



EUROPEAN SOUTHERN OBSERVATORY

Organisation Européenne pour des Recherches Astronomiques dans l'Hémisphère Austral

Europäische Organisation für astronomische Forschung in der südlichen Hemisphäre

VERY LARGE TELESCOPE

Reflex GRAVITY Tutorial and Cookbook

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

Issue 1.5.0

Date 2021-02-20

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Released: —
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Change record

Issue/Rev.	Date	Section/Parag. affected	Reason/Initiation/Documents/Remarks
0.1	21/06/2016	All	Initial Release
0.9.2	08/08/2016	All	Updated Release for pipeline version 0.9.2
0.9.3	29/09/2016	All	Updated Release for pipeline version 0.9.3
1.0.0	17/10/2016	All	Updated Release for pipeline version 1.0.0
1.0.5	26/05/2017	All	Change to Cookbook for pipeline version 1.0.5
1.0.11	14/11/2017	All	Change to Cookbook for pipeline version 1.0.11
1.2.5	01/05/2019	All	Change to Cookbook for pipeline version 1.2.5

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1 Introduction to `EsoReflex`

This document is a tutorial designed to enable the user to to reduce his/her data with the ESO pipeline run under an user-friendly environmet, called `EsoReflex`, concentrating on high-level issues such as data reduction quality and signal-to-noise (S/N) optimisation.

`EsoReflex` 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 for further support.

A workflow accepts science and calibration data, as downloaded from the archive using the CalSelector tool¹ (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 pipeline manual and the GRAVITY user manual ([2]²) and to the ESO instrument web pages³ 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.

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

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

³<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 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

Esoreflex 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 macOS 10.11 to 10.14, while the `rpm/yum` repositories support Fedora 28 to 31, CentOS 7, Scientific Linux 7. For any other operating system it is recommended to use the `install_esoreflex` script.

The installation from package repository requires administrative privileges (typically granted via `sudo`), as it installs files in system-wide directories under the control of the package manager. If you want a local installation, or you do not have `sudo` privileges, or if you want to manage different installations on different directories, then use the `install_esoreflex` script. Note that the script installation requires that your system fulfill several software prerequisites, which might also need `sudo` privileges.

Reflex 2.10 needs java JDK 11 to be installed.

Please note that in case of major or minor (affecting the first two digit numbers) Reflex upgrades, the user should erase the `$HOME/KeplerData`, `$HOME/.kepler` directories if present, to prevent possible aborts (i.e. a hard crash) of the `esoreflex` process.

3.1 Installing Reflex workflows via `macports`

This method is supported for the macOS operating system. It is assumed that `macports` (<http://www.macports.org>) is installed. Please read the full documentation at <http://www.eso.org/sci/software/pipelines/installation/macports.html>.

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

This method is supported for Fedora 26 to 29, CentOS 7, Scientific Linux 7 operating systems, and requires `sudo` rights. To install, please follow these steps

1. Configure the ESO repository (This step is only necessary if the ESO repository has not already been previously configured).

- If you are running Fedora 26 or newer, run the following commands:

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

- If you are running CentOS 7, run the following commands:

```
sudo yum install yum-utils ca-certificates yum-conf-repos
sudo yum install epel-release
sudo yum-config-manager --add-repo=ftp://ftp.eso.org/pub/dfs/
pipelines/repositories/stable/centos/esorepo.repo
```

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- If you are running SL 7, run the following commands:

```
sudo yum install yum-utils ca-certificates yum-conf-repos
sudo yum install yum-conf-epel
sudo yum-config-manager --add-repo=ftp://ftp.eso.org/pub/dfs/
pipelines/repositories/stable/sl/esorepo.repo
```

2. Install the pipelines

- The list of available top level packages for different instruments is given by:

```
sudo dnf list esopipe-\*-all # (Fedora 26 or newer)
sudo yum list esopipe-\*-all # (CentOS 7, SL 7)
```

- To install an individual pipeline use the following (This example is for X-Shooter. Adjust the package name to the instrument you require.):

```
sudo dnf install esopipe-xshoo-all # (Fedora 26 or newer)
sudo yum install esopipe-xshoo-all # (CentOS 7, SL 7)
```

- To install all pipelines use:

```
sudo dnf install esopipe-\*-all # (Fedora 26 or newer)
sudo yum install esopipe-\*-all # (CentOS 7, SL 7)
```

For further information, please read the full documentation at
<http://www.eso.org/sci/software/pipelines/installation/rpm.html>.

3.3 Installing Reflex workflows via `install_esoreflex`

This method is recommended for operating systems other than what indicated above, or if the user has no sudo rights. Software dependencies are not fulfilled by the installation script, therefore the user has to install all the prerequisites before running the installation script.

The software pre-requisites for Reflex 2.11.0 may be found at:
http://www.eso.org/sci/software/pipelines/reflex_workflows

To install the Reflex 2.11.0 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:

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```
./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. Follow all the script instructions; you will be asked whether to use your Internet connection (recommended: yes), the pipelines and demo-datasets to install (note that the installation will remove all previously installed pipelines that are found in the same installation directory).
5. 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 ~ 5 GB, ~ 9 GB and ~ 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 `esoreflex 2.11.0` release. By following these steps, the user should have enough information to perform a reduction of his/her own data without any further reading:

1. First, type:

```
esoreflex -l
```

If the `esoreflex` executable is not in your path, then you have to provide the command with the executable full path `<install_dir>/bin/esoreflex -l`. For convenience, we will drop the reference to `<install_dir>`. A list with the available `esoreflex` workflows will appear, showing the workflow names and their full path.

2. Open the GRAVITY by typing:

```
esoreflex gravity_wkf&
```

Alternatively, you can type only the command `esoreflex` the empty canvas will appear (Figure 5.1) and you can select the workflow to open by clicking on `File -> Open File`. Note that the loaded workflow will appear in a new window. The GRAVITY workflow is shown in Figure 8.1.

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. Change directories set-up. Under “Setup Directories” in the workflow canvas there are seven parameters that specify important directories (green dots).

By default, the `ROOT_DATA_DIR`, which specifies the working directory within which the other directories are organised, is set to your `$HOME/reflex_data` directory. All the temporary and final products of the reduction will be organized under sub-directories of `ROOT_DATA_DIR`, therefore make sure this parameter points to a location where there is enough disk space. To change `ROOT_DATA_DIR`, double click on it and a pop-up window will appear allowing you to modify the directory string, which you may either edit directly, or use the button to select the directory from a file browser. When you have finished, click to save your changes.

Changing the value of `RAW_DATA_DIR` is the only necessary modification if you want to process data other than the demo data

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

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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 `esoreflex` 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 keywords⁴. 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. A full description of the options offered by the `Data Set Chooser` will be presented in Section 7.2.2.
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 8.7 shows the *Product Explorer* window. A full description of the *Product Explorer* will be presented in Section 7.2.3.
10. After the workflow has finished, all the products from all the datasets can be found in a directory under `END_PRODUCTS_DIR` named after 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.

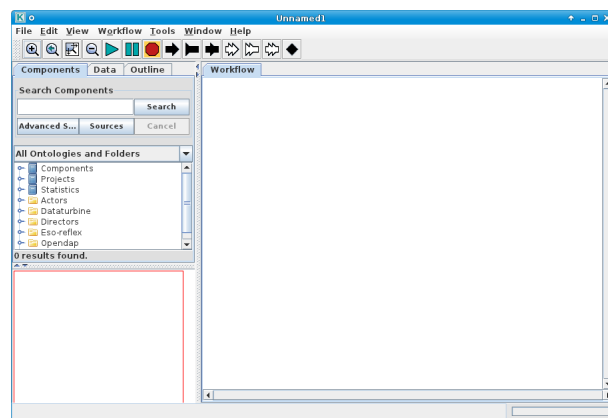


Figure 5.1: *The empty Reflex canvas.*

⁴The keywords listed can be changed by double clicking on the `DataOrganiser` Actor and editing the list of keywords in the second line of the pop-up window. Alternatively, instead of double-clicking, you can press the right mouse button on the `DataOrganiser` Actor and select `Configure Actor` to visualize the pop-up window.

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6 About the main `esoreflex` 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 `esoreflex` 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 `esoreflex` 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; [4]).

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 (note that this does not work for all instrument workflows).

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 7.2.5), reusing the previous pipeline recipe outputs if 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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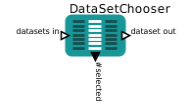
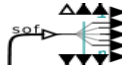
windows are disabled in the default configuration and therefore are not affected by this parameter.

