# Processing of AMBER data

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**Abstract**

This practice work session introduces the participants to the ESO tools available for the reduction of VLTI/AMBER data. They include Gasgano and Reflex. These tools are provided by ESO, and are based on amdlib, provided by the AMBER consortium.

## 1 Introduction

Interferometric data reduction, due to its inherent complexity, is especially subject to the "Black Box" approach, which offers peace of mind if you trust the authors of the package and the quality of the data delivered. However, because the result is affected by so many variables, it is important to demand of the packages to display intermediate results and allow the user to interact with the reduction. To some extent, this has been honored by some reduction packages, notably the nice graphical user interface (GUI) of MIA for MIDI (http://www.strw.leidenuniv.nl/∼nevec/MIDI/index.html). Amdlib itself has been transformed from just a library into an interactive data reduction package (http://www-laog.obs.ujf-grenoble.fr/amber/article.php3?id_article=157). A very good manual can be downloaded from http://www.jmmc.fr/doc/approved/JMMC-MAN-2720-0001.pdf.

Here we describe new tools under development by ESO, which are based on amdlib. The new Reflex tool is designed to assemble a data reduction recipe from smaller processors, allowing one to examine intermediate results. The theory of AMBER data reduction has been described by Tatulli et al. (2007), and a summary including a brief tutorial by the same author can also be found at http://vltischool.obs.ujf-grenoble.fr/.

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### *1.1 Reference documents*

When using ESO instruments, like AMBER or MIDI, it is important to read the very detailed manuals written by the instrumentation teams. In particular, the User and Template Manuals as well as the calibration plan, are all available at *http://www.eso.org/instruments/amber/doc/*.

### *1.2 Where to find help and learn about interferometry*

Here is a non-exhaustive list of starting points for your endeavours in interferometry.

- VLTI: http://www.eso.org/projects/vlti/
- AMBER at LAOG: http://www-laog.obs.ujf-grenoble.fr/amber/
- Jean-Marie Mariotti Center (JMMC): http://www.mariotti.fr/
- Optical Long Baseline Interferometry News: http://olbin.jpl.nasa.gov/index.html

## 2 AMBER FITS Information

### *2.1 AMBER file structure*

A complete, i.e. self contained, AMBER data set consists of 10 3P2V (or 5 2P2V, i.e. Pixel-to-Visibility) calibration files, one or more fringe exposures, and one DARK and one SKY exposure. Optionally, there are four spectral calibration files (WAVE) to register the photometric and interferometric channels with respect to each other. There will be more files contained in your AMBER data package, but they are of lesser importance to your data reduction.

Each file is in FITS format and contains several HDUs (header-data units) that can be visualized using **fv** (see below). The structure of an AMBER file is the following:

- HDU1: Primary FITS header containing information about the observation.
- HDU2 (IMAGING_DATA): Header + table containing the frame data (each row contains the pixel values for all five detector windows of a frame, and information about the frame like the time).
- HDU3 (IMAGING_DETECTOR): Header + table of detector setup description.
- HDU4 (ARRAY_DESCRIPTION): Header + description of port IDs of installed optical elements.

- HDU5 (ARRAY_GEOMETRY): Header + table giving the telescope coordinates
- HDU6 (OPTICAL_TRAIN): Header + table giving the port IDs for each optical element encountered by the three beams.
- HDU7 (AMBER_WAVEDATA): Header + table giving wavelengths of the spectrometer

### *2.2 Extracting FITS Information*

There are many tools to extract and parse FITS headers. One convenient way of extracting FITS information and displaying it on a terminal or re-directing it to a text file, is to use two stand-alone programs called dfits and fitsort. Both are included into the ESO eclipse distribution (http://www.eso.org/eclipse).

**dfits** dumps a FITS header on stdout. You can use it to dump the FITS headers of many files and to allow the parsing of the output. Example: `dfits *.fits | grep "TPL ID"`

Usually, you want to get the value of a list of given FITS keywords in a list of FITS files. **fitsort** reads the output from **dfits**, classifies the keywords into columns, and prints out in a readable format the keyword values and file names. Example:

```
dfits *.fits | fitsort NAXIS1 NAXIS2 BITPIX
```

**fitsort** also understands the shortFITS notation, where e.g. `HIERARCH ESO TPL ID` is shortened to `TPL.ID`. A classification example could be (both commands are equivalent, since **fitsort** is case-insensitive):

```
dfits *.fits | fitsort TPL.ID DPR.TYPE OBS.TARG.NAME
dfits *.fits | fitsort tpl.id dpr.type obs.targ.name
```

