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## VERY LARGE TELESCOPE

### Reflex GRAVITY Tutorial and Coobook

VLT-MAN-ESO-19500-....

Issue 1.2.1

Date 2018-11-01

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## 1 Introduction And Scope

Reflex is the ESO Recipe Flexible Execution Workbench, an environment to run ESO VLT pipelines which employs a workflow engine to provide a real-time visual representation of a data reduction cascade, called a workflow, which can be easily understood by most astronomers. The basic philosophy and concepts of Reflex have been discussed by Freudling et al. (2013A&A...559A..96F). Please reference this article if you use Reflex in a scientific publication.

Reflex and the data reduction workflows have been developed by ESO and instrument consortia and they are fully supported. If you have any issue, please contact [usd-help@eso.org](mailto:usd-help@eso.org) for further support.

This document is a tutorial designed to enable the user to employ the GRAVITY workflow to reduce his/her data in a user-friendly way, concentrating on high-level issues such as data reduction quality and signal-to-noise (S/N) optimisation.

A workflow accepts science and calibration data, as downloaded from the archive using the CalSelector tool<sup>1</sup> (with associated raw calibrations) and organises them into DataSets, where each DataSet contains one science object observation (possibly consisting of several science files) and all associated raw and static calibrations required for a successful data reduction. The data organisation process is fully automatic, which is a major time-saving feature provided by the software. The DataSets selected by the user for reduction are fed to the workflow which executes the relevant pipeline recipes (or stages) in the correct order. Full control of the various recipe parameters is available within the workflow, and the workflow deals automatically with optional recipe inputs via built-in conditional branches. Additionally, the workflow stores the reduced final data products in a logically organised directory structure employing user-configurable file names.

This tutorial deals with the reduction of GRAVITY single and dual mode observations only via the GRAVITY Reflex workflow. For more detail on the pipeline, the user is referred to the (preliminary) pipeline manual and the GRAVITY user manual ([2]<sup>2</sup>) and to the ESO instrument web pages<sup>3</sup> for more information on the instrument itself as well as a summary of available documentation, recent news, and tools. The cookbook aspects derive from further guidance on GRAVITY data reduction and analysis in general.

The quick start section (see Section 5) describes the minimum effort to get started, and it makes up only two pages of text in this tutorial. User support for this software is available by sending enquiries to [usd-help@eso.org](mailto:usd-help@eso.org).

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<sup>1</sup><http://www.eso.org/sci/archive/calselectorInfo.html>

<sup>2</sup>available at: <http://www.eso.org/sci/facilities/paranal/instruments/gravity/doc>

<sup>3</sup><http://www.eso.org/sci/facilities/paranal/instruments/gravity.html>

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## 2 Workflow Status

The GRAVITY Reflex workflow, in its current version, is preliminary but is capable, together with its underlying GRAVITY pipeline, of delivering calibrated data products. The Reflex workflows are built upon the GRAVITY pipeline delivered by LESIA, Observatoire de Paris.

The first step of the GRAVITY Reflex workflow is to organise the data of this instrument into an associated, organised, and classified structure including for each science or interferometric calibrator file the required instrument calibration files with matching spectral resolution and integration time. The user will be warned if any calibration frames are missing.

The GRAVITY Reflex workflow, *gravity\_wkf*, will correct the frames for their dark level and structure, flat-field the data, and compute a wavelength solution. A large number of data products are created and retained for the user to assess the quality of the pipeline processing.

An alternative workflow, *gravity\_mastercalib*, allows to reduce data with the P2VM master calibration file which can be downloaded from the archive. This allows the user to skip the resource-intensive P2VM computation step (you would need at least 8GB of RAM in high resolution mode).

Calibrating the science observations is done with a separate workflow, *gravity\_viscal*.

During the processing within the Reflex workflow, the user has the ability to modify a number of pipeline parameters in order to optimise the data processing.

During the pipeline development and the experience of GRAVITY use, the pipeline parameters have been set to default values that deliver the best results for the most cases. However, the user should make an effort to adjust and experiment with the parameters to optimize the results.



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### 3 Software Installation

Reflex and the workflows can be installed in different ways: via package repositories, via the `install_esoreflex` script or manually installing the software tar files.

The recommended way is to use the package repositories if your operating system is supported. The `macports` repositories support OS X, while the `rpm/yum` repositories support Fedora 20 to 25. For any other operating system it is recommended to use the `install_esoreflex` script.

#### 3.1 Installing Reflex workflows via `macports`

This method is supported for the OS X operating system. It is assumed that `macports` (<http://www.macports.org>) and `java` are installed. If you have any problem with this installation method, please read the full documentation at <http://www.eso.org/sci/software/pipelines/installation/macports.html>.

For a quick installation, the following steps will install the ESO pipeline `macports` repository, the GRAVITY pipeline, including the Reflex workflow support and Reflex itself:

- Set up the repository:

```
# curl ftp://ftp.eso.org/pub/dfs/pipelines/repositories/macports/setup/Portfile -o Portfile
# sudo port install
# sudo port sync
```

- Install the GRAVITY pipeline:

```
# sudo port install esopipe-gravity-all
```

#### 3.2 Installing Reflex workflows via `rpm/yum`

This method is supported for Fedora 20/21/22/23/24/25 operating systems. If you have any problem with this installation method, please read the full documentation at <http://www.eso.org/sci/software/pipelines/installation/rpm.html>.

For a quick installation, the following steps will install the ESO pipeline `rpm` repository, the GRAVITY pipeline, including the Reflex workflow support and Reflex itself:

- Set up the repository for Fedora 20/21:

```
# sudo yum install yum-utils
# sudo yum-config-manager \
  --add-repo=ftp://ftp.eso.org/pub/dfs/pipelines/repositories/fedora/esorepo.repo
```

- Set up the repository for Fedora 22/23/24/25:

```
# sudo dnf install dnf-plugins-core
# sudo dnf config-manager \
  --add-repo=ftp://ftp.eso.org/pub/dfs/pipelines/repositories/fedora/esorepo.repo
```

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- Install the GRAVITY pipeline (Fedora 20/21):  
# `sudo yum install esopipe-gravity-all`
- Install the GRAVITY pipeline (Fedora 22/23/24/25):  
# `sudo dnf install esopipe-gravity-all`

### 3.3 Installing Reflex workflows via `install_esoreflex`

The software pre-requisites for Reflex 2.9 may be found at:  
[http://www.eso.org/sci/software/pipelines/reflex\\_workflows](http://www.eso.org/sci/software/pipelines/reflex_workflows)

To install the Reflex 2.9 software and demo data, please follow these instructions:

1. From any directory, download the installation script:

```
wget ftp://ftp.eso.org/pub/dfs/reflex/install_esoreflex
```

2. Make the installation script executable:

```
chmod u+x install_esoreflex
```

3. Execute the installation script:

```
./install_esoreflex
```

and the script will ask you to specify three directories: the download directory `<download_dir>`, the software installation directory `<install_dir>`, and the directory to be used to store the demo data `<data_dir>`. If you do not specify these directories, then the installation script will create them in the current directory with default names.

4. You will be asked whether you want to use your Internet connection. Unless you want to reuse already downloaded packages (only advanced users), use the default Yes.
5. You will be given a choice of pipelines (with the corresponding workflows) to install. Please specify the numbers for the pipelines you require, separated by a space, or type “A” for all pipelines.
6. For the pipelines to be installed you will be prompted for the demo data sets to be installed. Type “A” for all demo datasets. Take into account that if you are installing in a directory that already contains data, it won’t be removed.
7. The script will also detect whether previous versions of the workflows or Reflex were installed and in this case you have the option to update links or remove obsolete cache directories. It is advised to use the defaults.
8. If some of the prerequisite binaries for Reflex are not under one of the paths indicated by the command,

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```
getconf PATH
```

then you will need to add the appropriate paths as a colon separated list to the `esoreflex.path` parameter in the configuration file `<install_dir>/etc/esoreflex.rc`. This will usually be necessary when the FITS viewer (`fv`) is installed outside of `/usr/bin`. As an example, assume `fv` is installed into the directory `/usr/local/fv5.4`, the file `esoreflex.rc` should then have the line setting `esoreflex.path` look similar to the following:

```
esoreflex.path=/usr/local/fv5.4
```

In the case of OS X `/Applications/fv.app/Contents/MacOS/` is the typically installation directory. Thus, this should be similar to the following line instead:

```
esoreflex.path=/opt/local/bin:/Applications/fv.app/Contents/MacOS
```

9. To start Reflex, issue the command:

```
<install_dir>/bin/esoreflex
```

It may also be desirable to set up an alias command for starting the Reflex software, using the shell command `alias`. Alternatively, the `PATH` variable can be updated to contain the `<install_dir>/bin` directory.

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## 4 Demo Data

Together with the pipeline you can also choose to receive a demo data set that allows you to run the `Reflex GRAVITY` workflow without any changes in parameters. This way you have data sets to experiment with before you start to work on your own data.

Note that you will need a minimum of  $\sim 5$  GB,  $\sim 9$  GB and  $\sim 8$  GB of free disk space for the directories `<download_dir>`, `<install_dir>` and `<data_dir>`, respectively.

The raw input consists of OBJ-SKY-OBJ-SKY sequences of:

1. two calibrator OBs of HIP 64314, and
2. one science OB of a double star, HD 114529 ( $\rho = 143.0$  mas,  $\theta = 132.6^\circ$ , secondary flux fraction = 24%).

The data set also includes the DARK, P2VM, FLAT, WAVE, and WAVESC files. The raw tutorial data sets are summarized in Table 4.1. The list of files as shown in the table can be obtained by executing the following command (part of the ESO SciSoft collection) in the demo data directory:

