

HAWC+ Imaging Pipeline Tutorial

This tutorial is designed to help guide users through the steps of processing HAWC+ imaging data, from raw data files (Level 0) to the final, calibrated data product. The information in this tutorial can also be found in more detail in the [Data Reduction Pipeline \(DRP\) User's Manual](#).

https://www.sofia.usra.edu/sites/default/files/2022-02/hawc_users_revJ_0.pdf

Retrieve the Data

In this tutorial, we use observations of NGC 2273 in total intensity (imaging) mode. This galaxy has been observed in total intensity mode across all available HAWC+ filters: A, C, D, E. Here, we will reduce the data for Band C.

To retrieve the data from the SOFIA Science Archive at IRSA, enter the following criteria in the main SOFIA search page (<https://irsa.ipac.caltech.edu/applications/sofia/>):

Spatial Constraints → All-Sky

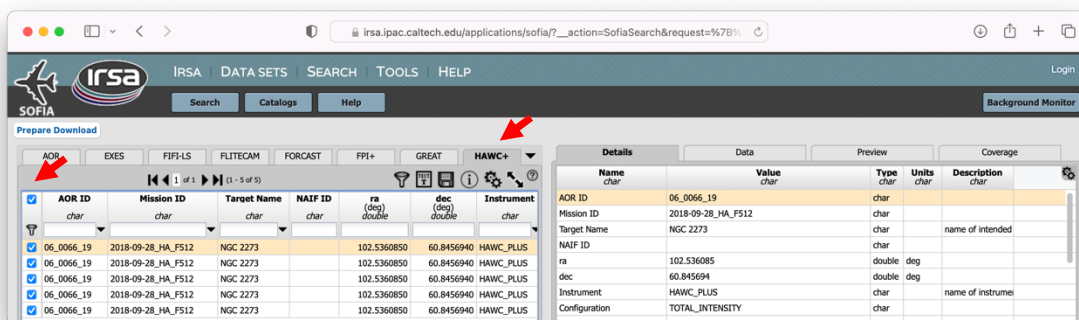
Observation Constraints → AOR ID → 06_0066_19

Data Product Constraints → Select Level 0 only (de-select Level 3 and Level 4)

or follow this link:

https://irsa.ipac.caltech.edu/applications/sofia/?api=search&spatialConstraints=allsky&execute=true&processingLevel=LEVEL_0&aorid=06_0066_19

On the search results page, click on the HAWC+ tab. On the HAWC+ tab, select all 5 data files, either individually or by selecting the box next to the AOR ID column header.



The screenshot shows the IRSA SOFIA search results page. The browser address bar shows the URL: irsa.ipac.caltech.edu/applications/sofia/?_action=SofiaSearch&request=%7B%7D. The page has a navigation bar with 'IRSA', 'DATA SETS', 'SEARCH', 'TOOLS', and 'HELP'. Below the navigation bar, there are tabs for 'Search', 'Catalogs', and 'Help'. The main content area is titled 'Prepare Download' and shows a table of search results. The table has columns for 'AOR ID', 'Mission ID', 'Target Name', 'NAIF ID', 'ra (deg)', 'dec (deg)', and 'Instrument'. The 'AOR ID' column has a checkbox next to each row, and the 'Instrument' column has a dropdown menu. A red arrow points to the 'HAWC+' dropdown menu. The table shows 5 rows of data for AOR ID 06_0066_19, Mission ID 2018-09-28_HA_FS12, Target Name NGC 2273, NAIF ID 102.5360850, ra (deg) 60.8456940, dec (deg) 60.8456940, and Instrument HAWC_PLUS. To the right of the table is a 'Details' panel with tabs for 'Details', 'Data', 'Preview', and 'Coverage'. The 'Details' tab is active, showing a table with columns for 'Name', 'Value', 'Type', 'Units', and 'Description'. The table shows details for the selected AOR ID, including Mission ID, Target Name, NAIF ID, ra, dec, Instrument, Configuration, and Control Element 1.

Name	Value	Type	Units	Description
AOR ID	06_0066_19	char		
Mission ID	2018-09-28_HA_FS12	char		
Target Name	NGC 2273	char		name of intended
NAIF ID	102.5360850	double	deg	
ra	60.8456940	double	deg	
dec	60.8456940	double	deg	
Instrument	HAWC_PLUS	char		name of instrume
Configuration	TOTAL_INTENSITY	char		
Control Element 1	HAW_C	char		

Click on Prepare Download to open a download dialog box, and then select Prepare Download within the dialog box. After a few moments, you will be asked to save a zip file to disk (about 1.43GB in size). Save this file wherever you wish, unzip it, and navigate to the subfolders to locate the 5 HAWC+ raw FITS files. You may either leave these files in the directory or move them to another location of your choice; the folder containing the 5 FITS files will be referred to as the 'input' directory for the remainder of the tutorial.

Download and Install the Pipeline

Instructions on how to download and install the SOFIA data reduction pipeline, *sofia_redux* package can be found at https://github.com/SOFIA-USRA/sofia_redux. If you need assistance, you can contact us through GitHub or the SOFIA Helpdesk (sofia_help@sofia.usra.edu).