The output from this combination is something like:

```
FILE                                TPL.ID                      DPR.TYPE    OBS.TARG.NAME
AMBER.2005-02-25T07:41:23.925.fits  AMBER_3Tstd_acq             WAVE,3TEL   betcen
AMBER.2005-02-25T07:41:36.616.fits  AMBER_3Tstd_acq             WAVE,3TEL   betcen
AMBER.2005-02-25T07:41:51.649.fits  AMBER_3Tstd_acq             WAVE,3TEL   betcen
AMBER.2005-02-25T07:42:01.825.fits  AMBER_3Tstd_acq             WAVE,3TEL   betcen
AMBER.2005-02-25T07:42:41.554.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:43:01.338.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:43:16.401.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:43:31.509.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:43:46.570.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:44:03.045.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:44:18.171.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:44:33.120.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:44:48.267.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T07:45:11.354.fits  AMBER_3Tstd_acq             3P2V        betcen
AMBER.2005-02-25T09:22:40.696.fits  AMBER_3Tstd_obs_1row        DARK        alfara
AMBER.2005-02-25T09:24:22.488.fits  AMBER_3Tstd_obs_1row        OBJECT      alfara
AMBER.2005-02-25T09:26:02.281.fits  AMBER_3Tstd_obs_1row        OBJECT      alfara
AMBER.2005-02-25T09:27:39.957.fits  AMBER_3Tstd_obs_1row        OBJECT      alfara
AMBER.2005-02-25T09:29:45.946.fits  AMBER_3Tstd_obs_1row        SKY         alfara
AMBER.2005-02-25T10:02:35.241.fits  AMBER_3Tstd_obs_1row        DARK        hd165024
AMBER.2005-02-25T10:04:10.020.fits  AMBER_3Tstd_obs_1row        OBJECT      hd165024
AMBER.2005-02-25T10:05:45.944.fits  AMBER_3Tstd_obs_1row        OBJECT      hd165024
AMBER.2005-02-25T10:07:19.877.fits  AMBER_3Tstd_obs_1row        OBJECT      hd165024
AMBER.2005-02-25T10:09:20.178.fits  AMBER_3Tstd_obs_1row        SKY         hd165024
AMBER_BPM_fuzzy_img.fits            AMBER_gen_tec_badPixelMap   BADPI
AMBER_FFM_img.fits                  AMBER_gen_tec_badPixelMap   FLATFIELD
```

This kind of table is useful in getting an idea of what is present in a directory or list of directories. Loading such a summary table into a spreadsheet program also makes it conveniently readable. In this example, we see files related to an observation with AMBER including fringe exposures (DPR type OBJECT) on both science and calibrator targets, as well as P2VM calibration files (DPR type 3P2V). The last two files, which are also delivered in the data package, are the bad pixel and the flat field maps. For a full list of keywords available, check the header of HDU1.

## *2.3 Visualizing FITS Tables*

Similarly, a FITS table can be visualized on the command-line using the **dtfits** command. Alternatively, we recommend using **fv**, available from http://heasarc.gsfc.nasa.gov/docs/software/ftools/fv/.

**dfits** and **fitsort** will help you classify tables and see ancillary data attached to them, but **dtfits** will display all information contained in the table itself, in ASCII format on the command-line. There are various options to help make the output readable on a terminal, or by a spreadsheet program.

See the dtfits manual page to get more information.

## 3 The AMBER Pipeline

### *3.1 Purpose*

Pipelines can serve two purposes: First, to allow a quick and automatic reduction of data as it comes from the instrument, in order to make an assessment of the data quality almost in real time. Second: a science-grade pipeline produces optimally calibrated products which can be analyzed scientifically without any further manipulation.

The AMBER pipeline is of the first type, i.e. final data reduction for scientific analysis will be done using other reduction packages, which will be described in the following.

### *3.2 Downloading and installing*

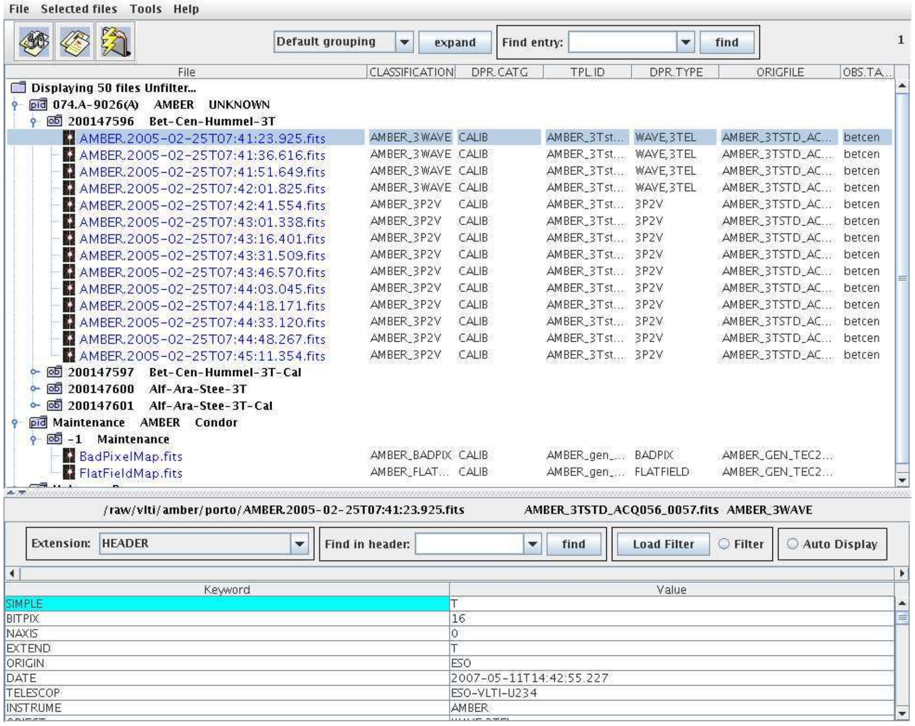
The AMBER pipeline is currently available for download. For up-to-date information, please check http://www.eso.org/projects/dfs/dfs-shared/web/vlt/vlt-instrument-pipelines.html.

