



TITLE : Document Title
 REF. : **VLT-BBB-SPH-xxxxx-xxxxx**
 ISSUE : 1
 DATE: Date of issue PAGE 1/43

SPHERE-DC

Interface user manual

A01 Contr	A02 Man-PA	A03 Sci	A04 Syst	A05 INS	A06 DRH	A11 CPI	A12 IRD	A13 IFS	A14 ZIM
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TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 2/43

Change Record

Issue	Rev.	Paragr.	Page	Date	Observations
1	0	all	all	XX XX 2013	First issue



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 3/43

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Table of Contents

1 Overview.....6

1.1 Scope of the interface.....6

1.2 Servers.....6

1.3 Users.....6

1.4 Overview of the document.....6

1.5 Applicable Documents.....6

1.6 Reference Documents.....7

1.7 Acronyms.....7

2 Client Installation.....8

2.1 Prerequisite.....8

2.2 Procedure for a server outside IPAG.....8

3 Quickstart.....9

3.1 Usual Vocabulary.....9

3.2 Importing Data.....9

3.3 Launching the SPHERE DC client.....9

3.4 Browsing data.....10

3.5 Running a pipeline recipe through SPHERE DC client.....11

3.5.1 Selecting a recipe.....11

3.5.2 Running a recipe.....12

4 ACCOUNTS.....14

5 Data transfer.....15

5.1 Raw data : from observations to the Data Center.....15

5.2 Reduced data : from the Data Center to the user.....15

6 NIRSUR-like data reduction cookbook.....17

6.1 General principles about launching recipes from the DC.....17

6.1.1 No risks of data loss, but some cleaning habits to get.....17

6.1.2 Use of “optimised” data selection in routines.....17

6.1.3 Automatic reductions of most data.....18

6.2 IRDIS reduction.....18

6.2.1 Master dark recipe (automated).....18

6.2.2 Instrument flat (automated).....21

6.2.3 Star center (automated).....23

6.2.4 Distortion calibration.....24

6.2.5 Irdi DBI reduction (automated).....25

6.2.6 Irdi PSF (FLUX_CALIB) reduction (automated).....25

6.2.7 ird_convert_dc (automated).....25

6.2.8 ird_sortframes_dc.....26

6.2.9 ird_specal_dc.....27

6.2.10 ird_specalcharac_dc.....27

6.3 IFS Reduction.....1

6.3.1 Produce master darks frames (automated).....1

6.3.2 Clean raw science data from badpixels and cross talk (automated).....3

6.3.3 Produce master detector flats (automated).....4



6.3.4 Clean reduced flats data from badpixels (automated).....	5
6.3.5 Calibrate position of spectra (automated).....	6
6.3.6 Calibrate wavelength solution (automated).....	7
6.3.7 Produce IFU flats (automated).....	8
6.3.8 Reduce science data: SPH_IFS_SCIENCE_DR (automated).....	10
6.3.9 IFS PSF (FLUX_CALIB) reduction (automated).....	11
6.3.10 ifs_convert_dc (automated).....	11
6.3.11 ifs_sortframes_dc.....	12
6.3.12 ifs_specal_dc.....	12
7 Calendar.....	14
7.1.1 Objective.....	14
7.1.2 How to proceed.....	14
7.1.3 Limitations and assumptions.....	14
8 Instrument monitoring.....	15
8.1.1 Objective.....	15
8.1.2 How to proceed.....	15
8.1.3 Limitations and assumptions.....	15
9 Appendix.....	16

List of Tables



1 Overview

1.1 Scope of the interface

This document provides a description of the user interface that is currently being developed for the SPHERE data center.

The interface allows the following capabilities:

- Processing of a large volume of data (including file selection, parameter choices, validation), either using a homogeneous procedure (especially for NIRSUR, but also for other surveys), with reference recipes/parameters or using several recipes / parameters until convergence toward the best result(s), with the possibility of archiving several results for a given observation, either on short term or long term.
- Reprocessing of old data using new versions of the pipeline
- Archiving of all information relevant to the processing (recipes, input files, parameters)
- Instrument monitoring

1.2 Servers

The main server is located at the data center.

The main server is used for:

- File system : data, recipes
- Database : data, recipes, workflows, parameters sets, processes (= execution of a recipe on given inputs files), data status
- Interface
- Visualization software

The client launch the interface from his laptop/desktop using the client server. There are as many client servers as there are users. Tasks are executed on the main server, located at the data center.

1.3 Users

There are different levels of users. Duty service members (a limited number of people working for the data center) have access to all the functionalities. Some specific accounts can be created for the use of the interface in the frame of specific cases (e.g. WP2 GTO).

PI requesting processing of their data (including consortium members for their IP data) have no access to the interface, and are not concerned by the manual except for section 5 (data transfer) if they ask the data center to process their data.

1.4 Overview of the document

1.5 Applicable Documents

no.	document name	document number, Iss./Rev.
AD1		



1.6 Reference Documents

no.	document name	document number, Iss./Rev.
RD1	SPHERE – IFS Data Reduction Library Design	VLT-TRE-SPH-14690-0350
RD2	SPHERE – IRDIS Data Reduction Library Design	VLT-TRE-SPH-14690-0351
RD3	SPHERE – ZIMPOL Data Reduction Library Design	VLT-TRE-SPH-14690-0352
RD4	SPHERE – Data Flow System Impact	VLT-TRE-SPH-14690-0241
RD5	Plan for use of consortium GTO	VLT-PLA-SPH-14690-0282
RD6	Plan for Large Surveys in Open Time	VLT-PLA-SPH-14690-0283
	Data Center implementation and operation	VLT-BBB-SPH-14690-GGGG

1.7 Acronyms

GTO	Guaranteed Time Observations
IFS	Integral Field Spectrometer
IRDIS	IR Differential Imaging Spectrometer
NIRSUR	Near Infrared Survey
SPHERE	Spectro-Polarimetric High Contrast Exoplanet REsearch
TBD	To Be Defined
TBC	To Be Confirmed
ZIMPOL	Zurich Polarimetric POLarimeter



2 Client Installation

Click on <http://wsrdata.obs.ujf-grenoble.fr:8080/sphere-server/sphere-client/sphere-client.jnlp> and open with java

“use javaws” works as long as the javaws used by you browser points to your installation of java8. Might work with java 7, but is not guaranteed.

You do not need to desinstall the old Java version, you have: you can have several java version installed at the same timeselect the one used by default with the following command:

```
sudo update-alternatives --config javaws
```

this shows you all the installed version and gets you to choose the version you want as default.

As an instance of a java version that works, here is what i get when i type java -version:

```
java version "1.8.0_25"
```

```
Java(TM) SE Runtime Environment (build 1.8.0_25-b17)
```

```
Java HotSpot(TM) 64-Bit Server VM (build 25.25-b02, mixed mode)
```

In case you have issues **here is a step by step troubleshooting guide:**

1- First thing to try is to use the following command, to check whether your system is indeed using the newest version of the javaws, even if you have just installed a brand new version:

```
- sudo update-alternatives --config javaws
```

2- If it was already using the latest version, then try:

```
javaws http://wsrdata.obs.ujf-grenoble.fr:8080/sphere-server/sphere-client/sphere-client.jnlp
```

to be sure your browser is not set manually to an earlier version.

3- If it still does not work go to

```
http://wsrdata.obs.ujf-grenoble.fr:8080/sphere-server/sphere-client/
```

and download sphere-client.jar + lib.zip in a local repertory, uncompress the lib repertory and launch it manually with:
java -jar sphere-client.jar

2.1 Prerequisite

Java 8 up to date. Might work with earlier versions, but not guaranteed.

2.2 Procedure for a server outside IPAG

TO BE DONE LATER: not possible at the moment



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 9/43

3 Quickstart

3.1 Usual Vocabulary

- **Data** refers to all files (Science data, Calibration data and Standard data) acquired with the SPHERE instrument and loaded into the SPHERE DC database.
- **A recipe** is a routine from the SPHERE data reduction pipeline
- **A process** is a set of (data + recipe + input parameters) that refers to a single data reduction operation on the data center.
- **A workflow** is a series of routines, usually starting with the creation of basic calibration files and ending with the final reduced science product.

3.2 Importing Data

The first step is to import your data (science, calibrations and standards files) onto the DC server. In most of the cases, this will be done directly by DC staff. Otherwise consult section data import of this manual.

3.3 Launching the SPHERE DC client

External user can use a java applet to access the SPHERE DC client. Their usernames and passwords are also communicated personally:

Click on <http://wsrdata.obs.ujf-grenoble.fr:8080/sphere-server/sphere-client/sphere-client.jnlp> and open it with java (or “javaws”).

The welcome virtual desktop (Figure 1) offers 7 utilization modes of the client :

- **Data Import:** to import data from the server local data storage to the database. Only for use by local DC staff.
- **Data Browse:** to browse and view your data that has been imported to the data center.
- **Recipe Manual:** Direct link to the documentation for any pipeline recipe
- **Recipe Launch:** Enable to easily use any pipeline recipe on your DC data.
- **Process Browse :** To consult the archive of your previous routine use. Useful to easily check and improve the result of a given routine without starting from scratch again.
- **Validation Browse:** Data quality validation interface. Only for use by local DC staff.
- **Validation Calendar:** Direct access to data and processes by observation date and execution date. Only for use by local DC staff.



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 10/43



Figure 1: Welcome virtual desktop, as seen just after the launch of the DC interface.

3.4 Browsing data

Either when in “data browse” or when selecting input or output data when reducing data using the DC interface, you will have the same browsing interface. It uses an interactive tree on the its left panel. This is like a regular graphical repertory-based file-browser tree (like Data/IRDIS/2013-01-21/files for instance) but the repertory architecture is not hard coded by customizable. You can therefore instantly re-organize it into the tree architecture you want (i.e. IRDIS/DATA_TYPE/2013-01-21 /files). You can choose various architectures using the rolling selection at the bottom of the left panel (Fig.2).

Another option, perhaps more powerful, for sorting data is to use the “filter” panel (top left) that allows you to sort the data according to many criteria (like name of IRDIS/IFS/ZIMPOL, filter, exptime, RA, Dec and such). Note that some short time lag can happen when the sorting criteria used return many files.

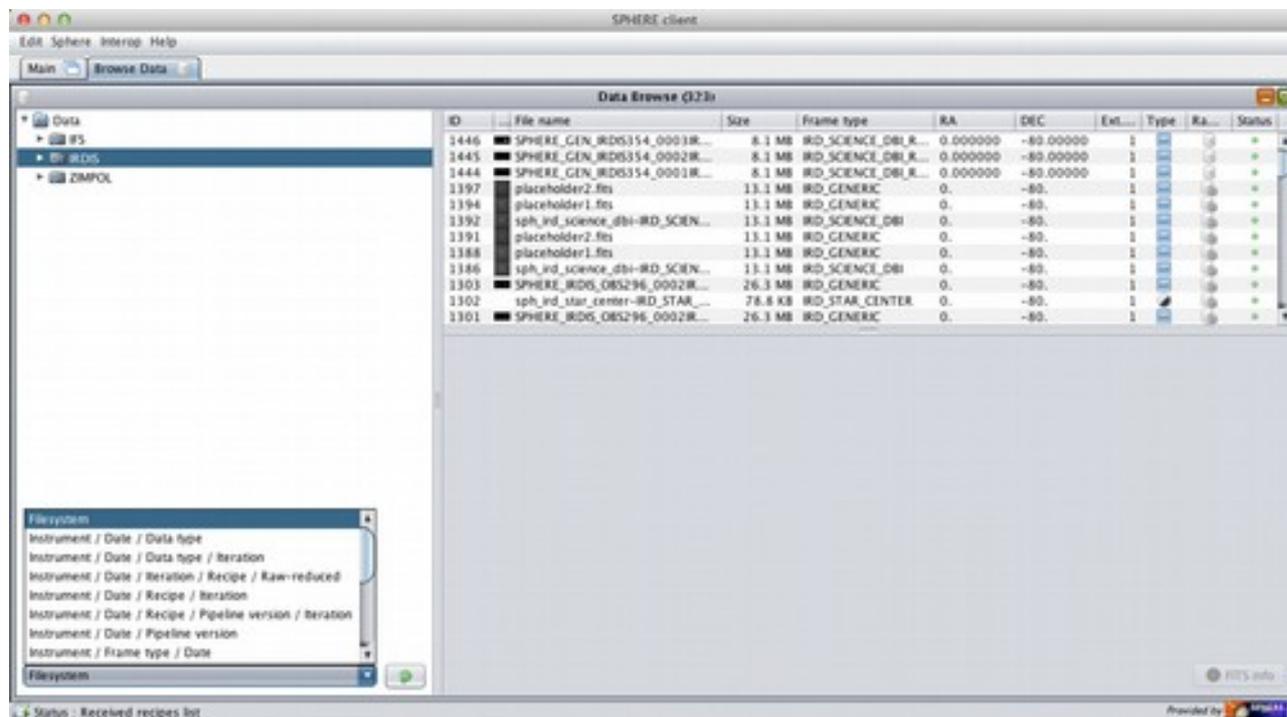


Figure 2: Rolling selection to change the browsing data architecture.

