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Reflex VIMOS/MOS Tutorial

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

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ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	3 of 34

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ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	5 of 34

Contents

1	Introduction And Scope	7
2	Software Installation	8
3	Demo Data	9
4	Quick Start: Reducing The Demo Data	10
5	About The Reflex Canvas	14
5.1	Saving And Loading Workflows	14
5.2	Buttons	14
5.3	Workflow States	14
6	The VIMOS Workflow	15
6.1	Workflow Canvas Parameters	15
6.2	Workflow Actors	16
6.2.1	Simple Actors	16
6.2.2	Composite Actors	16
6.2.3	Recipe Execution within Composite Actors	16
6.2.4	Lazy Mode	19
6.3	Workflow Steps	20
6.3.1	Step 1: Data Organisation And Selection	20
6.3.2	Step 2: Creation Of Master Calibration Files	21
6.3.3	Step 3: Response Computation	21
6.3.4	Step 4: Science Reduction	23
6.3.5	Step 5: Output Organisation	23
6.4	Interactive Windows	24
6.4.1	vmmoscalib	24
6.4.2	vmmosscience (Response)	25
6.4.3	vmmosscience (Science)	25

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	6 of 34

7	Improving Your Results Through Workflow Interaction	28
7.1	Demo Data	28
7.2	Wavelength Calibration	28
8	Frequently Asked Questions	29
8.1	VIMOS specific questions	30
9	Troubleshooting	33

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	7 of 34

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 for further support.

This document is a tutorial designed to enable the user to employ the VIMOS 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 delivered to PIs in the form of PI-Packs (until October 2011) or downloaded from the archive using the CalSelector tool¹ 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 VIMOS MOS spectroscopic observations only via the VIMOS/MOS workflow. The user is referred to the VIMOS web page (<http://www.eso.org/sci/facilities/paranal/instruments/vimos/>) for more information on the instrument itself, and the VIMOS pipeline user manual for the details of the pipeline recipes (<http://www.eso.org/sci/software/pipelines/>).

The workflow uses association rules known to work with files downloaded from the ESO archive with the CalSelector tool (from year 2009 onwards).

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

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	8 of 34

2 Software Installation

The software pre-requisites for Reflex 2.8 may be found at:

http://www.eso.org/sci/software/pipelines/reflex_workflows

To install the Reflex 2.8 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. 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.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	9 of 34

3 Demo Data

Together with the pipeline you will also receive a demo data set, that allows you to run the `Reflex VIMOS` workflow without any changes in parameters. This way you have a data set to experiment with before you start to work on your own data. The demo data for VIMOS includes both data for the IFU and MOS workflows, but a given workflow will only use the data for that mode.

Note that you will need a minimum of ~ 1.3 GB, ~ 0.6 GB and ~ 7.0 GB of free disk space for the directories `<download_dir>`, `<install_dir>` and `<data_dir>`, respectively. The VIMOS demo data have been retrieved with the CalSelector tool².

²<http://www.eso.org/sci/archive/calselectorInfo.html>

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	10 of 34

4 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 VIMOS demo data set supplied with the Reflex 2.8 release. By following these steps, the user should have enough information to attempt a reduction of his/her own data without any further reading:

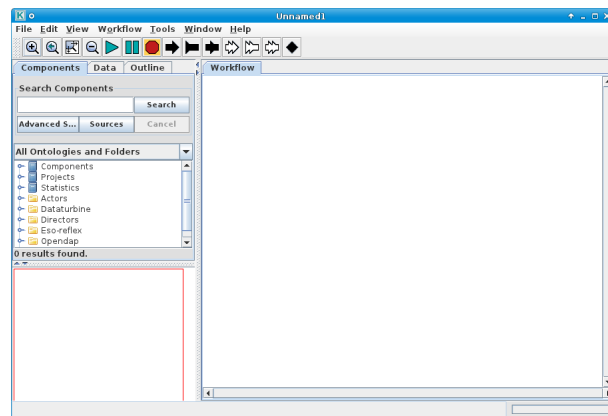


Figure 4.1: *The empty Reflex canvas.*

1. Start the Reflex application:


```
reflex &
```

The empty Reflex canvas as shown in Figure 4.1 will appear.

2. Now open the VIMOS workflow by clicking on File -> Open File, selecting first vimos-3.0.0 and then the file VimosMos.xml in the file browser. You will be presented with the workflow canvas shown in Figure 4.2. 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). Setting the value of ROOT_DATA_DIR is the only necessary modification if you want to process data other than the demo data³, 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 button to select the directory from a file browser. When you have finished, click to save your changes.

³If you used the install script install_reflex, then the value of the parameter ROOT_DATA_DIR will already be set correctly to the directory where the demo data was downloaded.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	11 of 34

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 `RAWDATA_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 `RAWDATA_DIR` or in `CALIB_DATA_DIR`, otherwise DataSets may be incomplete and cannot be processed. However, if the same reference file was downloaded twice in 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 4.3) 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, and by default all complete DataSets are 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. When the reduction of the current DataSet finishes, a pop-up window called *Product Explorer* will appear showing the datasets which have been so far 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 4.5 shows the Product Explorer window.
10. The workflow will continue with the remaining DataSets following the same steps described above.
11. 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 `VIMOS` workflow that merit a look at the rest of this tutorial.

⁴The 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.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	12 of 34

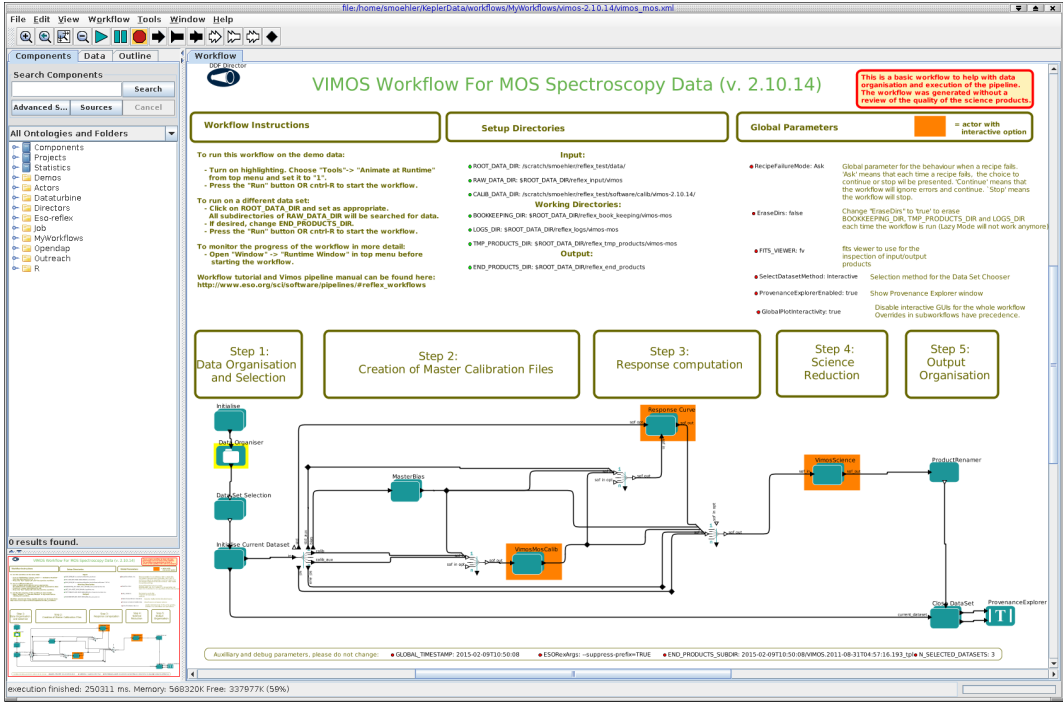


Figure 4.2: *VIMOS/MOS workflow general layout.*

The screenshot shows the "Select Datasets" pop-up window. It contains a table with the following data:

Selected	Data Set	#Files	OBS.TARG.NAME	OCS.CON...
<input checked="" type="checkbox"/>	VIMOS.2011-08-31T04:57:16.193	27	ELAIS-S1	1
<input checked="" type="checkbox"/>	VIMOS.2011-10-01T00:40:42.327	34	W4P081	2
<input checked="" type="checkbox"/>	VIMOS.2011-12-23T02:40:35.987	15	MOS-aLESS-Point7-1111-3	3

Below the table, there are buttons for "Select complete", "Select all", "Deselect all", "Save all", "Continue", and "Stop".