Start the GUI

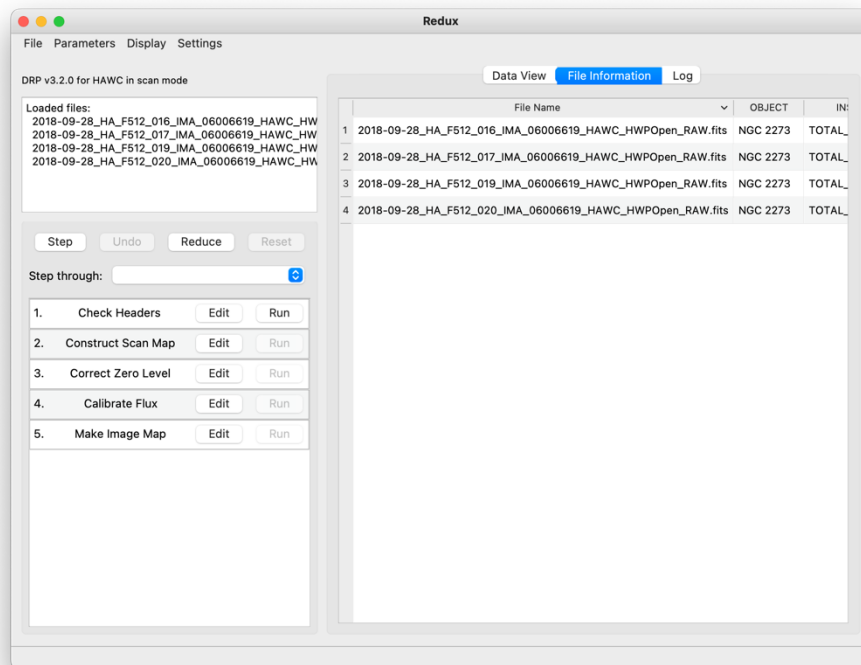
The pipeline can be executed in either Automatic Mode (on the command line) or in Manual Mode (through a GUI). In this tutorial, we will focus on running the pipeline through the GUI. To begin, open a terminal and navigate to a scratch directory.

Launch the GUI by typing:

```
> redux
```

The pipeline will write output files and logs to your current working directory, by default. If desired, the output directory may be modified from the File menu after a reduction is loaded.

In the Redux GUI, load the NGC 2273 data for the desired filter by selecting File → Open New Reduction, and navigating to the input directory where you saved the data. Select all 5 FITS files by clicking on the first file and shift-clicking on the last file, and then click Open. After clicking Open, the software reads the FITS headers and extracts relevant information, such as the instrument name for determining which pipeline the software will call. Some additional FITS header information is shown on the “File Information” tab on the right side of the GUI.



When the pipeline runs, it is possible to automatically display the intermediate data using SAO DS9 if the connection between the pipeline/python and DS9 is set up properly. To use DS9 with the pipeline, see the pipeline documentation for [download and installation instructions](#); the ds9 executable must be available in the PATH environment variable for the pyds9 interface to be able to find and control it. Alternatively, the automatic display can be disabled. Each pipeline module can optionally produce FITS file output, for use with a different FITS viewer if preferred. Options for displaying images in DS9 are found under Display Settings on the Data View tab.

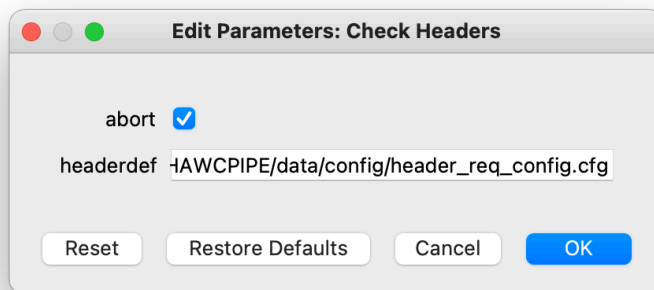
Run the Pipeline

There are 5 modules in the HAWC+ imaging pipeline, shown in the bottom-left panel of the GUI. Each pipeline module can be configured by clicking the 'Edit' button for that module. The entire pipeline can be executed by clicking the 'Reduce' button. Alternatively, the modules can be run individually by clicking on the 'Run' button for that module, or in a small group by selecting an end point in the 'Step Through' dropdown menu, then clicking 'Step.' In this tutorial, we'll run the modules one by one and examine their output.

1. Check Headers

This module examines the FITS headers to make sure that they have the keywords required by the pipeline.

Options: Click on the Edit button next to Check Headers module. A popup window for Edit Parameters for Check Headers will open up. In the popup window, if the 'abort' option is selected, the pipeline will abort the reduction if FITS headers do not match requires specifications. If it is not set, the pipeline may fail in unexpected ways (as always: garbage in, garbage out!).



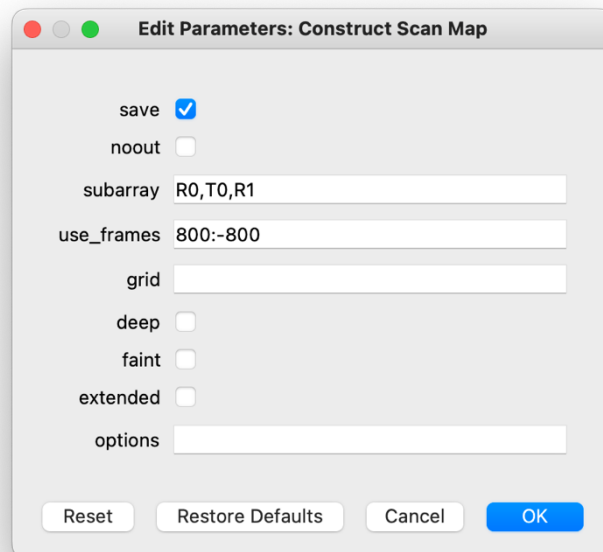
Output: This module creates no output; it allows the data set to pass through to the next modules in the reduction.

