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

v 2.6

USER MANUAL

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Prerequisites

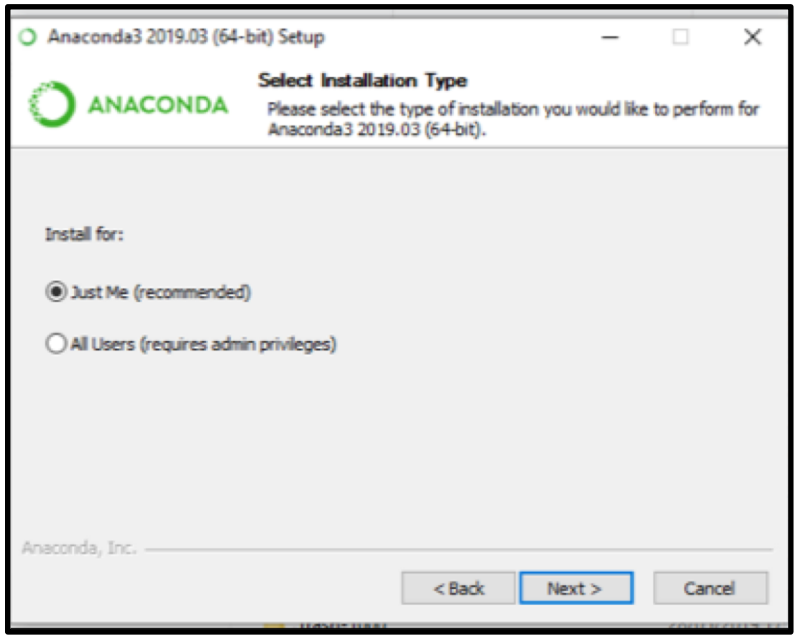
- A computer with any operating system:
  Windows, MAC OSX or Linux.
- A minimum RAM of 4 GB.
- Free space of about 4 GB to install Python and HOPS.

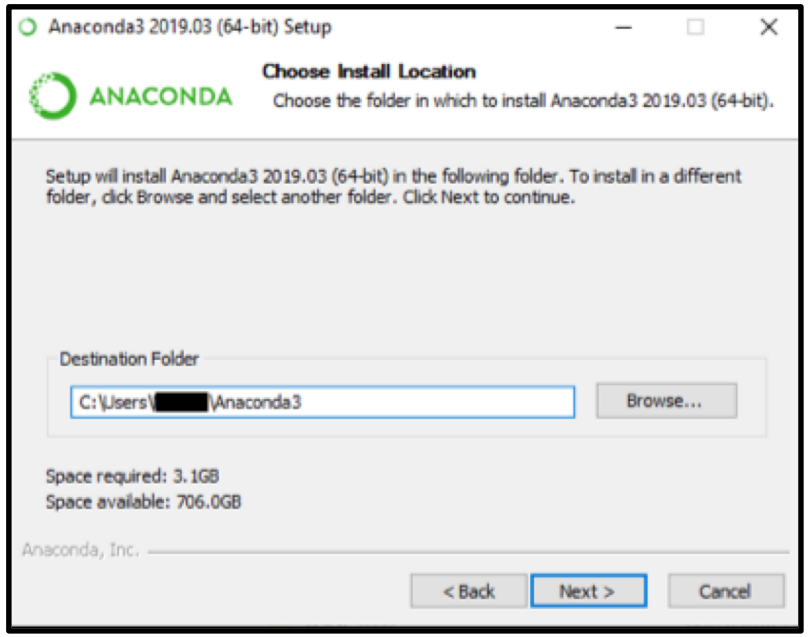
Installing Anaconda (Python)

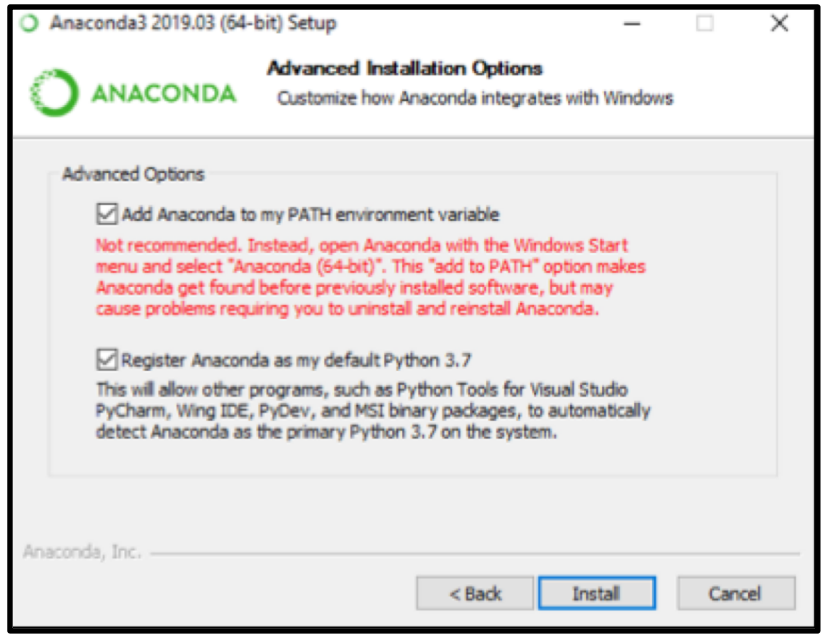
- Visit the Anaconda website (https://www.anaconda.com/distribution/#download-section)
- Click on Download under Python 3.7 version.
- For windows users, during installation, be careful to install Python in your home directory (for you only, not for all users) and add python as a system variable.

Installing Anaconda (Python)

For windows users, during installation:







Installing HOPS

To install the software:

- Download the code from GitHub

(https://github.com/HolomonAstronomicalStation/hops/archive/master.zip)

- Unzip the file hops-master.zip
- Double click on one of the appropriate files inside the subfolder, depending on your operating system:
  - windows_installer.cmd
  - osx_installer.command
  - linux_installer.sh
- After installing the program, an executable file named hops.x (.cmd for windows, .sh for linux, .command for OSX) will be created on your desktop

Known issues

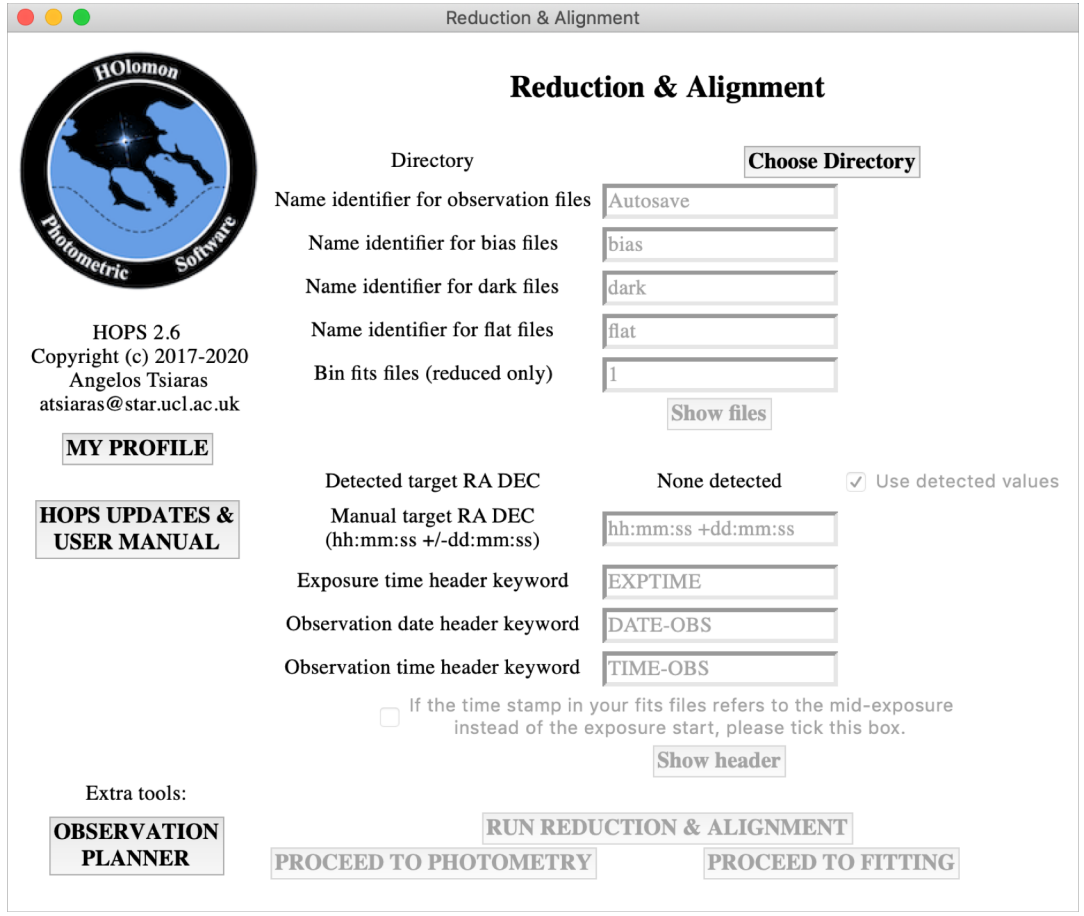
- For Windows users, if windows_installer.cmd is not working, this means that Python is not installed as a system variable. In this case, either try installing Python again with Anaconda, or include Python to your system variables manually (https://geek-university.com/python/add-python-to-the-windows-path).

- For Mac OS MOJAVE 10.14.6 users, TkIner, the GUI backend used by HOPS is not working properly on this OSX version, causing a user log out. To solve this issue you will need to upgrade your Mac OS to Catalina.

Reduction

Reduction window

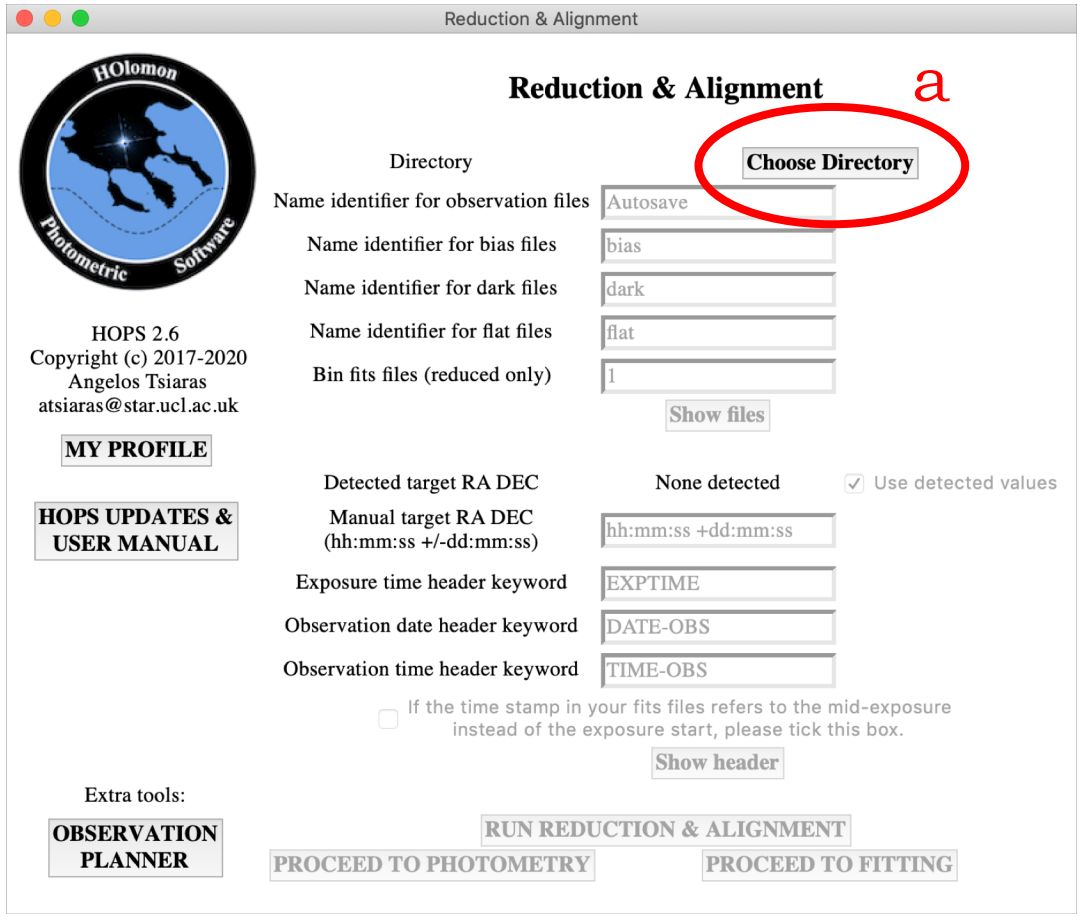
The first window to appear is where the data analysis starts – reduction. If you have used the software before, the latest setup will be loaded.

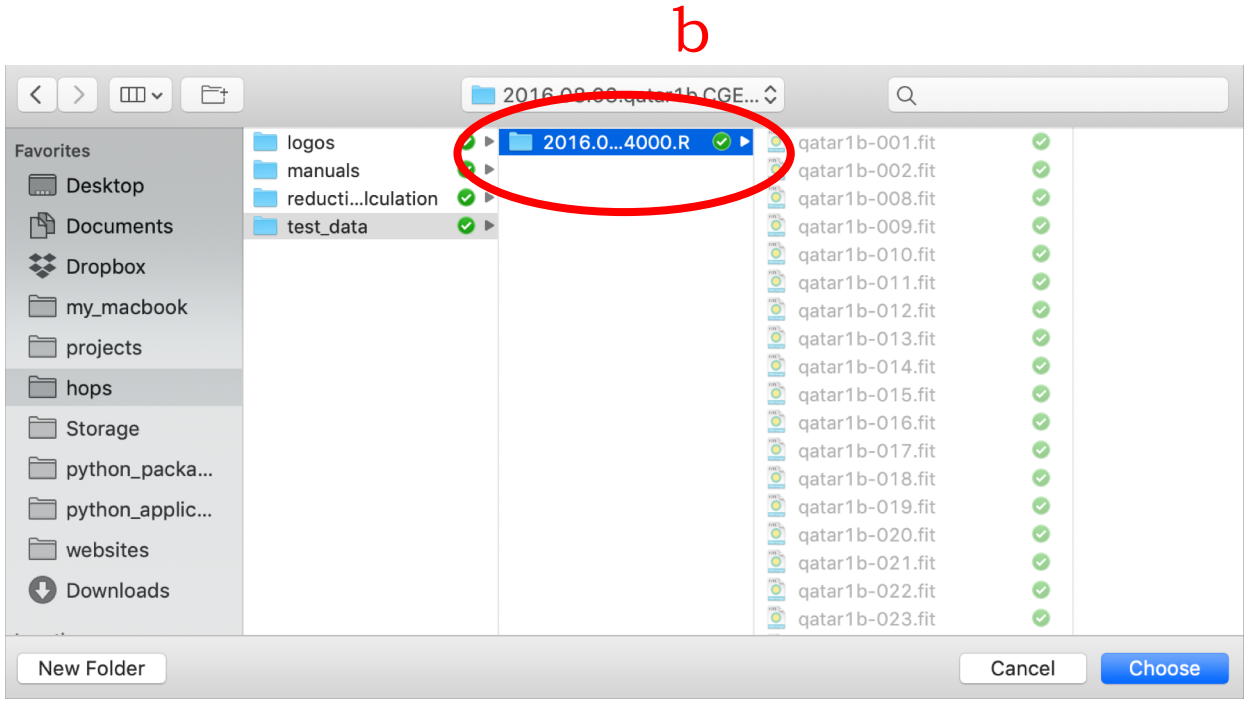


Select your data directory

a. Click on Choose Directory

b. Select your directory from the secondary window





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…

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.

