HOPS
HOlomon **P**hotometric **S**oftware

v3.0
USER MANUAL

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Prerequisites

To run HOPS properly you need:

- a computer with any of the major operating systems: Windows, MacOS or Linux;
- 4 GB or more of available RAM;
- 4 GB or more of free disk space.

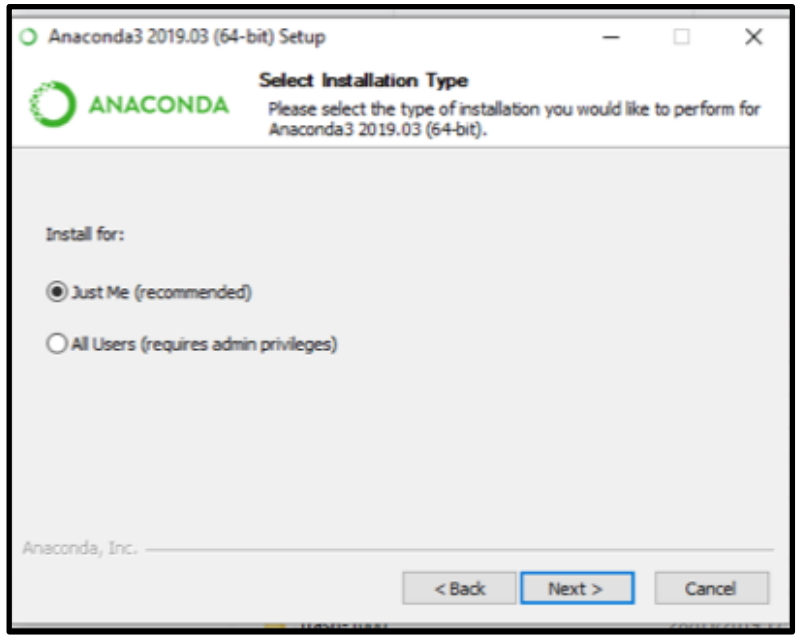
Python installation

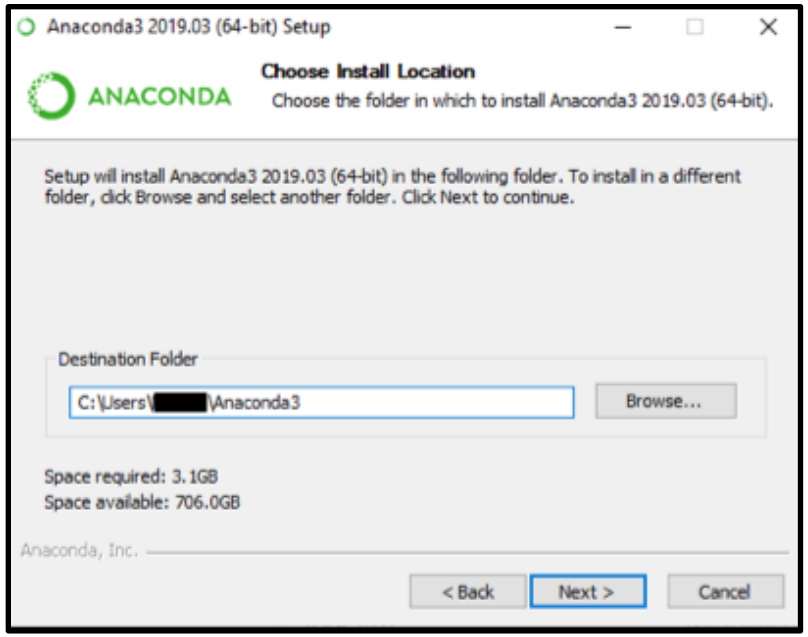
If you have Python installed on your computer, you can skip this step, otherwise:

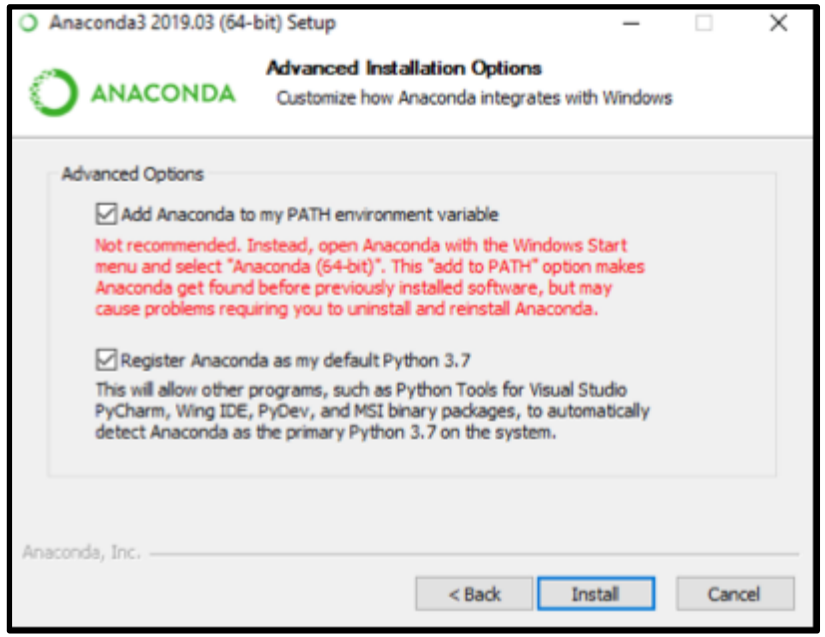
- visit the Anaconda website (www.anaconda.com/products/individual#download-section);
- choose the version you want to download depending on your operating system (I suggest going for the Graphical installers for version 3.8, version 3.7 has also been tested);
- follow the on-screen installation instructions;
- **(for Windows users)** during installation be careful to (next page):

Python installation

- install Python for you only (as recommended);
- use any destination that you prefer (if the default is not suitable for you);
- add python as a system variable (despite not being recommended).







Python installation verification

This is an important step for Windows users, while no problems are expected for MacOS and Linux users:

- open a Terminal (Command Prompt for Windows users);
- type python
- check that the Terminal enters a python environment, something like this:

```
Python 3.8.5 (default, Sep 4 2020, 02:22:02)
[Clang 10.0.0] :: Anaconda, Inc. on darwinType "help",
"copyright", "credits" or "license" for more information.
>>>
```

Python installation verification

- **(for Windows users)** if the command is not recognised it means that python is not installed as a system variable, you will need to:
  a. close the Command Prompt;
  b. add python to the system variables manually, as explained in this webpage https://geek-university.com/python/add-python-to-the-windows-path/;
  c. start the verification step again.

Installing HOPS

To install HOPS:

- visit the software webpage on GitHub (github.com/ExoWorldsSpies/hops);
- click on “Code” (green button), and on “Download ZIP”;
- unzip the file "hops-master.zip";
- double click on one of the “installer” files inside the extracted "hops-master" folder, depending on your operating system;
- after installation, an executable file named "hops" will be created on your desktop, double-click on it to start HOPS.

Known issues

- **For MacOS Mojave 10.14.6 users:**
  TkIner, the GUI backend used by HOPS, is not working properly on this MacOS version, causing a user log out. To solve this issue, you will need to either upgrade your MacOS to Catalina or downgrade your Python to 3.7.0.

TIPS SECTION

Reduction frames are important! Obtain them with extra care:

- Use the same **camera temperature**, **binning** and **subframe** as the science frames.
- Obtain at least five bias frames (**zero exposure, using a cover**), and check that there is no external light contaminating them.
- Obtain at least five dark frames (**same exposure time as the science frames, using a cover**), and check that there is no external light contaminating them.
- Obtain at least five flat frames (**pointing to a uniformly illuminated surface, with the counts at 2/3 of the full well-depth of your camera**), if your are using the sky, check that stars are not visible in your frames.
- **Do not apply any pre-processing** (for example do not create master frames) HOPS will create the master frames on the fly, and use them appropriately.

DANGER ZONE

TIPS SECTION

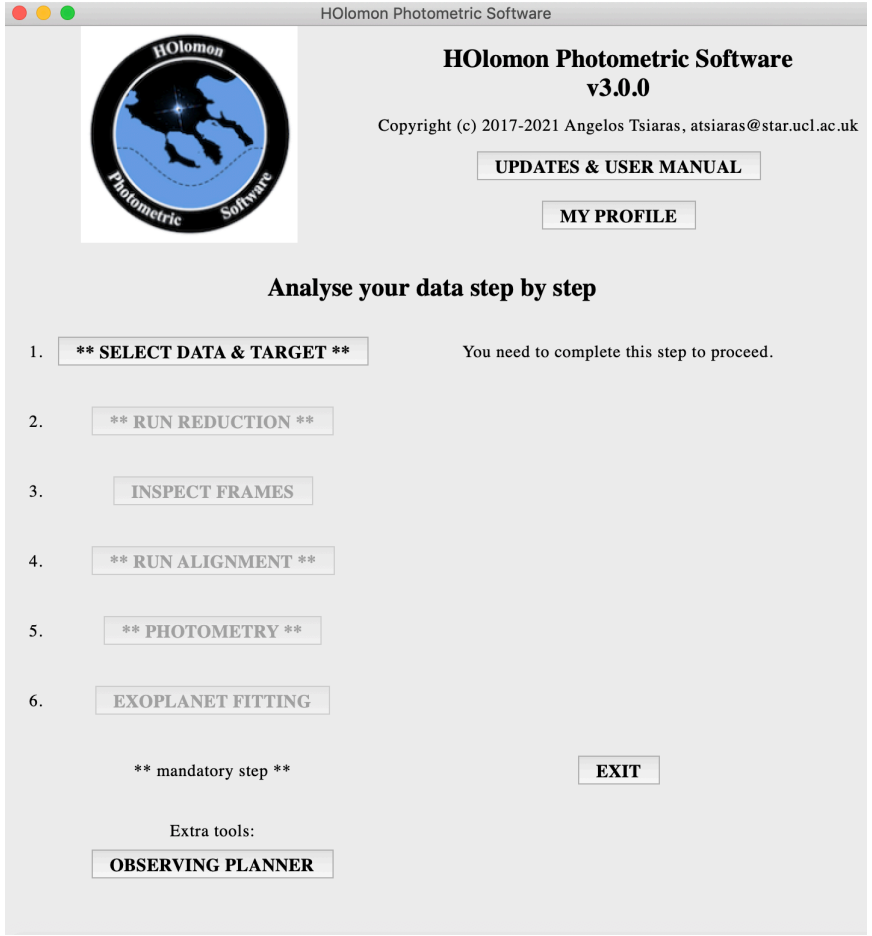
Organise your data in a way that you can have easy access to them from HOPS. The following strategy has been proven very convenient:

- Keep all scientific and reduction frames in one folder without subfolders.
- Use a specific identifier for the scientific frames, for example:
  “WASP-10b-001.fits”, “WASP-10b-002.fits”, etc…
- Use a specific identifier for the bias frames, not containing the same identifier as the scientific frames, for example:
  “bias-001.fits”, “bias-002.fits” etc…
- Use a specific identifier for the dark frames, not containing the same identifier as the scientific or the bias frames, for example:
  “dark-001.fits”, “dark-002.fits” etc…
- Use a specific identifier for the flat frames, not containing the same identifier as the scientific, the bias, or the dark frames, for example:
  “flat-001.fits”, “flat-002.fits”etc…

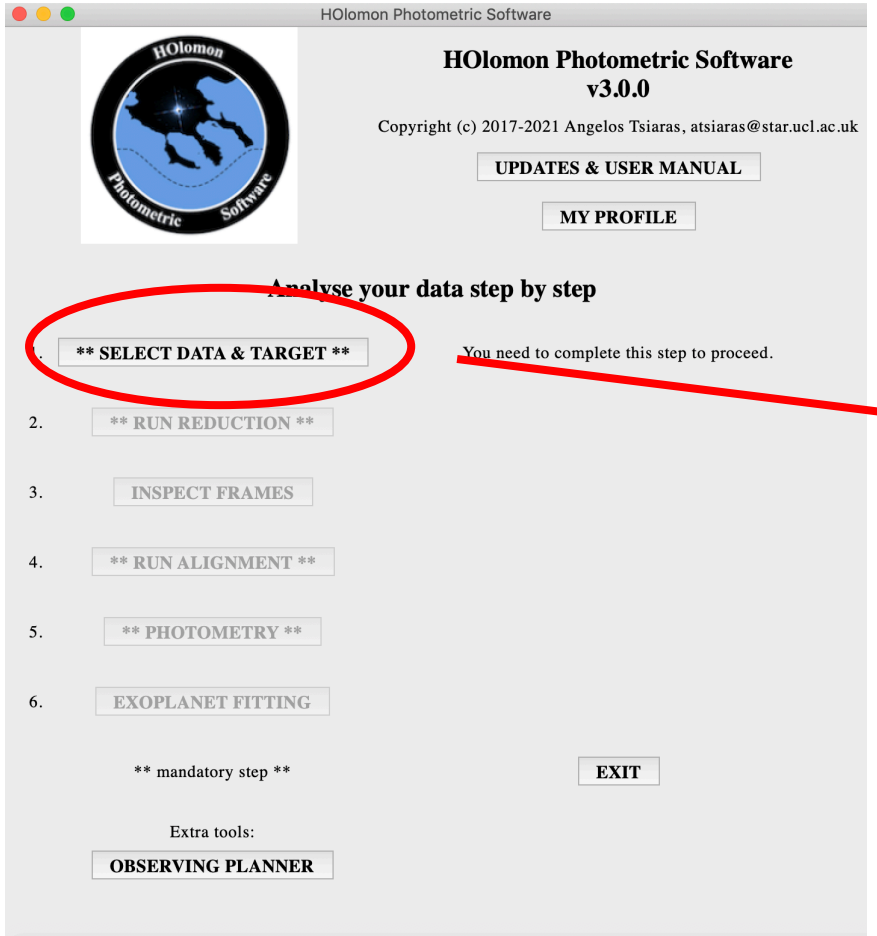
Running HOPS

Main menu

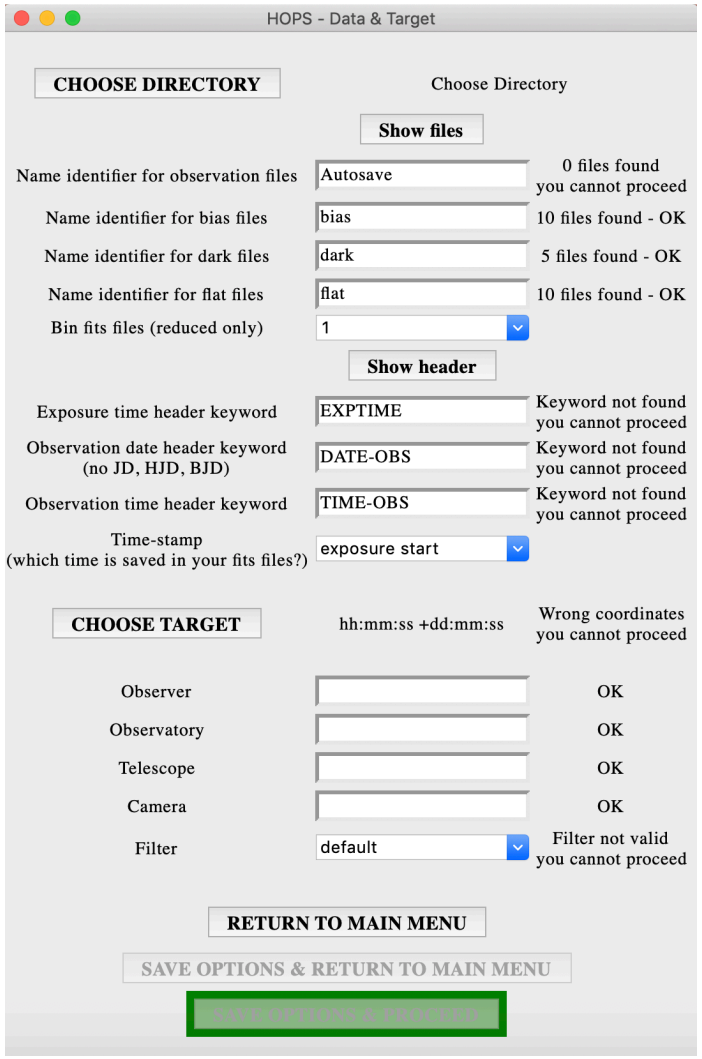
The first window to appear is the main control window from where you can initiate the different analysis steps. Some of them are mandatory so you will not be able to proceed before completing them.



1. Select Data & Target



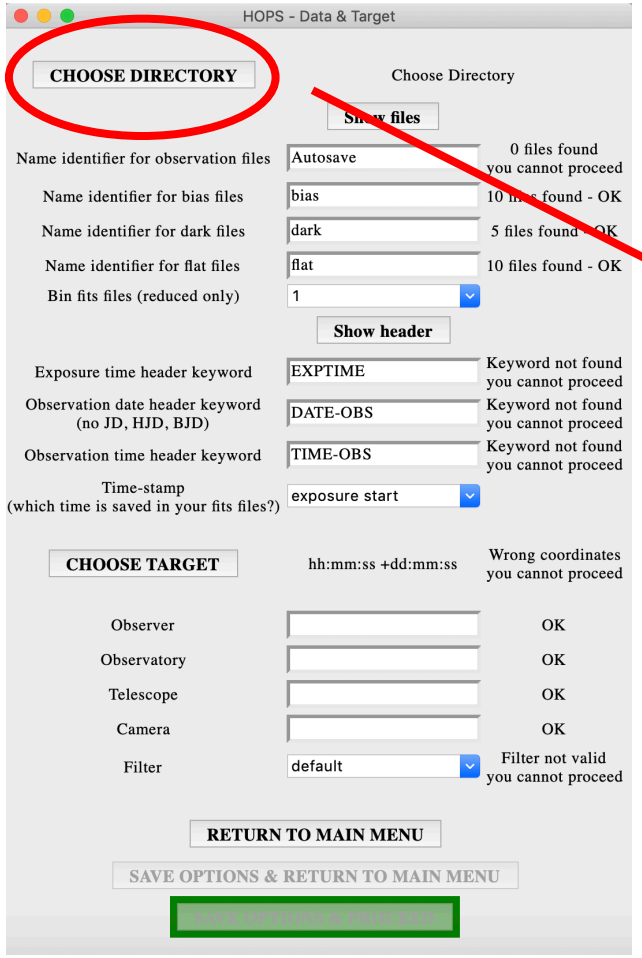
opens



Select your data directory

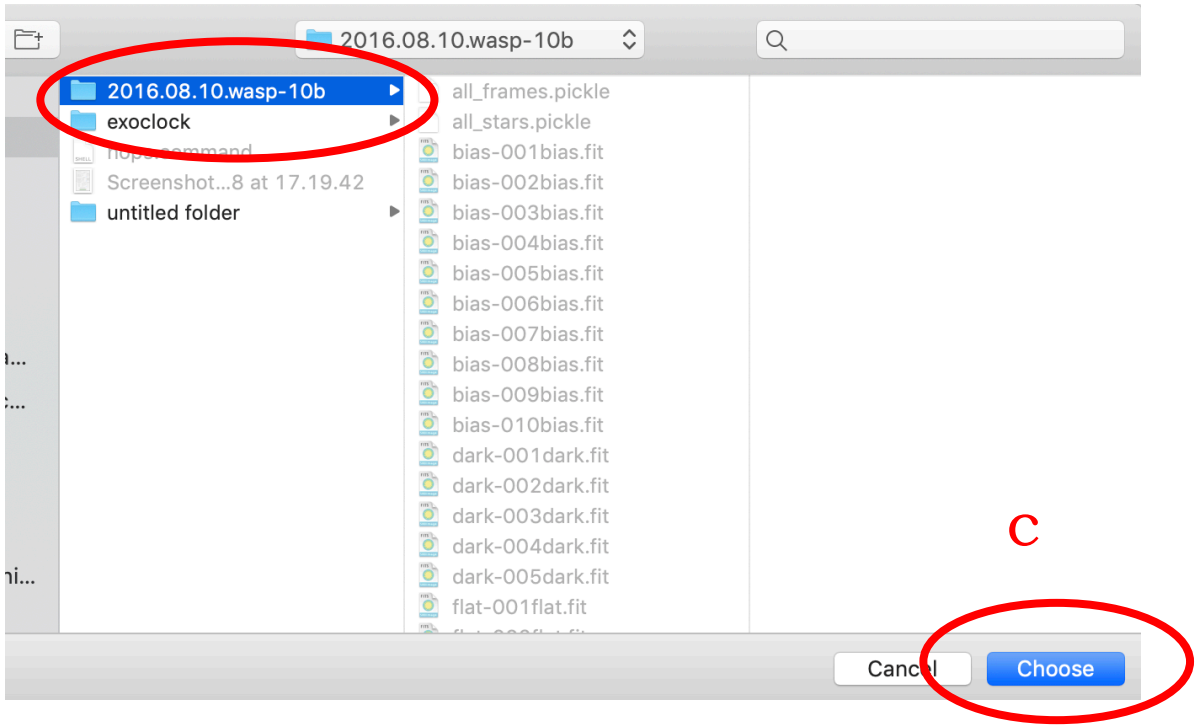
a. Click on Choose Directory, a second window will appear.
b. On the second window, select the directory containing your data.
c. On the second window, click on Choose.

a



opens

b

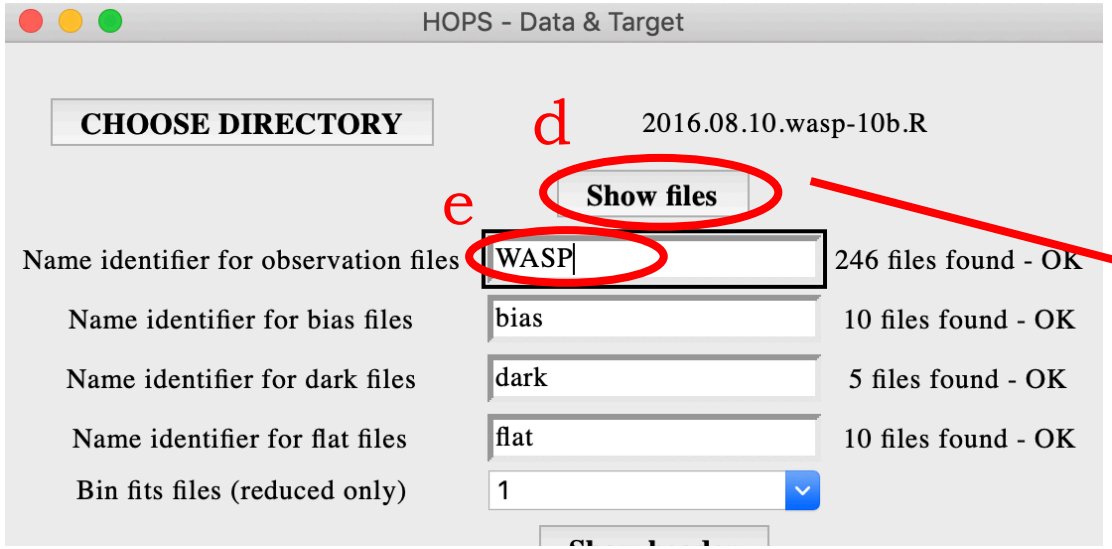


c

Enter the name of your observation files

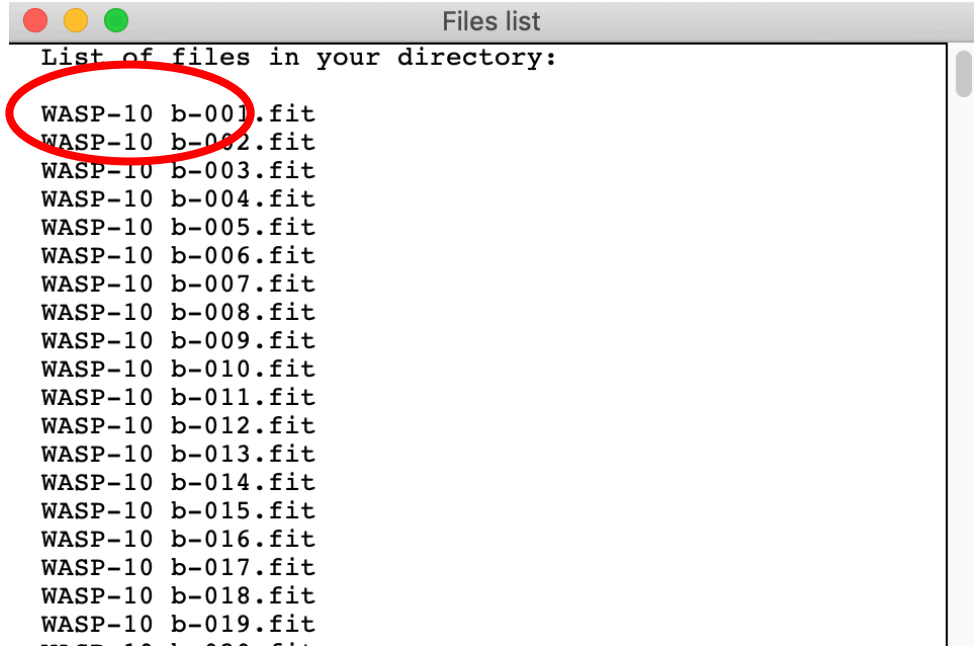
d. Click on Show files to see the files in your data directory on a second window.

e. Type in Name identifier for observation files the identifier for your observation files (i.e. the science frames).



