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VERY LARGE TELESCOPE

SPHERE ZIMPOL Imaging EDPS-GUI tutorial

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Issue 1

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1 Introduction

1.1 Scope

This document describes how to reduce SPHERE ZIMPOL Imaging data with the `edps-gui` (Graphic User Interface), the dashboard of the ESO Data Processing System (EDPS), which is the recommended interface to reduce data from ESO telescopes. Details on the SPHERE ZIMPOL Imaging data reduction stream and how to configure the reduction to meet specific scientific needs are also given.

For a more extensive documentation on the `edps-gui` itself, consult the dedicated manual [here](#).

For a description of the SPHERE ZIMPOL Imaging pipeline itself, consult the pipeline manual available at: https://www.eso.org/sci/software/pipe_aem_table.html.

Note: this tutorial refers to:

- SPHERE ZIMPOL Imaging instrument pipeline named `zpl-img`, version 0.59.1.
- SPHERE ZIMPOL Imaging workflow: `sphere.sphere_zimpol_imaging_wkf`
- EDPS version 1.6.0.
- `edps-gui` version 0.91.

1.2 What is EDPS?

The ESO Data Processing System (EDPS) is a framework to run ESO's data processing pipelines and it is meant to eventually replace the previous [ESOReflex environment](#). The general principles of EDPS have been described by [Freudling, Zampieri, Coccato et al. \[2024, A&A, 681, A93\]](#). Please refer to that paper if you have used EDPS for research resulting in a scientific publication.

Each of ESO's data processing pipeline consists of a series of standalone programs called *recipes*. Each recipe is designed to process certain type(s) of input data. The processing of these input data typically requires a range of auxiliary files such as calibration files. EDPS is designed to select appropriate input data for the different recipes of a pipeline, and execute them in sequence. This is done by specifying for each pipeline the workflow for organizing data and executing the recipes. Then, the workflow can be used to process a set of data fully automatically.

1.3 Main concepts

EDPS is an environment designed to execute the recipes of an instrument pipeline according to a series of instructions. The main concepts in EDPS are:

- **Workflow and reduction cascades.** A workflow is a series of instructions designed to reduce data with an instrument pipeline in potentially multiple ways, by carrying on a sequence of tasks. Each workflow can define multiple reduction cascades, depending on the scientific needs. For example, the same workflow

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can be used to process data following different strategies that trigger different reduction steps (e.g. in one strategy flux calibration can be omitted) or different end-points (e.g., combine different science exposures, or stop after the reduction of individual exposures without combining them). Each of these "strategies" defines a "reduction cascade".

- **Task, jobs, and recipes.** A task is an element in the workflow that performs a given step of the data reduction cascade. Tasks are often associated to a recipe of the underlying instrument pipeline. A job is a work unit in a processing environment, that runs a recipe on a set of input data with a set of recipe parameters. A single task can generate several jobs: for example, a "bias" task, can generate multiple jobs, each of the running the bias recipe on a different set of input files.
- **Dataset.** A dataset is a collection of files, that are needed to perform the data reduction as specified by the workflow. It consists, for example, of one or more science files plus the calibrations needed to process them. In EDPS, datasets have a hierarchical structure, which highlights the connections between the various files and tasks (e.g., task A is an input to task B).
- **Target and Target category.** The "target", or the "target task" is the end point of the reduction cascade. When specifying a target, EDPS will process all and only the files needed to execute it. For example, if my target is "science", and the science files need the bias files, EDPS will process only the biases that have been selected to process those science files; then it processes the science using the product of the bias reduction. However, if my target is bias, then EDPS will process all and only the bias files, regardless they are not used by any science. In this case, EDPS does not process the science, as it has already reached the end reduction point (e.g., process all biases). The "Target category" is a group of targets that have similar purposes. For example, the target category "science", includes all the tasks that deliver final scientific products, the target category "qc1calib" includes all and only the tasks that processes calibrations (e.g., bias, flat fields, standard stars).

1.4 Installation

1.4.1 Prerequisites

Prerequisites for a well functioning installation of EDPS and EDPS-gui are:

- Recent Firefox or Chrome browser, Python 3.11 or higher (but there are issues with Python 3.14).
- At least one ESO pipeline with EDPS workflow should be in your system. To install the desired ESO pipelines, follow the instructions in the ESO pipelines pages. NOTE: the `apptainer` installation method is currently not supported. After the installation, the `esorex` command must be in the path. To test whether the installation was successful, type

```
esorex --recipes
```

A list of available recipes should appear.

- Install `graphviz`, `fv`, and `ds9`, which have to be included in the system path (defining aliases not enough). On linux, `Graphviz` can be easily installed via:

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```
sudo apt install graphviz (Debian, Ubuntu)
sudo dnf install graphviz (Fedora)
```

Check the [Graphviz webpage](#) for installation instructions for other OS.

`fv` and `ds9`, are optional. To install them, follow the instructions in corresponding webpages. You can test whether these three packages are installed and their paths are correctly set by typing on a terminal:

```
dot -V
fv -version
ds9 -version
```

1.4.2 Installation steps

To install EDPS follow these steps:

- Create a new Python virtual environment and activate it:

```
python3 -m venv edpsgui
. edpsgui/bin/activate
```

Make sure the `python3` version is 3.11 or higher, but not 3.14.

- Install the required packages:

```
pip install --extra-index-url \
  https://ftp.eso.org/pub/dfs/pipelines/repositories/stable/src \
  edps edpsgui edpsplot adari_core
```

To run the `edps-gui` type from a terminal (with the active environment):

```
edps-gui
```

Important note. The first time `edps-gui` is executed, you will be asked to specify the directory where the reduction products (fits files and quality plots) will be stored. The default location is `$HOME/EDPS_data`. During the first execution, a configuration file named `application.properties` will also be saved in the directory (newly created) `$HOME/.edps`.

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2 Reducing demo data

Follow this procedure to quickly reduce SPHERE ZIMPOL Imaging demo data. We assume that the EDPS, `edps-gui`, the SPHERE ZIMPOL Imaging pipeline and its associated demo data are installed in your system. For general instructions on how to install EDPS and the pipeline, see Section 1.4 or please visit: <https://www.eso.org/sci/soft>

2.1 Setting the workflow

Proceed as follows:

1. If not done already, activate the EDPS virtual environment, defined during installation (Sect. 1.4).
2. Start the `edps-gui` dashboard by typing:

