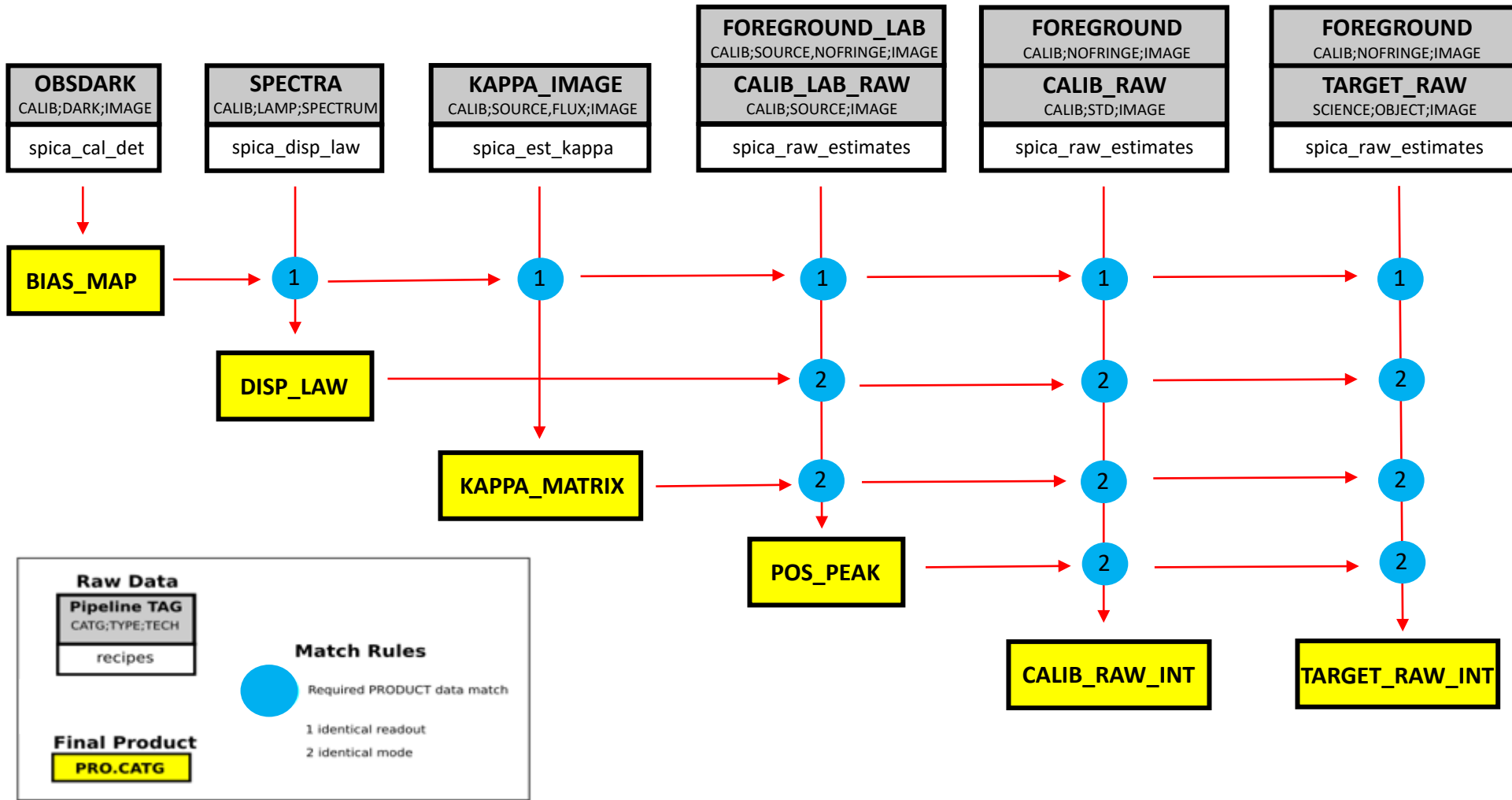
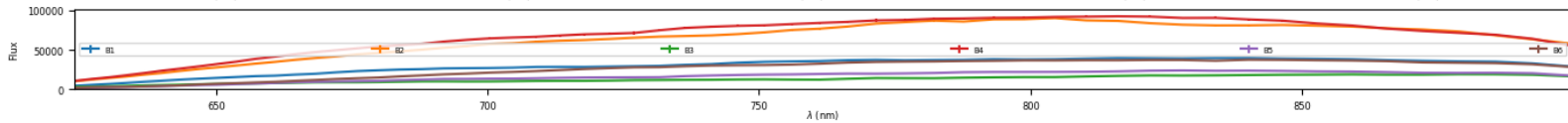
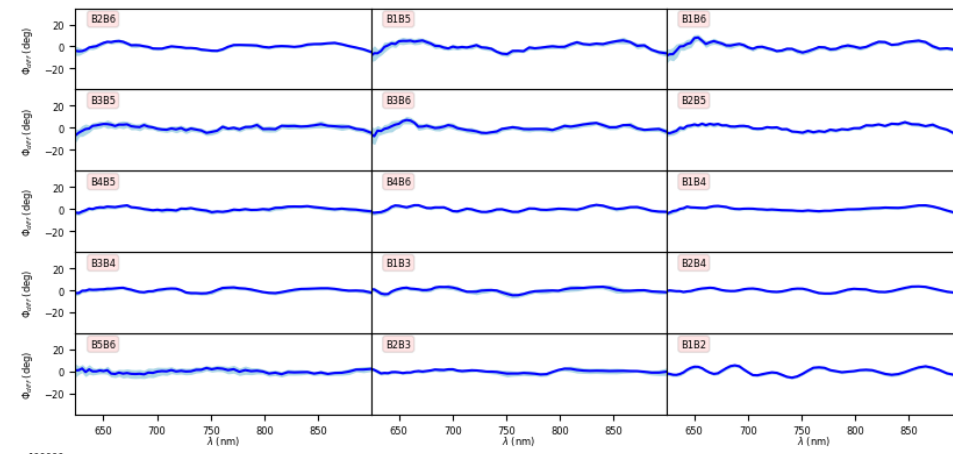