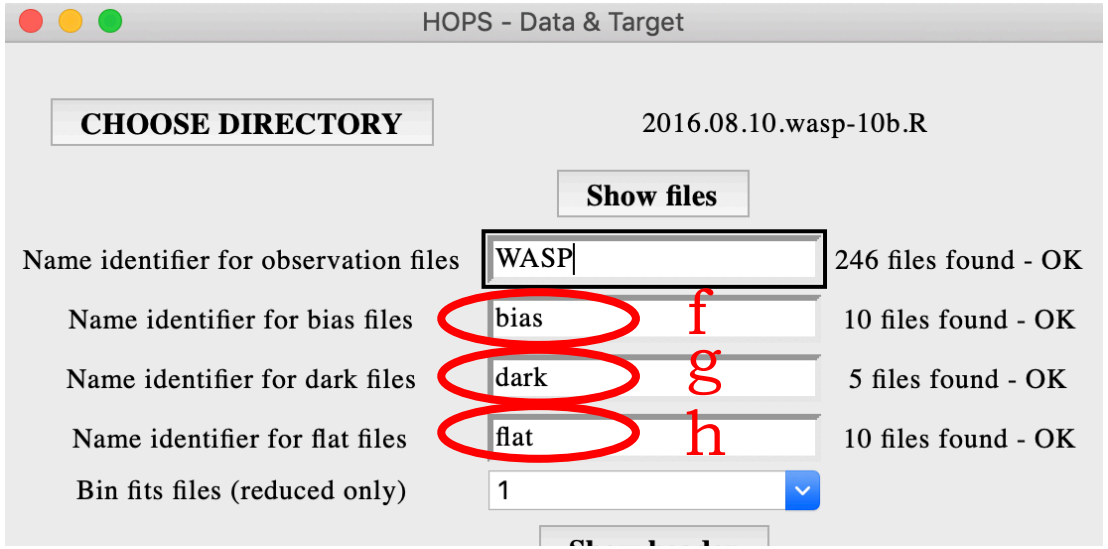
opens

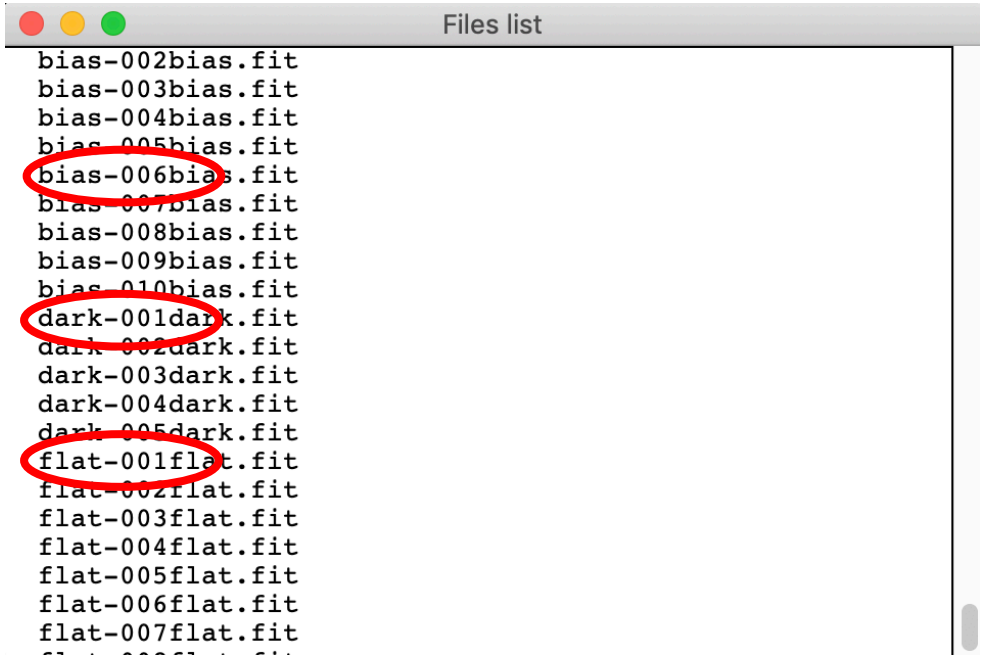
e



Enter the name of your reduction files

f. Type in Name identifier for bias files the identifier for your bias files.
g. Type in Name identifier for dark files the identifier for your dark files.
h. Type in Name identifier for flat files the identifier for your flat files.





TIPS SECTION

You should not proceed without any reduction frames but there are cases when is is unavoidable.

- If your observatory provides fully reduced data, you can safely proceed without any bias, dark, or flat frames.
- If your observatory provides bias-subtracted data, you can safely proceed without any bias frames.
- If your observatory provides bias- and dark-subtracted data, you can safely proceed without any bias or dark frames.

DANGER ZONE

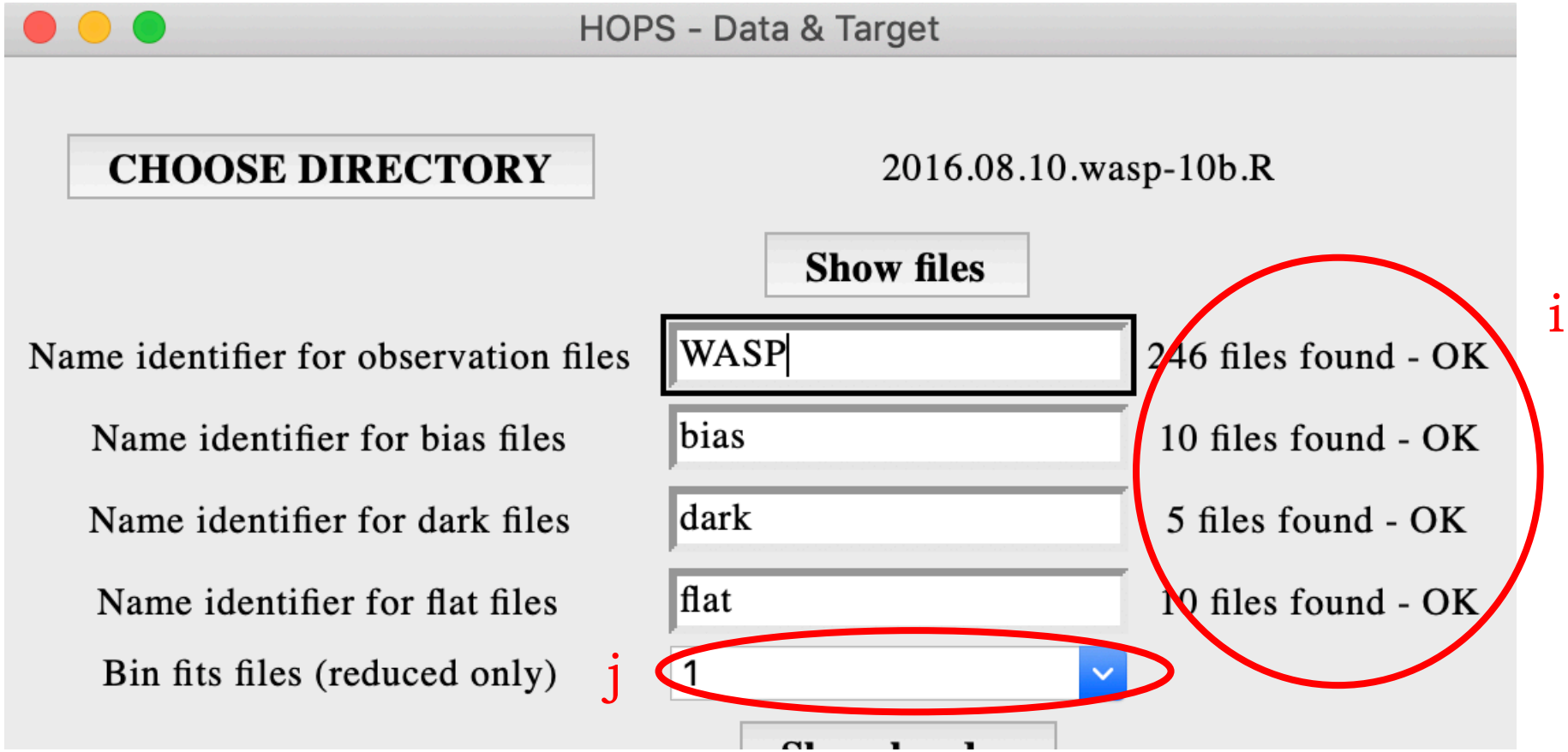
Do not proceed if:

- you have raw data, dark and flat frames only. In absence of bias frames your reduced images will be distorted.
- you have raw data and flat frames only. Flat frames not corrected for bias and dark will cause problems to your reduced frames.

Check your data

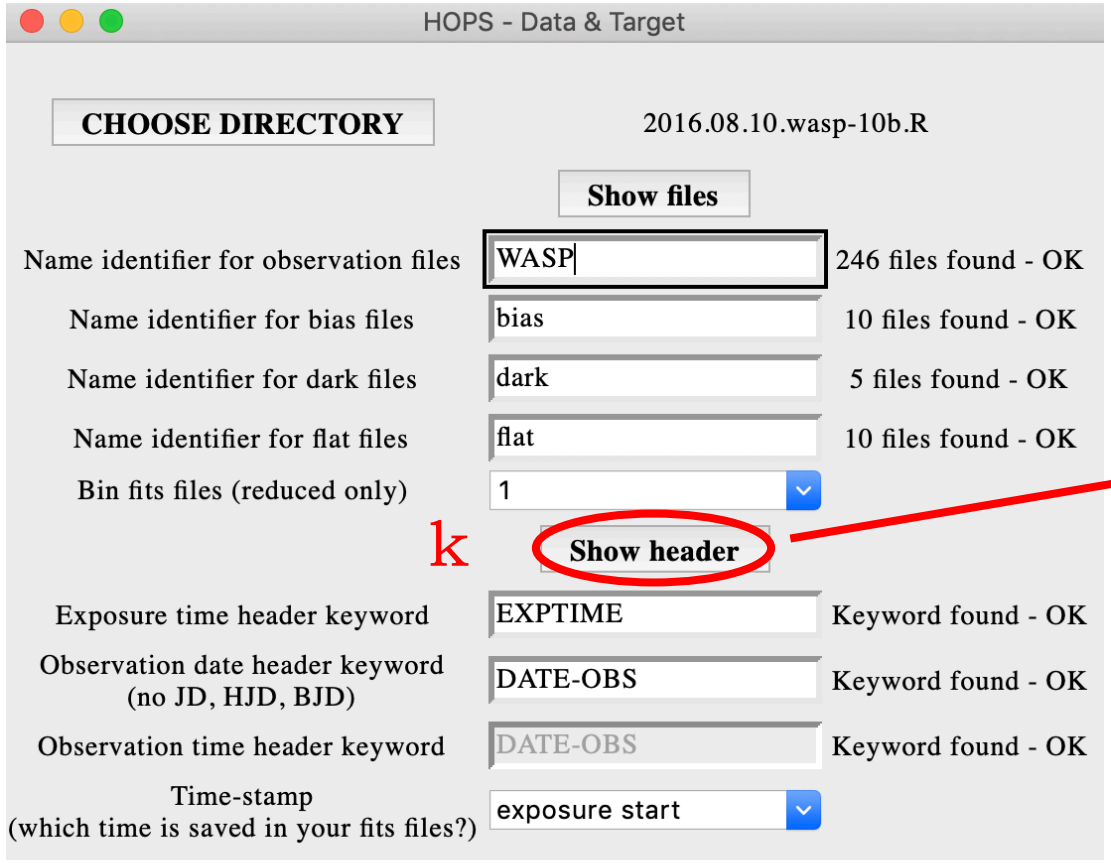
i. Check that files are found, you cannot proceed with 0 observation files but you can with 0 bias dark or flat files (not recommended!).

j. Select whether you want to bin down the reduced images by selecting an option from the Bin fits files drop-down menu (not recommended!).

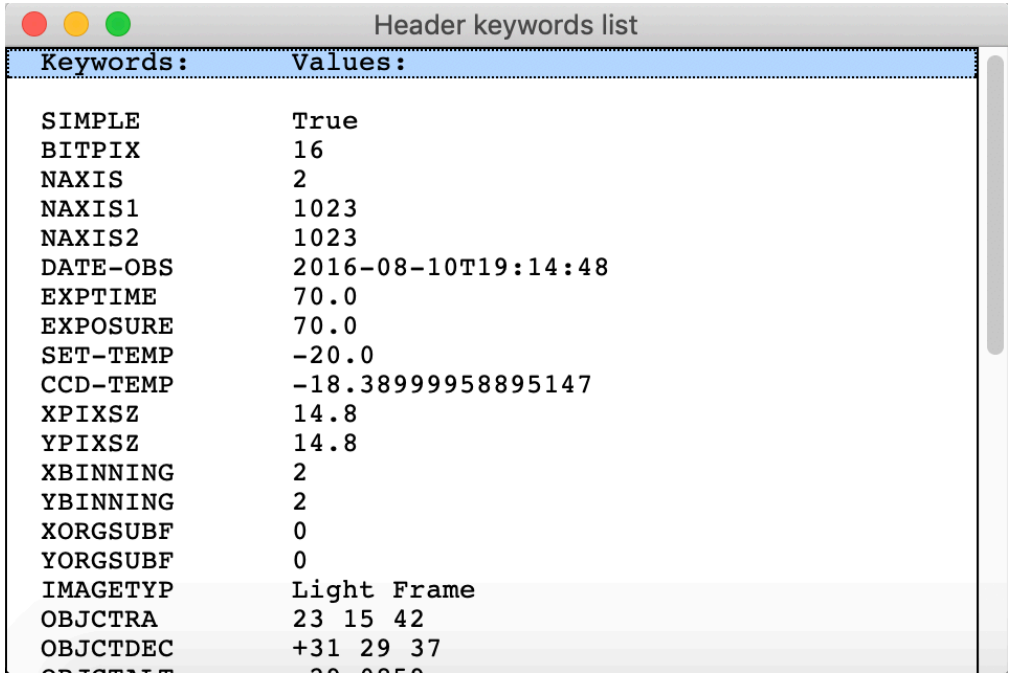


Enter your header keywords about time

k. Click on Show header to see the header of your observation files on a second window.



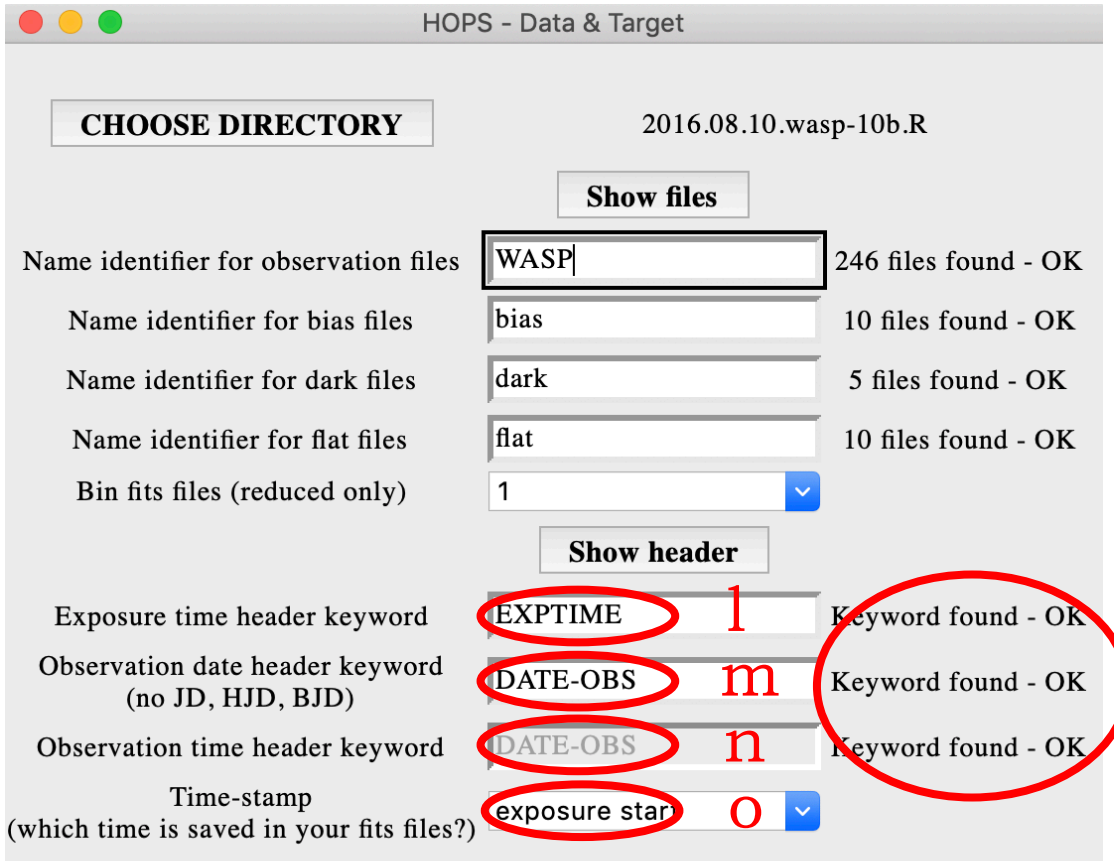
opens

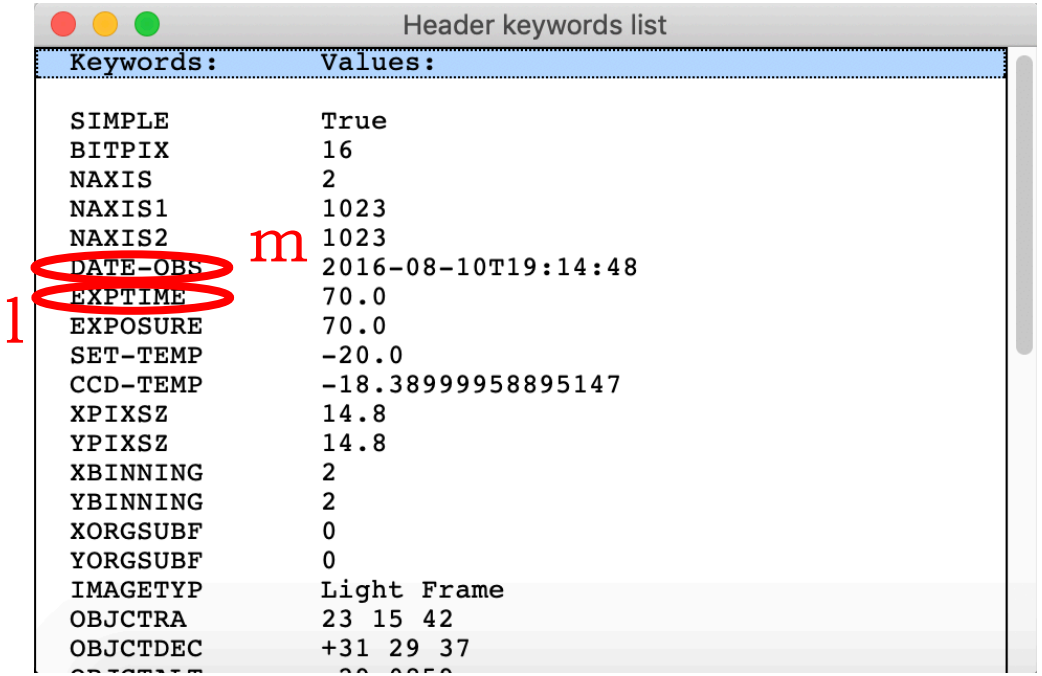


Enter your header keywords about time

l. Type in Exposure time header keyword the header keyword indicating the exposure time of each image.
m. Type in Observation date header keyword the header keyword indicating the date of each image.
n. Type in Observation time header keyword the header keyword indicating the time of each image. If the observation date keyword contains both the observation date and the observation time (for example 2016-08-03T19:08:10) then Observation time header keyword will be deactivated.
o. Select the time-stamp of your data from the Time-stamp drop-down menu. Usually, the time saved in the fits header represents the exposure start time, but this may not be the case for you. Be careful to choose the correct time stamp!
p. Check that the header keywords are all found, you cannot proceed without these information.

Enter your header time keywords



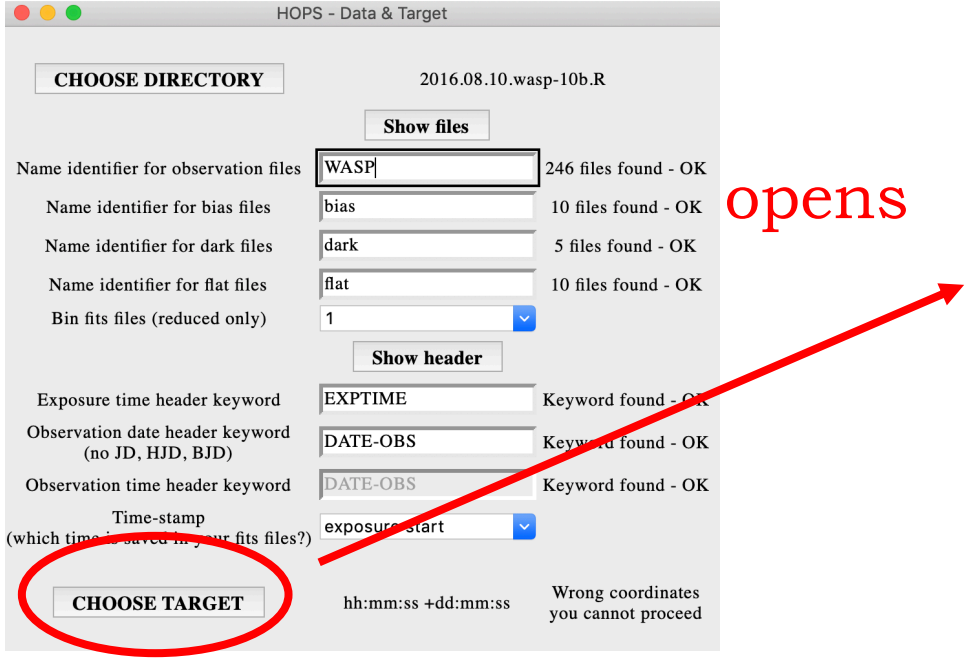


Select your target

q. Click on Choose target, a second window will appear.

r. On the second window, select one of the three options. Option 1 will be available only if the RA/DEC are included in the header of your images. Option 2 will be available only if your computer is connected to the internet, and the name that you will provide will be accepted only if it can be resolved by SIMBAD. Option 3 will always be available, but you have to provide the RA/DEC in the form hh:mm:ss +/-dd:mm:ss.