The right panel shows the files present in the selected repertory. Left click on any file shows file information, a right click shows possible actions (*show fits details*, *save as*, or *preview image with ds9*).

3.5 Running a pipeline recipe through SPHERE DC client

3.5.1 Selecting a recipe

The latest version of the ESO pipeline is installed on the DC server and automatically accessible through the SPHERE DC client. The interface offers an easy way to relevantly use the pipeline recipe (*Recipe launch*, Fig.3):

- On the left hand panel, all SPHERE recipes are available, arrayed following the instrument used (IFS, IRDIS and ZIMPOL)
- Click on the recipe you want to use and **double-click** or press the button “select”. This launches the recipe interface.

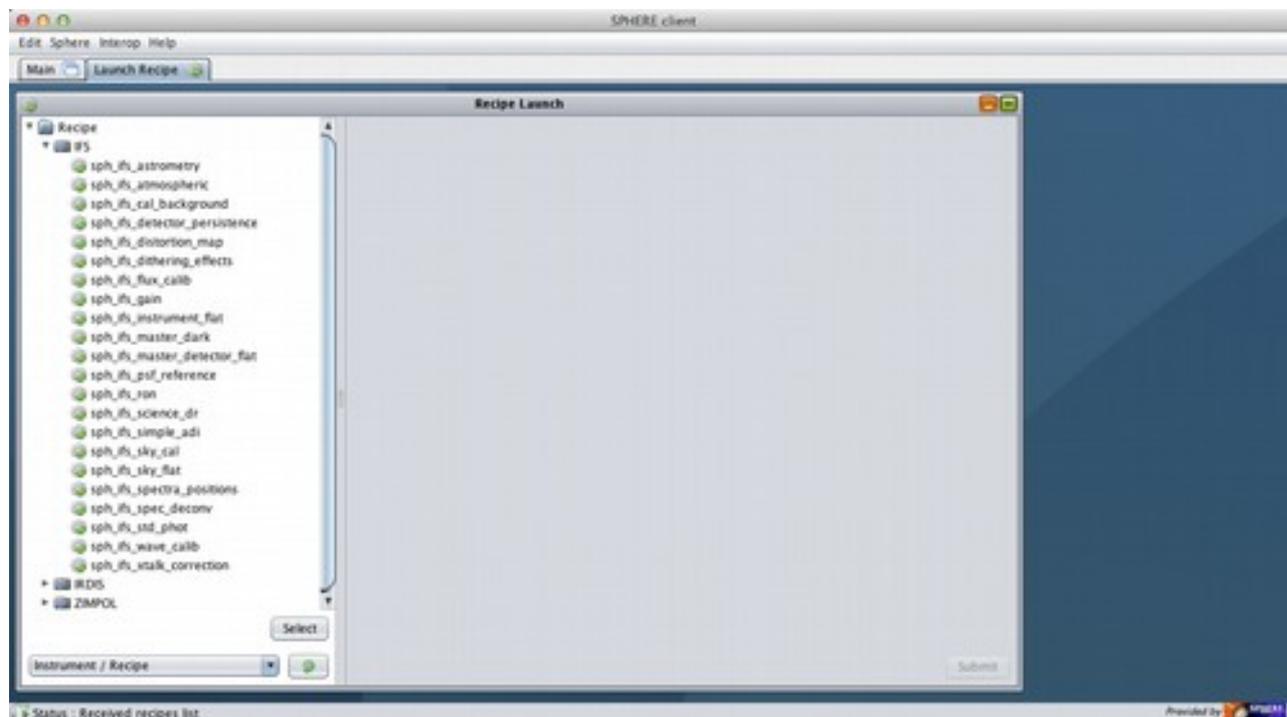


Figure 3: Recipe launching interface.

3.5.2 Running a recipe

The running recipe interface is shown on Figure 4.

- The top panel of the interface displays the routine version information, and enables you to custom-name the process by filling “process reference”. By default “process reference” is left blank and has no impact on running a recipe.
- The detail panel, if selected, shows the full pipeline manual entry related to the selected routine.
- The input frame panel shows all inputs types necessary (regular font) or optional (Italic font) to run the selected routine. If you click on the blue icon on any input line you will be presented with a data browsing interface (see previous subsection) for which only the data relevant to the selected input are presented, i.e., only raw flats if you need raw flats. You can then select your input files and add them as input either by hitting the “add input data” button or right clicking on a file and choosing “add input data”. **Note that for the calibrations, you can click on the left panel to choose the relevant observing date, the data are then automatically classified by integration time and type (filter, mode etc..).**
- The option panel shows all possible options for the routine. Default parameters from the pipeline are loaded by default. You can view a description of each option by briefly setting the mouse pointer on its input form. Custom-made, pre-registered full option sets will be available by clicking on **the “value” roller menu**.
- Once all mandatory input files have been selected, you can click on “submit” at the bottom right to launch the recipe. Note that an error message will be sent if you click on submit before all mandatory inputs are selected, but not if you forgot to enter an optional one. To make sure your process has been launched, you can check *process browse* from the opening interface and check that your process is running (note that this window does not refresh automatically)
- A “process information” window appears, showing the information given when the recipe runs, as well as possible warning or error messages in “log”. Raw input, reduced input and output files are shown. A “refresh”

button appears (bottom right) to refresh the status of the status of the ongoing reduction and has to be selected to see the newly produced files (and error messages) as they are produced by the running routine. The “status” entry shows how the reduction is going, green meaning well and red meaning bad. You can check the results of working (green) processes by right clicking on the output file, and see the details of error messages (useful in red status cases...) on the “log” panels.

Output data can then be directly downloaded or previewed with ds9 by right clicking on the output files.

- You can close/reduce the process information file and directly modify the input files and/or option settings on the original “recipe launch” panel to improve your results if you desire.

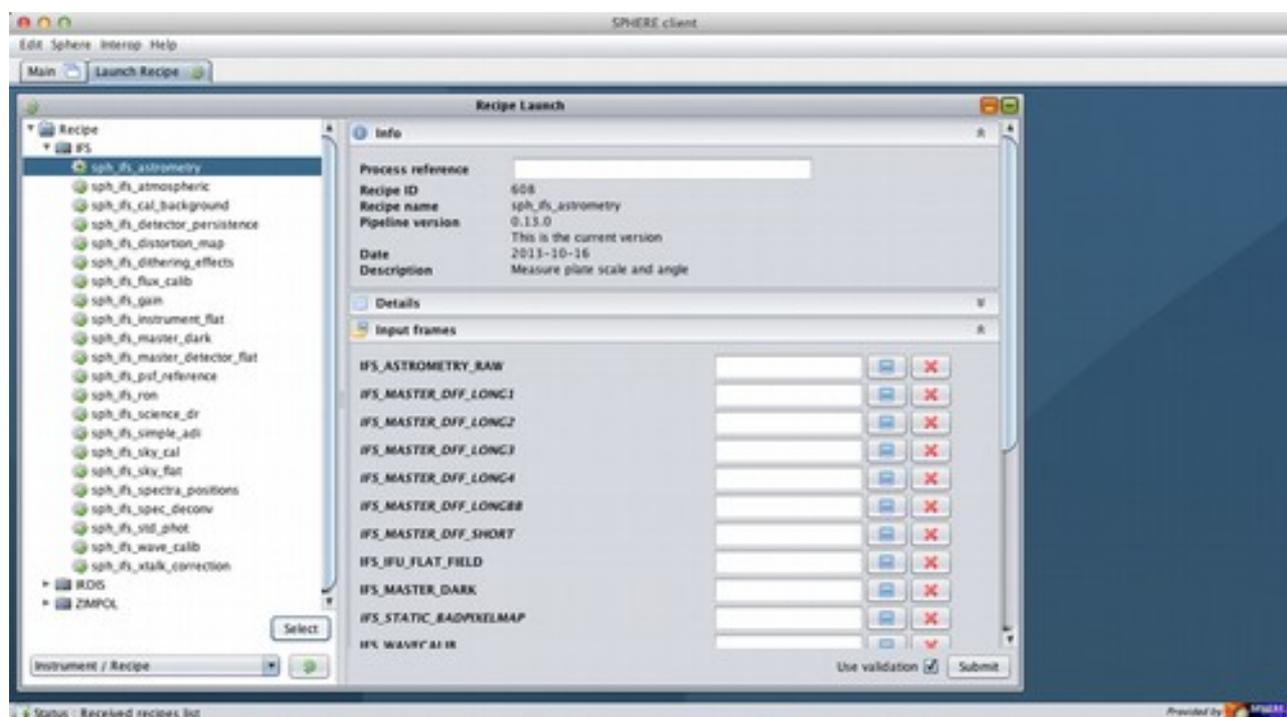


Figure 4: Interface to launch a recipe and select parameters.



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 14/43

4 ACCOUNTS

Access restrictions concern data, functionalities, and recipes.

Done by DC staff. An account can be requested by launching the client and clicking on the “?” near the login field. Remember the password you enter with you account request: this will be your future DC user password.



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 15/43

5 Data transfer

5.1 Raw data : from observations to the Data Center

Done by DC staff

5.2 Reduced data : from the Data Center to the user

You can use the DC client to download data by making a selection of files using the quite efficient « *filter* » *tool of the « browse data » tab of the DC client*, and then download your selection. You need to connect to the DC client for this, so you have to have a computer with java 8 installed and then simply to click on this link : wsrdata.obs.ujf-grenoble.fr:8080/sphere-server/sphere-client/sphere-client.jnlp

You can filter data similarly to what you can do on the ESO archive, just *always think to click on the « submit » button* after doing your selection, even if it seems the selection has been actualised. For instance, if you want to see all the IRDIS master reduced cube available for GJ_285 during the night of 2015-12-25 (which, like all DC nights goes from 2015-12-25 at 20:00 UT to 2015-12-26 at 19:59 UT, so that the morning calibs are within the same night as their obs) you need to :

- set the « Observation night » to 2015-12-25
- set the « frametype » to IRD_SCIENCE_REDUCED_MASTER_CUBE
- set the « Object » to GJ_285

If you want to see all reduced IFS and IRDIS data for this object you let the « frametype » empty and you put the « raw/reduced » tab to « reduced ». You can see more information on the browsing and filtering options within the DC client by reading section 3,4 of the DC manual, or just *hover your mouse on any field in the « filtering » tab to get dedicated info on this filtering parameter*. Also for most parameters *you can enter partial info and the DC will propose you relevant completion*, so it is better to look for GJ_285 by typing “285” and selecting GJ_285 rather than typing GJ285, without the “_” and getting nothing that matches! “Object” comes from the fits header, hence what was written in the OB. Some typos can have been made during the observation, so if you do not find your target, use the box “target”, which will look in the database for the simbad resolved name. Note that you can only see files for which your user has access right.

Once you get your selection you have 2 solutions to download data :

1- *You can conveniently and efficiently download hundreds of Go if necessary*, by right clicking on your selection and *select the « download script » option*. You can either download all files that are displayed by your filtering or select a subset with the regular ctrl or shift clicks to do your homemade subselection. Saving the download script is almost instantaneous since it is only a txt file. *Copy it* in the repertory where you want to download your data, *make it executable* (chmod u+x sphere_dl_script.sh), and then *execute it* (./sphere_dl_script.sh) so that all your files are efficiently downloaded, like with an eso download script, through wget. You can also mail the script to somebody you want to share the data with, instead of sending loads of data, but note that the script has a time-limited validity (typically 1 month) and use with care to avoid dissemination of data to unauthorised people.

2- *To download a single or a few file of small size (<50Mo)*, you might want to just right click on each file and select « save as ». Since this goes through java this is not at all an optimised download so please use it only for small files.

Web service enabling requests on the data base / file system :

<http://wsrdata.obs.ujf-grenoble.fr:8182/sitools/client-user/Sphere/project-index.html>



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 16/43

User account necessary to access data. At some point, reduced calibrations should be available with default user.



6 NIRSUR-like data reduction cookbook

If you are part of a large program DRT (Data Reduction Team), you might have access directly to the DC with a given user account and with the availability to see a set of data associated with a given workspace on which you are allowed to work.