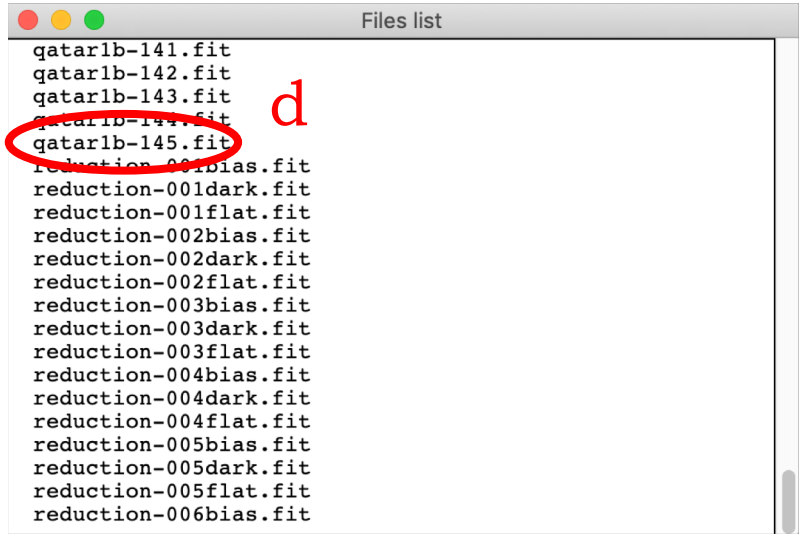
DANGER ZONE

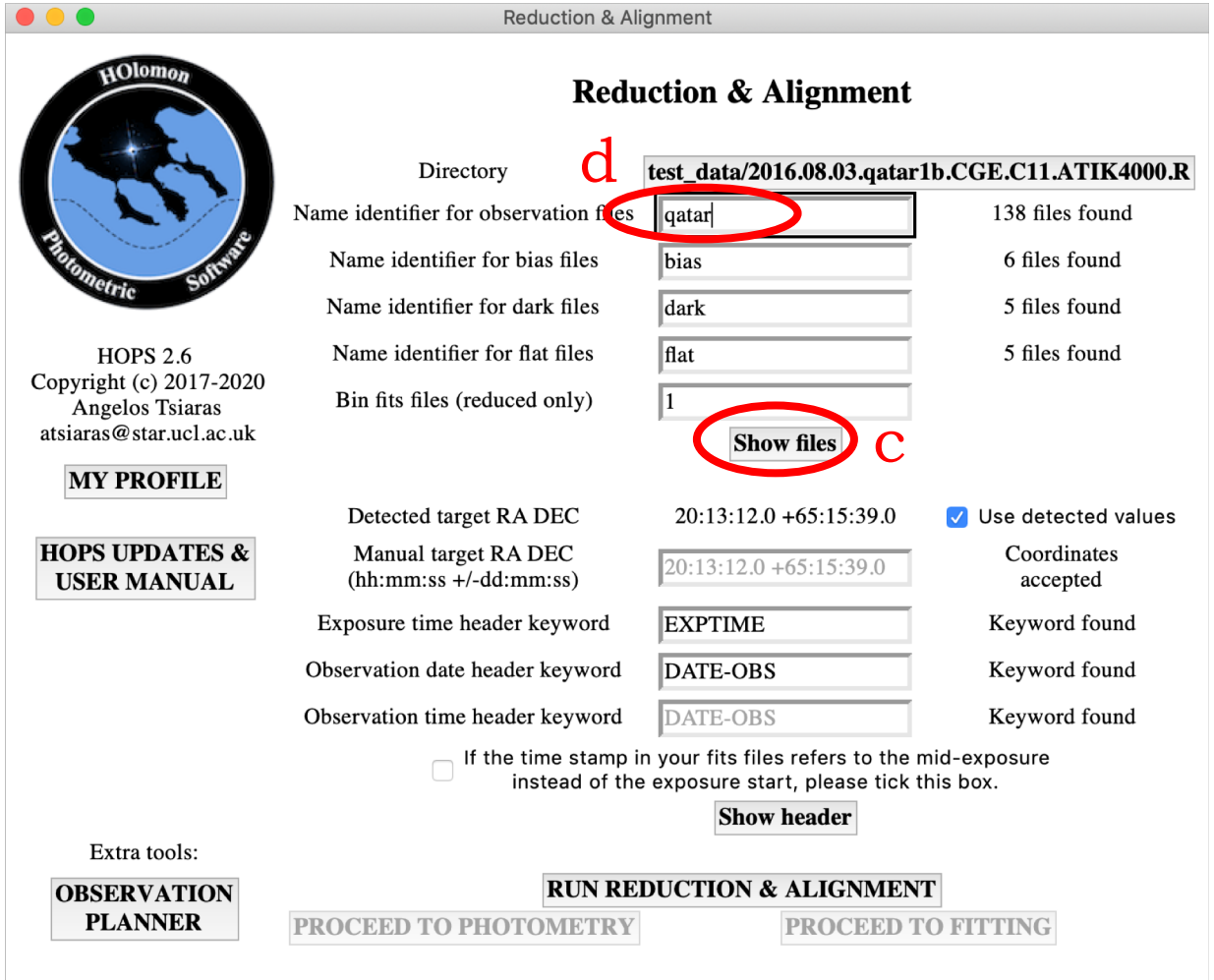
- **Do not apply any pre-processing** (for example do not create master frames) HOPS will create the master frames on the fly, and use them appropriately.

Select your observation files

c. Click on Show files to see the files in your data directory in the secondary window

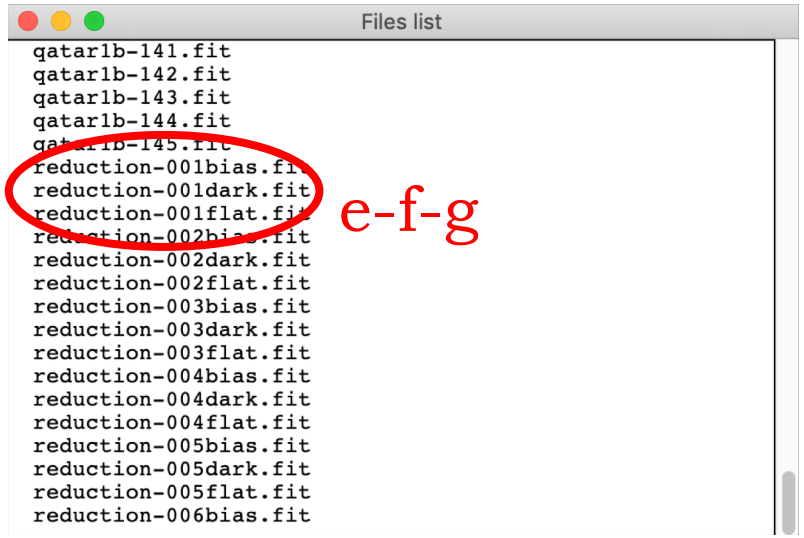
d. Type in Name identifier for observation files the identifier for your observation files (i.e. science frames)

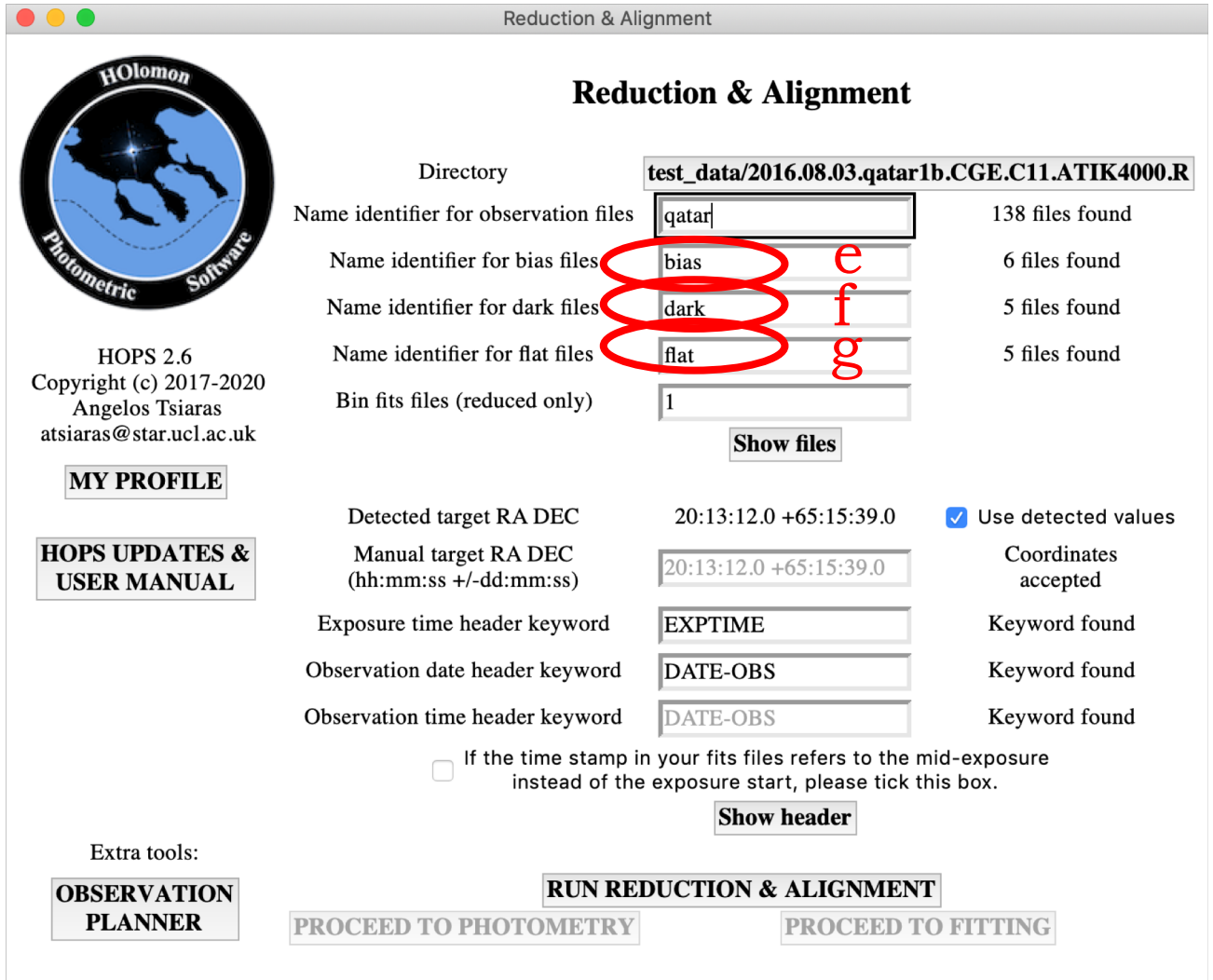




Select your reduction files

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

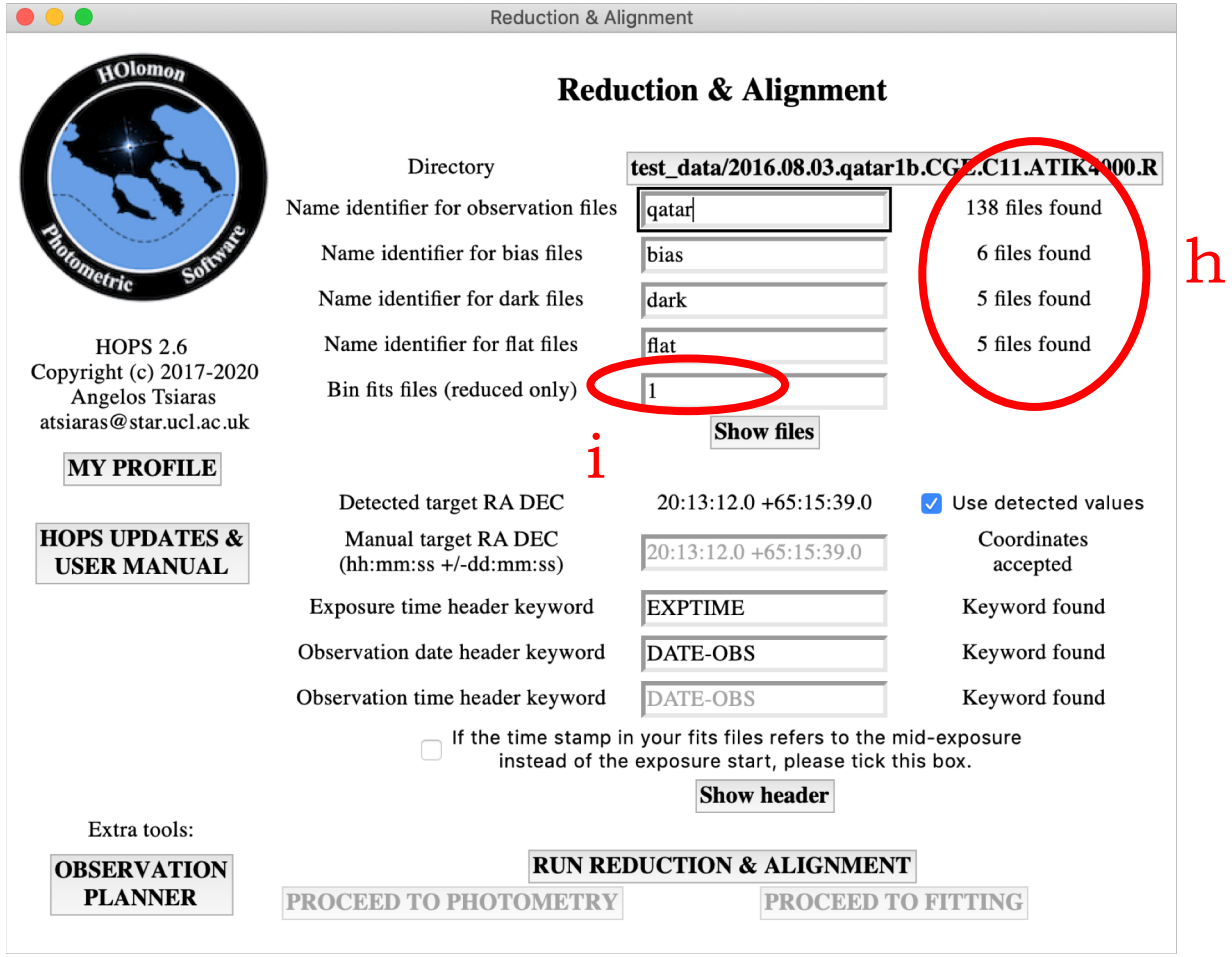




Check your selections

h. Check that files are found, you cannot proceed with 0 observation files but you can without bias dark or flat files (not recommended!)

i. Select whether you want to bin down the reduced images by typing in Bin fits files your preferred binning (not recommended, again!)