2. Construct Scan Map

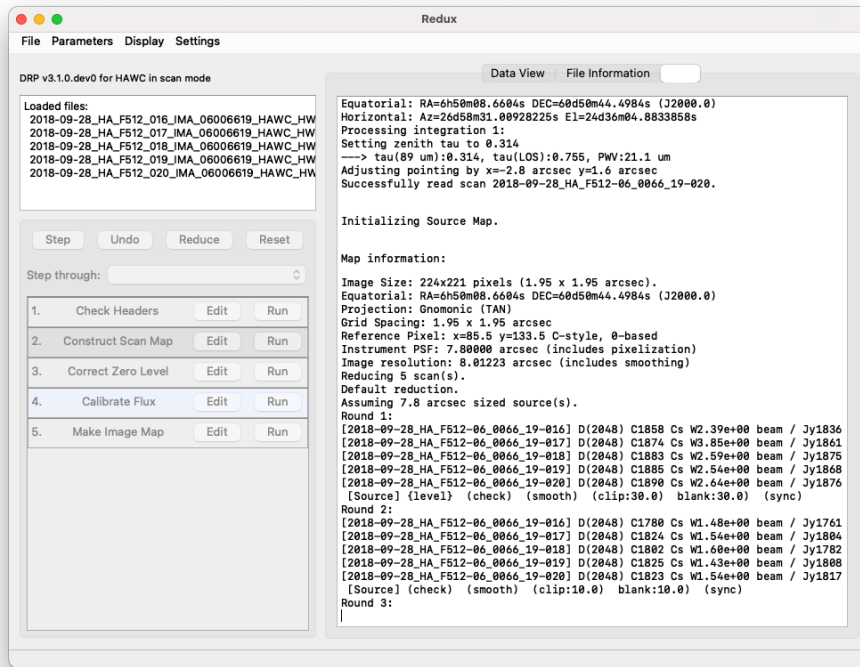
This module constructs the scan map by modeling the measured detector timestreams using a number of contributions such as $1/f$ drifts, correlated noise components, detector gains, and the observed source structure. An initialization and validation step takes place prior to beginning iterative solution for the model components. During the initialization, the pipeline reads in the raw FITS table, assigns positional offsets to every detector pixel, and sky coordinates to every time frame in the scan. The input timestream is then checked for inconsistencies such as discontinuous “jumps” in flux levels or “gaps” in the timestream, gyro drifts over the course of observation, or extreme low or high scan speeds that may affect the per-pixel-exposure and distort the image.

Options:

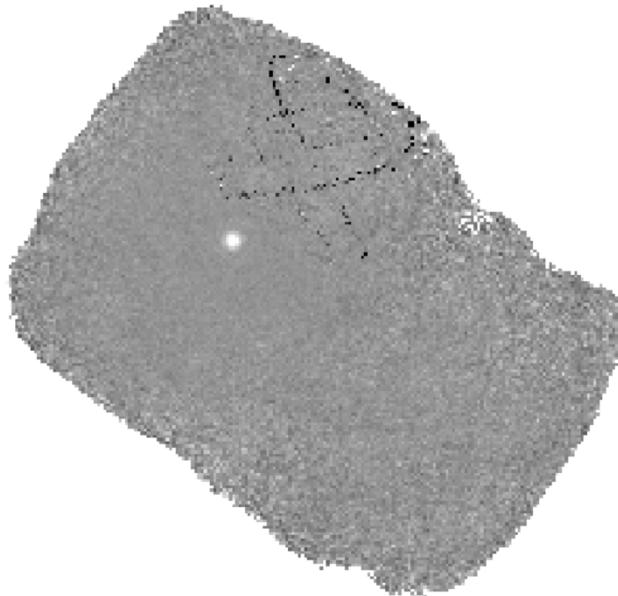
In most cases, users will want to use the default values in this module.



The “Log” tab in the GUI as well as the terminal dialog summarize the map information before attempting to iteratively solve for each of the modeled signal components.



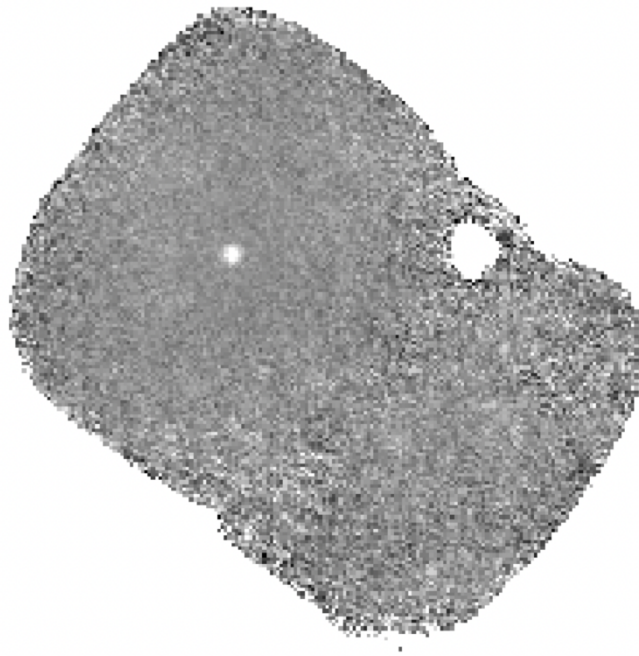
Output: By default, the pipeline stores the scan map (can be spotted in the output directory via “SMP” in the fits file name).



F0512_HA_IMA_06006619_HAWCHWPOpen_SMP_016-020.fits without attempted corrections for the artifact seen in at the top of the image.