The parameter `ProductExplorerMode` controls whether the `ProductExplorer` actor will show its window or not. The possible values are `Enabled`, `Triggered`, and `Disabled`. `Enabled` opens the `ProductExplorer` GUI at the end of the reduction of each individual dataset. `Triggered` (default and recommended) opens the `ProductExplorer` GUI when all the selected datasets have been reduced. `Disabled` does not display the `ProductExplorer` GUI.

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 `DataOrganiser` actor.
- 
 - The `DataSetChooser` actor (inside a composite actor).
- 
 - The `FitsRouter` actor Redirects files according to their categories.
- 
 - The `ProductRenamer` actor.
- 
 - The `ProductExplorer` 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 DataSetChooser

The `DataSetChooser` displays the `DataSets` available in the “Select Data Sets” window, activating vertical and horizontal scroll bars if necessary (Fig. 8.4).

Some properties of the `DataSets` are displayed: the name, the number of files, a flag indicating if it has been successfully reduced (a green OK), if the reduction attempts have failed or were aborted (a red FAILED), or if

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it is a new dataset (a black "-"). The column "Descriptions" lists user-provided descriptions (see below), other columns indicate the instrument set-up and a link to the night log.

Sometimes you will want to reduce a subset of these DataSets rather than all DataSets, and for this you may individually select (or de-select) DataSets for processing using the tick boxes in the first column, and the buttons `Deselect All` and `Select Complete` at the bottom, or configure the "Filter" field at the bottom left. Available filter options are: "New" (datasets not previously reduced will be selected), "Reduced" (datasets previously reduced will be selected), "All" (all datasets will be selected), and "Failed" (dataset with a failed or aborted reduction will be selected).

You may also highlight a single DataSet in blue by clicking on the relevant line. If you subsequently click on `Inspect Highlighted`, then a "Select Frames" window will appear that lists the set of files that make up the highlighted DataSet including the full filename⁵, the file category (derived from the FITS header), and a selection tick box in the right column. The tick boxes allow you to edit the set of files in the DataSet which is useful if it is known that a certain calibration frame is of poor quality (e.g: a poor raw flat-field frame). The list of files in the DataSet may also be saved to disk as an ASCII file by clicking on `Save As` and using the file browser that appears.

By clicking on the line corresponding to a particular file in the "Select Frames" window, the file will be highlighted in blue, and the file FITS header will be displayed in the text box on the right, allowing a quick inspection of useful header keywords. If you then click on `Inspect`, the workflow will open the file in the selected FITS viewer application defined by the workflow parameter `FITS_VIEWER`.

To exit from the "Select Frames" window, click `Continue`.

To add a description of the reduction, press the button `...` associated with the field "Add description to the current execution of the workflow" at the bottom right of the Select Dataset Window; a pop up window will appear. Enter the desired description (e.g. "My first reduction attempt") and then press `OK`. In this way, all the datasets reduced in this execution, will be flagged with the input description. Description flags can be visualized in the `SelectFrames` window and in the `ProductExplorer`, and they can be used to identify different reduction strategies.

To exit from the "Select DataSets" window, click either `Continue` in order to continue with the workflow reduction, or `Stop` in order to stop the workflow.

7.2.3 The ProductExplorer

The `ProductExplorer` is an interactive component in the `esoreflex` workflow whose main purpose is to list the final products with the associated reduction tree for each dataset and for each reduction attempt (see Fig. 8.7).

Configuring the ProductExplorer

You can configure the `ProductExplorer` GUI to appear after or before the data reduction. In the latter case you can inspect products as reduction goes on.

1. To display the `ProductExplorer` GUI at the end of the data reduction:

⁵keep the mouse pointer on the file name to visualize the full path name.

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- Click on the global parameter “ProductExplorerMode” before starting the data reduction. A configuration window will appear allowing you to set the execution mode of the Product Explorer. Valid options are:
 - "Triggered" (default). This option opens the ProductExplorer GUI when all the selected datasets have been reduced.
 - "Enabled". This option opens the ProductExplorer GUI at the end of the reduction of each individual dataset.
 - “Disable”. This option does not display the ProductExplorer GUI.
- Press the  button to start the workflow.

2. To display the ProductExplorer GUI “before” starting the data reduction:

- double click on the composite Actor "Inspect previously reduced data". A configuration window will appear. Set to "Yes" the field "Inspect previously reduced data (Yes/No)". Modify the field "Continue reduction after having inspected the previously reduced data? (Continue/Stop/Ask)". "Continue" will continue the workflow and trigger the DataOrganizer. "Stop" will stop the workflow; "Ask" will prompt another window deferring the decision whether continuing or not the reduction after having closed the Product Explorer.
- Press the  button to start the workflow. Now the ProductExplorer GUI will appear before starting the data organization and reduction.

Exploring the data reduction products

The left window of the ProductExplorer GUI shows the executions for all the datasets (see Fig. 8.7). Once you click on a dataset, you get the list of reduction attempts. Green and red flags identify successful or unsuccessful reductions. Each reduction is linked to the “Description” tag assigned in the “Select Dataset” window.

1. To identify the desired reduction run via the “Description” tag, proceed as follows:

- Click on the symbol at the left of the dataset name. The full list of reduction attempts for that dataset will be listed. The column Exec indicates if the reduction was successful (green flag: "OK") or not (red flag: "Failed").
- Click on the entries in the field "Description" to visualize the description you have entered associated to that dataset on the Select Dataset window when reducing the data.
- Identify the desired reduction run. All the products are listed in the central window, and they are organized following the data reduction cascade.

You can narrow down the range of datasets to search by configuring the field "Show" at the top-left side of the ProductExplorer (options are: "All", "Successful", "Unsuccessful"), and specifying the time range (Last, all, From-to).

2. To inspect the desired file, proceed as follows:

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- Navigate through the data reduction cascade in the ProductExplorer by clicking on the files.
- Select the file to be inspected and click with the mouse right-hand button. The available options are:
 - Options available always:
 - * Copy full path. It copies the full name of the file onto the clipboard. Shift+Ctrl+v to past it into a terminal.
 - * Inspect Generic. It opens the file with the fits viewer selected in the main workflow canvas.
 - * Inspect with. It opens the file with an executable that can be specified (you have to provide the full path to the executable).
 - Options available for files in the TMP_PRODUCTS_DIR directory only:
 - * command line. Copy of the environment configuration and recipe call used to generate that file.
 - * Xterm. It opens an Xterm at the directory containing the file.
 - Options available for products associated to interactive windows only:
 - * Display pipeline results. It opens the interactive windows associated to the recipe call that generated the file. Note that this is for visualization purposes only; the recipe parameters cannot be changed and the recipe cannot be re-run from this window.

7.2.4 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.
- 
 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.

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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 9 in table 9.2. The intermediate pipeline calibration products can be found in subdirectories of the `TMP_PRODUCT_DIR` and are summarized in section 9 and in table

7.2.5 Lazy Mode

By default, all `RecipeExecutor` 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`.

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. *Note: The option `EraseDirs = true` does not work in esoreflex version 2.9.x and makes the workflow to crash.*

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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.