The first step after you have logged in the DC client is to select your working workspace by using the “select/update” workspace (the first left of the three buttons at the bottom of the welcome menu). It should be something like 'GTO_Run_May'.

Though you have the administrative rights to create sub-workspaces, please don't do so on a regular basis because it makes data administration much more difficult when multiple users create multiple sub-workspaces.

Note that some more detailed information on the algorithms used by the pipeline are available on the DRH manual:

http://www.mpia.de/SPHERE/Releases/drh_manual14.pdf

Note that as of October 2015 all calibrations are automatically reduced: see 6.1.3 for details

6.1 General principles about launching recipes from the DC

6.1.1 No risks of data loss, but some cleaning habits to get

- Since the local interface you use is really just an interface, don't worry if your connection is broken or if the interface crashes: your work is safe and running on the DC server.

- Remember that the vocation of the DC is to keep data safe, *so if you run the wrong process or just do a test, this will stay on the hard drive unless you tell the DC*. Please do it :-). You have two ways of doing so:

- 1 If you realise the process you have just ran is not useful you can remove it definitively by selecting the process, choosing the **“admin” tab and then click on “delete process”**
- 2 If you have already used the outputs from the process before you realised it was wrong, you cannot remove the process, but *you can tag it as “rejected” (click on “reject” button on the lower right of the process panel)* so that the DC knows it can erase it when running its regular cleaning and maintenance tasks

6.1.2 Use of “optimised” data selection in routines

As of September 2015 a new semi-automatised way to launch recipe is available from the DC:

- 1- **Select the routine you want to use** in “launch recipe”
- 2- **Select one file of the main input** (always the first input) corresponding to the data set you want to reduce. If all the necessary calibs and data that you need to run the recipe are on the DC it should be the only manual file selection you have to do to launch it.
- 3- **click on the “optimize” button** (see Fig5): the DC will automatically select the calibrations closest in time with your file and select the full stack of main input. (meaning that for instance if you selected only 1 raw flat file, it will automatically select the 4 other matched raw flat files that are necessary to launch the flat recipe)
- 4- **Check that no inputs are missing**: the “optimize” button only selects optimal calibs (i.e. darks with exactly the exposure time of you data), but if nothing optimal is available you might want to select sub-optimal calibs manually.
- 4- **Check that the routine parameters that the DC pre-selected are fine** for you
- 5- **Click on “submit”** launch the recipe

Note that if for any reason you want to change the “optimised” inputs files that the DC selected, you can do it manually using the regular file selection option for each input “browse input frames” or **look among the 10 best pre-selected files using the “browse compatible frames” button** (see Fig.5). If you don't see the optimize button it means the associations rules have not yet been coded into the DC for this recipe.

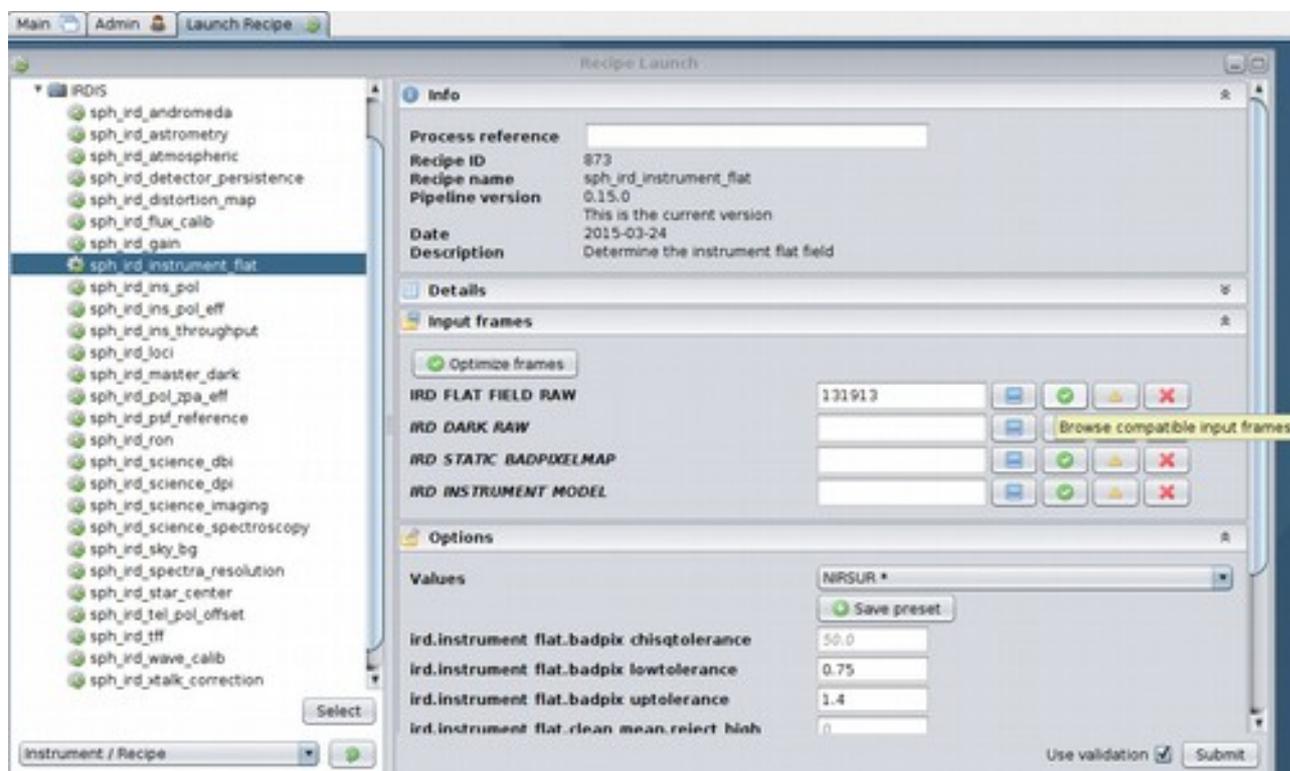


Figure 5: "optimize" and "browse compatible input frames" buttons

6.1.3 Automatic reductions of most data

As of the end of October 2015 the DC runs an automated reduction on all calibrations, and carry out pre-reduction steps on raw science data (like cross-talk correction of IFS raw images). **Manual reductions therefore only consist in the science reductions of science and PSF frames**, both for IRDIS (IRD_SCIENCE_DBI) and IFS (IFS_SCIENCE_DR).

So for a first glance at data analysis you can directly jump to 6.2.5 and 6.3.8, and launch them with the assisted “optimised” mode (see previous section), **after carefully checking the proposed inputs, notably the quality of the IRD_STAR_CENTER (see 6.2.3, on how to estimate its quality).**

The automated pipeline for IRDIS stops after the ird_convert_dc step. You can check if your target has been reduced by using “browse process” and filter using either your object name and/or the ird_convert routines.

The automated pipeline for IFS stops after the ifs_sortframes_dc step. You can check if your target has been reduced by using “browse process” and filter using either your object name and/or the ifs_sortframes routines.

6.2 IRDIS reduction

6.2.1 Master dark recipe (automated)

Routine: *sph_ird_master_dark*

Note that recipe uses “IRD_DARK_RAW” frame types, that can be of various types depending on the wavelength

First check that relevant reduced “IRD_MASTER_DARK” files are not already available by using browse data with option filter.

Specification for inputs in YJH bands

- Relevant dark calibrations are usually taken the morning after the corresponding science data: date-obs within 1 day of science



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 19/43

- OBJECT= "DARK,BACKGROUND"
- Same filter
- Same exptime
- Same readout mode (should be the same for same exptime, but better check)
- Same neutral density
- Relevant dark calibration are usually taken the morning after the corresponding science

Specification for inputs in K band : (since thermal background is not negligible)

- *Same as above or, alternatively:*

- Raw frames with OBJECT= target name. DPR.TYPE="sky,background" can be used instead of DPR.TYPE="dark,background" raw frames (that have non null RA and Dec, that should be close to the target)
- Same filter
- Same neutral density
- Same exptime
- Same readout mode (should be the same for same exptime, but better check)

Use recipe sph_ird_master_dark with "launch recipe" with as as many relevant(see above) inputs dark raw frames as available to produce a reduced master dark.

Following parameters are advised:

- * "save.addproduct=true". For the badpixel map to be created
- * "sigma clip" =3 . in case too many badpixels would be created, you can reverted to default value of 5.
- * Use default of "max acceptable"=3500 to avoid the issue detailed below

In K band for long exposures, (32s, and 64s, perhaps for 16s) the use of the default absolute threshold "max acceptable" of 1000 leads to have strong part of the detector tagged as "badpixel", if thermal noise overshoot 1000ADU. Use higher values of "max acceptable" of ~1600 for 32s and 3500 for 64s.

* Others parameters can be left to their default values

The routine produces two files that will be used later, a dark (frame type: IRD_MASTER_DARK) and a bad pixels map (frame type: IRD_STATIC_BADPIXEL_MAP).