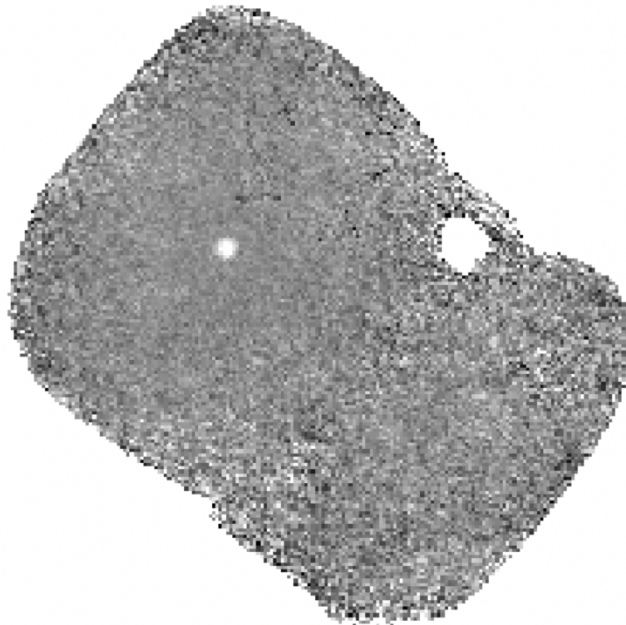
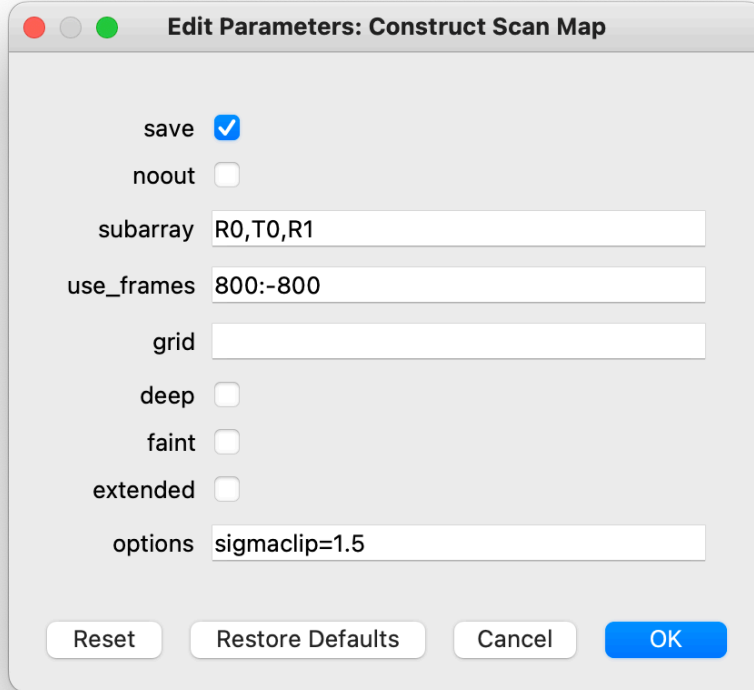
The dark Lissajous pattern in the top of the map is the result of incomplete or corrupted Lissajous scans or poor coverage of the area on a single array side. This effect is sporadically seen in HAWC+ data from early science flights, but as in this scan map, it does not typically affect the central region of the map where the source is located.

To fix the artifact, the first step is to reduce the images one by one to determine the image(s) that are affected. To reduce each file by itself, from the GUI, go to File -> Open New Reduction, select one file, then run the first two steps in the pipeline. In this example, only one input file, 2018-09-28_HA_F512_018_IMA_06006619_HAWC_HWPOpen_RAW.fits, showed this pattern. If your observations include multiple scans and you can reach your SNR by excluding one file, then in such cases the off-nominal scan(s) can be excluded from processing.



F0512_HA_IMA_06006619_HAWCHWPOpen_SMP_016-020.fits, reduced with 4 scans only (file 18 excluded). The artifact is not present, but the SNR over the source may be reduced.

On the other hand, if you do not reach the expected SNR with the exclusion of the off-nominal scan(s) then you can try to mitigate this artifact by adding a parameter in the “options” section of the Construct Scan Map module: ***sigmaclip=1.5***. This option iteratively clips samples with anomalous telescope speeds from the timestream, leaving only samples with telescope speeds within 1.5 sigma of the mean value. This is the option we will use in this tutorial.

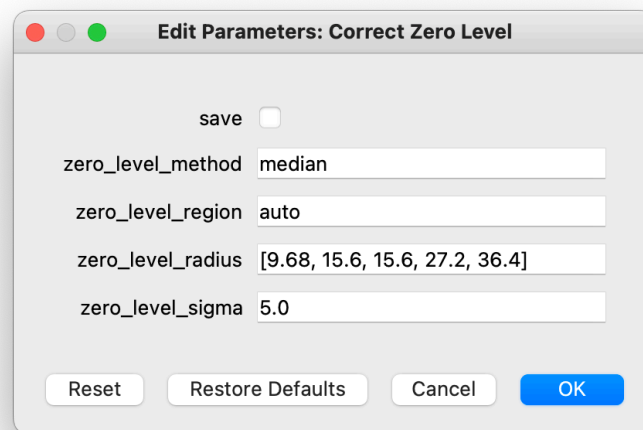


F0512_HA_IMA_06006619_HAWCHWPOpen_SMP_016-020.fits, reduced with option sigmaclip=1.5. The artifact is mostly corrected, but there is also more missing data in low coverage areas and SNR may also be reduced over the source.

3. Correct zero level

Since the scan map step sets the background level independently for each observation set from the median of the full map, there may be inconsistencies in the zero-level between separate observations if there is significant diffuse emission across the map. In this case, the pipeline may optionally correct the zero-level in each image by identifying a sky region with no emission and subtracting the median level in this region from each image. The sky region can be identified manually or automatically.

Options: The performance summary of this step is stored in the log. The method for zero-level correction is median or mean of individual pixels within the regions specified by 'zero_level_region' and 'zero_level_radius.' In most cases, users will want to use the default values in this module.