```
edps-gui
```

The `edps-gui` dashboard will start in a browser window (Figure 1).

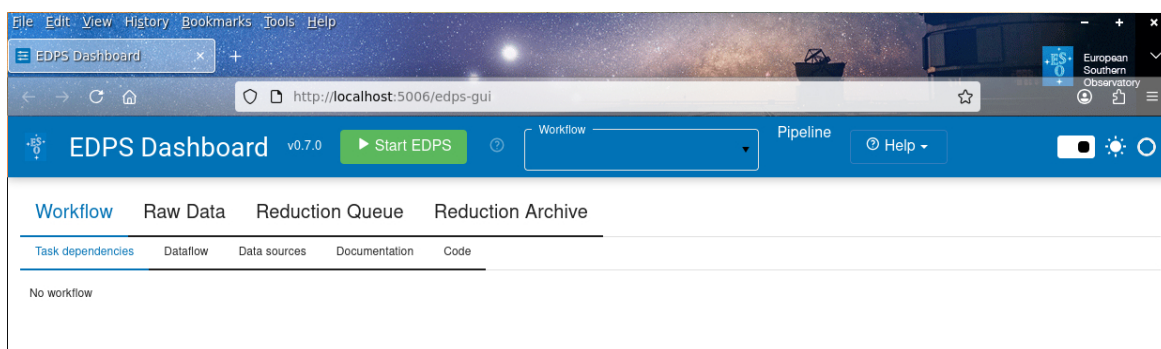


Figure 1: The empty `edps-gui` Dashboard; the underlying EDPS engine has not yet been started and no workflow has been loaded.

3. Optionally, before starting EDPS, one can specify new settings by pressing Help → Settings (Figure 2).

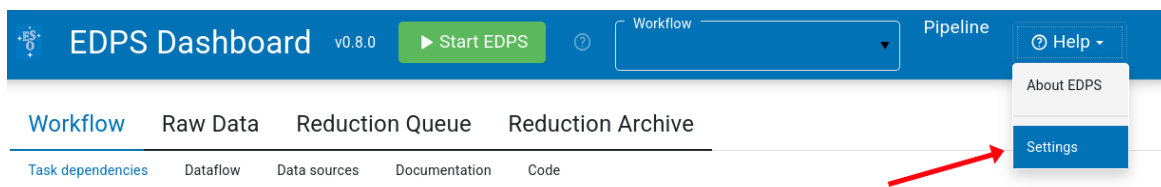


Figure 2: The “Help” → “Settings” menu.

4. On the browser window with the dashboard, press the button ‘Start EDPS’.
5. Choose the `sphere.sphere_zimpol_imaging_wkf` workflow from the list in the ‘Workflow’ field. The workflows offered in this selector depend on the installed pipelines. The graphic workflow representation will appear as in Figure 4.

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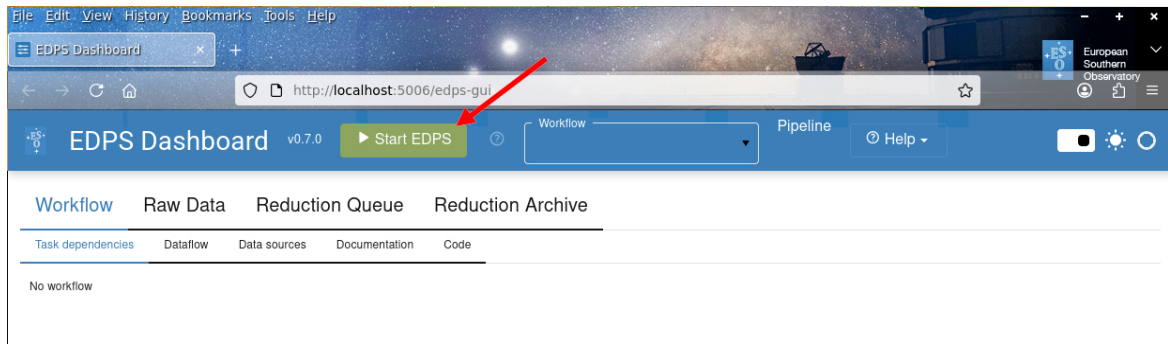


Figure 3: The “Start EDPS” button.

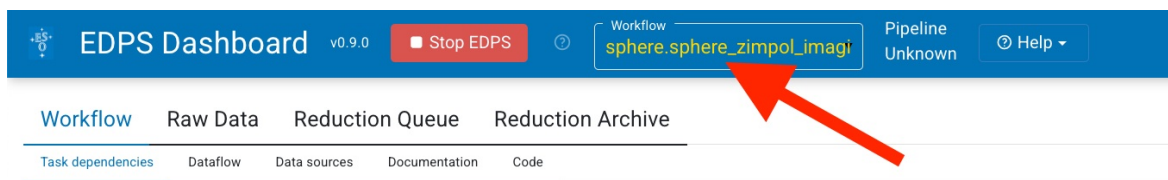


Figure 4: The edps-gui with the SPHERE ZIMPOL Imaging workflow loaded.

2.2 Selecting the input data

1. Press ‘Raw Data’ to enter the corresponding tab, as in Figure 5.

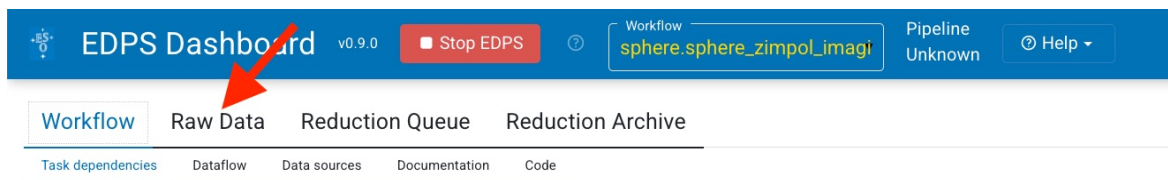


Figure 5: How to select RAW data Tab.

2. Press ‘Select Inputs’. A selection window will appear that allows to select data that are stored on a local disk (Figure 6).
3. (Optional). Select the reduction target, configure the workflow parameter and specify the association preferences. These steps are optional. For more information see Section ??.
4. Press ‘Create Datasets’. A list of datasets appears, one line for each set of science data (Figure 7).
5. Choose the datasets that should be processed (Figure 8) and send them to the data reduction queue by pressing ‘Submit to Reduction Queue’. Note that this action does not start the reduction automatically.

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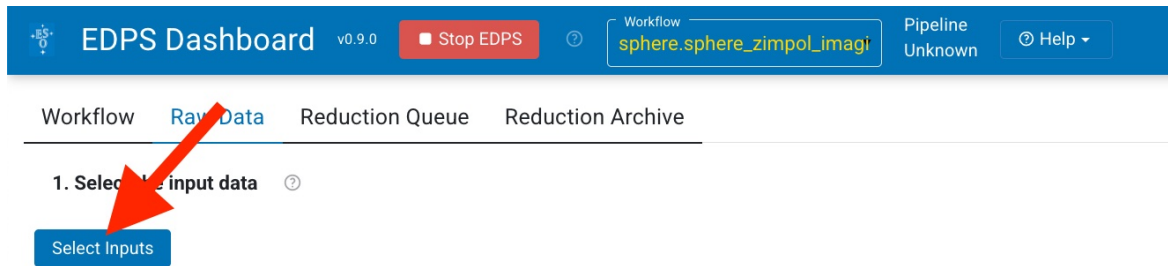


Figure 6: How to select input data.

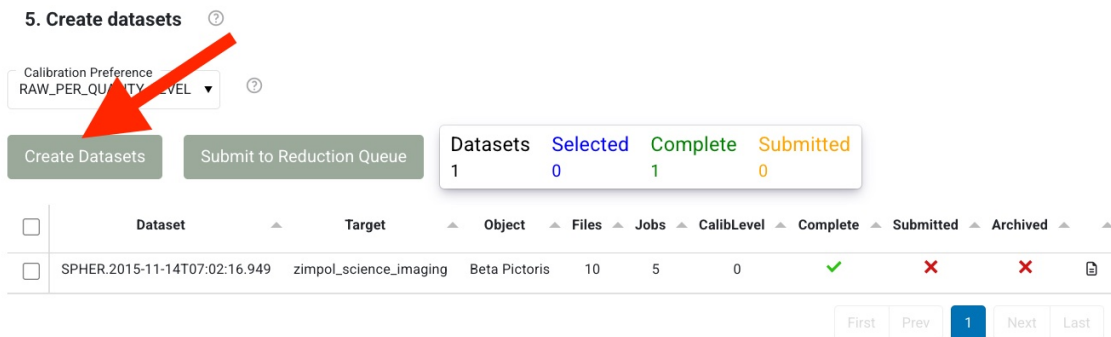


Figure 7: How to inspect the input data directory to create datasets.

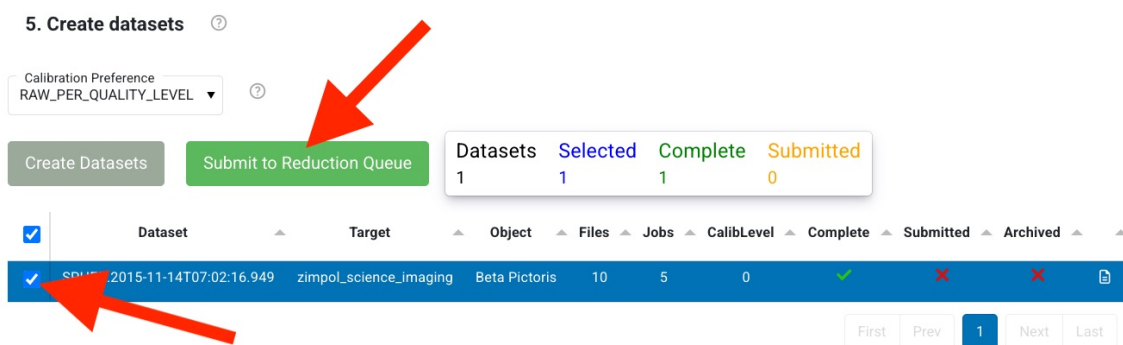



Figure 8: How to send the selected datasets to the Reduction Queue for processing.

2.3 Start the reduction

1. Press the 'Reduction Queue' tab (Figure 9).
2. Select the datasets you'd like to reduce.

3. (Optional). Configure the workflow and recipe parameters by pressing the wheel button  to open the

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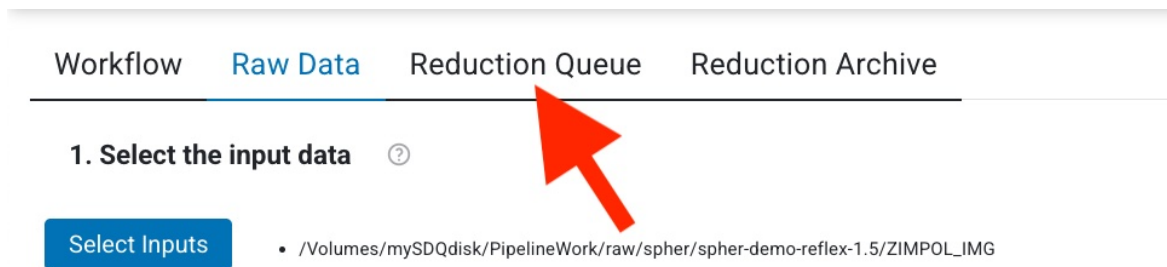


Figure 9: How to select Reduction Queue tab.

configuration editor. See Section 4.2 for more information on the configuration editor.

4. Press the 'Reduce' button (Figure 10). The selected data will now be processed with the configured parameters.

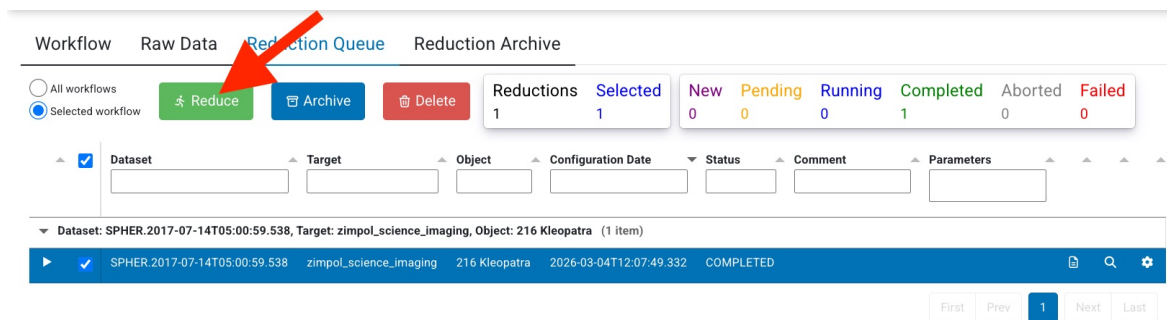


Figure 10: Reduce.

Congratulations! You reduced your first data with the EDPS dashboard! All the reduced data are saved in the EDPS_data directory specified when executing `edps-gui` for the first time.

2.3.1 Quality plots

It is possible to inspect the information on each job, such as quality plots showing the products (for the most important jobs and products), the list of inputs and output files, the recipe parameters and logs. All the information on the job processing can be inspected from the 'Reduction Queue' window. While quality plots are produced only for completed jobs, the other relevant information is available also for failed jobs.

The information associated for the main product can be inspected by pressing the magnifying glass symbol at the right side of each dataset. To inspect the information associated to other individual jobs (e.g., calibrations), proceed as follows:

- Expand the desired dataset by pressing the black arrow on its left. The list of jobs will appear with the associated status (COMPLETED, RUNNING, PENDING, MISSING, ABORTED, FAILED)

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- Press the magnifying glass symbol at the right side of the job you want to inspect.

Figure 11: How to look for job information from the Reduction Queue tab.

2.4 Exporting the final products

Completed reductions can be 'Archived' (i.e. declared 'completed' because no more work is needed) and removed from the Reduction Queue. Additionally, even if all products for all tasks are saved in the EDPS_data directory, the most important products can be 'exported' to a desired location.