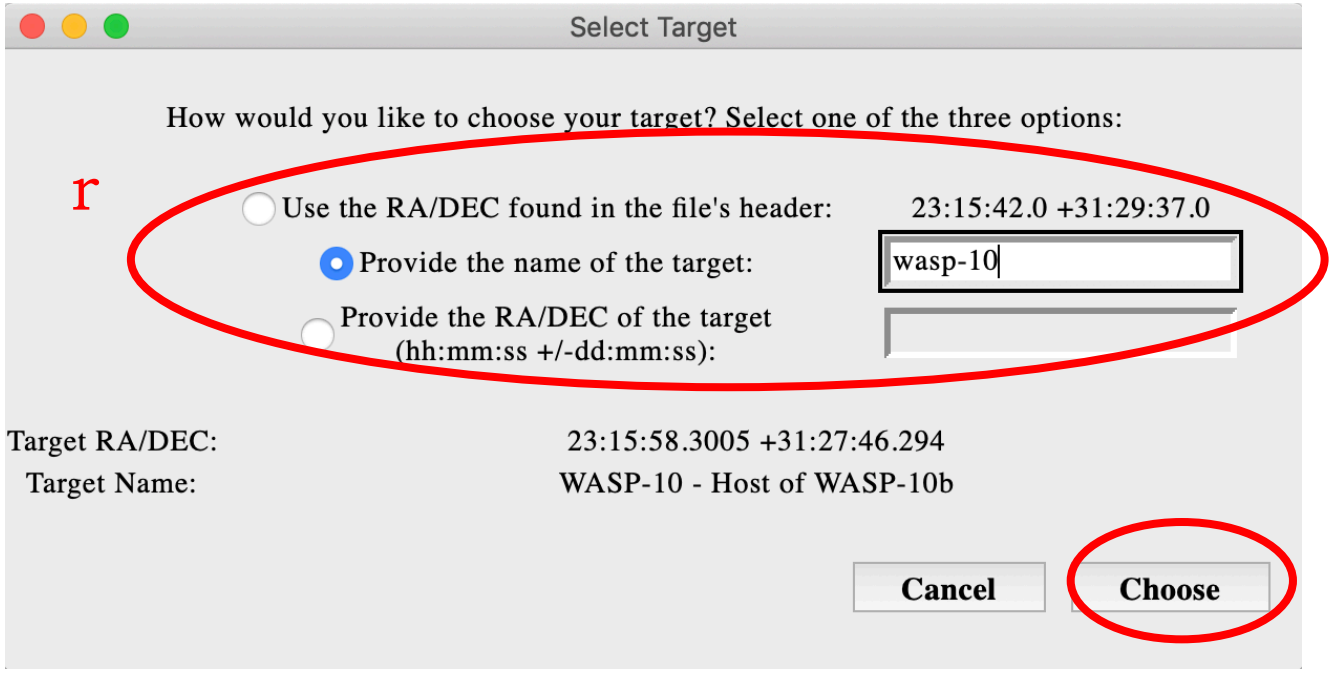
s. On the second window, click on Choose.



q

opens

r

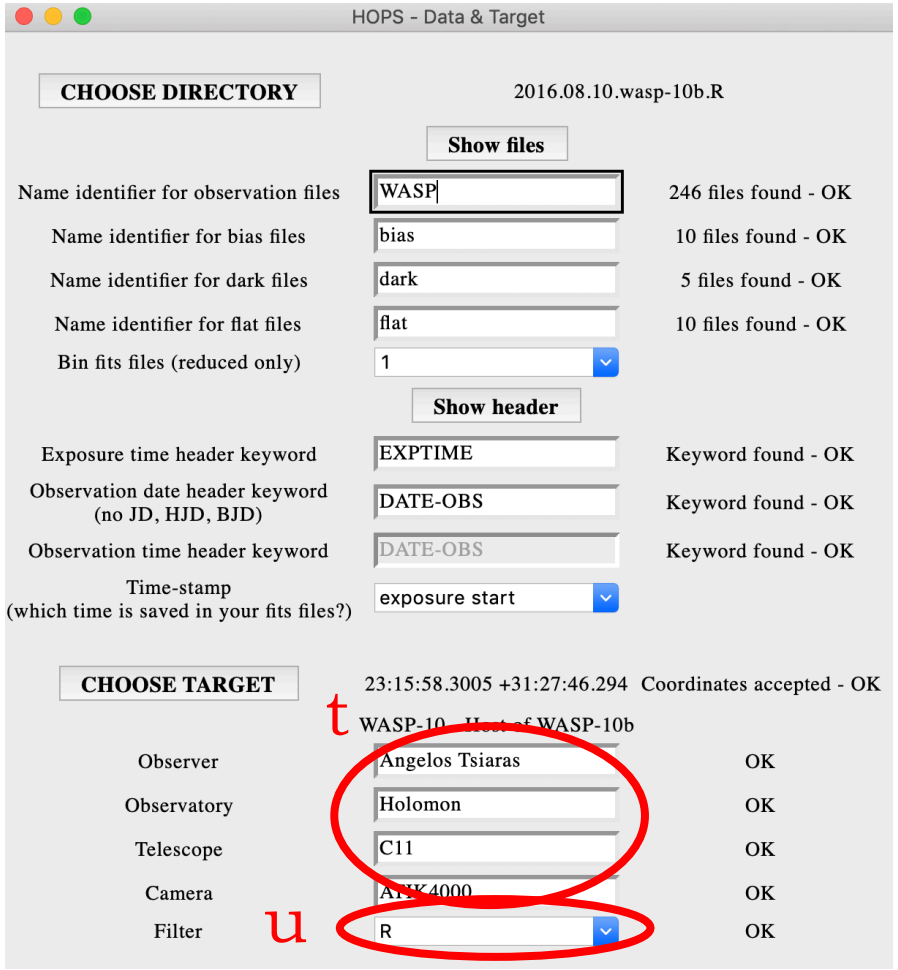


s

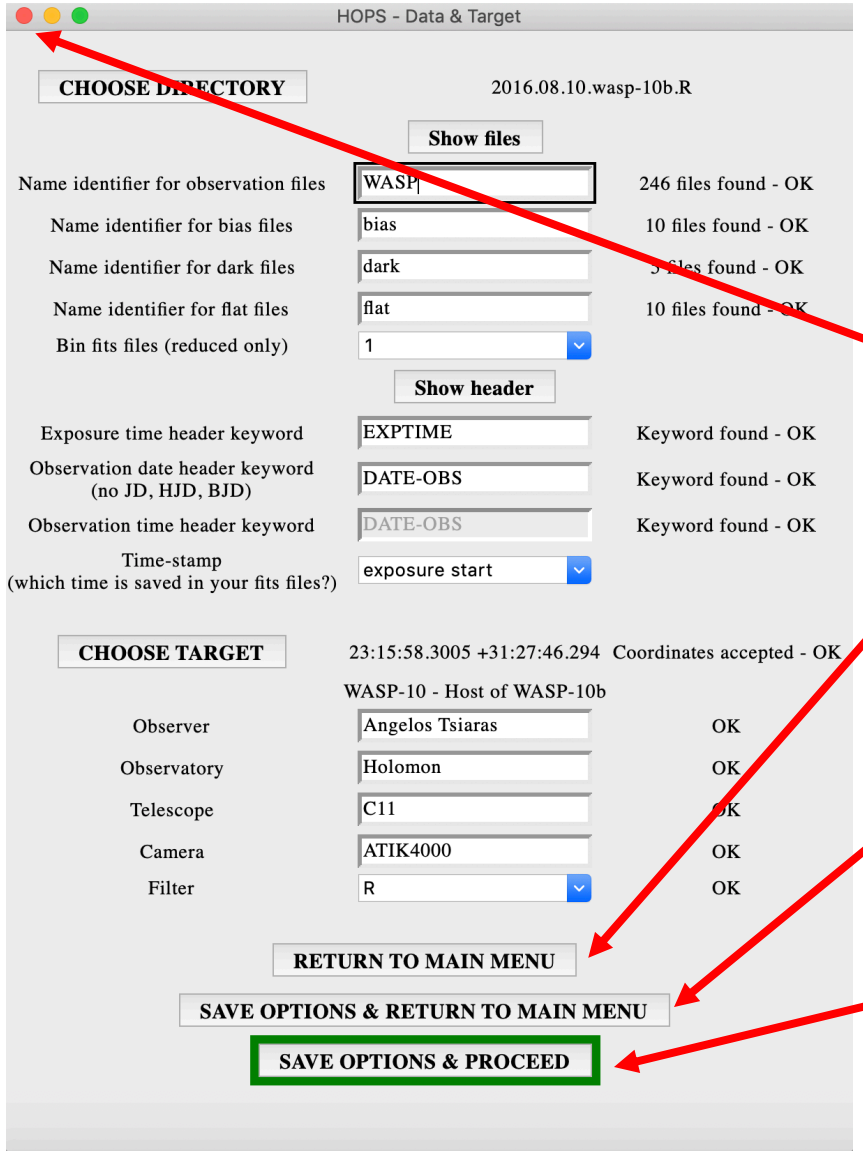
Enter your personal and system information

t. Optional: Enter the name of the observer, the observatory, the telescope and the camera. These are not necessary for the analysis but will only be printed in the final image with the fitting results.

u. Mandatory: Choose the name of the filter used from the Filter drop-down menu.



Proceed

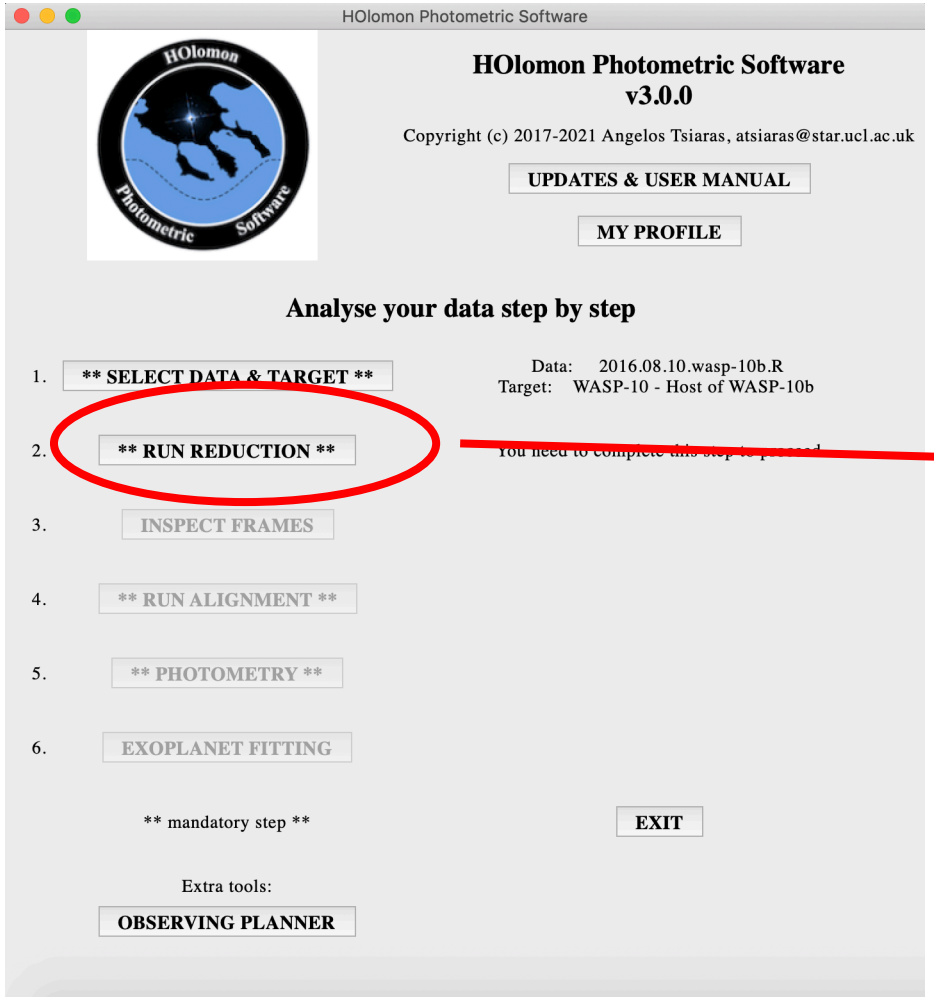


Return to the main menu without saving the current options.

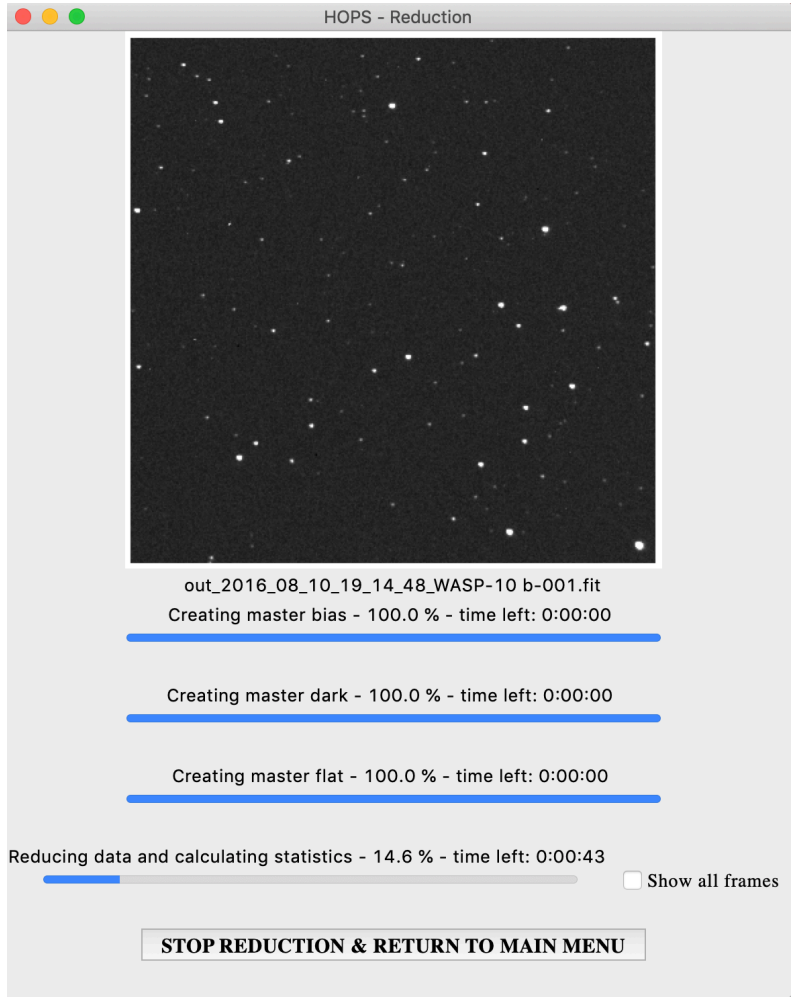
Saves the current options and returns to the main menu.

Saves the current options and proceeds to the next step – reduction.

2. Run Reduction



opens

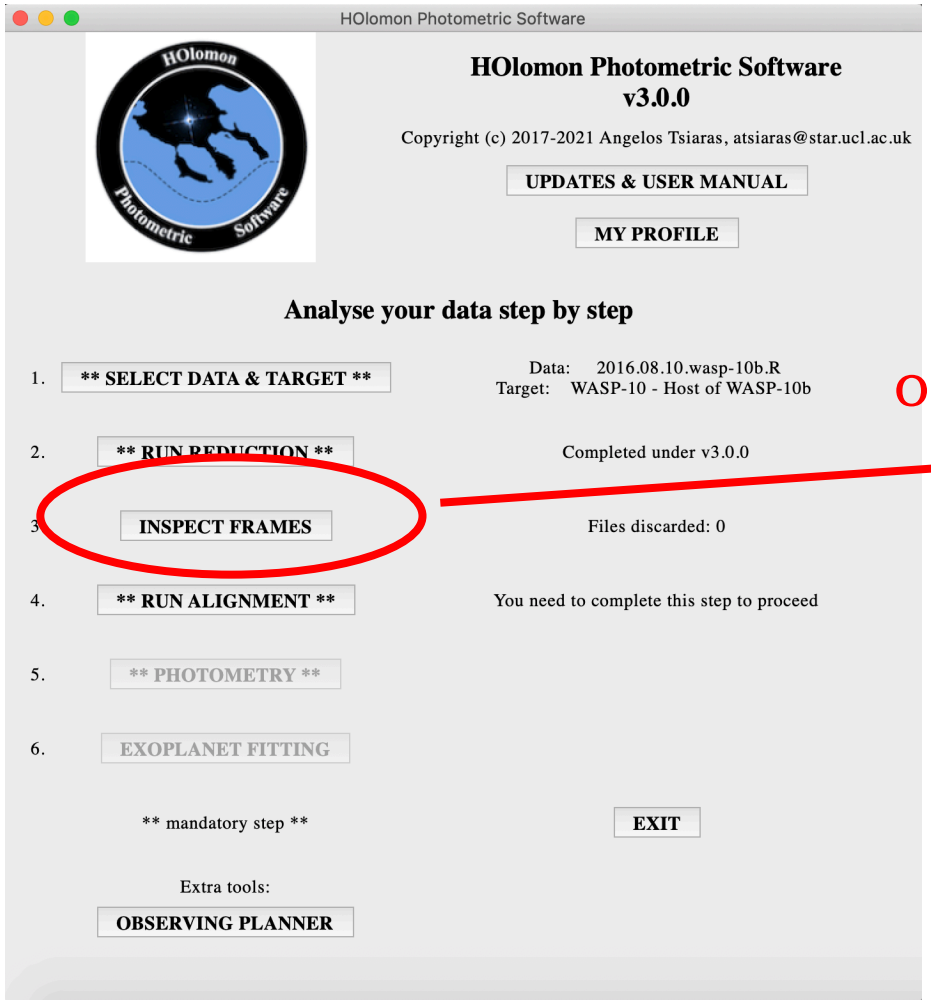


Run reduction

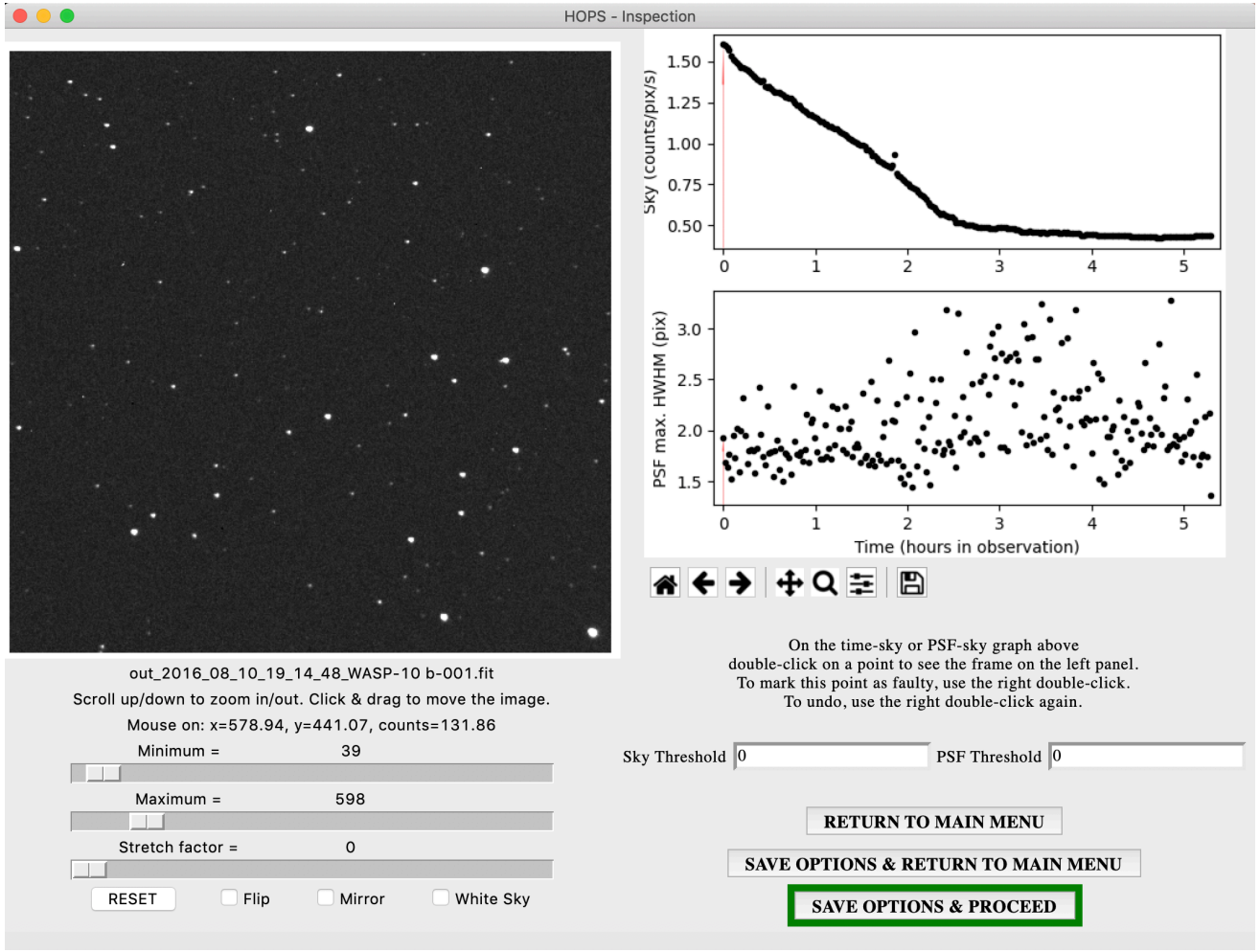
At this step you don't have to do anything but wait for the reduction process to finish. On completion HOPS will proceed to the nest step – inspection. Here, you can:

a. Select the Show all frames option if you want to display all of your images (it is useful if you want to visually inspect them while the reduction is being performed, but the process will get slower).
b. Interrupt reduction process by clicking on Stop reduction and return to main menu.

3. Inspect Frames

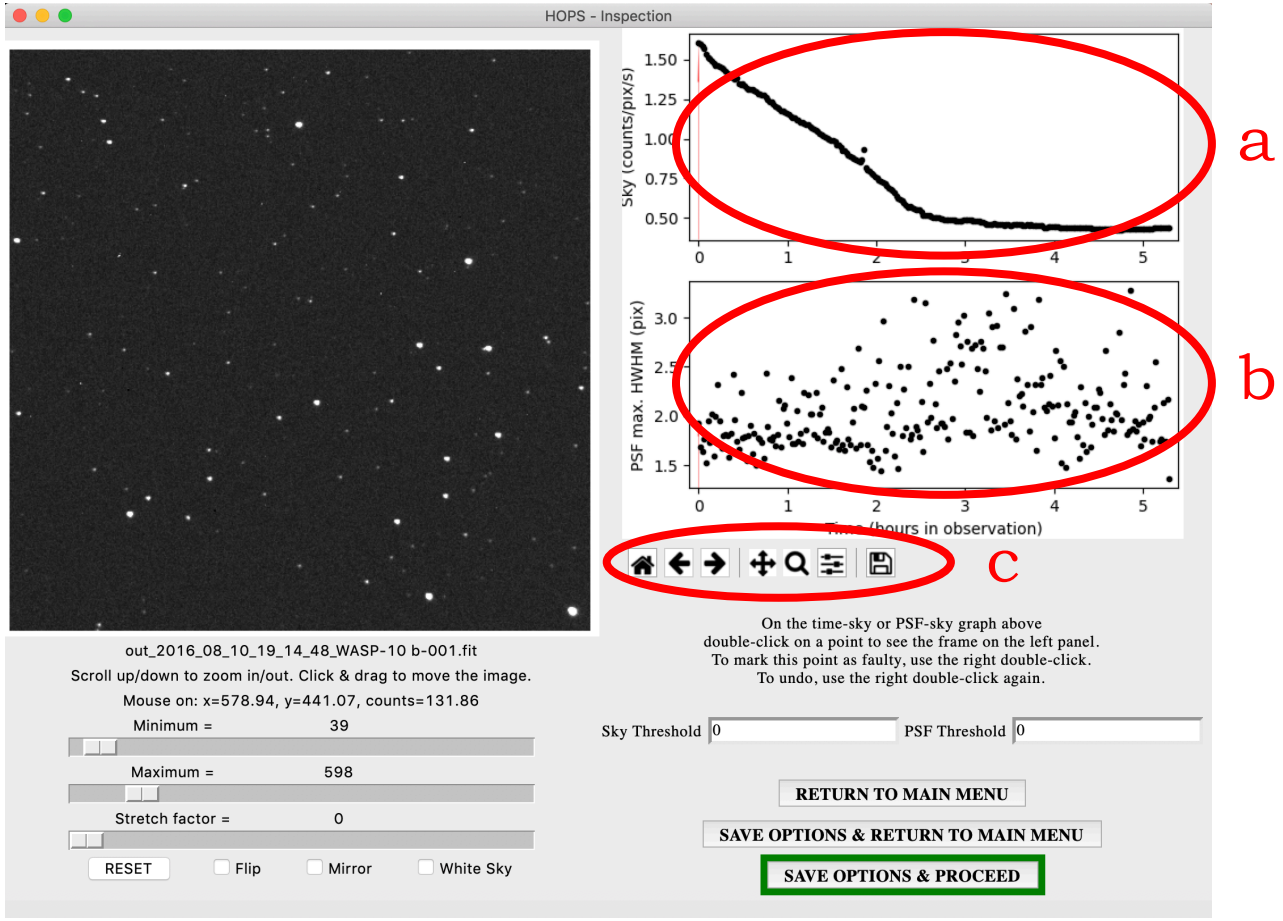


opens



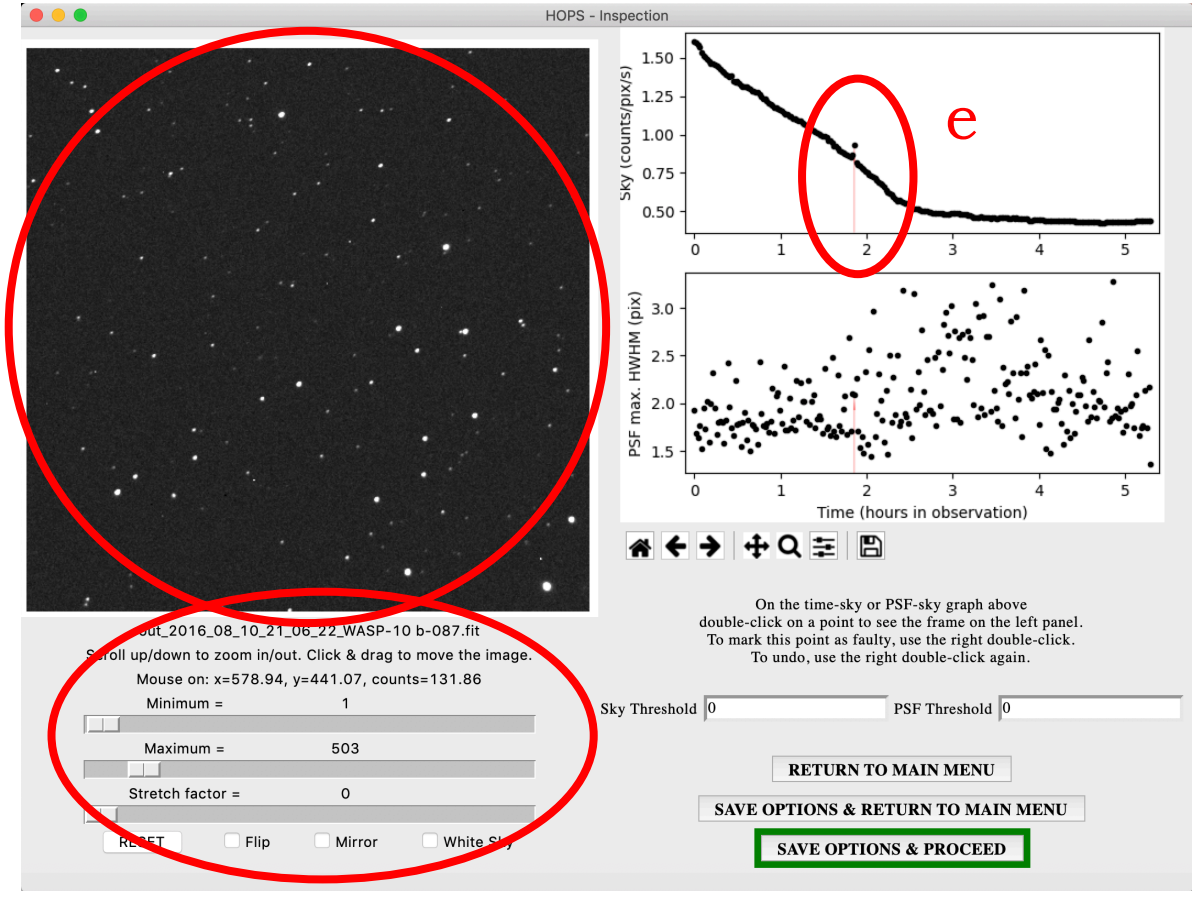
Inspect frames

At this step you can filter out faulty images from the rest of the process. On the top right, you can see two diagnostics plotted over the course of your observation. These are the Sky (a) and the HWHM (b). You can zoom, move, or rest these graphs using the panel beneath them (c).