Output: By default, this module creates no output; it allows the data set to pass through to the next modules in the reduction. If the user chooses to save the output, a file with "ZLC" tag that indicates the zero-level corrected scan map will be saved in the designated output directory (e.g., F0512_HA_IMA_06006619_HAWCHWPOpen_ZLC_016-020.fits)

4. Calibrate flux

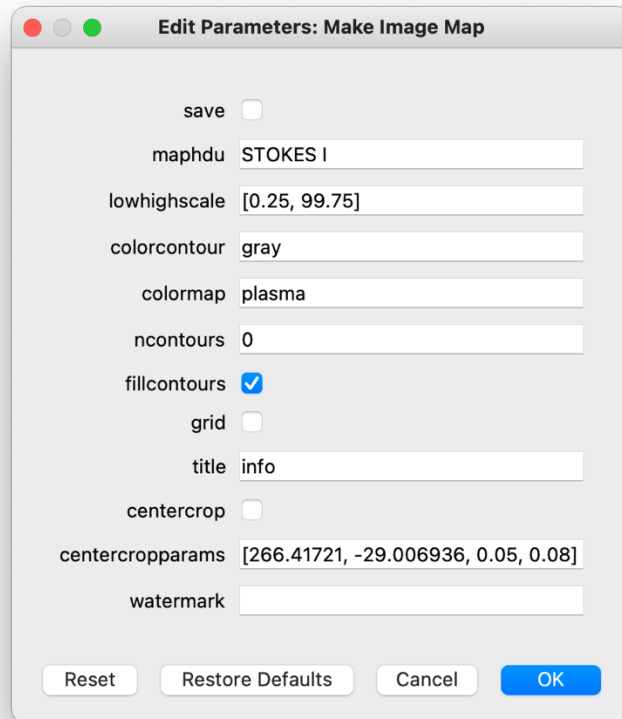
In this step, a calibration factor is calculated and applied to the zero-level corrected scan maps to convert the flux from counts to the physical units of the received energy from the mapped source per detector pixel. The pipeline requires several additional auxiliary files to perform flux calibration. The required files include instrumental response, opacity corrections, and reference calibration factors, which are used to flux calibrate the data. The calibration factors for each flight series are calculated from fluxes of standard sources that are observed on multiple flights

in an observing series. The log tab shows the applied calibration factor for your data (e.g. for this reduction example: 826.4140).

Output: This module by default stores the flux calibrated scan map in the designated output directory (e.g. F0512_HA_IMA_06006619_HAWCHWPOpen_CAL_016-020.fits).

5. Make image map

Options:



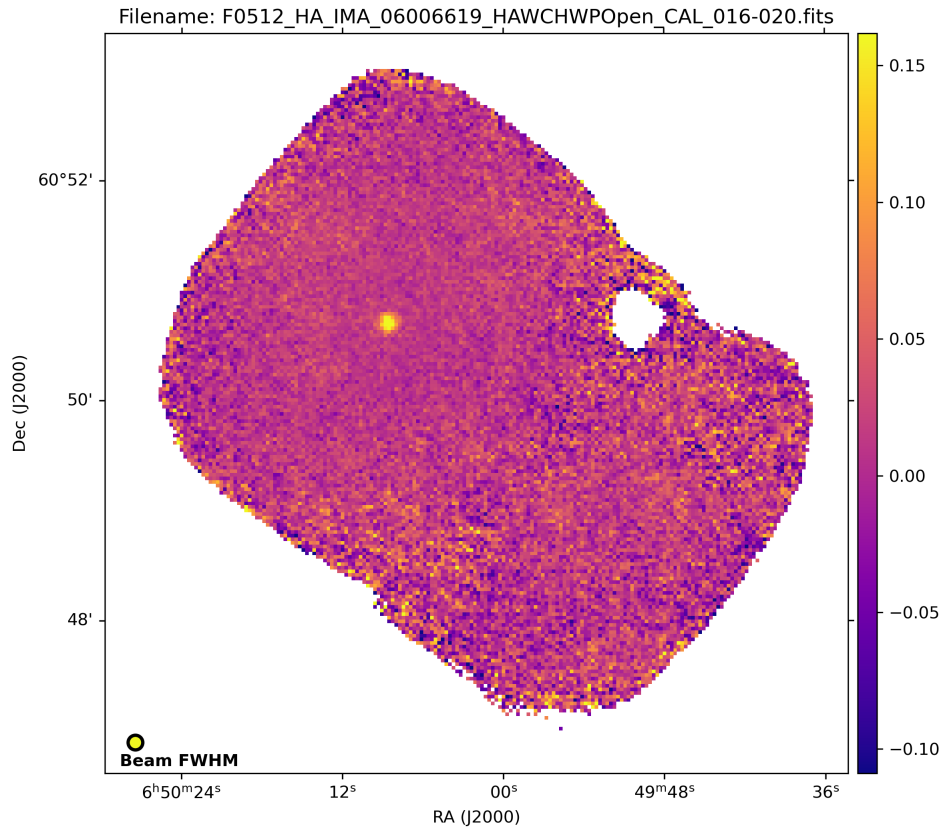
The image shows a dialog box titled "Edit Parameters: Make Image Map". It contains several parameters and checkboxes:

- save:
- maphdu: STOKES I
- lowhighscale: [0.25, 99.75]
- colorcontour: gray
- colormap: plasma
- ncontours: 0
- fillcontours:
- grid:
- title: info
- centercrop:
- centercropparams: [266.41721, -29.006936, 0.05, 0.08]
- watermark: (empty text field)

At the bottom of the dialog box, there are four buttons: "Reset", "Restore Defaults", "Cancel", and "OK".

Output: The pipeline by default creates the final image map in the form of a PNG image of the target.