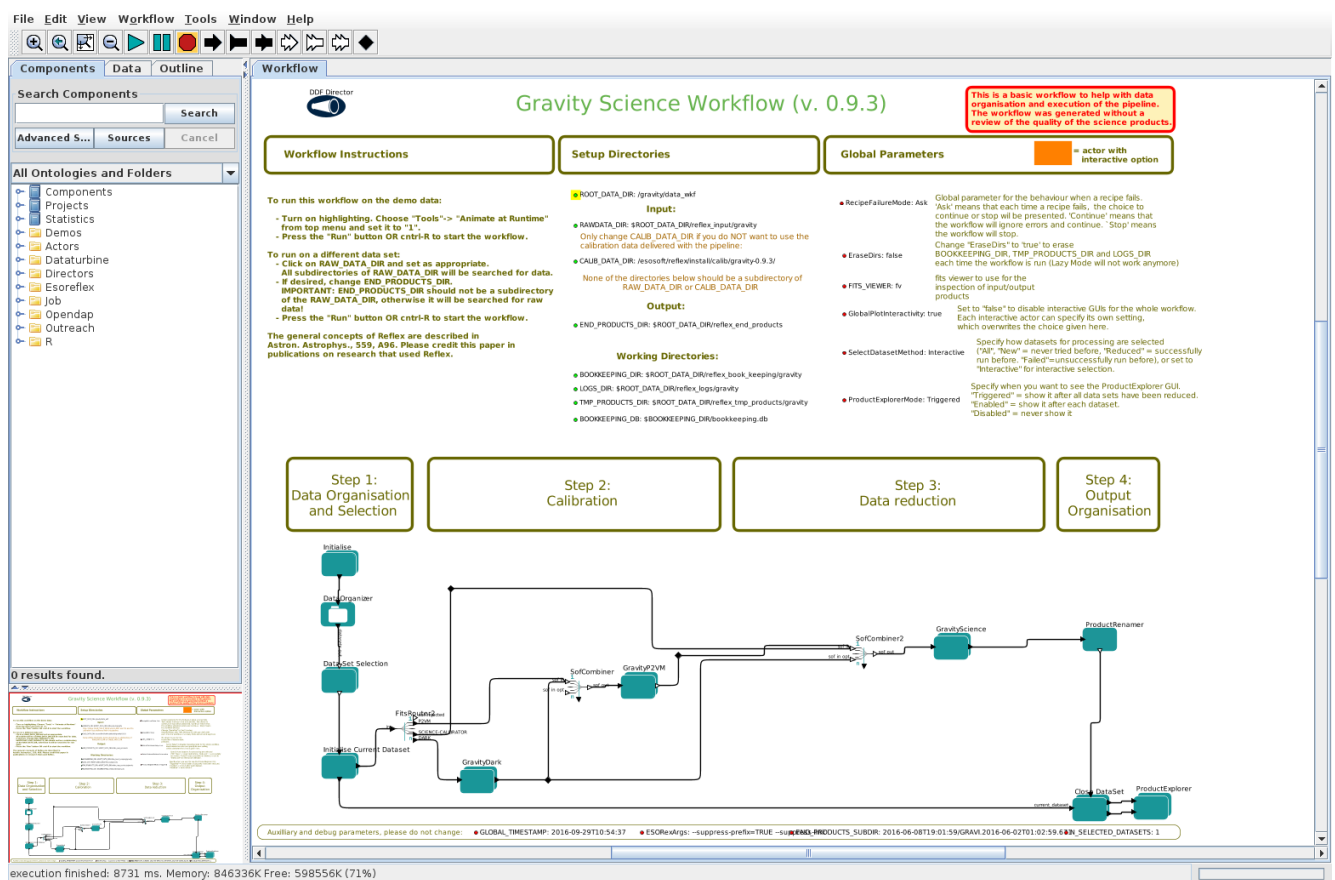


Figure 8.1: *gravity_wkf* workflow layout.

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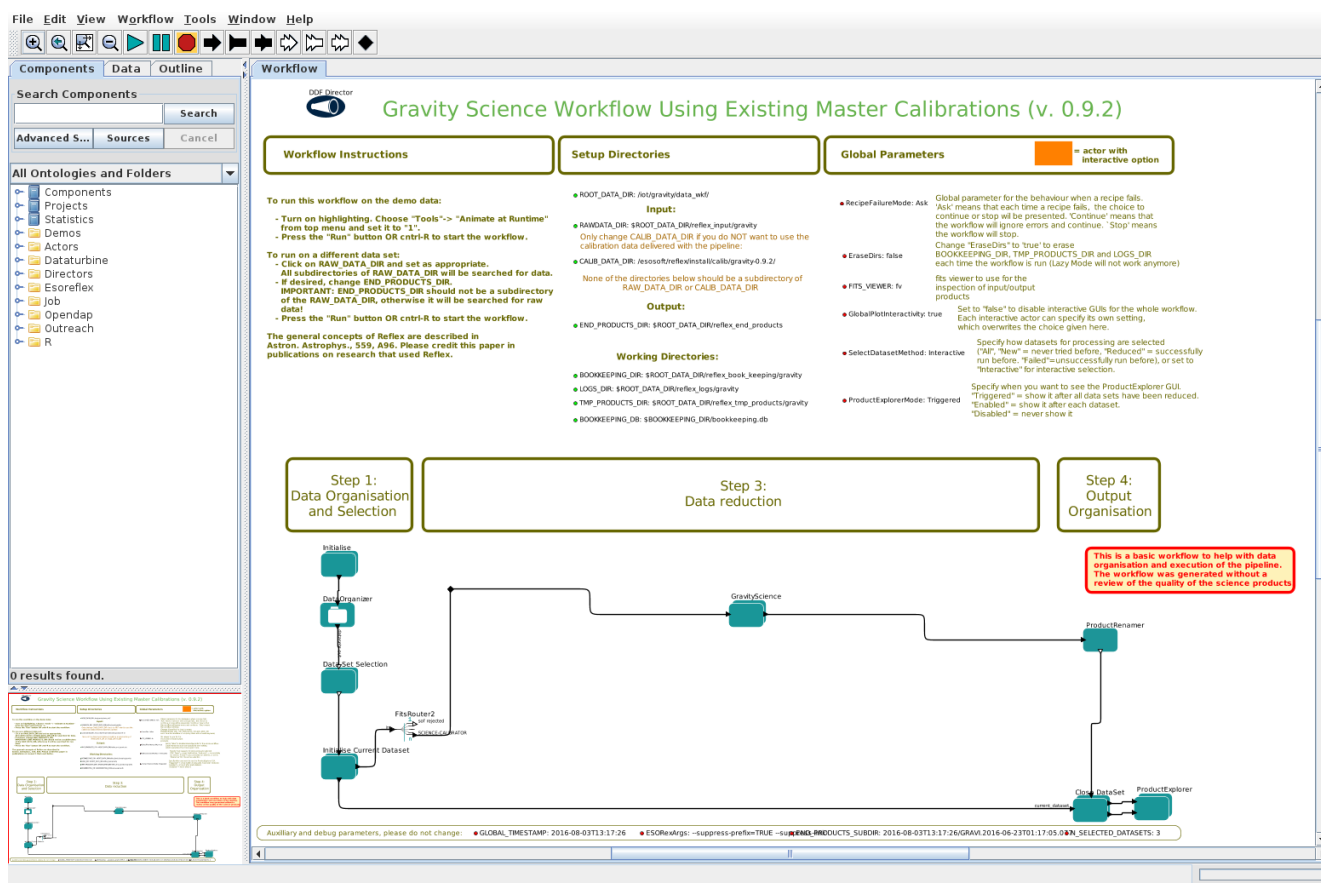


Figure 8.2: gravity_mastercalib workflow layout.

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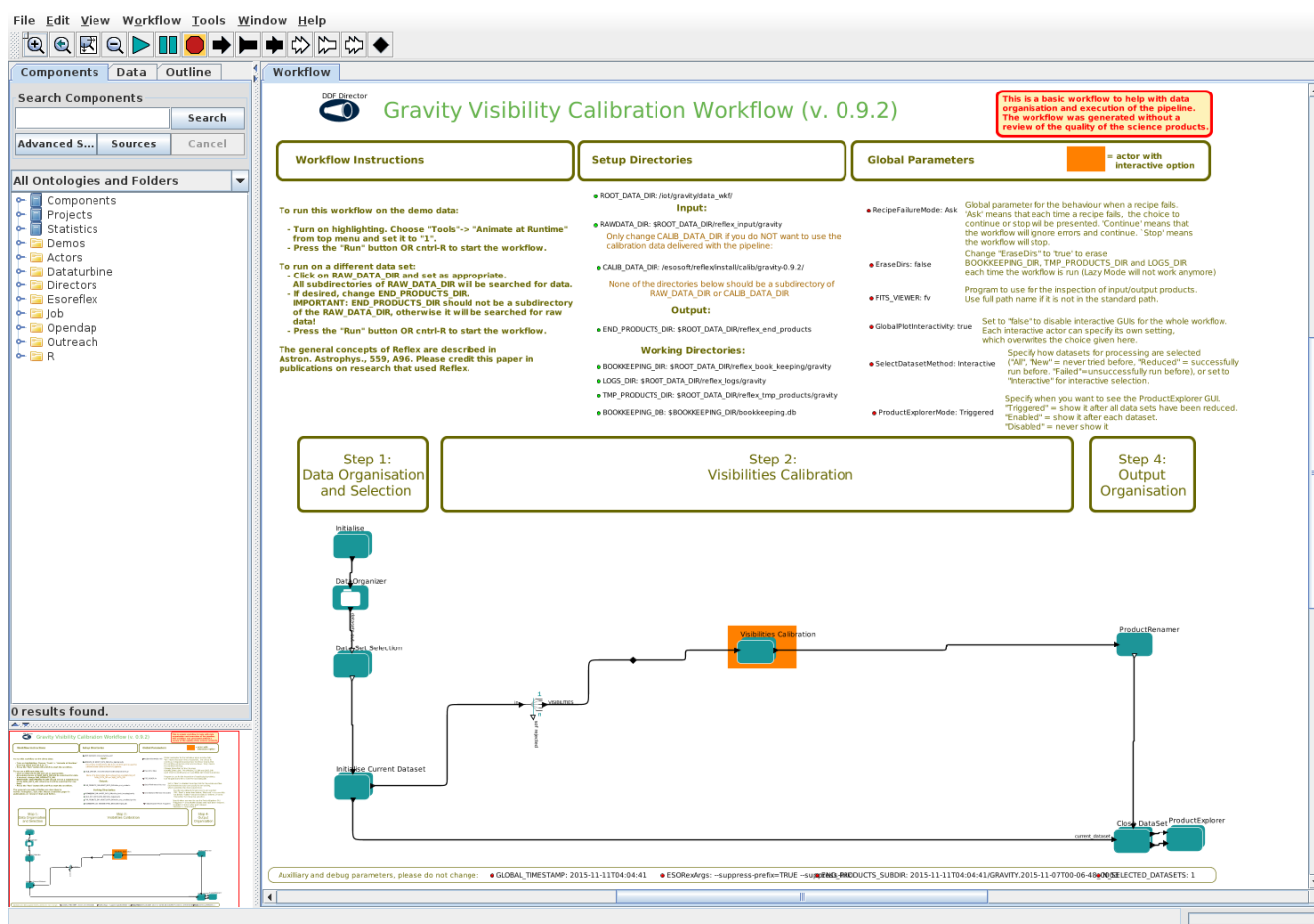