## 4 AMBER interactive reduction

### *4.1 Exercise 1: Gasgano.*

Download and install Gasgano from
http://www.eso.org/sci/data-processing/software/gasgano/.

Change the working directory to where your raw data are located. Here you type `gasgano` to start the GUI.



| File | CLASSIFICATION | DPR.CATG | TPL.ID | DPR.TYPE | ORIGFILE | OBS.TA... |
|---|---|---|---|---|---|---|
| Displaying 50 files Unfilter... | | | | | | |
| 074.A-9026(A) AMBER UNKNOWN | | | | | | |
| 200147596 Bet-Cen-Hummel-3T | | | | | | |
| AMBER.2005-02-25T07:41:23.925.fits | AMBER_3WAVE | CALIB | AMBER_3Tst... | WAVE,3TEL | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:41:36.616.fits | AMBER_3WAVE | CALIB | AMBER_3Tst... | WAVE,3TEL | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:41:51.649.fits | AMBER_3WAVE | CALIB | AMBER_3Tst... | WAVE,3TEL | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:42:01.825.fits | AMBER_3WAVE | CALIB | AMBER_3Tst... | WAVE,3TEL | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:42:41.554.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:43:01.338.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:43:16.401.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:43:31.509.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:43:46.570.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:44:03.045.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:44:18.171.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:44:33.120.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:44:48.267.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| AMBER.2005-02-25T07:45:11.354.fits | AMBER_3P2V | CALIB | AMBER_3Tst... | 3P2V | AMBER_3TSTD_AC... | betcen |
| 200147597 Bet-Cen-Hummel-3T-Cal | | | | | | |
| 200147600 Alf-Ara-Stee-3T | | | | | | |
| 200147601 Alf-Ara-Stee-3T-Cal | | | | | | |
| Maintenance AMBER Condor | | | | | | |
| -1 Maintenance | | | | | | |
| BadPixelMap.fits | AMBER_BADPIX | CALIB | AMBER_gen_... | BADPIX | AMBER_GEN_TEC2... | |
| FlatFieldMap.fits | AMBER_FLAT... | CALIB | AMBER_gen_... | FLATFIELD | AMBER_GEN_TEC2... | |

/raw/vlti/amber/porto/AMBER.2005-02-25T07:41:23.925.fits AMBER_3TSTD_ACQ056_0057.fits AMBER_3WAVE

Extension: HEADER

| Keyword | Value |
|---|---|
| SIMPLE | T |
| BITPIX | 16 |
| NAXIS | 0 |
| EXTEND | T |
| ORIGIN | ESO |
| DATE | 2007-05-11T14:42:55.227 |
| TELESCOP | ESO-VLTI-U234 |
| INSTRUME | AMBER |

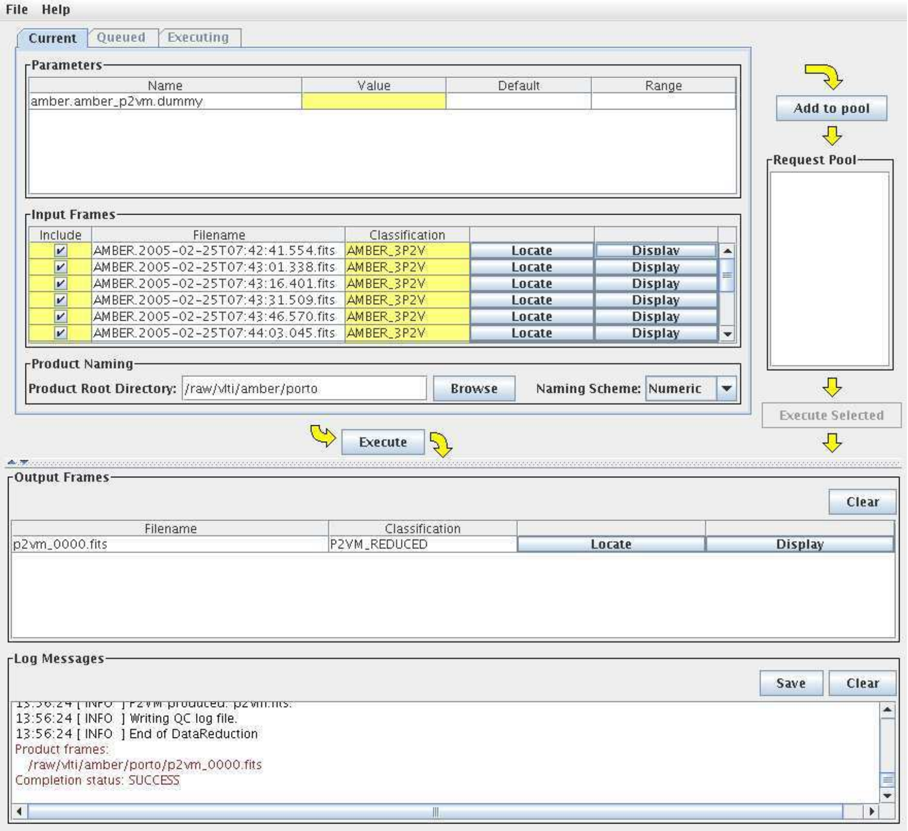
Fig. 1. Gasgano file display. Other files might be displayed too in your specific application.