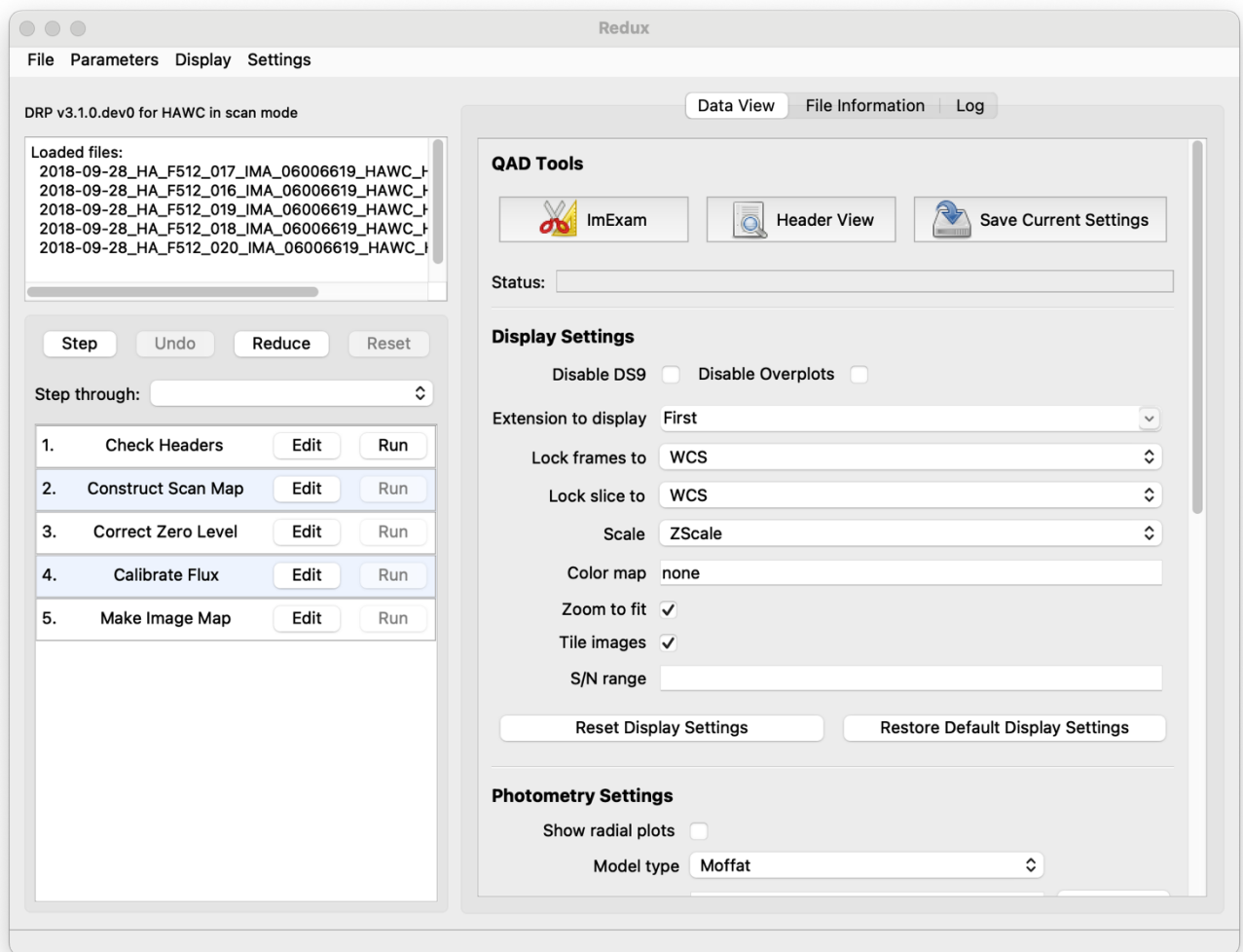
Object: NGC 2273, Band: C



Quality Assessment

After the final step of the pipeline is completed, the flux calibrated image is ready for quality checks. The Redux GUI displays images for **quality analysis and display (QAD)** in the DS9 FITS viewer.

It is good practice to *deselect* the “Disable DS9” box in **Display Settings** of the Redux GUI which allows the products of each reduction step to be automatically displayed in your locally installed DS9.



From the Redux interface, the **Display Settings** can be used to:

- Set the FITS extension to display (**First**, or edit to enter a specific extension), or specify that all extensions should be displayed in a cube or in separate frames.
- Lock individual frames together, in image or WCS coordinates.
- Lock cube slices for separate frames together, in image or WCS coordinates.
- Set the image scaling scheme.
- Set a default color map.
- Zoom to fit image after loading.
- Tile image frames, rather than displaying a single frame at a time.

Changing any of these options in the Data View tab will cause the currently displayed data to be reloaded, with the new options. Clicking **Reset Display Settings** will revert any edited options to the last saved values. Clicking **Restore Default Display Settings** will revert all options to their default values.

In the **QAD Tools** section of the **Data View** tab, there are several additional tools available.

Clicking the **ImExam** button (scissors icon) launches an event loop in DS9. After launching it, bring the DS9 window forward, then use the keyboard to perform interactive analysis tasks:

- Type 'a' over a source in the image to perform photometry at the cursor location.
- Type 'p' to plot a pixel-to-pixel comparison of all frames at the cursor location.
- Type 's' to compute statistics and plot a histogram of the data at the cursor location.
- Type 'c' to clear any previous photometry results or active plots.
- Type 'h' to print a help message.
- Type 'q' to quit the ImExam loop.

The photometry settings (the image window considered, the model fit, the aperture sizes, etc.) may be customized in the **Photometry Settings**. Plot settings (analysis window size, shared plot axes, etc.) may be customized in the **Plot Settings**. After modifying these settings, they will take effect only for new apertures or plots (use 'c' to clear old ones first). As for the display settings, the reset button will revert to the last saved values and the restore button will revert to default values. For the pixel-to-pixel and histogram plots, if the cursor is contained within a previously defined DS9 region (and the **regions** package is installed), the plot will consider only pixels within the region. Otherwise, a window around the cursor is used to generate the plot data. Setting the window to a blank value in the plot settings will use the entire image.