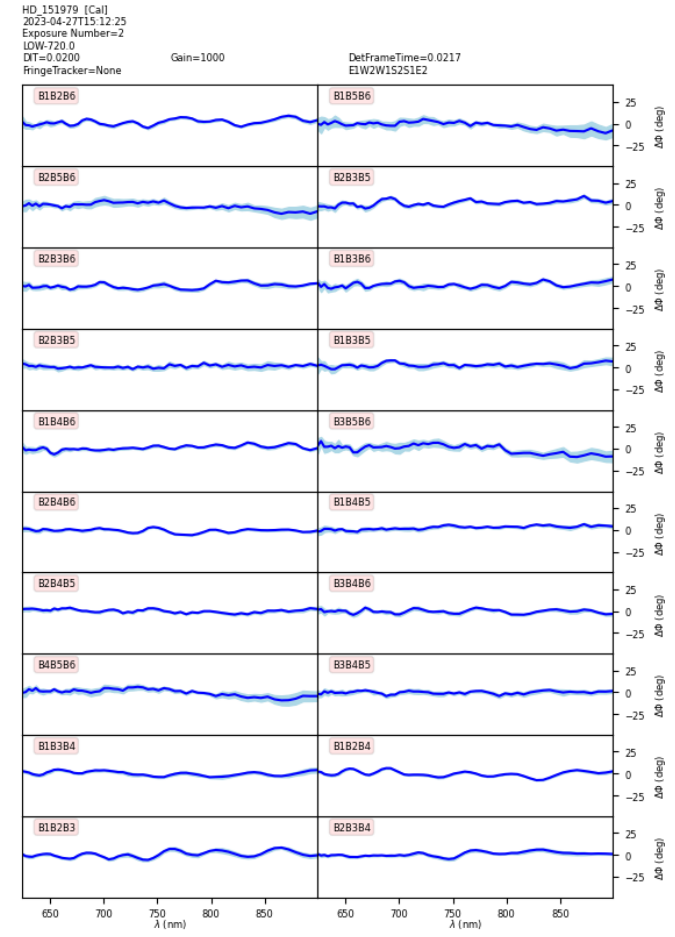
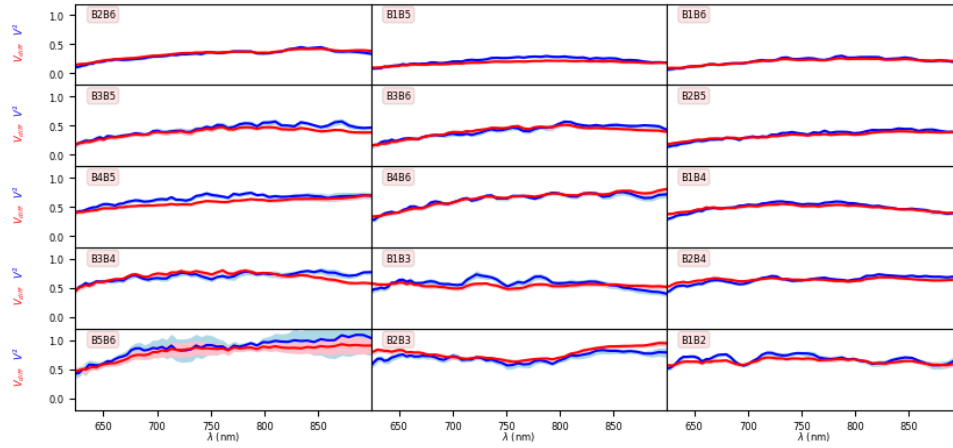
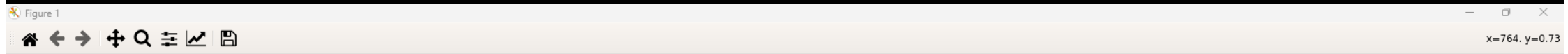