First, you have to add files to the display using the Add/Remove Files GUI on the File menu. In the GUI, select Add File, click your data directory (you might have to select a different "Look In" directory), and click Add File in the lower right. (Even though it says File, what is actually meant is a directory.) The file selection GUI will disappear and you click OK to finish. All the files of the selected directory will be displayed.

Familiarize yourself with the Gasgano GUI. Expand directory and file trees by clicking on the handles on the left. Select individual files and study the FITS file headers displayed at the bottom of the GUI. Use the Preferences menu to change the selection of displayed keywords.

### *4.1.1 Examine AMBER data files.*

Learn in what sequence AMBER data are recorded. Note the classification of the files based on keywords. (To see the classification rules, look under the Tools menu.) Note the grouping of the files by OB identification number. Check that the frame integration time is the same for all data files (DIT keyword). Sending files to the external viewer (button in the upper left corner of the Gasgano GUI) will open the **fv** utility (provided that this tool is specified as the Fits Viewer in the File Display & Grouping tab of the Preferences GUI).



Parameters

| Name | Value | Default | Range |
|---|---|---|---|
| amber.amber_p2vm.dummy | | | |

Input Frames

| Include | Filename | Classification | | |
|---|---|---|---|---|
| ☑ | AMBER.2005-02-25T07:42:41.554.fits | AMBER_3P2V | Locate | Display |
| ☑ | AMBER.2005-02-25T07:43:01.338.fits | AMBER_3P2V | Locate | Display |
| ☑ | AMBER.2005-02-25T07:43:16.401.fits | AMBER_3P2V | Locate | Display |
| ☑ | AMBER.2005-02-25T07:43:31.509.fits | AMBER_3P2V | Locate | Display |
| ☑ | AMBER.2005-02-25T07:43:46.570.fits | AMBER_3P2V | Locate | Display |
| ☑ | AMBER.2005-02-25T07:44:03.045.fits | AMBER_3P2V | Locate | Display |

Product Naming

Product Root Directory: /raw/vlti/amber/porto

Naming Scheme: Numeric

Output Frames

| Filename | Classification | | |
|---|---|---|---|
| p2vm_0000.fits | P2VM_REDUCED | Locate | Display |

Log Messages

```
13:56:24 [ INFO  ] P2VM produced: p2vm.fits.
13:56:24 [ INFO  ] Writing QC log file.
13:56:24 [ INFO  ] End of DataReduction
Product frames:
  /raw/vlti/amber/porto/p2vm_0000.fits
Completion status: SUCCESS
```

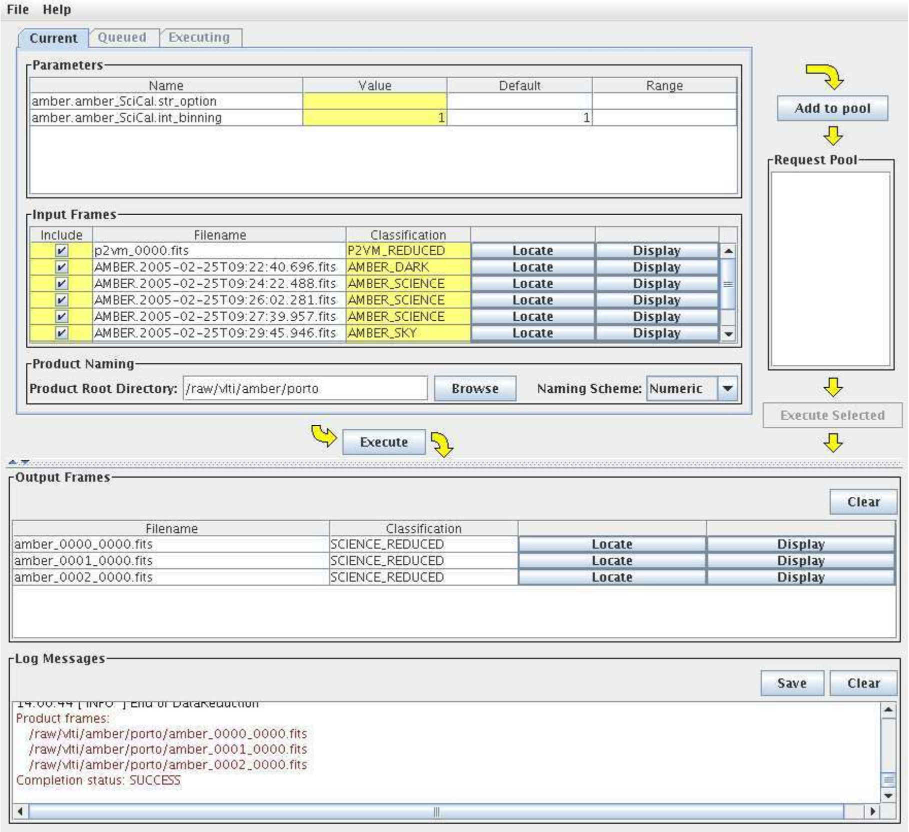
Fig. 2. Recipe amber_p2vm run from Gasgano. The output (P2VM) was written into p2vm_0000.fits.