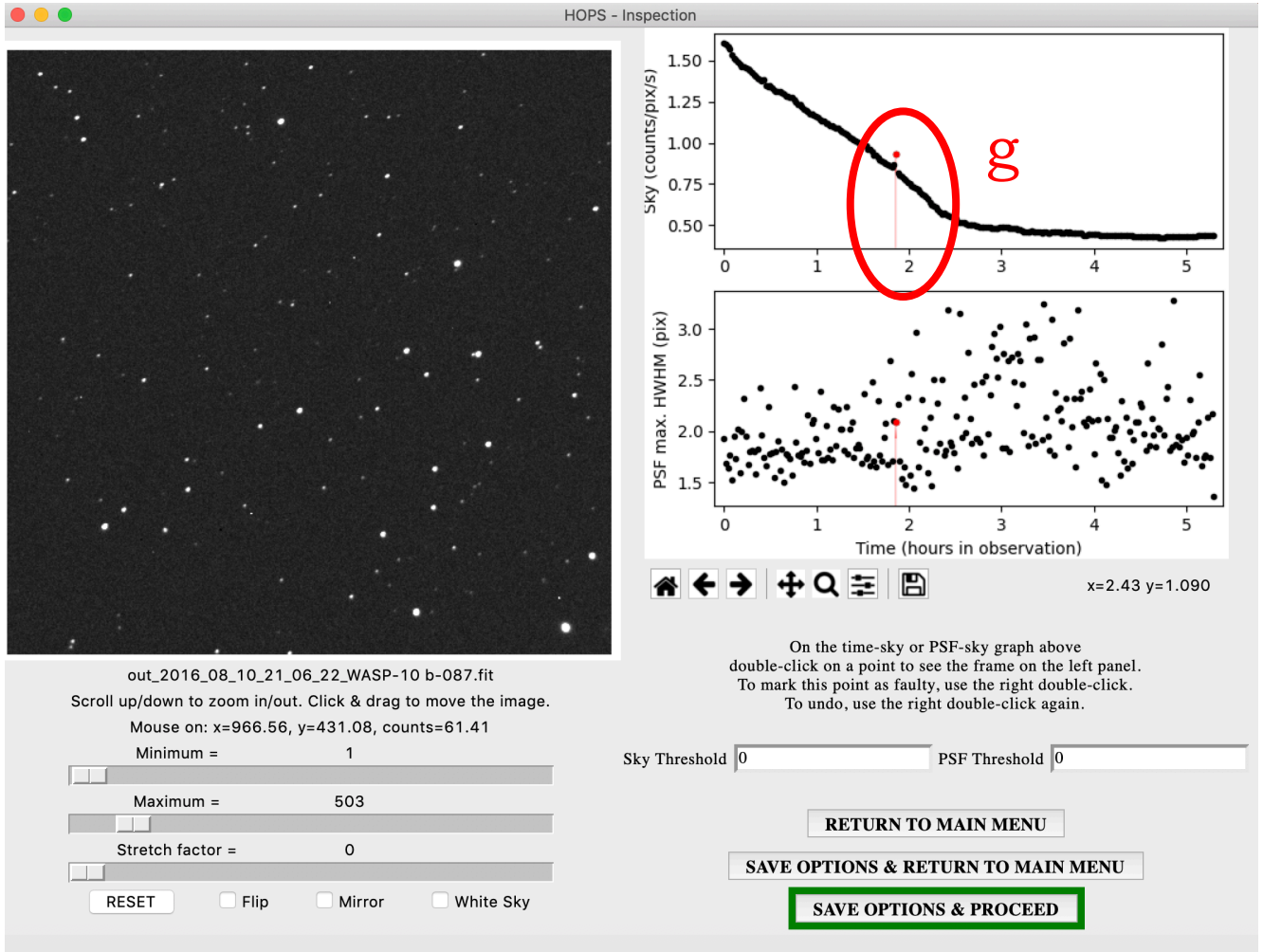
Inspect frames

The scope of these graphs is to help you identify frames that have been affected by clouds or twilight (high sky value) or by pointing issues (high value of HWHM). To visualize an image on the left panel (d), double click on a point on either the Sky or the HWHM graph and the vertical red arrow will point to it (e). You can zoom, move, flip, mirror, adjust the contrast or rest your image using the panel beneath it (f).



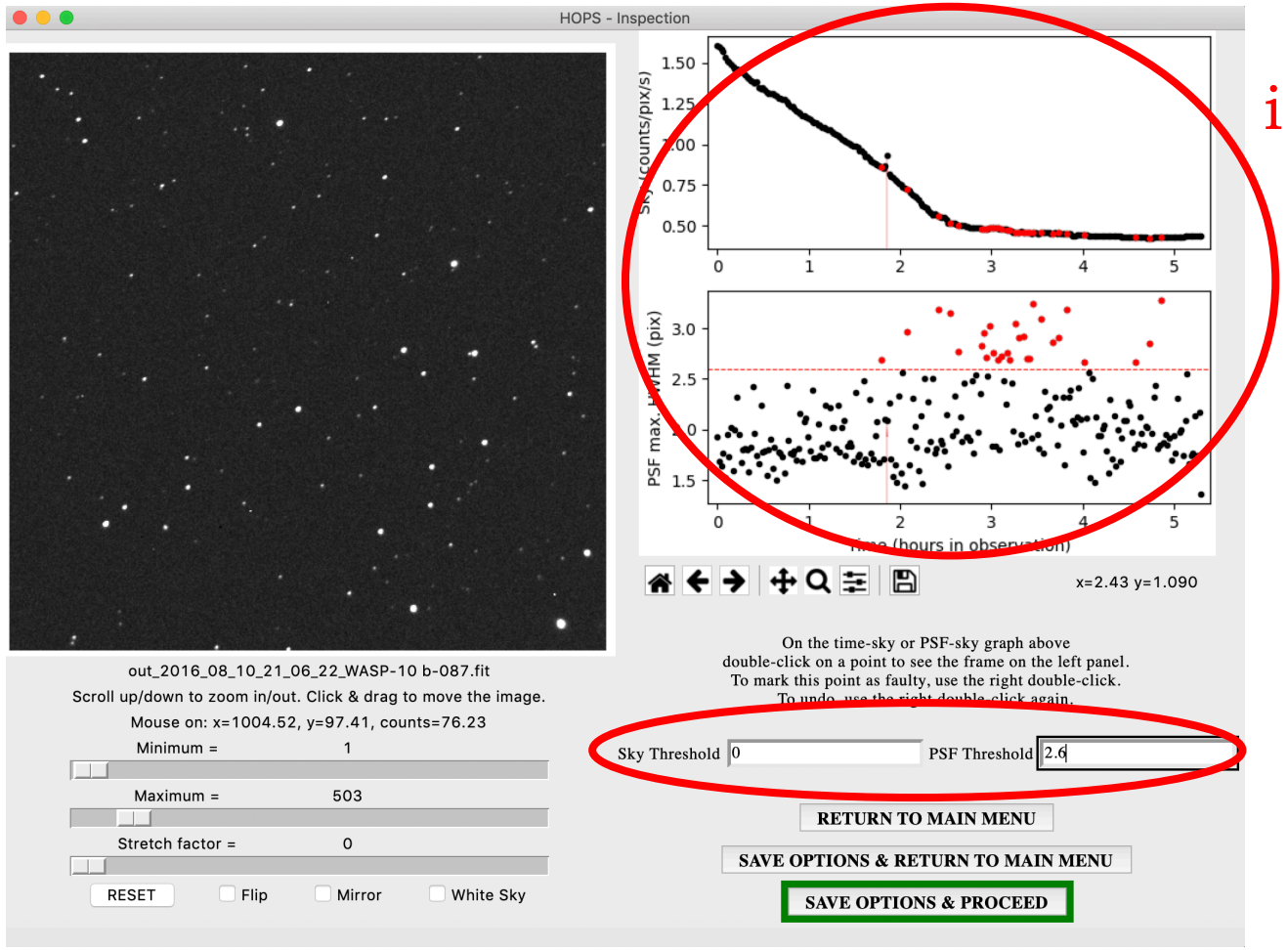
Inspect frames

If you decide to filter this image out, use the right double click - it will turn red on both graphs (g). To revive a filtered image, use the right double click again - it will turn black again on both graphs .



Inspect frames

To filter out many images at once you can set a threshold on the Sky and/or the HWHM using the relative entries (h). The filtered images will turn into red on both the Sky and the HWHM graphs (i). To remove these thresholds, set them to 0.

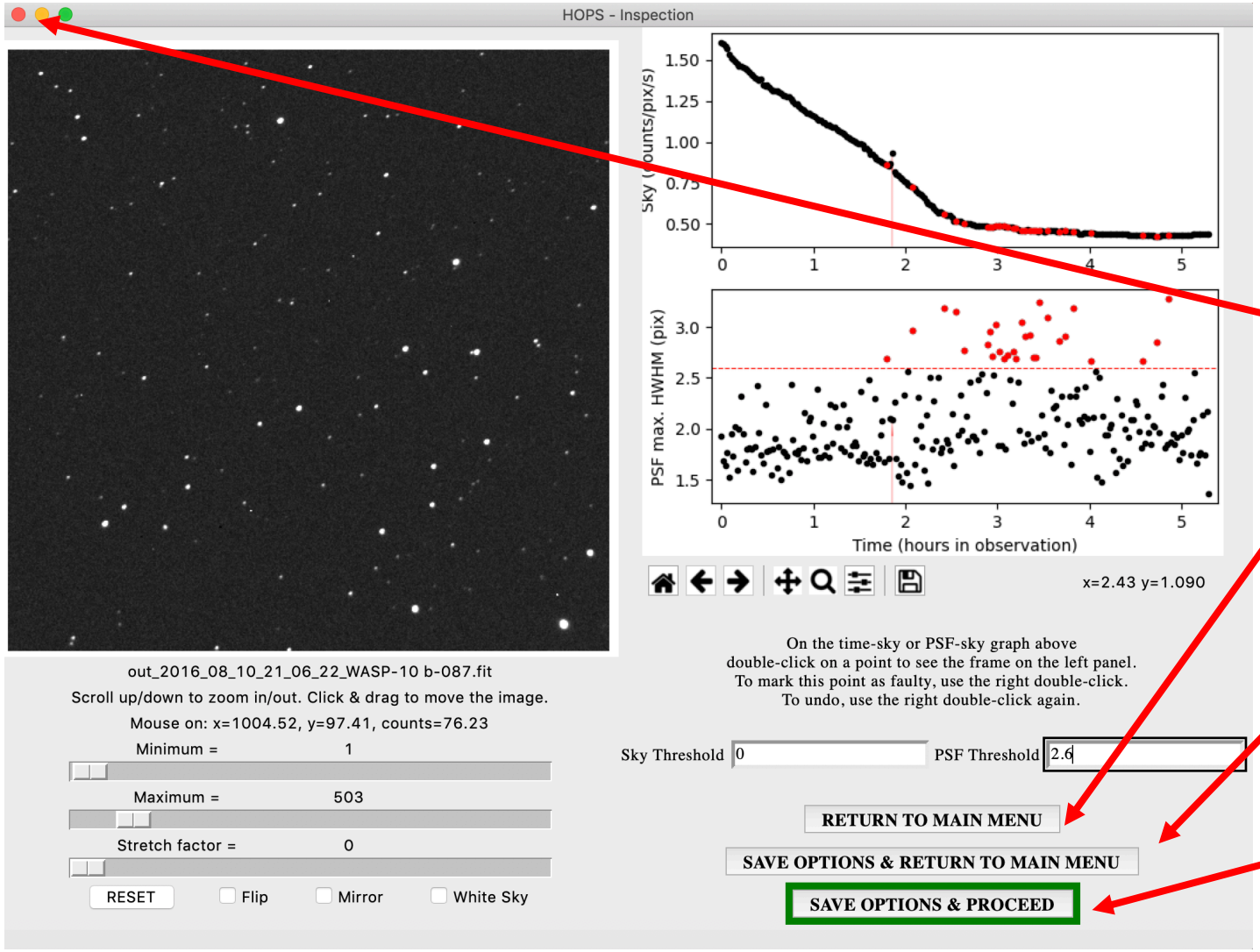


TIPS SECTION

The alignment process relies heavily on your first image. This is a good moment to check your first image again and verify that it is not overexposed and that the tracking is representative of your observation in total.

If your first image is not of good quality, select it as faulty here (step d on the next slide), it will save you a lot of time!

Proceed

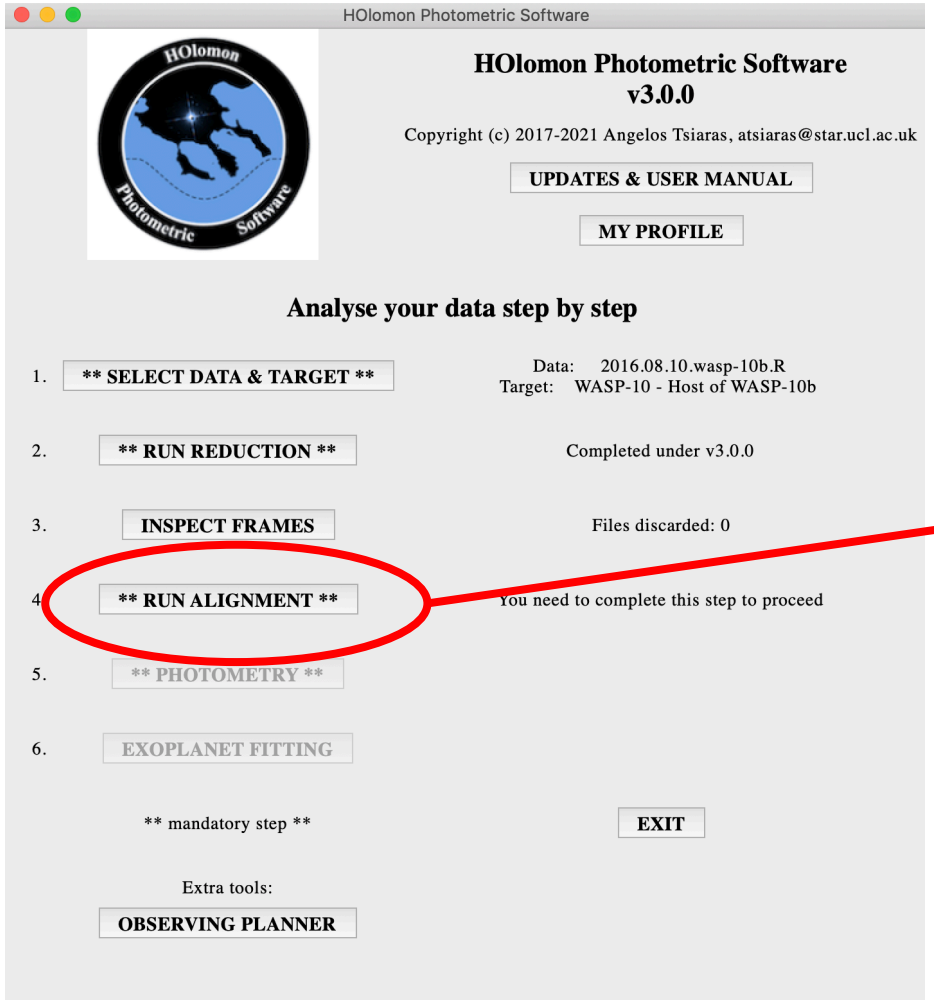


Return to the main menu without saving the current options.

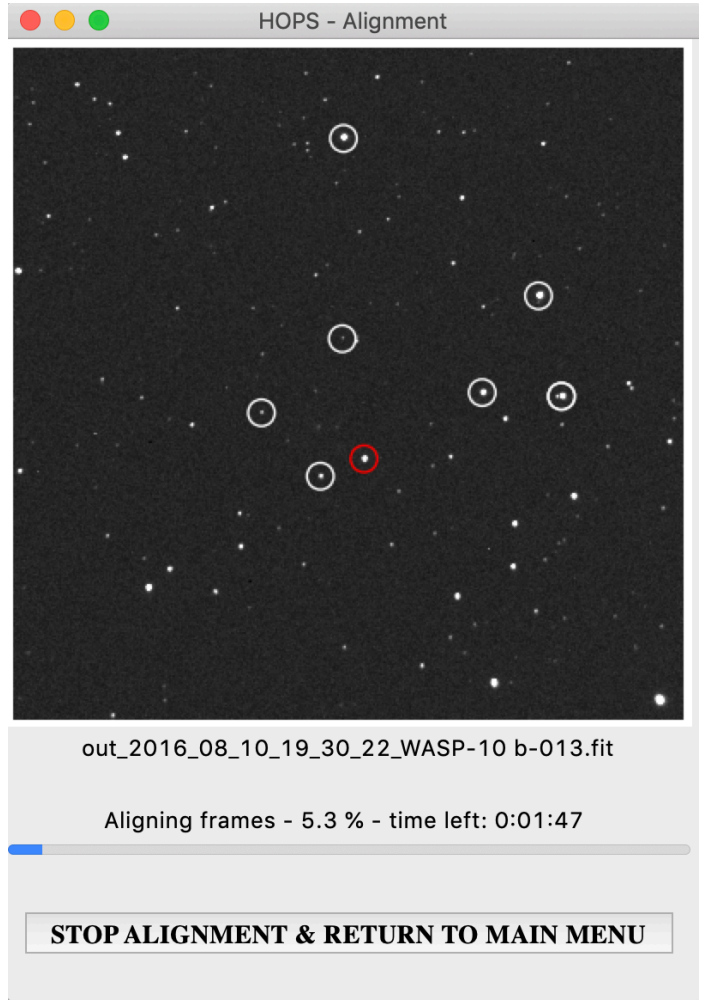
Saves the current options and returns to the main menu.

Saves the current options and proceeds to the next step – alignment.

4. Run Alignment

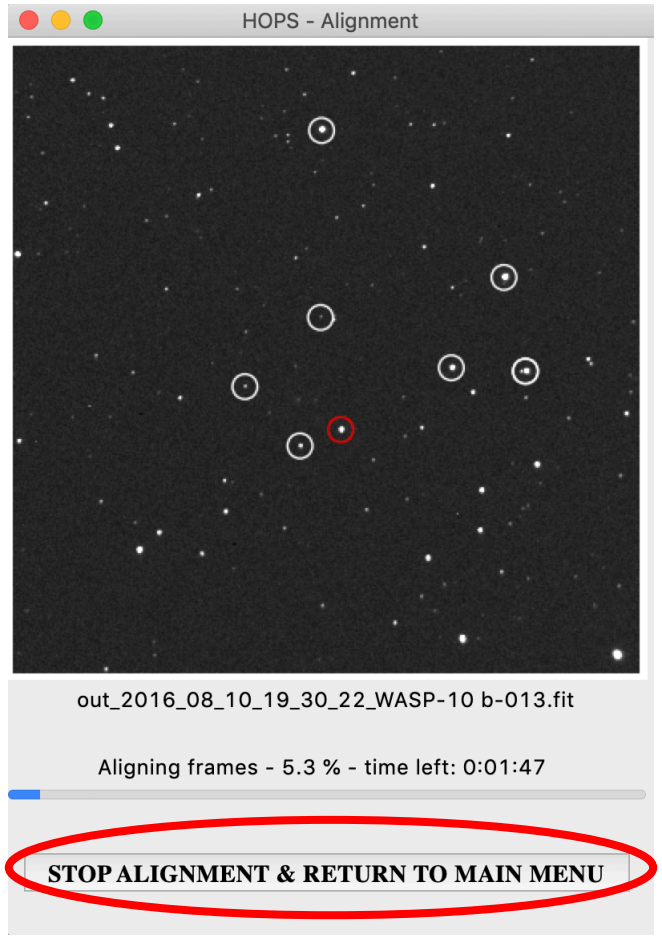


opens



Run reduction

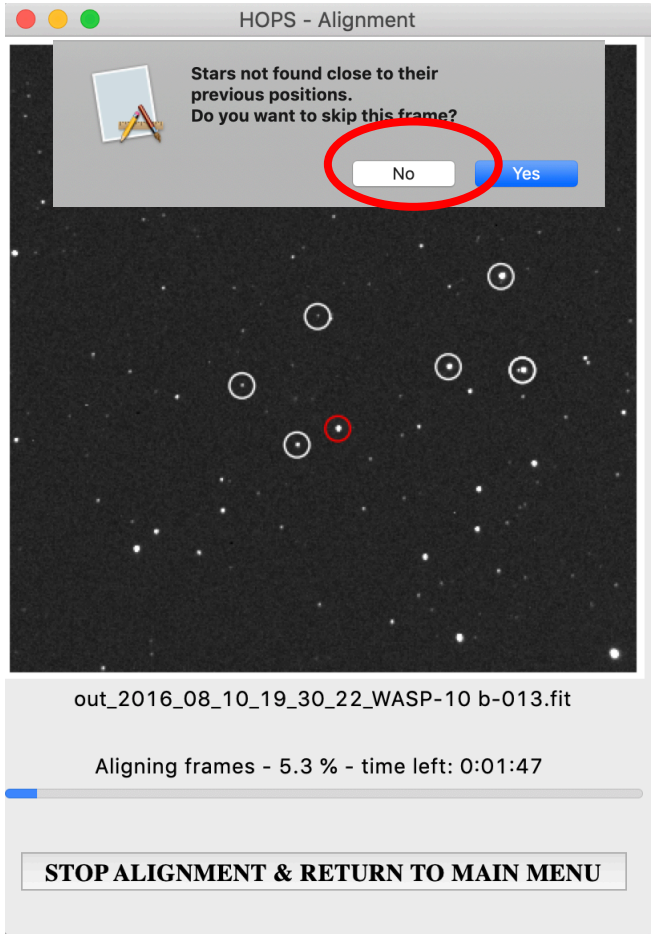
At this step you don’t have to do anything but wait for the alignment process to finish. On completion HOPS will proceed to the nest step – photometry. Here, you can only interrupt the alignment process by clicking on Stop alignment and return to main menu (a).