Figure 4.3: *The “Select Datasets” pop-up window.*

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	13 of 34

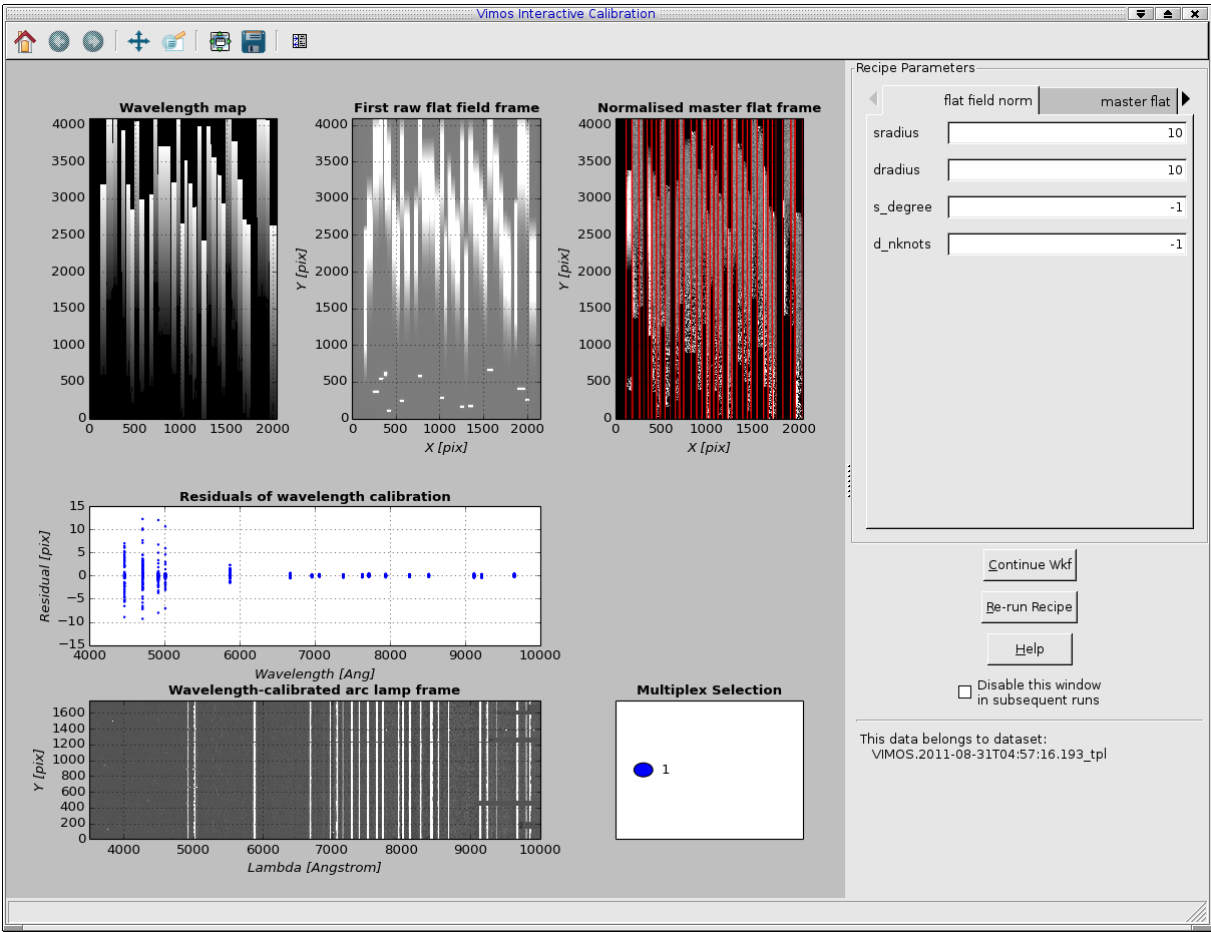


Figure 4.4: The interactive window of the `for_calib` actor for the first demo DataSet..

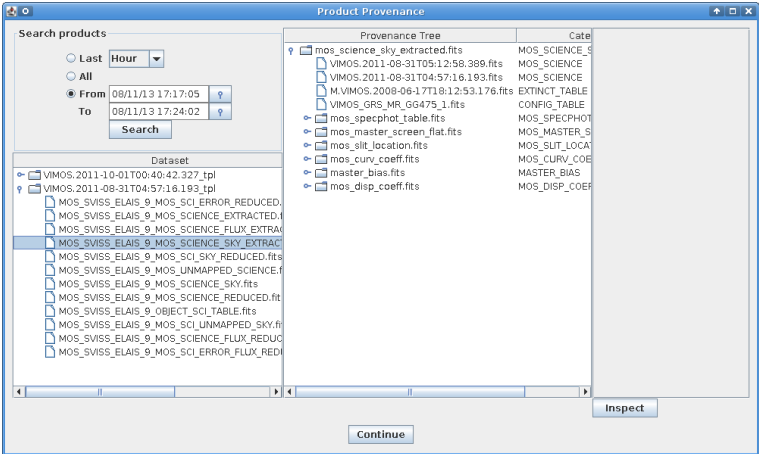


Figure 4.5: The Provenance Explorer shows all datasets reduced in previous executions together with the full reduction chain for all the pipeline products.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	14 of 34








5 About The Reflex Canvas

5.1 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 format (.kar) is only advised if you do not plan to use the workflow in another computer.








5.2 Buttons

At the top of the Reflex canvas are a set of buttons which have the following useful 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.

5.3 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.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	15 of 34

6 The VIMOS Workflow

The VIMOS 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.

6.1 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 `RAWDATA_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 `RAWDATA_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; [Forchi \(2012\)](#)).

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.

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 6.2.4), 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 rereduce 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 fails 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. Additionally, the `Stop` mode will stop the workflow execution immediately.

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



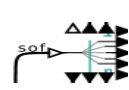
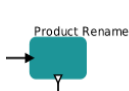

The parameter `ProductExplorerEnabled` controls whether the `ProductExplorer` actor will show its window or not. The possible values are `true`, `false`.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	16 of 34

6.2 Workflow Actors

6.2.1 Simple Actors

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

-  - The Data Organiser actor.
-  - The Data Set Chooser actor.
-  - The Fits Router actor
-  - The Product Renamer actor.
-  - The Product Explorer 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).

6.2.2 Composite Actors

Composite Actors have workflow symbols that consist of multiply-layered green-blue rectangles. They generally do not have a logo within the rectangle. A Composite Actor represents a combination of more Simple or Composite Actors which hides over-complexity from the user in the top-level workflow.

Composite Actors may also be expanded for inspection. To do this, right-click on the actor and select `Open Actor`, which will expand the Composite Actor components in a new `Reflex` canvas window. If the Composite Actor corresponds to a pipeline recipe, then the corresponding `RecipeExecutor` actor will be present as a Simple Actor, and its parameters are accessible as for any other Simple Actor. Alternatively you may still find Composite Actors, on which you need to repeat the first step to access the `Recipe Executor`.