### *4.1.2 Produce the Pixel-to-Visibility Matrix.*

Select the 10 P2VM files (taken on Bet Cen, in this example) by clicking the first, then the last one while holding down the Shift key. Be sure to also select the files containing the bad pixel map (BPM) and the flat field map (FFM), under the Maintenance header. (These two files are also delivered with the data reduction software and may therefore reside in a different location.) (If you want to compute the spectral calibration too, then also select the four WAVE files.) Then use the Selected files—To Recipe—Load Recipe menu to select the amber_p2vm recipe. When you click Execute, it will compute the P2VM which you will need later to run the Sci_cal recipe. Note the file name of the P2VM.

### *4.1.3 Run SCICAL.*

Now select files of a science observation, including SKY and DARK frames, as well as the P2VM computed in the previous step (now displayed in red in the main file display), and the BPM and FFM. Use the Selected files—To Recipe—Load Recipe menu to select the amber_SciCal recipe, and execute



| Name | Value | Default | Range |
|---|---|---|---|
| amber.amber_SciCal.str_option | | | |
| amber.amber_SciCal.int_binning | 1 | 1 | |

| Include | Filename | Classification | | |
|---|---|---|---|---|
| ☑ | p2vm_0000.fits | P2VM_REDUCED | Locate | Display |
| ☑ | AMBER.2005-02-25T09:22:40.696.fits | AMBER_DARK | Locate | Display |
| ☑ | AMBER.2005-02-25T09:24:22.488.fits | AMBER_SCIENCE | Locate | Display |
| ☑ | AMBER.2005-02-25T09:26:02.281.fits | AMBER_SCIENCE | Locate | Display |
| ☑ | AMBER.2005-02-25T09:27:39.957.fits | AMBER_SCIENCE | Locate | Display |
| ☑ | AMBER.2005-02-25T09:29:45.946.fits | AMBER_SKY | Locate | Display |

Product Root Directory: /raw/vlti/amber/porto

Naming Scheme: Numeric

| Filename | Classification | | |
|---|---|---|---|
| amber_0000_0000.fits | SCIENCE_REDUCED | Locate | Display |
| amber_0001_0000.fits | SCIENCE_REDUCED | Locate | Display |
| amber_0002_0000.fits | SCIENCE_REDUCED | Locate | Display |

```
14:00:44 [ INFO ] End of DataReduction
Product frames:
  /raw/vlti/amber/porto/amber_0000_0000.fits
  /raw/vlti/amber/porto/amber_0001_0000.fits
  /raw/vlti/amber/porto/amber_0002_0000.fits
Completion status: SUCCESS
```

Fig. 3. Recipe amber_scical run from Gasgano. Three output files (amber_0000_0000.fits, etc.) have been produced, one for each selected file of type OBJECT.

it. (Note that some parameters can be defined, such as the binning. For now, we leave it at the default.)

### *4.1.4 Plot results.*

Upon successfull completion of the amber_SciCal recipe, select the output file file (e.g. amber_0000_0000.fits) and open the Script Board using the Tools menu. Double-click the amber_OI_FITS_plot.sh entry, and confirm the command. This will startup MIDAS, which will create a customized plot containing various results such as fringe SNR, piston, and average visibility spectrum. Re-run the amber_SciCal recipe with a different binning parameter to study the effects on the results. Type `quit` into the MIDAS terminal to quit MIDAS, which unlocks Gasgano. Use the external viewer to look at the contents of the OI_FITS file produced.

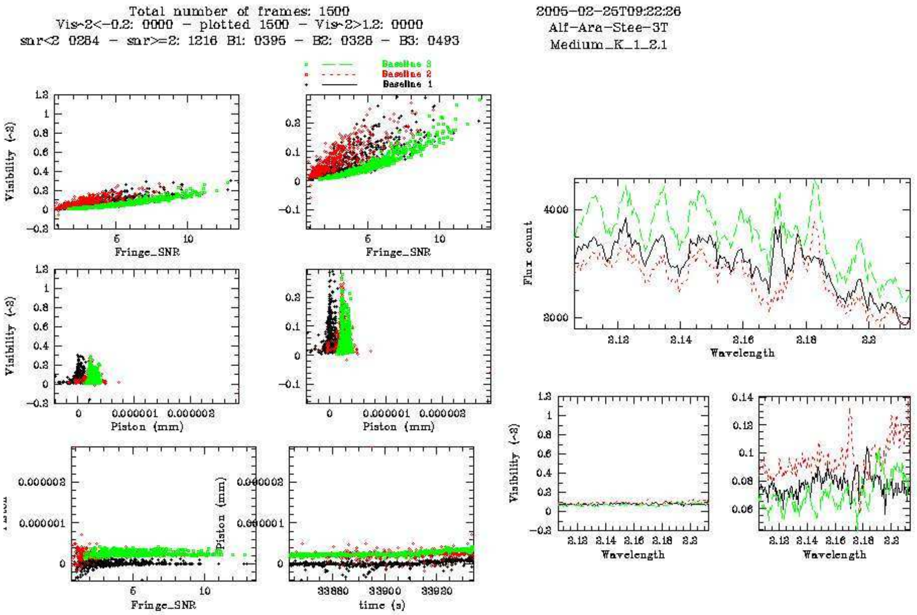


Fig. 4. MIDAS graph of the frame results. The three baselines are colored in red, green, and blue. On the left, each data point corresponds to a single frame. The visibility is plotted versus the fringe SNR and one can see the typical increase with SNR. In the plot visibility versus piston, note that visibility measurements taken away from the mean piston are decreased. In the plot piston versus fringe SNR (bottom panel), note how the piston converges to the mean at high SNR. On the right, mean results for photometry and visibilities are displayed. The strong wiggles are a result of the missing spectral calibration for this older data set, and the results including this calibration are shown further below in the reduction using Reflex.