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:

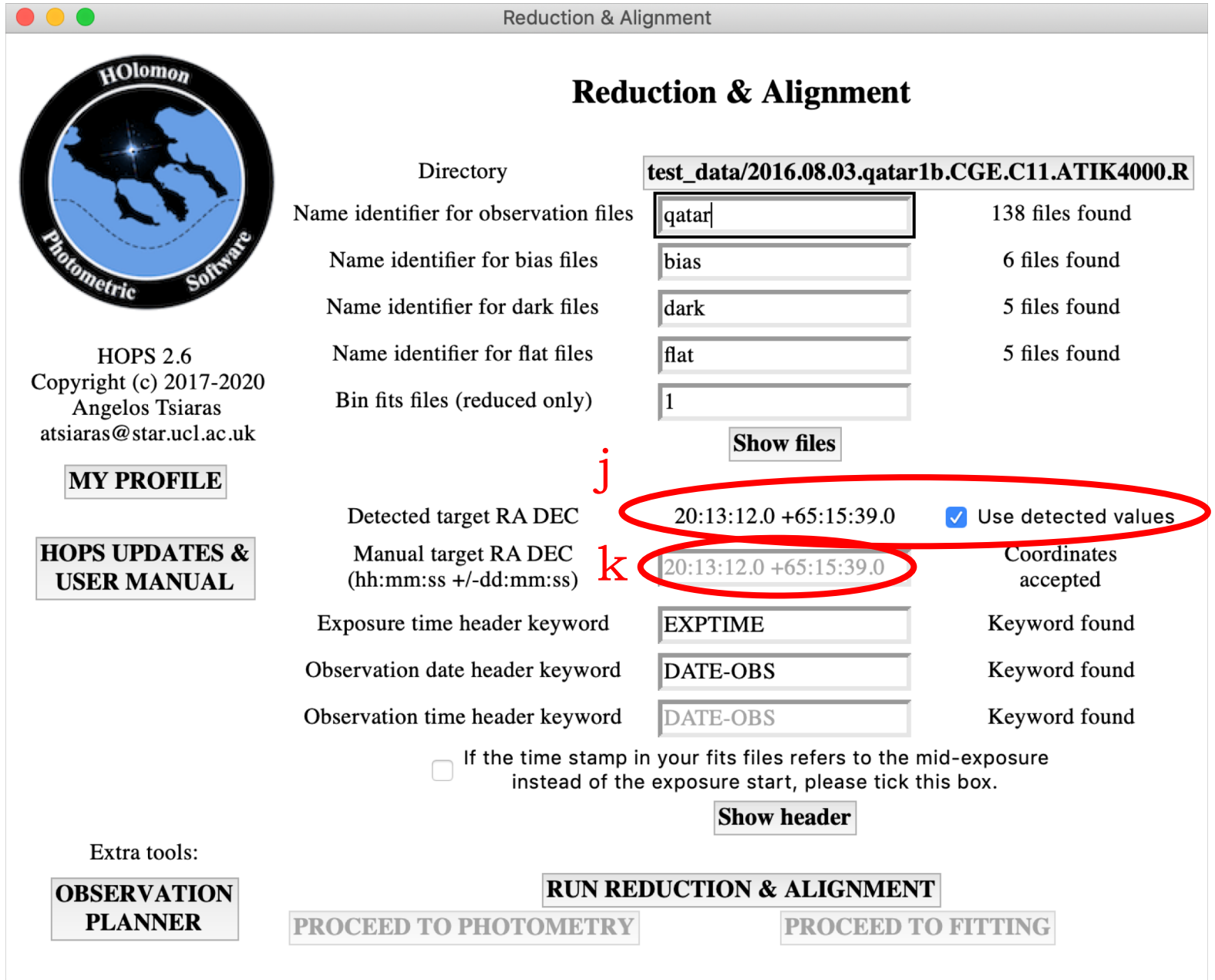
- you have raw data, dark and flat frames only. In absence of bias frames your reduced images will be distorted.
- you have raw data and flat frames only. Flat frames not corrected for bias and dark will cause problems to your reduced frames

Enter your target coordinates RA / DEC

j. If your header includes RA/DEC information, it will be detected and shown in Detected target RA DEC and Use detected values will be checked. If your header does not include this information Detected target RA DEC will be None and Use detected values will be unchecked. If you wish to enter different values manually, uncheck Use detected values.

k. When Use detected values is unchecked, you can type the coordinates in Manual target RA DEC, using the requested format.

Enter your target coordinates RA/ DEC



Enter your header time keywords

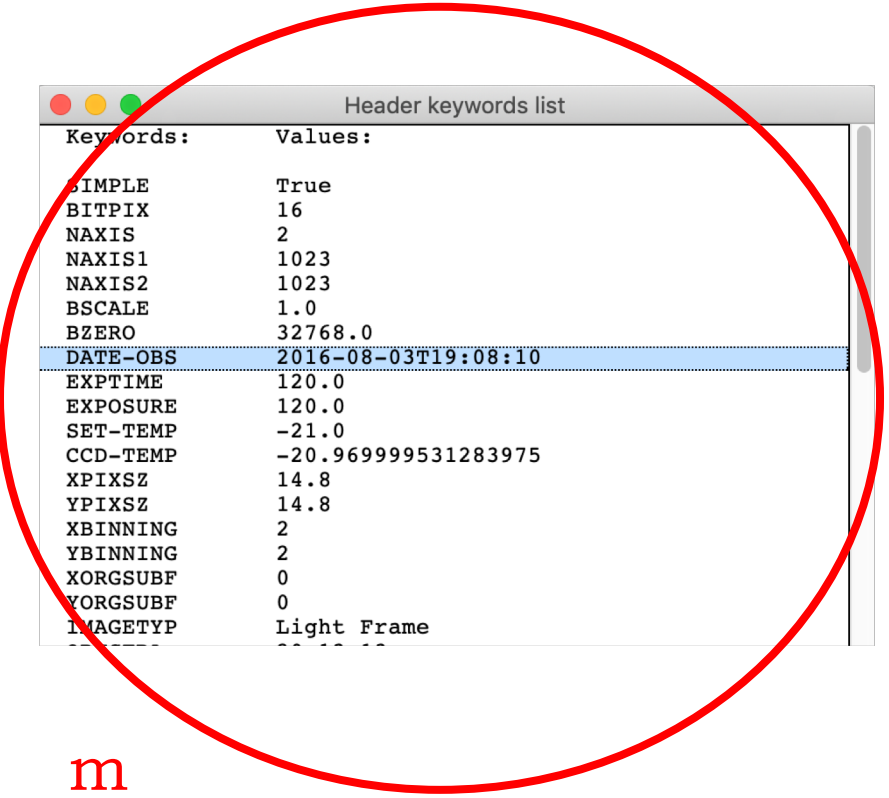
l. For the Exposure time header keyword, the Observation date header keyword and the Observation time header keyword the default values are EXPTIME, DATE-OBS, TIME-OBS, respectively. If these are not found in your header, you will need to enter the respective keywords manually.

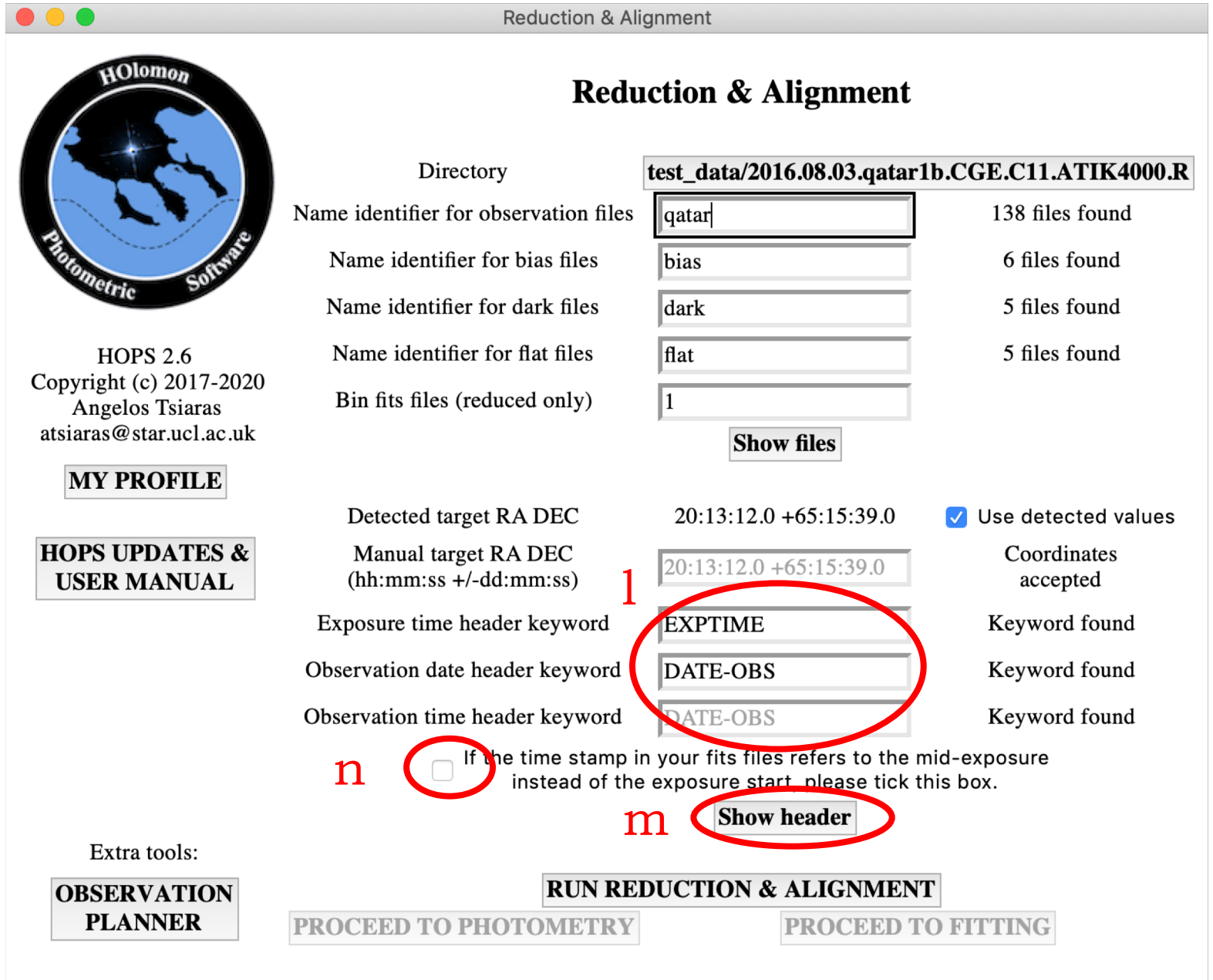
m. To check your header click on Show header, and a secondary window will appear

NOTE: If the observation date (usually DATE-OBS) contains also the observation time (in our example it is 2016-08-03T19:08:10) then Observation time header keyword will be deactivated.

n. Usually the time saved in the fits header represents the exposure start time. If this is not the case for you, and the save time represents the exposure mid-time, check the box below Observation time header keyword.

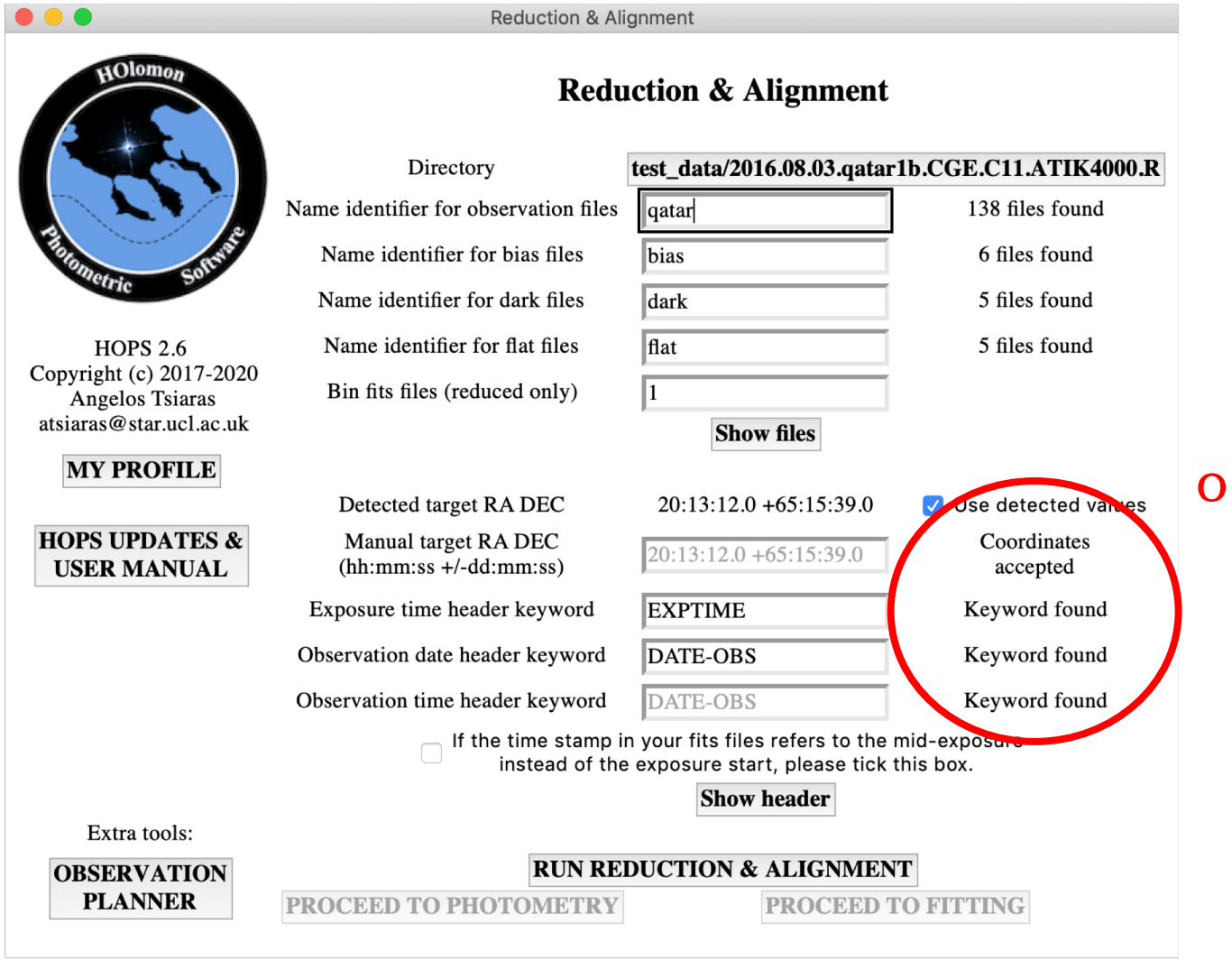
Enter your header time keywords





Check your header information

o. Check that the target coordinates are accepted and that the header keywords are all found, you cannot proceed without these information