6.2.3 Recipe Execution within Composite Actors

The VIMOS workflow contains Composite Actors to run pipeline recipes. This is in the most simple case due to the `SoF Splitter/SoF Accumulator`⁵, which allow to process calibration data from different setting

⁵SoF stands for Set of Files, which is an ASCII file containing the name (and path) of each input file and its category (e.g. `BIAS`).

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	17 of 34

within one given DataSet (e.g. lamp frames taken with different slits/masks). More complex Composite Actors contain several actors (e.g. Recipe Executer).

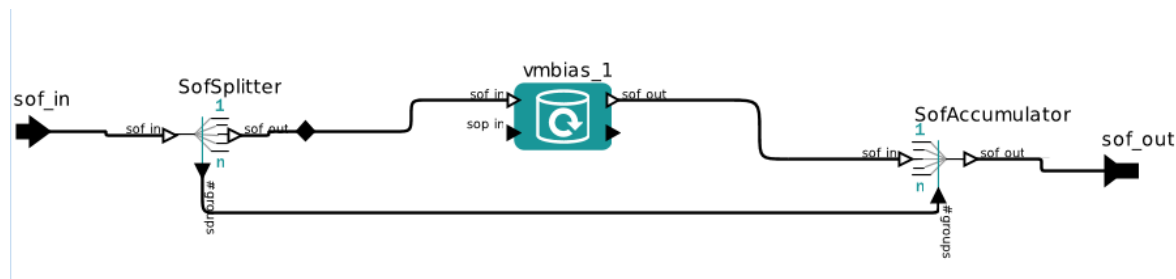


Figure 6.1: This is the window you get when you choose `Open Actor` for the `Composite ActorMasterBias`. This is the most simple case for a `Composite Actor`. Using `Configure Actor on vimos_bias_1` gives you Fig. 6.2.

The central elements of any Reflex workflow are the `RecipeExecutor` actors that actually run the recipes. One basic way to embed a `RecipeExecutor` in a workflow is shown in Fig 6.1, which is the most simple version of a `Composite Actor`. The `RecipeExecutor` is preceded by an `SofSplitter`, and followed by an `SofAccumulator`. The function of the `SofSplitter` is to investigate the incoming SoFs, sort them by “purpose”, and create separate SoFs for each purpose. The `RecipeExecutor` then processes each of the SoFs independently (unless they are actually the same files). Finally, the `SofAccumulator` packs all the results into a single output SoF. The direct relation between the `SofSplitter` and `SofAccumulator` is used to communicate the number of different SoFs created by the `SofSplitter`. A workflow will only work as intended if the purpose of all the files a recipe needs as input is identical. The only exception to this rule is that a purpose can also be “default”. In this case, the file is included in any output SoF created by the `SoFsplitter` and `SofAccumulator`.

The reason for this scheme is best explained by an example. For a complex DataSet, the `Data Organiser` might have selected a large number of individual raw lamp frames (arc and flat field). The different lamp frames are to be used to calibrate different frames, e.g. the science frames and the standard star frames. The `Data Organiser` determines and records this “purpose” of each lamp frame, and this information is included in the DataSet and each SoF created from this DataSet. The `FitsRouter` directs all raw lamp frames to the calibration `Composite Actor`. The `SofSplitter` then creates SoFs, one for the lamp frames to be used for the science frames, and (probably) separate ones for the lamp frames to be used for the standard star observations. The calibration recipe creates one master flat field (and other products) for each SoF, and the `SofAccumulator` then creates a SoF that contains all the products.

A `RecipeExecutor` actor is used in the workflow to run a single VIMOS pipeline recipe (e.g: in the `MasterBias` actor the recipe `vmbias` is executed). In order to configure the `RecipeExecuters`, one has to first use `Open Actor` to get to the level of the recipe executors (see Fig. 6.1).

In Figure 6.2 we show the “Edit parameters” window for a typical `RecipeExecutor` actor, which can be displayed by right-clicking on the actor and selecting `Configure Actor`. In the following we describe in more detail the function of some of the parameters for a `RecipeExecutor` actor:

- The “recipe” parameter states the VIMOS pipeline recipe which will be executed.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	18 of 34

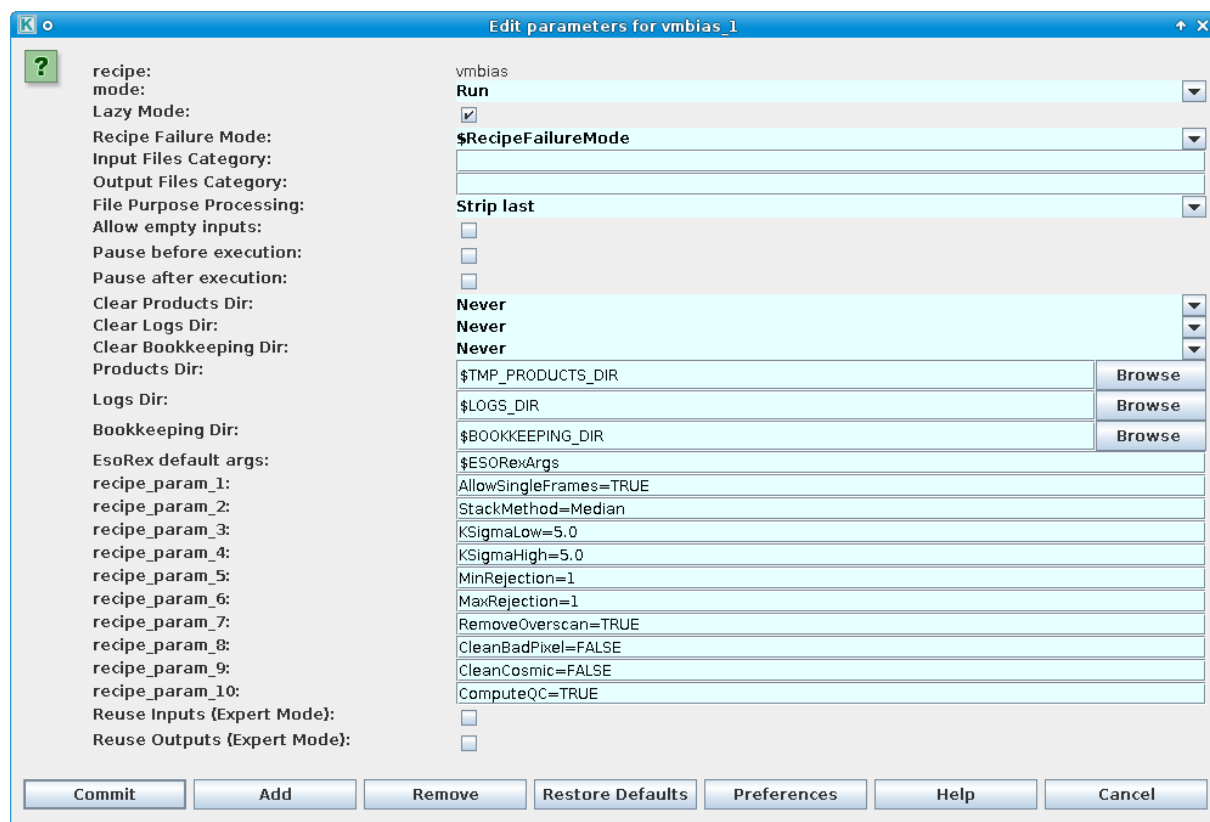


Figure 6.2: The “Edit parameters” window for a typical `RecipeExecutor` actor, the `vmbias_1` actor which runs the `vmbias` pipeline recipe.