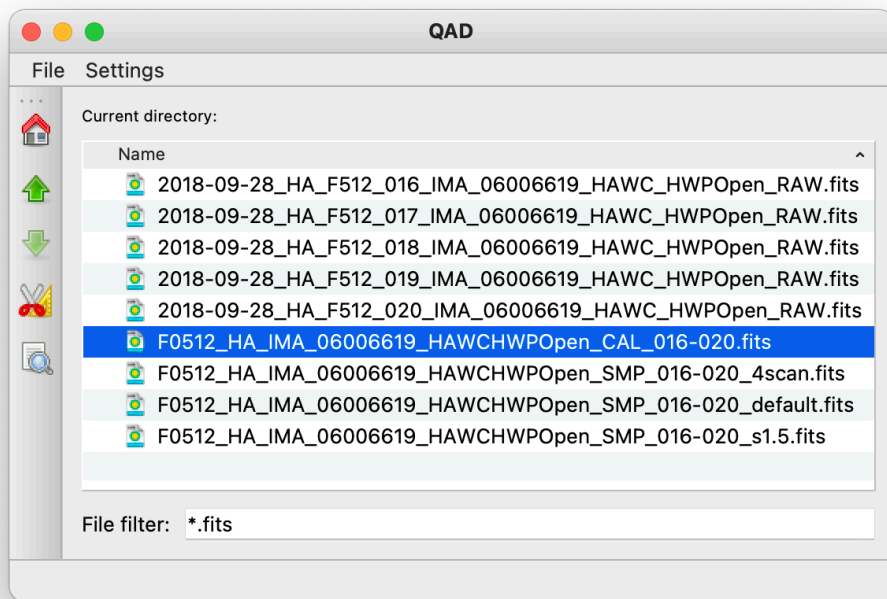
Clicking the **Header** button (magnifying glass icon) from the **QAD Tools** section opens a new window that displays headers from currently loaded FITS files in text form. The number of extensions displayed depends on the extension setting selected (in **Extension to Display**). If a particular extension is selected, only that header will be displayed. If all extensions are selected (either for cube or multi-frame display), all extension headers will be displayed. The buttons at the bottom of the window may be used to find or filter the header text or generate a table of header keywords. For filter or table display, a comma-separated list of keys may be entered in the text box.

Clicking the **Save Current Settings** button (disk icon) from the **QAD Tools** section saves all current display and photometry settings for the current user. This allows the user's settings to persist across new Redux reductions, and to be loaded when Redux next starts up.

The QAD tools can also be launched independently from the Redux GUI by simply typing:

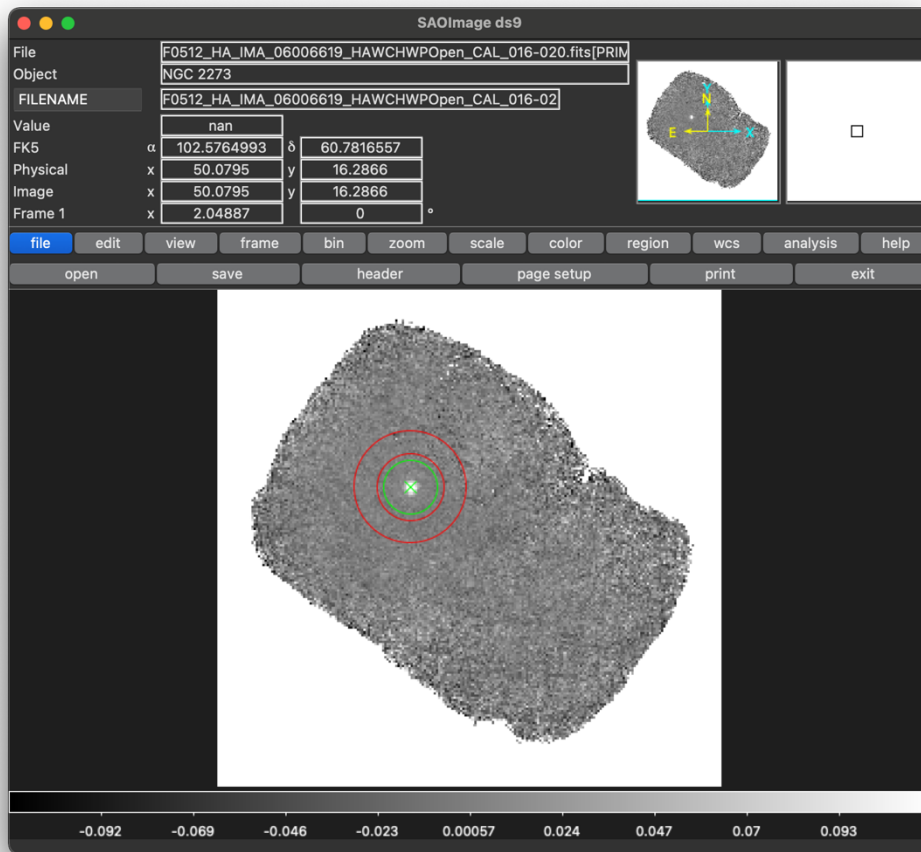
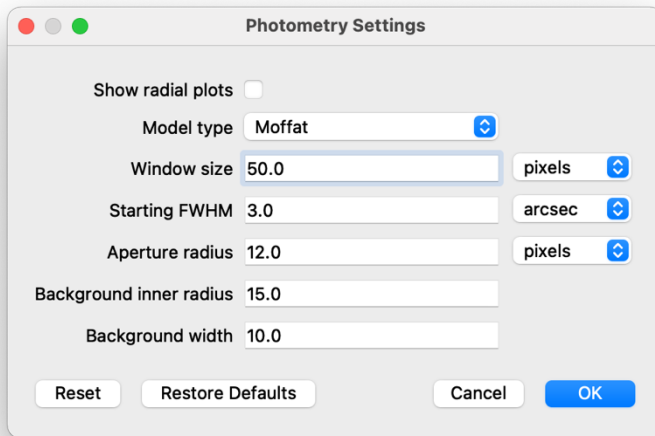
```
> qad
```

in the terminal.