```
dfits *.fits | fitsort obs.name dpr.catg dpr.type tpl.expno
ins.filt1.name ins.filt2.name dit
```

FILT1 refers to the Wollaston prism, which is “IN” when recording both polarizations and “OUT” when recording the sum of both signals. FILT2 refers to the spectral resolution. Note the two DARK frames with different DIT, one belonging to the science frames, the other one to the P2VM frames.

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Table 4.1: The GRAVITY Reflex workflow tutorial data set, single field mode data with medium spectral resolution and no polarization.

File	OBS.NAME	DPR.CATG	DPR.TYPE	EXPNO	FILT1.NAME	FILT2.NAME	DIT
GRAVI.2016-06-22T16:26:14.536.fits	Calibration	CALIB	DARK	1	OUT	MED	0.3
GRAVI.2016-06-22T16:27:29.540.fits	Calibration	CALIB	FLAT	2	OUT	MED	0.3
GRAVI.2016-06-22T16:28:05.542.fits	Calibration	CALIB	FLAT	3	OUT	MED	0.3
GRAVI.2016-06-22T16:28:41.544.fits	Calibration	CALIB	FLAT	4	OUT	MED	0.3
GRAVI.2016-06-22T16:29:17.546.fits	Calibration	CALIB	FLAT	5	OUT	MED	0.3
GRAVI.2016-06-22T16:30:02.549.fits	Calibration	CALIB	WAVE,SC	6	OUT	MED	0.3
GRAVI.2016-06-22T16:35:38.568.fits	Calibration	CALIB	WAVE	7	OUT	MED	0.3
GRAVI.2016-06-22T16:40:23.583.fits	Calibration	CALIB	P2VM	8	OUT	MED	0.3
GRAVI.2016-06-22T16:42:59.592.fits	Calibration	CALIB	P2VM	9	OUT	MED	0.3
GRAVI.2016-06-22T16:45:35.601.fits	Calibration	CALIB	P2VM	10	OUT	MED	0.3
GRAVI.2016-06-22T16:48:11.610.fits	Calibration	CALIB	P2VM	11	OUT	MED	0.3
GRAVI.2016-06-22T16:50:47.619.fits	Calibration	CALIB	P2VM	12	OUT	MED	0.3
GRAVI.2016-06-22T16:53:23.628.fits	Calibration	CALIB	P2VM	13	OUT	MED	0.3
GRAVI.2016-06-22T17:11:47.690.fits	Calibration	CALIB	DARK	1	OUT	MED	10.0
GRAVI.2016-06-23T00:19:55.884.fits	CAL_HIP64314	CALIB	OBJECT,SINGLE	1	OUT	MED	10.0
GRAVI.2016-06-23T00:24:37.900.fits	CAL_HIP64314	CALIB	SKY,SINGLE	2	OUT	MED	10.0
GRAVI.2016-06-23T00:29:22.916.fits	CAL_HIP64314	CALIB	OBJECT,SINGLE	3	OUT	MED	10.0
GRAVI.2016-06-23T00:34:04.932.fits	CAL_HIP64314	CALIB	SKY,SINGLE	4	OUT	MED	10.0
GRAVI.2016-06-23T00:47:52.978.fits	SCI_HD114529	SCIENCE	OBJECT,SINGLE	1	OUT	MED	10.0
GRAVI.2016-06-23T00:52:34.994.fits	SCI_HD114529	SCIENCE	SKY,SINGLE	2	OUT	MED	10.0
GRAVI.2016-06-23T00:57:20.010.fits	SCI_HD114529	SCIENCE	OBJECT,SINGLE	3	OUT	MED	10.0
GRAVI.2016-06-23T01:02:02.026.fits	SCI_HD114529	SCIENCE	SKY,SINGLE	4	OUT	MED	10.0
GRAVI.2016-06-23T01:17:05.077.fits	CAL_HIP64314	CALIB	OBJECT,SINGLE	1	OUT	MED	10.0
GRAVI.2016-06-23T01:21:47.092.fits	CAL_HIP64314	CALIB	SKY,SINGLE	2	OUT	MED	10.0
GRAVI.2016-06-23T01:26:35.108.fits	CAL_HIP64314	CALIB	OBJECT,SINGLE	3	OUT	MED	10.0
GRAVI.2016-06-23T01:31:20.125.fits	CAL_HIP64314	CALIB	SKY,SINGLE	4	OUT	MED	10.0

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## 5 Quick Start: Reducing The Demo Data

For the user who is keen on starting reductions without being distracted by detailed documentation, we describe the steps to be performed to reduce the science data provided in the GRAVITY demo data set supplied with the Reflex 2.9 release. By following these steps, the user should have enough information to perform a reduction of his/her own data without any further reading:

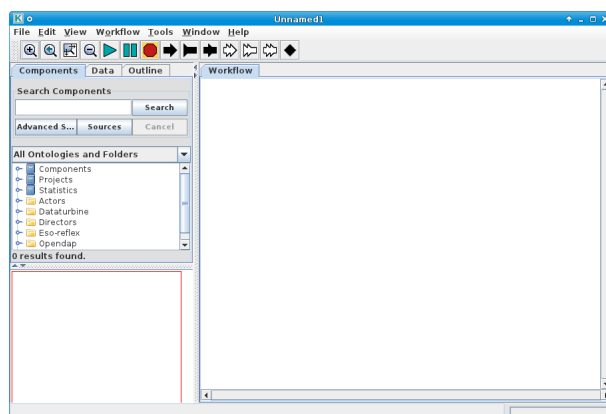


Figure 5.1: *The empty Reflex canvas.*

1. Start the Reflex application:

```
esoreflex &
```

If `install_esoreflex` was used or manual installation was performed then the start command is:


```
<install_dir>/bin/esoreflex &
```

The empty Reflex canvas as shown in Figure 5.1 will appear.

2. Now open the GRAVITY workflow by clicking on `File -> Open File`, selecting first `gravity-1.2.1` and then the file `gravity_wkf.xml` in the file browser. You will be presented with the workflow canvas shown in Figure 8.1. Note that the workflow will appear as a canvas in a new window.
3. To aid in the visual tracking of the reduction cascade, it is advisable to use component (or actor) highlighting. Click on `Tools -> Animate at Runtime`, enter the number of milliseconds representing the animation interval (100 ms is recommended), and click .
4. Under “Setup Directories” in the workflow canvas there are seven parameters that specify important directories (green dots). Changing the value of `ROOT_DATA_DIR` and/or `RAW_DATA_DIR` is the only

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necessary modification if you want to process data other than the demo data<sup>4</sup>, since the value of this parameter specifies the working directory within which the other directories are organised. Double-click on the parameter `ROOT_DATA_DIR` and a pop-up window will appear allowing you to modify the directory string, which you may either edit directly, or use the `Browse` button to select the directory from a file browser. When you have finished, click `OK` to save your changes.

5. Click the  button to start the workflow
6. The workflow will highlight the `Data Organiser` actor which recursively scans the raw data directory (specified by the parameter `RAW_DATA_DIR` under “Setup Directories” in the workflow canvas) and constructs the DataSets. Note that the raw and static calibration data must be present either in `RAW_DATA_DIR` or in `CALIB_DATA_DIR`, otherwise DataSets may be incomplete and cannot be processed. However, if the same reference file was downloaded twice to different places this creates a problem as `Reflex` cannot decide which one to use.
7. The `Data Set Chooser` actor will be highlighted next and will display a “Select Datasets” window (see Figure 8.4) that lists the DataSets along with the values of a selection of useful header keywords<sup>5</sup>. The first column consists of a set of tick boxes which allow the user to select the DataSets to be processed. By default all complete DataSets which have not yet been reduced will be selected.
8. Click the `Continue` button and watch the progress of the workflow by following the red highlighting of the actors. A window will show which DataSet is currently being processed.
9. Once the reduction of all DataSets has finished, a pop-up window called *Product Explorer* will appear, showing the datasets which have been reduced together with the list of final products. This actor allows the user to inspect the final data products, as well as to search and inspect the input data used to create any of the products of the workflow. Figure 8.5 shows the Product Explorer window.
10. After the workflow has finished, all the products from all the DataSets can be found in a directory under `END_PRODUCTS_DIR` with the named with the workflow start timestamp. Further subdirectories will be found with the name of each DataSet.

Well done! You have successfully completed the quick start section and you should be able to use this knowledge to reduce your own data. However, there are many interesting features of `Reflex` and the GRAVITY workflow that merit a look at the rest of this tutorial.

<sup>4</sup>If you used the install script `install_esoreflex`, then the value of the parameter `ROOT_DATA_DIR` will already be set correctly to the directory where the demo data was downloaded.

<sup>5</sup>The keywords listed can be changed by right-clicking on the `DataOrganiser Actor`, selecting `Configure Actor`, and then changing the list of keywords in the second line of the pop-up window.

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## 6 About The Reflex Canvas

### 6.1 Saving And Loading Workflows

In the course of your data reductions, it is likely that you will customise the workflow for various data sets, even if this simply consists of editing the `ROOT_DATA_DIR` to a different value for each data set. Whenever you modify a workflow in any way, you have the option of saving the modified version to an XML file using `File -> Export As` (which will also open a new workflow canvas corresponding to the saved file). The saved workflow may be opened in subsequent Reflex sessions using `File -> Open`. Saving the workflow in the default Kepler format (.kar) is only advised if you do not plan to use the workflow with another computer.

### 6.2 Buttons

At the top of the Reflex canvas are a set of buttons which have the following functions:

-  - Zoom in.
-  - Reset the zoom to 100%.
-  - Zoom the workflow to fit the current window size (Recommended).
-  - Zoom out.
-  - Run (or resume) the workflow.
-  - Pause the workflow execution.
-  - Stop the workflow execution.

The remainder of the buttons (not shown here) are not relevant to the workflow execution.

### 6.3 Workflow States

A workflow may only be in one of three states: executing, paused, or stopped. These states are indicated by the yellow highlighting of the , , and  buttons, respectively. A workflow is executed by clicking the  button. Subsequently the workflow and any running pipeline recipe may be stopped immediately by clicking the  button, or the workflow may be paused by clicking the  button which will allow the current actor/recipe to finish execution before the workflow is actually paused. After pausing, the workflow may be resumed by clicking the  button again.



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## 7 The GRAVITY Workflow

The GRAVITY workflow canvas is organised into a number of areas. From top-left to top-right you will find general workflow instructions, directory parameters, and global parameters. In the middle row you will find five boxes describing the workflow general processing steps in order from left to right, and below this the workflow actors themselves are organised following the workflow general steps.

### 7.1 Workflow Canvas Parameters

The workflow canvas displays a number of parameters that may be set by the user. Under “Setup Directories” the user is only required to set the `RAW_DATA_DIR` to the working directory for the `DataSet(s)` to be reduced, which, by default, is set to the directory containing the demo data. The `RAW_DATA_DIR` is recursively scanned by the `Data Organiser` actor for input raw data. The directory `CALIB_DATA_DIR`, which is by default within the pipeline installation directory, is also scanned by the `Data Organiser` actor to find any static calibrations that may be missing in your `DataSet(s)`. If required, the user may edit the directories `BOOKKEEPING_DIR`, `LOGS_DIR`, `TMP_PRODUCTS_DIR`, and `END_PRODUCTS_DIR`, which correspond to the directories where book-keeping files, logs, temporary products and end products are stored, respectively (see the Reflex User Manual for further details; [3]).

There is a mode of the `Data Organiser` that skips the built-in data organisation and uses instead the data organisation provided by the `CalSelector` tool. To use this mode, click on `Use CalSelector associations` in the `Data Organiser` properties and make sure that the input data directory contains the XML file downloaded with the `CalSelector` archive request.

Under the “Global Parameters” area of the workflow canvas, the user may set the `FITS_VIEWER` parameter to the command used for running his/her favourite application for inspecting FITS files. Currently this is set by default to `fv`, but other applications, such as `ds9`, `skycat` and `gaia` for example, may be useful for inspecting image data. Note that it is recommended to specify the full path to the visualization application (an alias will not work).

By default the `EraseDirs` parameter is set to `false`, which means that no directories are cleaned before executing the workflow, and the recipe actors will work in Lazy Mode (see Section 7.2.3), reusing the previous pipeline recipe outputs where input files and parameters are the same as for the previous execution, which saves considerable processing time. Sometimes it is desirable to set the `EraseDirs` parameter to `true`, which forces the workflow to recursively delete the contents of the directories specified by `BOOKKEEPING_DIR`, `LOGS_DIR`, and `TMP_PRODUCTS_DIR`. This is useful for keeping disk space usage to a minimum and will force the workflow to fully re-reduce the data each time the workflow is run.