- The “mode” parameter has a pull-down menu allowing the user to specify the execution mode of the actor. The available options are:
 - Run: The pipeline recipe will be executed, possibly in Lazy mode (see Section 6.2.4). This option is the default option.
 - Skip: The pipeline recipe is not executed, and the actor inputs are passed to the actor outputs.
 - Disabled: The pipeline recipe is not executed, and the actor inputs are not passed to the actor outputs.
- The “Lazy Mode” parameter has a tick-box (selected by default) which indicates whether the `RecipeExecutor` actor will run in Lazy mode or not. A full description of Lazy mode is provided in Sect. 6.2.4.
- The “Recipe Failure Mode” parameter has a pull-down menu allowing the user to specify the behaviour of the actor if the pipeline recipe fails. The available options are:
 - Stop: The actor issues an error message and the workflow stops.
 - Continue: The actor creates an empty output and the workflow continues.
 - Ask: The actor displays a pop-up window and asks the user whether he/she wants to continue or stop the workflow. This option is the default option.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	19 of 34

Table 6.1: The VIMOS/MOS pipeline actors and their contents

actor	recipe	description
MasterBias	vmbias	create master bias
VimosMosCalib	vmmoscalib	create master flat, determine coefficients for wave-length calibration and correction of spatial distortion
Response Curve	vmmosscience	determine response function
VimosScience	vmmosscience	reduce science data

- The set of parameters which start with “recipe param” and end with a number or a string correspond to the parameters of the relevant VIMOS pipeline recipe. By default in the `RecipeExecutor` actor, the pipeline recipe parameters are set to their pipeline default values. If you need to change the default parameter value for any pipeline recipe, then this is where you should edit the value. For more information on the VIMOS pipeline recipe parameters, the user should refer to the VIMOS pipeline user manual ([Izzo et al. 2012⁶](#)).

The description of the remainder of the `RecipeExecutor` actor parameters are outside the scope of this tutorial, and the interested user is referred to the Reflex User Manual for further details ([Forchì 2012](#)). Any changes that you make in the “Edit parameters” window must be saved in the workflow by clicking the `Commit` button when you have finished to take effect. If you want to reuse the parameters you have to save the workflow with the saved parameters.

6.2.4 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 rereduction where it is not necessary.

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

The forced rereduction of data at each execution may of course be desirable. To force a rereduction of all data for all `RecipeExecutor` actors in the workflow (i.e. to disable Lazy mode for the whole workflow), set the `EraseDirs` parameter under the “Global Parameters” area of the workflow canvas to `true`. This will then remove all previous results as well. To force a rereduction of data for any single `RecipeExecutor` actor in the workflow (which will be inside the relevant composite actor), right-click the `RecipeExecutor` actor, select `Configure Actor`, and uncheck the Lazy mode parameter tick-box in the “Edit parameters” window


⁶ Available at <ftp://ftp.eso.org/pub/dfs/pipelines/vimos/vimos-pipeline-manual-6.11.pdf>

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	20 of 34

that is displayed. If the Lazy mode is switched off for an actor, all subsequent actors that use products from that one will also reprocess the data, as they see new products.

6.3 Workflow Steps

6.3.1 Step 1: Data Organisation And Selection

On clicking the  button on the Reflex canvas, the workflow will highlight and execute the `Initialise` actor, which among other things will clear any previous reductions if required by the user (see Section 6.1).

1. The `DataOrganiser` (DO) is the first crucial component of a Reflex workflow. The DO takes as input `RAWDATA_DIR` and `CALIB_DATA_DIR` and it detects, classifies, and organises the files in these directories and any subdirectories. The output of the DO is a list of “DataSets”. A DataSet is a special Set of Files (SoF). A DataSet contains one or several science (or calibration) files that should be processed together, and all files needed to process these data. This includes any calibration files, and in turn files that are needed to process these calibrations. Note that different DataSets might overlap, i.e. some files might be included in more than one DataSet.

A DataSet lists three different pieces of information for each of its files, namely 1) the file name (including the path), 2) the file category, and 3) a string that is called the “purpose” of the file. The DO uses OCA⁷ rules to find the files to include in a DataSet, as well as their categories and purposes. The file category identifies different types of files. A category could for example be `MOS_SCREEN_FLAT`, `MOS_ARC_SPECTRUM` or `MOS_SCIENCE`. The purpose of a file identifies the reason why a file is included in a DataSet. The syntax is `action_1.action_2.action_3.action_n`, where each `action_i` describes an intended processing step for this file. The actions are defined in the OCA rules and contain the recipe together with all file categories required to execute it (and predicted products in case of calibration data). For example, a workflow might include two actions `BIAS` and `MOS_CAL`. The former creates a master bias from raw biases, and the later creates (among other products) a master flat from raw flats and arcs. The `MOS_CAL` action needs raw lamp frames (arc and flat field) and the master bias (or a set of raw biases) as input. In this case, these biases will have the purpose `BIAS.MOS_CAL`. The same DataSet might also include biases with a different purpose, e.g. `BIAS.MOS_SCIENCE`. Irrespective of their purpose the file category for all these biases will be `BIAS`.

Take into account that currently the Data Organizer cannot handle .xml files created by CalSelector. See the FAQ for details.

2. Next the `DataSet Chooser` displays the DataSets available in the “Select Data Sets” window⁸, activating a vertical scroll bar on the right if necessary (see Figure 4.3). 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 `Select All` and `Deselect All` at the bottom left.

⁷OCA stands for OrganisationClassificationAssociation and refers to rules, which allow to classify the raw data according to the contents of the header keywords, organise them in appropriate groups for processing, and associate the required calibration data for processing. They can be found in the directory `<install_dir>/share/esopipes/<pipeline-version>/reflex/`, carrying the extension `.oca`

⁸If you run the Data Organizer in Lazy Mode, changes in the Keywords to be displayed list will have no effect on the output shown in the DataSet Chooser.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	21 of 34

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 filename and path for each file, the file category (from the FITS header), and a selection tick box in the right column (see Figure 6.3). 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 (see Figure 6.3), 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`, and 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.

The categories and purposes of raw files are set by the DO, whereas the categories and purpose of products generated by recipes are set by the `RecipeExecutor` (see Sect. 6.2.3). The file categories are used by the `FitsRouter` to send files to particular processing steps or branches of the workflow (see below). The purpose is used by the `SofSplitter` to generate input SoFs for the `RecipeExecutor` and the results are collected by the `SofAccumulator`. Note that while the DO includes files into a DataSet for a reason, and records this reason as the “purpose” of the file, the workflow itself can use these files in a different manner. The `SofSplitter` and `SofAccumulator` accept several SoFs as simultaneous input. The `SofAccumulator` creates a single output SoF from the inputs, whereas the `SofSplitter` creates a separate output SoF for each purpose.

6.3.2 Step 2: Creation Of Master Calibration Files

In this step of the workflow, the following VIMOS recipes are executed in the order listed below. Please refer to the VIMOS pipeline user manual (Izzo et al. 2012: Sections 9 and 10) for the details of each recipe and the algorithms employed:

1. The `MasterBias` actor will execute the VIMOS pipeline recipe `vmbias` in order to create a combined master bias frame from the set of raw bias frames
2. The `VimosMosCalib` actor will execute the VIMOS pipeline recipe `vmmoscalib` in order to create from the set of raw flat and arc frames a combined master flat frame as well as coefficients for wavelength calibration and correction of spatial distortions.