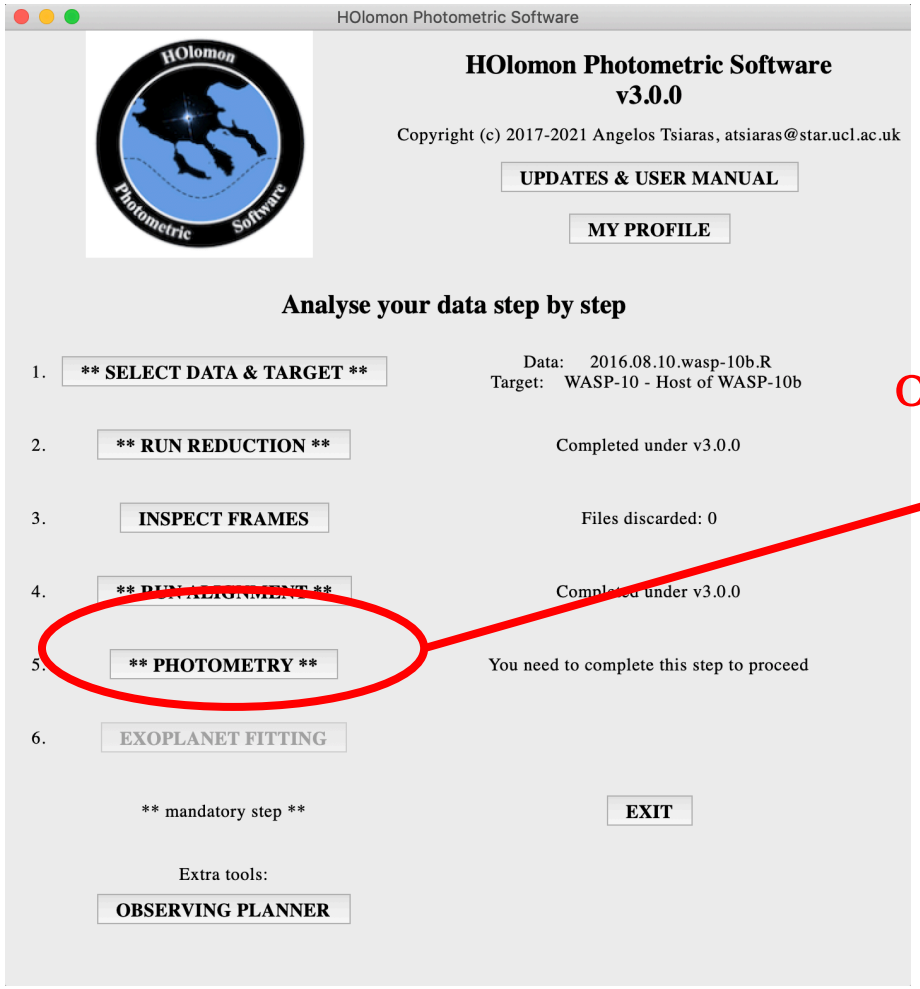
a

Running alignment

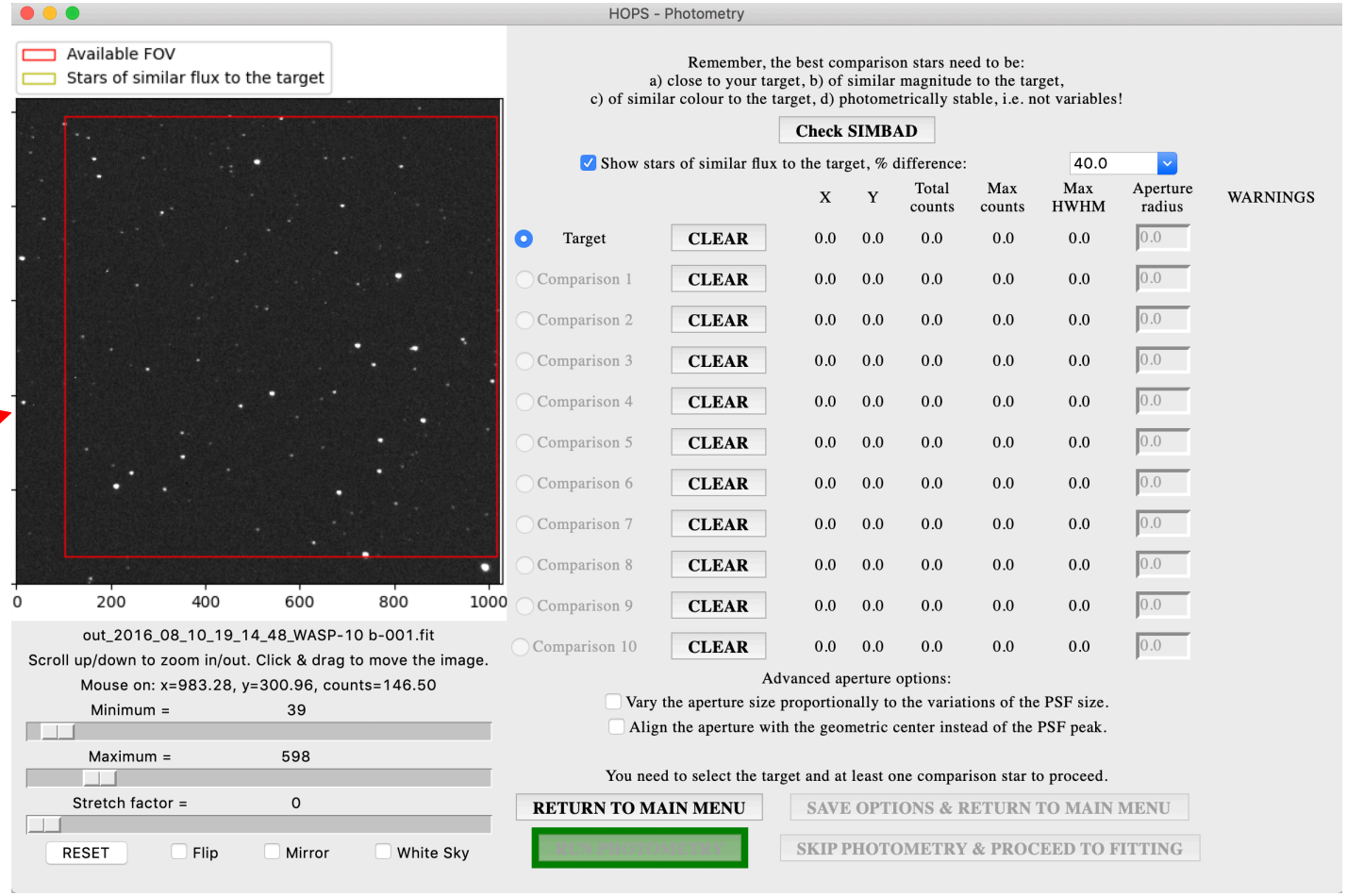
NOTE: If there is an image where stars cannot be detected, you will be asked whether you want to skip it. If the image is just shifted of flipped select No, otherwise, if the image is faulty, select Yes. (you won't be asked for small shifts or meridian flips without large shifts)



5a. Photometry (selection)



opens

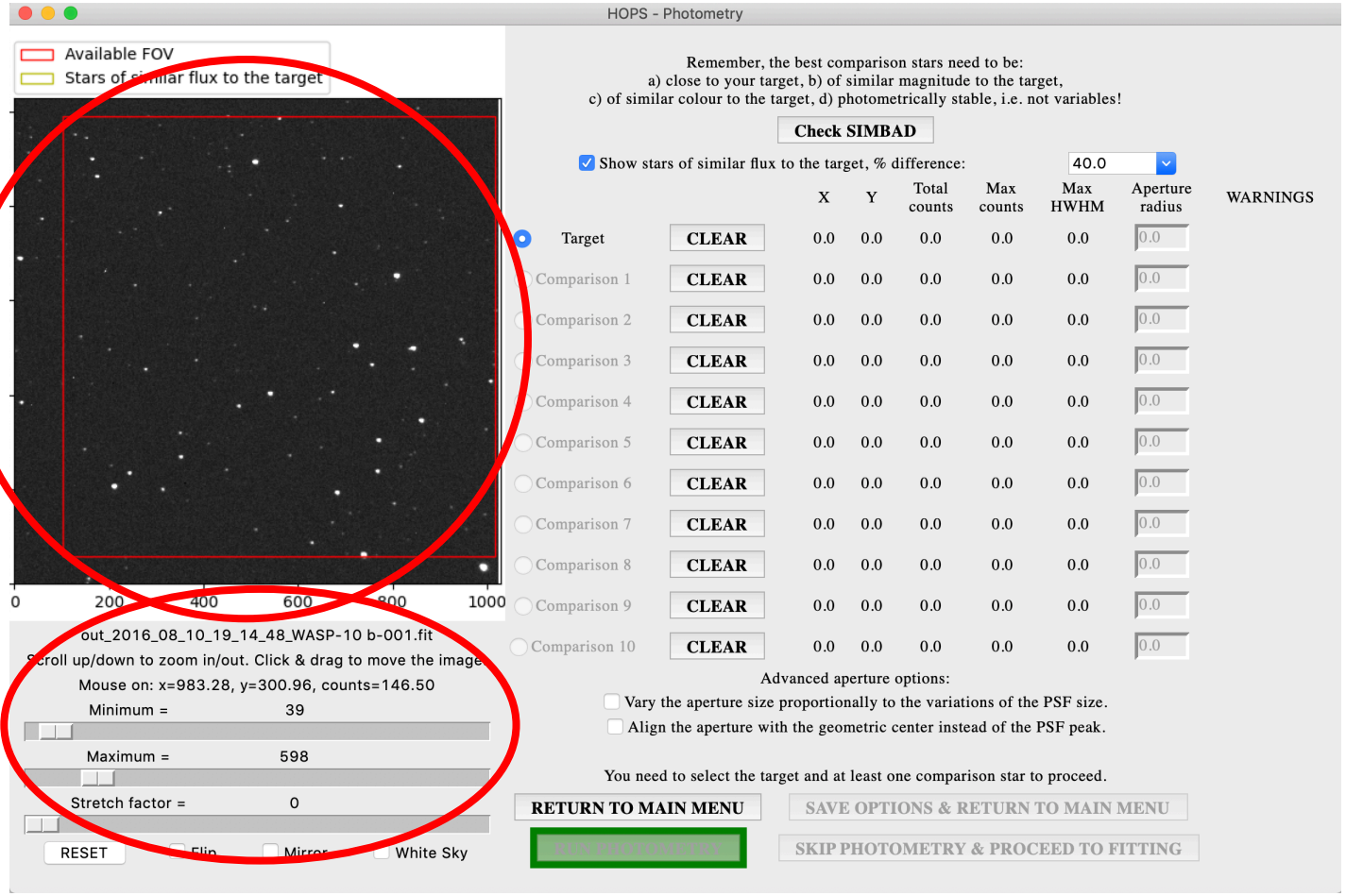


Photometry (selection)

At this stage you will can select your target and comparison stars. The graph on the left (a) shows your first image, with a red box indicating the stars that were inside your FOV for the whole observation (available FOV). You can zoom, move, flip, mirror, adjust the contrast or rest your image using the panel beneath it (b).

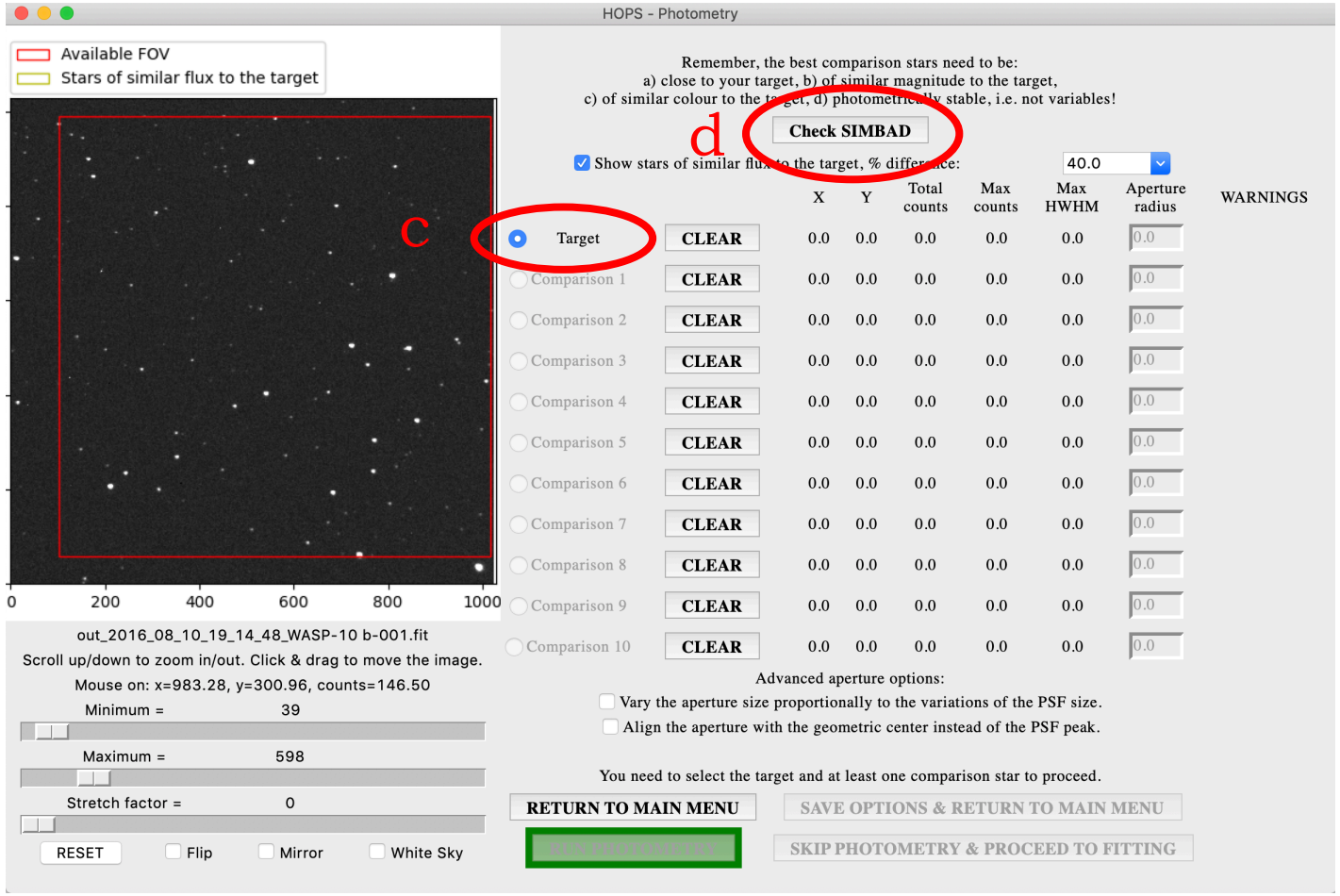
a

b



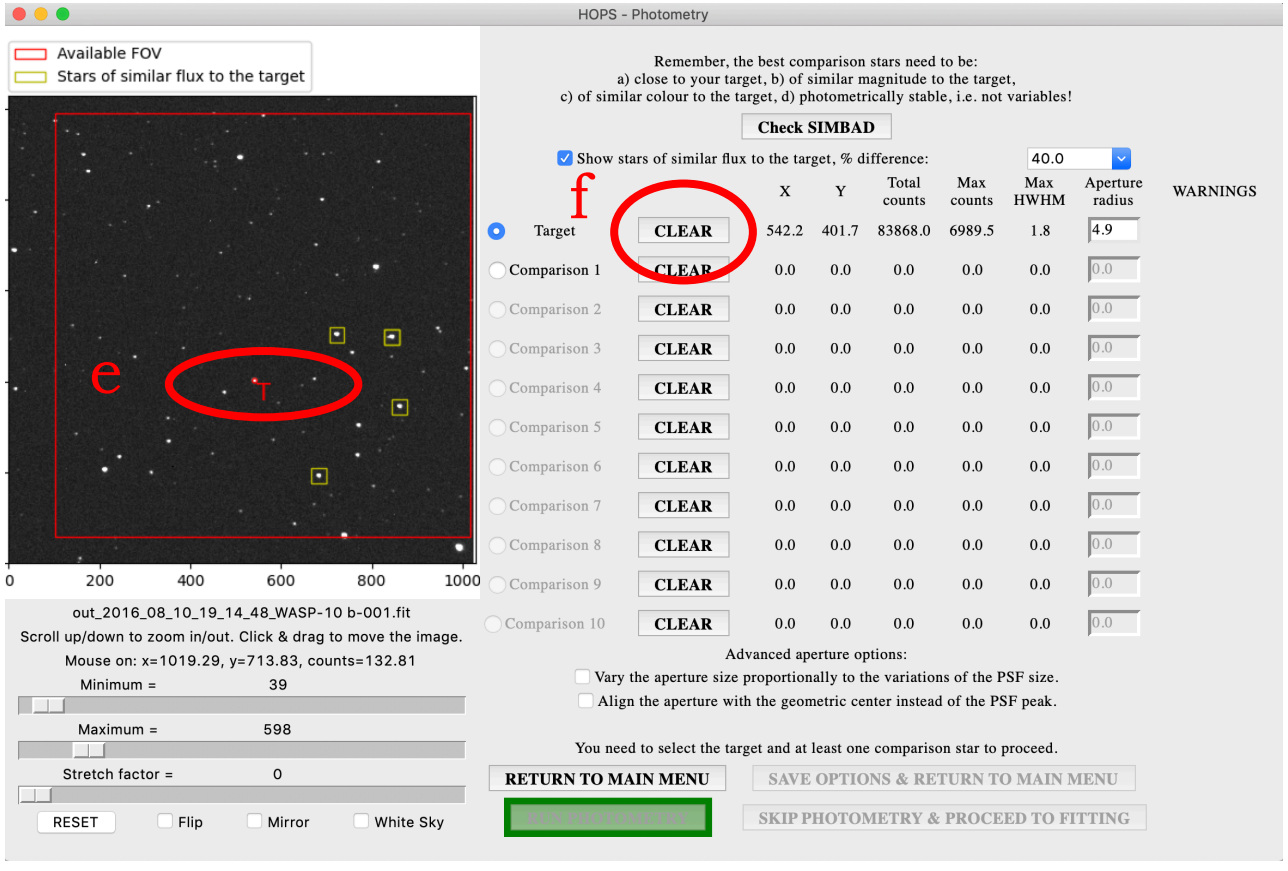
Select your target

Select the Target option (c), and try to identify your target in your image. If you cannot identify your target, you can cross-check your image with SIMBAD by clicking on Check SIMBAD (d).



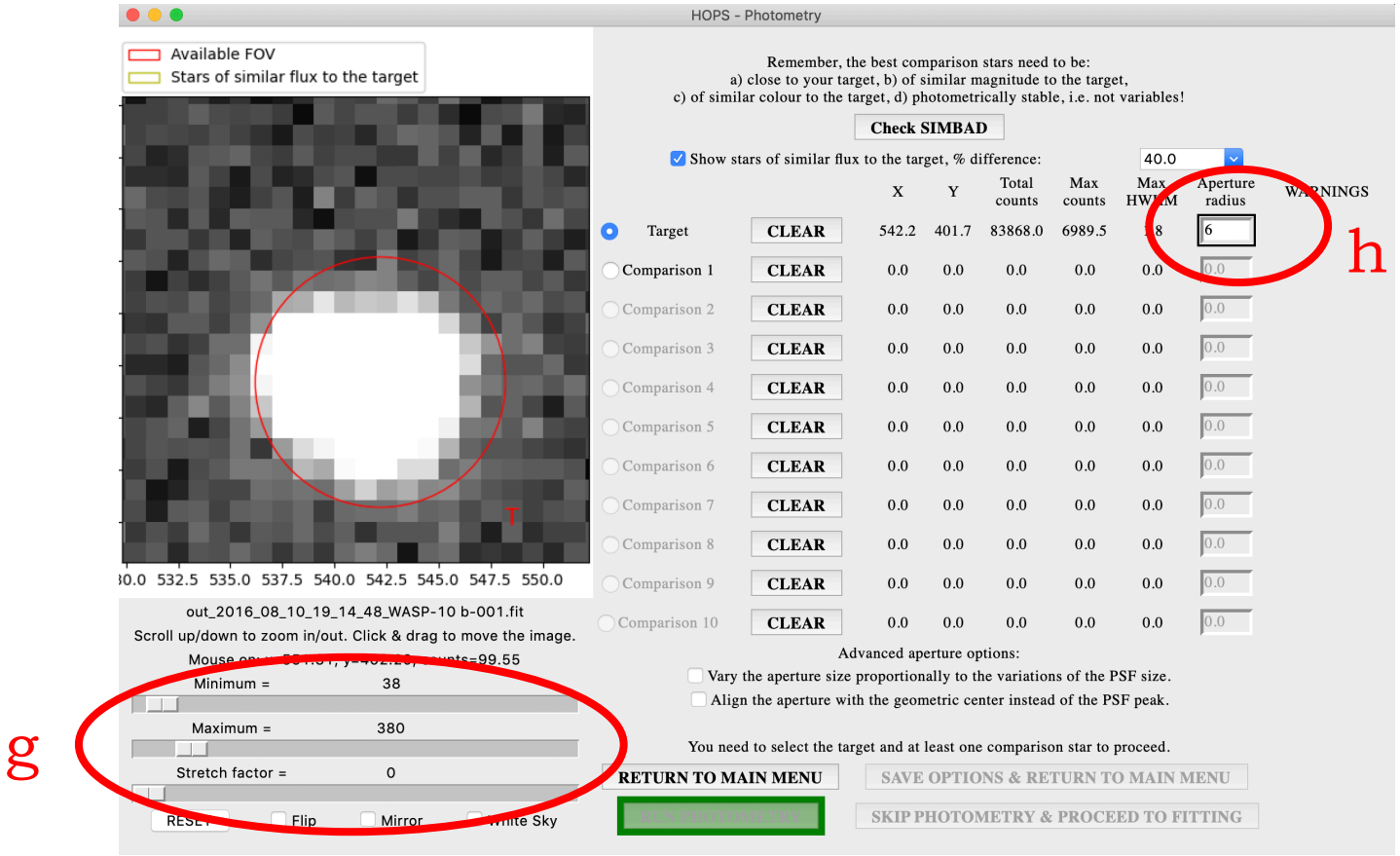
Select your target

Once you have identified your target double click on it (e) and a red circle will appear around it and the X, Y position, the total ana maximum counts and the max HWHM will be displayed next to the Target option. To replace your target double click on a different star. To clear your selection, click on Clear, next to the Target option (f).



Select your target aperture

Use the control panel beneath the image (g) to zoom-in to your target and modify the contrast so that you can see the full extend of your PSF. Enter your preferred aperture in the Aperture radius, next to the Target option (h). The aperture should enclose completely the star but avoid nearby stars (the default value is 1.4 times the collective FWHM of the stars in the image.



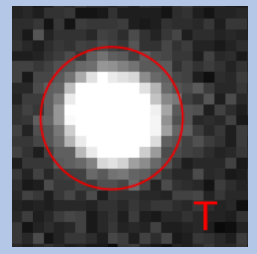
TIPS SECTION

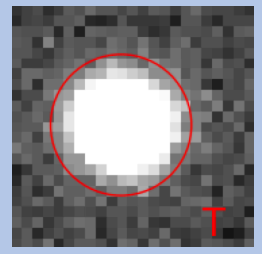
Select your target aperture carefully

Default aperture
Low contrast

Default aperture
high contrast

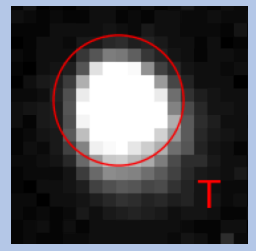
Well-shaped PSF



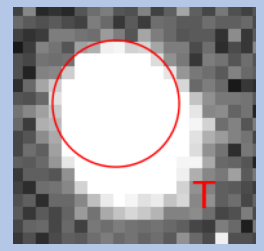


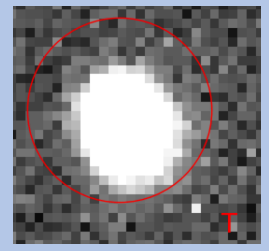
In this best case, even if you increase the contrast you will see that the aperture is including all of your star.

Trails

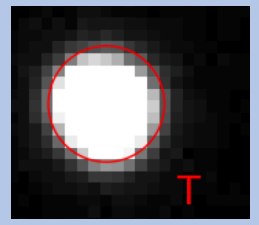


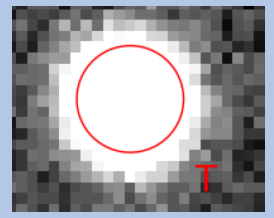
Increase the contrast to see the real extend of your PSF

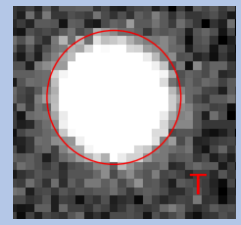




Extended PSF wings



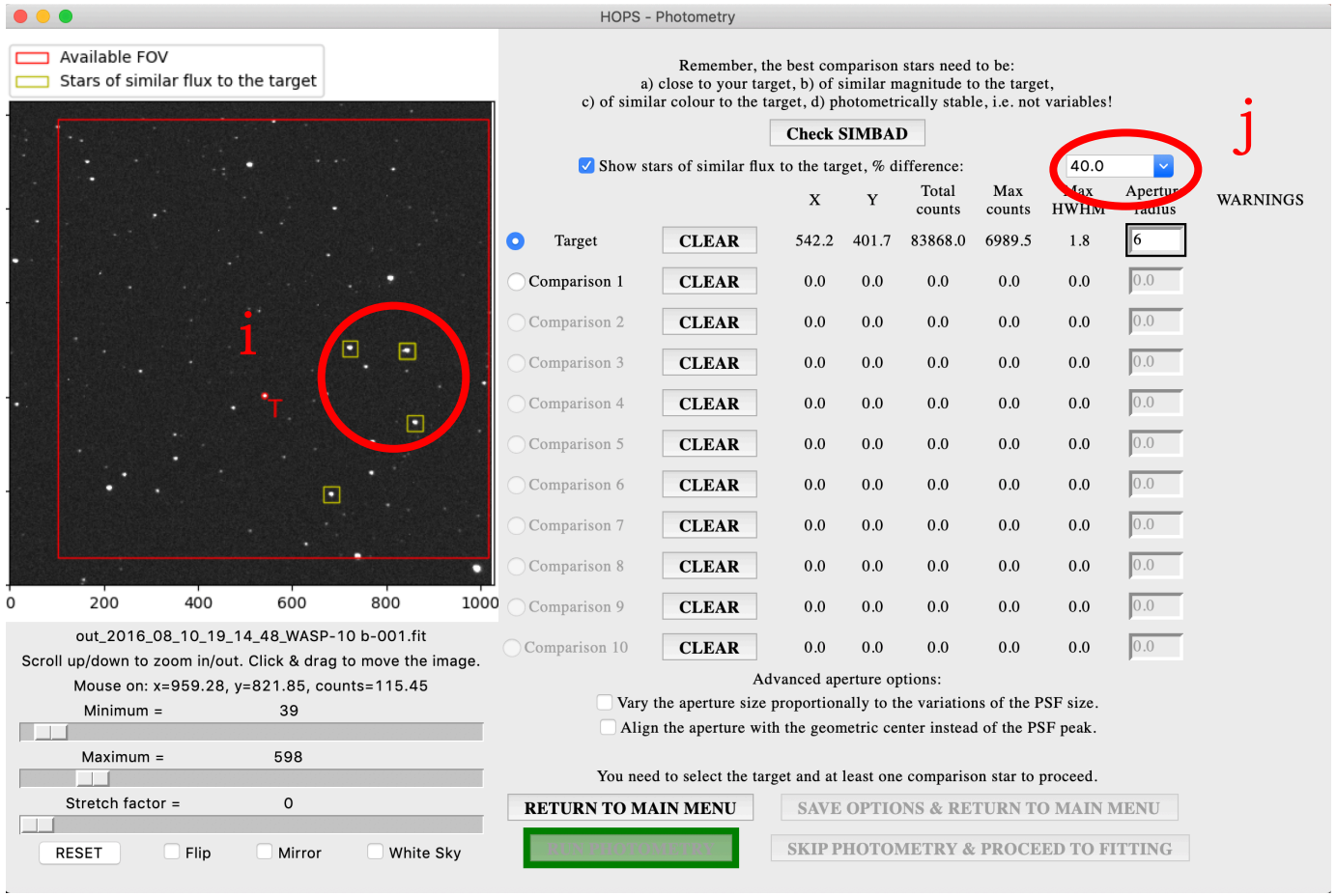




In these two cases, a larger aperture will give you better results. Experiment with it to find the best solution.