Figure 8.3: gravity_viscal workflow layout.

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8.2 Specifying data directories and selecting files

To reduce your own science data, simply change the paths to the root (optional) and data directories. Under the root directory, Reflex will create sub-directories which will contain temporary and end products, as well as book keeping and log files. The data directory, 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 start 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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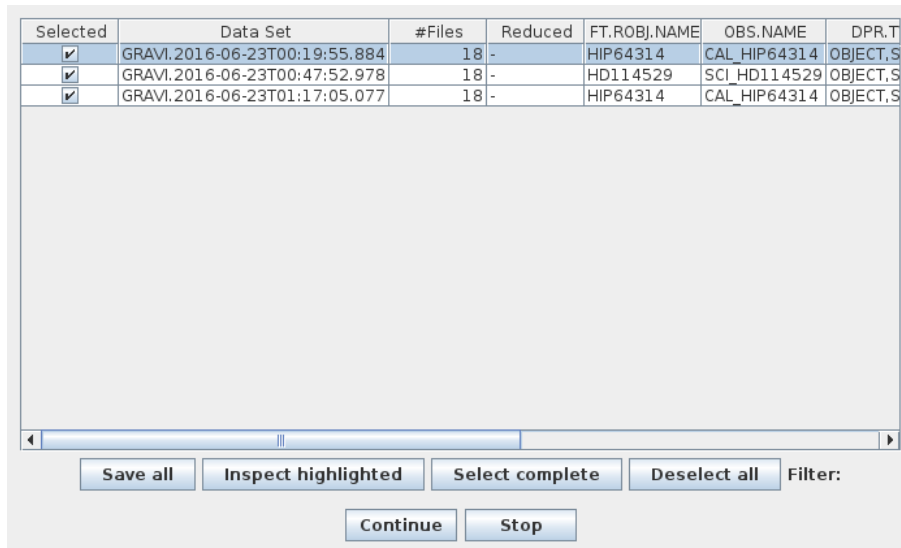


Figure 8.4: The “Select Datasets” pop-up window.

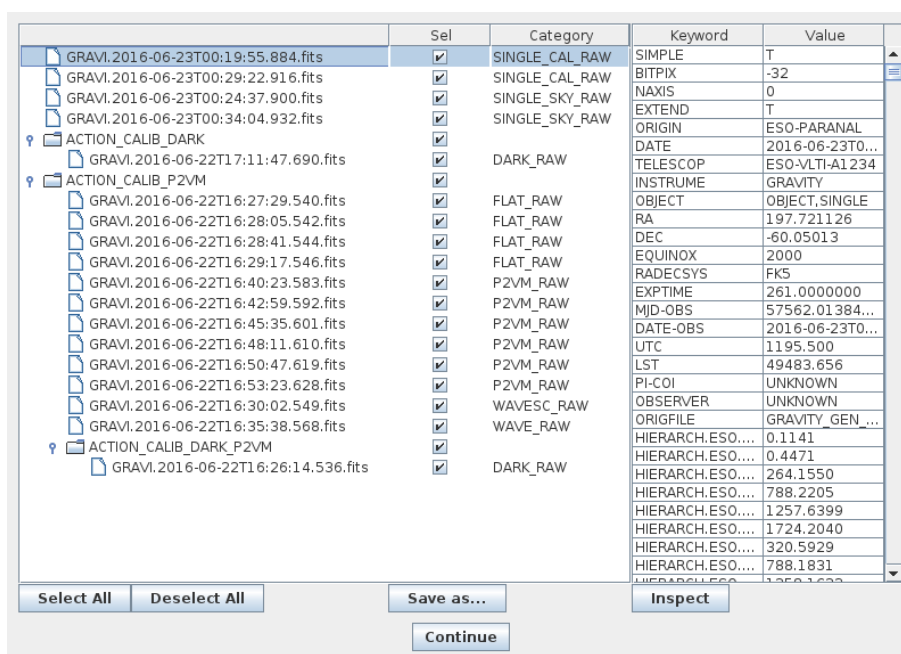


Figure 8.5: The “Select Frame” pop-up window, obtained after pressing the “Inspect highlighted” button in the “Select Datasets” window.

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8.3 Correction of systematic errors in the 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 1.5.0 of the pipeline, if the vFactor correction results in visibilities significantly larger than unity, the correction must be switched off. 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. 8.6. To disable the vFactor correction, change the value of vis-correction-sc (recipe_param_26) from VFATOR to NONE. Please note that turning the vFactor correction off is not recommended in general.

Likewise, if you needed to disable the bias correction, you would set the value of parameter debias-sc (recipe_param_23) 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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8.4 Removing instrumental signatures from the source spectrum

GRAVITY records the source spectrum in addition to the source fringes. The former is affected by the wavelength-dependent throughput, and to correct for this, the value of the parameter flat-flux (recipe_param_29) must be set to "true".

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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:

recipe_param_16:

recipe_param_17:

recipe_param_18:

recipe_param_19:

recipe_param_20:

recipe_param_21:

recipe_param_22:

recipe_param_23:

recipe_param_24:

recipe_param_25:

recipe_param_26:

recipe_param_27:

recipe_param_28:

recipe_param_29:

recipe_param_30:

recipe_param_31:

recipe_param_32:

gravity_vis

Run

☒

\$RecipeFailureMode

Strip last

☒

☐

☐

☐

\$TMP_PRODUCTS_DIR	Browse	Configure
\$LOGS_DIR	Browse	Configure
\$BOOKKEEPING_DIR	Browse	Configure
\$ESORexArgs		
\$BOOKKEEPING_DB	Browse	Configure

static-name=false

bias-subtracted-file=false

spectrum-file=false

preproc-file=false

p2vmreduced-file=false

astro-file=false

average-vis=false

bias-method=MEDIAN

ditshift-sc=0

acq-correction-delay=0.1

interp-3pixels=false

nsmooth-snr-ft=5

snr-min-ft=3

global-state-min-ft=2

global-state-max-ft=4

state-min-ft=1

tracking-min-sc=0.8

vfactor-min-sc=0.1

use-met-zero=true

use-met-zero=true

max-frame=10000

force-same-time=false

debias-sc=true

debias-ft=true

nboot=20

vis-correction-sc=VFACTOR

phase-ref-sc=AUTO

output-phase-sc=AUTO

flat-flux=true

average-sky=false

reduce-acq-cam=false

color-wave-correction=false

Commit
Add
Remove
Defaults
Preferences
Help
Cancel

Figure 8.6: The interactive window to edit parameters of recipe gravity_vis.

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8.5 Examining the workflow results

When the workflow has finished, the Product Explorer window opens (Fig. 8.7). 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. 8.8) and a master dark frame (Fig. 8.9) are shown below.