To do so, proceed as follows:

1. In the 'Reduction Queue' tab, select the dataset and the dataset for which you want to export the final products, and press the 'Archive' button.
2. Go in the Reduction Archive tab and click on the 'Export' button. A new tab window appears where you can indicate the directory you want to copy your final products; finally press "Export" to copy the data.

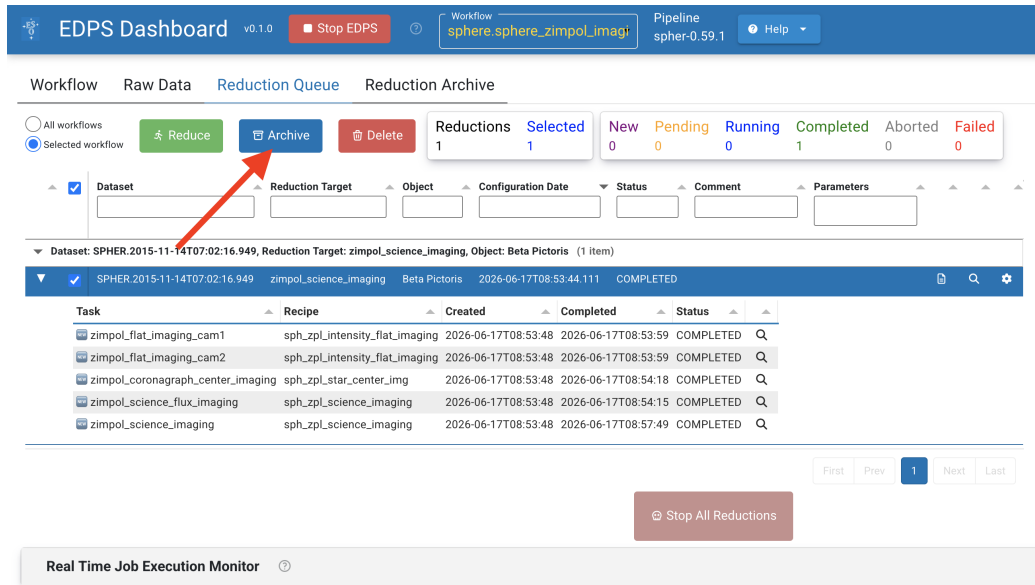


Figure 12: How to archive a completed reduction from the Reduction Queue tab.

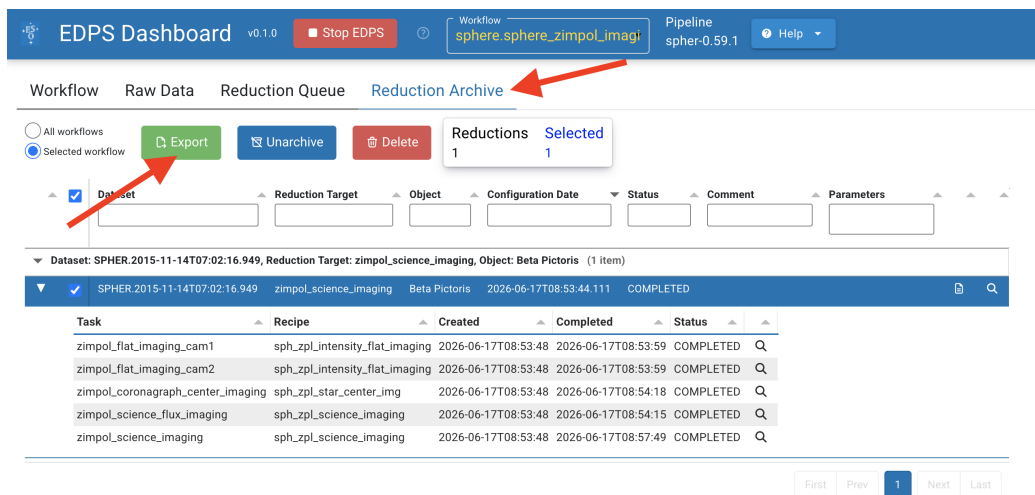


Figure 13: The reduction archive tab. This table contains all the different configurations of datasets that are declared "finished" and removed from the Reduction Queue. From this page, the user can export the most important files into a desired local directory.

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Selected reductions

Dataset ▲	Configuration Date ▲	Status ▲	Parameters ▲
▼ Dataset: SPHER.2015-11-14T07:02:16.949 (1 item)			
SPHER.2015-11-14T07:02:16.949	2026-06-17T08:53:44.111	COMPLETED	

Export all selected reductions
 Export the latest reduction for each selected dataset

Output directory

Figure 14: The EXPORT dialogue window, where the user can decide which reduced configuration to save and where.

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Exported products are organized by ‘DATASET’ (named as the first scientific exposure of the dataset), and ‘TIMESTAMP’ (time of start of reduction).

The final products saved in the specified directory are the reduced and combined images from the two ZIMPOL cameras, with name format ZIMPOL_ followed by the observing mode (IMAGE_), camera number (CAM1_ or CAM2_), and archive file name (corresponding to header keyword ARCFIELD). Each file contains eight FITS extensions. The first four correspond to the combined science intensity image and include the science image itself, a bad-pixel map, a number-of-combined-frames (ncomb) map, and an RMS map. The remaining four extensions contain the combined dark-current image together with its associated bad-pixel map, ncomb map, and RMS map.

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3 The SPHERE ZIMPOL Imaging data reduction flow.

The overall data flow of the SPHERE ZIMPOL Imaging pipeline is displayed in Figure 15.

The reduction cascade is organized in tasks, which represent well-defined steps in the process. Tasks can be grouped inside sub-workflows. Each task runs a recipe; the detailed description of the algorithms, input, outputs and recipe parameters used in each recipe are available in the pipeline manual. Here, we present only the description of most important features.

The EDPS workflow is designed to execute the tasks that deliver the final reduced data for each dataset. It can be either the product of a single exposure, or the combination of multiple exposures. Only calibrations needed by the selected scientific exposures are processed.

It is possible to set EDPS to perform the data reduction until a certain step of the reduction chain (e.g. to reduce only standard stars, or only flat fields). This is done by specifying the desired tasks in the field **Select reduction target** of the **Raw Data** tab.

The reduction steps of the workflow are listed below. Before starting the reduction, the parameters of the recipes associated to each task can be configured by pressing the button  close to each dataset configuration. See Section 4 for more information.

The reduction steps are:

3.1 Subworkflow Internal Calibrations Imaging

Recipes:

`sph_zpl_intensity_flat_imaging`

`sph_zpl_master_dark_imaging`

`sph_zpl_master_bias_imaging`

This subworkflow generates the camera master flats, the master dark and bias. It consists of the following tasks:

- **zimpol_flat_imaging_cam2**: uses `sph_zpl_intensity_flat_imaging` to produce intensity flat-field calibration frames for camera 2.
- **zimpol_flat_imaging_cam1**: uses `sph_zpl_intensity_flat_imaging` to produce intensity flat-field calibration frames for camera 1.
- **zimpol_dark_imaging**: uses `sph_zpl_master_dark_imaging` to generate master dark calibration frames.
- **zimpol_bias_imaging**: uses `sph_zpl_master_bias_imaging` to produce the master bias calibration frame.