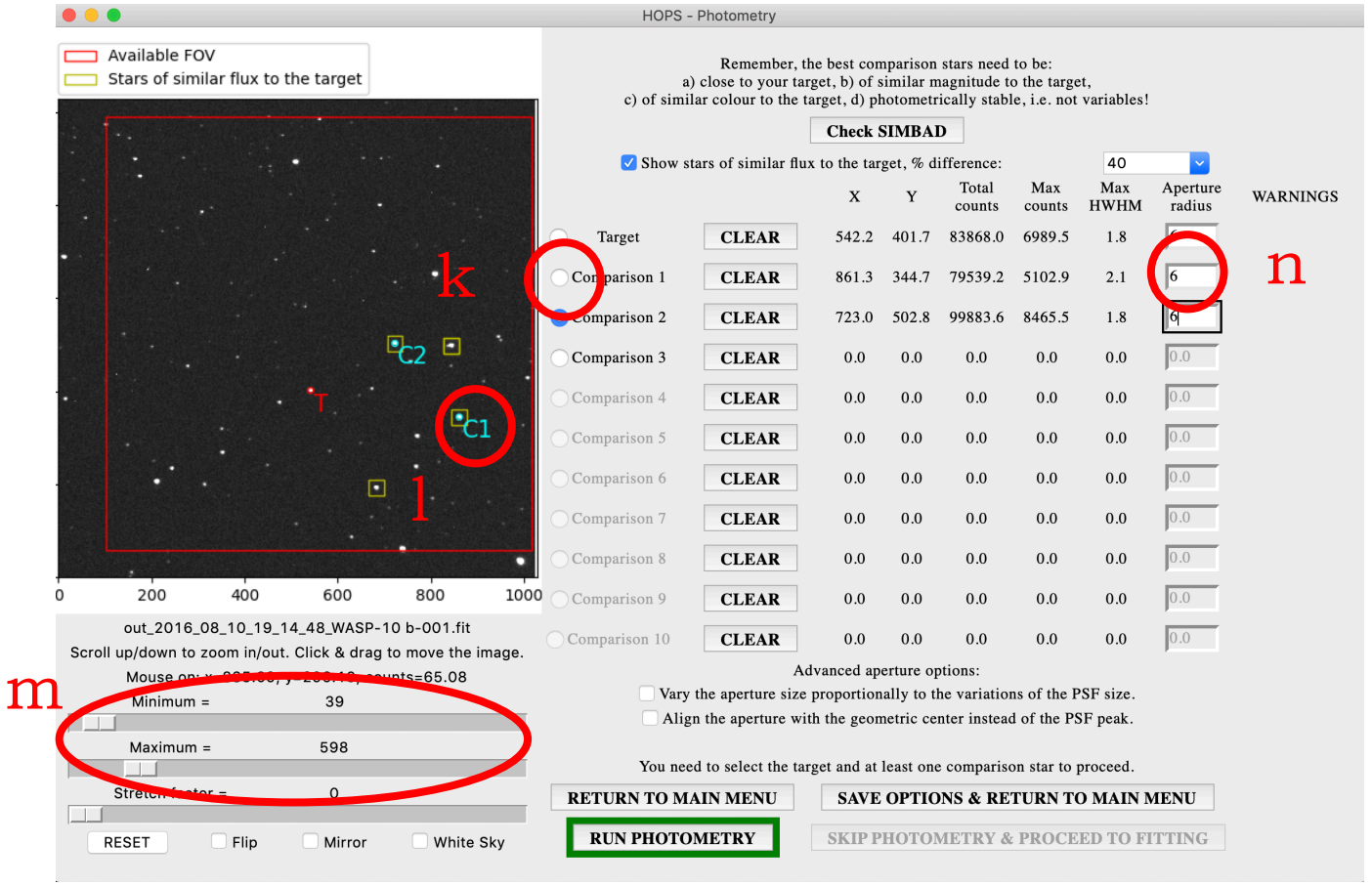
Select your comparison stars and their apertures

After selecting a target, a number of yellow boxes will appear, indicating stars of similar flux, as potential comparisons (i). You can adjust the level of similarity between the target and the proposed comparison stars from the % difference drop-down menu (j). The default is +/- 40 %.



Select your comparison stars and their apertures

Follow the same procedure as for the target and select between 1 - suggested minimum is 2 - and 10 comparison stars: select the Comparison X option (k), double click on the star you wish to select (l), adjust zoom and contrast to see the full extend of the star (m), and enter the aperture (n).



TIPS SECTION

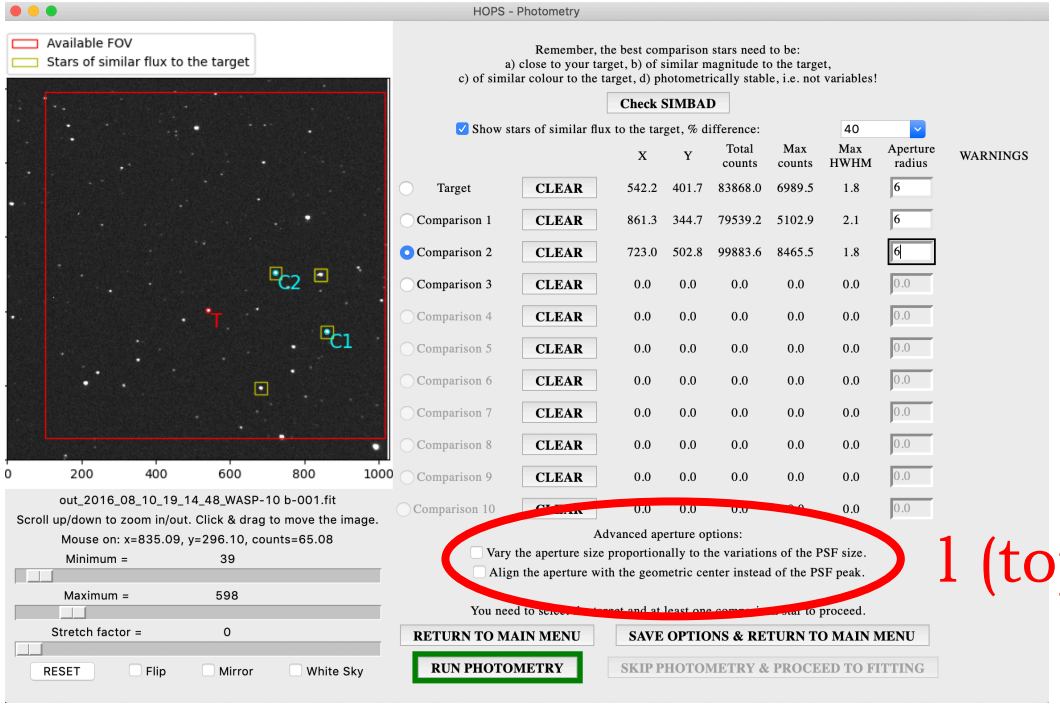
Choose your comparison stars carefully, as they affect significantly the quality of the final result. The general rules are that the comparison stars need to be:

- close to the target star;
- of similar magnitude to the star;
- of similar colour to the target star (check with SIMBAD of GAIA);
- stable, i..e not variables (check with SIMBAD or AAVSO or from the comparison light curves on a few pages later).

There is always the possibility that no good comparison stars exist. In this case you have to proceed with on-ideal comparison stars (very faint or very bright).

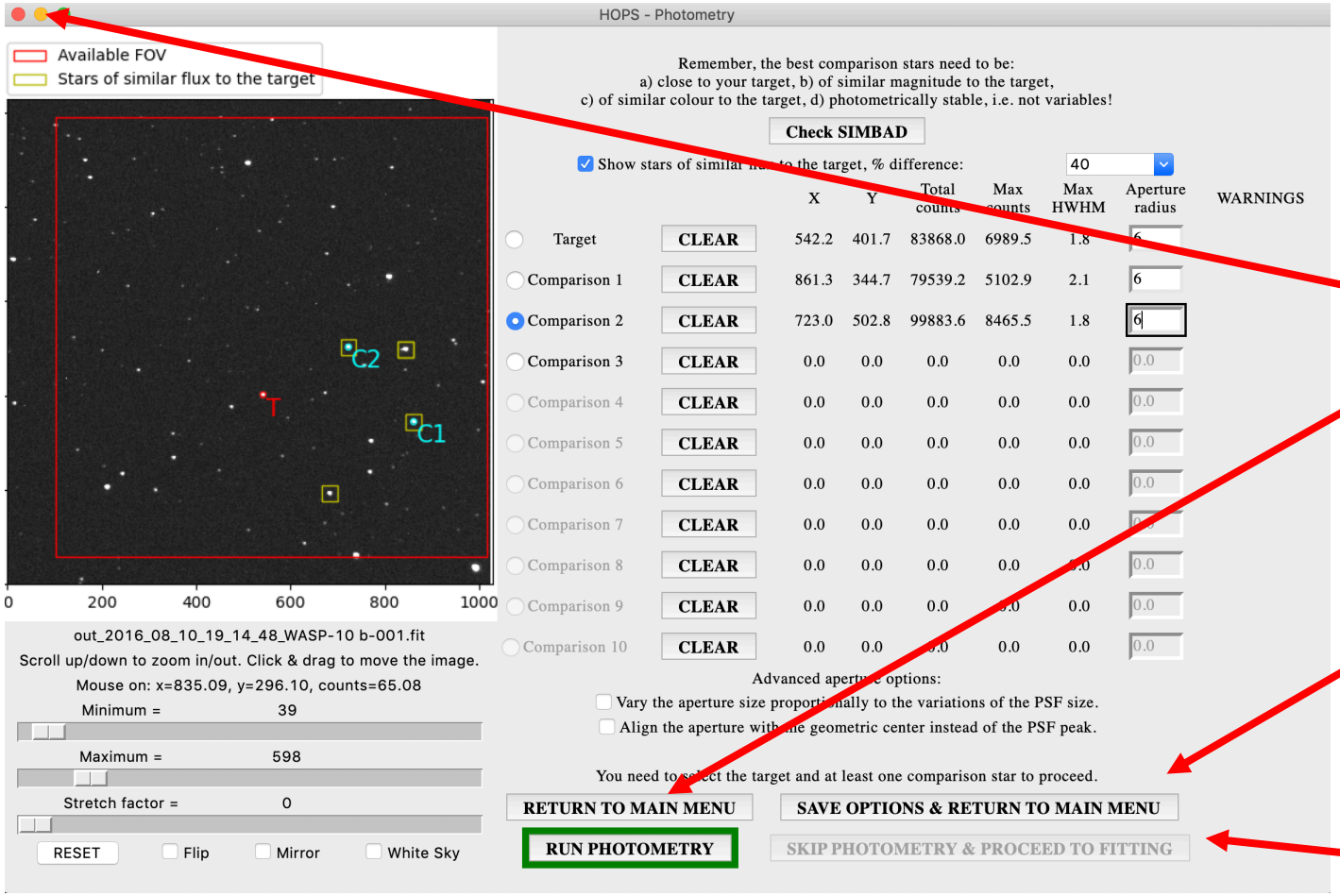
Advanced aperture options

If you believe that the PSF size is changing considerably during the observation you may wish to select the option to vary the aperture size proportionally to the variations of the PSF size (l). If your PSF suffers from strong asymmetries, you can select the option to align the aperture with the geometric centre of the star instead of the PSF peak (m).



l (top)-m (bottom)

Run photometry or proceed



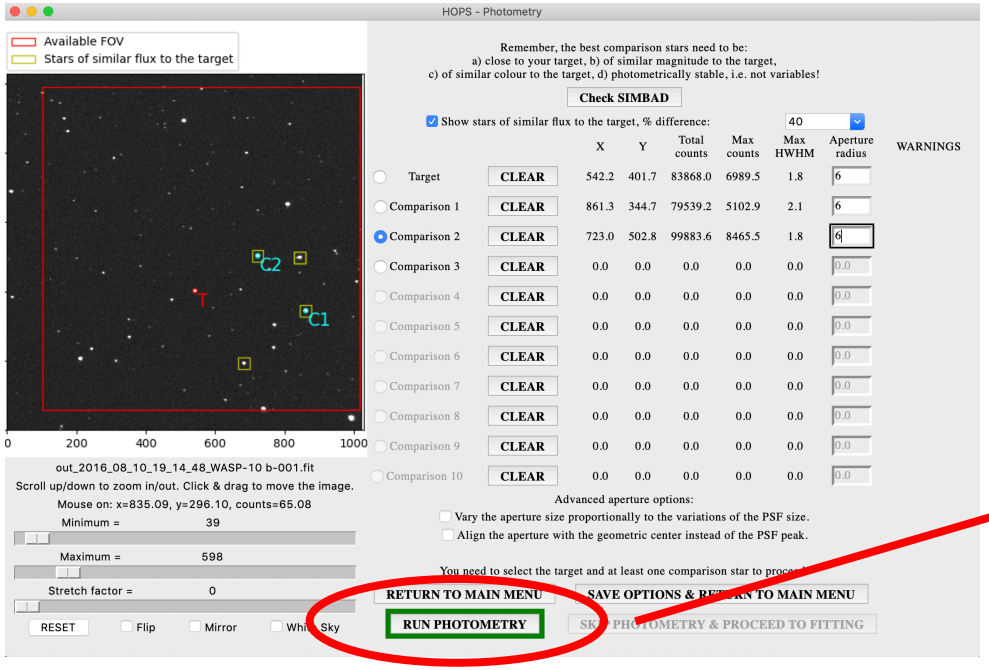
Return to the main menu without saving the current options.

Saves the current options and returns to the main menu.

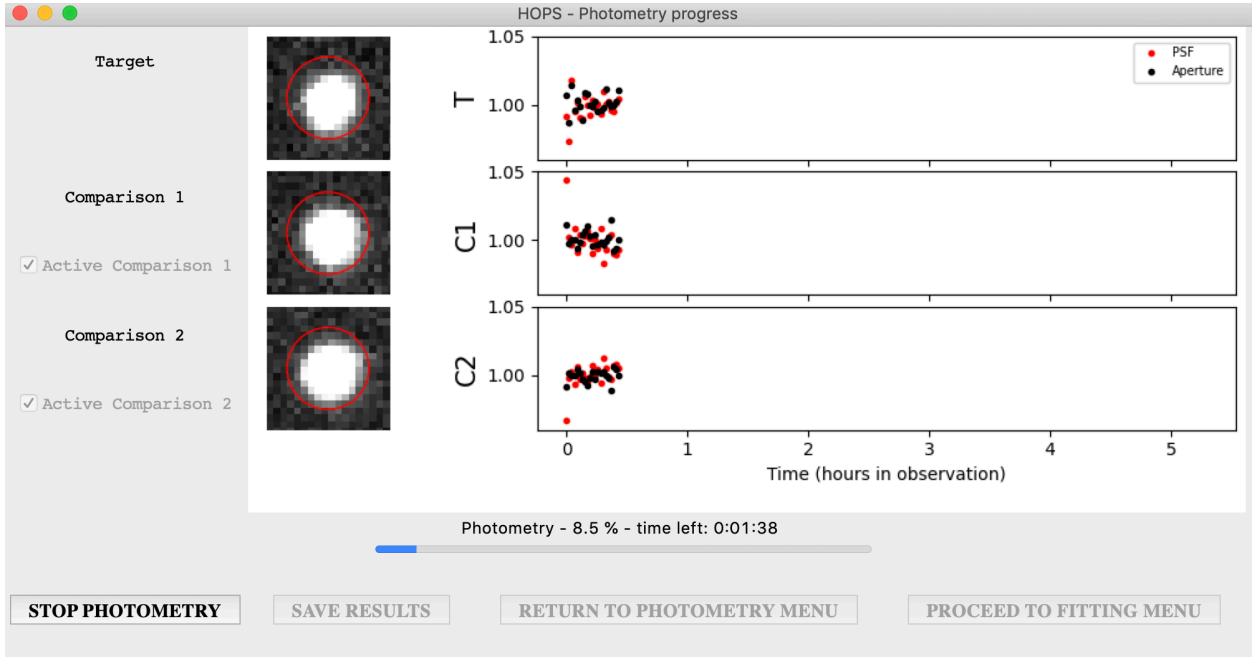
If photometry has been completed in the past, proceeds to the next step - fitting.

Runs photometry.

5b. Photometry (running)

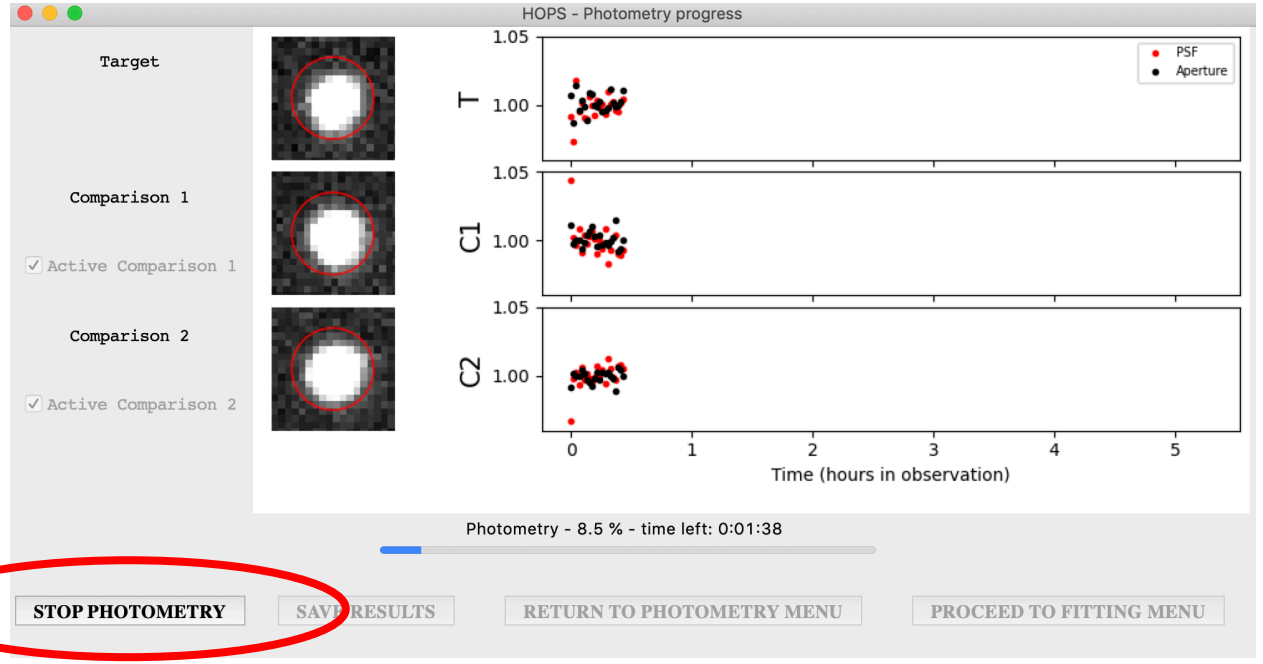


opens



Photometry (running)

At this step you don't have to do anything but wait for the photometry process to finish. Here, you can only interrupt photometry by clicking on Stop photometry (a), which will get you back to the main photometry menu, where you selected the target and comparison stars.



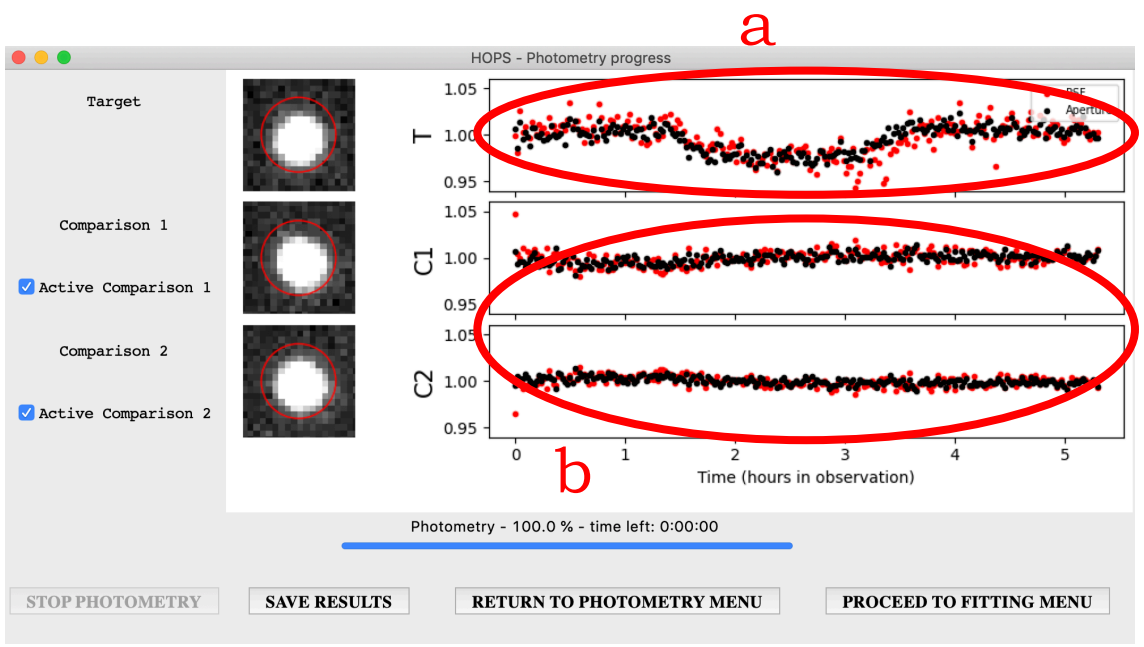
a

5c. Photometry (inspection)

on completion

Photometry (inspection)

At this step you can remove one or more of your comparison stars if you believe that their light curves have a negative impact on the light curve of the target. On the right, you can see a number of light curves, one for every star selected. The first (a) is the light curve of the target divided by the sum of the light curves of all the comparison stars. Every other one (b) is the light curve of one comparison star divided by the sum of the light curves of all the other comparison stars.