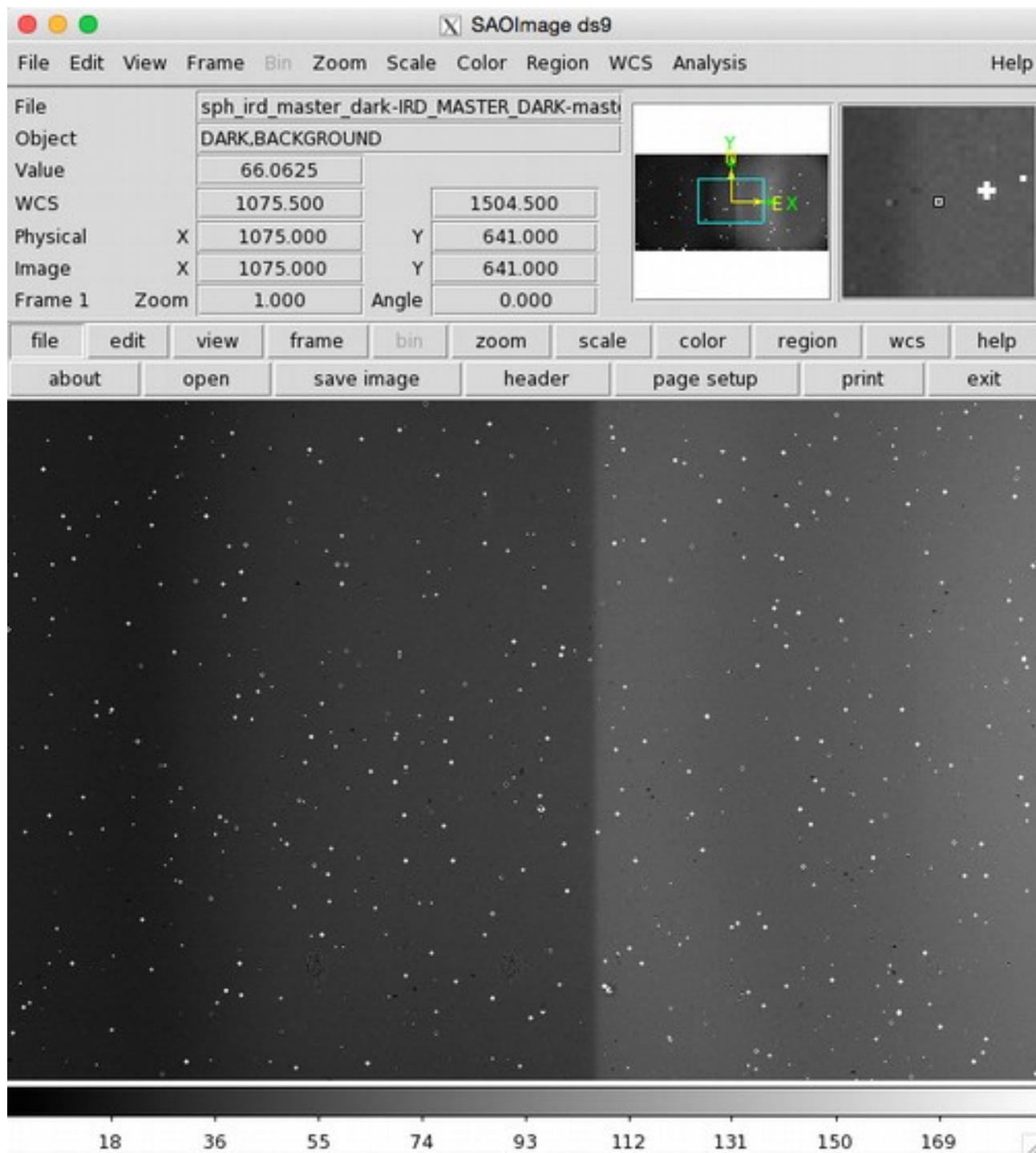


Figure 6: IRDIS dark frame, as obtained with the sph_ird_master_dark

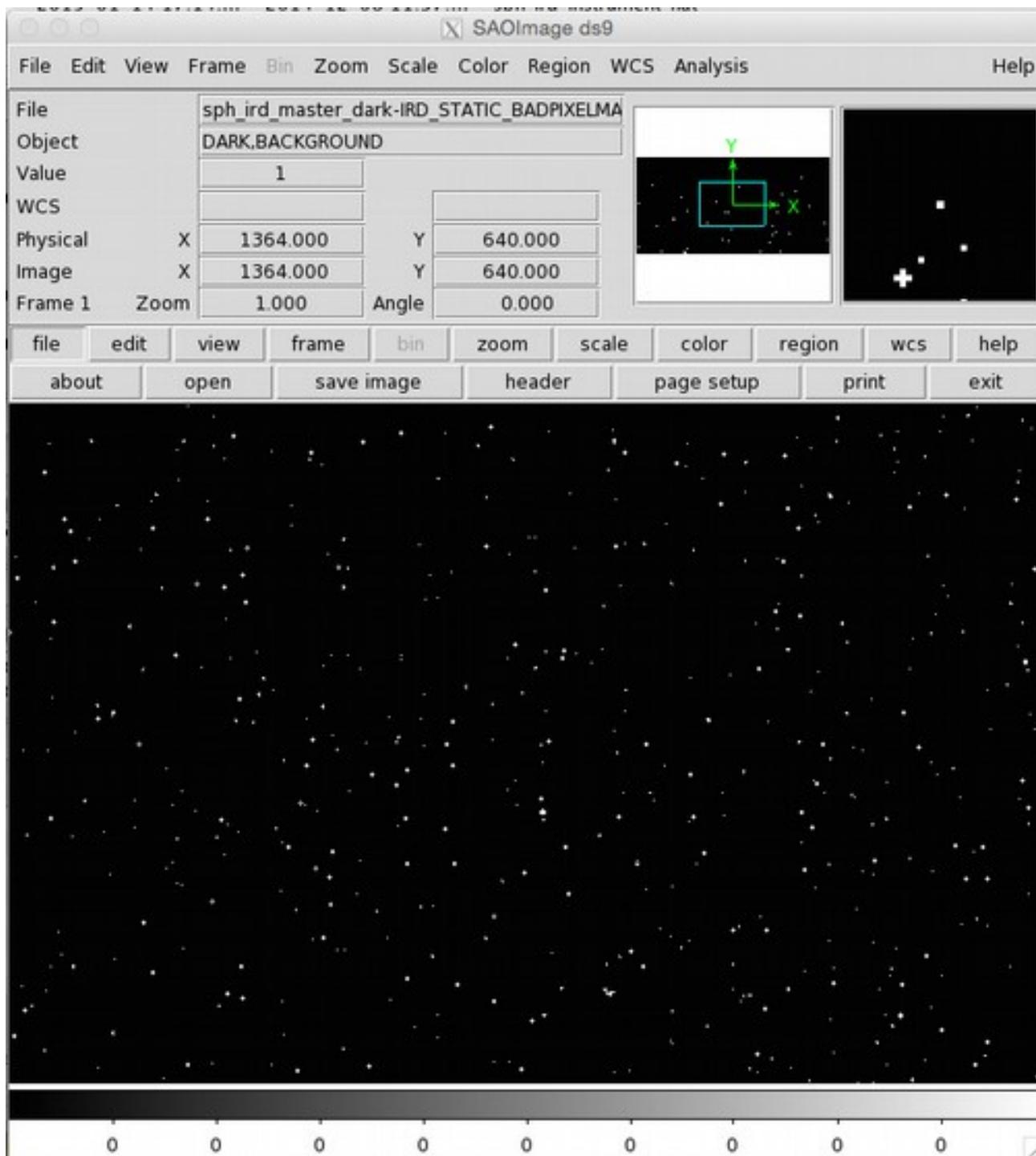


Figure 7: IRDIS bad pixel map as produced by the sph_ird_master_dark recipe

6.2.2 Instrument flat (automated)

Routine: *sph_ird_instrument_flat*

If relevant reduced “IRD_FLAT_FIELD” files are already available in DC (check by using browse data with option filter) you don't need to reduce it again.

Specification for input files:



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 22/43

- Relevant flat calibration are usually taken the morning after the corresponding science data: date-obs within 1 day of science
- Same filter
- Preferably from the same night or as close as possible in time

Additional specifications for raw flats:

- Raw flats used as input of sph_ird_instrument_flat need to span a range of exposure times (typically 2,4,6,8 and 10s) and at least 2 different exposure times are necessary.
- Raw darks (Not necessary for NIRSUR) with same exposure time sequence (eg: 2,4,6,8,10s) as raw flats are an optional inputs that might improve data reduction in cas of faint extended objects (To be confirmed).
- Static badpixel map from relevant dark procedure (see previous subsection, beware to have same readout mode as raw flat) is required **! NOT from a flat !**
- No instrument model needs to be used

Parameters:

If needed run sph_ird_instrument_flat with relevant inputs. Advised parameters are default plus the following tuning:

* badpix_low_tolerance = 0.75

* badpix_high_tolerance = 1.25 (more 1.5 in K-band)

This routine will create a flat field (frame type: IRD_FLAT_FIELD).

Note that the flat field file itself also store the bad pixel map that combine the badpix from the dark and the non linear pixel identified in the flat in the second extension of the MEF flat. All subsequent DRH routines mainly use this extension to correct badpixels.

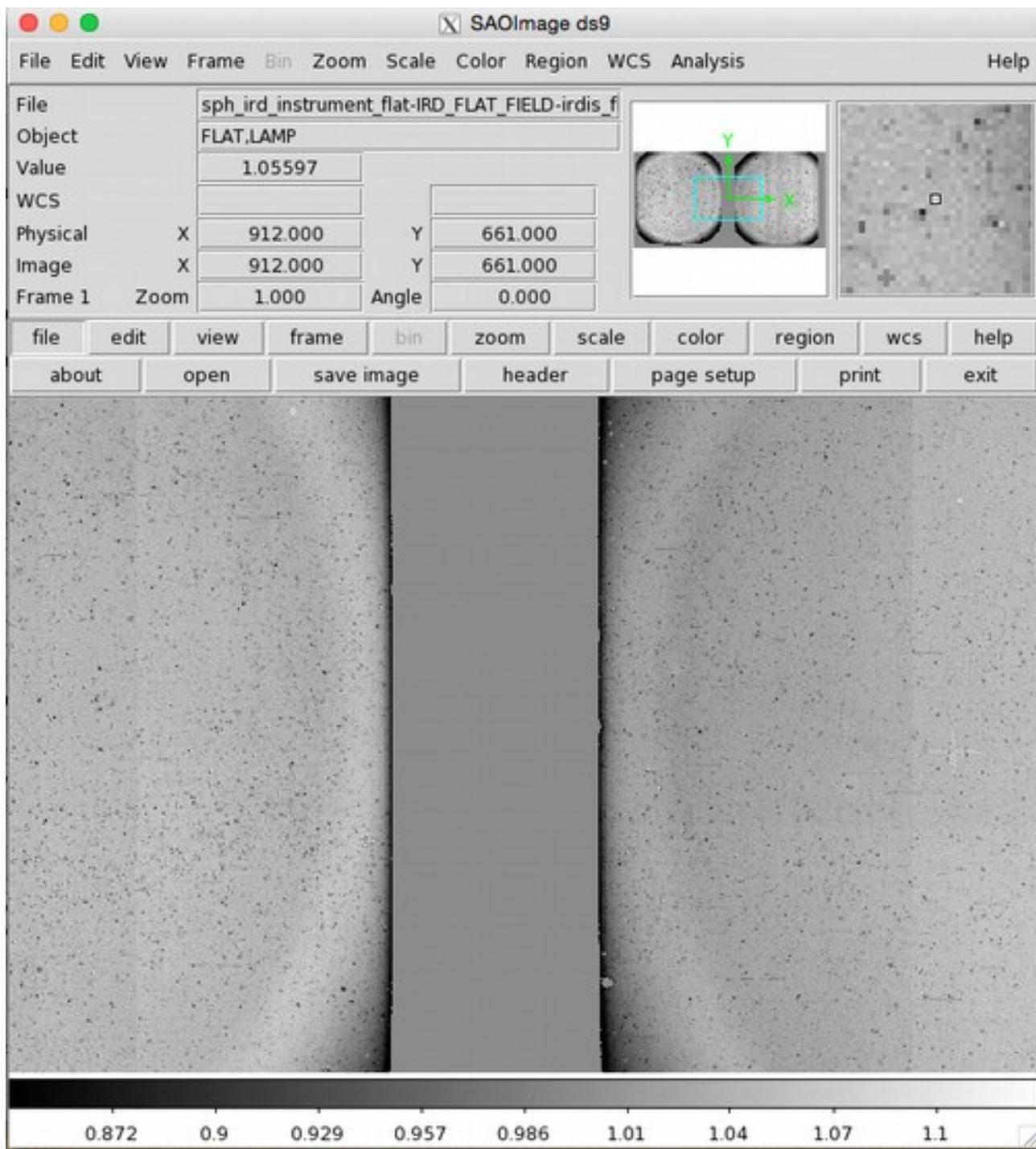


Figure 8: Flat field obtained with the sph_ird_instrument_flat recipe

6.2.3 Star center (automated)

Routine: *sph_ird_star_center*

Specifications for star center inputs:

- IRD_STAR_CENTER_WAFFLE_RAW Need to be images of the target itself, preferably with waffles
- Only one cube is to be used (otherwise the following SCIENCE routine that follows, crashes) and it is best to take a waffle cube acquired in the middle or after the observations



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 24/43

- *The use of a special "STATIC_BADPIXEL_MAP" is strongly recommended* so that waffles are looked after only where they can be. The relevant file is 96856 with name "waffle_lowmaskgoodIRD_STATIC_BADPIXELMAP.fits". File 68803 also works.

- MASTER_DARK with same filter as waffle raw frame, and same exptime .

- FLAT_FIELD with same filter as waffle raw frame

Parameters:

Advised parameters are default plus the following tuning:

center.sigma=100, unless the waffles are very faint

This routine creates a fits table (frame type: IRD_STAR_CENTER). The quality of the centring can be assessed efficiently by looking at the first lines of the log, which are written by a DC applet and look like this:

star_center IDL check patch finds:

Unweighted left center is: 485.85, 520.45

distance between center estimates on left detector is: 0.007

Unweighted right center is: 488.13, 511.42

distance between center estimates on right detector is: 0.028

The value to check is the "distance between center estimates" for each detector, which is a measure of the uncertainty (or rather of sqrt(2) of it). If below ~0.5pixels your star center is good. between 0.5 and 0.9pix you should check the raw image to see whether it is saturated or if it simply has a very low SNR and try to find a better raw if it exist. If it is >0.9 pixel the DC automatically decides the star center is bad and stops the workflow for this target at this step, meaning that no convert will exist for this target.

SPECIAL CASE FOR non-coronographic data:

On non-coro data there is no need for waffles because the star itself is visible, meaning you can use any raw science cube as input for the star center recipe. To do this you need to select "non-standard" input using the yellow triangle button to select the IRD_SCIENCE_DBI_raw file that you will use instead of the IRD_STAR_CENTER_WAFFLE_RAW.

You will need to untick the parameter "use_waffle" to tell the routine to look for a star and not 4 waffles, and usually to set a high threshold of detection like 500 sigma in "center.sigma", because non-coro stars are usually very bright.

You can use "OPTIMIZE", but **BEWARE, optimize will always use the "donut" mask as static bad pixel map, which is very bad for non-coro**, because it excludes the center of the image from the research area, while your star usually sits right in the center. Since this will never work, either use a "normal" STATIC_BADPIXEL_MAP" or use none.

6.2.4 Distortion calibration

Routine: *sph_ird_distortion_map*

BEWARE: If you don't use the right settings/parameters/inputs, this will completely distort the final image: proceed only if you know what you are doing: No distortion calibration is OK, a bad one is definitively not OK...

First check that relevant reduced "IRD_DISTORTION_MAP" files are not already available by using browse data with option filter: this calibration is done weekly, or once per run.

- **This routine needs a static calibration in "IRD_POINT_PATTERN"**. This is a unique files that gives the expected position of the points in the calibration grid **its file ID is 71272**

- Necessary to have the same coronagraph

- Same filter (Broad Band filter at similar wavelength might better)

- Closest in time (supposed to be weekly calib or so)

"Master dark" is not necessary? Flat

Parameters:

- **Use only default parameters**



The routine will create a distortion map (frame type: IRD_DISTORTION_MAP).