# SPICA-VIS PIPELINE

Philippe Berio & Arnaud Caci

# SPICA-VIS PIPELINE





## Differential Visibility

- $V_i \cdot \sum_{j \neq i} V_j$

## Closure Phase

- $\phi_{ij} + \phi_{jk} - \phi_{ik}$

## Differential Phase

- Phase per spectral channel
- $\sum_i \phi_i = 0$

## Run the Pipeline from the GUI

SPICA Pipeline --- /DATA/RawData/2023-04-09

Data Type	Tpl.Start	Obs.Targ.Name	Det.Dit	Det.Gain	Ins.Resol	Ins.Central.Wl	Chara.Baseline	Tpl.Nexp
OBSDARK	2023-04-09T04:08:00		0.0199999995529652	3	LOW	720.0	S1S2E1E2W2	1
SPECTRA	2023-04-09T04:08:49		0.0199999995529652	3	LOW	720.0	S1S2E1E2W2	1
OBSDARK	2023-04-09T04:09:24		0.0199999995529652	1000	LOW	720.0	S1S2E1E2W2	1
KAPPA_IMAGE	2023-04-09T04:10:02		0.0199999995529652	1000	LOW	720.0	E1W2W1S2S1E2	6
CALIB_LAB_RAW	2023-04-09T04:13:46		0.0199999995529652	1000	LOW	720.0	E1W2W1S2S1E2	2
TARGET_RAW	2023-04-09T11:03:41	HD_147394	0.0199999995529652	1000	LOW	720.0	S1S2E1E2W2	11
TARGET_RAW	2023-04-09T12:26:18	HD_147394	0.0199999995529652	1000	LOW	720.0	S1S2E1E2W2	21

Select All OBs | Deselect All OBs

Working Directory: /home/pbe/WorkingDirectory/test

Calibration Directory: /home/pbe/WorkingDirectory/test

Science Spectral Bands (nm):

Spectral Binning (in pixels): 2

Phot Filter Kernel (in pixels):