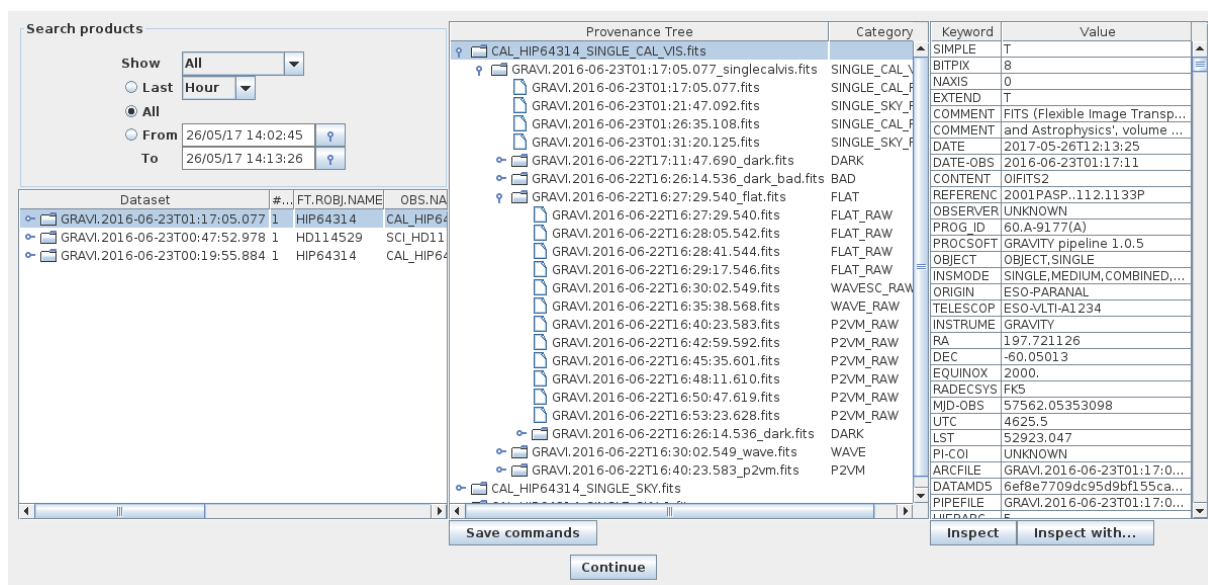


Figure 8.7: The GRAVITY product explorer for the gravity_vis workflow.

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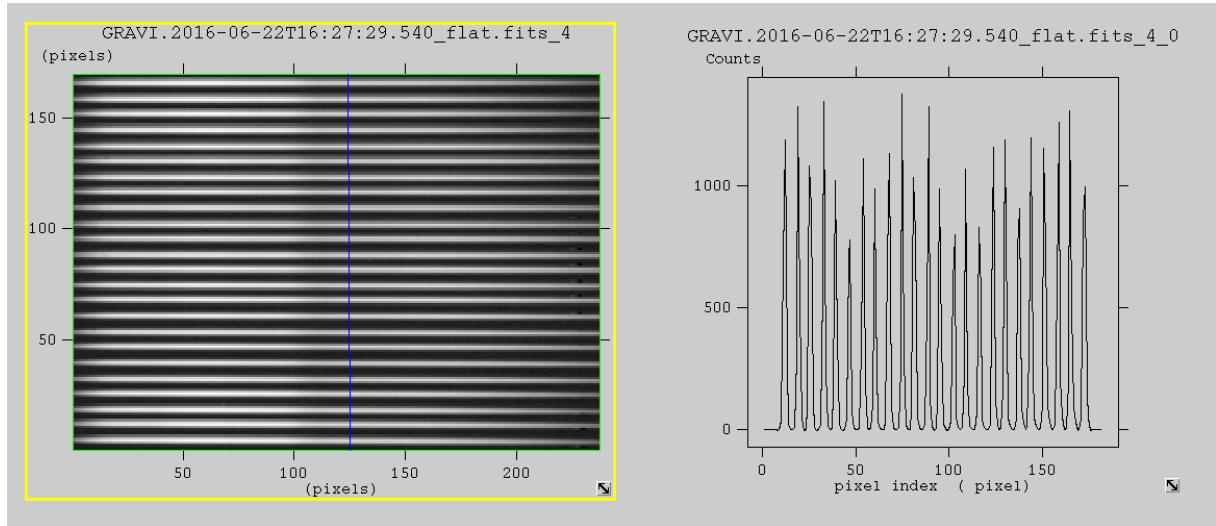


Figure 8.8: *GRAVITY* master flat image, stored in the *IMAGING_DATA_SC* binary extension. The horizontal axis is the wavelength axis, the 24 output channels are arranged along the vertical axis.

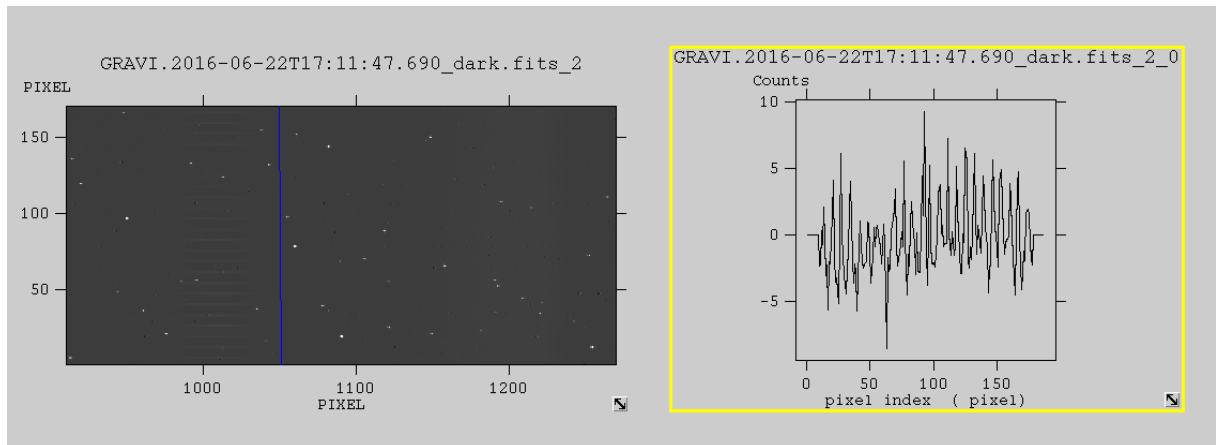


Figure 8.9: *GRAVITY* master dark image, stored in the *IMAGING_DATA_SC* binary extension. The horizontal axis is the wavelength axis, the 24 output channels are arranged along the vertical axis.

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8.6 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 plot window showing the TF for each of the six baselines of GRAVITY, as shown in Fig. 8.10. The calibrator diameter information is taken from *GRAVI_FAINT_CALIBRATORS.fits* in the Reflex directory *install/calib/gravity-1.1.2/cal*. Please note that the calibrated data files are not in the *reflex_end_products* directory, but under the *reflex_tmp_products/gravity_viscal/gravity_v* directory, in a folder named with the date and time when it was created.