6.2.5 Irdis DBI reduction (automated)

Routine: *sph_ird_science_dbi*

Manual reduction of data might start at this step. If this is the case, please check the quality of your IRD_STAR_CENTER automatic calibration (see 6.2.3 on how to assess this quality). If not good, you should tune the star center recipe manually, or ask DC staff to help with this.

If you don't have any IRD_STAR_CENTER frames it is an issue. It probably means that your data are non-coronographic and that you should manually run the IRD_STAR_CENTER recipe using a science raw as input (see dedicated paragraph in section 6.2.3)

Specifications for irdis science dbi inputs:

- IRD_SCIENCE_DBI_RAW need to have same exptime, same filter and ND and are a single serie of uninterrupted observation is preferable.
- flat, dark, star center and distortion as described just above.
- Static bapixel map is not necessary because the info on badpixels is already in the 2nd extension of the flat.
- Even if you don't use the SDI option, a filter table is required. These are static calibrations that should be readily available from the DC.
- Input "FC_table" should not be used.

Parameters:

Standard NIRSUR reduction us default parameters, plus:

* "use adi" =TRUE

In case you use SDI, parameter "min r" should be set to 20pix and "max r = 70" pix for 1,6 micron observation, scalable with lambda.

6.2.6 Irdis PSF (FLUX_CALIB) reduction (automated)

Routine: *sph_ird_science_dbi*

Same as previous one, but in this case you have to force the data center to accept raw inputs that have a FRAMETYPE different from the regular IRD_SCIENCE_DBI_RAW. Instead of clicking on the usual "browse input files", use the yellow triangle just besides that is tagged "browse any input files". Use this to select files of the same object, but with frametype IRD_FLUX_CALIB_CORO_RAW.

- Use any working star center file from any previous reduction. You need this file for the recipe to work, but you don't actually care about the centering since PSF files are offsetted.
- flat, dark, and distortion map as described just above. Note that some calibrations might be missing because calibrations for calibrations such as PSF are not automatically taken. In this case use the closest calib available, perhaps with just a different exptime. **NOTE that exptime and neutral density are different than for the science, hence different calibs are necessary.**
- Note that given the purpose of PSF observations you should **never use the ADI, nor the SDI options**
- Even if you don't use the SDI option, a filter table is required. These are static calibrations that should be readily available from the DC.

6.2.7 ird_convert_dc (automated)

Directly derived from Anthony Boccaletti's "convert" routine. This IDL routine converts the DRH outputs into a single master reduced cube ("center_im.fits") along with the parallactic angle of each of its frame ("rotnth.fits"), a table the wavelengths ("lam.fits", table of 2 wavelength for IRDIS DBI) and a PSF reference cube "median_unsat.fits".



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 26/43

This routine has 4 inputs:

- IRD_SCIENCE_DBI_CUBE_RIGHT: extra outputs of a single IRD_science_dbi recipe executed on science data, right channel
- IRD_SCIENCE_DBI_CUBE_LEFT: extra outputs of a single IRD_science_dbi recipe executed on science data, left channel
- IRD_SCIENCE_PSF_CUBE_RIGHT: extra outputs of a single IRD_science_dbi recipe executed on PSF (flux_calib coro) data, right channel
- IRD_SCIENCE_PSF_CUBE_LEFT: extra outputs of a single IRD_science_dbi recipe executed on PSF (flux_calib coro) data, left channel

Parameters:

Default are fine, please note the following

- TN is the true north calibration value. Let it empty unless you really want to use a specific value for TN. By default it is read from the astrometric calibration table at the DC. For old data this table will always be up to date. For the reduction of an ongoing run, please wait until DC staff tell you this table has been updated before running ird_convert.
- /anamorph correct the first order distortion which is an anamorphism of 1.006 in the Y direction, ***dont use it if you use DRH distortion maps otherwise it will correct anamorphism twice.***

Note that as of 2016-03-23 the frame selection part of convert has been removed and is now used in a dedicated routine detailed below.

6.2.8 ird_sortframes_dc

Directly derived from Anthony Boccaletti's "sortframes" routine. The automatic sort is based on the statistics of the central diffraction spot behind the mask of the coronagraph. **NOTE that if you don't actually set any of the various automated sorting parameters to a value, no automatic sorting will be done.**

Inputs:

One center_im.fits (IRD_SCIENCE_REDUCED_MASTER_CUBE) and one rothn.fits (IRD_SCIENCE_PARA_ROTATION_CUBE) coming from the same convert process.

Parameters :

- select : requires a vector of frame index to be retained in the INPUT data cube. e.g. [0, 7,148]
- reject : requires a vector of frame index to be removed from the INPUT data cube. e.g. [0, 7,148]

Note: you can reject a whole serie of frames by using inputs such as: [[0, 7,130+indgen(6),148]] which is equivalent but shorter to :[0, 7,130,131,132,133,134,135,148] . Note the "[[" and "]"".

- sortsym : This parameter is the number of sigma you allow to keep in the automated sorting. If set to a numerical value it selects the frames for which the flux of the central spot is within :

*median(flux) +/- sortsym * sigma. A value of sortsym=0,5 will be aggressive, 1 is moderate and 3 is very soft.*

- sortgt : This parameter is the number of sigma above which frames are rejected in the automated sorting. If set to a numerical value it selects the frames for which the flux of the central spot is greater than:

*median(flux) - sortgt * sigma. A value of sortgt=0,5 will be aggressive, 1 is moderate and 3 is very soft.*

- sortraffaele Sorting developed by Raffaele Gratton for IFS data. Numerical value of X for automatically rejecting frames that have flux ratio outer/inner gt X*median. Keep blank if you don't want to use it. Can be used in combination with /sortgt or/sortsym. Raffaele's recommended setting for IFS sorting is ***sortraffaele=1.3 and is a very soft sorting.***

select and reject and sortraffaele and either sortsym/sortgt can be combined while sortsym and sortgt are exclusive

- special_reject_output_frames : Rejects frames using the numeration of the OUTPUT cube. This parameter is supposed to be used only with the "duplicate process" option because it supposes you know which frames are kept by sortframe



for a given set of parameter. You are supposed to visualize the output cube of the first “sortframe” instance, run without this special parameter. You can note the additional frames you would want to reject in this output cube and this parameter allows you to reject them using the frame number of this first output cube. For the frame number to match correctly, you need to use exactly the same inputs and parameters (save for this one of course) as those of the previous instance of sortframe, which enabled you to identify the remaining bad frames that you want to reject here.

6.2.9 ird_specal_dc

Directly derived from Raphael Galicher “specal” routine. **Note that this routine might change somewhat in 2017, while the information provided here is valid as of June 2017.**

Detailed information on specal might be found here: /opt/idl/lib/GTO_routines/Specal/*README.pdf

Inputs:

One center_im.fits sorted (IRD_SCIENCE_REDUCED_MASTER_CUBE_SORTED), one rothn.fits (IRD_SCIENCE_PARA_ROTATION_CUBE_SORTED), one lambda info file (IRD_SCIENCE_LAMBDA_INFO) and one PSF file (IFS_SCIENCE_PSF_SPECTRAL_MASTER_CUBE) **coming from the same convert/sortframe process.**

“optimize” button works to do that for you.

You can also use directly the outputs of ird_convert without doing any sorting, but you need to use the “browse any input frame” yellow triangle button. In this case optimize will fetch the lambda info and the SPF file, but you will need to look for the good IRD_SCIENCE_PARA_ROTATION_CUBE file manually.

Parameters :

- Quicklook: **SHOULD NOT BE USED during a DRT.** This “quicklook” is in fact very long because it runs all algorithms in a row. Outside of DRT, and on small and average size data cubes (less than ~200) frames it might be used, providing that the server is not very much used. For DRT it is better to choose which algo you want with the following parameter. **If you want several algos, you can do that easily by doing “duplicate process” on you first** and change the algorithm. Again control the load of the server (using the manual bash command htop for instance), before launching in parallel several reduction of a big datacube (median value of center_im cube on DC is ~80 frames).
- algorithm: choose your reduction algorithm, such as “TLOC1” or “CADI”
- adionly: choose whether you use only the rotation information (“ADI”, advised for IRDIS) or rotation AND spectral information (“ADI+SDI”)
- pcamode: specify the number of modes to be subtracted during a pca analysis. You can ask the routine to subtract different number of mode by using a vector of several integers (such as [5, 10,30]) into this parameter
- other parameters are OK as default.

Note that as for all DC routine a detailed help is available when you let you mouse on any of these parameters

6.2.10 ird_specalcharac_dc

Directly derived from Raphael Galicher “specacharac” routine. **Note that this routine might change somewhat in 2017, while the information provided here is valid as of June 2017.**

Detailed information on specal might be found here: /opt/idl/lib/GTO_routines/Specal/*README.pdf

Inputs:

All the Specal outputs are necessary inputs for specalcharac. With the client, you only use to enter the first input, IRD_SPECAL_MISC_TARGZ and **click on optimize, and the DC will find all the correct inputs SAVED ONE special input.**

SPECIAL Input of ds9 detection region:

This region file (.reg) must be created manually on your local terminal (see below). The first time you use a given region on the DC, you need to upload it to the DC, from the **parameter field 'regionfile'**. Click on the field and it opens a standard browsing windows that allows you to select your local region file. Once imported on DC, you can sue this region again through the regular client “input” field.



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 1/43

How to create a local ds9 region file:

right click on the main specal output IRD_SPECAL_MISC_TARGZ and select save as to save it locally. Untar it (tar -xzf filename.tar.gz). The detected point-like sources are identified by eye looking at cube*.fits and/or snrmap*.fits orreduced_image*.fits using SAOImage DS9. There is no efficient automatic procedure yet.

1/ In the Edit menu of SAOImage DS9, choose Pointer, and in the Region menu, set Form to Circle.

In French, Edition/Pointeur/Région/Forme(or Shape)/Cercle.

In Deutsch, Bearbeiten/Zeiger/Region/Form/Kreis.

In Spanish, Editar/Indicador/Region/circulo.

2/ Open the image and click all the detected sources with an accuracy of <1 pixel (one circle per detection). The pipeline will adjust the position around the clicked pixel but it scans only 1 to 2 pixels.

3/ In the Region menu, Select All.

4/ In the Region menu, Save Regions in the Reduction_XXXX/ folder using:

Format : X Y

Coordinate : Image

Parameters :

Defaults are recommended, and as for all DC routine a detailed help is available when you let you mouse on any of these parameters.

Go to specal manual to get even more detailed information

6.3 IFS Reduction

6.3.1 Produce master darks frames (automated)

Routine: *sph_ifs_master_dark*

- Relevant dark calibration are usually taken the morning after the corresponding science data: date-obs within 1 day of science

- OBJECT= "DARK,BACKGROUND" or "SKY,BACKGROUND" (in this case with same OBJECT name or ra/dec as the target)

- Same readout mode

- **Same exptime is preferable.**

- Filter is always "CAL_DARK" and Neutral density need to be the same as science for "DARK, BACKGROUND" files

- Filter and Neutral density need to be the same as science for "SKY, BACKGROUND" files

Use recipe *sph_ifs_master_dark* with "launch recipe" with as as many relevant(see above) inputs dark raw frames as available to produce a reduced master dark.

Following parameters are advised:

* "sigma clip" =3 . in case too many badpixels would be created, you can reverted to default value of 5.

* Default parameters are fine, but the "max acceptable" and "min acceptable" parameters can be tuned to a narrower range in case too many badpixels are not correctly registered as possible (min=0, max=800 are good alternatives).

This recipe produces two files that will be used later, a dark (frame type: IFS_MASTER_DARK) and a bad pixel map (frame type: IFS_STATIC_BADPIXELMAP).

