Practice Work Session

AMBER data reduction

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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.

Overview.

Today, we will use Gasgano and Reflex to reduce AMBER data. These tools are provided by ESO, and are based on amdlib. ESO provides pipelines, but is not responsible for general data reduction software.

Exercise 1: Gasgano.

Change directory to *data*. Here you type `gasgano` to start the GUI.

First, you have to add files to the display using the File—Add/Remove Files menu. In that menu, select Add File, click the *data* directory, and click Add File in the lower right. The file selection GUI will disappear and you click OK to finish. All the files of the selectd 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.

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, use 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.

Produce P2VM.

Select the 10 P2VM files (taken on Bet Cen) by clicking the first, then the last one by 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. 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.

Run SCICAL.

Now select files of a science observation, including SKY and DARK frames, as well as the P2VM computed in the previous step, and the BPM and FFM. Use the SELECTED FILES—TO RECIPE—LOAD RECIPE menu to select the amber_SciCal recipe, and execute it. (Note that some parameters can be defined, such as the binning. For now, we leave it at the default.)

Plot results.

Upon successfull completion of the amber_SciCal recipe, select the file 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.

AMBER selector.

This recipe takes a reduced file containing individual frame results, and selects all those frames meeting certain selection criteria.

Exercise 2: REFLEX.

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 */home/student/data*. Make sure (important!) that the check box next to "Perform housekeeping on startup" is *not* selected.

Load a workflow

Use LOAD—LOAD FROM A FILE to navigate to */opt/reflex/reflex-0.9.3/examples* to select the amber_workflow_3_telescopes_science.xml workflow.

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 create 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.

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.

If you have problems defining the inputs, you can also load a predefined inputs file, inputs.xml, using the LOAD INPUTS button.

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. 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.

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 the general purpose interferometry analysis package called OYSTER. A current version has been installed, and can be invoked by typing "oyster" at the command prompt.

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"q 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.