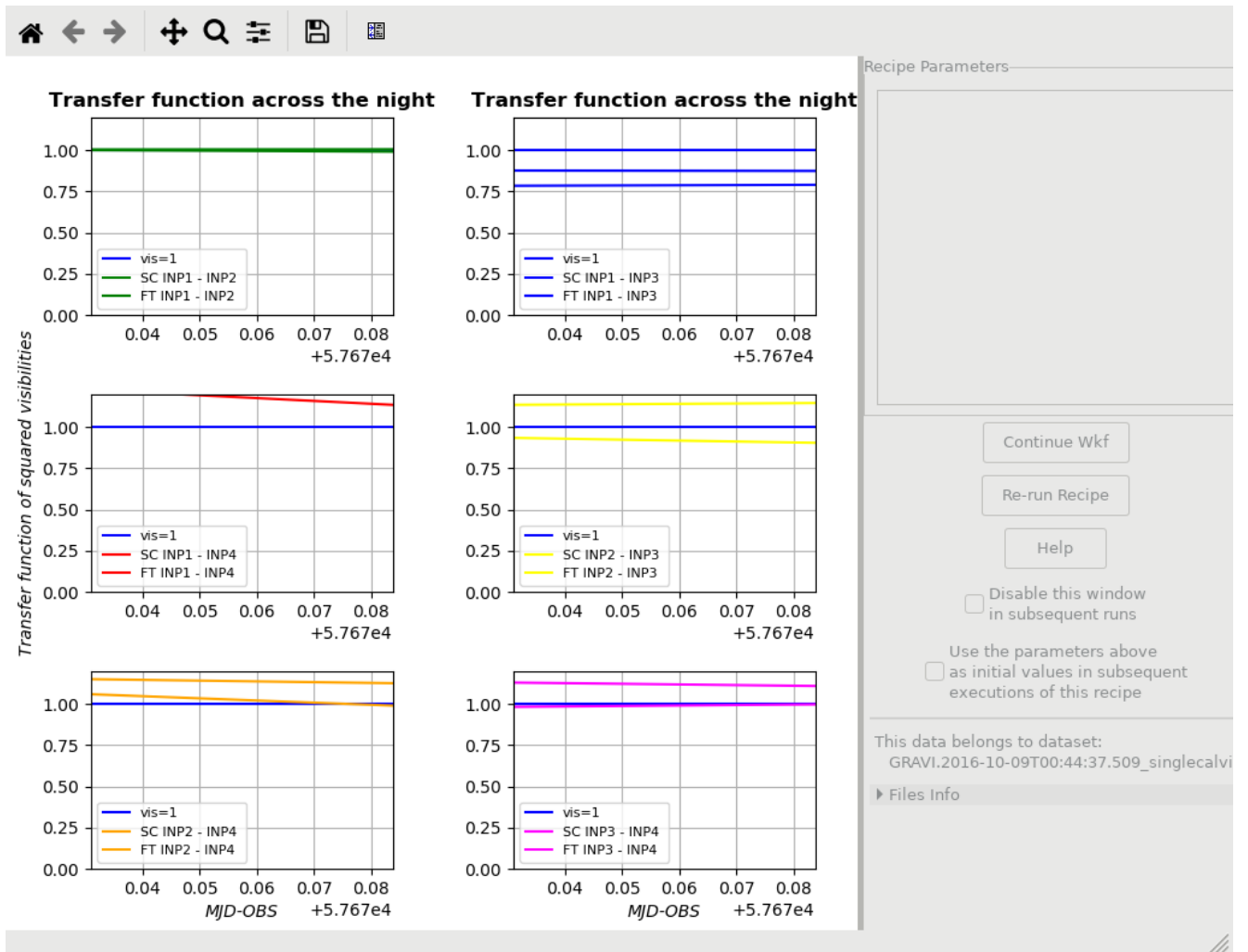


Figure 8.10: *gravity_viscal* workflow plot of the FT and SC channel transfer functions.

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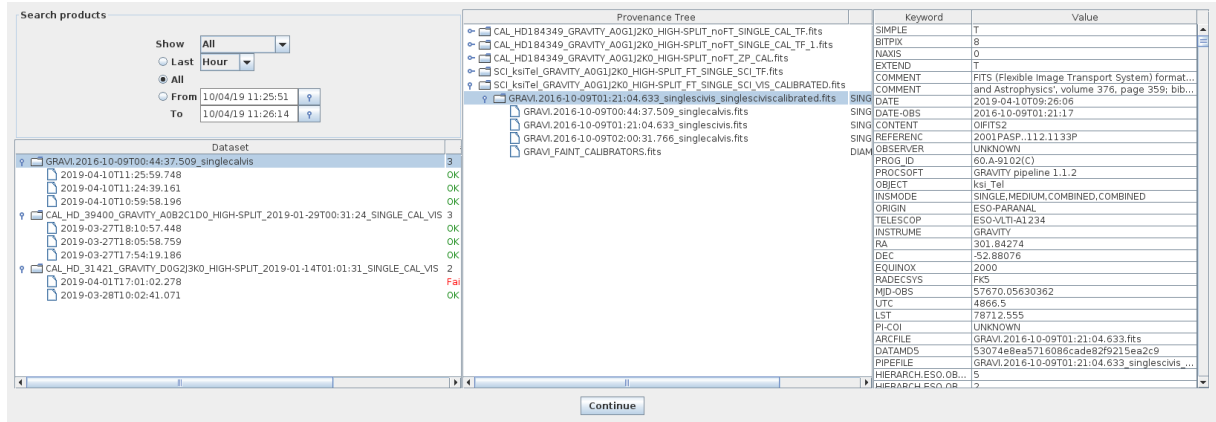


Figure 8.11: The GRAVITY product explorer for the gravity_viscal workflow.

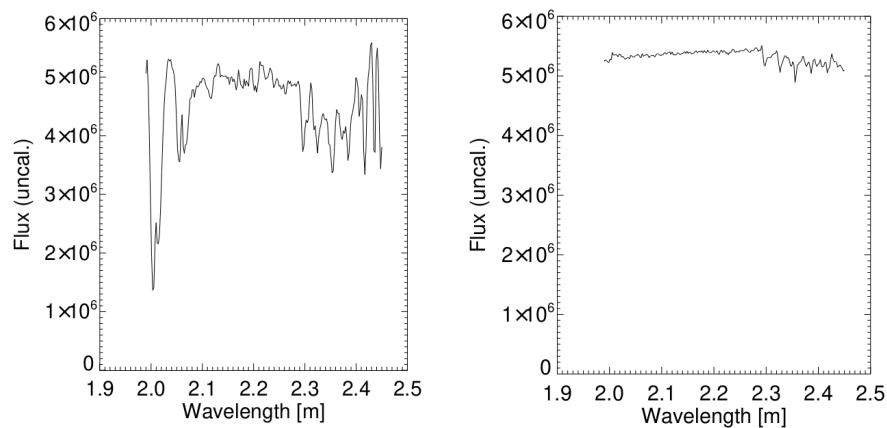


Figure 8.12: Uncalibrated (left) and calibrated (right) medium resolution spectra of the science target, produced by gravity_viscal. The deep absorption lines in the uncalibrated spectrum are telluric features of CO₂ and H₂O.

8.7 Calibrating your flux spectra

The workflow *gravity_viscal* also allows you to divide the science spectrum by the calibrator spectrum. If your calibrator had a featureless spectrum, you would get the best correction of the telluric features possible. However, this is almost never the case since nearly featureless spectra are only displayed by early-type stars, and these are usually poor calibrators due to the high fraction of multiples in these classes. To have the workflow do the division, you should set the value of the parameter `calib-flux` to `true` (recipe_parameter_7).

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8.8 Telluric corrections of the flux spectra with Molecfit

Molecfit⁶ is a tool to fit abundances of atmospheric molecules to their telluric absorption lines in astronomical spectra. These can then be used in turn to compute the telluric absorption over the entire wavelength range covered by the spectrum for the purpose of removing the telluric absorption lines. In the following, we show an example computed for the high resolution mode of GRAVITY. In this example, the data file (*gravity.dat*) is a text file with two columns, wavelength (in microns) and flux. In the *K* band we only fit the carbondioxide, water, and methane lines. A Gaussian line profile is adopted, whose width changes with wavelength. Atmospheric parameters such as temperature, pressure, humidity, can be extracted from the FITS headers of the GRAVITY data files. An example parameter file is given below. The only parameter values which need to be updated are `cont_const`, the approximate level of the continuum flux, observation date and time, telescope altitude (i.e., pointing), and the weather parameters.

```
filename: gravity.dat
trans: 1
columns: Wavelength Flux NULL NULL
default_error: 1.0
wlgto micron: 1.0
vac_air: air
wrange_include: gravity_include.dat
wrange_exclude: gravity_exclude.dat
ftol: 0.01
xtol: 0.01
list_molec: H2O CO2 CH4
fit_molec: 1 1 1
relcol: 1.0 1.06 1.0
flux_unit: 0
fit_back: 0
telback: 0.1
fit_cont: 1
cont_n: 1
cont_const: 110000.0
fit_wlc: 1
wlc_n: 1
wlc_const: 0.0
fit_res_box: 0
relres_box: 0.0
fit_res_gauss: 1
res_gauss: 1.4
fit_res_lorentz: 0
res_lorentz: 0.5
kernmode: 0
kernfac: 30.0
varkern: 1
```

⁶<http://www.eso.org/sci/software/pipelines/skytools/molecfit>

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```

obsdate: 57849.000
obsdate_key: MJD-OBS
utc: 5826.8243
utc_key: UTC
telalt: 68.923724
telalt_key: ESO TEL ALT
rhum: 32.0000
rhum_key: ESO TEL AMBI RHUM
pres: 744.380
pres_key: ESO TEL AMBI PRES START
temp: 14.4900
temp_key: ESO TEL AMBI TEMP
mltemp: 14.4900
mltemp_key: ESO TEL TH M1 TEMP
geoelev: 2635.0
geoelev_key: ESO TEL GEOELEV
longitude: -70.4032
longitude_key: ESO TEL GEOLON
latitude: -24.6258
latitude_key: ESO TEL GEOLAT
slitw: 0.4
slitw_key: ESO INS SLIT1 WID
pixsc: 0.086
pixsc_key: NONE
ref_atm: equ.atm
gdas_dir: data/profiles/grib
gdas_prof: auto
layers: 1
emix: 5.0
pwv: -1.
end

```

The file *gravity_include.dat* is shown below. It contains the wavelength intervals including the most prominent CO₂, CH₄, and H₂O lines for the fit of the abundances of these species.