# of co added frames: 1

# of merged exposures: 1

Compute POS\_PEAK  
 Debug Plots  
 Intermediate products

Run | Quit

## Run the Pipeline in command line

```
(palmier3) pbe@spica-vis-oca:~/WorkingDirectory/2023-04-27$ spica_autoPipeline_func.py --help
usage: spica_autoPipeline_func.py [-h] [--caldir CALDIR] [--wdir WDIR] [--sb SB [SB ...]] [--binning BINNING] [--kernel KERNEL] [--frames FRAMES]
                                   [--expo EXPO] [--pospeak POSPEAK] [--plots PLOTS] [--products PRODUCTS] [--tplstart TPLSTART]
                                   rawdir

positional arguments:
  rawdir                Raw Data Directory (your_path)

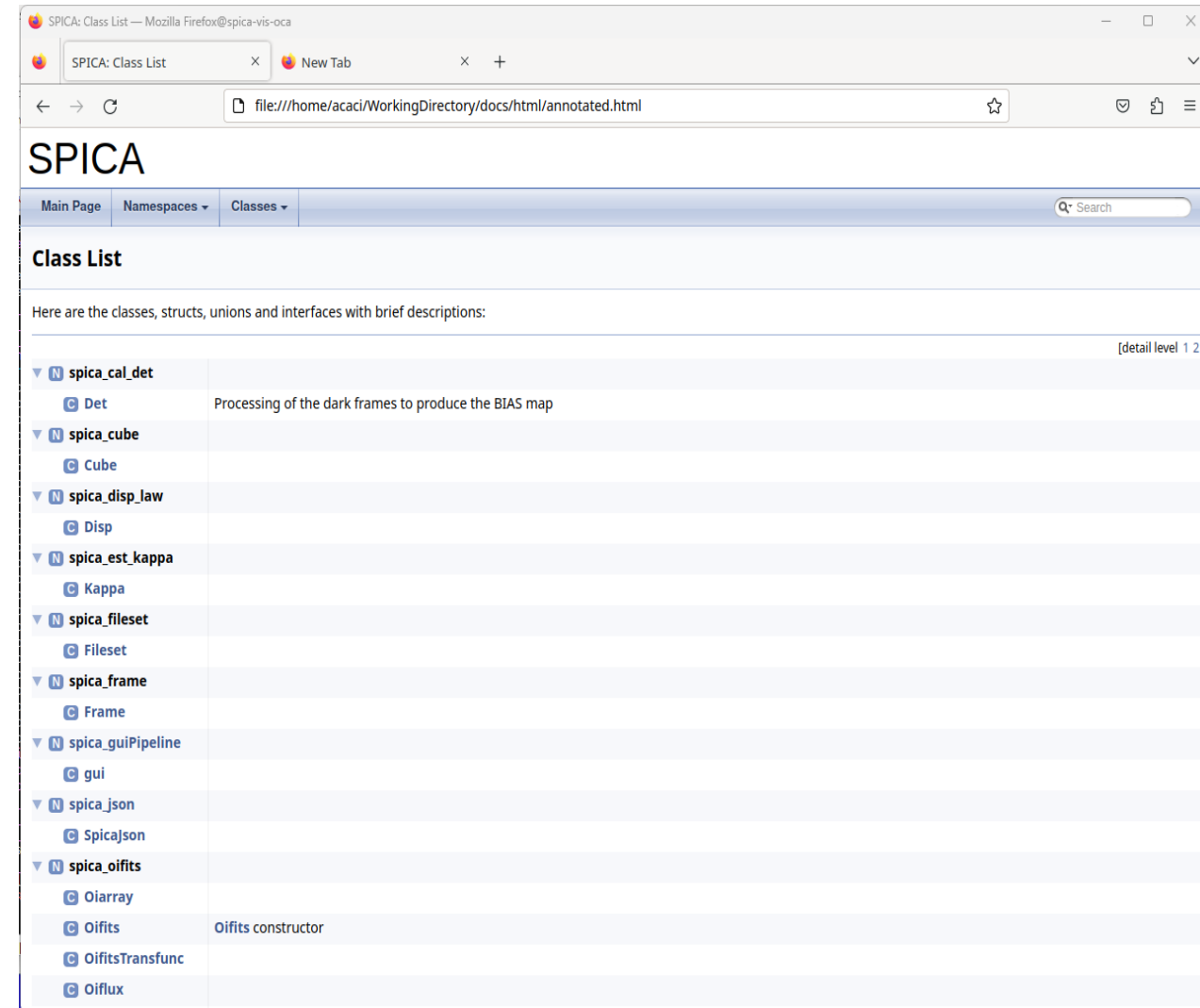
optional arguments:
  -h, --help            show this help message and exit
  --caldir CALDIR       Calibration Map Directory (--caldir your_path)
  --wdir WDIR           Working Directory (--wdir your_path)
  --sb SB [SB ...]     Science spectral bands (--sb lmin1 lmax1 lmin1 lmax2 ...)
  --binning BINNING    Number of spectral pixels to bin (--binning 3)
  --kernel KERNEL       Photometry Filter Kernel (--kernel 3)
  --frames FRAMES      Number of added frames (--frames 3)
  --expo EXPO          Number of merged exposures (--expo 3)
  --pospeak POSPEAK    Compute POS_PEAK (--pospeak 3)
  --plots PLOTS        Debug plots (--plots 3)
  --products PRODUCTS  Intermediate products (--products 3)
  --tplstart TPLSTART  Process the specified TPLSTART only (--tplstart 2020-11-05T09:26:57.316633)
```

## Pipeline Coding

- Python 3
- Object Oriented Programming
- Pipeline run on Linux (never tested on Windows)
- OCA GITLAB versionning
- Code Quality Checked with Pylint
- Doxygen Code Documentation
- Regression Tests