The parameter `RecipeFailureMode` controls the behaviour in case that a recipe fails. If set to `Continue`, the workflow will trigger the next recipes as usual, but without the output of the failing recipe, which in most of the cases will lead to further failures of other recipes without the user actually being aware of it. This mode might be useful for unattended processing of large number of datasets. If set to `Ask`, a pop-up window will ask whether the workflow should stop or continue. This is the default. Alternatively, the `Stop` mode will stop the workflow execution immediately.

The parameter `GlobalPlotInteractivity` controls whether the interactive windows will appear for those windows which are *enabled* by default. The possible values are `true`, `false`. Take into account that some

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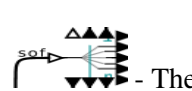
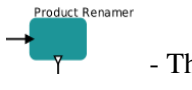

windows are disabled in the default configuration and therefore are not affected by this parameter.

The parameter `ProductExplorerMode` controls whether the `ProductExplorer` actor will show its window or not. The possible values are `Enabled`, `Disabled` and `Triggered`. The latter, recommended, means that the `ProductExplorer` actor will be shown only at the end of the workflow execution.

## 7.2 Workflow Actors

### 7.2.1 Simple Actors


Simple actors have workflow symbols that consist of a single (rather than multiple) green-blue rectangle. They may also have an icon within the rectangle to aid in their identification. The following actors are simple actors:

- 
 • - The Data Organiser actor.
- 
 • - The Data Set Chooser actor (inside a composite actor).
- 
 • - The Fits Router actor
- 
 • - The Product Renamer actor.
- 
 • - The Product Explorer actor (inside a composite actor).




Access to the parameters for a simple actor is achieved by right-clicking on the actor and selecting `Configure Actor`. This will open an “Edit parameters” window. Note that the `Product Renamer` actor is a jython script (Java implementation of the Python interpreter) meant to be customised by the user (by double-clicking on it).

### 7.2.2 GRAVITY-specific actors: the workflow data-reduction cascade

The present GRAVITY workflow is designed to process the datasets according to a specific data reduction cascade. This cascade triggers a series of pipeline recipes, which are associated to the following composite actors:

- 
 • GravityDark: it executes the recipe *gravity\_dark* . It processes the dark frames to create a master dark needed both for the recipe *gravity\_p2vm* and for *gravity\_vis*. The master dark frames need to have the same DIT as the corresponding science/calibration frames.

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- 
 GravityP2VM: it executes the recipe *gravity\_p2vm*. It requires products of *gravity\_dark* as input, as well as raw P2VM, FLAT, and WAVE files.
- 
 GravityScience: it executes the recipe *gravity\_vis*. It requires products of *gravity\_dark* as input, as well as reduced BAD, P2VM, FLAT, and WAVE files.
- 
 Visibilities Calibration: it executes the recipe *gravity\_viscal*. It requires products of *gravity\_vis* as input, for a science target and one or more calibrator observations.

This is an interactive actor, meaning that an apposite interacting window will appear allowing the used to inspected the products and, eventually, to re-run the recipe with modified parameters.

We refer the user to the GRAVITY pipeline manual for a complete description of the recipes and their parameters.

As noted in the Quick Start Section 5, the workflow will then proceed through its remaining processing steps and write out all pipeline products to the end products directory (specified by the parameter `END_PRODUCTS_DIR` under “Setup Directories” in the workflow canvas). The science data products from the tutorial data set are summarized in section 10 in table 10.2. The intermediate pipeline calibration products can be found in subdirectories of the `TMP_PRODUCT_DIR` and are summarized in section 10 and in table 10.

### 7.2.3 Lazy Mode

By default, all recipe executor actors in a pipeline workflow are “Lazy Mode” enabled. This means that when the workflow attempts to execute such an actor, the actor will check whether the relevant pipeline recipe has already been executed with the same input files and with the same recipe parameters. If this is the case, then the actor will not execute the pipeline recipe, and instead it will simply broadcast the previously generated products to the output port. The purpose of the Lazy Mode is therefore to minimise any reprocessing of data by avoiding data re-reduction where it is not necessary.

One should note that the actor’s Lazy Mode depends on the contents of the directory specified by the parameter `BOOKKEEPING_DIR` and the relevant FITS file checksums. Any modification to the directory contents and/or the file checksums will cause the corresponding actor to run the pipeline recipe again when executed, thereby re-reducing the input data.

The re-reduction of data at each execution may sometimes be desirable. To force a re-reduction of data for any single `RecipeExecutor` actor in the workflow, right-click the actor, select `Configure Actor`, and uncheck the Lazy mode parameter tick-box in the “Edit parameters” window that is displayed. For many workflows the `RecipeExecutor` actors are actually found inside the composite actors in the top level workflow. To access such embedded `RecipeExecutor` actors you will first need to open the sub-workflow by right-clicking on the composite actor and then selecting `Open Actor`.

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To force the re-reduction of all data in a workflow (i.e. to disable Lazy mode for the whole workflow), you must uncheck the Lazy mode for every single `RecipeExecutor` actor in the entire workflow. It is also possible to change the name of the bookkeeping directory, instead of modifying any of the Lazy mode parameters. This will also force a re-reduction of the given dataset(s). A new reduction will start (with the lazy mode still enabled), but the results of previous reduction will not be reused. Alternatively, if there is no need to keep any of the previously reduced data, one can simply set the `EraseDirs` parameter under the “Global Parameters” area of the workflow canvas to `true`. This will then remove all previous results that are stored in the bookkeeping, temporary, and log directories before processing the input data. In effect, starting a new clean data reduction and re-processing every input dataset.

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## 8 Reducing and Calibrating Your Own Science Data with Reflex

### 8.1 Available Reflex workflows

There are two workflows available for the reduction and one workflow for the calibration of the visibility data. While the workflow *gravity\_wkf* shown in Fig. 8.1 performs all reduction steps using the raw data, the workflow *gravity\_mastercalib* shown in Fig. 8.2 uses the P2VM master calibration files downloaded from the ESO archive (associated *processed* calibrations), allowing you to bypass the resource-heavy step of the P2VM computation. The workflow *gravity\_viscal* in Fig. 8.3 calibrates the reduced science files.

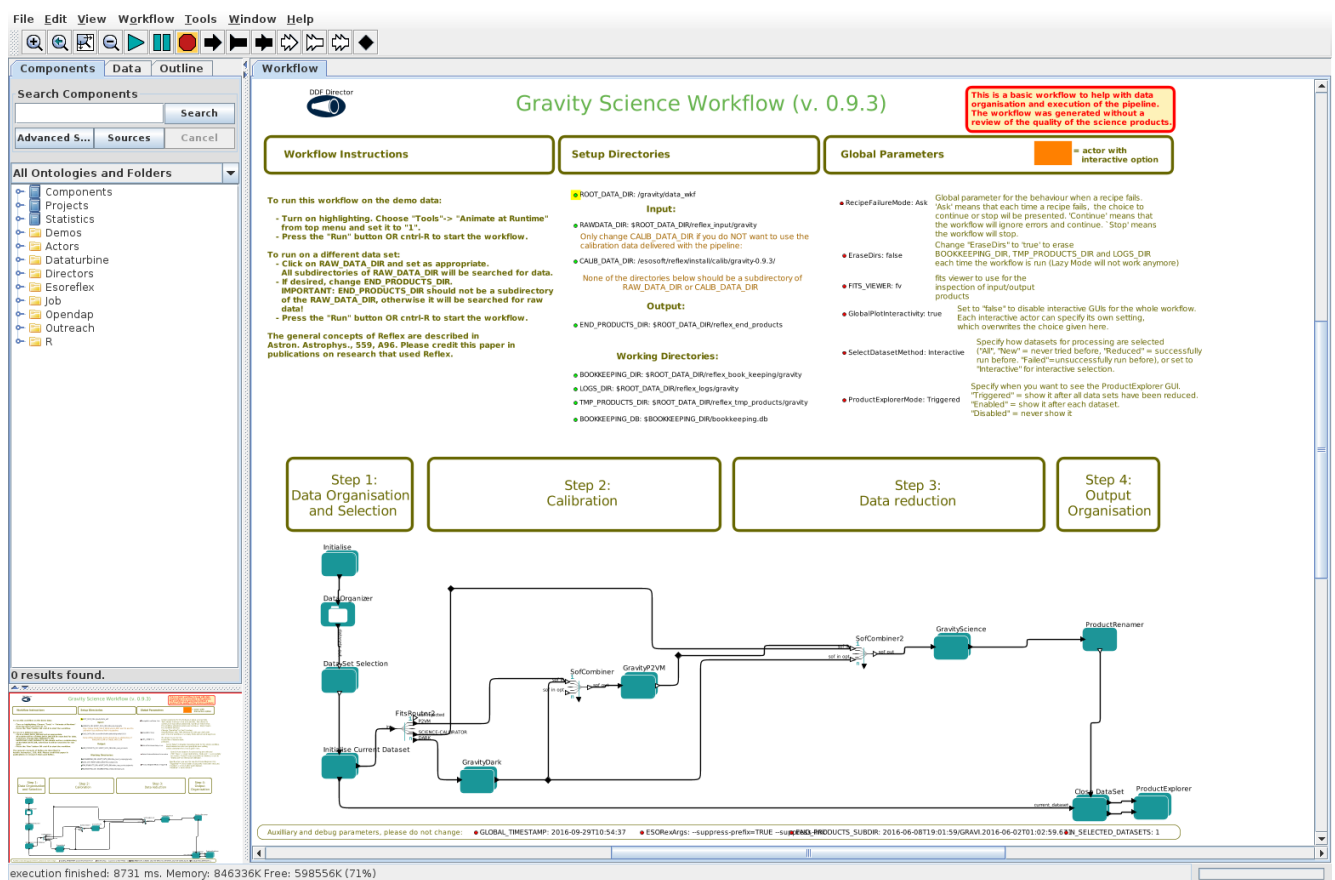


Figure 8.1: *gravity\_wkf* workflow layout.

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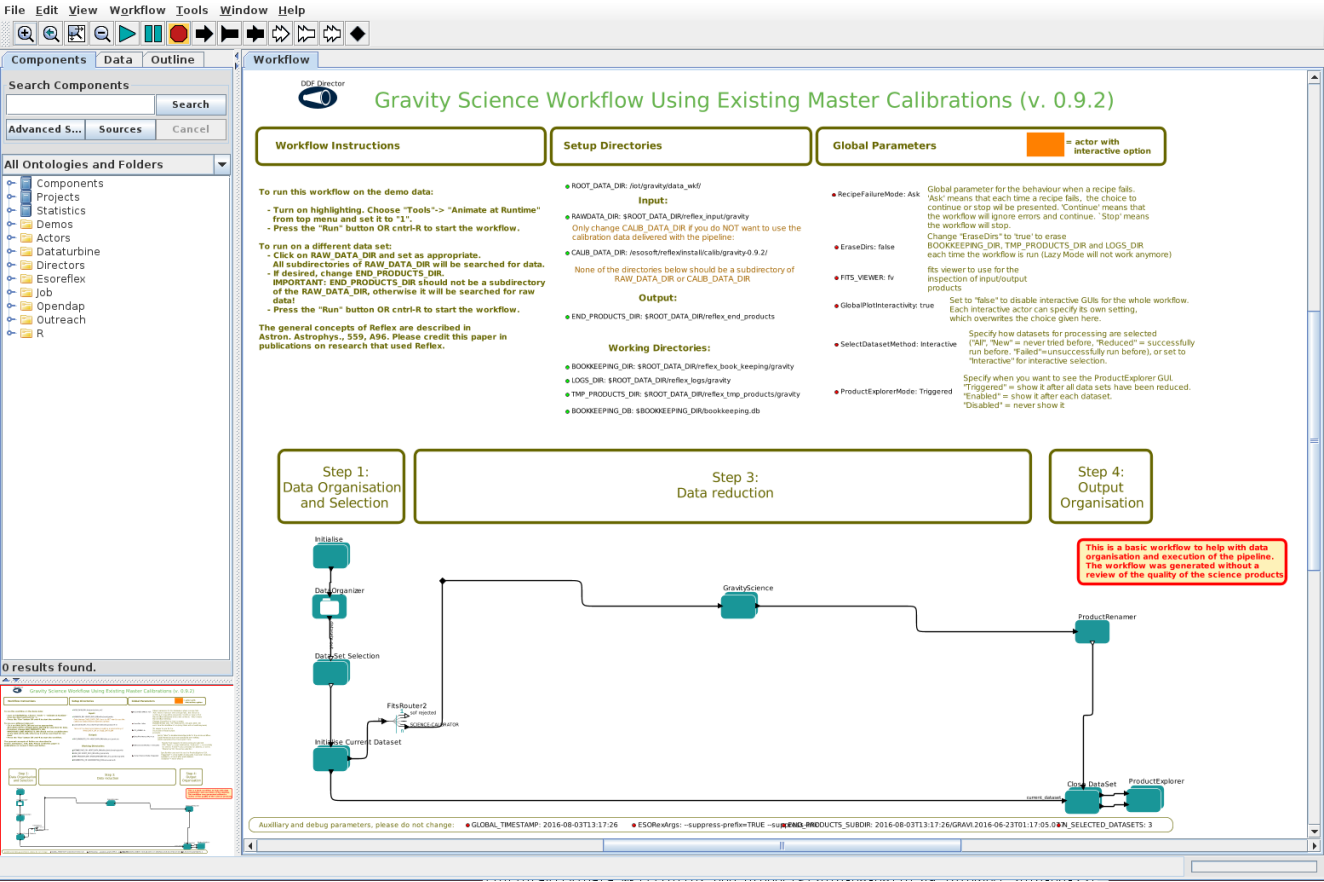


Figure 8.2: gravity\_mastercalib workflow layout.

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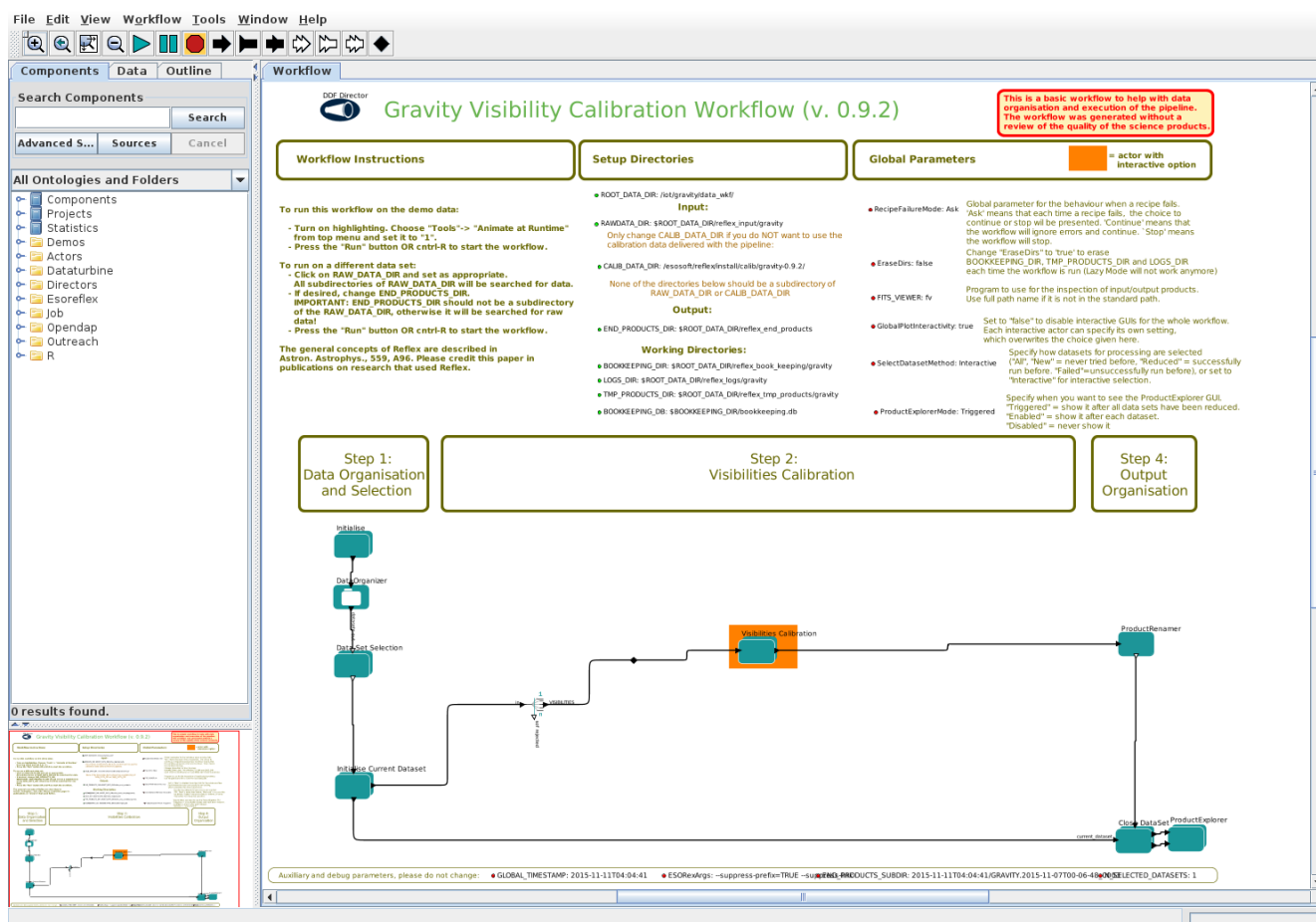


Figure 8.3: gravity\_viscal workflow layout.

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## 8.2 Specifying data directories

To reduce your own science data, simply change the paths to the root (optional) and data directories. Under the former, Reflex will create sub-directories which will contain temporary and end products, as well as book keeping and log files. The latter, normally also under the root directory, contains directories with your raw files downloaded from the ESO archive. The paths are defined at the top of the workflow window in the area labeled `Setup Directories`. Simply double click on the `RAWDATA_DIR`, enter the path to your raw science directory and then re-run the workflow in the same way as you did for the tutorial demo data. In case the data sets listed in the first window created by the work flow (Fig. 8.4) are greyed out, calibration files are missing (hovering with the mouse over the grey file entry will give more details). You can click the entry and a GUI opens up showing the dependency tree of the science (or calibrator) file on calibrations (Fig. 8.4). Please note that the pipeline step which computes the P2VM calibration file requires about 8 GB of memory for the demo data (medium resolution, no polarization), about 12 GB for high resolution (no polarization), and up to about 20 GB for high resolution with polarization.