```

# CO2
1.99 2.08
# CH4
2.315 2.321
2.363 2.380
#
# H2O
2.41 2.45

```

The file *gravity_exclude.dat* is shown below. It contains the wavelength intervals including the most common intrinsic lines of the late-type calibrators or science targets which must not be fit.

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```
# He line
2.058 2.060
# Br-g line
2.150 2.190
# CO band heads
2.292 2.298
2.321 2.327
2.350 2.356
2.381 2.387
```

The result of an application of Molecfit is shown in Fig. [8.13](#). Even though the most prominent telluric features have been removed from the spectra, the result shows that instrumental residuals from the flat-fielding remain, which are only removed if one divides the science spectrum by the one of the calibrator.

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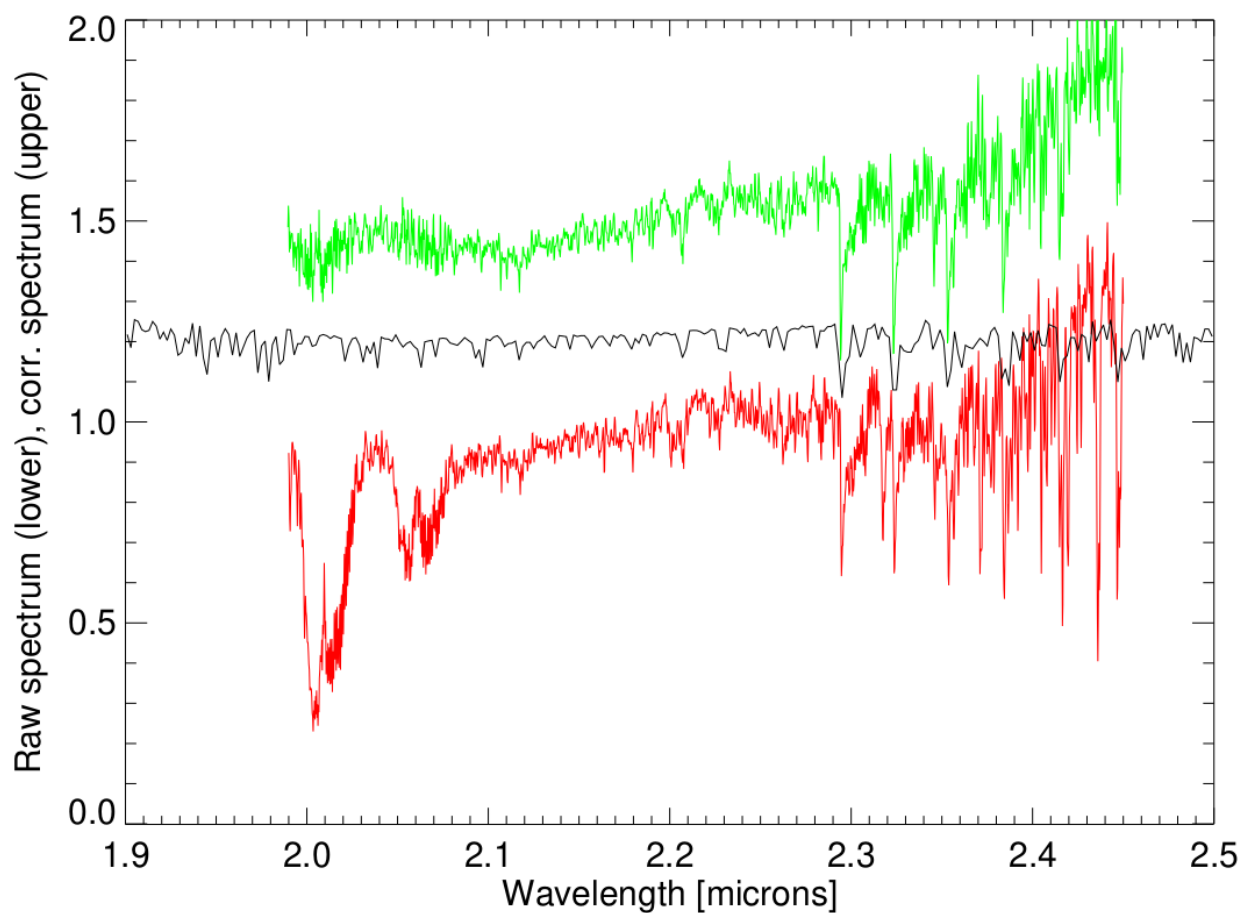


Figure 8.13: Telluric correction computed with Molecfit. The lower (red) spectrum is of the raw flux, the upper (green) spectrum is the raw flux divided by the atmospheric transmission fit to the telluric lines. The middle line is a (lower resolution) spectrum from the NextGen library [3] for the spectral type of the observed star.

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9 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 9.1.

Table 9.1: 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 9.2. Their description will be done in Section 9.1.

Table 9.2: 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 9.3: 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

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9.1 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 information, 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. 9.1 shows the structure of an OIFITS2 file and Figs. 9.2 and 9.3 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				
☐ 0	Primary	Image	0	Header	Image		Table	
☐ 1	OI_ARRAY	Binary	6 cols X 4 rows	Header	Hist	Plot	All	Select
☐ 2	OI_TARGET	Binary	17 cols X 1 rows	Header	Hist	Plot	All	Select
☐ 3	OI_WAVELENGTH	Binary	2 cols X 210 rows	Header	Hist	Plot	All	Select
☐ 4	OI_WAVELENGTH	Binary	2 cols X 5 rows	Header	Hist	Plot	All	Select
☐ 5	OI_VIS	Binary	18 cols X 6 rows	Header	Hist	Plot	All	Select
☐ 6	OI_VIS2	Binary	10 cols X 6 rows	Header	Hist	Plot	All	Select
☐ 7	OI_T3	Binary	14 cols X 4 rows	Header	Hist	Plot	All	Select
☐ 8	OI_FLUX	Binary	8 cols X 4 rows	Header	Hist	Plot	All	Select
☐ 9	OI_VIS	Binary	27 cols X 6 rows	Header	Hist	Plot	All	Select
☐ 10	OI_VIS2	Binary	10 cols X 6 rows	Header	Hist	Plot	All	Select
☐ 11	OI_T3	Binary	14 cols X 4 rows	Header	Hist	Plot	All	Select
☐ 12	OI_FLUX	Binary	13 cols X 4 rows	Header	Hist	Plot	All	Select

Figure 9.1: 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	21	210L	
Invert	Modify	Modify	Modify	Modify	Modify	Modify	Modify	Modify	Modify	Modify	
1	1	3.004850001074E+03	S.756203477836E+04	2.500000000000E+02	Plot	Plot	1.184747173728E+01	1.401293942436E+01	Plot	F	
2	1	3.004850001074E+03	S.756203477836E+04	2.500000000000E+02	Plot	Plot	-5.907509238401E+00	-7.006687578612E+00	Plot	F	
3	1	3.004850001074E+03	S.756203477836E+04	2.500000000000E+02	Plot	Plot	-1.848589227815E+01	1.265930368203E+01	Plot	F	
4	1	3.004850001074E+03	S.756203477836E+04	2.500000000000E+02	Plot	Plot	-1.775498097568E+01	-2.101962700297E+01	Plot	F	
5	1	3.004850001074E+03	S.756203477836E+04	2.500000000000E+02	Plot	Plot	-3.03336401543E+01	-1.353635742328E+00	Plot	F	
6	1	3.004850001074E+03	S.756203477836E+04	2.500000000000E+02	Plot	Plot	-1.257838303975E+01	1.966599126064E+01	Plot	F	

Figure 9.2: OIVIS2 table.