Each time, the calibration (flat, dark or bias) is generated separately for the odd (informative) and even (dark current) ZIMPOL sub-frames and stored in a DOUBLE IMAGE FITS format. Inputs can be raw frames, or

SPHERE ZIMPOL imaging workflow

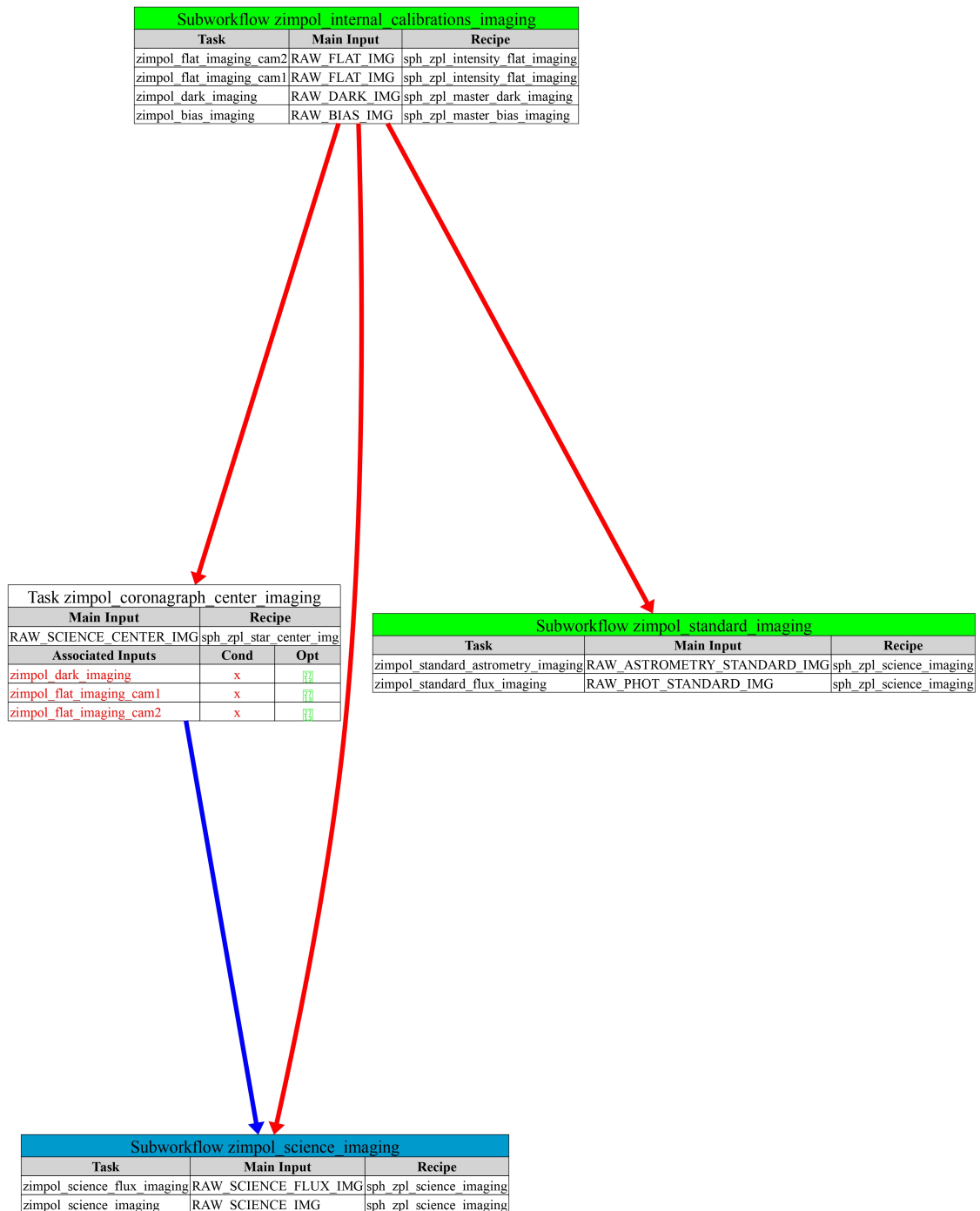


Figure 15: The data reduction cascade of the SPHERE ZIMPOL Imaging workflow.

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pre-processed frames. If raw frames are provided, a pre-processing step on the raw cubes is performed with `sph_zpl_preproc_imaging` to generate pre-processed frames. Outputs include the master calibration (flat, dark or bias), as well as a bad-pixel map, a number-of-combined (ncomb) frames map, and an RMS map.

In practice, bias and darks are rarely used in the current workflow:

- Bias frames are used only for Fast Polarimetry readout mode (`DET.READ.CURNAME = FastPolarimetry`).
- Dark frames are used only for long exposures, defined as `EXPTIME > 30 s`.

Customization

Recipe parameters:

- `zpl.intensity_flat.coll_alg`: collapse algorithm (0 = Mean, 1 = Median; default, 2 = Clean Mean).

3.2 Coronagraph Center

Recipe: `sph_zpl_star_center_img`

The task **zimpol_coronagraph_center_imaging** executes the pipeline recipe to determine the stellar center position behind the coronagraph and produce a table of frame centers. If raw frames are provided, a pre-processing step on the raw cubes is performed with `sph_zpl_preproc_imaging` to generate pre-processed frames.

The combined images are analyzed with an aperture detection algorithm that identifies bright regions (e.g., waffle satellite spots or a single star) and computes their geometric center, which defines the frame center. The resulting center coordinates are stored in the FITS header.

Customization

Recipe parameters:

- `zpl.star_center.coll_alg`: collapse algorithm (0 = Mean; default, 1 = Median, 2 = Clean Mean).
- `zpl.star_center.sigma`: the sigma threshold for source detection (default = 10.0).
- `zpl.star_center.save_interprod`: enable to produce a field center table containing the calculated center positions (default = FALSE).

3.3 Subworkflow Standard Imaging

Recipe: `sph_zpl_science_imaging`

This subworkflow processes imaging standard-star observations used for calibration and monitoring of the ZIMPOL imaging mode. It reduces observations of astrometric and photometric (flux) standard stars to verify the instrument's astrometric and photometric performance.

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Two tasks are executed:

- **zimpol_standard_astrometry_imaging**: Processes observations of astrometric standard fields to assess the astrometric calibration, including the plate scale and detector orientation.
- **zimpol_standard_flux_imaging**: Processes observations of photometric standard stars to monitor the photometric response of the instrument.

Both tasks run the corresponding imaging pipeline recipes and may use available calibration products such as master dark frames and intensity flat fields. These calibrations are optional, as the pipeline can process the data without them.

The resulting products are used primarily for quality control and instrument monitoring (qc0, qc1calib, calchecker) and are not required for the reduction of science imaging observations.

Customization

Recipe parameters:

- `zpl.science_imaging.coll_alg`: collapse algorithm (0 = Mean; default, 1 = Median, 2 = Clean Mean).
- `zpl.imaging.save_interprod`: enable to produce a field center table containing the calculated center positions (default = FALSE).

3.4 Subworkflow Science Imaging

Recipe: `sph_zpl_science_imaging`

The task **zimpol_science_flux_imaging** uses the pipeline recipe to reduce and combine science frames. Optional calibration inputs include master bias, master dark, and intensity flat-field frames for each camera. If raw frames are provided, a pre-processing step on the raw cubes is performed with `sph_zpl_preproc_imaging` to generate pre-processed frames.

The pre-processed science frames are then calibrated by subtracting the master bias and master dark frames and dividing by the appropriate flat field, if available.