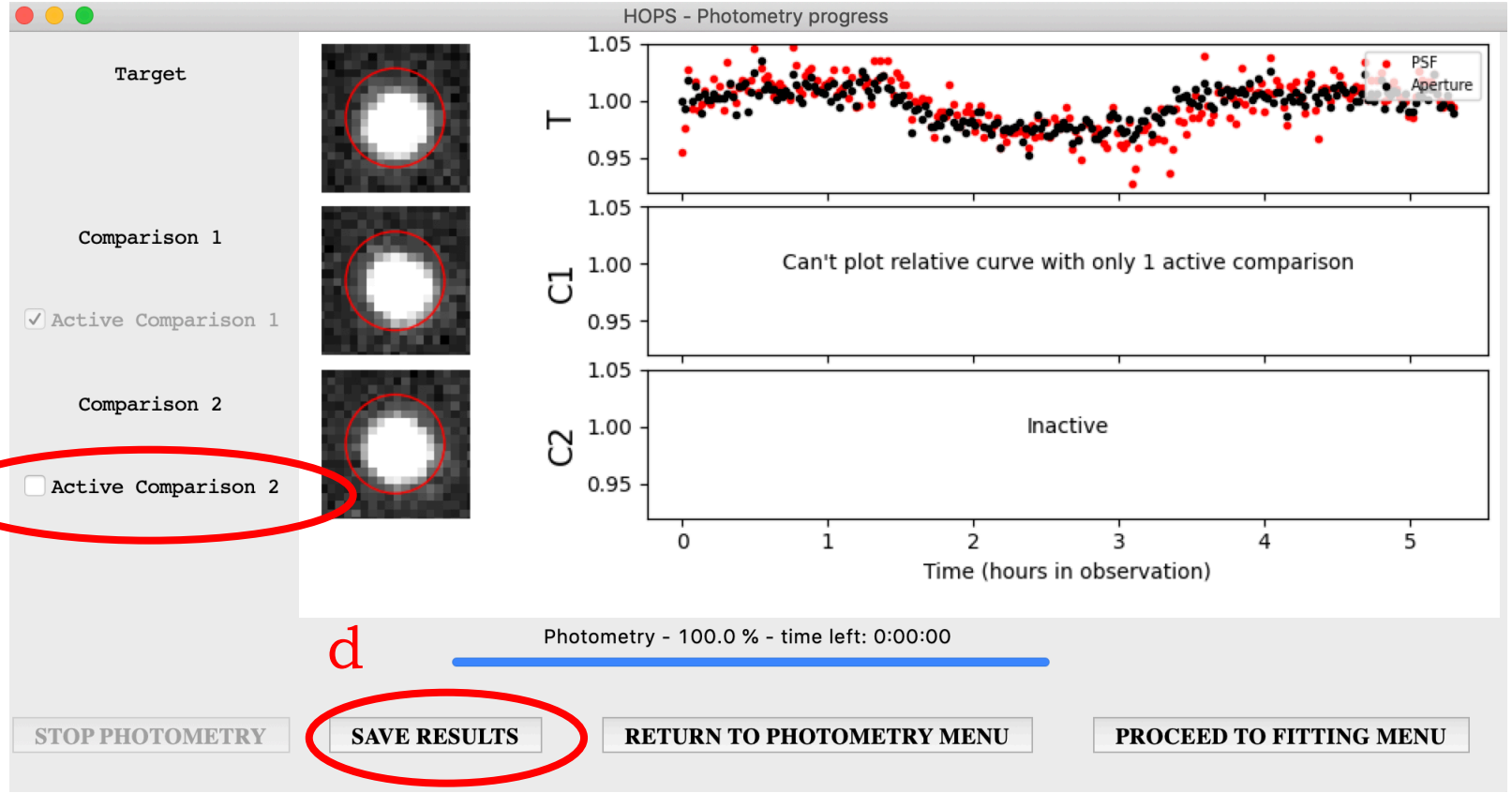
Target / (Comp.1 + Comp.2)

Comp.1 / Comp.2

Comp.2 / Comp.1

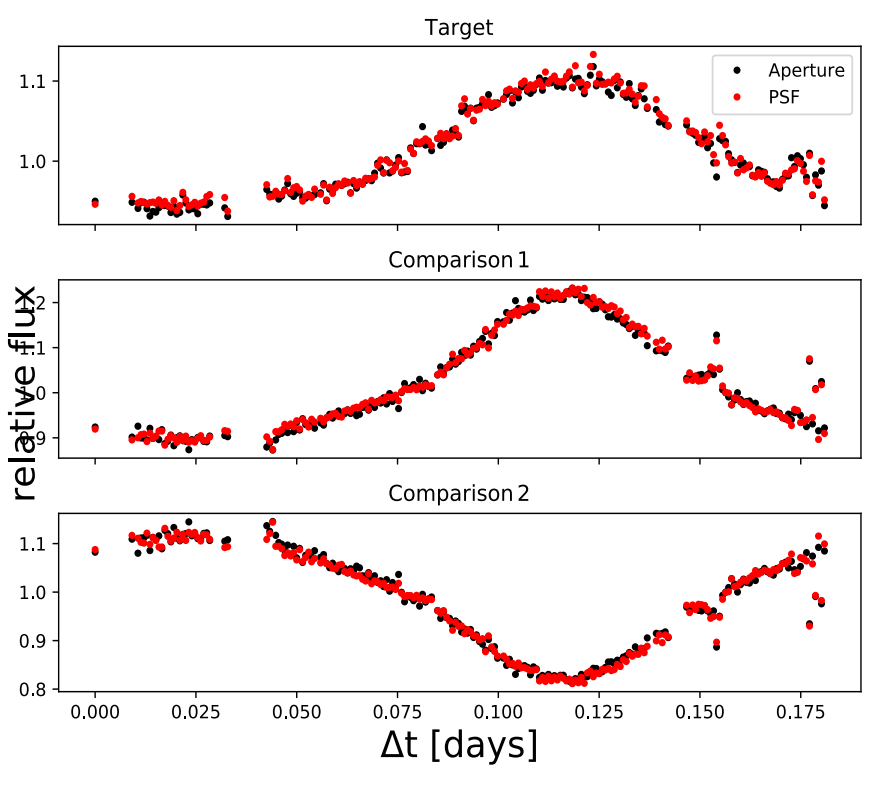
Remove comparison stars

To remove one comparison star you can de-select the respective option Active Comparison X, on the left (c). The results will be plotted again. Note that if only one comparison star is active, you will only see one light curve (the target's light curve). **If you remove one or more comparison stars, do not forget to save the new photometry results (d)!**



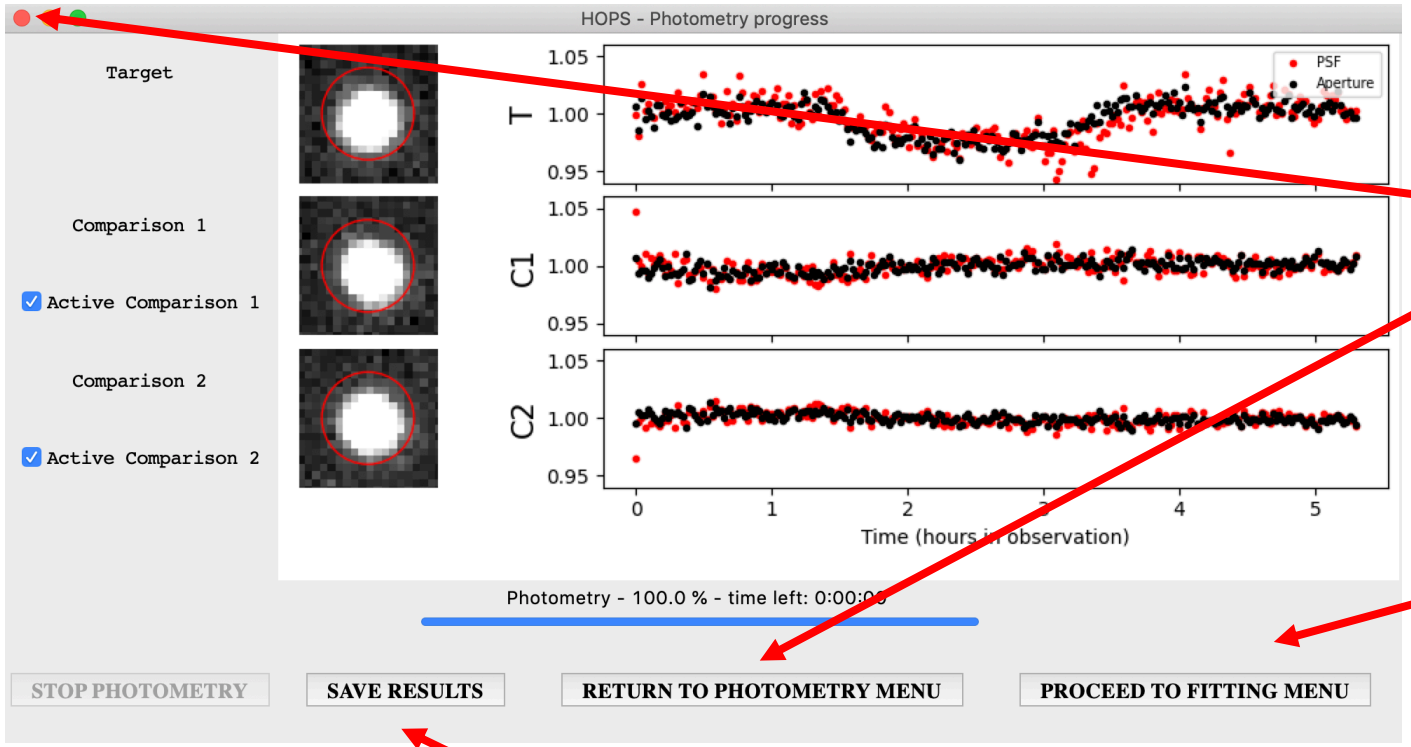
TIPS SECTION

If one comparison star is variable, you will see its light curve is **anti-corelated to all the other light curves, including the target's light curve**.



In this example from a difference dataset, the variable star is Comparison 2

Proceed

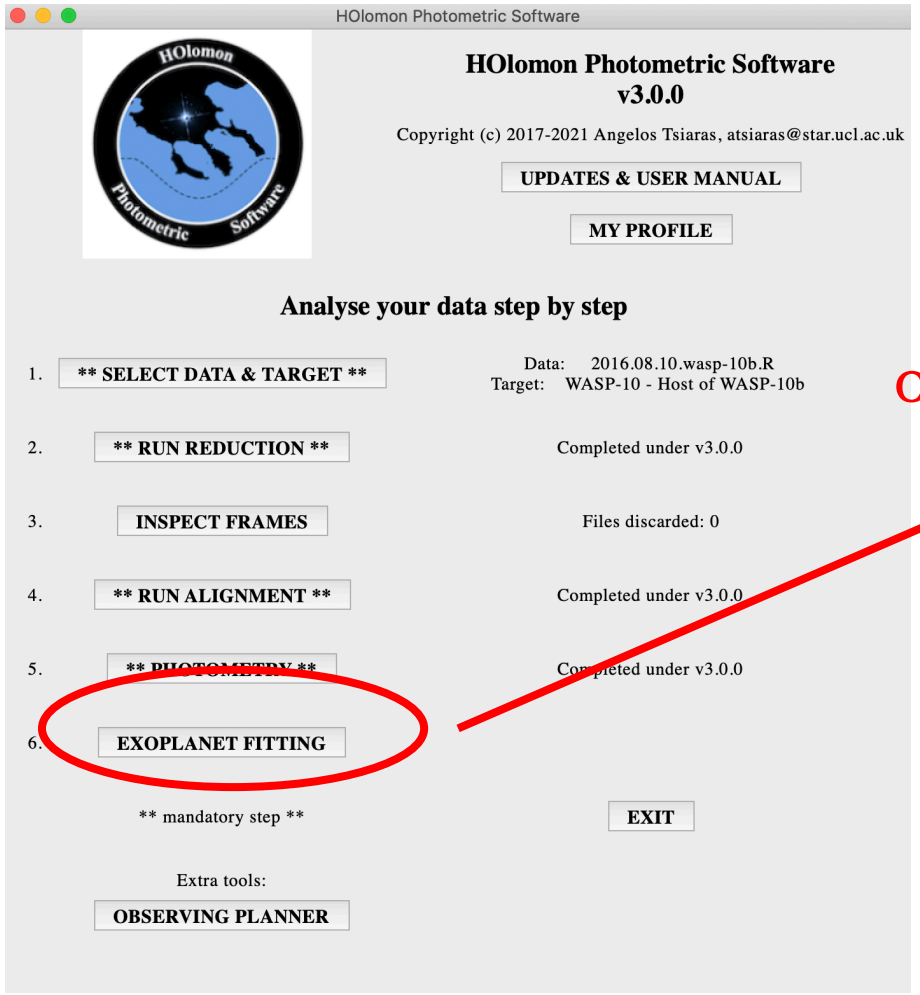


Return to the main photometry menu, where you selected the target and comparison stars.

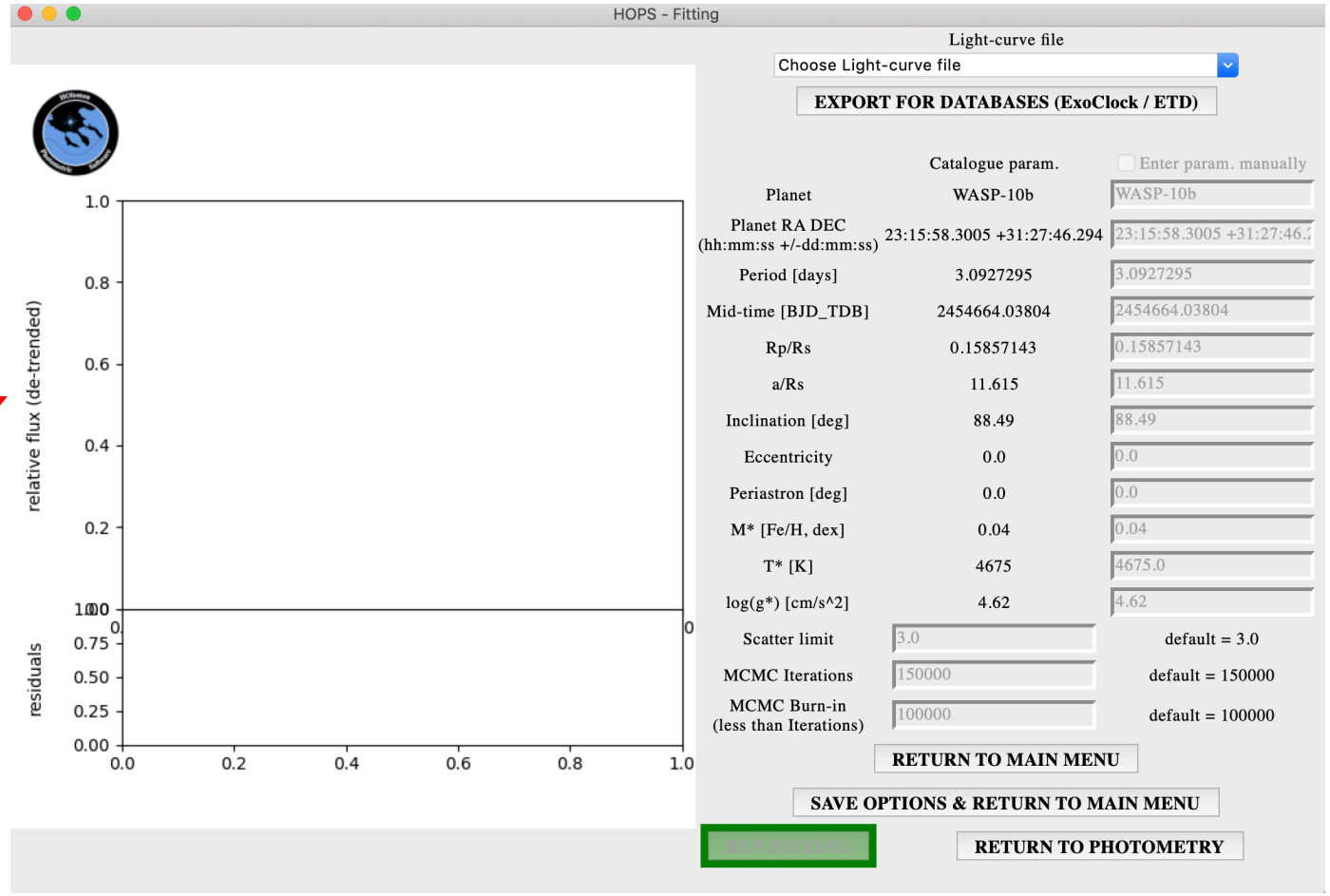
Proceeds to the next step - fitting.

Saves new results.

6a. Fitting (selection)

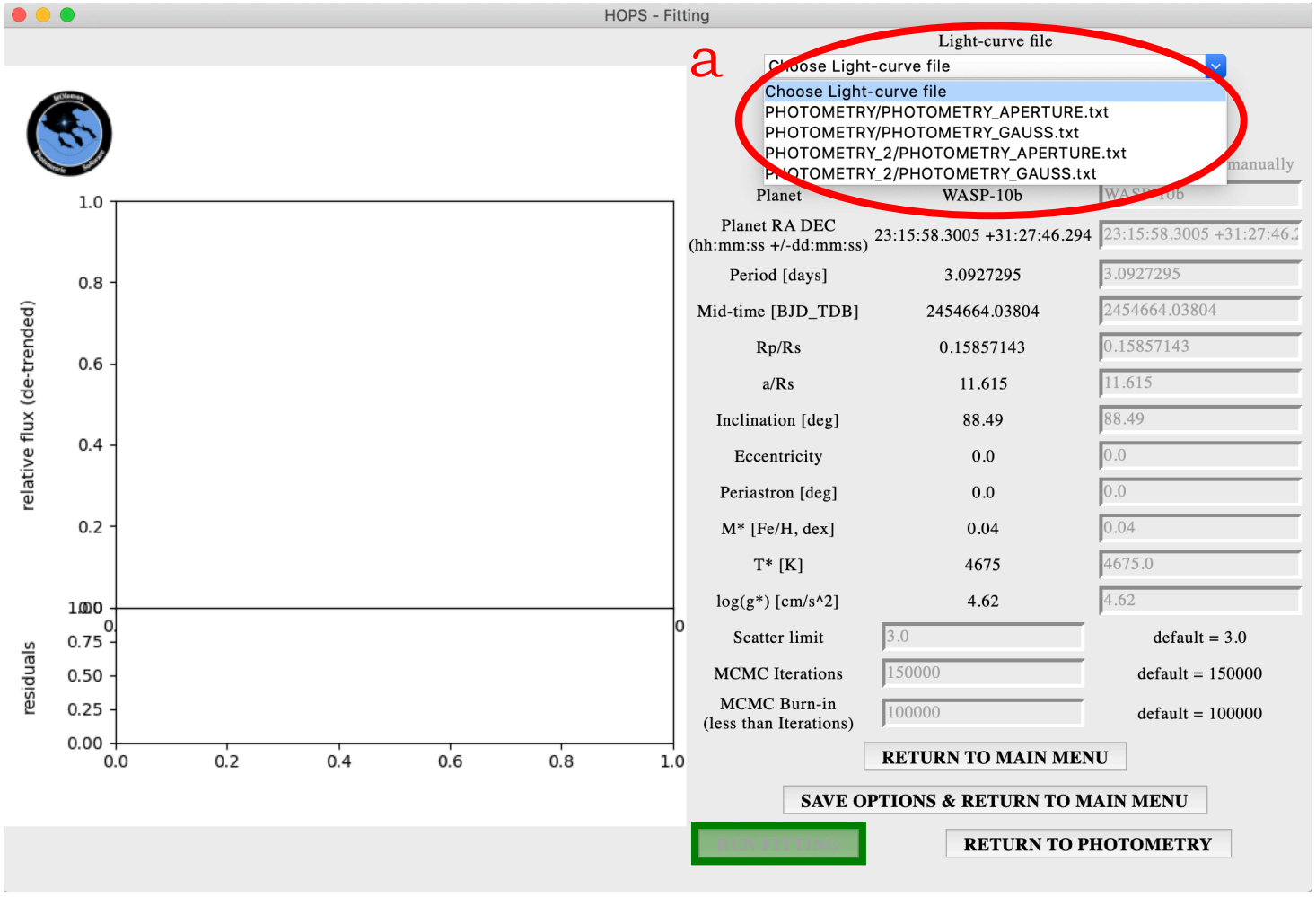


opens



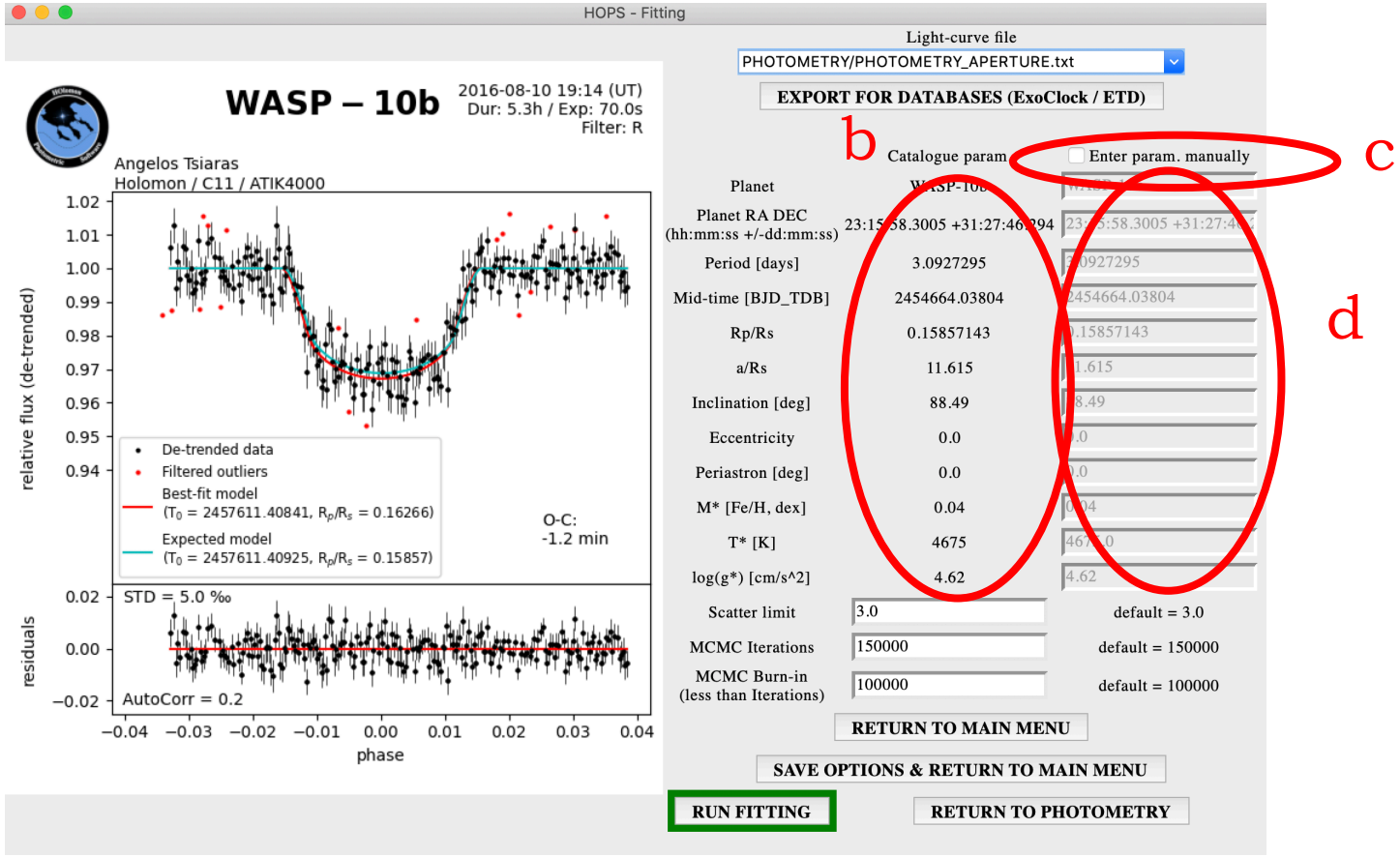
Select a light curve

Choose the light curve you want to fit form the Light-curve file drop-down menu (a), you can choose between aperture of PSF fitting (GAUSS) and the different attempts of photometry that you tried.



Enter the planet parameters

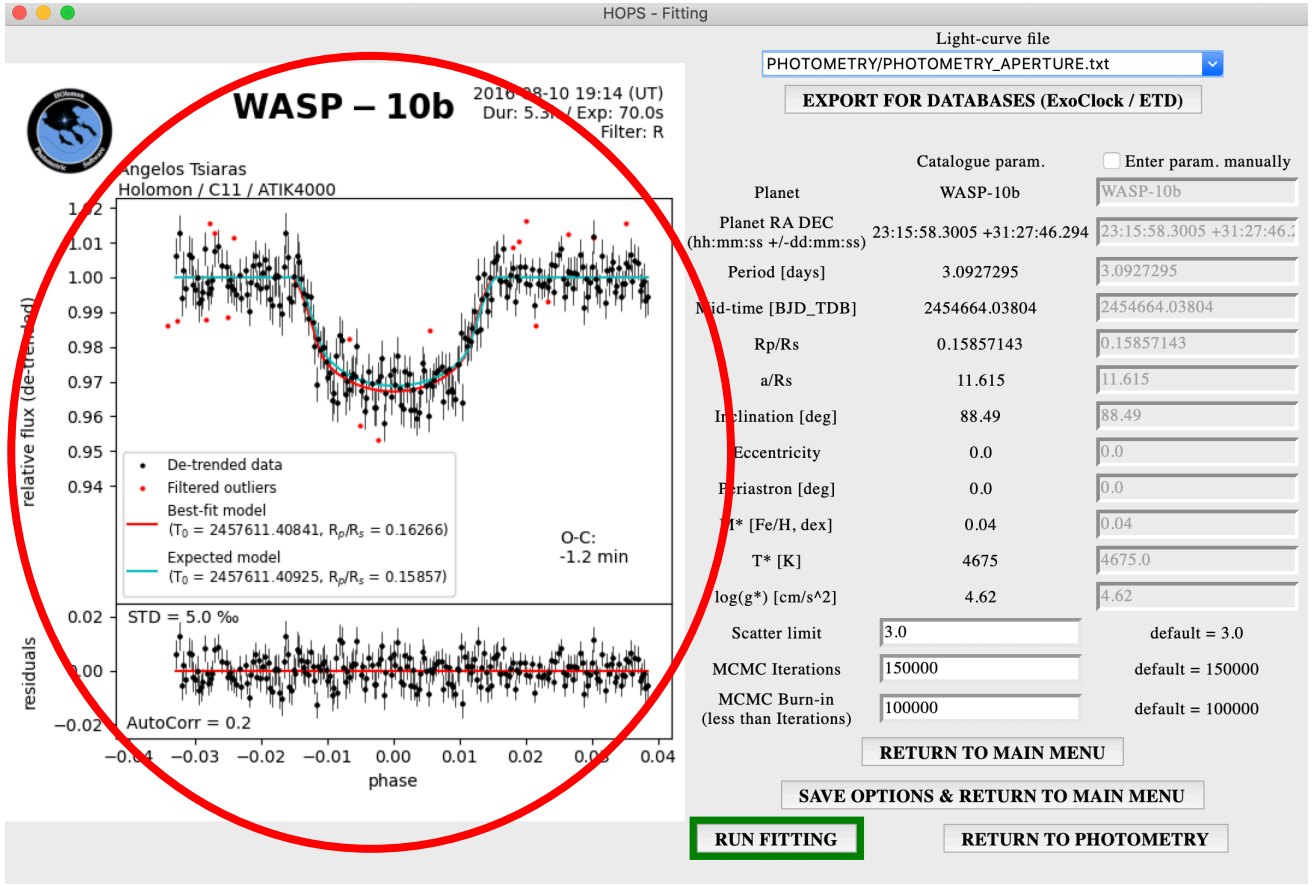
The parameters of the exoplanet that is the closest to your coordinates will be chosen from a built-in catalogue (b). This catalogue contains about 400 exoplanets but not all of them. If this is not your target, or if you want to change the default values, select the Enter param. Manually option (c) to activate the manual entries (d).