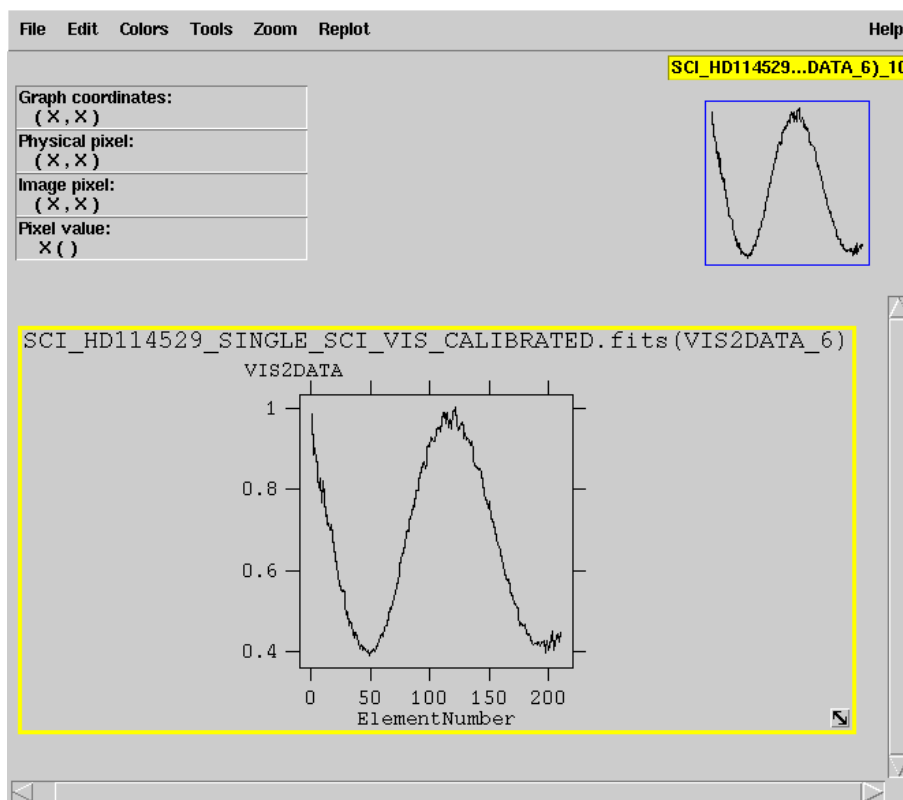


Figure 9.3: Plot of the squared visibility amplitude for baseline 6.

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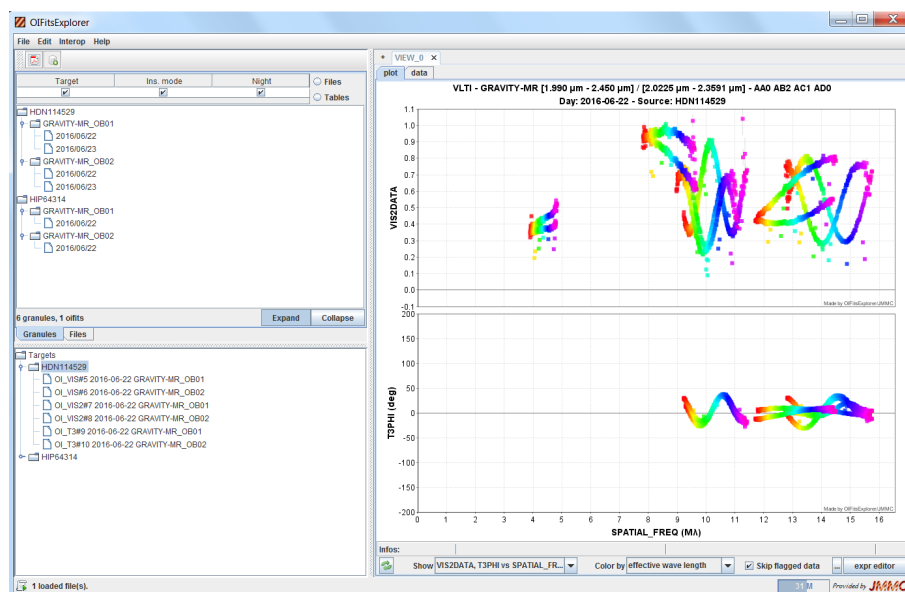


Figure 9.4: OIFitsExplorer view of the demo data (all science files combined).

One can use the OIFitsExplorer (Fig. 9.4)

(http://www.jmmc.fr/oifitsexplorer_page.htm) to examine the data and LitPro

(http://www.jmmc.fr/litpro_page.htm) to fit simple models.

9.2 Calibration of flux spectra

The column named “FLUX” in the “OI_FLUX” table (of the science detector) contains the reduced fluxes from each of the four telescopes for every integration.

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10 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/ 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. 10.1).

```
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.

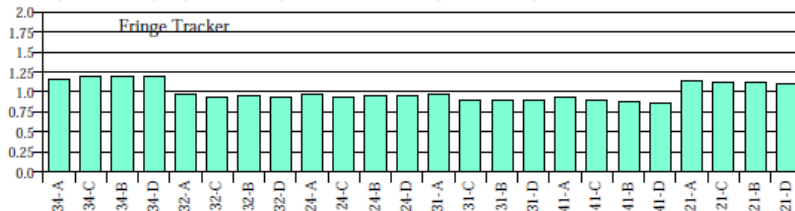
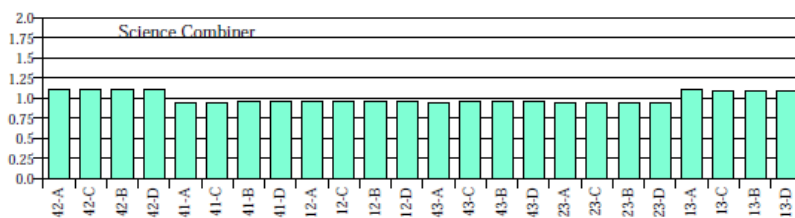
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GRAVITY P2VM Quality Control Report

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).



Coherence transmission per baseline

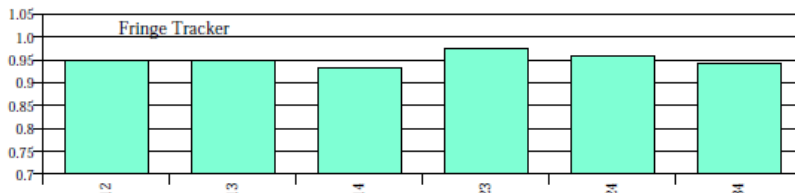
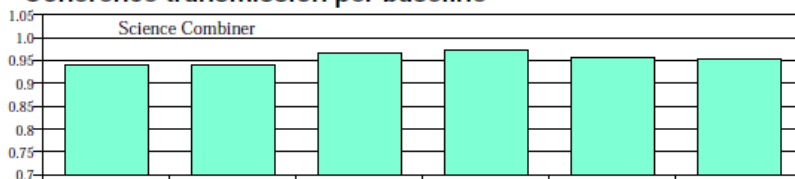


Figure 10.1: The first page of the P2VM report produced by `run_gravi_visual.py`. Note the overall quality rating box near the top of the page.

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11 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 ([4]). 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 ([4]) 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 ([4]) 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.

- **How to insert negative values into a textbox?**

Due to a bug in wxPython, the GUI might appear to freeze when attempting to enter a negative number in a parameter's value textbox. This can be worked around by navigating away to a different control in the GUI with a mouse click, and then navigating back to the original textbox. Once focus is back on the original textbox the contents should be selected and it should be possible to replace it with a valid value, by typing it in and pressing the enter key.

- **I've updated my Reflex installation and when I run esoreflex the process aborts. How can I fix this problem?**

As indicated in Section 3, in case of major or minor (affecting the first two digit numbers) Reflex upgrades, the user should erase the `$HOME/KeplerData`, `$HOME/.kepler` directories if present, to prevent possible aborts (i.e. a hard crash) of the esoreflex process.

- **How can include my analysis scripts and algorithms into the workflow?**

EsoReflex is capable of executing any user-provided script, if properly interfaced. The most convenient way to do it is through the Python actor. Please consult the tutorial on how to insert Python scripts into a workflow available here: www.eso.org/sci/data-processing/Python_and_esoreflex.pdf

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12 Troubleshooting

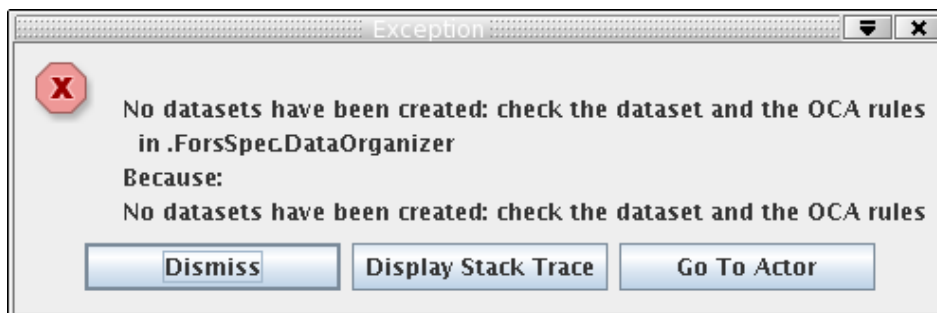


Figure 12.1: *TheDataOrganizer* interactive window reports an error “:No DataSets have been created, check the data set and the OCA rules.”.

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 12.1.)

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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