The calibrated frames are subsequently de-dithered and de-rotated, and saved as intermediate products. The center of rotation is taken from the star-center calibration frames (`SPH_ZPL_TAG_STAR_CENTER_IMG_CALIB_CAM*/2`) when available; otherwise, the geometric center of the frame (`xc=512, yc=512`) is used.

In the final step, all calibrated, de-dithered, and de-rotated frames are combined using a mean algorithm. The resulting products for each camera are written in DOUBLE IMAGE format (8 FITS extensions), containing:

- a combined science intensity image, bad-pixel map, ncomb frames map, and RMS map;
- a combined dark-current image, with corresponding bad-pixel map, ncomb map, and RMS map.

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These outputs constitute the final reduced science products for both ZIMPOL cameras.

For point sources, the recipe can also estimate the Strehl ratio if a filter-table calibration frame is available. When successful, Strehl-related quality-control parameters are written into the product headers.

Customization

Recipe parameters:

- `zpl.science_imaging.coll_alg`: collapse algorithm (0 = Mean; default, 1 = Median, 2 = Clean Mean).
- `zpl.imaging.save_interprod`: enable to produce a field center table containing the calculated center positions (default = FALSE).

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4 Overview of all the data reduction configuration options

4.1 Selection of most appropriate calibrations

By default, EDPS associates raw calibrations to the reduction process. It is also possible to use pre-processed calibrations (a.k.a. master calibrations) if available, in order to speed up the reduction. The preference can be specified in the Raw Data tab, before creating the datasets.

Possible values of the Calibration Preferences are:

- **raw_per_quality_level:** At equal quality of reduction, association of raw calibrations is preferred. This is the default.
- **master_per_quality_level:** At equal quality of reduction, association of master calibrations is preferred.
- **raw:** Association of raw calibration is preferred, despite the quality of results.
- **master:** Association of master calibration is preferred, despite the quality of results.

When master calibrations are used, the reduction step needed to process raw calibrations are not executed. The reduction then moves directly to the process of scientific exposures.

For example, if reduction speed for a quick check is preferred over a high quality reduction, one can select "master". In this case, old master calibrations are associated even if there are raw calibrations closer in time (and therefore more likely to ensure better quality products).

The quality level that the selected calibrations deliver is indicated close to each dataset in the 'Raw input' tab, under the column 'CalibLevel'. CalibLevel=0 indicates that calibrations that follow the rules of the instrument calibration plans have been selected. The higher the number, the poorer the quality of the products.

4.2 Configuration of parameters: the configuration editor

The data reduction of each dataset can be configured according to the scientific needs using an appropriate configuration editor.

The EDPS workflows contain two types of parameters and they both have default values that can be modified to improve the data reduction.


- **Workflow parameters** (for some workflows only) are global and they are applied to the entire workflow. They are accessible both in the 'Raw Data' tab, prior to the creation of a dataset, and in the 'Reduction Configuration' editor, in the 'Reduction queue' tab. Note: some workflow parameters were already configured before creating the dataset and sending it to the reduction queue. Here, they can be changed again. Please, note that the parameters have an effect only on the files that are already in the dataset. If one specifies a parameter that should include extra files in the dataset (e.g., the inclusion of more calibrations), files are not added and the reduction might fail. If you need to change a parameter that modifies the dataset content, please go back to the Raw data tab and create a new dataset.

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- **Recipe parameters** are specific to the individual recipes and can be configured per task. They are accessible in the ‘Reduction Configuration’ editor, in the ‘Reduction queue’ tab.