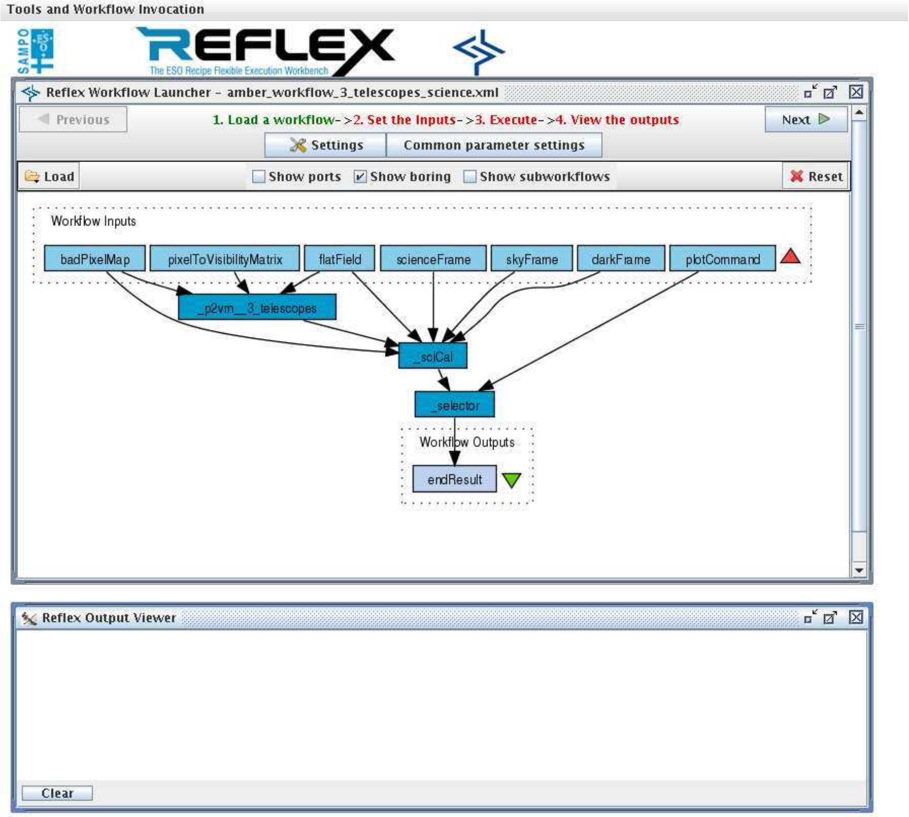


Fig. 5. The main Reflex GUI with the selected workflow. The workflow contains a sequence of processors (called recipes in Gasgano), in dark blue color. The processor inputs are in light blue, or are connected to the outputs of previously executed recipes.

### *4.2 Exercise 2: Reflex.*

At the time of writing, Reflex has not been publicly released yet, but a preliminary and unsupported version is available at http://www.eso.org/sampo/reflex/instructions/.

Type `reflex` at the command prompt to start the Reflex tool. Click settings to make sure the recipe executor is set to “jni”, and that all directory options are set to working dirctory, e.g. */home/student/data*. Make sure (important!) that the check box next to “Perform housekeeping on startup” is *not* selected.

#### *4.2.1 Load a workflow*

Use Load—Load from a file to navigate to *reflex/reflex-0.9.3/examples* (actual path may vary) to select the amber_workflow_3_telescopes_science.xml workflow. Note: if you accidentally selected the wrong one, reset first (button near upper right of GUI), then load again.

### *4.2.2 Editing a workflow*

This exercise, which can be skipped, is just for those who are interested in some information on the underlying principles of Reflex. Instead of loading the workflow mentioned above, choose the amber_workflow_3_telescopes.xml workflow. Tip: if you selected another workflow previously, reset it first before loading a new one.

Now open the Advanced Model Explorer under the Tools menu. This tool allows you to modify workflows, or even create new ones. For now, since the workflow we loaded does not contain inputs for the SKY and DARK frames to SciCal, we will add them manually. Right-click the Workflow inputs line, and select CREATE NEW INPUT... Name it darkFrame, click OK, then also add skyFrame in the same way.

To link the newly created inputs (which are now displayed on the workflow window) to the sciCal recipe, right-click (in the model explorer) the newly created input, and click the darkFrame input in the inputs menu for the sciCalprocessor. Do the same for the skyFrame. Note that now these inputs have been connected to the SciCal recipe in the workflow display.