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Selected	Data Set	#Files	Reduced	FT.ROBJ.NAME	OBS.NAME	DPR.T
<input checked="" type="checkbox"/>	GRAVI.2016-06-23T00:19:55.884	18	-	HIP64314	CAL_HIP64314	OBJECT,S
<input checked="" type="checkbox"/>	GRAVI.2016-06-23T00:47:52.978	18	-	HD114529	SCI_HD114529	OBJECT,S
<input checked="" type="checkbox"/>	GRAVI.2016-06-23T01:17:05.077	18	-	HIP64314	CAL_HIP64314	OBJECT,S

	Sel	Category	Keyword	Value
GRAVI.2016-06-23T00:19:55.884.fits	<input checked="" type="checkbox"/>	SINGLE_CAL_RAW	SIMPLE	T
GRAVI.2016-06-23T00:29:22.916.fits	<input checked="" type="checkbox"/>	SINGLE_CAL_RAW	BITPIX	-32
GRAVI.2016-06-23T00:24:37.900.fits	<input checked="" type="checkbox"/>	SINGLE_SKY_RAW	NAXIS	0
GRAVI.2016-06-23T00:34:04.932.fits	<input checked="" type="checkbox"/>	SINGLE_SKY_RAW	EXTEND	T
ACTION_CALIB_DARK	<input checked="" type="checkbox"/>		ORIGIN	ESO-PARANAL
GRAVI.2016-06-22T17:11:47.690.fits	<input checked="" type="checkbox"/>	DARK_RAW	DATE	2016-06-23T0...
ACTION_CALIB_P2VM	<input checked="" type="checkbox"/>		TELESCOP	ESO-VLT-A1234
GRAVI.2016-06-22T16:27:29.540.fits	<input checked="" type="checkbox"/>	FLAT_RAW	INSTRUME	GRAVITY
GRAVI.2016-06-22T16:28:05.542.fits	<input checked="" type="checkbox"/>	FLAT_RAW	OBJECT	OBJECT,SINGLE
GRAVI.2016-06-22T16:28:41.544.fits	<input checked="" type="checkbox"/>	FLAT_RAW	RA	197.721126
GRAVI.2016-06-22T16:29:17.546.fits	<input checked="" type="checkbox"/>	FLAT_RAW	DEC	-60.05013
GRAVI.2016-06-22T16:40:23.583.fits	<input checked="" type="checkbox"/>	P2VM_RAW	EQUINOX	2000
GRAVI.2016-06-22T16:42:59.592.fits	<input checked="" type="checkbox"/>	P2VM_RAW	RADECSYS	FK5
GRAVI.2016-06-22T16:45:35.601.fits	<input checked="" type="checkbox"/>	P2VM_RAW	EXPTIME	261.0000000
GRAVI.2016-06-22T16:48:11.610.fits	<input checked="" type="checkbox"/>	P2VM_RAW	MJD-OBS	57562.01384...
GRAVI.2016-06-22T16:50:47.619.fits	<input checked="" type="checkbox"/>	P2VM_RAW	DATE-OBS	2016-06-23T0...
GRAVI.2016-06-22T16:53:23.628.fits	<input checked="" type="checkbox"/>	P2VM_RAW	UTC	1195.500
GRAVI.2016-06-22T16:30:02.549.fits	<input checked="" type="checkbox"/>	WAVESC_RAW	LST	49483.656
GRAVI.2016-06-22T16:35:38.568.fits	<input checked="" type="checkbox"/>	WAVE_RAW	PI-COI	UNKNOWN
ACTION_CALIB_DARK_P2VM	<input checked="" type="checkbox"/>		OBSERVER	UNKNOWN
GRAVI.2016-06-22T16:26:14.536.fits	<input checked="" type="checkbox"/>	DARK_RAW	ORIGFILE	GRAVITY_GEN_...
			HIERARCH.ESO....	0.1141
			HIERARCH.ESO....	0.4471
			HIERARCH.ESO....	264.1550
			HIERARCH.ESO....	788.2205
			HIERARCH.ESO....	1257.6399
			HIERARCH.ESO....	1724.2040
			HIERARCH.ESO....	320.5929
			HIERARCH.ESO....	788.1831

Figure 8.4: Upper panel: the “Select Datasets” pop-up window; Lower panel: the “Select Frame” pop-up window, obtained after pressing the “Inspect highlighted” button in the “Select Datasets” window.

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When the workflow has finished, the Product Explorer window opens (Fig. 8.5). Select a data file and unfold the file tree in the “Provenance Tree” window. This provides information on the dependency of product files on the calibration files and other files from recipes executed before. You can inspect a data file by clicking the “Inspect with...” button, and entering the path to your favourite FITS file viewer (e.g., *fv*). Examples of the master flat frame (Fig. 8.6) and a master dark frame (Fig. 8.7) are shown below.

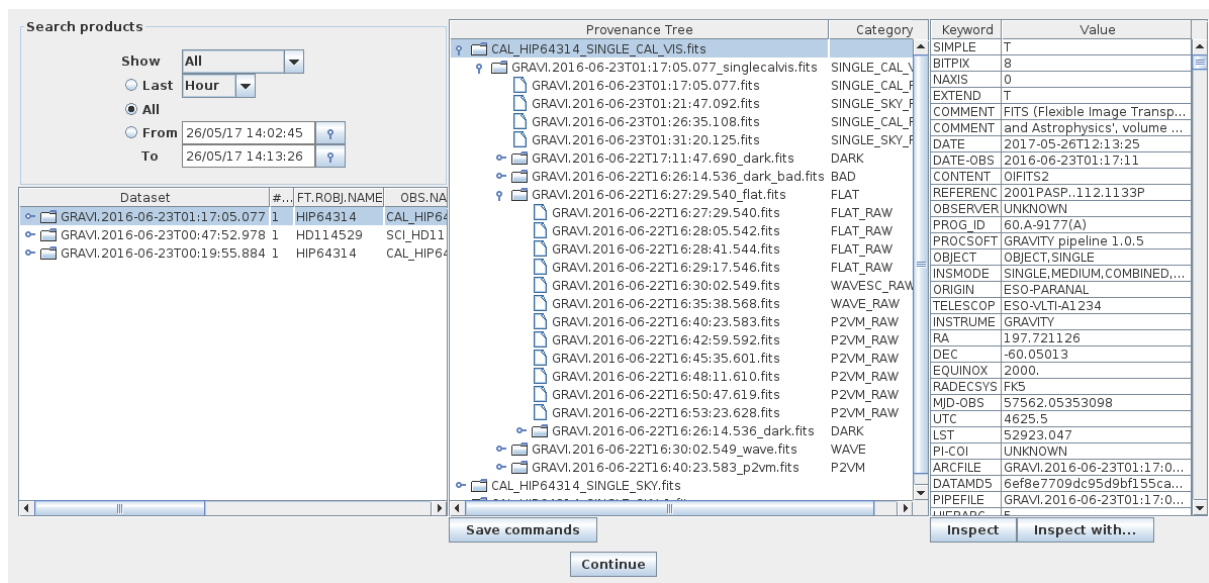


Figure 8.5: The GRAVITY product explorer.

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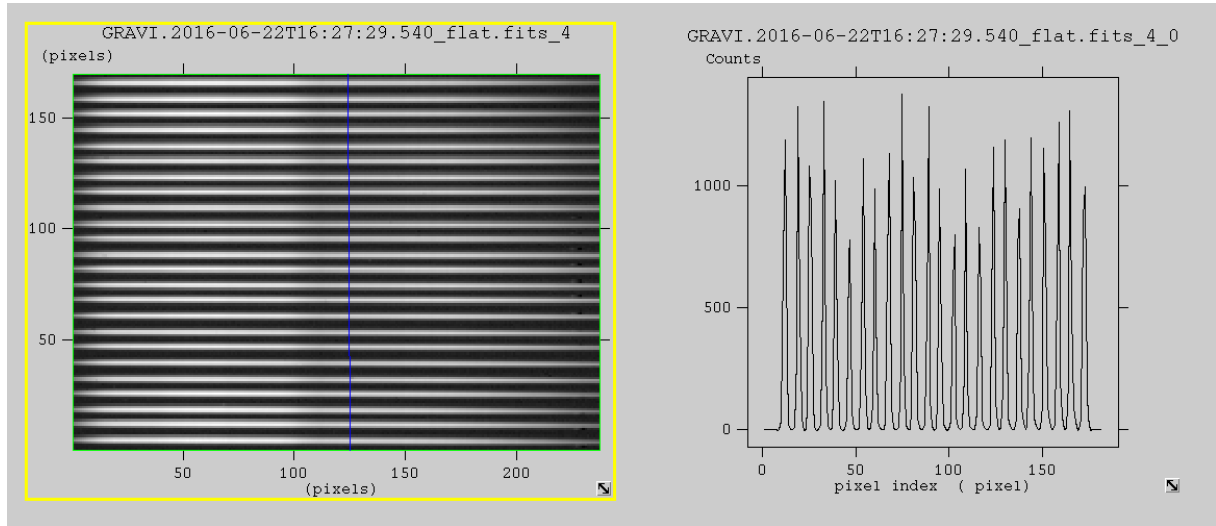


Figure 8.6: *GRAVITY* master flat image, stored in the *IMAGING\_DATA\_SC* binary extension. The horizontal axis is the wavelength axis, the 24 output channels are arranged along the vertical axis.

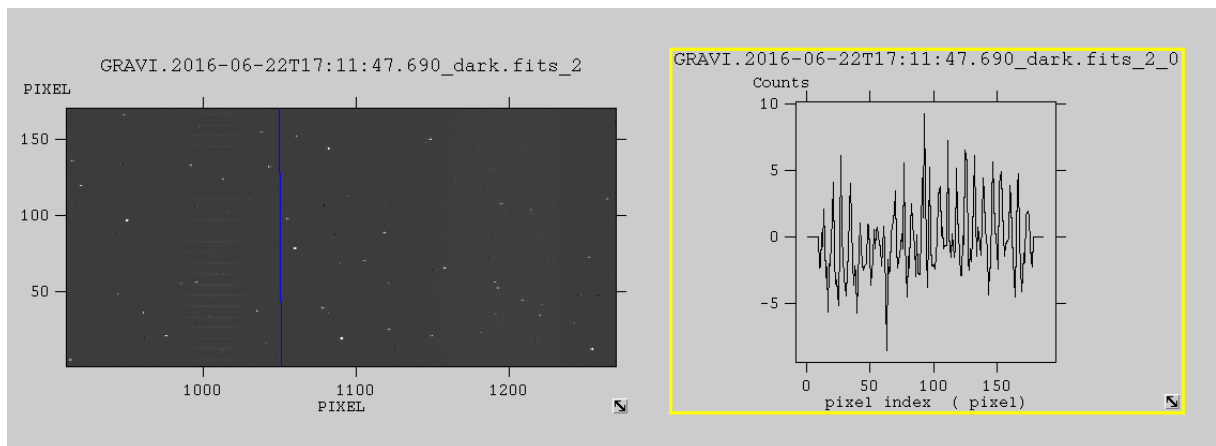


Figure 8.7: *GRAVITY* master dark image, stored in the *IMAGING\_DATA\_SC* binary extension. The horizontal axis is the wavelength axis, the 24 output channels are arranged along the vertical axis.

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### 8.3 Calibrating your visibility data

The workflow *gravity\_viscal* allows you to select (aside from the science file) one or more calibrator files which will define the transfer function (TF, i.e., the visibility measured on a calibrator, corrected for the effect of a non-zero diameter of the calibrator). The demo data set includes two calibrators, one measured before and one after the science target. Thus, the TF will be linearly interpolated to the epoch of the science observations. When running this recipe, you will be presented with a (not yet interactive) plot window showing the TF for each of the six baselines of GRAVITY, as shown in Fig. 8.8. The calibrator diameter information is taken from file *GRAVI\_FAINT\_CALIBRATORS.fits* in the Reflex installation directory *install/calib/gravity-1.0.0/cal*.

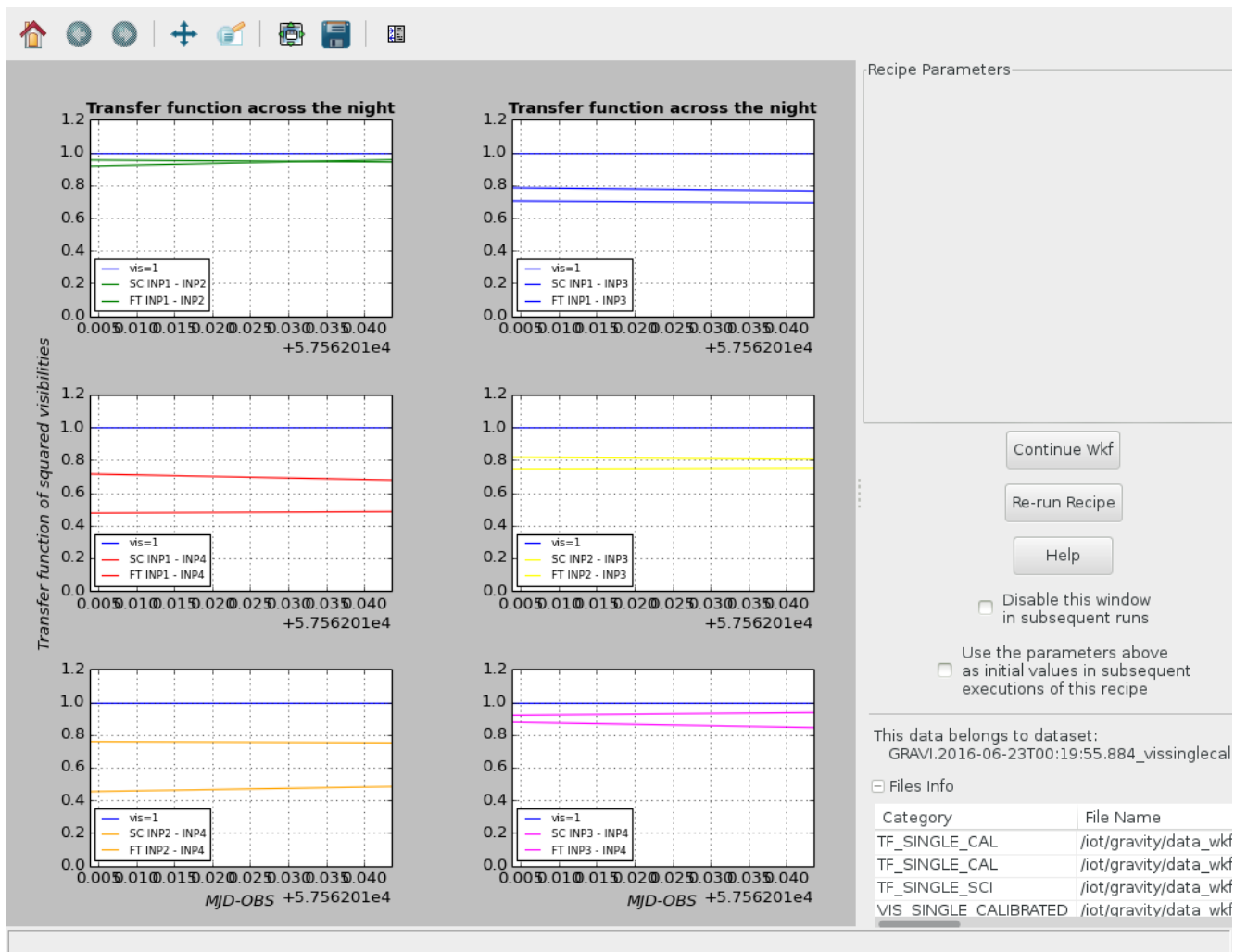


Figure 8.8: *gravity\_viscal* workflow plot of the FT and SC channel transfer functions.

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## 9 Optimising Your Results Through Workflow Interaction

In this Section, we use the information from Section 5 along with the GRAVITY demo data set supplied with pipeline version 1.2.1 to illustrate how to optimise the scientific products in terms of quality and signal-to-noise ratio.

This is work in progress and the contents of this section will grow as we gain experience and add functionality. Optimising the results is achieved by interaction with the workflow actors via interactive windows displayed at key data reduction points in the data flow, which enable iteration of certain recipes in order to obtain better results.

We recommend that the user has already carried out the reductions for the demo data set as described in Section 5, although this is not a pre-requisite to following this section. By doing this, the user will be taking advantage of the workflow Lazy Mode, with minimal waiting time between various pipeline recipe executions.

As discussed previously, the first operation the GRAVITY workflow does is to group the raw data (science, raw calibrations, and static calibrations) into datasets to be reduced. The datasets will be then processed in series.

The second operation is to direct all the files of a dataset to the correct pipeline recipe, so that the data reduction could start and the various recipes can be triggered in the correct order with the correct set of input files. The data reduction cascade operated by the GRAVITY workflow triggers the recipes according to the data reduction cascade outlined in Section 7.2.2.

### 9.1 Bias and vFactor correction of visibilities

The visibility amplitudes are affected by bias and coherence time. The former is related to photon noise and needs to be subtracted from the (square) modulus of the complex visibility, the latter can be corrected by multiplying the visibility with a factor larger than 1, called vFactor, which is derived from the GRAVITY fringe tracker phase RMS.

In version 1.2.1 of the pipeline, the vFactor correction sometimes results in visibilities significantly larger than unity and therefore must be switched off in those cases. To do this, right-click with the mouse on the GravityScience actor and select "Open actor". The workflow canvas of this actor will be displayed, and here you right-click on the gravity\_vis actor to select "Configure actor". This will display a window like the one shown in Fig. 9.1. To disable the vFactor correction, change the value of vis-correction (recipe\_param\_8) from VFAC-TOR to NONE.

Likewise, if you needed to disable the bias correction, you would set the value of parameter debias-sc (recipe\_param\_13) to "false". However, please note that the bias correction is a fundamental and well established correction which should only be disabled if you have very good evidence for it not to work in your specific case.

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?

recipe:

mode:

Lazy Mode:

Recipe Failure Mode:

Input Files Category:

Output Files Category:

File Purpose Processing:

Allow empty inputs:

Pause before execution:

Pause after execution:

Clean Temporary Directories:

Products Dir:

Logs Dir:

Bookkeeping Dir:

EsoRex default args:

Bookkeeping DB:

recipe\_param\_1:

recipe\_param\_2:

recipe\_param\_3:

recipe\_param\_4:

recipe\_param\_5:

recipe\_param\_6:

recipe\_param\_7:

recipe\_param\_8:

recipe\_param\_9:

recipe\_param\_10:

recipe\_param\_11:

recipe\_param\_12:

recipe\_param\_13:

recipe\_param\_14:

recipe\_param\_15:

gravity\_vis

Run

☒

Stop

Strip last

☒

☐

☐

☐

\$TMP\_PRODUCTS\_DIR

\$LOGS\_DIR

\$BOOKKEEPING\_DIR

\$ESORexArgs

\$BOOKKEEPING\_DB

static-name=false

bias-subtracted-file=false

preproc-file=false

p2vmreduced-file=false

snr-min-ft=3

state-min-ft=1

tracking-min-sc=0.8

vfactor-min-sc=0.1

nboot=20

vis-correction=VFACTOR

flat-flux=false

astro-file=false

debias-sc=true

debias-ft=true

coadd-vis=false

Browse

Configure

Browse

Configure

Browse

Configure

Browse

Configure

Commit

Add

Remove

Defaults

Preferences

Help

Cancel

Figure 9.1: The interactive window to edit parameters of recipe gravity\_vis.

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## 10 GRAVITY Reduced Data Description

A number of intermediate pipeline products from the tutorial data set can be found in subdirectories of the `TMP_PRODUCT_DIR`. These master calibration files are summarized in Table 10.

Table 10.1: The GRAVITY Reflex workflow tutorial data set: calibration products

File	PRO.CATG	Description
<i>gravity_p2vm:</i>		
GRAVI.2016-06-22T16:26:14.536_dark_bad.fits	BAD	bad pixel map
GRAVI.2016-06-22T16:27:29.540_flat.fits	FLAT	flat field
GRAVI.2016-06-22T16:35:38.568_wave.fits	WAVE	wavelength calibration
GRAVI.2016-06-22T16:40:23.583_p2vm.fits	P2VM	p2vm
<i>gravity_dark:</i>		
GRAVI.2016-06-22T16:26:14.536_dark.fits	DARK	dark frame

The final products of the reduction pipeline can be found in the directory `END_PRODUCT_DIR` that is defined in the “Setup Directories” section at the top of the workflow.

The science data products from the two tutorial data sets are summarized in tables 10.2. Their description will be done in Section 10.1.

Table 10.2: The GRAVITY Reflex workflow tutorial data set: uncalibrated visibility products

File	PRO.CATG	Description
GRAVI.2016-06-22T23:07:43.639/CAL_HIP64314_SKY.fits	SKY	sky frame
GRAVI.2016-06-22T23:07:43.639/CAL_HIP64314_SINGLE_CAL_VIS.fits	SINGLE_CAL_VIS	uncalibrated averaged visibility data
GRAVI.2016-06-22T23:35:46.735/CAL_HIP64314_SKY.fits	SKY	sky frame
GRAVI.2016-06-22T23:35:46.735/CAL_HIP64314_SINGLE_CAL_VIS.fits	SINGLE_CAL_VIS	uncalibrated averaged visibility data
GRAVI.2016-06-22T23:52:43.791/SCI_HD114529_SKY.fits	SKY	sky frame
GRAVI.2016-06-22T23:52:43.791/SCI_HD114529_SINGLE_SCI_VIS.fits	SINGLE_SCI_VIS	uncalibrated averaged visibility data
GRAVI.2016-06-23T00:19:55.884/CAL_HIP64314_SKY.fits	SKY	sky frame
GRAVI.2016-06-23T00:19:55.884/CAL_HIP64314_SINGLE_CAL_VIS.fits	SINGLE_CAL_VIS	uncalibrated averaged visibility data
GRAVI.2016-06-23T00:47:52.978/SCI_HD114529_SKY.fits	SKY	sky frame
GRAVI.2016-06-23T00:47:52.978/SCI_HD114529_SINGLE_SCI_VIS.fits	SINGLE_SCI_VIS	uncalibrated averaged visibility data
GRAVI.2016-06-23T01:17:05.077/CAL_HIP64314_SKY.fits	SKY	sky frame
GRAVI.2016-06-23T01:17:05.077/CAL_HIP64314_SINGLE_CAL_VIS.fits	SINGLE_CAL_VIS	uncalibrated averaged visibility data

Table 10.3: The GRAVITY Reflex workflow tutorial data set: calibrated visibility of the science target

File	PRO.CATG	Description
<i>gravity_viscal:</i>		
CAL_HIP64314_SINGLE_CAL_TF_1.fits	SINGLE_CAL_TF	Transfer function of calibrator
CAL_HIP64314_SINGLE_CAL_TF.fits	SINGLE_CAL_TF	Transfer function of calibrator
CAL_HIP64314_ZP_CAL.fits	ZP_CAL	Zero-point calibration (photometry)
SCI_HD114529_SINGLE_SCI_TF.fits	SINGLE_SCI_TF	Transfer function interpolated for science target
SCI_HD114529_SINGLE_VIS_CALIBRATED.fits	SINGLE_SCI_VIS_CALIBRATED	calibrated science visibility

### 10.1 Description of final products

In this section we provide a very brief description of the workflow science products that are stored in the `reflex_end_products` directory. They are produced by the pipeline recipes *gravity\_vis*. For further infor-

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mation, please consult the GRAVITY pipeline manual. In the list, the products are identified by their PRO.CATG keyword.

- **SINGLE\_CAL\_VIS**. Product of the recipe *gravity\_vis* for a CAL observation. This file should conform to the OIFITS2 file format used for interferometric data [1]. If the visibilities of the calibrator are corrected for the non-zero diameter of the calibrator star, the resulting visibility amplitudes are called the *transfer function* (TF).
- **SINGLE\_SCI\_VIS**. Product of the recipe *gravity\_vis* for a SCI observation. This file should conform to the OIFITS2 file format used for interferometric data [1]. The visibility data are averaged, but not calibrated.
- **SINGLE\_SCI\_VIS\_CALIBRATED**. Product of the recipe *gravity\_viscal* for a SCI observation. This file should conform to the OIFITS2 file format used for interferometric data [1]. The visibility data are averaged and were calibrated by dividing the science target visibilities by the calibrator transfer function interpolated for the epoch of the science observation. Fig. 10.1 shows the structure of an OIFITS2 file and Figs. 10.2 and 10.3 show the extension table for the (squared) visibility amplitudes and a plot for one of the baselines.

File Edit Tools				Help				
Index	Extension	Type	Dimension	View				
<input type="checkbox"/> 0	Primary	Image	0	Header	Image	Table		
<input type="checkbox"/> 1	OI_ARRAY	Binary	6 cols X 4 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 2	OI_TARGET	Binary	17 cols X 1 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 3	OI_WAVELENGTH	Binary	2 cols X 210 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 4	OI_WAVELENGTH	Binary	2 cols X 5 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 5	OI_VIS	Binary	18 cols X 6 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 6	OI_VIS2	Binary	10 cols X 6 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 7	OI_T3	Binary	14 cols X 4 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 8	OI_FLUX	Binary	8 cols X 4 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 9	OI_VIS	Binary	27 cols X 6 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 10	OI_VIS2	Binary	10 cols X 6 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 11	OI_T3	Binary	14 cols X 4 rows	Header	Hist	Plot	All	Select
<input type="checkbox"/> 12	OI_FLUX	Binary	13 cols X 4 rows	Header	Hist	Plot	All	Select

Figure 10.1: Main structure of OIFITS2 file with binary extension tables.



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File Edit Tools Help											
Select	TARGET_ID	TIME	MJD	INT_TIME	VIS2DATA	VIS2ERR	UCOORD	VCOORD	STA_INDEX	FLAG	
All	11	1D	1D	1D	210D	210D	1D	1D	2I	210L	
Invert	Modify	Modify	Modify	Modify	Modify	Modify	Modify	Modify	Modify	Modify	
1	1	3.004850001074E+03	5.756203477836E+04	2.500000000000E+02	Plot	Plot	1.184747173728E+01	1.401293942436E+01	Plot	F	
2	1	3.004850001074E+03	5.756203477836E+04	2.500000000000E+02	Plot	Plot	-5.907509238401E+00	-7.006687578612E+00	Plot	F	
3	1	3.004850001074E+03	5.756203477836E+04	2.500000000000E+02	Plot	Plot	-1.048589227815E+01	1.265930368203E+01	Plot	F	
4	1	3.004850001074E+03	5.756203477836E+04	2.500000000000E+02	Plot	Plot	-1.775498097568E+01	-2.101962700297E+01	Plot	F	
5	1	3.004850001074E+03	5.756203477836E+04	2.500000000000E+02	Plot	Plot	-3.033336401543E+01	-1.353635742328E+00	Plot	F	
6	1	3.004850001074E+03	5.756203477836E+04	2.500000000000E+02	Plot	Plot	-1.257838303975E+01	1.966599126064E+01	Plot	F	

Figure 10.2: OIVIS2 table.

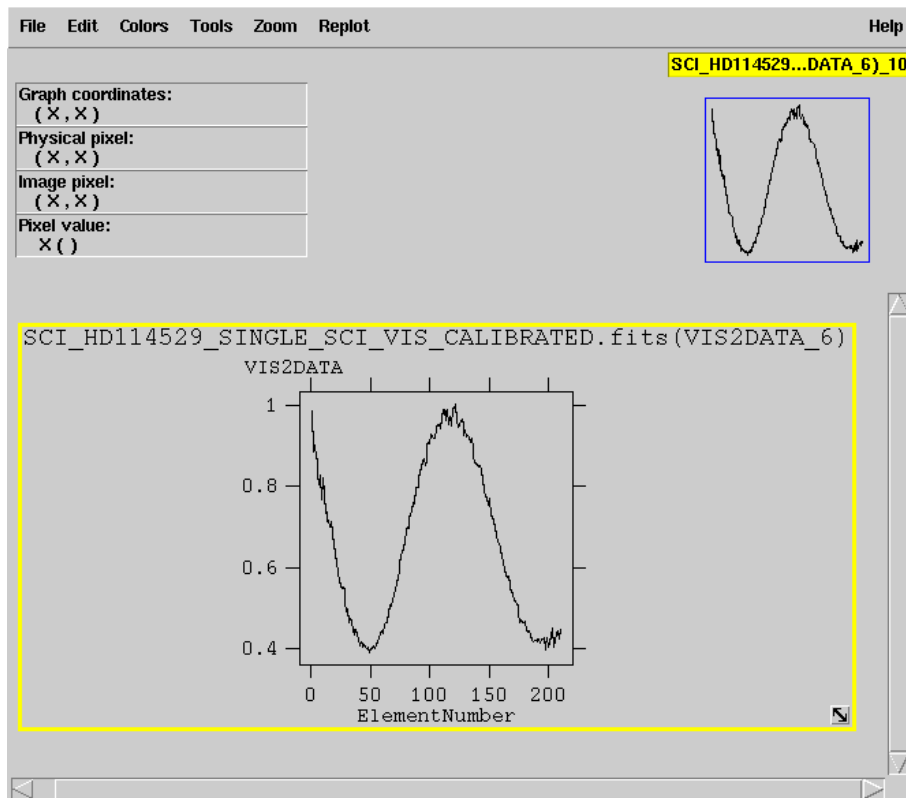


Figure 10.3: Plot of the squared visibility amplitude for baseline 6.

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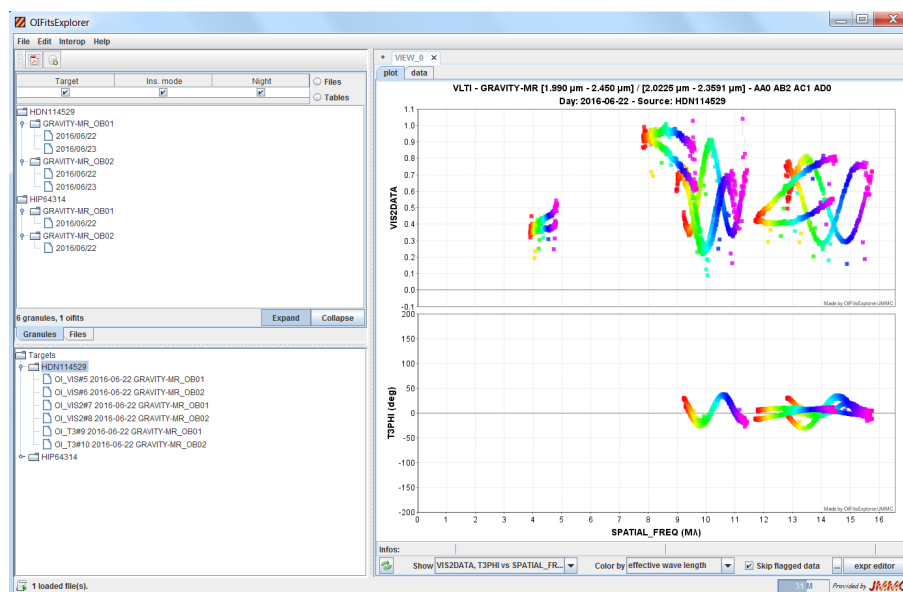


Figure 10.4: OIFitsExplorer view of the demo data (all science files combined).

One can use the OIFitsExplorer (Fig. 10.4)

([http://www.jmmc.fr/oifitseexplorer\\_page.htm](http://www.jmmc.fr/oifitseexplorer_page.htm)) to examine the data and LitPro

([http://www.jmmc.fr/litpro\\_page.htm](http://www.jmmc.fr/litpro_page.htm)) to fit simple models.

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## 11 Reducing Your Own Science Data with Python tools

The GRAVITY consortium developed a set of Python scripts which interface with pipeline recipes to reduce and analyze data. These tools are not maintained by ESO and no support is provided by ESO. The scripts can be downloaded from [http://version-lesia.obspm.fr/repos/DRS\\_gravity/python\\_tools/](http://version-lesia.obspm.fr/repos/DRS_gravity/python_tools/) or with the following command:

```
svn co https://version-lesia.obspm.fr:/repos/DRS_gravity/python_tools
```

The scripts will be located in a local directory name *python\_tools*. Please consult the README file in that directory for instructions on how to change the PATH environment variable so that the scripts can be found by python.

To reduce all demo data at once, change the working directory to the *data\_wkf/reflex\_input/gravity/gravity-demo-reflex-0.5* created when you downloaded the data. Since the science and calibration data files are located in various sub-directories, create symbolic links to them in the working with the following command (include the “dot” at the end!):

```
ln -s */*.fits .
```

Then run the following command to reduce all files and store the results in a local directory named *reduced*:

```
python run_gravi_reduce.py
```

The following command, if run in the reduced files directory, produces very informative PDF files on the (uncalibrated) results. The same command, when run in *reflex\_tmp\_products/gravity/gravity\_p2vm\_1* (then choosing the sub-directory with the date/time stamp corresponding to the desired execution of the work flow), produces a PDF file with various plots useful for quality control of the P2VM (see the first page in Fig. 11.1).

```
python run_gravi_visual.py
```

A useful script is also *quicklook.py* (<http://github.com/amerand/GRAVIQL>) which plots visibilities, phases, and fluxes for re-reduced data files.

Finally, the following command calibrates the visibilities of the science targets:

```
python run_gravi_trend.py
```

It creates two directories, *trends* and *calibrated*. Files *GRAVI.????-??-??T??:??:??:??\*\_singleisciviscalibrated.fits* contain the calibrated visibilities of the science targets. Alternatively, the reduced data can be calibrated using the Reflex it gravity\_viscal workflow.

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## GRAVITY P2VM Quality Control Report

file name:	GRAVI.2016-06-22T16:40:23.583_p2vm.fits
Observing date:	2016-06-22T16:40:28
Processing/report date:	2017-05-26T13:33:48 2017-06-01T09:47:03
Product category:	P2VM
SC & Polar setup:	MEDIUM, COMBINED, COMBINED
SC NDIT x DIT:	256 x 0.3 s
FT DIT freq.:	0.00085 s, 909 Hz
P2VM overall quality	GOOD

### Relative photometric transmission per output

Normalized to average transmission over all outputs. Cyan=Pol.1(P) or COMB, Blue=Pol.2(S).

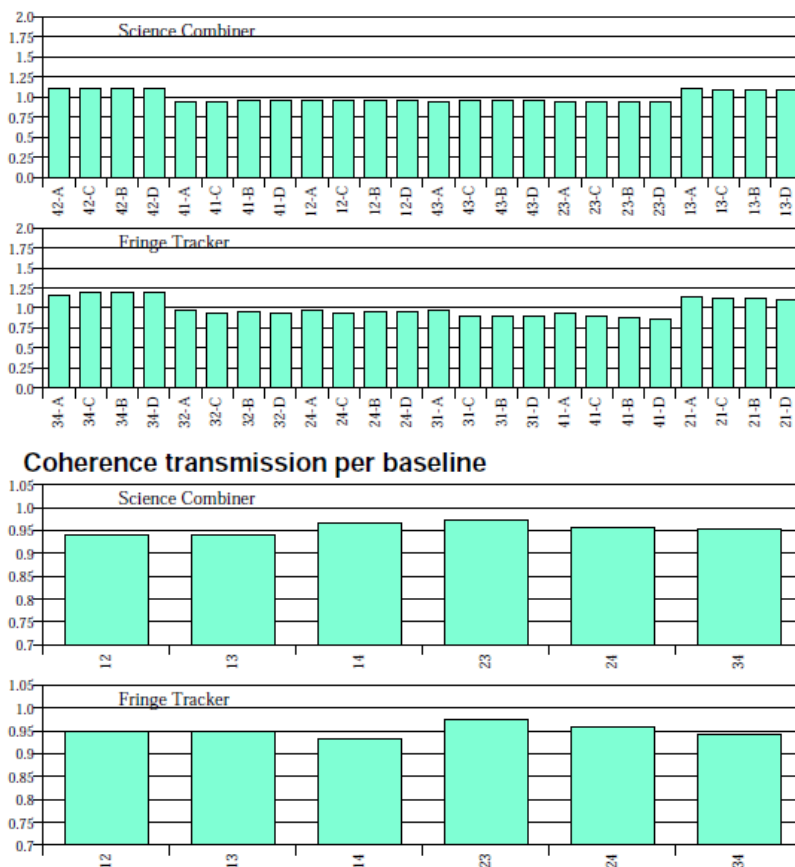


Figure 11.1: The first page of the P2VM report produced by `run_gravi_visual.py`. Note the overall quality rating box near the top of the page.

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## 12 Frequently Asked Questions

- **The error window fills the whole screen - how can I get to the `Continue`/`Stop` buttons?**

Press the `Alt` key together with your left mouse button to move the window upwards and to the left. At the bottom the `Continue`/`Stop` buttons will be visible. This bug is known but could not yet be fixed.

- **I tried to Open (or Configure) an Actor while the workflow is running and now it does not react any more. What should I do?**

This is a limitation of the underlying Kepler engine. The only way out is to kill the workflow externally. If you want to change anything while a workflow is running you first need to pause it.

- **After a successful reduction of a data set, I changed this data set in some way (e.g. modified or removed some files, or changed the rules of the Data Organizer). When I restart Reflex, the Data Set Chooser correctly displays my new data set, but marks it as “reduced ok”, even though it was never reduced before. What does this mean?**

The labels in the column “Reduced” of the Data Set Chooser mark each dataset with “OK”, “Failed” or “-”. These labels indicate whether a data set has previously successfully been reduced at least once, all previous reductions failed, or a reduction has never been tried respectively. Data sets are identified by their name, which is derived from the first science file within the data set. As long as the data set name is preserved (i.e. the first science file in a data set has not changed), the Data Organizer will consider it to be the same data set. The Data Organizer recognizes any previous reductions of data sets it considers to be the same as the current one, and labels the current data set with “OK” if any of them was successful, even if the previously reduced data set differs from the current one.

Note that the Product Explorer will list all the previous reductions of a particular data set only at the end of the reduction. This list might include successful and/or unsuccessful reduction runs with different parameters, or in your case with different input files. The important fact is that these are all reductions of data sets with the same first raw science file. By browsing through all reductions of a particular raw science file, the users can choose the one they want to use.

- **Where are my intermediate pipeline products?** Intermediate pipeline products are stored in the directory `<TMP_PRODUCTS_DIR>` (defined on the workflow canvas, under Setup Directories) and organised further in directories by pipeline recipe.
- **Can I use different sets of bias frames to calibrate my flat frames and science data?** Yes. In fact this is what is currently implemented in the workflow(s). Each file in a DataSet has a purpose attached to it ([3]). It is this purpose that is used by the workflow to send the correct set of bias frames to the recipes for flat frame combination and science frame reduction, which may or may not be the same set of bias frames in each case.

- **Can I run Reflex from the command line?** Yes, use the command:

```
esoreflex -n <workflow_path>/<workflow>.xml
```

The `-n` option will set all the different options for Kepler and the workflows to avoid opening any GUI elements (including pipeline interactive windows).

It is possible to specify workflow variables (those that appear in the workflow canvas) in the command line. For instance, the raw data directory can be set with this command:

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```
esoreflex -n -RAW_DATA_DIR <raw_data_path> \
          <workflow_path>/<workflow>.xml
```

You can see all the command line options with the command `esoreflex -h`.

Note that this mode is not fully supported, and the user should be aware that the path to the workflow must be absolute and even if no GUI elements are shown, it still requires a connection to the window manager.

- **How can I add new actors to an existing workflow?** You can drag and drop the actors in the menu on the left of the Reflex canvas. Under `Eso-reflex -> Workflow` you may find all the actors relevant for pipeline workflows, with the exception of the recipe executer. This actor must be manually instantiated using `Tools -> Instantiate Component`. Fill in the “Class name” field with `org.eso.RecipeExecuter` and in the pop-up window choose the required recipe from the pull-down menu. To connect the ports of the actor, click on the source port, holding down the left mouse button, and release the mouse button over the destination port. Please consult the Reflex User Manual ([3]) for more information.
- **How can I broadcast a result to different subsequent actors?** If the output port is a multi-port (filled in white), then you may have several relations from the port. However, if the port is a single port (filled in black), then you may use the black diamond from the toolbar. Make a relation from the output port to the diamond. Then make relations from the input ports to the diamond. Please note that you cannot click to start a relation from the diamond itself. Please consult the Reflex User Manual ([3]) for more information.
- **How can I manually run the recipes executed by Reflex?** If a user wants to re-run a recipe on the command line he/she has to go to the appropriate `reflex_book_keeping` directory, which is generally `reflex_book_keeping/<workflow>/<recipe_name>_<number>`. There, subdirectories exist with the time stamp of the recipe execution (e.g. `2013-01-25T12:33:53.926/`). If the user wants to re-execute the most recent processing he/she should go to the `latest` directory and then execute the script `cmdline.sh`. Alternatively, to use a customized `esorex` command the user can execute

```
ESOREX_CONFIG="INSTALL_DIR/etc/esorex.rc"
PATH_TO/esorex --recipe-config=<recipe>.rc <recipe> data.sof
```

where `INSTALL_DIR` is the directory where Reflex and the pipelines were installed.

If a user wants to re-execute on the command line a recipe that used a specific raw frame, the way to find the proper `data.sof` in the bookkeeping directory is via `grep <raw_file> */data.sof`. Afterwards the procedure is the same as before.

If a recipe is re-executed with the command explained above, the products will appear in the directory from which the recipe is called, and not in the `reflex_tmp_products` or `reflex_end_products` directory, and they will not be renamed. This does not happen if you use the `cmdline.sh` script.

- **If I enter “-” into an empty integer parameter of an interactive window it is automatically completed to “-1”. Why?**

The parameters are validated for correctness according to their type (e.g. string, integer, float). In the case of an integer or float parameter “-” alone is considered an invalid input and is therefore automatically completed to “-1”. This is part of the validation of input done by the WxPython library.

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- **Can I reuse the bookkeeping directory created by previous versions of the pipeline?**

In general no. In principle, it could be reused if no major changes were made to the pipeline. However there are situations in which a previously created bookkeeping directory will cause problems due to pipeline versions incompatibility. This is especially true if the parameters of the pipeline recipes have changed. In that case, please remove the bookkeeping directory completely.

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## 13 Troubleshooting

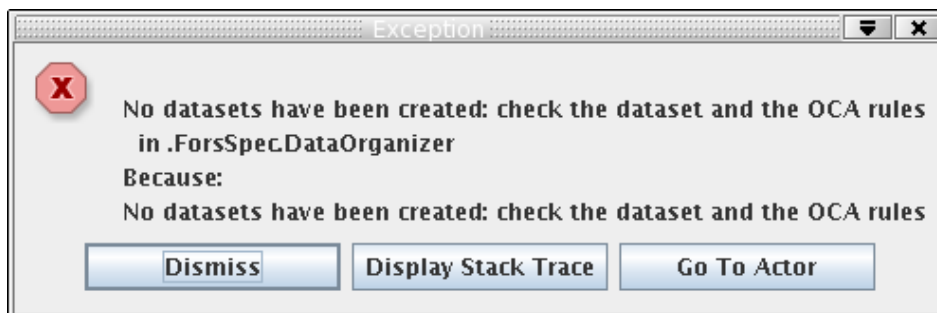


Figure 13.1: *TheDataOrganizer* interactive window reports an error “:No DataSets have been created, check the data set and the OCA rules.”.

1. **I downloaded the data from the ESO archive, put them into a new directory, tried to run `Reflex` on them, but**

- (a) **it crashes**

This may happen if one of the files was downloaded only partially (check for a file with the extension `fits.Z.part`. You will have to download that file again in order to have an uncorrupted file (and remove the partial one).

- (b) **it fails with error message “:No DataSets have been created, check the data set and the OCA rules.”(see Figure 13.1.)**

This error may be due to the fact that the data provided by the ESO archive are compressed (`<filename>.fits.Z`). Please remember to uncompress the data before executing `Reflex`.

- (c) **all DataSets are greyed out in the DataSets interactive window.**

The ESO archive used with `CalSelector` does not always supply all static calibration files. As a consequence some/all DataSets are greyed out because they were missing such required data.

Missing static calibration should be found by `reflex` in

`<install_directory>/calib/<pipeline_version>/cal`.

2. **The “Select DataSets” window displays my DataSets, but some/all of them are greyed out. What is going on?**

If a DataSet in the “Select DataSets” window is greyed out, then it means that the DataSet that was constructed is missing some key calibration(s) (i.e. the DataSet is incomplete). To find out what calibration(s) are missing from a greyed out DataSet, click on the DataSet in question to highlight it in blue, and then click on the button `Inspect Highlighted`. The “Select Frames” window that appears will report the category of the calibration products that are missing (e.g. DARK). From this the user has then to determine the missing raw data (in this case dark frames). If static calibrations are missing the mechanism unfortunately does not work, but should be found by `reflex` in

`<install_directory>/calib/<pipeline_version>/cal`



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**3. The plots in the interactive windows does not allow me to properly inspect the products; how can I change or measure what it is plotted?**

The plots in the interactive window are meant to provide a general visualization of the product. However, it is possible to inspect each file (input or output) with other visualization tools, or process them via custom scripts to evaluate the quality.

At the bottom right corner of each interactive window, the list of inputs/outputs files is given. Select with the mouse the file you would like to inspect and press Ctrl-C to copy its full path name.

It is also possible to change the general visualization tool in the Global Parameter section of the workflow, by editing the `FITS_VIEWER` variable.

**4. The workflow crashes with a message "...output file could not be moved..."**

This is a memory allocation error during execution of the *gravity\_p2vm* recipe due to insufficient memory installed. Try exiting other application and rerun the recipe. If this fails, try to use *gasgano* to reduce the P2VM. Unfortunately, this means that you have to use *gasgano* also for the rest of the data reduction of the related science files.

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## Acknowledgements

This tutorial has contributions from the GRAVITY IOT.

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- [1] G. Duvert, J. Young, and C.A. Hummel. OIFITS 2: the 2nd version of the Data Exchange Standard for Optical (Visible/IR) Interferometry. *Astronomy & Astrophysics*, 597:A8, 2015. 32
- [2] GRAVITY IOT GRAVITY Consortium. *GRAVITY 2016 User Manual*, 2016. VLT-MAN-ESO-XXXXX-XXX. 7
- [3] Forchì V. *Reflex User's Manual*. ESO/SDD/DFS, <http://www.eso.org/gasgano/>, 0.7 edition, 2012. VLT-MAN-ESO-19000-5037. 17, 37, 38