6.3.3 Step 3: Response Computation

In this step of the workflow, the `ResponseCurve` actor will determine the response function (if a flux standard star is provided) using the recipe `vmmosscience`, which will subsequently be used to flux-calibrate the science observation. Please refer to the VIMOS pipeline user manual (Izzo et al. 2012: Sections 9 and 10) for the details of this recipe.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	22 of 34

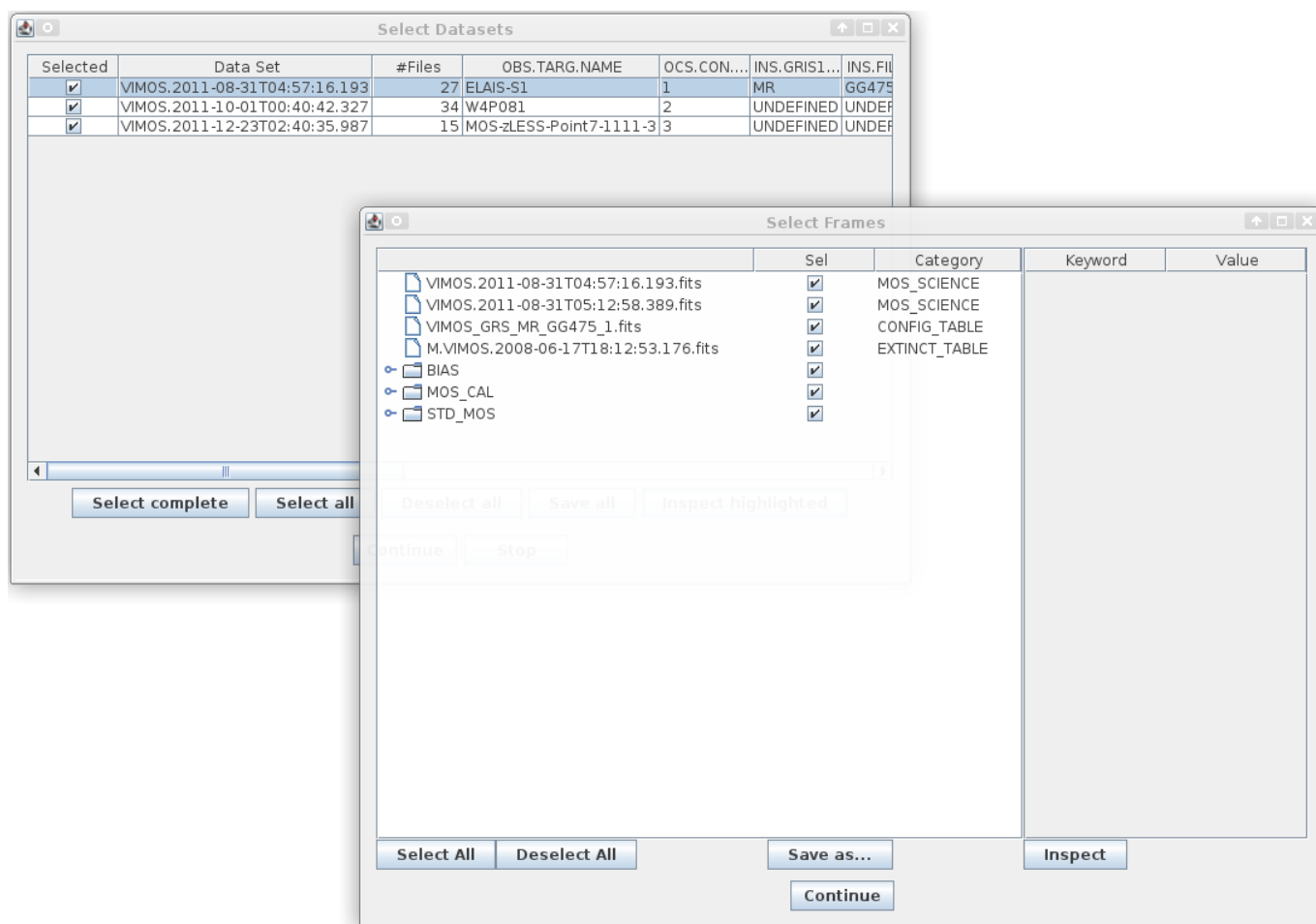


Figure 6.3: The “Select Frames” window with a single file from the current Data Set highlighted in blue, and the corresponding FITS header displayed in the text box on the right. Hidden partially behind the “Select Frames” window is the “Select DataSets” window with the currently selected DataSet highlighted in blue.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	23 of 34

Note that this actor will be skipped if there are no observations of a standard star in the current DataSet. A standard star observation is only included in the DataSet for a science observation if it was taken within ± 7 nights of the science observation. For some combinations of grism and filter, VIMOS PI-Packs as well as CalSelector data sets are supplied with master instrument response curves. These are currently not included in the data set for a science observation.

6.3.4 Step 4: Science Reduction

The `VimosScience` actor will execute the VIMOS pipeline recipe `vmmosscience` to apply sky subtraction and extract the spectra. Please refer to the VIMOS pipeline user manual (Izzo et al. 2012: Sections 9 and 10) for the details of this recipe and the extraction algorithms employed. The VIMOS/MOS workflow will flux-calibrate the science observation using the instrument response curve derived from the standard star observation if it exists in the current DataSet. If no standard star observation exists in the current DataSet, then the science observation will not be flux-calibrated.

6.3.5 Step 5: Output Organisation

After having processed the input data for a DataSet, the `Data Filter` actor allows the user to inspect the results and select which files to save. By default this actor is set to skip and all products will be saved. Next the workflow highlights and executes the `Product Renamer` actor, which, by default, will copy the defined final products of the `VimosScience` actor to the directory specified by `END_PRODUCTS_DIR` and rename them with names derived from the values of certain FITS header keywords. Specifically, final products are renamed by default with names of the form `<HIERARCH.ESO.OBS.NAME>_<HIERARCH.ESO.PRO.CATG>.fits`, where `<HIERARCH.ESO.OBS.NAME>` and `<HIERARCH.ESO.PRO.CATG>` represent the values of the corresponding FITS header keywords. These names are fully configurable by right-clicking on the `Product Renamer` actor, selecting `Configure Actor`, and then editing the string as appropriate.

The final products that are copied and renamed are:

- `<HIERARCH.ESO.OBS.NAME>_MOS_SCIENCE_REDUCED.fits` Extracted 1D scientific spectra
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCI_ERROR_REDUCED.fits` Errors on extracted 1D spectra
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCI_SKY_REDUCED.fits` Extracted 1D sky spectra
- `<HIERARCH.ESO.OBS.NAME>_MOS_UNMAPPED_SCIENCE.fits` Sky subtracted scientific spectra unrectified
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCIENCE_EXTRACTED.fits` Rectified scientific spectra with sky subtracted
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCIENCE_SKY_EXTRACTED.fits` Rectified science spectra with sky
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCIENCE_SKY.fits` Rectified sky spectra

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	24 of 34

- `<HIERARCH.ESO.OBS.NAME>_MOS_SCI_UNMAPPED_SKY.fits` Sky on CCD unrectified
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCI_GLOBAL_SKY_SPECTRUM.fits` Global sky spectrum (only if parameter `–skyglobal` is set)
- `<HIERARCH.ESO.OBS.NAME>_OBJECT_SCI_TABLE.fits` Positions of detected objects
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCIENCE_FLUX_REDUCED.fits` If flux calibration is done (if an standard star is present): Flux calibrated scientific 1D spectra
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCI_ERROR_FLUX_REDUCED.fits` If flux calibration is done (if an standard star is present): Errors on flux calibrated 1D spectra
- `<HIERARCH.ESO.OBS.NAME>_MOS_SCIENCE_FLUX_EXTRACTED.fits` If flux calibration is done (if an standard star is present): Flux calibrated 2D slit spectra

All products with `<HIERARCH.ESO.OBS.NAME>_REDUCED` are created only if spectra are identified and can be extracted. All products `<HIERARCH.ESO.OBS.NAME>_<type>_FLUX` are created only if flux standard star observations are provided and the standard star flux table is available.

The remaining actors in this step of the workflow are concerned with the termination of the data flow for the current DataSet and will highlight briefly as they are executed.