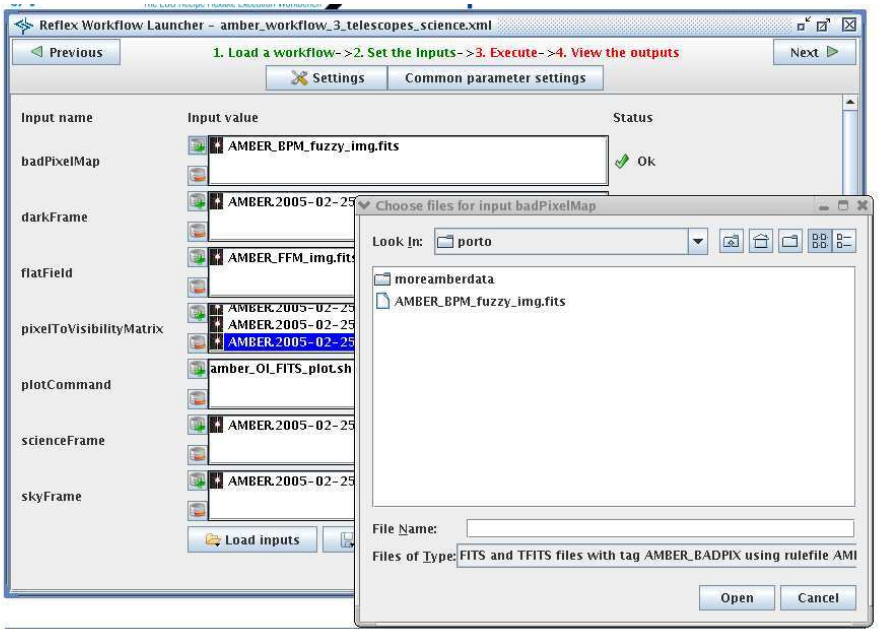
### *4.2.3 Defining the inputs*

Click the *Next* button (in the upper right of the workflow GUI), to display the GUI for defining the input files. Each window has a green colored icon button to add files, and a red colored to remove files from the input section. Reflex uses the classification rules also used by Gasgano to display only those files with the appropriate classification, e.g. only files with DPR.CATG=DARK when defining the inputs for DARK files. To specify the files used for the computation of the P2VM, you might want to display all files in order to select the four WAVE files used to determine the spectral calibration in addition to the 10 3P2V files.

A current lack of functionality of Reflex is a file display similar to Gasgano. Therefore, be a little careful to select the correct files, e.g. if two DARK and two SKY files are displayed, select either the first or second one in *both* of them, because they correspond to two different observations.

This time select, in addition to the 10 3P2V files for the computation of the P2VM also the four WAVE files. You have to display all files in order to see the WAVE files since, at the time of writing, the classification rules do not include them.

You can save the inputs selection to an XML file in order to load it quickly for subsequent execution of only slightly modified selections.


Reflex Workflow Launcher - amber_workflow_3_telescopes_science.xml
◁ Previous
1. Load a workflow->2. Set the Inputs->3. Execute->4. View the outputs
Next ▷
Settings
Common parameter settings
Load inputs
Choose files for input badPixelMap
Open
Cancel

| Input name | Input value | Status |
|---|---|---|
| badPixelMap | AMBER_BPM_fuzzy_img.fits | ✓ Ok |
| darkFrame | AMBER.2005-02-25 | |
| flatField | AMBER_FFM_img.fits | |
| pixelToVisibilityMatrix | AMBER.2005-02-25<br>AMBER.2005-02-25<br>AMBER.2005-02-25 | |
| plotCommand | amber_OI_FITS_plot.sh | |
| scienceFrame | AMBER.2005-02-25 | |
| skyFrame | AMBER.2005-02-25 | |

Look In: porto

moreamberdata
AMBER_BPM_fuzzy_img.fits

File Name:
Files of Type: FITS and TFITS files with tag AMBER_BADPIX using rulefile AMI

Fig. 6. Inputs definition GUI with the selection for the bad pixel map displayed.

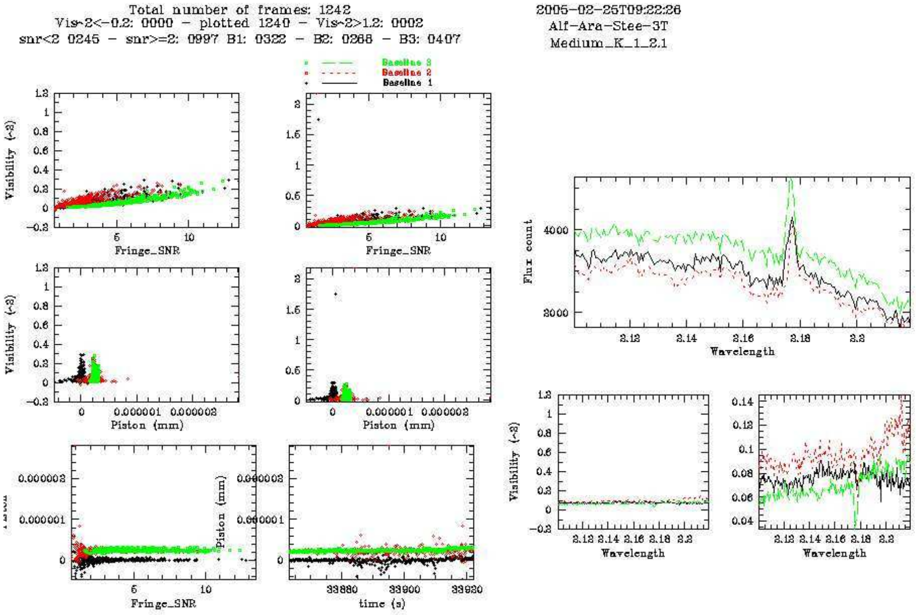


Fig. 7. MIDAS display of frame results. Note the absence of the artifacts in the photometry and mean visibilities when using the spectral calibration.