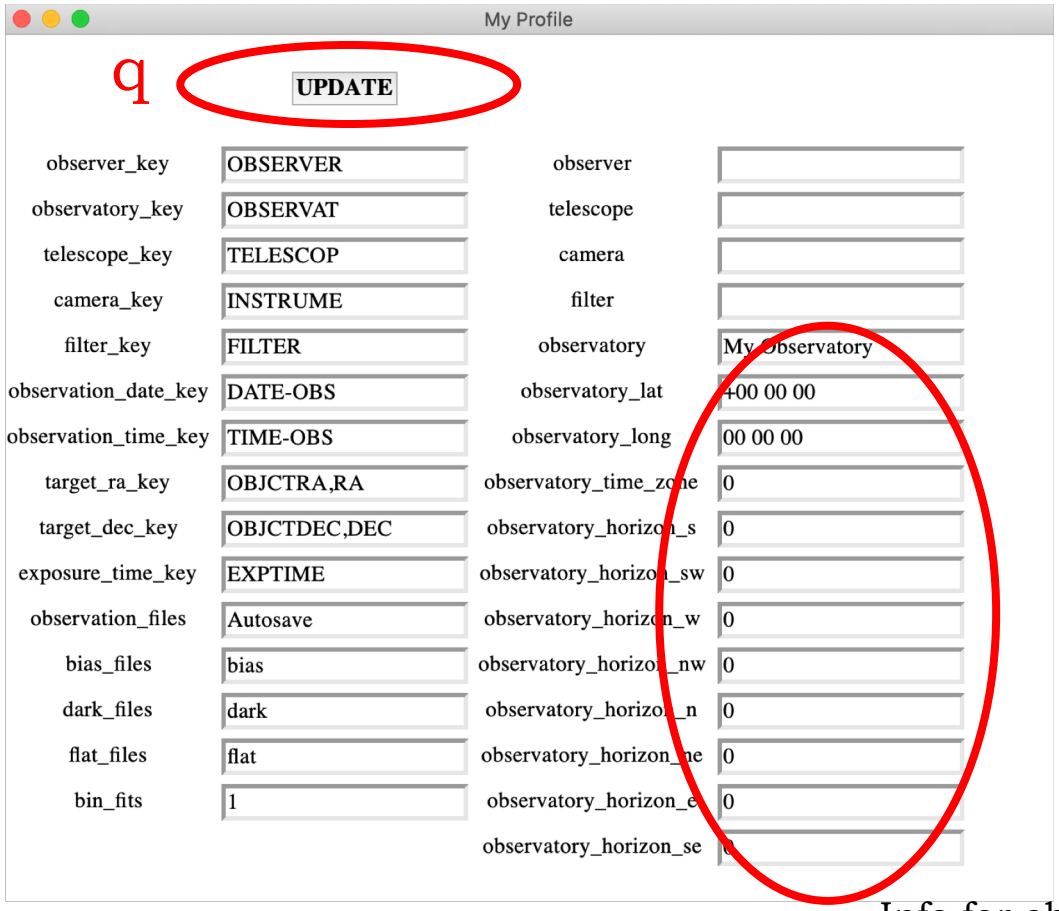


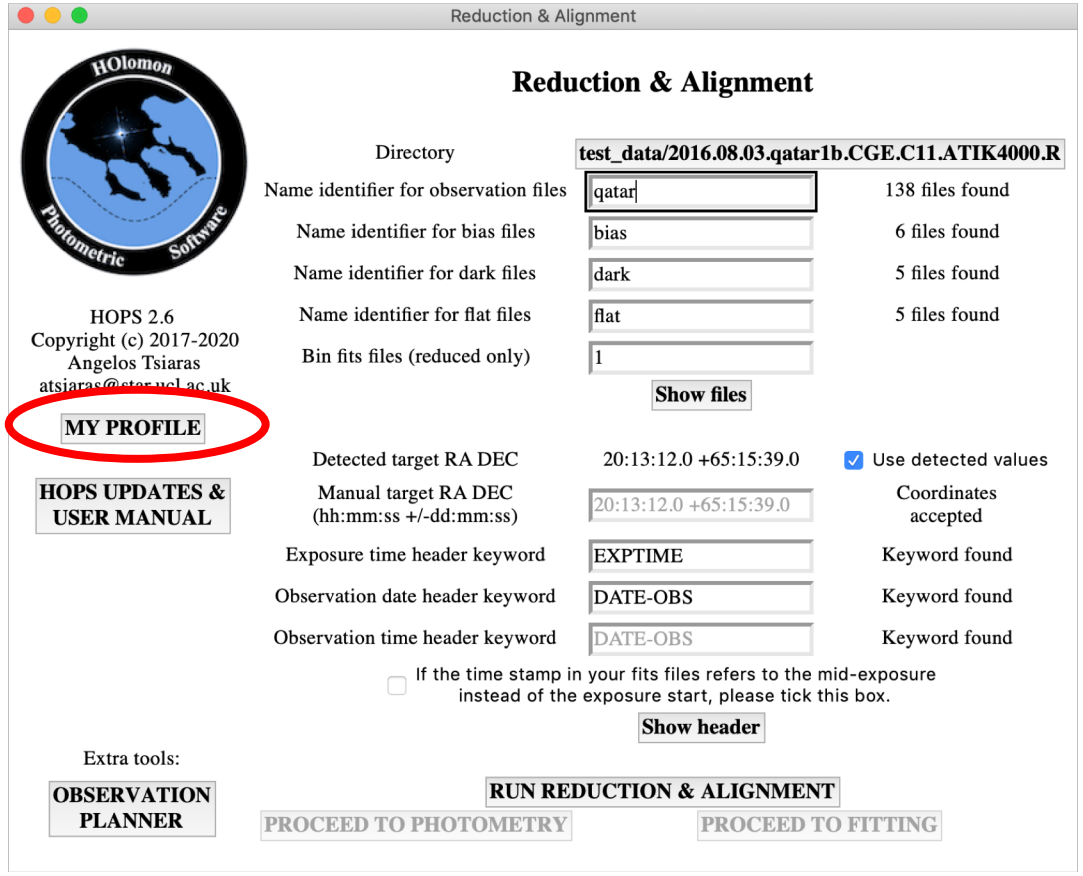
o

Set you profile – saves time for next runs!

p. If you follow a consistent way of saving your data you can click on MY PROFILE to change your default settings

q. Type the information in the secondary window (for multiple RA/DEC keys use commas without spaces) and click on UPDATE

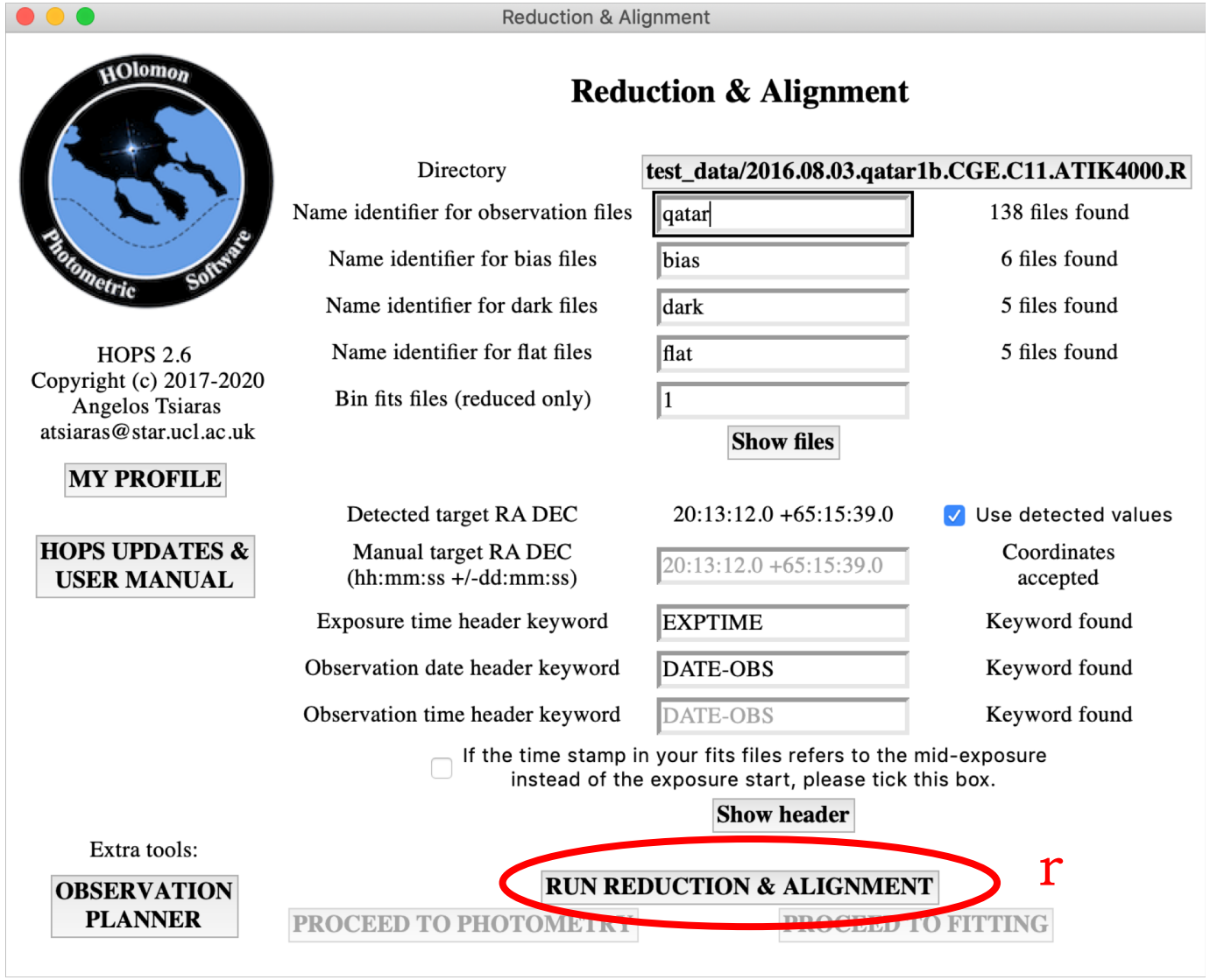




Info for obs. planner, not relevant at this stage

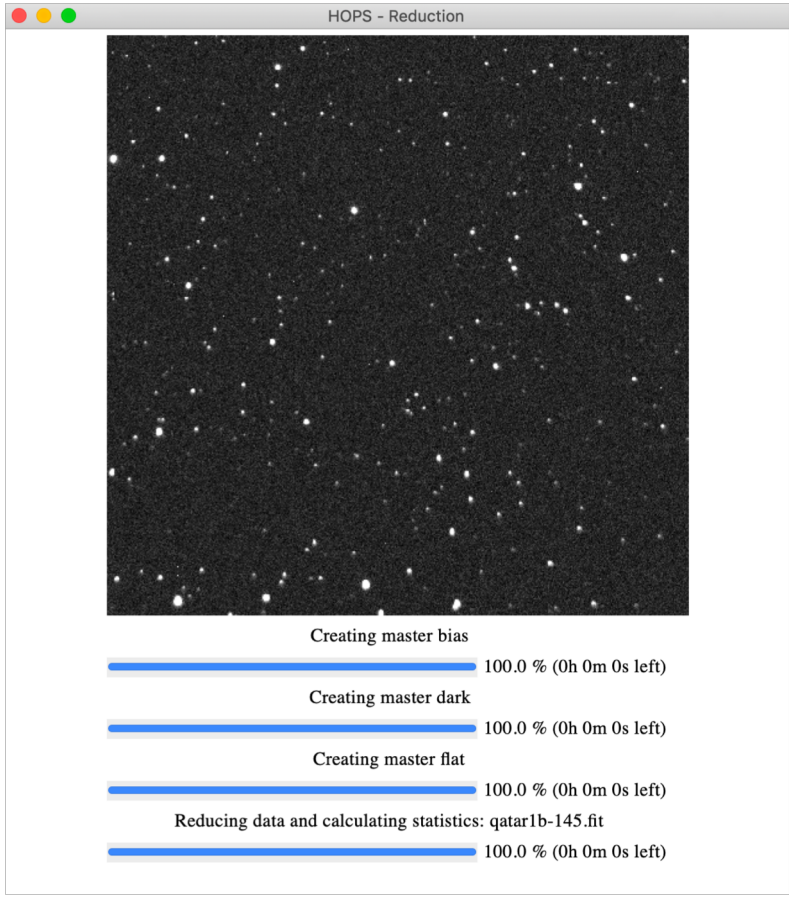
Run reduction

r. proceed by clicking on RUN REDUCTION & ALIGNMENT



Running reduction

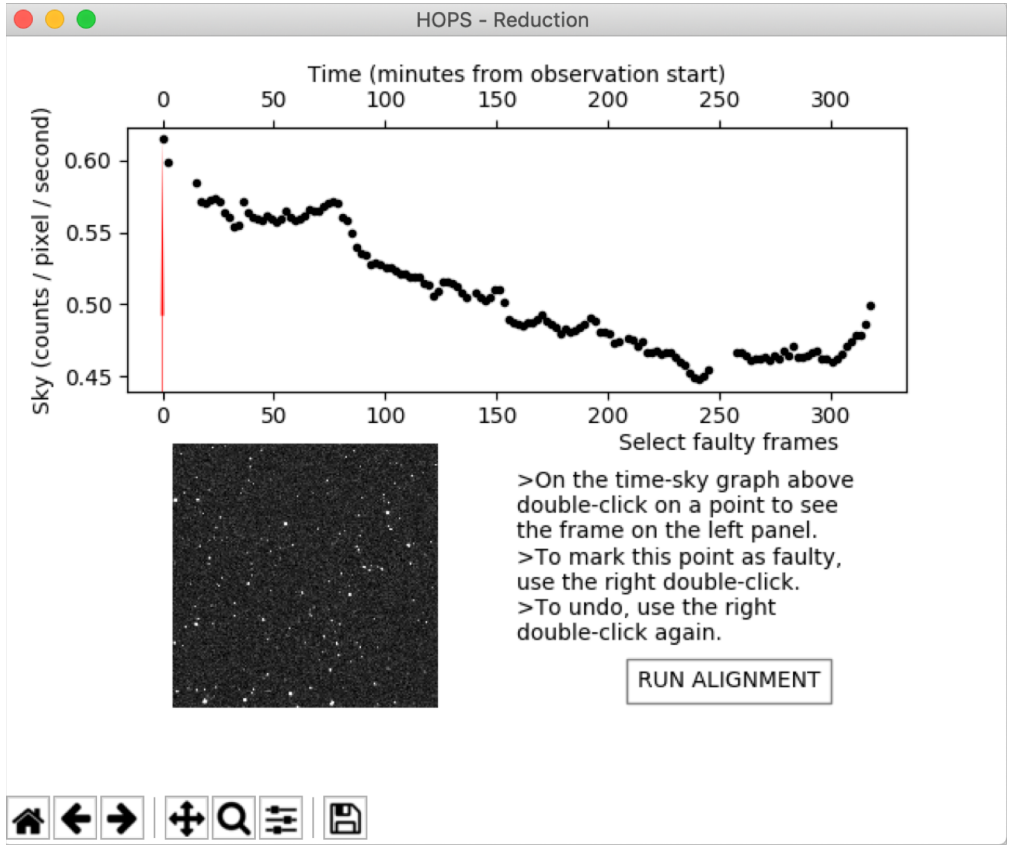
A window showing the progress of the reduction will appear. Note that even if you have not given any reduction frames, this process will take a few. This is because during this time, some statistics on your images are calculated.



Alignment

Sky-Time window

After reduction, a window will appear, showing how the sky background is changing during your observation. Any cloudy images will appear as outliers and at this stage you can filter them out. Its not mandatory though, as bad frames will be identified in the next step of alignment, too.



TIPS SECTION

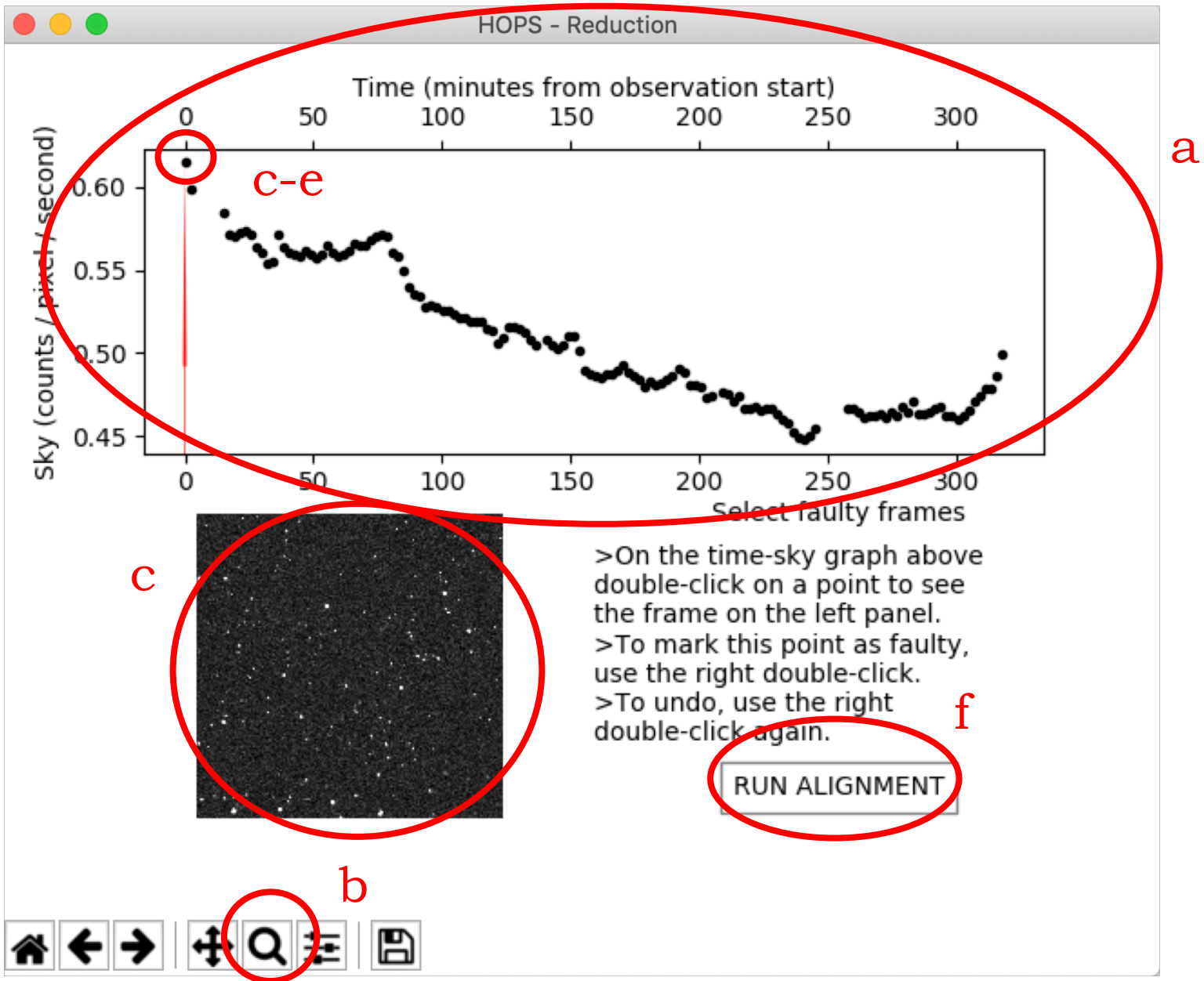
The alignment process relies heavily on your first image. This is a good moment to check your first image again and verify that it is not overexposed and that the tracking is representative of your observation in total.