6.4 Interactive Windows

The VIMOS MOS workflow contains three interactive windows that allow the user to iterate on the processing of their data. They are described below.

6.4.1 vmmoscalib

The interactive window shown in Fig. 4.4 (p. 13) provides information about the quality of the wavelength calibration (left column), distortion correction (top right and center plot) and the flat field combination and normalization (bottom right plot). The plots contain in detail:

Top Left *Wavelength map* The wavelength map has as pixel values the wavelength of a pixel. All slitlets should be present, the regions of the slitlets should not be strongly curved nor should regions of different slitlets overlap with each other.

Top Center *First raw flat* This plot is mostly of interest in comparison to the **Top Right** and **Top Left** one, as the number of slitlets and the areas covered by them should be identical.

Top Right *Normalized master flat* The normalized master flat field should have the same number of slitlets as the first raw flat and their areas should also be identical. The red lines show the traces of the slitlet edges. They should therefore follow the slit edges and not cut across slitlets. All slitlets should be detected and there should be no spurious detections (e.g. one slitlet detected as several).

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	25 of 34

Center Left *Residuals between predicted and detected arc line position* The residuals should generally be below 0.5 pixel. If they show systematic variations the polynomial degree used to fit the dispersion relation may be too low (or in rare cases too high). If the scatter appears very large one should zoom in, because there are often only a few outliers and the majority of the residuals are within ± 0.5 pixels. Middle-clicking with the mouse on a line will add the catalogue line nearest to this position to `-ignore_lines`. Doing this again after re-running the recipe, however, will overwrite previously ignored lines.

Center Right *Detected (black), identified (green) and rejected lines (red)*. If you see a large number of rejected lines zoom in to verify that this is really a problem. The limited plot size can give a wrong impression.

Bottom *Wavelength-calibrated arc lamp frame*: In this plot the arc lamp lines should run straight from top to bottom without any empty rows between them. Some arc lines may show gaps due to the placement of the slits, but empty rows without any lines point towards problems with the detection of the arc lamp lines.

The buttons in the **bottom right** window allow to switch between extensions for multiplexed data. For multiplex data one should always verify the results for all extensions, as parameters which improve some extension may give worse results for others.

6.4.2 vmossience (Response)

The interactive window shown in Fig. 6.4 provides information about the quality of the response curve fit:

Top *Extracted standard star spectrum*: The extracted standard star spectrum should show no jumps or sky emission lines. Strong gradients due to order separating filters are valid but may cause problems with the fit of the response curve.

Center *Raw response and fit*: The dots show the raw response (ratio of reference spectrum and observed spectrum integrated over same bins as reference spectrum) and the blue line shows the corresponding fit. Blue dots are masked (`ignore_resp_mode`, `ignore_resp_points`) and not used for the fit.

Bottom *Flux-calibrated standard star spectrum and reference*: The red line marks the observed standard star spectrum calibrated with its own response curve and the green and blue points indicate the reference data (blue points were masked during the fitting of the response). Differences between the green points and the red line indicate a problem with the flux calibration, usually features on a scale smaller than the bins of the reference data. Differences between the red line and blue points indicate problems with inter- and/or extrapolation.

The buttons in the **bottom right** window allow to switch between extensions for multiplexed data.

6.4.3 vmossience (Science)

The interactive window shown in Fig. 6.5 provides information about the quality of the sky subtraction and spectrum extraction. It shows the spectra in ADU/sec, i.e. not flux-calibrated:

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	26 of 34

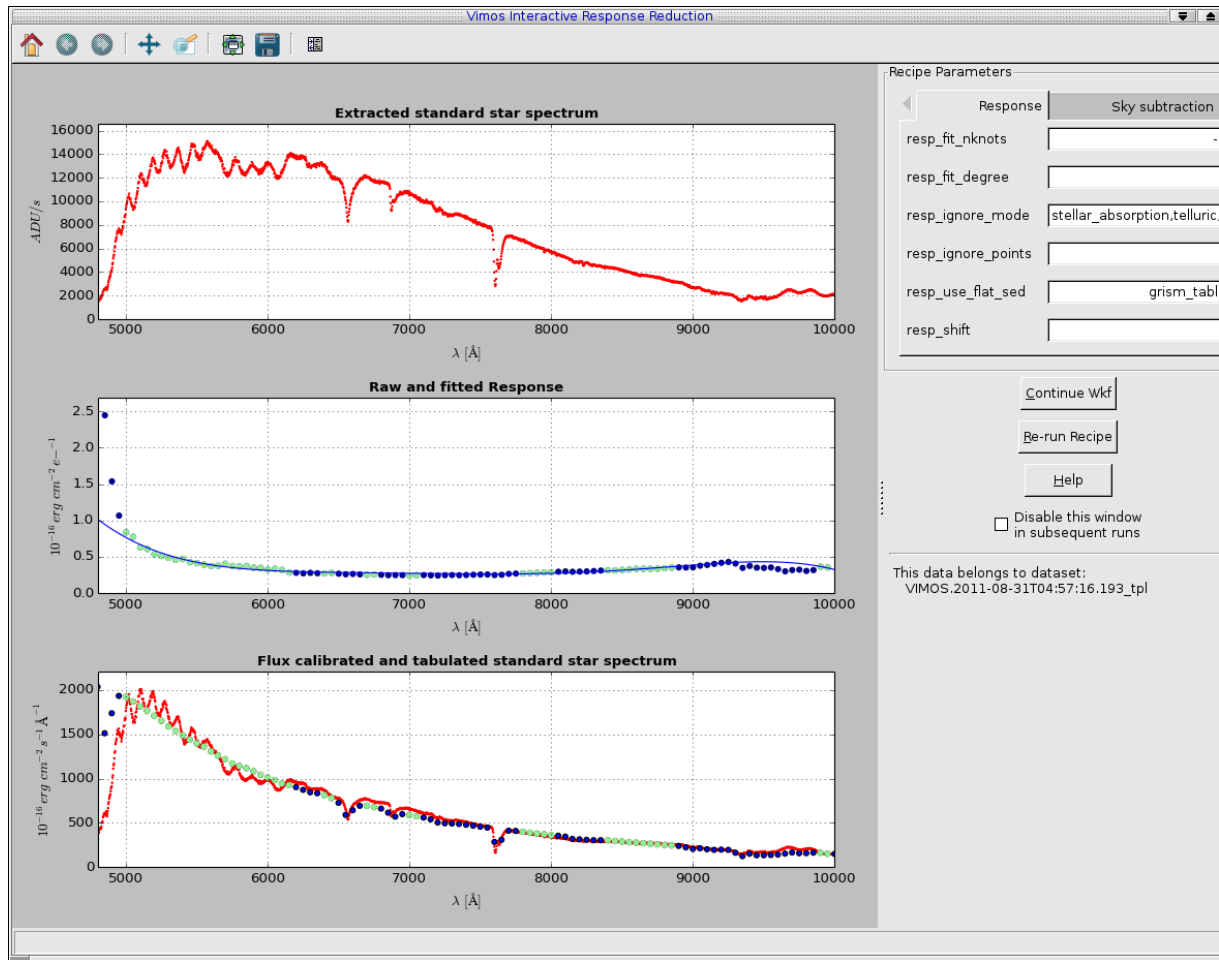


Figure 6.4: The interactive window of the ResponseCurve actor for the first demo DataSet.

Top *Mapped sky-subtracted 2-dimensional spectrum*: The wavelength-calibrated, rectified frame is shown after sky subtraction. The yellow and red lines mark the lower/upper extraction limits of the detected spectra. Right-clicking on such a range will plot the extracted spectrum in the **Bottom** plot.

Bottom *Extracted science spectrum*: The spectrum should not show strong residuals of sky lines.