This editor allows to configure the data reduction for a given dataset by specifying workflow and recipe parameters.

Note: some workflow parameters were already configured before creating the dataset and sending it to the reduction queue. Here, they can be changed again. Please, note that the parameters have an effect only on the files that are already in the dataset. If one specifies a parameter that should include extra files in the dataset (e.g., the inclusion of more calibrations), files are not added and the reduction might fail. If you need to change a parameter that modifies the dataset content, please go back to the Raw data tab and create a new dataset.

To open the editor, click on the wheel button  next to the dataset you desire to configure the reduction for. A window with the configuration editor appears as shown Figure 16.

×

Dataset Configuration Editor

Current Configuration ? ^

<input checked="" type="checkbox"/> Dataset	Target	Object	Configuration Date	Status
<input checked="" type="checkbox"/> SPHER.2015-11-14T07:02:16.949	zimpol_science_imaging	Beta Pictoris	2026-06-17T08:53:44.111	COMPLETED

Other Configurations ? v

Comment ? v

Parameters ? v

Figure 16: The Reduction Configuration editor. It contains 4 sections, that indicate the current configuration, list of other configurations to set, comments to insert, and the parameters to modify.

The editor is divided into 4 parts, which can be accessed pressing the corresponding expansion arrow.

- **Current configuration.** It indicates the name of the selected configuration for a given dataset (Figure 17).
- **Other configurations.** It allows to specify other configurations, to which the changes shall be copied to (Figure 18).
- **Comment.** It allows to specify a comment to describe the configuration. It is possible to append or replace a comment (Figure 19). Comments can be changed on all configurations. It is possible to save the comment for the current configuration only, or for all the selected configurations.

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- **Parameters.** A window as in Figure 20 appears.

The window allows to:

- Select the parameter set. A pre-determined list of workflow parameters and recipe parameters for a given use case. For the majority of the cases, the "science" parameter set can be used.
- Edit the workflow parameters. These are parameters that regulates the reduction strategy, e.g. whether to use a given calibration or not, or to trigger a certain reduction step. Note that if the changes imply that some files not in the dataset are needed, the reduction might fail. In case, go back to the raw data tab, edit the workflow parameters there, and recreate the datasets.
- Edit the recipe parameters. These are parameters associated to the recipe of a given task. Note: the same recipe parameters can be configured differently for the tasks that run the same recipe. Default parameters are shown (albeit some parameters can be dynamic, e.g. 'EDPS' changes their value depending on the type of input data).

Change the values according to the needs and then select whether to save it to the current or the selected configurations. Note, complete configurations cannot be modified, new configurations will be automatically created instead.

<input checked="" type="checkbox"/> Dataset	Target	Object	Configuration Date	Status
<input checked="" type="checkbox"/> SPHER.2015-11-14T07:02:16.949	zimpol_science_imaging	Beta Pictoris	2026-06-17T08:53:44.111	COMPLETED

Figure 17: The first part of the Reduction Configuration Editor, that indicates the selected configuration.

Other Configurations ?

<input type="checkbox"/> Dataset	Target	Object	Configuration Date	Status
▼ Dataset: SPHER.2018-12-23T07:18:33.119, Target: zimpol_science_p1, Object: CS Cha (1 item)				
<input type="checkbox"/> SPHER.2018-12-23T07:18:33.119	zimpol_science_p1	CS Cha	2026-03-05T14:12:51.534	COMPLETED
▼ Dataset: SPHER.2024-06-07T08:08:48.228, Target: zimpol_science_p2, Object: 16_Psyche (1 item)				
<input type="checkbox"/> SPHER.2024-06-07T08:08:48.228	zimpol_science_p2	16_Psyche	2026-03-05T09:45:53.067	COMPLETED

Figure 18: The second part of the Reduction Configuration Editor, that indicates other configurations for which we'd like to apply the changes.

4.3 Troubleshooting

This section provides guidance for diagnosing and resolving common issues encountered during the SPHERE-ZIMPOL Imaging data-reduction cascade.