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!

Discard bad frames

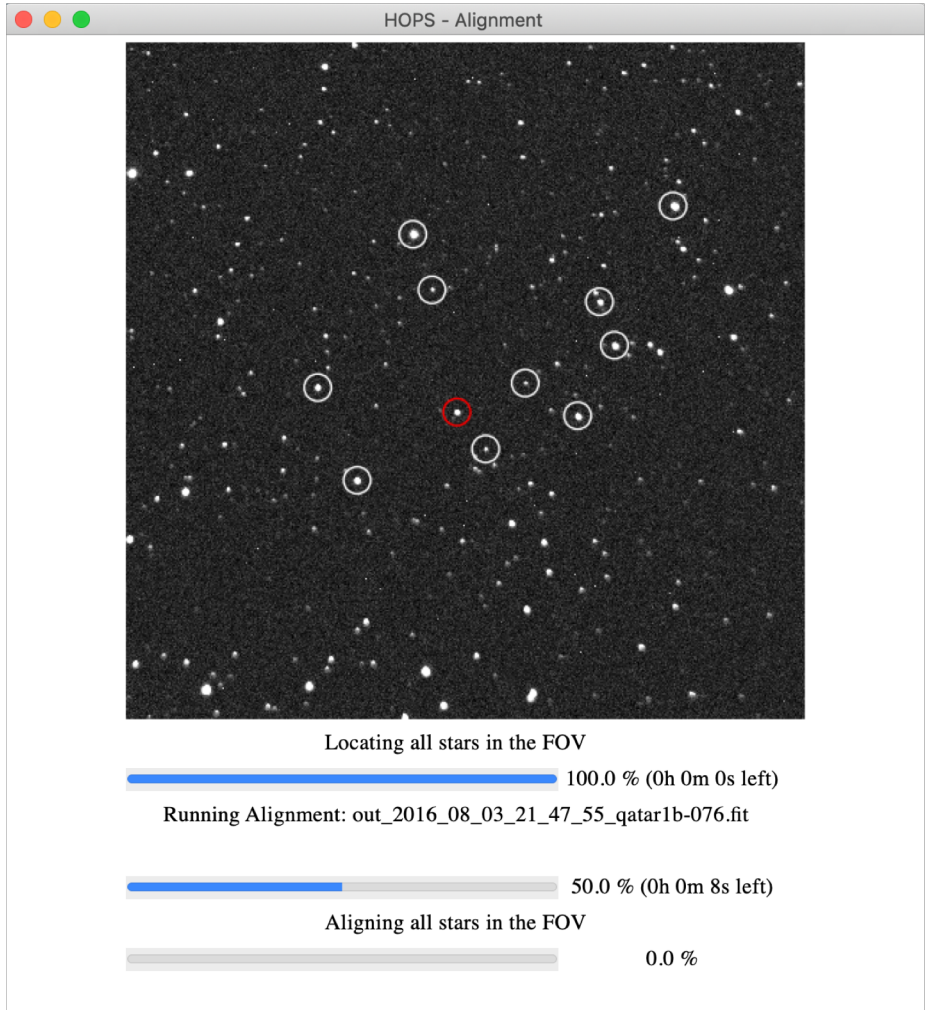
a. Inspect the sky counts vs time plot for outliers
b. Zoom-in if necessary using the tool at the bottom of the window
c. Double click on a point to view the frame.
d. Double right click on a point if you want to exclude it (it will turn red)
e. Double right click on a red point again to include it again (it will turn black again)
f. Click on RUN ALIGNMENT to proceed

Discard bad frames



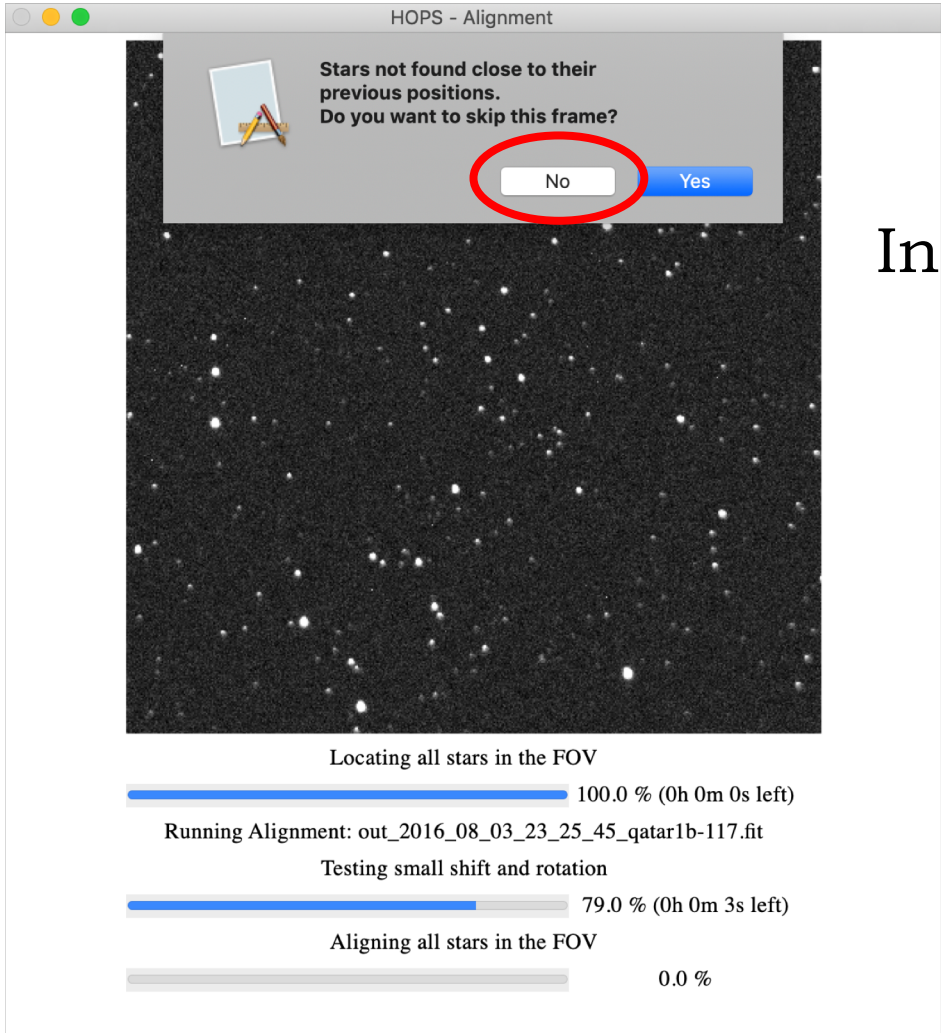
Running alignment

A window showing the progress of the alignment will appear. If there are no bad frames or large shifts and rotations, you will not need to do anything else.



Running alignment

g. If there is a frame where stars cannot be detected, you will be asked whether you want to skip it. If the frame is just shifted of flipped select No. (you won't be asked for small shifts or meridian flips without large shifts)



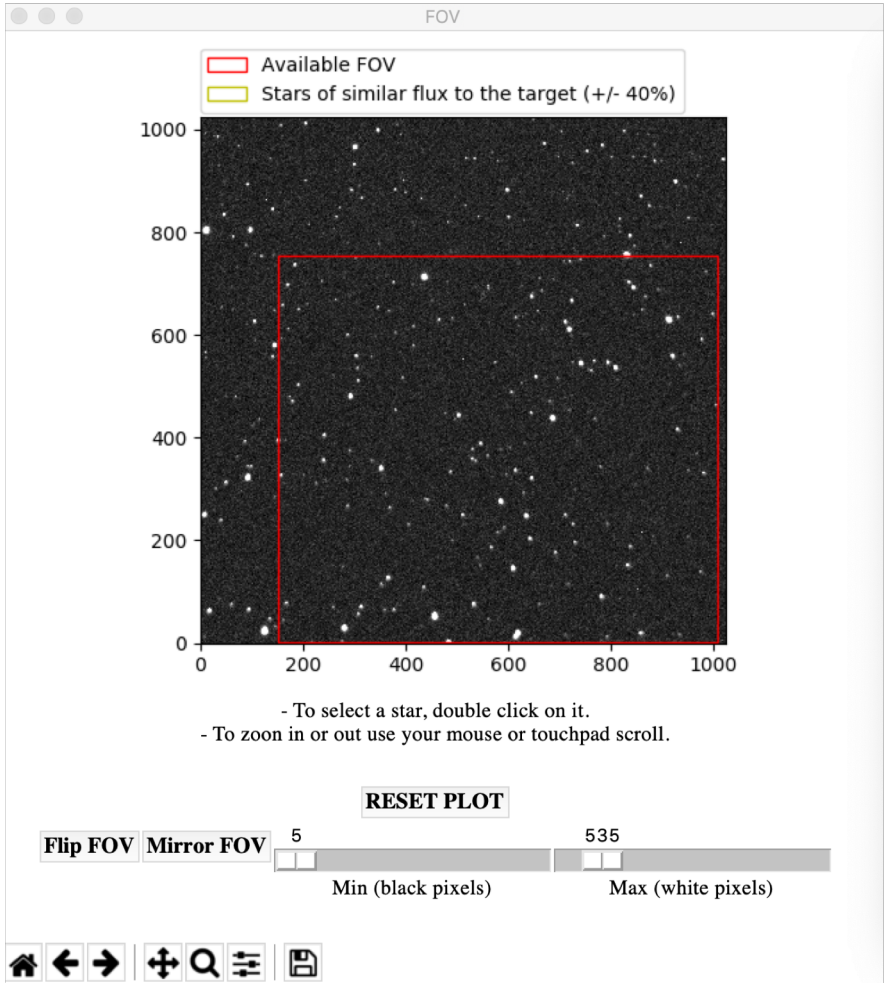
g

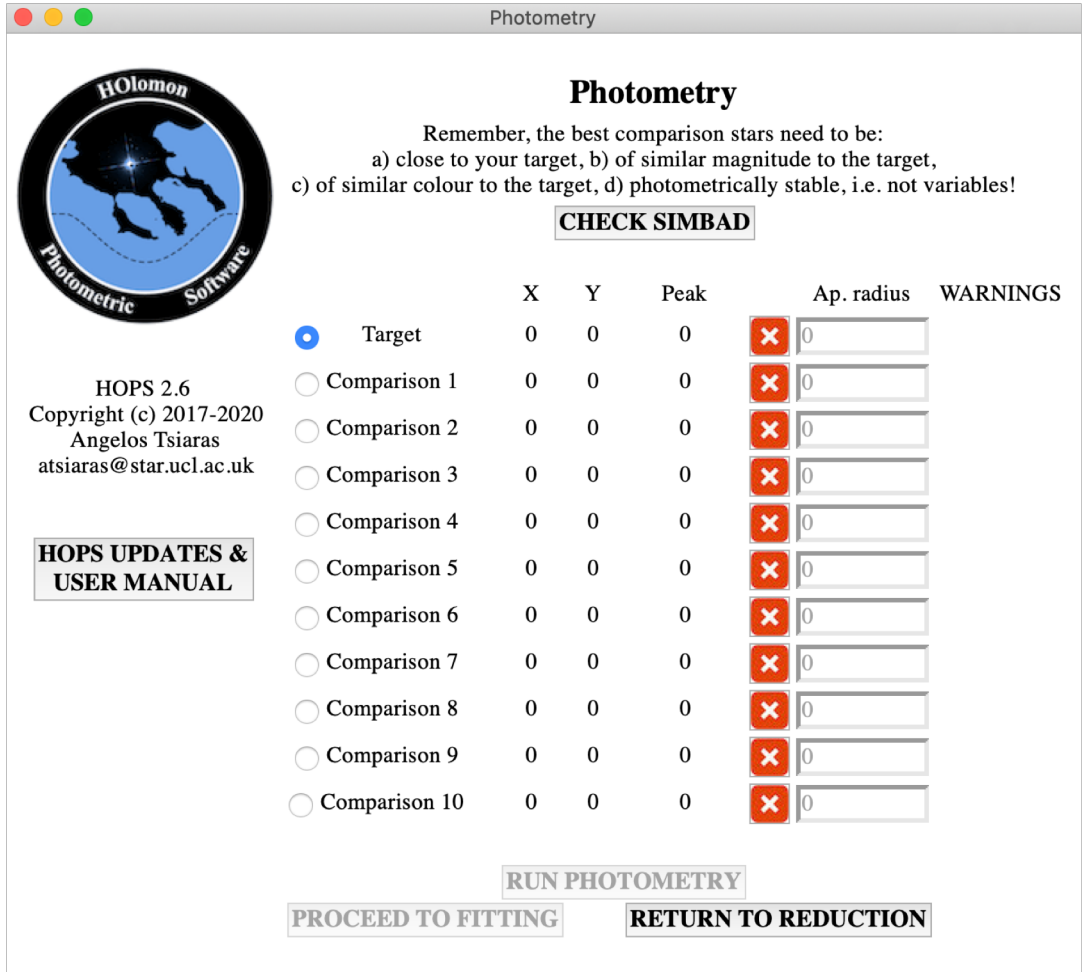
In this example the FOV here is flipped

Photometry

Photometry window

After alignment, two windows will appear: one showing your first observation file and one where you will be able to select your target and comparison stars. If you have analysed this dataset before, the latest setup will be loaded.