The buttons in the **bottom right** window allow to switch between extensions for multiplexed data.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	27 of 34

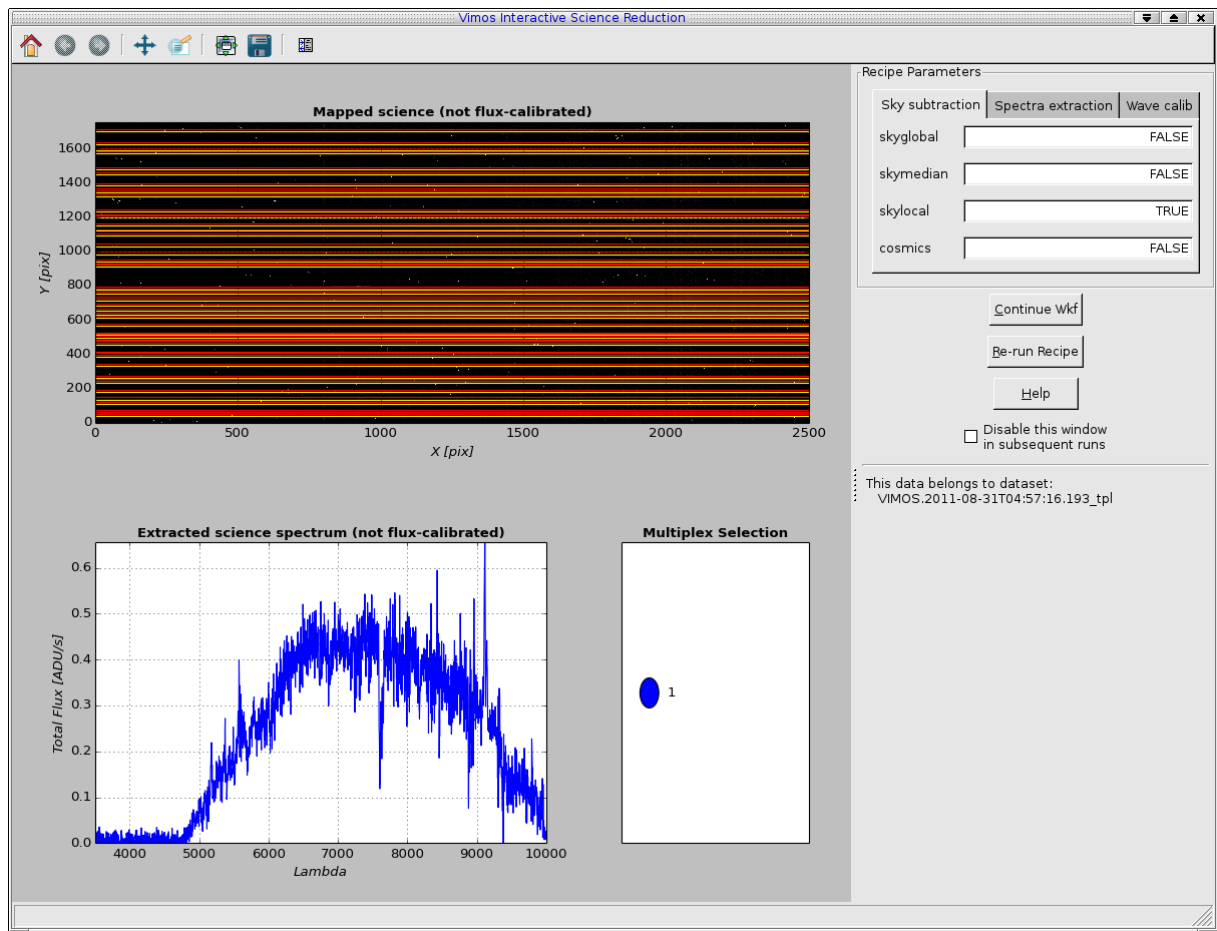


Figure 6.5: The interactive window of the VimosScience actor for the first demo DataSet.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	28 of 34

7 Improving Your Results Through Workflow Interaction

In this section we provide information on how to improve your results by changing the parameters of the `vmmoscalib` and `vmmosscience` recipes.

7.1 Demo Data

DataSet 1 The response curve ends in a masked telluric region. In order to avoid extrapolation the response is only fit between the bluest and the reddest unmasked points. To see the effect of the masking you can change `resp_ignore_mode` from `stellar_absorption, telluric, command_line` to `stellar_absorption, command_line` and rerun the recipe. Now the fit is less good because more (and deviating) points need to be fit, so the fit parameters need to be changed as well.

DataSet 2 The wavelength calibration of the flux standard shows some distortions in the wavelength calibrated arc frame. This can be improved by setting `wreject=0.7`.

The spectrum of the flux standard star is shifted by 90 Å, relative to the tabulated values. Setting `resp_shift` to -90 corrects this offset.

7.2 Wavelength Calibration

For multiplex data one should always verify the results for all extensions, as parameters which improve some extension may give worse results for others.

Failures for the various grisms can be recovered in many cases by the following parameter changes:

- `LR_red` reduce `wreject` to 0.4
- `HR_blue` reduce `peakdetection` to 30 and/or increase `wreject` to 2.5
- `HR_orange` reduce `wreject` to 0.4 and/or reduce `peakdetection` to 30
- `HR_red` decrease `wdegree` to 4 (reducing `wreject` to 0.7 or `peakdetection` to 2500 is also sometimes helpful)

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	29 of 34

8 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 a fix has not yet been found.

- **Where are my intermediate pipeline products?** Intermediate pipeline products are stored in the directory `<TMP_PRODUCTS_DIR>` (defined on the workflow canvas) 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 (Forchì (2012)). 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:

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

The `-n` option will set all the different options to Kepler and the workflows that avoid any graphical display (including pipeline interactive windows). 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 (Forchì (2012)) 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 (Forchì (2012)) for more information.
- **How can I run manually 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