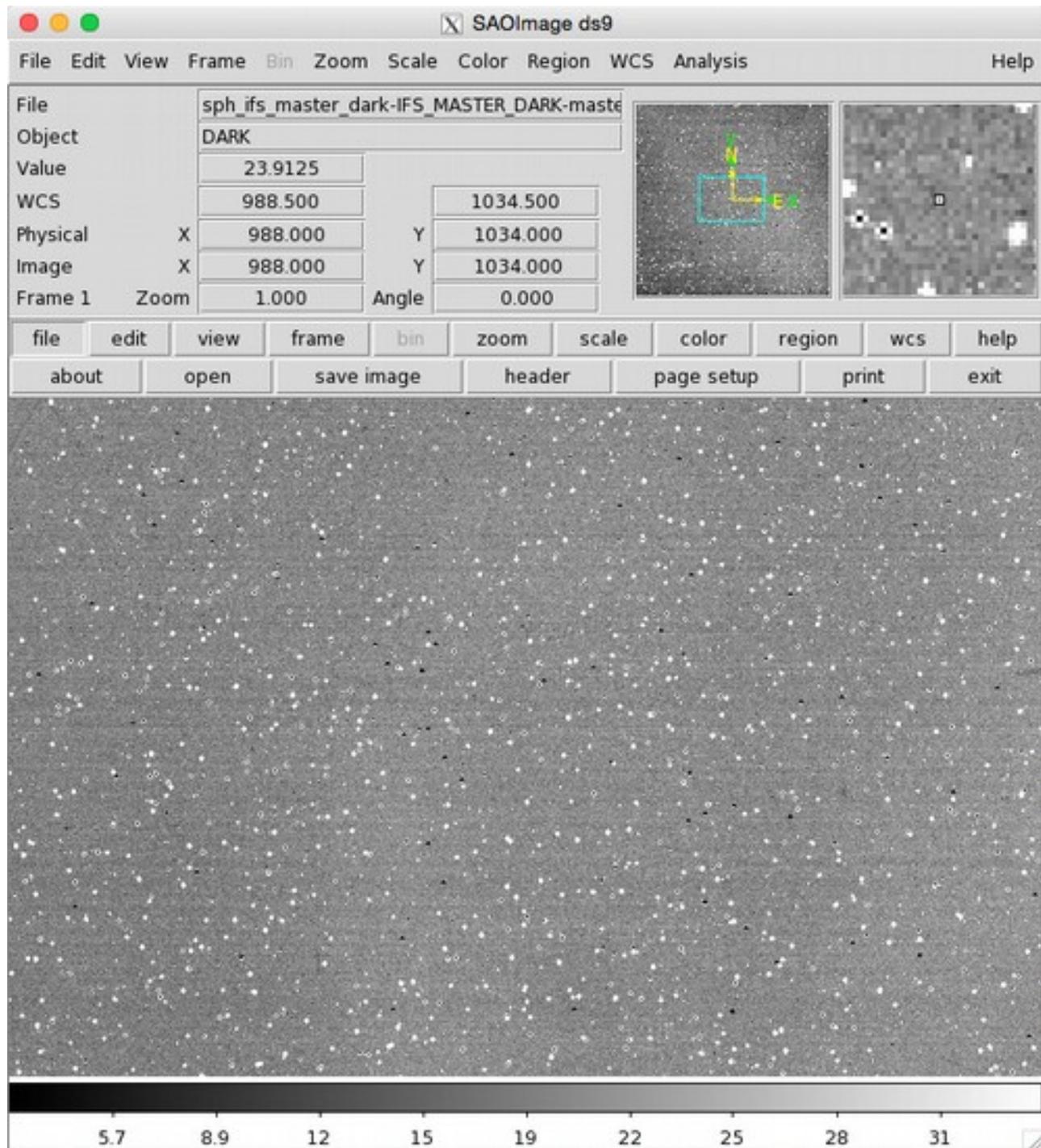


Figure 9: A dark frame obtained with the ifs_master_dark recipe, its frame type is MASTER DARK

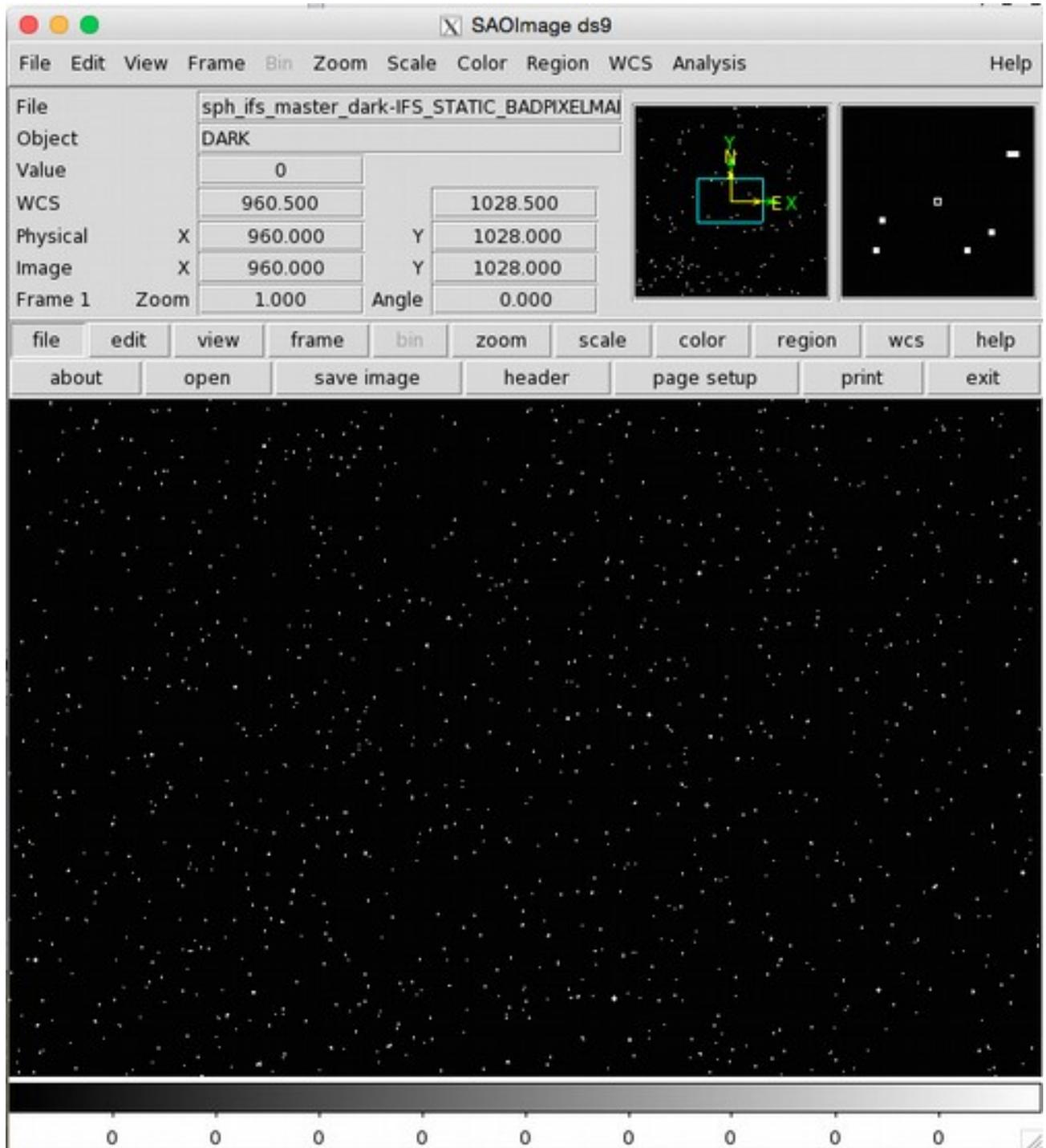


Figure 10: Bad pixel map obtained with the sph_ifs_master_dark_routine (frame type: IFS_STATIC_BADPIXELMAP)

6.3.2 Clean raw science data from badpixels and cross talk (automated)

Using Dino's routine *clean_ifs_raw_bp_ct_background*. This routine can only be seen using a selection tree including "version" since it is located in the "development pipeline" and not the regular DRH pipeline. It uses the badpixels frame (frame type: IFS_STATIC_BADPIXELMAP) and the master dark, produced according to the science data to reduce here, *with exactly the same exposure time as the science frame (no rescaling is performed)*. **Inputs must be of type "raw"**. Frame with "reduced" type have already been processed by this routine and applying it twice is erroneous.



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 4/43

This routine allows you to bin the inputs cubes in the time direction (the parameter nbin or “\$1” for now... is the binnig factor. Hence using nbin =2 on inputs cubes with 8 frames will produce a clean cube with only 4 frames). ***It is recommended to use the default value (“0”), that lets the routine automatically compute the maximal binning*** that does not lead to smearing, is an integral divisor of the initial cube size, and lets enough frames for a comfortable PCA analysis.

If you use the set the ***option largescale=true***, the large scale cross talk will be corrected, which can improve point source detection but ***might cause significant self-subtraction for extended structures such as discs***.

The output files are of the same frametype as the input files “IFS_SCIENCE_DR_RAW” or “IFS_FLUX_CALIB_RAW” if this routine is applied on PSFs rather than on standard science raw. Note that the files you used as input are tagged as “raw” while the output files are tagged as “reduced” and their name changed with bp_ct as a suffix.

6.3.3 Produce master detector flats (automated)

Recipe: *sph_ifs_master_detector_flat*

- Relevant flat calibration are usually taken the morning after the corresponding science data: date-obs within 1 day of science

- **Same filter (YJ or YH)**

- coronagraph, neutral density are indifferent

- This routine ***can reduce the flats for all calibration lamps (3 narrow bands and 1 broad band in YJ mode. 4 narrow bands and 1 broad band in YJ mode) at the same time***. It uses “IFS_DETECTOR_FLAT_FIELD_RAW” frames (2 frames with different exposure time per lamp) .

* Master dark must use the same neutral density as the raw flat use, and similar exptime, see 6.3.1

* Static badpixel just need same readout mode

* **Large scale flat and preamp flat are not necessary and should not be used as inputs.**

Parameters:

Lambda parameter using the default of -1 let the routine look for the relevant values in the header and this works well.

The output frames will have frame types:

IFS_MASTER_DFF_LONGBB

IFS_MASTER_DFF_LONG1

IFS_MASTER_DFF_LONG2

IFS_MASTER_DFF_LONG3

IFS_MASTER_DFF_LONG4

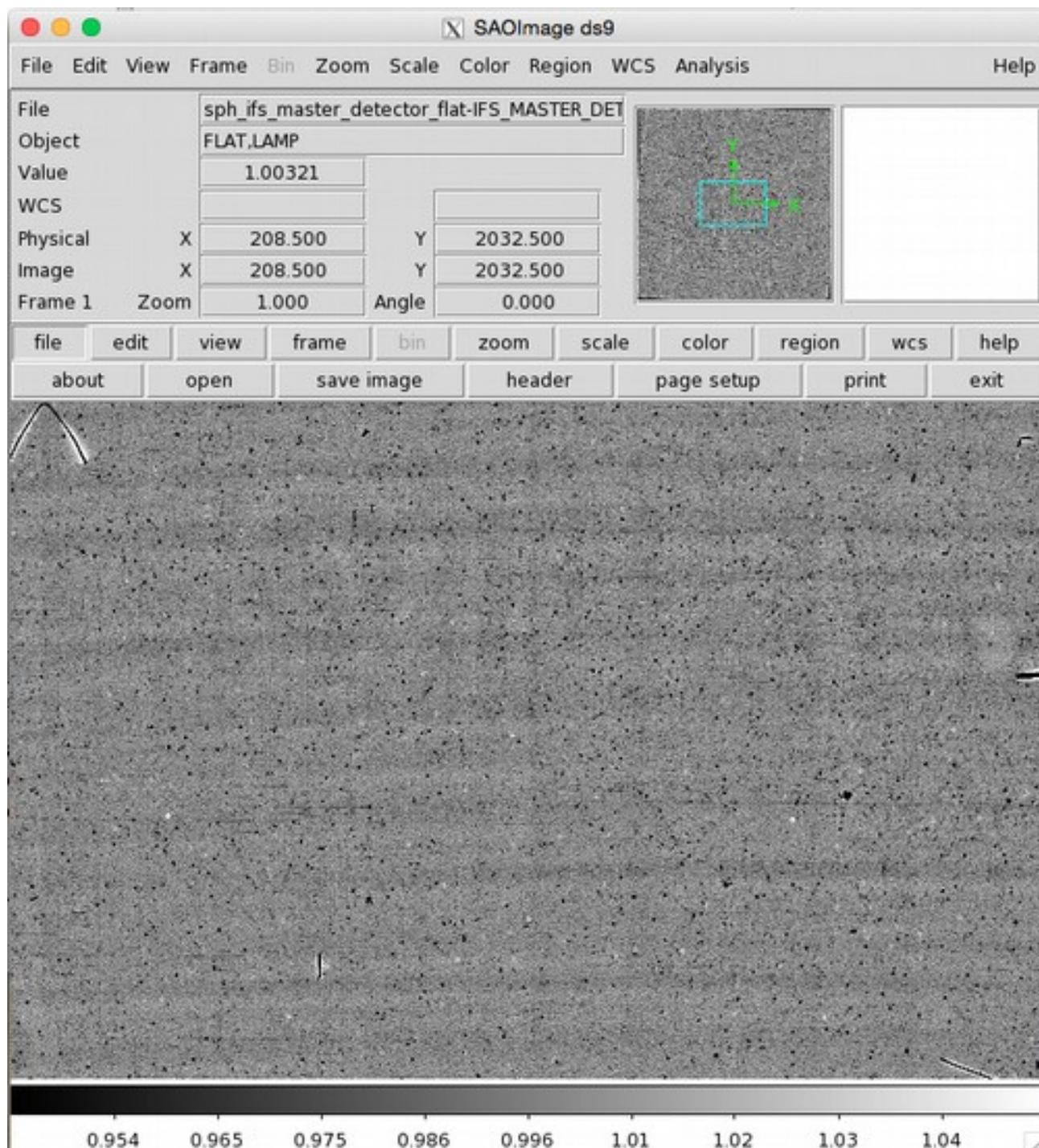


Figure 11: Master detector flat obtained with teh sph_ifs_master_detector_flat recipe. The frame type is of the style IFS_MASTER_DFF_LONG*

6.3.4 Clean reduced flats data from badpixels (automated)

Using Dino's routine *ifs_master_dff_bp_lampall* that can only be seen using a selection tree including "version" since it is located in the "development pipeline" and not the regular DRH pipeline. In the "Launch recipe" window, select e.g Version/ Instrument/ Recipe. You can then find it in the *dev_pipeline* folder. The output will have the same format as the input.