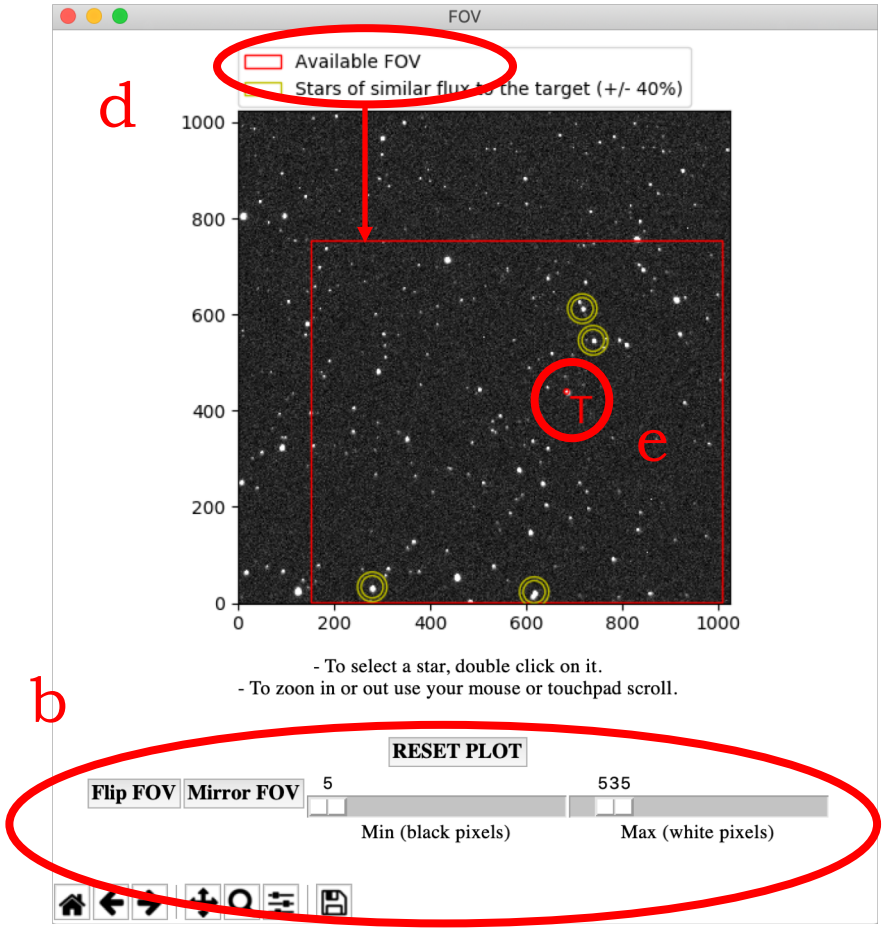


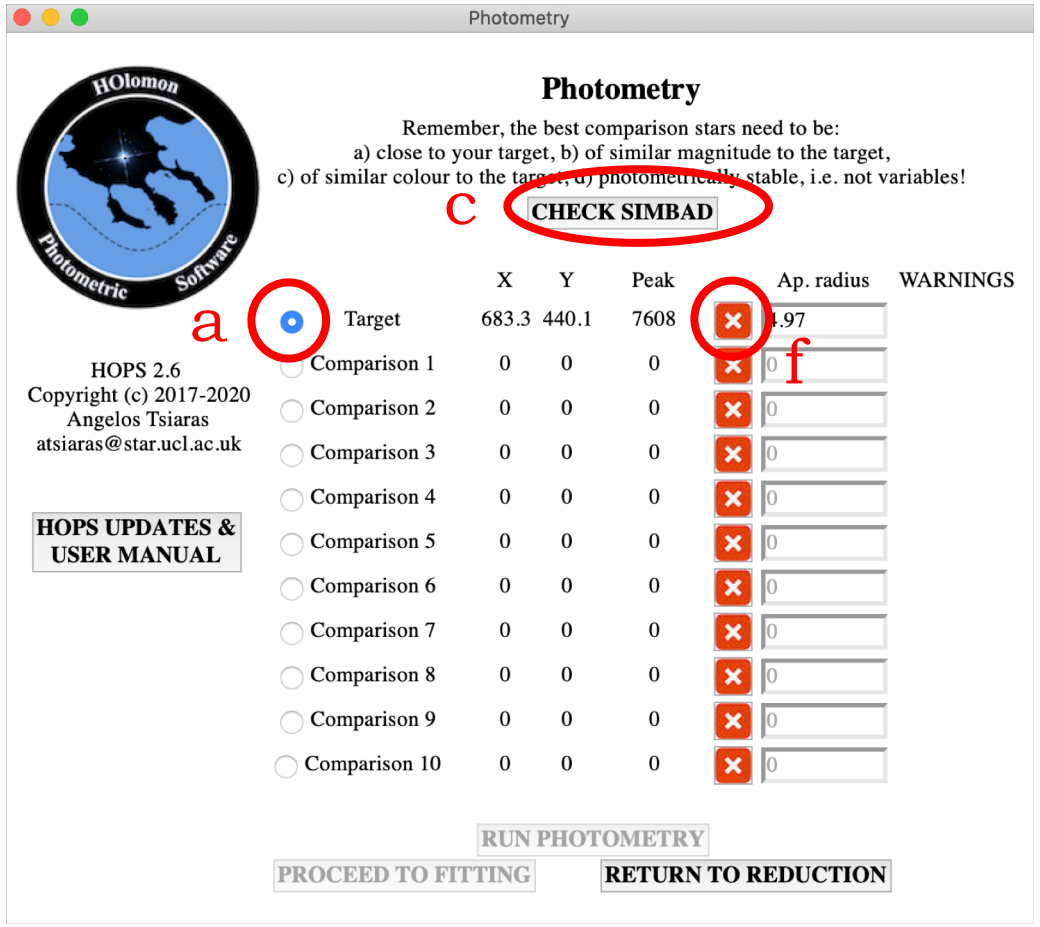


Select your target

a. Click on the radio-button next to Target.
b. In order to identify your target you can zoom-in and zoom-out using your mouse scroll, and use the plotting tools below the FOV to flip, mirror, or change the contrast of the image.
c. You can also check the FOV on by clicking CHECK SIMBAD.
d. A red box indicates the area that stays within your CCD throughout your observation, only stars within this box can be selected.
e. Double click on the star, on the FOV, you may need to zoom in using your mouse scroll (a red circle will appear around the star in the FOV and the X, Y position and peak counts will be shown on the main window).
f. To replace your target double click on another star and to delete it click on the X button next to target.

Select your target

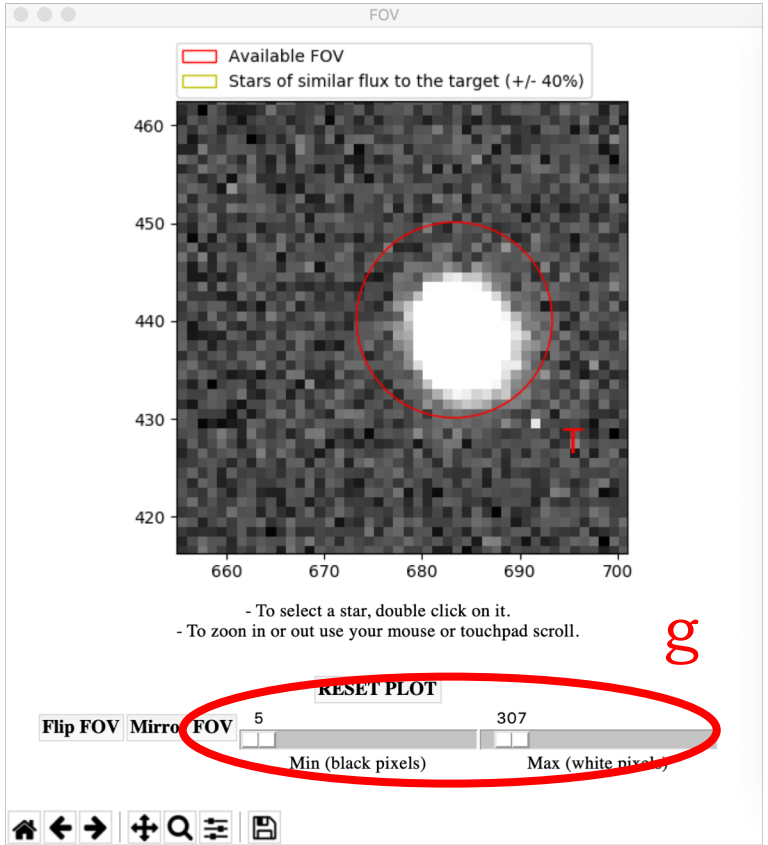


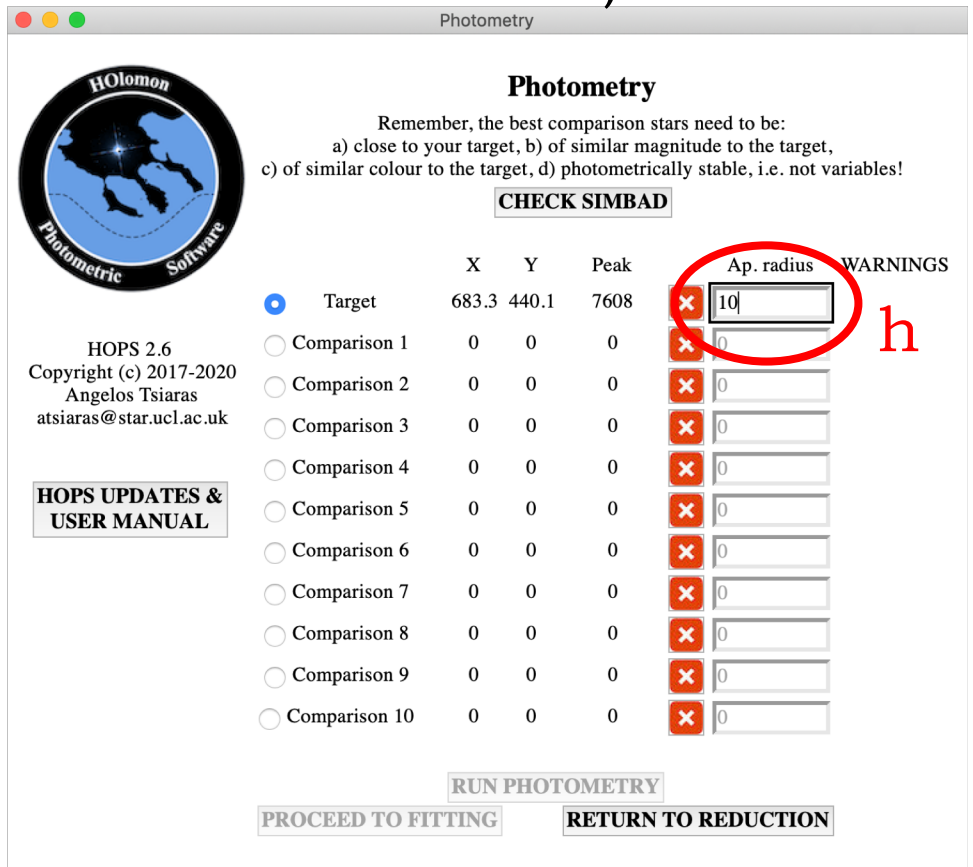


Select your target aperture

g. Zoom-in to your target and if needed, modify the black and white level to see the extend of your PSF.

h. Enter your preferred aperture in the Ap. radius next to the target in the main window (the size of the circle in the FOV will change accordingly). The aperture should include all of your star but not nearby stars (the default value is 1.4 times the fitted FWHM of the stars).





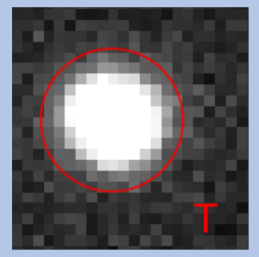
TIPS SECTION

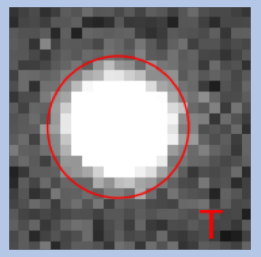
Select your target aperture carefully

Default aperture
Low contrast

Default aperture
high contrast

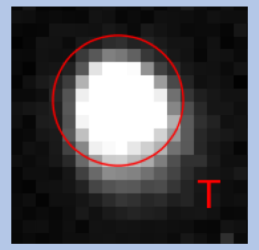
Well-shaped PSF



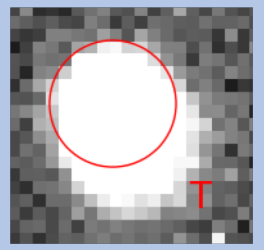


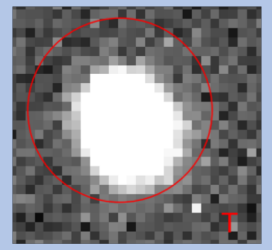
In this best case, even if you increase the contrast you will see that the aperture is including all of your star.

Trails

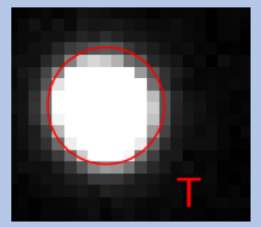


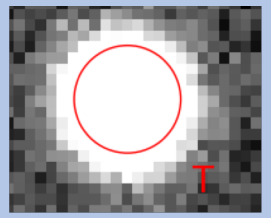
Increase the contrast to see the real extend of your PSF