## How to use the Pipeline ?

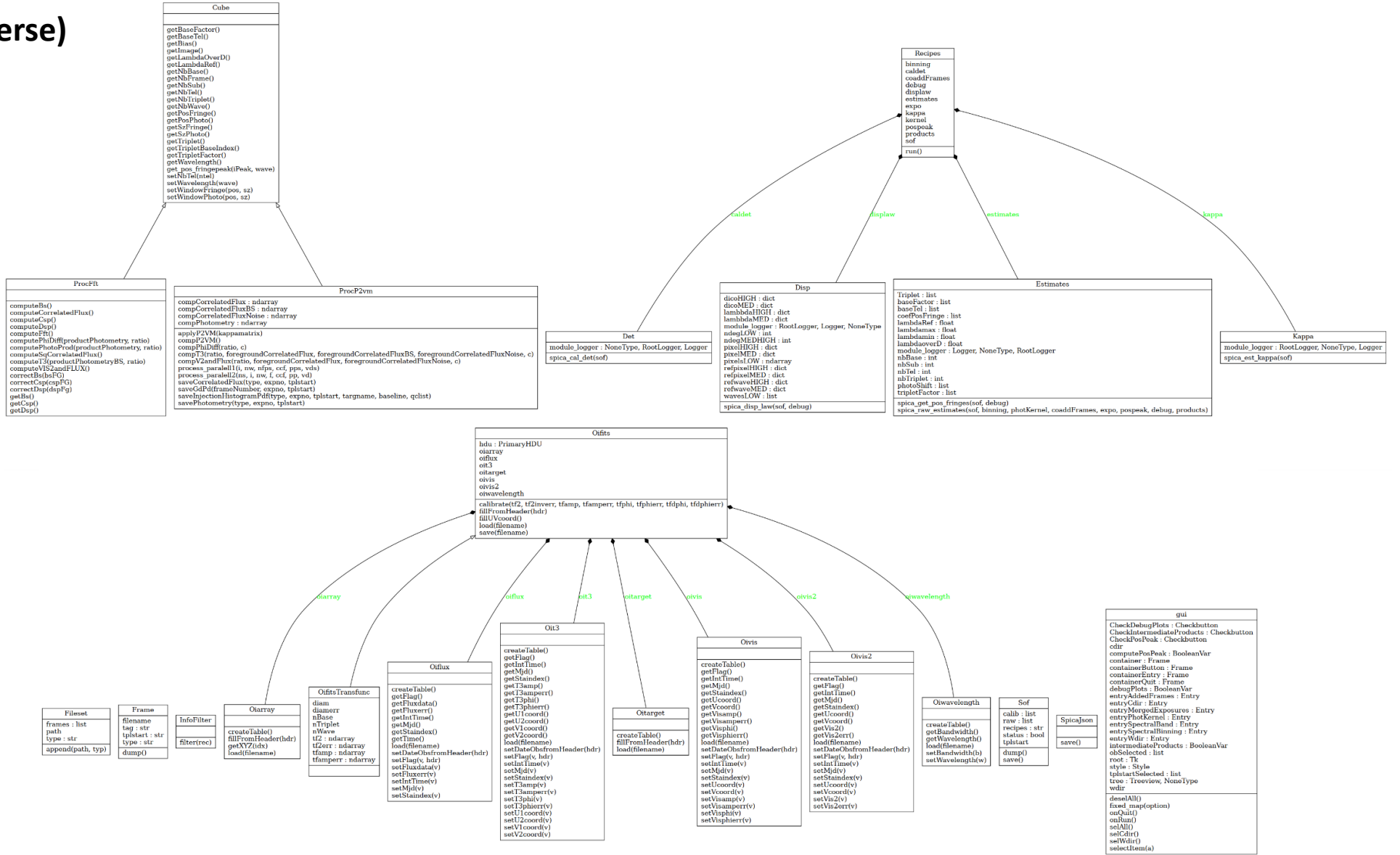
- Installed on spicavis server @CHARA and @Nice
- Current version: 1.0
- /DATA/Pipeline/V1.0  
/dev