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	30 of 34

recent processing he/she should go to the latest directory and then execute the script `cmdline.txt`. Alternatively, to ensure that the path to `esorex` is the correct one, the user can execute

```
ESOREX_CONFIG="INSTALL_DIR/etc/esorex.rc"
INSTALL_DIR/bin/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 in the command line a recipe that used a given 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 before, 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 doesn't happen if you use the `cmdline.txt` script.

- **If I enter "-" into an empty integer parameter 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.

8.1 VIMOS specific questions

- **If I click on "Use the parameters above as initial values in subsequent executions of this recipe", some changes are ignored**

The VIMOS pipeline has a special way to handle the parameters which are in the configuration tables. Basically, the initial values are always taken from the configuration table. Still, during the loop execution, the parameters can be changed to the desired values.

If you want to use different values as "initial values" for those parameters, edit the configuration tables (`VIMOS_GRS_*` to create your own version. The parameters affected are: `dispersion`, `peakdetection`, `wdegree`, `cdegree`, `reference`, `startwavelength`, `endwavelength`, `resp_use_flat_sed`, `resp_fit_degree`, and `resp_fit_nknots`.

- **Can I use the .xml file that is produced by CalSelector as an input of the DO?**

Currently no. As of current release the static calibrations in the ESO archive are not compatible with the pipeline. Therefore one has to use the static calibrations installed along with the pipelines. The `.xml` file produced by CalSelector contains only static calibrations from the archive, making the pipeline fail. This will be fixed in next releases, once the ESO archive has been updated with all the new calibrations.

- **I see small dark and bright regions in my normalized flat field - why?**

These features are caused by straylight from 0th order light in adjacent slitlets. As the pipeline no longer normalizes the flat fields column-by-column/row-by-row, but uses an average along the rows/column instead this effect is currently not corrected. This should be improved in a later release. The science data will also be contaminated by the 0th order light, but in a different way as the flat field spectra are all from one source while the science spectra are created by different sources.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	31 of 34

- **I am using the maximum number of knots for the spline fit of the response but the fit still does not go through all data points.**

The maximum number of knots for the spline is the number of unmasked data points – 2 (entering a higher number will cause the pipeline to reduce it to the allowed maximum). Since the knots are distributed at equal distances this means that the distance between two knots is always larger than the distance between two data points. This explains why even at a maximum number of knots the fit may not go through all data points. A polynomial of very high degree might achieve that, but is rather unstable.

- **I get a warning “Column STLLR_ABSORP not found in std star table. Value ‘stellar_absorption’ in ‘resp_ignore_mode’ is ignored” if I use the standard star tables that have been downloaded from the archive with CalSelector.**

This may happen for data from old PIPacks or for data that were downloaded before August 1, 2015, when old static calibration files were delivered. You should remove these files from your input files. Since the static calibrations are also delivered together with the latest version of the pipeline, you don’t really need them, Reflex will take the ones under directory `CALIB_DATA_DIR`.

- **Why do my flux-calibrated data not agree with independent photometric measurements?**

In order to have a true absolute flux calibration several requirements need to be fulfilled:

1. All flux of both the target and the standard star needs to be collected, i.e. a wide slit has to be used.
2. The transparency does not change between the observations of the target and the standard star.

With respect to the first condition one should keep in mind that the flux standard stars are observed with a 5” wide slit, while science data are typically observed with slit widths of 0.8” to 1”. For a seeing of 0.8” a slit width of 0.8”/1.0” means that some 33%/24%, respectively, of the target flux are lost (see also Fig. 8.1). This would result in a too low flux for the flux calibrated spectrum of the target.

If the second condition is not fulfilled, i.e. the standard star or the target or both are observed under non-photometric conditions (e.g. CLR or THN) their observed flux will be lower than it should be. If the standard star is observed under photometric conditions but the science target is not the flux in the flux calibrated target spectrum will be too low. The opposite happens if the target is observed under photometric conditions but the standard star is not. CLR/THN conditions allow for transparency variations of 10%/20%, respectively.

- **Does the pipeline combine different detectors chips into a common product?**

No. The spectroscopic pipeline and Reflex workflow works only on files from the same detector chip. Files from different detectors must not be mixed in the same sof.

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	32 of 34

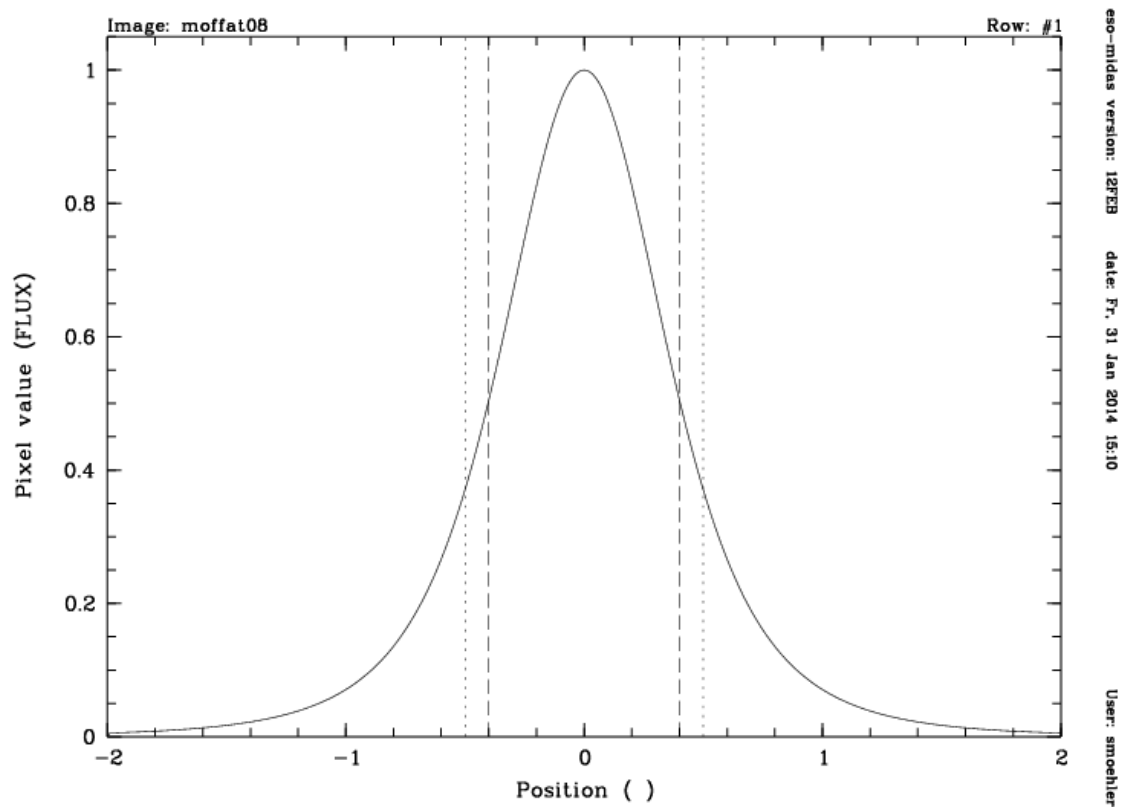


Figure 8.1: Here a Moffat profile with a FWHM of 0.8'' is shown. The dashed and dotted lines mark the limits of a 0.8''/1.0'' slit..

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	33 of 34

9 Troubleshooting

In this section we describe some of the problems that may occur when reducing the VIMOS/MOS with the ESOREX pipeline. For a more comprehensive description we refer the user to the VIMOS user manual (<http://www.eso.org/sci/software/pipelines/>).

1. I have data from the old PI packs

The data from the DVD have to be cleaned up:

- remove *all* the pipeline products i.e. master bias (whose filename contains the string MBIA), transmission response files (whose filename contains the string PTNF) and directories labelled as `proc` or `reduced`
- remove duplicate files (i.e. files with the same name, but stored in different directories, such as arc lamps).
- remove all old static calibrations.

2. Should I change the CALIB_DATA_DIR configuration?

This directory is setup automatically to point to the calibration database provided with the pipeline and in principle shouldn't be changed. However, if static calibration data are present in the RAWDATA_DIR (e.g. calibrations are downloaded from the archive, or copied from ESO-DVD distribution), then you might have to remove these data (otherwise an obsolete static calibration file may be selected instead of the most appropriate one).

3. If I set parameter `resp_ignore_mode` to empty in the response interactive window, the value `stellar_absorption, telluric, command_line` is taken

This is a known bug in Reflex that will be solved in next release. As a work-around, set `resp_ignore_mode` to `command_line` and `resp_ignore_points` to empty, in order to express that no masking has to be done.

4. Bug: MODE mismatch between BIAS frames and pixel tables

It can happen that the BIAS frames associated to the reduction flow of one MOS observation was taken in the imaging mode. The bias can be used, as there is no difference between bias taken in imaging or MOS modes. Nevertheless, the `vmbias` recipe requires the bias frame and the bad pixel table⁹ to have the same observing mode. This bug can be overcome by changing the `OBSMODE` in the bias frames from `IMG` to `MOS`. This bug is in the `vmbias` recipe, independent from the reflex workflow, and it may be solved in future VIMOS pipeline releases.

⁹CCD_TABLES are static calibration files, one per quadrant, one set per observing mode, containing the list of bad pixels. See Section 6.2 in the VIMOS pipeline user manual (version 6.5).

ESO	Reflex VIMOS/MOS Tutorial	Doc:	VLT-MAN-ESO-19500-....
		Issue:	Issue 1.2
		Date:	Date 2015-02-09
		Page:	34 of 34

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23