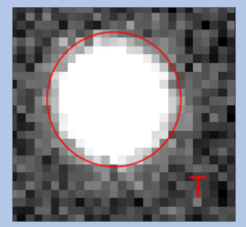




Extended PSF wings





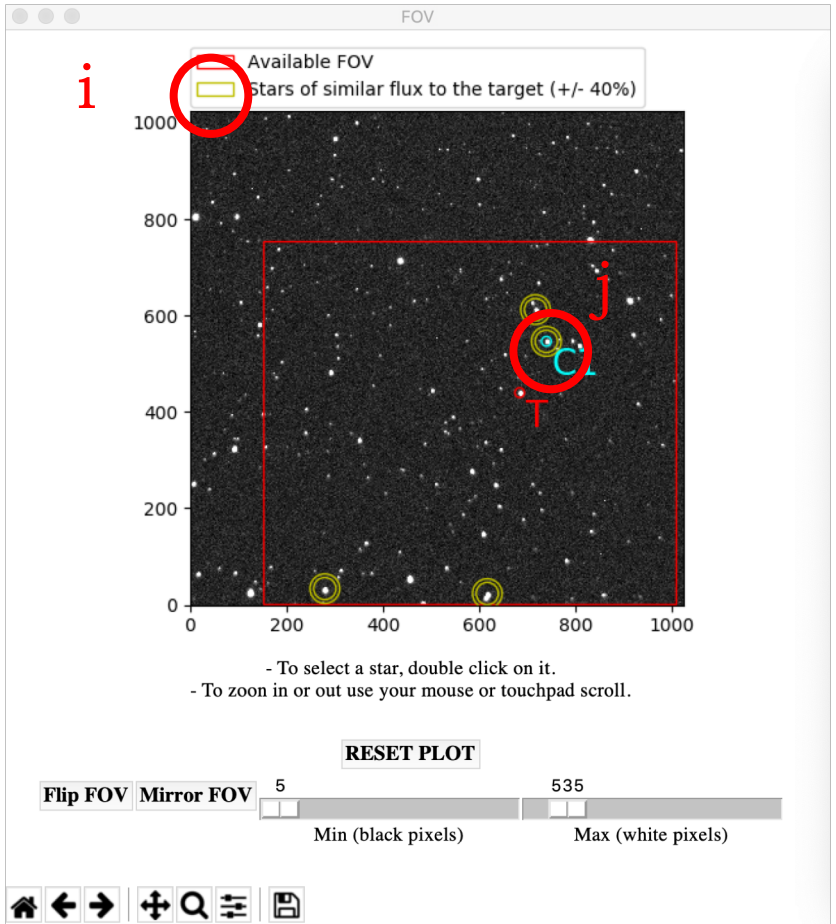


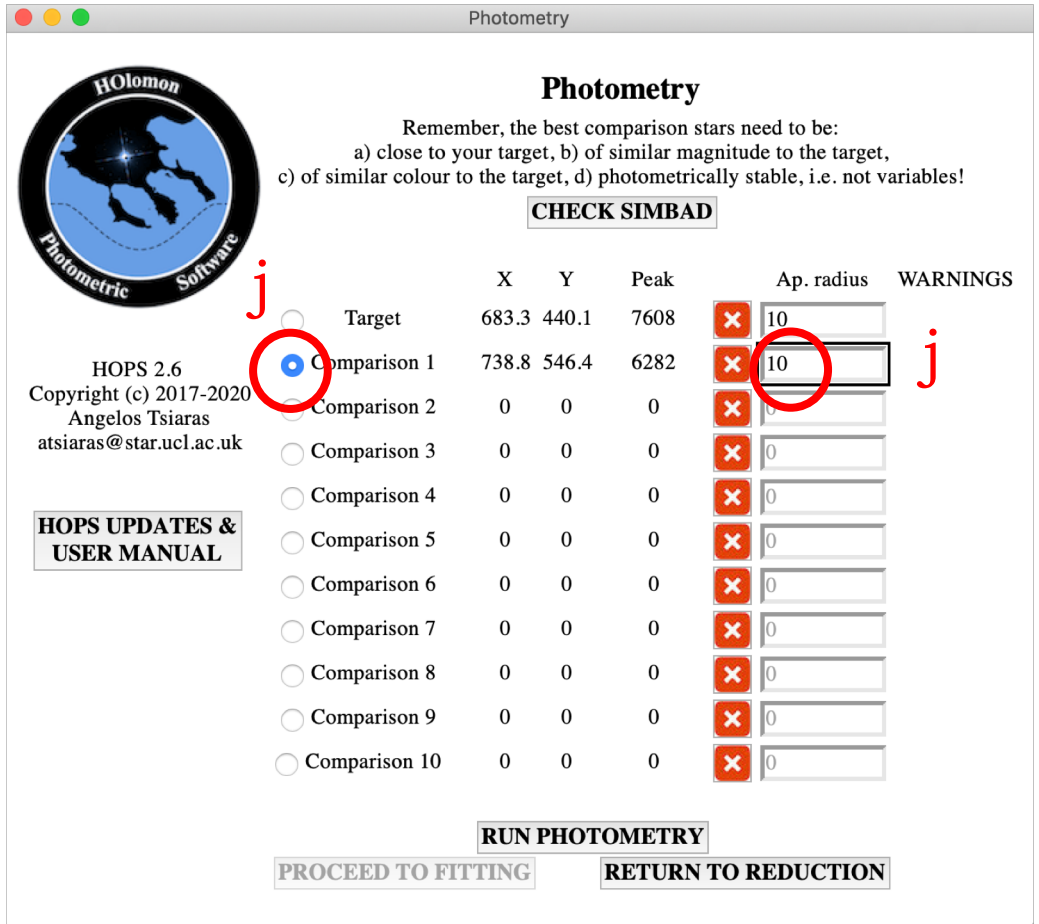
In these two cases, a larger aperture will give you better results. Experiment with it to find the best solution.

Select your comparison stars and their apertures

i. After selecting a target, a number of yellow circles will appear indicating stars of similar flux (+/- 40%).

j. Follow the same procedure as for the target and select between 1 and 10 comparison stars. There is, however, the possibility that no good comparisons exist. In this case you can proceed with other stars.

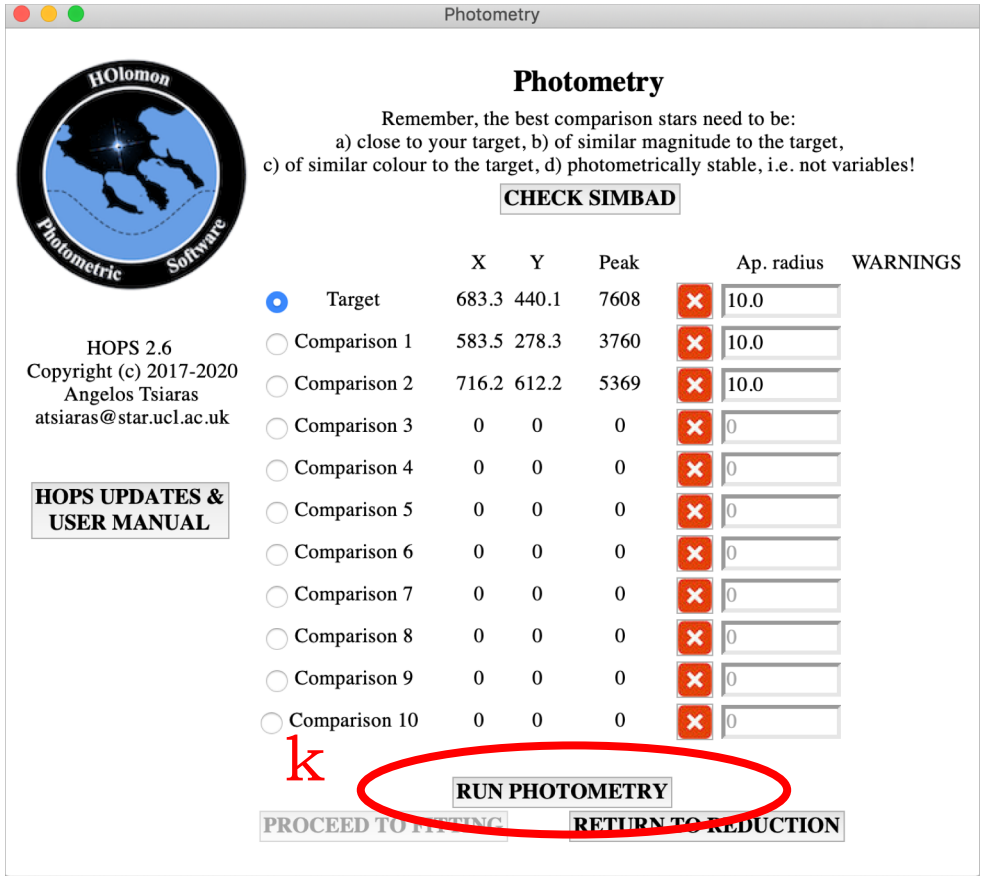




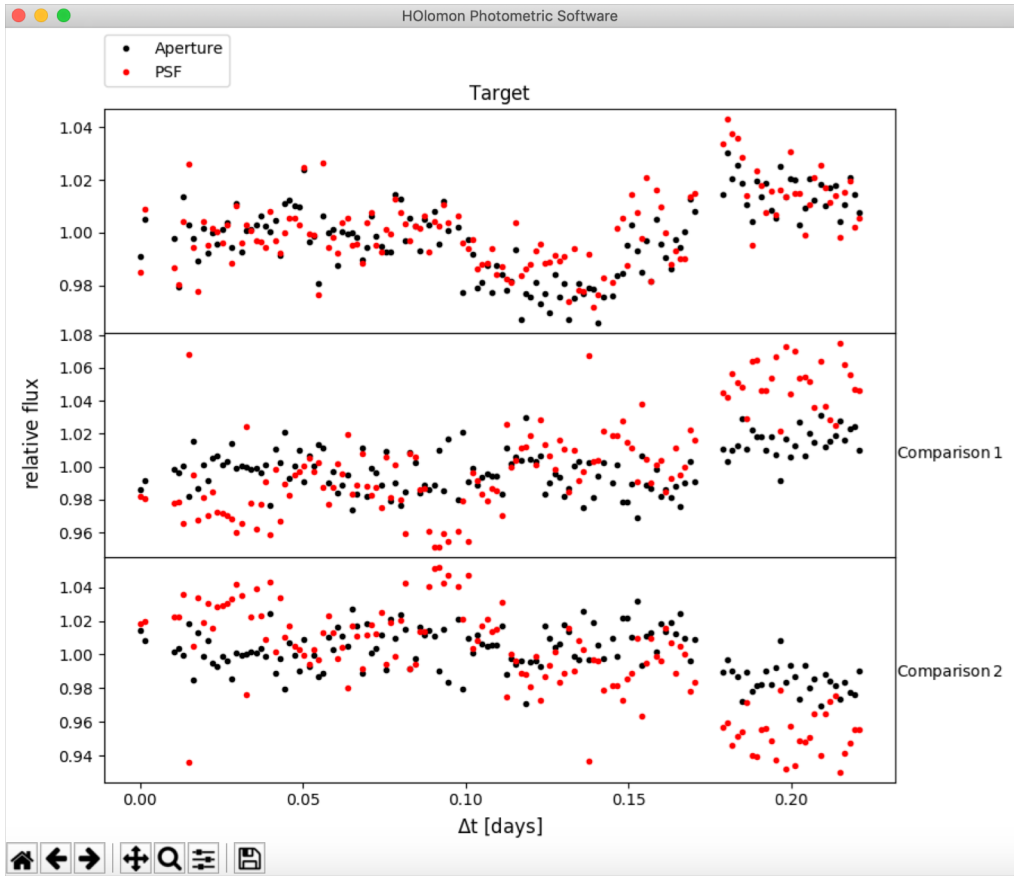
Run photometry

k. Once you have selected your comparisons, press RUN PHOTOMETRY.

l. After the calculation you can check the light curves in a secondary window. You will see as many light curves as the stars you selected.



l



Check your comparison stars for variability

Two curves will appear for every star, one calculated using your aperture (black), and one using a PSF fitting (red). If your stars are perfect circles and your aperture optimal, the two curves should be very similar (stars are not perfect circles in this example!).

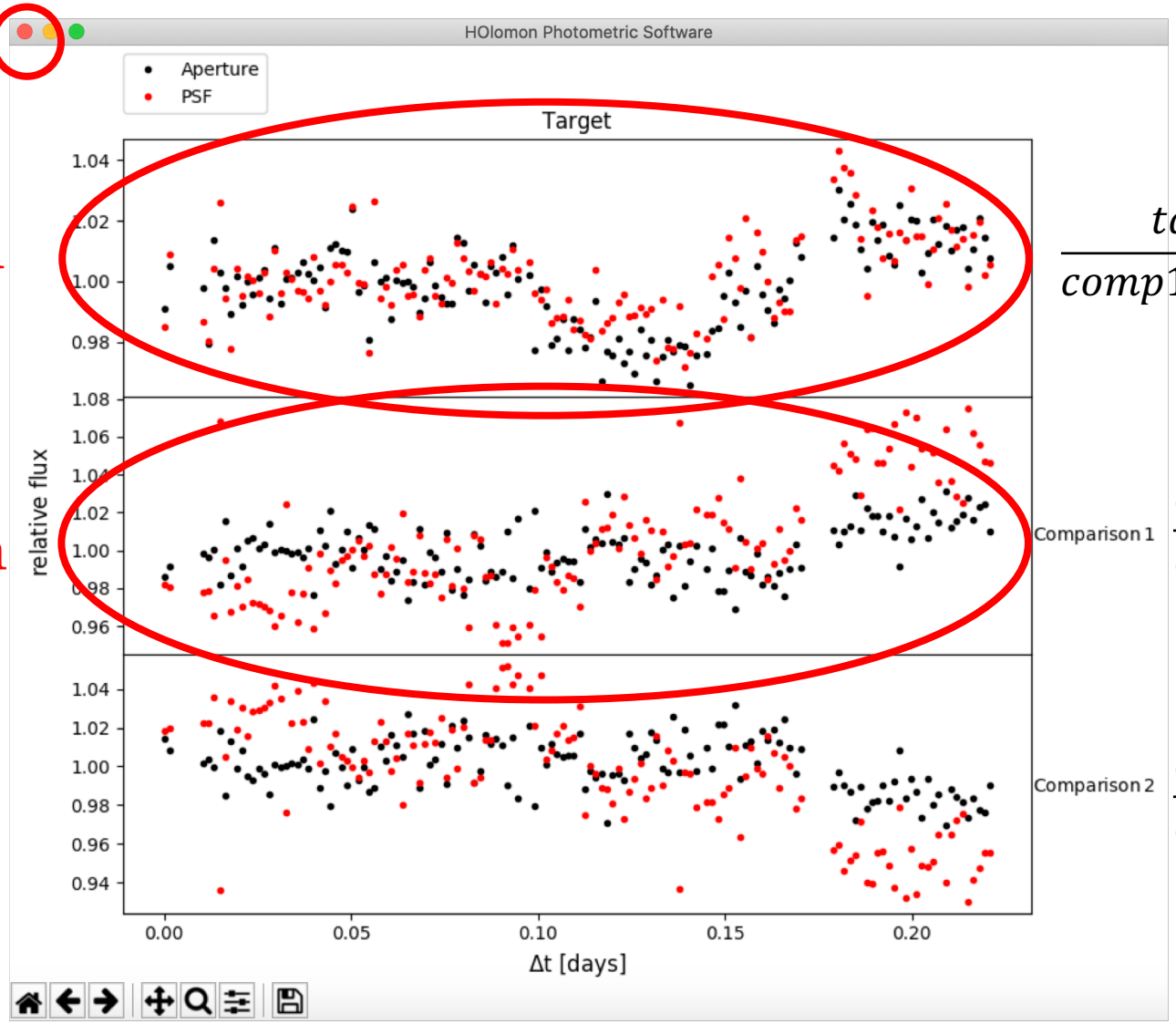
m. The top plot shows the light curve of the target divided by the sum of the light curves of all the comparison stars.
n. Every other plot shows the light curve of one comparison star divided by the sum of the light curves of all the other comparison stars, so if you have only two comparisons, their plots will look anti-correlated with each other.
o. If a comparison star is variable you will see its light curve **anti-corelated to all the other light curves including the target**.
p. To proceed close this window.