IFS_MASTER_DFF_LONGBB



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 6/43

IFS_MASTER_DFF_LONG1

IFS_MASTER_DFF_LONG2

IFS_MASTER_DFF_LONG3

IFS_MASTER_DFF_LONG4

and the name of the will be suffixed with “sb_processXXX” and will have 1 file extension instead of 4.

6.3.5 Calibrate position of spectra (automated)

Routine: *sph_ifs_spectra_positions*

- Relevant specpos calibrations are usually taken the morning after the corresponding science data: date-obs within 1 day of science

- Same filter is mandatory

* Use the Master dark that fits the specpos_raw file, following 6.3.1 guidelines

* **instrument flat and lenslet model are not necessary and should not be used as inputs**

Parameters:

- **use Hmode parameter =false if you are reducing YJ data.** (and true for YH)

- Use default values for the other parameters (question about the -370° angle instead of 10.7° documented in the manual)

The output frame type is IFS_SPEC_POS

You can also choose the preset parameters (field “values”) and set it to FILTER_OBS_YJ to reduce YJ data or FILTER_OBS_YJH to reduce YJH data.

IFS_SPECPOS_CORR

Note that the outputs of *ifs_spectra_positions* are automatically recalibrated by DC since DRH solution is inadequate. We use the recalibration by 2nd order polynomial fit as recommended by OAPD after commissioning data analysis. ***If executed manually the user needs to execute the dev_pipeline routine “IFS_SPECPOS_CORR” using the IFS_spectra_positions outputs as inputs.***

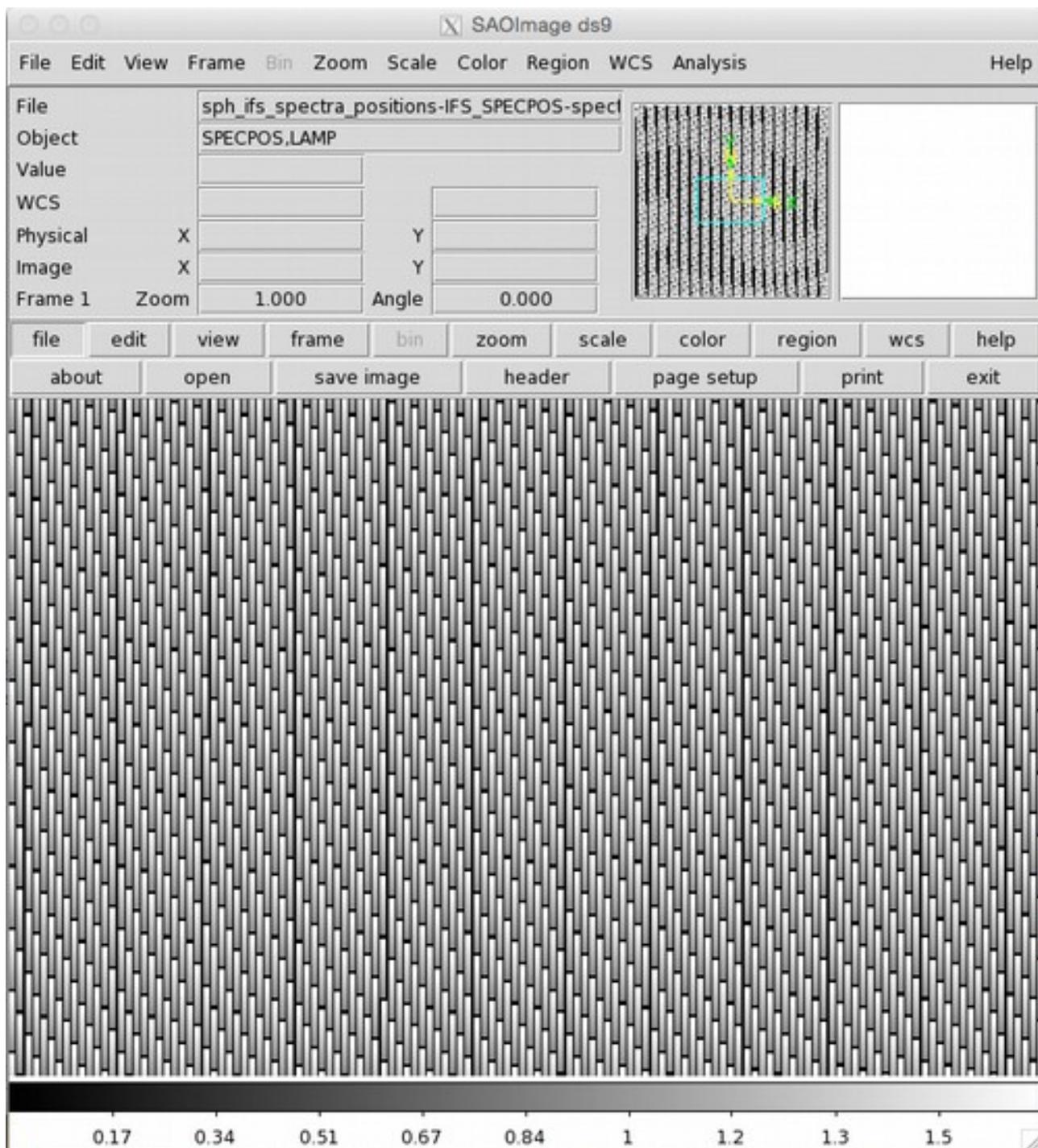


Figure 12: Position spectra frame as obtained from teh sph_ifs_spectra_positions recipe. Data frame type is IFS_SPECPOS

6.3.6 Calibrate wavelength solution (automated)

Recipe: *sph_ifs_wave_calib*

- Relevant wavecalib calibrations are usually taken the morning after the corresponding science data: date-obs within 1 day of science

- Same filter is mandatory

* Use relevant specpos file produced at previous step



* Use master dark that fits with the wave_calib_raw parameters following specification described in 6.3.1.

* Instrument flat input is not necessary and should not be used.

- **Need to change “number lines” parameter to 4 if in YH filter. In YJ you must keep 3**

- Use default value for other parameters.

You can also choose the preset parameters (field “values”) and set it to NIRSUR_YJ to reduce YJ data or NIRSUR_YJH to reduce YJH data.

The output file has a frame type IFS_WAVECALIB_RAW

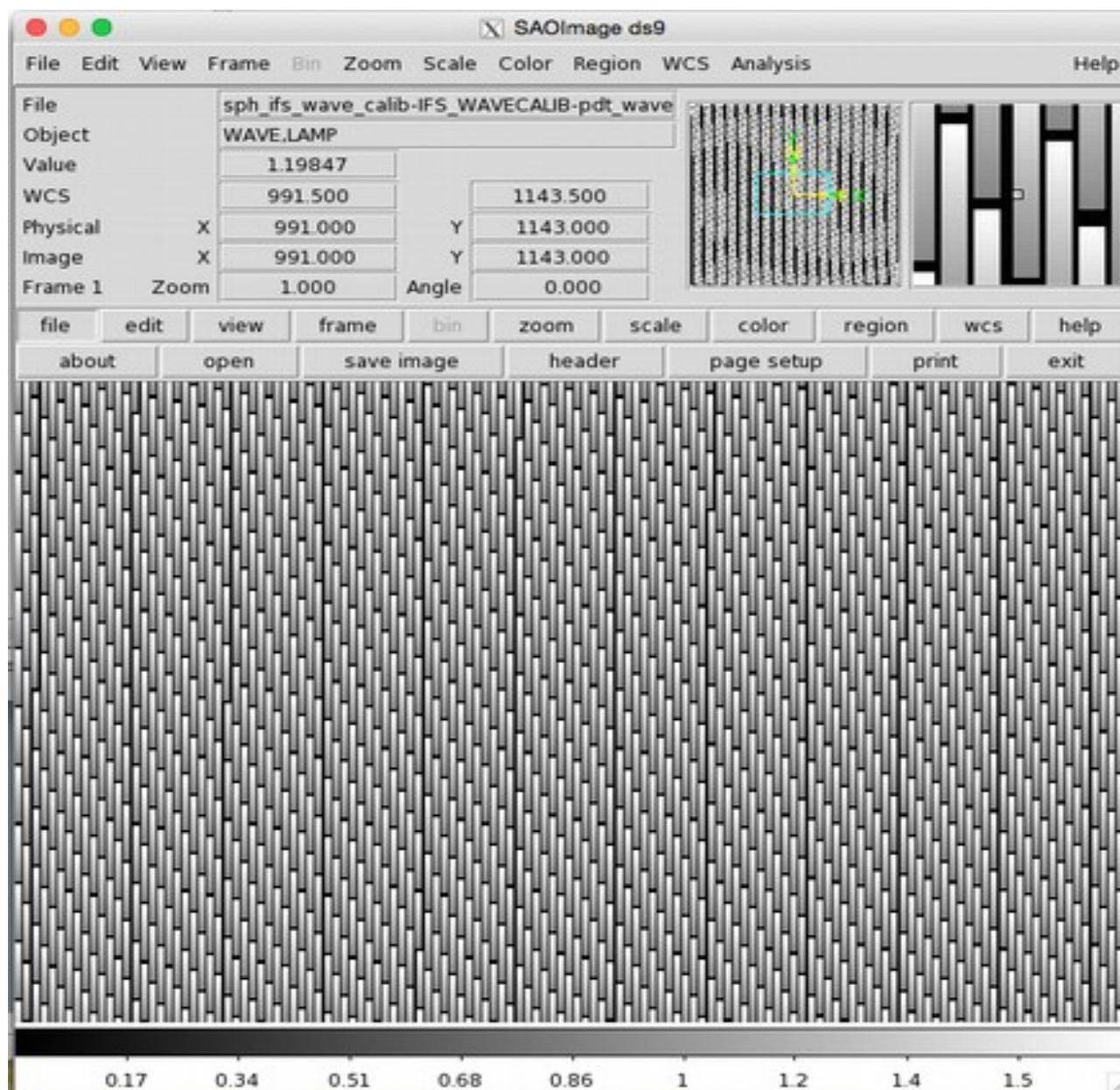


Figure 13: Wavelength solution frame obtained with the sph_ifs_wave_calib recipe. The frame type is IFS_WAVECALIB_RAW.

6.3.7 Produce IFU flats (automated)

Recipe: sph_ifs_instrument_flat



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 9/43

inputs:

- Relevant “ifs_instrument_flat_field_raw” calibrations are usually taken the morning after the corresponding science data: date-obs within 1 day of science.

- Use only one data cube

- Same filter is mandatory

* dark, reduced and badpixel-corrected (1 file extension instead of 4) master detector flats NB1,NB2,NB3 (NB4 for YH mode) and BB, as well wavecalib, that fits with the wave_calib_raw file according to the guideline described in previous section.

* preamp flat input is not necessary. If used you need to take the preamp flat produced when using the BB lamp as input.

*** DFFshort as well as SPEC_POS inputs are not needed and should not be used**

Parameters:

- **Use no-fit=TRUE as parameter.**

- All other parameters can be let to their default value, Particularly, don't change lowtolerance and up tolerance for badpixel, even if they sound way too permissive.