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Comment ⓘ

Comment

This is a comment about the reduction|

append
 replace ⓘ

Figure 19: The third part of the Reduction Configuration Editor, that allows to specify a comment to the selected configurations.

Recipe parameters

Task

zimpol_coronagraph_cente ▾

Parameter	Default value	Custom value
zpl.star_center_img.outfilename	zpl_star_center_img.fits	
zpl.star_center_img.outfilename_cam1	zpl_star_center_img_cam1.fits	
zpl.star_center_img.outfilename_cam2	zpl_star_center_img_cam2.fits	
zpl.science_p1.subtract_overscan	True	
zpl.star_center_img.coll_alg	0	
zpl.star_center_img.filter_radius	0.0	
zpl.star_center_img.sigma	10.0	
zpl.star_center_img.unsharp_window	4	
zpl.star_center_img.keep_intermediate	False	
zpl.star_center_img.save_interprod	False	
zpl.preproc.outfilename_cam1	preproc_cam1.fits	
zpl.preproc.outfilename_cam2	preproc_cam2.fits	

Figure 20: The fourth part of the Reduction Configuration Editor, that allows to specify the parameters sets and the recipe parameter per task. These settings can be applied to the "Selected Configuration" (Fig. 17) or to the "Other Configurations" (Fig. 18).

4.3.1 Image Incorrectly Rotated / Signal Smeared out

The task **zimpol_coronagraph_center_imaging** uses the instrument pipeline recipe `sph_zpl_star_center_img` to identify waffle spots and determine the position of the target behind the coronagraph. In some cases the detection threshold of 10σ is too high and the recipe cannot identify the target's position. In such a case the science recipe (`sph_zpl_science_imaging`) will rotate the frames around an incorrect position which will smear out the signal. If you see such behaviour you may try to reduce `star_center_img.sigma` to 5.

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5 List of workflow tasks

This is the list of all the tasks and associated recipes in the SPHERE ZIMPOL Imaging workflow. Only some of them are needed for scientific reduction, they are indicated by the flag “yes” (triggered by default) or “optional” (triggered only if requested by a workflow parameter). Other tasks are not used for scientific reduction (they are indicated by the flag “no”), they are mainly used for instrument monitoring and they can be executed only by specifying them as target. Note that, when a task is specified as target, all the tasks that generate the calibrations needed for it are automatically executed.

TASK	RECIPE	Used in science reduction	Notes
zimpol_bias_imaging	sph_zpl_master_bias_imaging	no	Creates master bias for both cameras.
zimpol_dark_imaging	sph_zpl_master_dark_imaging	optional	Produces master dark for both cameras.
zimpol_flat_imaging_cam1	sph_zpl_intensity_flat_imaging	optional	Generates intensity flat-field for camera 1.
zimpol_flat_imaging_cam2	sph_zpl_intensity_flat_imaging	optional	Generates intensity flat-field for camera 2.
zimpol_standard_astrometry_imaging	sph_zpl_science_imaging	optional	Reduces astrometric standard-field observations.
zimpol_standard_flux_imaging	sph_zpl_science_imaging	no	Reduces photometric standard-star observations.
zimpol_coronagraph_center_imaging	sph_zpl_star_center_img	optional	Determines stellar position behind the coronagraph.
zimpol_science_flux_imaging	sph_zpl_science_imaging	optional	Reduces off-axis flux frames.
zimpol_science_imaging	sph_zpl_science_imaging	yes	Reduces ZIMPOL imaging science.

Table 1: SPHERE ZIMPOL Imaging pipeline tasks overview

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6 Frequently Asked Questions

- **Q1) Where can I find the final reduced data?**

Answer: all the products of all the datasets and the reductions are saved into the EDPS_data directory, specified when executing the edps-gui for the first time. One can decide to export only the final products for selected datasets and only for the desired reduction attempts into another location for further analysis. See Section 2.4 for further instructions.

- **Q2) How do I stop the application?**

Answer: Proceed as follows:

1. Press “Stop EDPS” in the Dashboard.
2. Type Ctrl-C in the terminal where the application is running. If the application doesn’t terminate, type Ctrl-C again.
3. Alternatively, kill the ‘panel serve’ process on your system, for example:

```
ps -e | grep panel # get the process ID of the gui (<pid>).
kill -9 <pid>
```

- **Q3) I have closed the browser window where the application is running. How can I reopen the application?**

Answer: Point your browser to: `http://localhost:5006/edps-gui`

- **Q4) Where can I find some data that I can use to test the application?**

Answer: Install the ‘datademo’ package provided with the pipeline installation or download the “Demo Data” package from https://www.eso.org/sci/software/pipe_aem_table.html.

Please note that the demo data can be large (tens of Gigabytes).

A convenient script to download demo data for any pipeline is also available and can be used from the command line:

```
curl -O https://eso.org/sci/software/apptainer/eso_download_demodata.sh
bash ./eso_download_demodata.sh
```

- **Q5) How can I start the edps-gui if the following message appears?**

```
Cannot start Bokeh server, port 5006 is already in use
```

Answer: The panel server was not closed properly. Kill it by typing:

```
ps -e | grep panel # get the process ID of the gui (<pid>).
kill -9 <pid>
```

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- **Q6) How do I get additional support on EDPS or data reduction in general?**

Answer: For suggestions, questions, or feedback in general, please open a ticket with the EDPS Support team. This https://support.eso.org/new-ticket?ticket%5Bticket_field_13%5D%5Bdata%5D=227 should take you directly to a webpage for creating and EDPS feedback ticket, but in case you want to navigate there 'manually', go to <https://support.eso.org>, login, click on "Submit Helpdesk Ticket", and specify the Help topic: "Post Observations", "ESO Data Processing System [EDPS]".

- **Q7) I have a lot of disk space, but when I install EDPS with pip or an ESO pipeline with Homebrew I get the error message: Cannot mkdir: No space left on device. How do I fix it?**

Answer: This depends on how much disk space is allocated to the /home, /var, and /tmp directories. The final solution would be to resize the space allocated to the in the organization of the filesystem. However, we list here few tricks that might do the job.

- Clearing the pip .cache to make space for new packages. Type the command:

```
pip cache purge
```

before installing EDPS.

- Redirect the cache, Homebrew temporary build directories into a partition with enough space. Set some of the following environmental variables in your .bashrc file:

```
export HOMEBREW_CACHE=<path_to_new_cache_directory>
export XDG_CACHE_HOME=<path_to_new_cache_directory>
export HOMEBREW_TEMP=<path_to_new_temporary_directory>
export TMPDIR=<path_to_new_temporary_directory>
```

The first moves only the location of Homebrew cache, the second the cache of most applications (instead of the default /home/username/.cache), the third moves the directory where Homebrew builds, extracts, and saves temporary files (instead of the defaults /tmp and /var/tmp). The last changes the global system temporary directory and affects most of the linux commands.

- As extreme measure, one can move the /home/linuxbrew/.linuxbrew directory somewhere else, and create a symbolic link in /home/linuxbrew. For example:

```
cd /home/linuxbrew
mv -f .linuxbrew <path_to_new_directory>
ln -s <path_to_new_directory> .linuxbrew
```

Important note: this operation might break some internal links. Recipes requiring external packages such as telluriccorr might not work (impacts on KMOS, XSHOOTER, FORS2, and MOLECFIT pipelines).