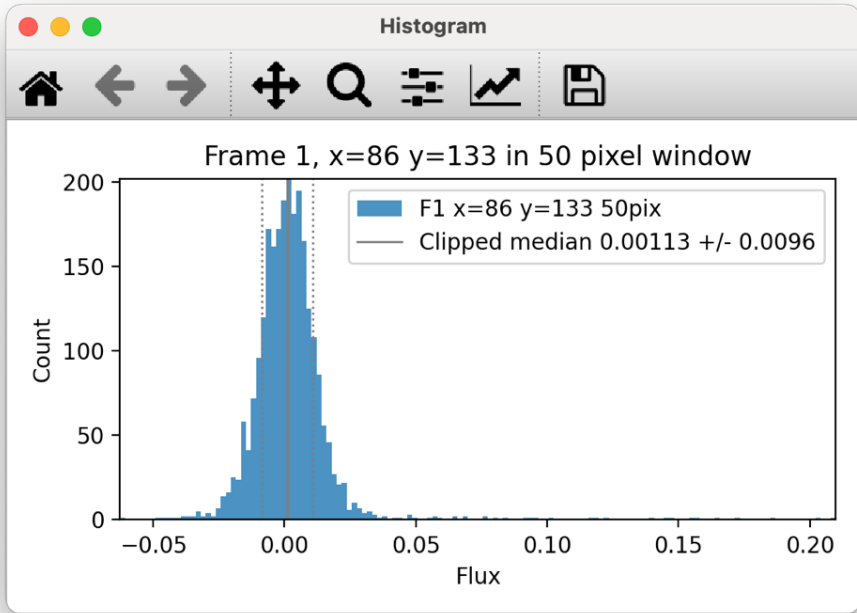


Double-clicking on the selected fits file will load the first extension of the image in DS9.

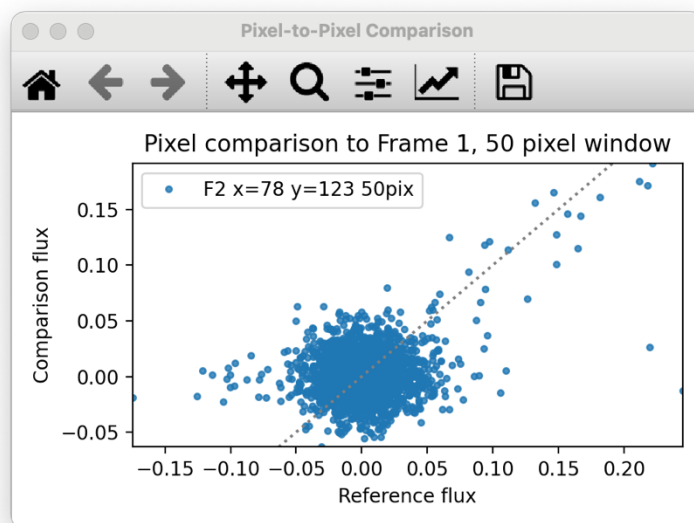
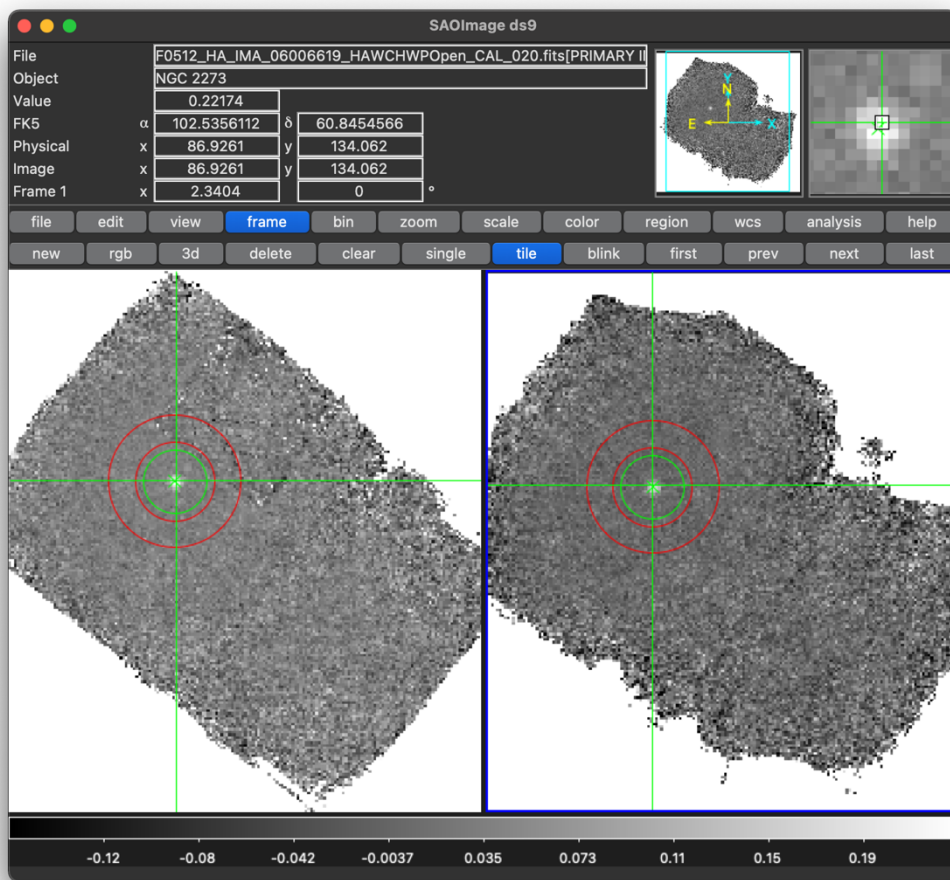
Once the image is loaded in DS9, click on the scissors icon which launches an event loop in DS9 with key commands that were described above and photometry setting that can be customized and stored.



Press 'a' for photometry. **NOTE:** the QAD photometry tools are intended for quick-look purposes. More accurate photometry tools are recommended for science analysis.



Press 's' for local image statistics and histogram plots.



Load two frames and press 'p' for a pixel-to-pixel comparison plot in the same area of both frames.