The output file has a frame type IFS_IFU_FLAT_FIELD

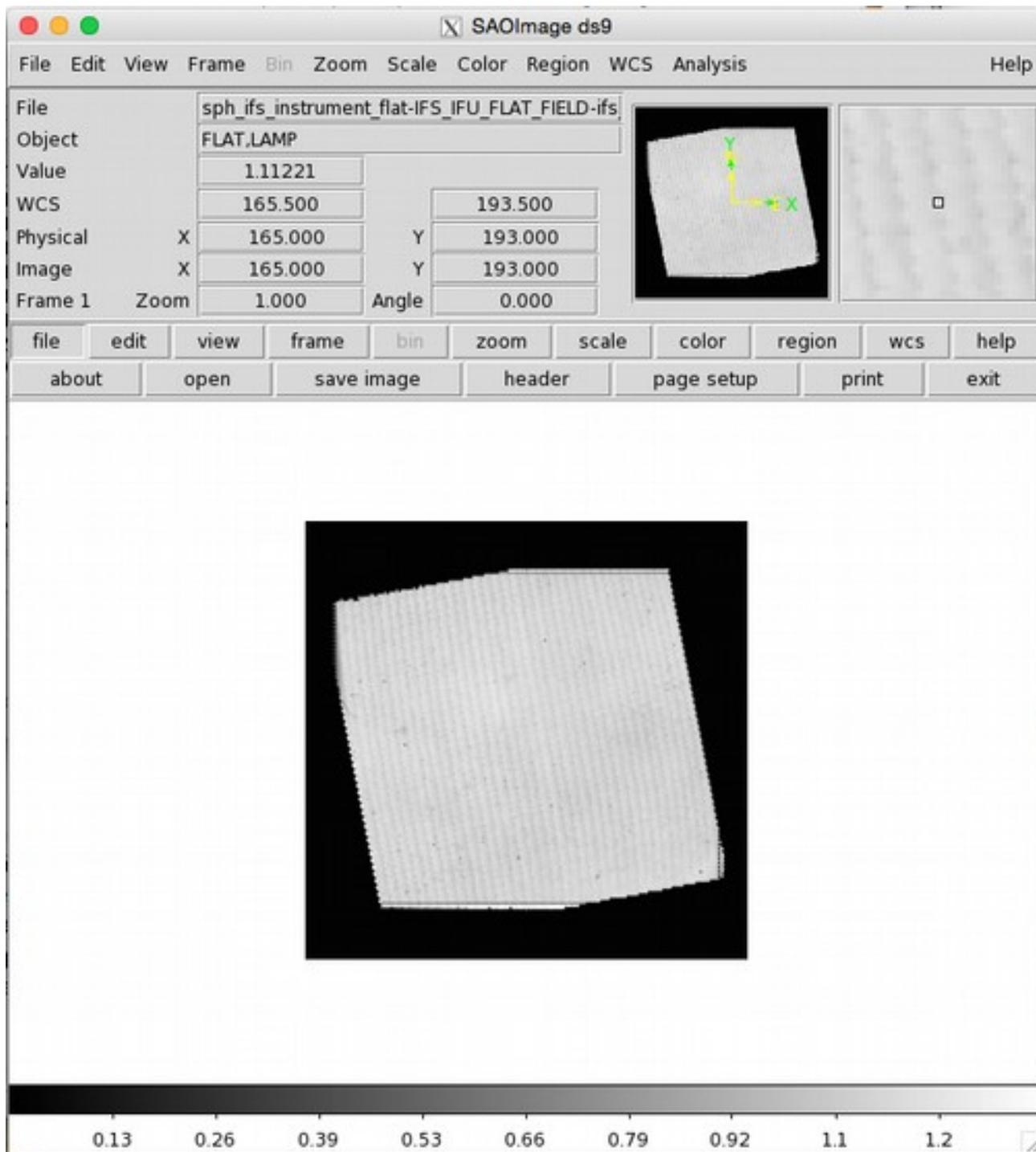


Figure 14: IFS IFU flat field obtained with the sph_ifs_instrument_flat recipe. The frame type is IFS_IFU_FLAT_FIELD

6.3.8 Reduce science data: SPH_IFS_SCIENCE_DR (automated)

Note: *the DRH version installed in October/November 2015 do crash* when combining frames at the end of the routine, *but this is not an issue since it produce correct reduced spectral cubes* before crashing :-). Note that *you specially need to validate or reject this crashed processes*: since they are in error, they will be erased if not “validated”.

- Use SCIENCE_DR_RAW files that have been corrected from BP and cross-talk (hence of datatype “reduced” and not “raw”) in section 6.3.2. they need to have:



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 11/43

- Same object
- Same filter
- Same coronagraph
- Same neutral density
- Same exposure time

*** DON'T USE DARKS or static badpixels maps if raw frames are already corrected from cross-talk (step 6.3.2)**

*ifs IFU flat, reduced and badpixel-corrected master detector flats NB1,NB2,NB3 (NB4 for YH mode) and BB , as well wavecalib

* preamp flat input is not necessary. If used you need to take the preamp flat produced when using the BB lamp as input.

*** DFFshort input is not needed and should not be used**

Parameters:

-Parameter “spec.deconvolution” should be set to false (faster, but it might cause bugs, then use “true)

-Parameter “use ADI” should be set to false (“0”)(Faster, but it might cause bugs, then use “2”)

The default can be used for the other parameters.

The output file has a frametype IFS_SCIENCE_DR.

6.3.9 IFS PSF (FLUX_CALIB) reduction (automated)

Routine: *sph_ifs_science_dr*

Same as previous one, but in this case you have to force the data center to accept raw inputs that have a FRAMETYPE different from the regular IFS_SCIENCE_DR_RAW. Instead of clicking on the usual “browse input files”, use the yellow triangle just besides that is tagged “browse any input files”. Use this to select files of the same object, but with frametype IFS_FLUX_CALIB_RAW. Note that these' raw frames also **need to be cleaned from cross talk and badpixels (see 6.3.2)**

- flat, dark, and distortion map as described just above, but of course adapted to the flux raw properties: **NOTE that exptime and neutral density are usually different than for the science, hence different calibs are necessary.**

6.3.10 ifs_convert_dc (automated)

This IDL routine converts the DRH outputs into a single master reduced cube (“center_im.fits”) along with the parallactic angle of each of its frame (“rotnth.fits”), a table the wavelengths (“lam.fits”, table of 39 wavelength for IFS YJ) and a PSF reference cube “median_unsat.fits”. This routine also provide a wavelength-dependent recentring using reduced waffle frames.

This routine has 3 inputs:

- IFS_SCIENCE_DR_SPECTRAL_CUBE: extra outputs of a single IFS_science_dr recipe executed on science data
- IFS_SCIENCE_WAFFLE_SPECTRAL_CUBE: extra outputs of a single IFS_science_dr recipe executed on waffle data
- IFS_SCIENCE_PSF_SPECTRAL_CUBE:extra outputs of a single IFS_science_dr recipe executed on PSF (flux_calib coro) data,

Parameters:

Default are fine, please note the following

- TN is the true north calibration value. Let it empty unless you really want to use a specific value for TN. By default it is read from the astrometric calibration table at the DC. For old data this table will always be up to date. For the reduction of an ongoing run, please wait until DC staff tell you this table has been updated before running ifs_convert.



- /anamorph correct the first order distortion which is an anamorphism of 1.006 in the Y direction, dont use it if you use DRH distortion maps otherwise it will correct anamorphism twice

Note that as of 2016-03-23 the frame selection part of convert has been removed and is now used in a dedicated routine detailed below.

6.3.11 ifs_sortframes_dc

Directly derived from Anthony Boccaletti's "sortframes" routine. The automatic sort is based on the statistics of the central diffraction spot behind the mask of the coronagraph.

Inputs:

One center_im.fits (IFS_SCIENCE_REDUCED_SPECTRAL_MASTER_CUBE) and one rothn.fits (IFS_SCIENCE_PARA_ROTATION_CUBE) coming from the same convert process.

Parameters :

- select : requires a vector of frame index to be retained in the data cube. e.g. [0, 7,148]

- reject : requires a vector of frame index to be removed from the data cube. e.g. [0, 7,148]

Note: you can reject a whole serie of frames by using inputs such as: [[0, 7,130+indgen(6),148]] which is equivalent but shorter to :[0, 7,130,131,132,133,134,135,148] . Note the "[[" and "]"".

- sortsym : if set to a numerical value it selects the frames for which the flux of the central spot is within $median(flux) +/- sortsym * sigma$. **A value of sortsym=0,5 will be aggressive, 1 is moderate and 3 is very soft.**

- sortgt : if set to a numerical value is selects the frames for which the flux of the central spot is greater than $median(flux) - sortgt * sigma$. A value of sortgt=0,5 will be aggressive, 1 is moderate and 3 is very soft.

- sortraffaele Sorting developed by Raffaele Gratton for IFS data. Numerical value of X for automatically rejecting frames that have flux ratio outer/inner gt $X * median$. Keep blank if you don't want to use it. Can be used in combination with /sortgt or/sortsym. Raffaele's recommended setting for IFS sorting is **sortraffaele=1.3 and is a very soft sorting.**

select and reject and sortraffaele and either sortsym/sortgt can be combined while sortsym and sortgt are exclusive

- special_reject_output_frames : Rejects frames using the numeration of the OUTPUT cube. This parameter is supposed to be used only with the "duplicate process" option because it supposes you know which frames are kept by sortframe for a given set of parameters. You are supposed to visualize the output cube of the first "sortframe" instance, run without this special parameter. You can note the additional frames you would want to reject from this output cube and this special parameter allows you to reject them using the frame number of this first output cube. For the frame number to match correctly, you need to use exactly the same inputs and parameters (save for this one of course) as those of the previous instance of sortframe, which enabled you to identify the remaining bad frames that you want to reject here.

6.3.12 ifs_specal_dc

Directly derived from Raphael Galicher "specal" routine. **Note that this routine might change somewhat in early 2017, while the information provided here is valid as of december 2016.**

Detailed information on specal might be found here: /opt/idl/lib/GTO_routines/Specal/*README.pdf

Inputs:

One center_im.fits sorted (IFS_SCIENCE_REDUCED_SPECTRAL_MASTER_CUBE_SORTED) one rothn.fits (IFS_SCIENCE_PARA_ROTATION_CUBE_SORTED), one lambda info file (IFS_SCIENCE_LAMBDA_INFO) and one PSF file (IFS_SCIENCE_PSF_SPECTRAL_MASTER_CUBE) **coming from the same convert/sortframe process.**

"optimize" button works to do that for you.



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 13/43

You can also use directly the outputs of ird_convert without doing any sorting, but you need to use the “browse any input frame” yellow triangle button. In this case optimize will fetch the lambda info and the SPF file, but you will need to look for the good IFS_SCIENCE_PARA_ROTATION_CUBE file manually.

Parameters :

- Quicklook: **SHOULD NOT BE USED during a DRT.** This “quicklook” is in fact very long because it runs all algorithms in a row. Outside of DRT, and on small and average size data cubes (less than ~200) frames it might be used, providing that the server is not very much used. For DRT it is better to choose which algo you want with the following parameter. **If you want several algos, you can do that easily by doing “duplicate process” on you first** and change the algorithm. Again control the load of the server (using the manual bash command htop for instance), before launching in parallel several reduction of a big datacube (median value of center_im cube on DC is ~80 frames).

- algorithm: choose your reduction algorithm, such as “TLOCI” or “CADI”

- adionly: choose whether you use only the rotation information (“ADI”) or rotation AND spectral information (“ADI+SDI”, advised for IFS)

- pcamode: specify the number of modes to be subtracted during a pca analysis. You can ask the routine to subtract different number of mode by using a vector of several integers (such as [5, 10,30]) into this parameter

- other parameters are OK as default.

Note that as for all DC routine a detailed help is available when you let you mouse on any of these parameters

Link with specalcarac: The outputs of specal from the DC are currently two big tar.gz files (this will evolve) that you can copy to your wsrdata repertory to carry on with specalcarac.



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 14/43

7 Calendar

7.1.1 Objective

7.1.2 How to proceed

7.1.3 Limitations and assumptions



TITLE : Document Title

REF. : VLT-BBB-SPH-xxxxx-xxxxx

ISSUE : 1

DATE: Date of issue

PAGE 15/43

8 Instrument monitoring

8.1.1 Objective

8.1.2 How to proceed

8.1.3 Limitations and assumptions



TITLE : Document Title

REF. : **VLT-BBB-SPH-xxxxx-xxxxx**

ISSUE : 1

DATE: Date of issue

PAGE 16/43

9 Appendix