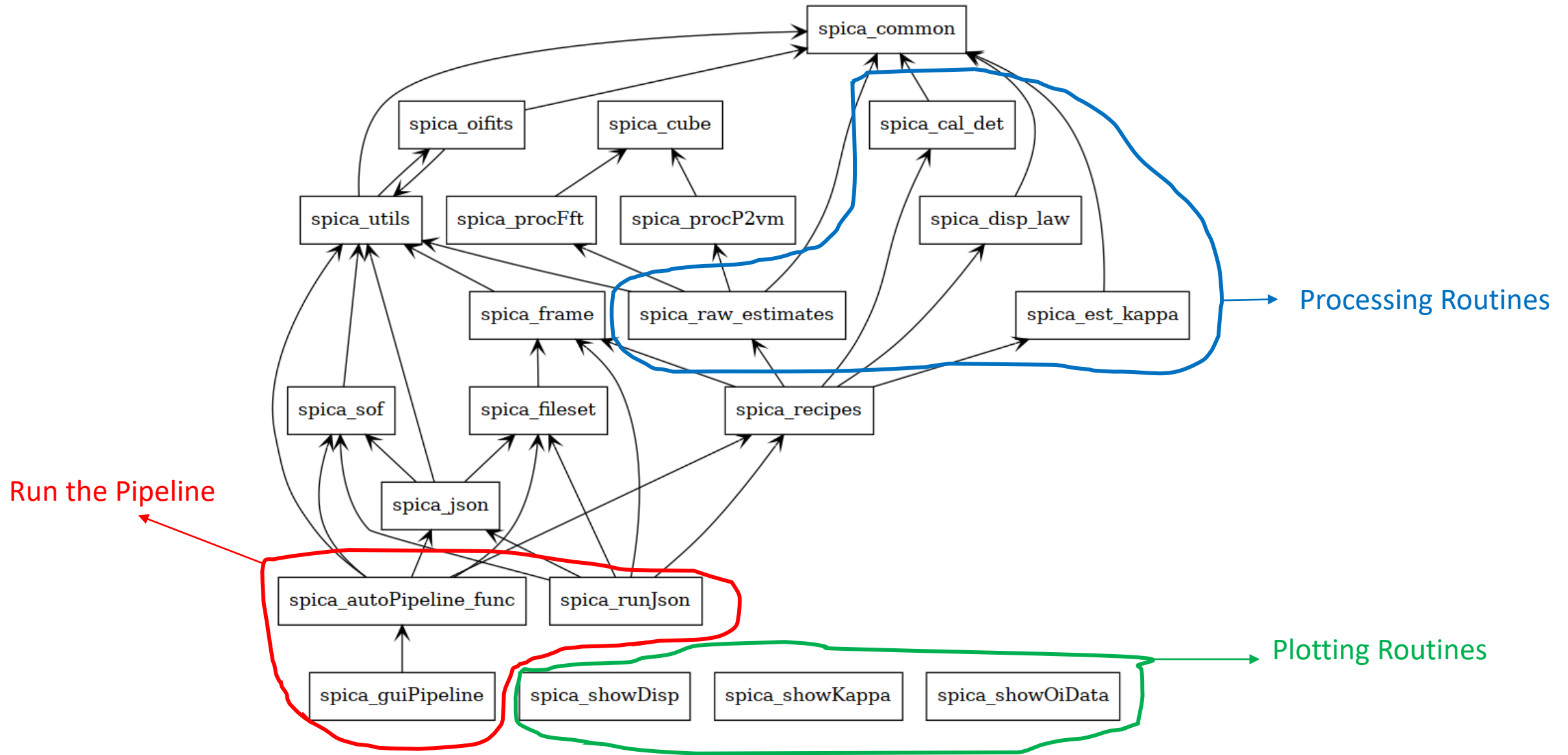
The screenshot shows a web browser window displaying the SPICA Class List. The browser title is "SPICA: Class List" and the address bar shows the file path: "file:///home/acaci/WorkingDirectory/docs/html/annotated.html". The page has a navigation bar with "Main Page", "Namespaces", and "Classes" tabs, and a search bar. The main content area is titled "Class List" and contains a list of classes, structs, unions, and interfaces with brief descriptions. The list is organized into a tree structure with expandable sections.

Class Name	Description
spica_cal_det	
Det	Processing of the dark frames to produce the BIAS map
spica_cube	
Cube	
spica_disp_law	
Disp	
spica_est_kappa	
Kappa	
spica_fileset	
Fileset	
spica_frame	
Frame	
spica_guiPipeline	
gui	
spica_json	
Spicajson	
spica_oifits	
Oiarray	
Oifits	Oifits constructor
OifitsTransfunc	
Oiflux	

## Class Diagram (pyreverse)



# SPICA-VIS PIPELINE





## Next Steps:

- Finalize the Regression tests
- Finalize the Doxygen documentation
- Tag version V1.1 (includes the work of Arnaud)
- Install V1.1 @CHARA and @Nice
- Test the pipeline on the data of the June Observing Run
  
- Pipeline User Manual