Check the fitting preview

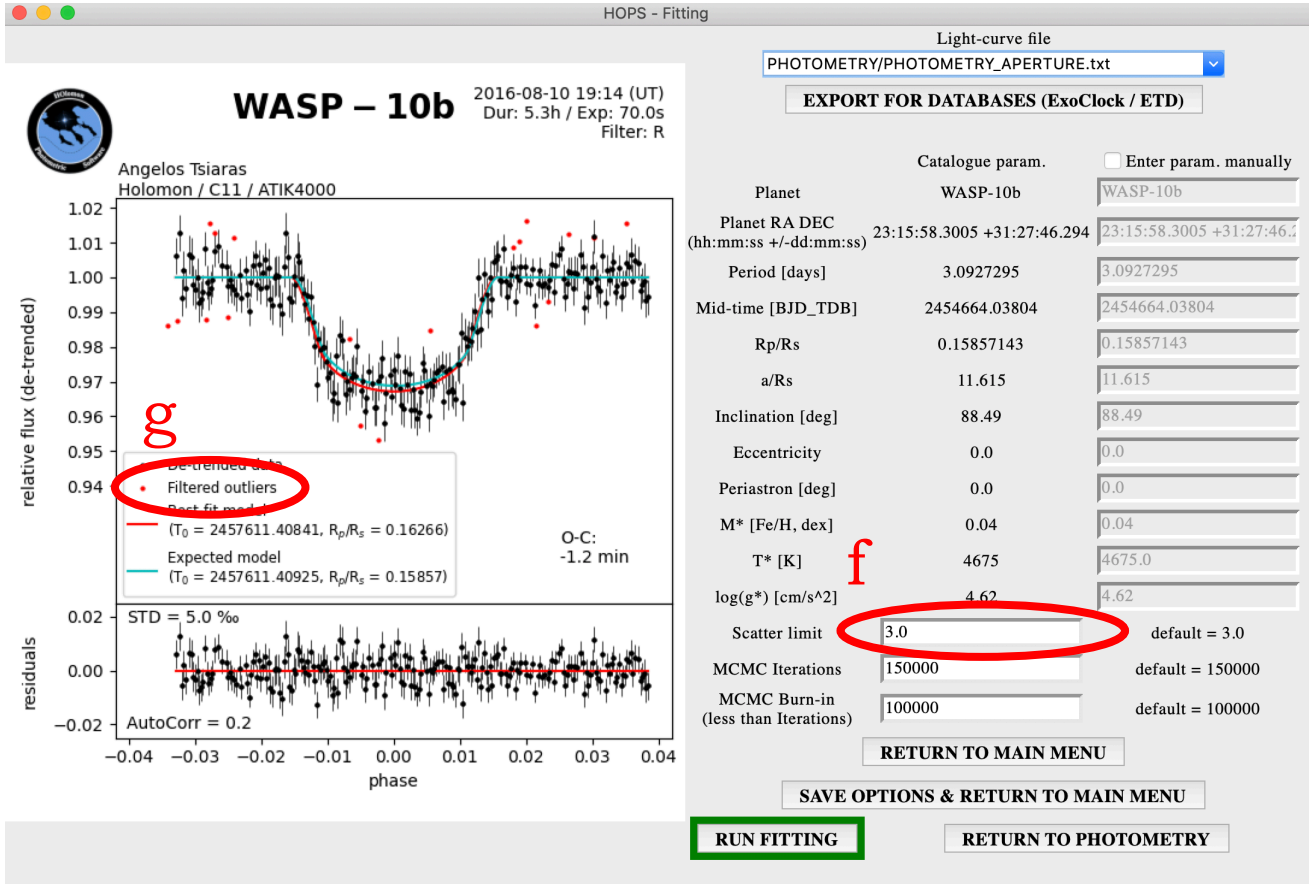
At this stage, you will be able to see the fitting preview on the left (e). In this graph, the data have been corrected for a quadratic term (de-trended). The models plotted represent the best-fit model on the data (not MCMC) with red, and the expected model based on the parameters you have provided with cyan. This graph also shows the fitting residuals and some diagnostics on them (STD and autocorrelation)

e



Filter outliers

Enter the Scatter limit (f), a parameter based on which the outliers are filtered out. The lower the value, the more sensitive the filtering process is (i.e. more point will be excluded). Reasonable values are above 3, otherwise too many point will be excluded. The excluded points appear red on the graph (g).



TIPS SECTION

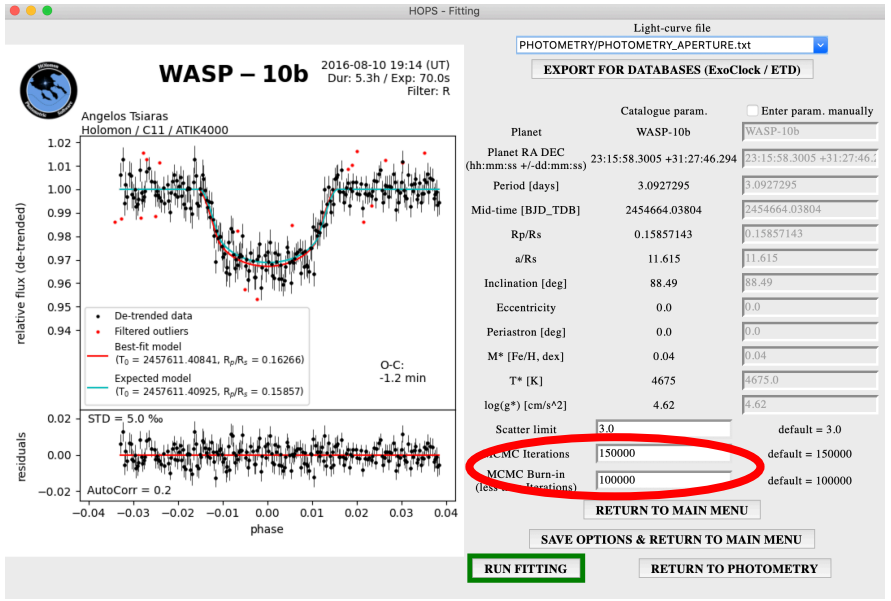
Evaluate the fitting preview before hitting the Run Fitting button. This is an important part of the process. It will tell you if your data are good to a level that results can be extracted.

First check the compatibility with the expected model, especially the transit depth. If you find large inconsistencies you may need to go back to photometry and pick deferent comparisons, or go back to reduction and check your flat frames. You will realise that changing comparisons can affect your final results a lot! **This is usually due to airmass effects caused by comparison stars of different spectral types. A way to be safe is to 1) get good flat fields, 2) observe long before and after the transit and 3) keep your stars within the linear response range of your camera.**

P.S.: The residuals are the difference between your data and the best model. STD and AutoCorr are the standard deviation and autocorrelation of the residuals, respectivelly. The smaller these numbers, the better the fitting!

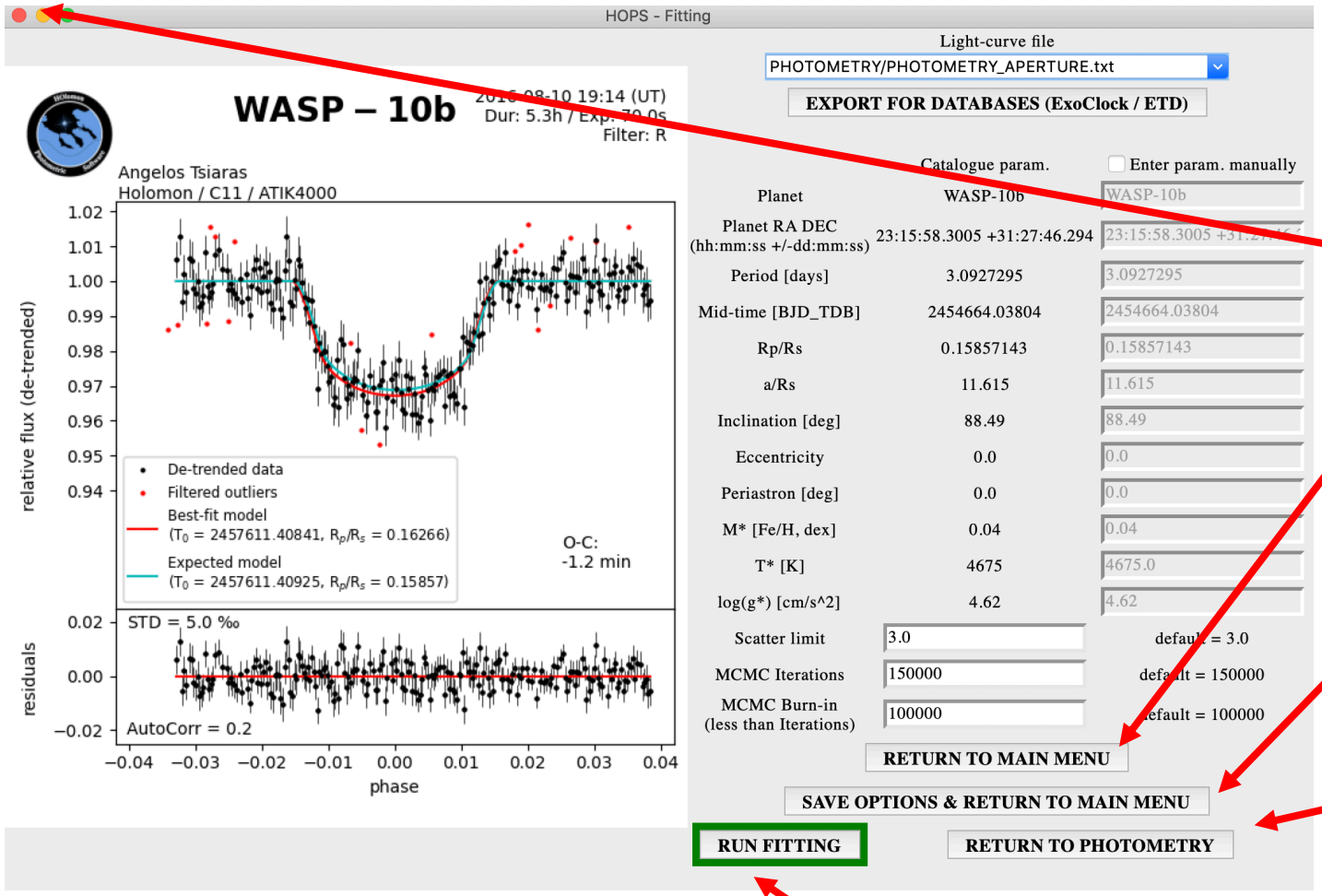
Adjust the MCMC parameters

HOPS uses MCMC fitting, which is a process that tries to reach the best result by approaching it in small steps. The number of steps is indicated by the MCMC iterations (h). The default value of 150000 should be sufficient but if the result is not good (very noisy light curve) you may need to increase it to 200000. The MCMC burn-in parameter states how many of the initial steps should be ignored and the default value is 100000. This is because in the beginning the algorithm is trying to "find its way towards the best solution" and the results are still unstable. If you increase MCMC iterations, increase MCMC burn-in accordingly but do not exceed The MCMC iterations value.



h

Proceed



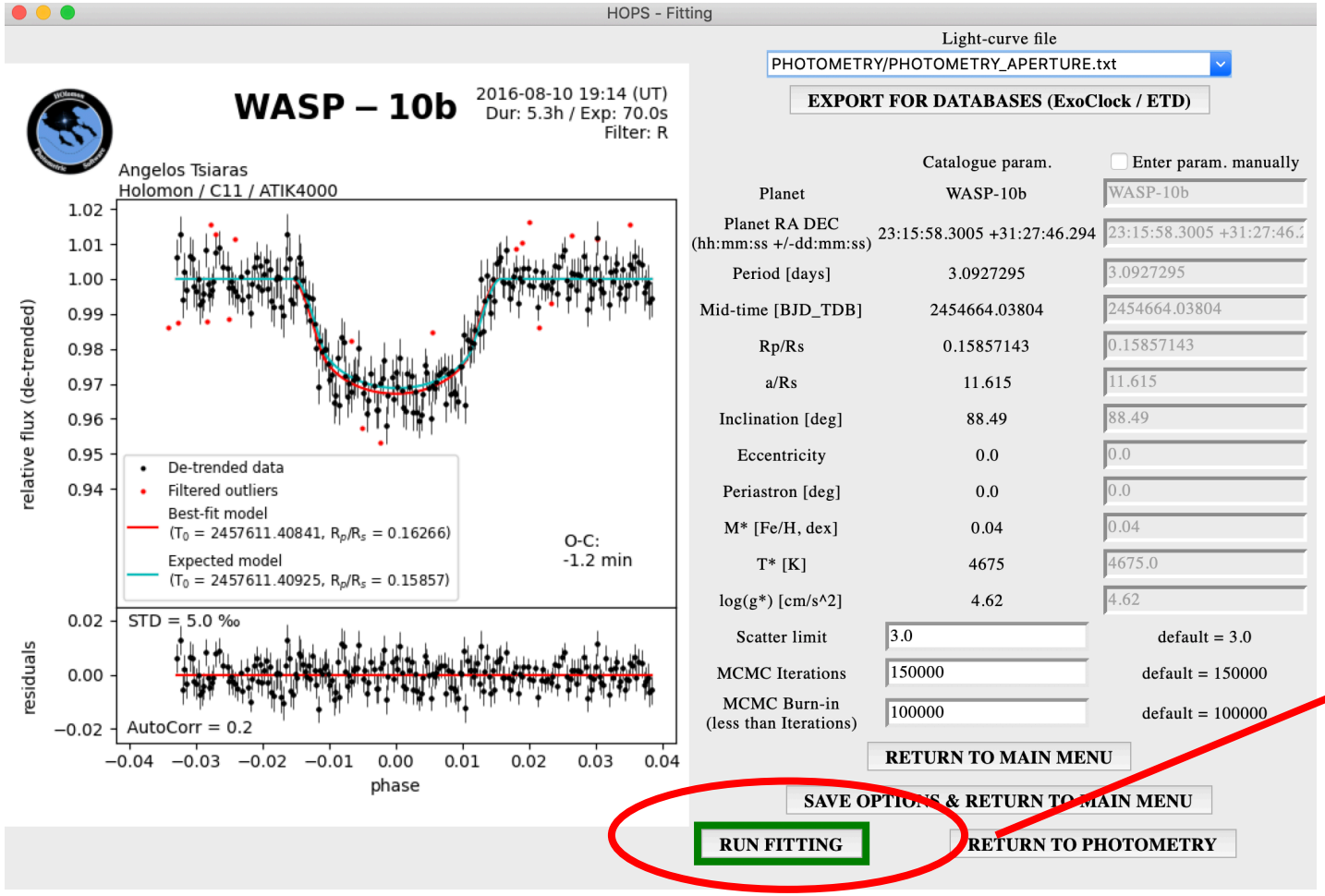
Return to the main menu without saving the current options.

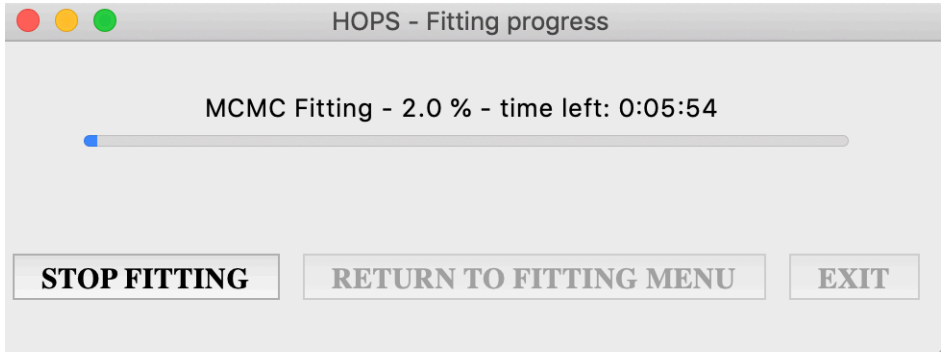
Saves the current options and returns to the main menu.

Saves the current options and return to the previous step – photometry.

Runs Fitting.

6b. Fitting (running)

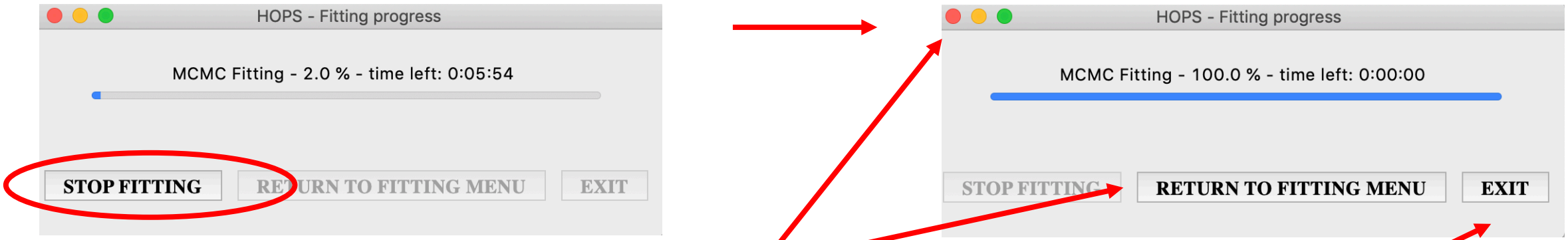




opens

Fitting (running)

At this step you don't have to do anything but wait for the fitting process to finish. Here, you can only interrupt fitting by clicking on Stop fitting (a), which will get you back to the main fitting menu, where you selected the light curve and the planet parameters.



a

Return to the main fitting menu, where you selected the light curve and the planet parameters.

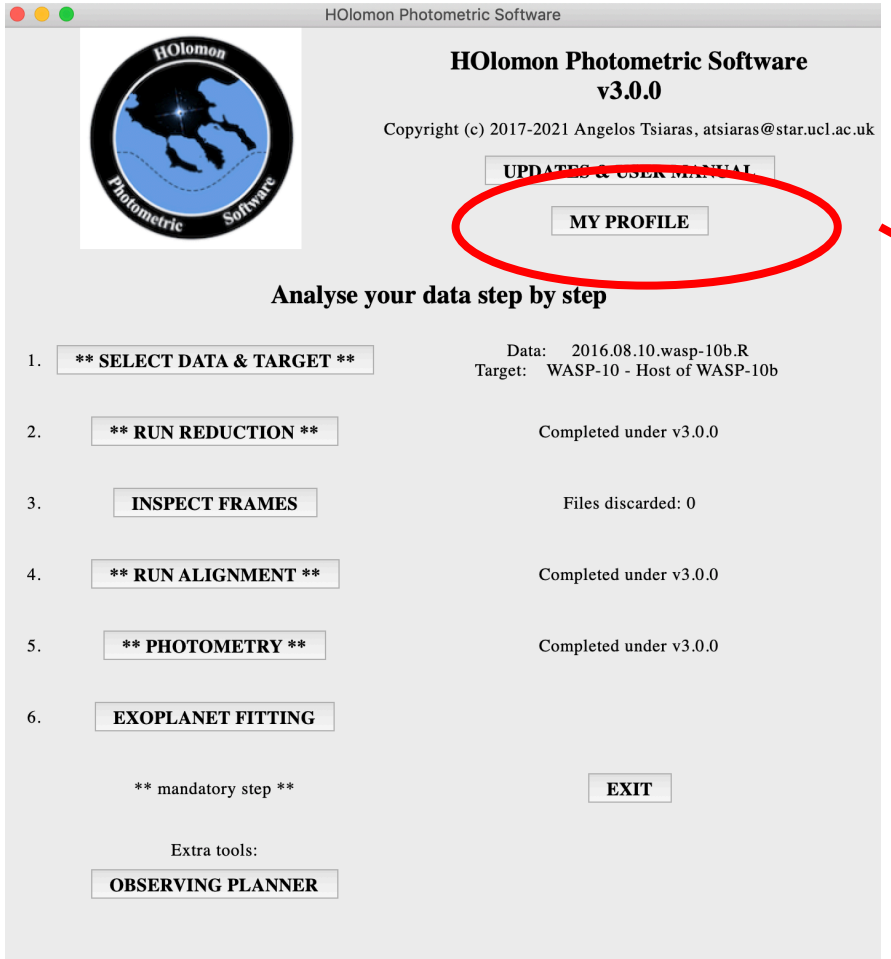
Return to the main menu.

Output

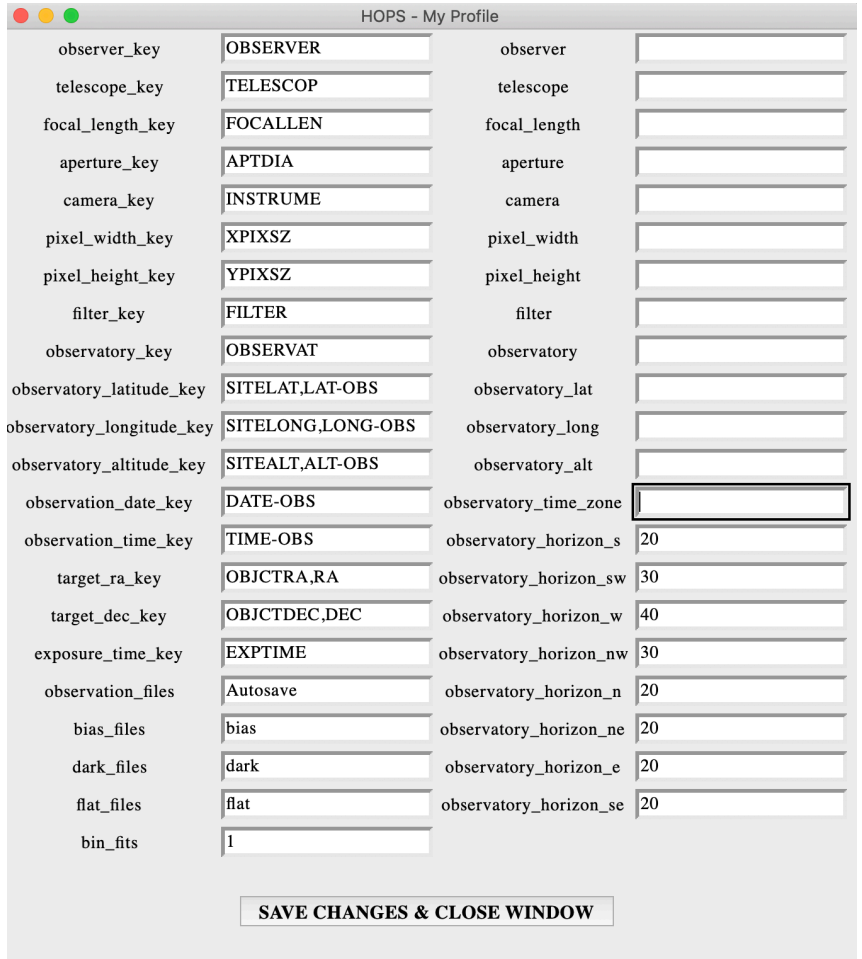
HOPS will create 3 new files and at least 2 new folders inside your initial data directory:

- log.yaml, all_frames.pickle, all_stars.pickle - supporting files (DO NOT DELETE THEM!)
- REDUCED_DATA – folder that contains the reduced data (DO NOT DELETE OR ANOTATE DATA in this folder, if you want to do so, work with the raw data and perform reduction again)
- PHOTOMETRY – folder that contains the photometry results, one for each time you run photometry or saved the photometry results.
- PHOTOMETRY_APERTURE_FITTING or PHOTOMETRY_GAUSS_FITTING (included in the photometry folder) – folders that contains the fitting results on the aperture or gauss light curves, respectively, one for each time you run fitting on this specific light curve.
- Included in the PHOTOMETRY and the FITTING folders you will find .txt files with more detailed descriptions of the output.

My Profile



opens



My Profile

If you want to save time when using HOPS you can set default values for some of the parameters used through the process, like the name identifier for the observation and reduction frames, of your personal data. At the moment only those encircled are actively used during the analysis.