE, or one at a time to disc, or many as a tarball.
- The data you get from the HSA is an **Observation Context**, which is a container for all the science data and all the auxiliary and calibration data that are associated with an observation, and includes

the **SPG** products. The entire observations is stored on disk as individual FITS files organised in a layered directory structure. The *ObservationContext* you load into HIPE contains links to all these files, and GUIs are provided to navigate through the layers.

There are several ways to **get and save observations from the HSA or disk** via HIPE. It does not matter which method you use.

- **Get the data directly from the HSA into HIPE on the command line, and then save to disk:**

```
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
# A: to save to the "MyHsa" directory (HOME/.hcss/MyHsa)
myobs = getObservation(obsid, useHsa=True, save=True)
# B: to save to your "local store" (usually HOME/.hcss/lstore)
myobs = getObservation(obsid, useHsa=True)
saveObservation(myobs)
# C: to save to another disk location entirely, use:
pool1 = "/Volumes/BigDisk/"
pooln = "NGC3333"
myobs = getObservation(obsid, useHsa=True)
saveObservation(myobs, poolLocation=pool1, poolName=pooln)
```

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. For full parameters of `getObservation`, see its [URM](#) entry.

- **To get the data back from disk into HIPE:**

*A and B:* If you saved the data to disk with the default name and location (either `[HOME]/.hcss/MyHSA` or `[HOME]/.hcss/lstore`) then you need only specify the `obsid`:

```
obsid = 134..... # enter your obsid here
myobs=getObservation(obsid)
```

*C:* If you used `saveObservation` with a `poolName` and/or `poolLocation` specified:

```
obsid = 134..... # enter your obsid here
pool1 = "/Volumes/BigDisk/"
pooln = "NGC3333"
myobs=getObservation(obsid, poolLocation=pool1, poolName=pooln)
```

To learn about the GUI methods for getting data, see chap. 1 of the [DAG](#).

### 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 (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"
- 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**)
- If there is a "level2\_5" then you can also look at any of the maps in there, these in fact being a combination of level2 maps from related observations, and hence of better sensitivity.

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

## 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?

It is unlikely that you will need to reprocess you data: normally if there is something wrong with the data, (i) there will be a qualitySummary comment discussing that, and (ii) you will be able to see if directly in the images. The final data in the archive have the best possible calibration and for the majority of observations, the JScanam or Unimap maps at Level 2.5 or the maps at Level 2 (where there is no Level 2.5) cannot be bettered: possible exceptions are observations of a field of very low intrinsic SNR or with complex structure, and these may benefit from a personal data reduction.

### 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 and the science target,

- *Chopped point source data*: see Sec. [3.3](#) for observations taken in chop-nod photometry mode (an old mode).
- scan-map and mini scan-map for point sources: *see Sec. [3.2.1](#) for observations containing mainly point sources and small extended sources*
- Extended sources using MADMap: *see Chap. [3.2.2](#) for observations of extended sources (only use when scan and cross scan data are taken).*
- Extended source using JScanam *see Sec. [3.2.3](#) for observations of extended sources (only use when scan and cross scan data are taken).*
- *Extended source using Unimap* see Sec. [3.2.4.2](#) for observations of 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 1 ((calibrated data cubes in Jy/detector pixel)) to Level 2 (fully-processed). 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)

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](#).

### 1.3.3. 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  $\geq 4$ 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*

- If you just want to look at the images you can use the **Standard Image Viewer**: see *Sec 4.4 of the DAG*:
- The **annularAperturePhotometry task**: (see *Sec 4.21 of the DAG*) Performs aperture photometry using simple circular aperture and a sky annulus. There are other aperture photometry tasks: fixed-Sky, pacsAnnularSky, rectangular.
- The **sourceExtractorDaophot and sourceExtractorSussextractor**: (see *Sec 4.19 of the DAG*) Extracts sources from a simple image using different algorithms.
- The **sourceFitter**: (see *Sec 4.20 of the DAG*) 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.