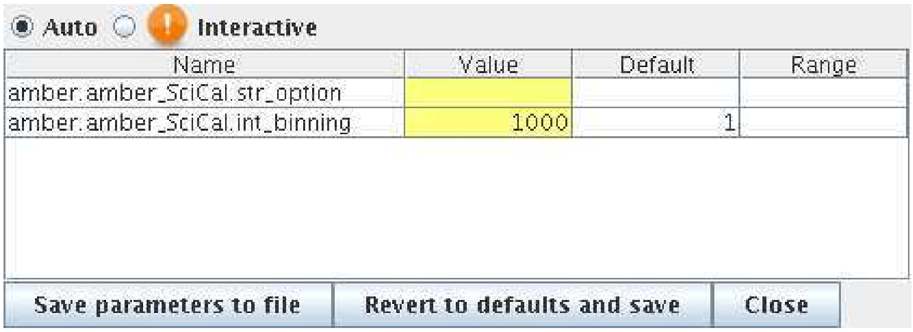
### *4.2.4 Executing the workflow*

Click NEXT, and you will be able to start execution by clicking the EXECUTE button. Parameters for the various recipes can be changed before execution by right-clicking the corresponding box, which will bring up a small GUI. Important: press “Return” to accept the new parameter value, and click “Save”.

Look at the messages during the workflow execution. (Click OK when prompted to proceed with amber_selector.) After the reduction, frame results will be displayed automatically using the same MIDAS procedure as used in Gasgano. Finally, acknowledge that you are happy with the results, and that will finish the workflow.

## *4.3 MyAmberGui*

This IDL based GUI wrapper for amdlib was originally written for Paranal Science Operations by C. Hummel to support an alternative to the AMBER ESO-pipeline for the quick-look data quality assessment. It has since been integrated into the OYSTER interferometry analysis software (http://www.eso.org/∼chummel/oyster/oyster.html) which provides astrometry, modeling, and plotting capabilities. MyAmberGui can be found at http://www.eso.org/∼chummel/amber/myambergui/myambergui.html (including HTML documentation). We list the software here to show different approaches to providing user friendly interactive data reduction software.


● Auto ○ Interactive

| Name | Value | Default | Range |
|---|---|---|---|
| amber.amber_SciCal.str_option | | | |
| amber.amber_SciCal.int_binning | 1000 | 1 | |

Fig. 8. Specifying parameters for processors (recipes). Make sure you hit Return after entering a new value, and Save the parameters to file.

OYSTER is based on IDL (ITT Industries Inc., http://www.ittvis.com/index.asp), also making use of a library of functions written in C.

## 5 A few words on AMBER data analysis

The reduction of the AMBER data should conclude with the calibrated visibility data written to disk in a suitable format, such as the OIFITS exchange format (http://www.mrao.cam.ac.uk/~jsy1001/exchange/). General analysis software will be based on this format due to its adoption by the IAU Working Group on Interferometry. For an overview of this software, see for example http://olbin.jpl.nasa.gov/software/index.html.

It is a good idea to obtain all calibrator data of the same night as the science target oberved with the same instrumental configuration from the public archive of ESO in order to study the consistency of their results. This is important for the assessment of the science reduction in terms of systematic errors. The analysis of the AMBER results in terms of astrophysical models can then be performed in a meaningful way.

### *5.1 Exercice 3: Analyzing the reduction output*

If the binning parameter of the SciCal recipe has been set to 1000 (i.e. all frames), the output OIFITS file will contain just averaged visibility and flux spectra. They can be examined and plotted using the Aspro OIFITS explorer.

Another option is to use a general purpose interferometry analysis package, e.g. OYSTER as mentioned above.

Within OYSTER, type `get_oifits,'amber_0000_0000.fits'` to read the data file (change file name if necessary).

Then bring up the main GUI by typing `oyster`. Select Calibrate—Visibility—PLOT to create the plot widget. In this widget, select "VisSq c" for the Y-axis, Wavelength for the X-axis, "ch" for the Slice. Select the "All" option for the channels in the widget called IndexSelection, and also select All baselines. Then plot the data Pl/E—Screen.

To plot the closure phase, select "TrplPhase c'.

You can also plot the uv-coverage using Plot—Interferometry—UV Data. Before you do this, enter the command `calcastrom` at the OYSTER prompt to recompute the uv coordinates, since they contain wrong values in the OIFITS file.

## References

Tatulli, E., Millour, F., Chelli, A., et al., Interferometric data reduction with AMBER/VLTI. Principle, estimators, and illustration, 2007, A&A, 464, 43