Check your comparison stars for variability

p

m

n



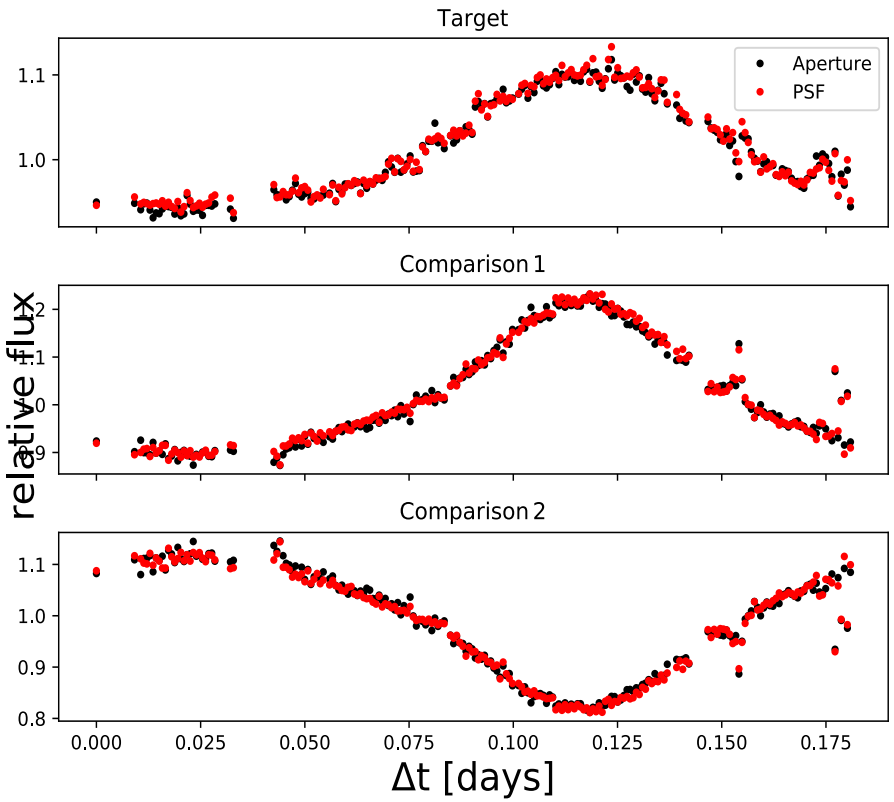
$$\frac{target}{comp1 + comp2}$$

$$\frac{comp1}{comp2}$$

$$\frac{comp2}{comp1}$$

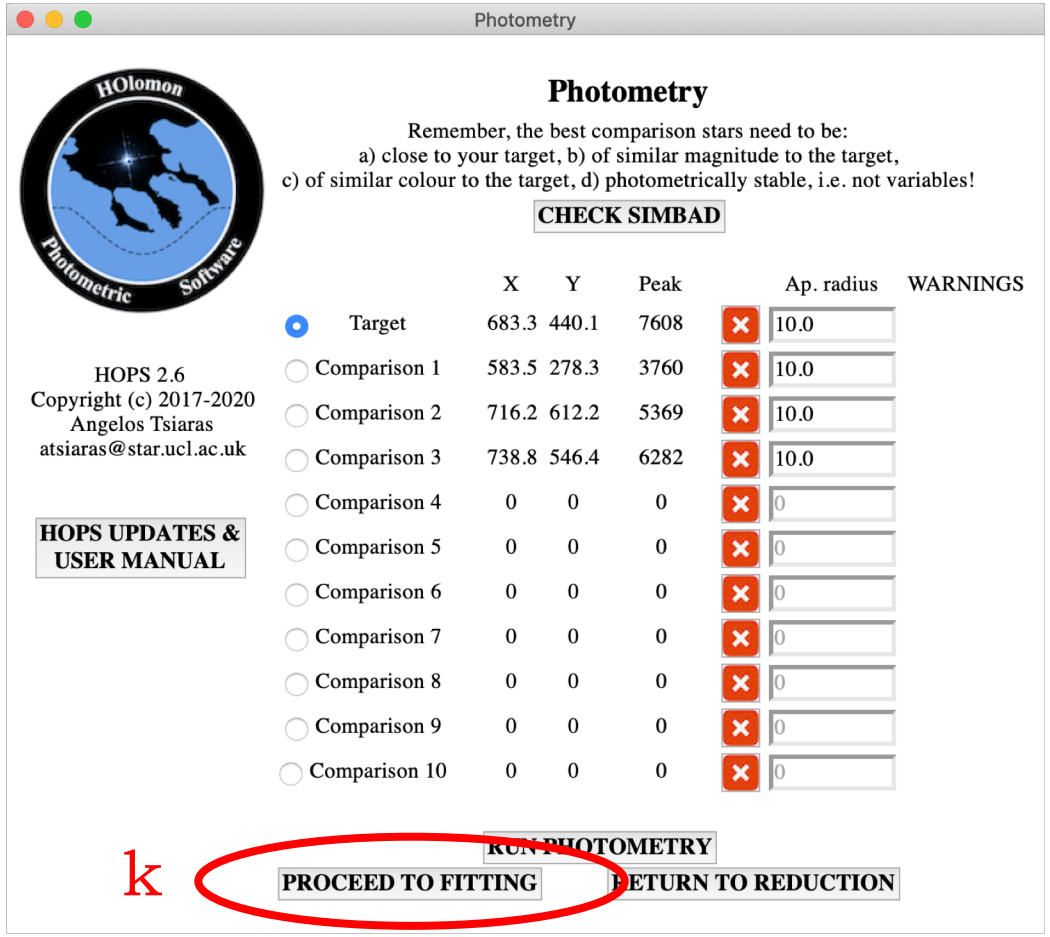
o

Example from a difference case – the variable star is Comparison 2



Proceed to fitting

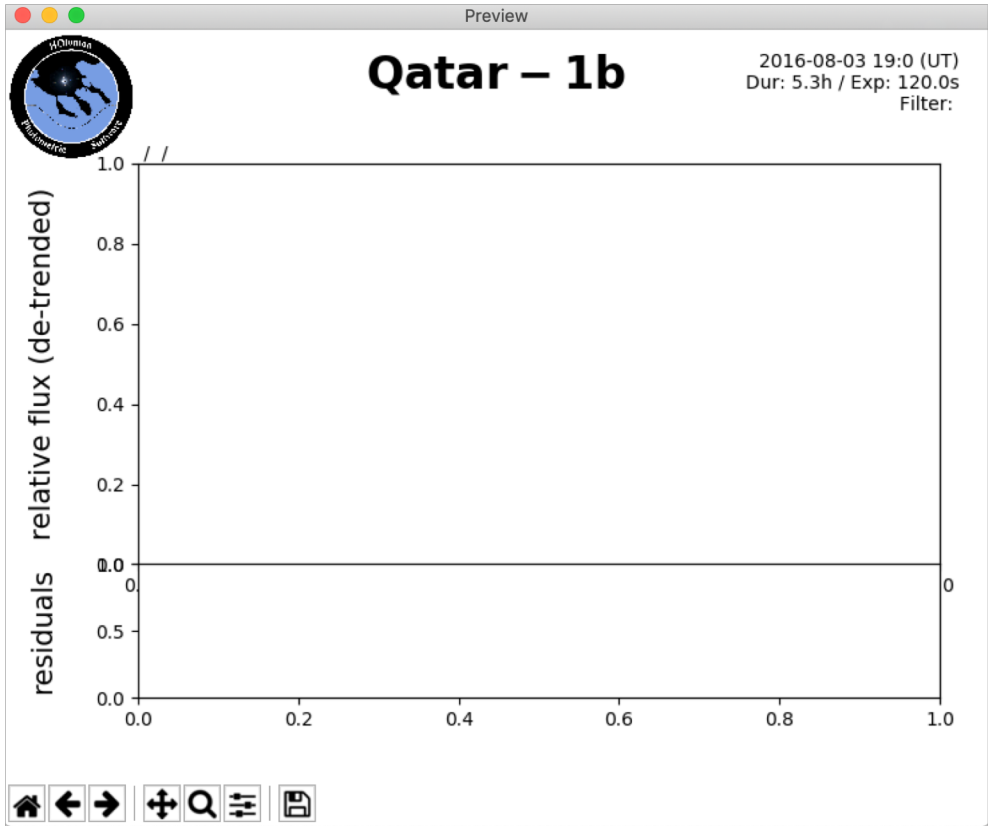
k. You can repeat the photometry part with different comparison stars or different aperture sizes as many times as you want. When you are satisfied with the result, click on PROCEED TO FITTING to continue to exoplanet transit modelling.

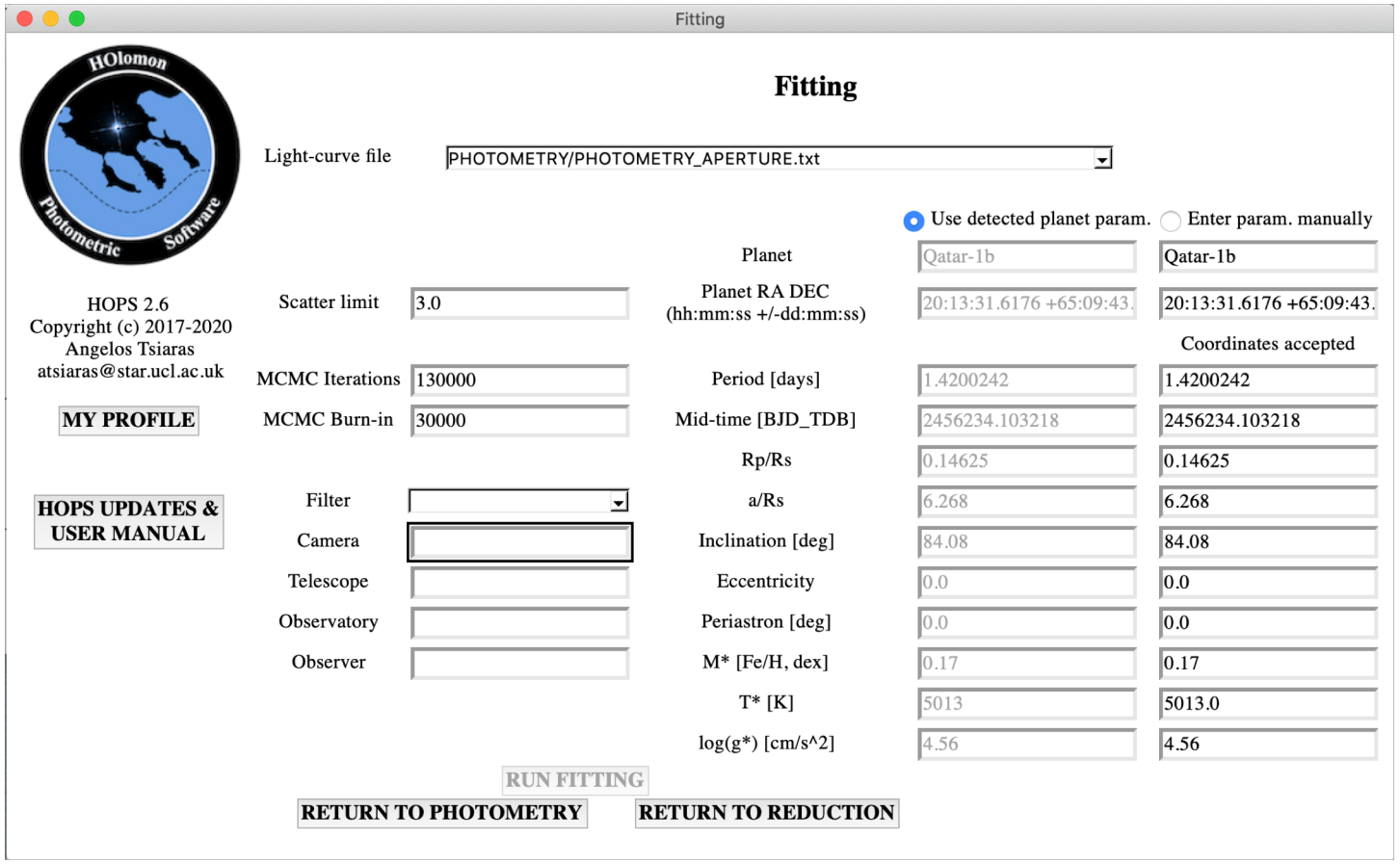


Fitting

Fitting window

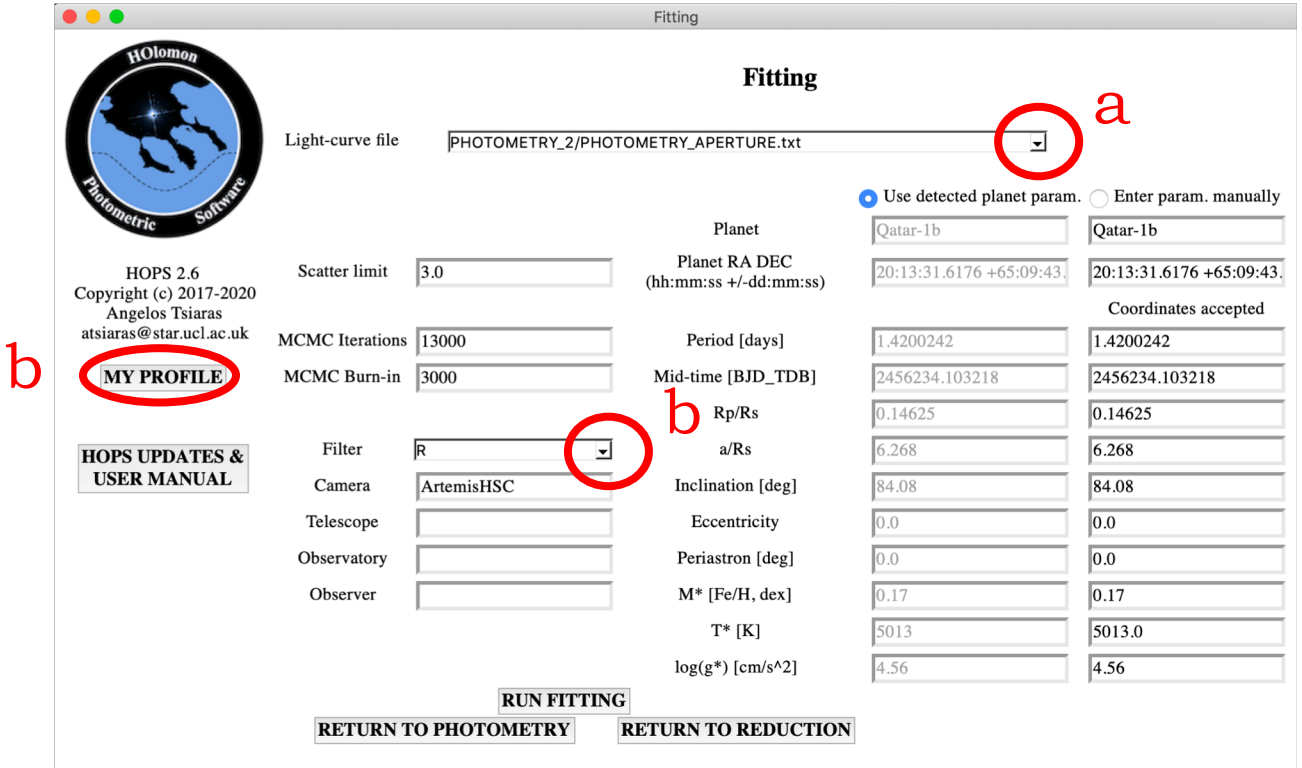
After photometry, two windows will appear: one showing a preview of your data with the results of a fast fitting (don't worry if it is totally blank in the beginning) and one where you can select the fitting parameters.





Choose your photometry file and filter

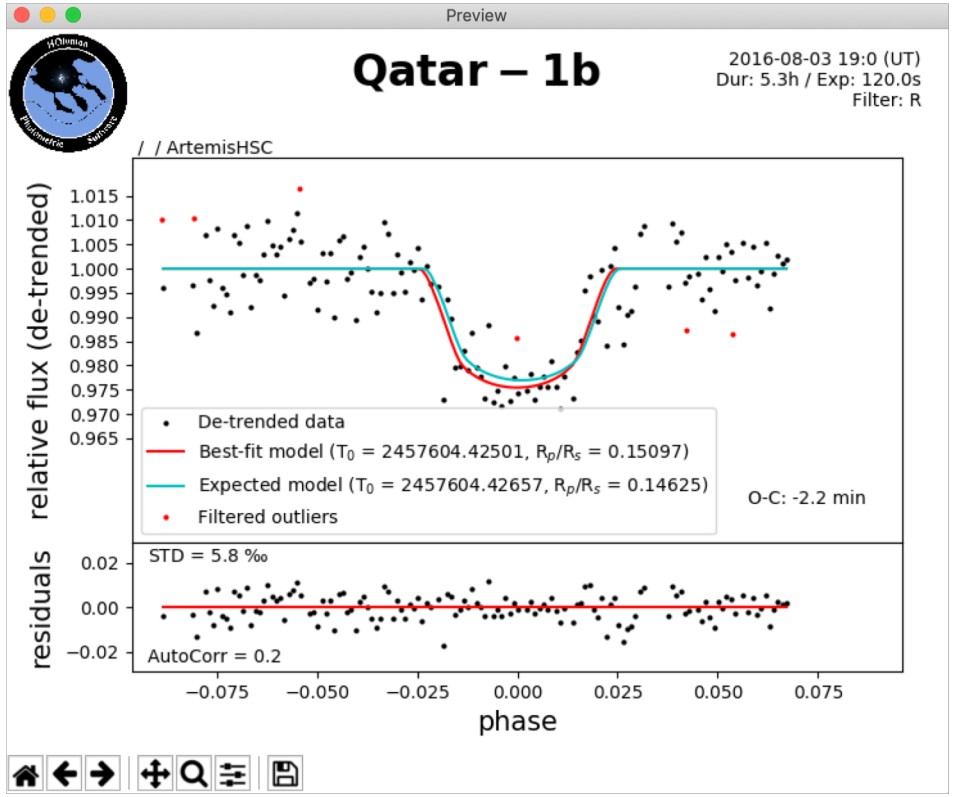
a. Choose the light curve you want to fit form the drop-down menu Light-curve file, you can choose between aperture of PSF fitting (GAUSS) and the different attempts of photometry that you tried.
b. Choose your filter form the drop-down menu Filter (you cannot procced without a filter, and the fitting preview will be empty).
c. If your filter is saved in the files header and it is compatible with the list you can set it up in MY PROFILE for the future.

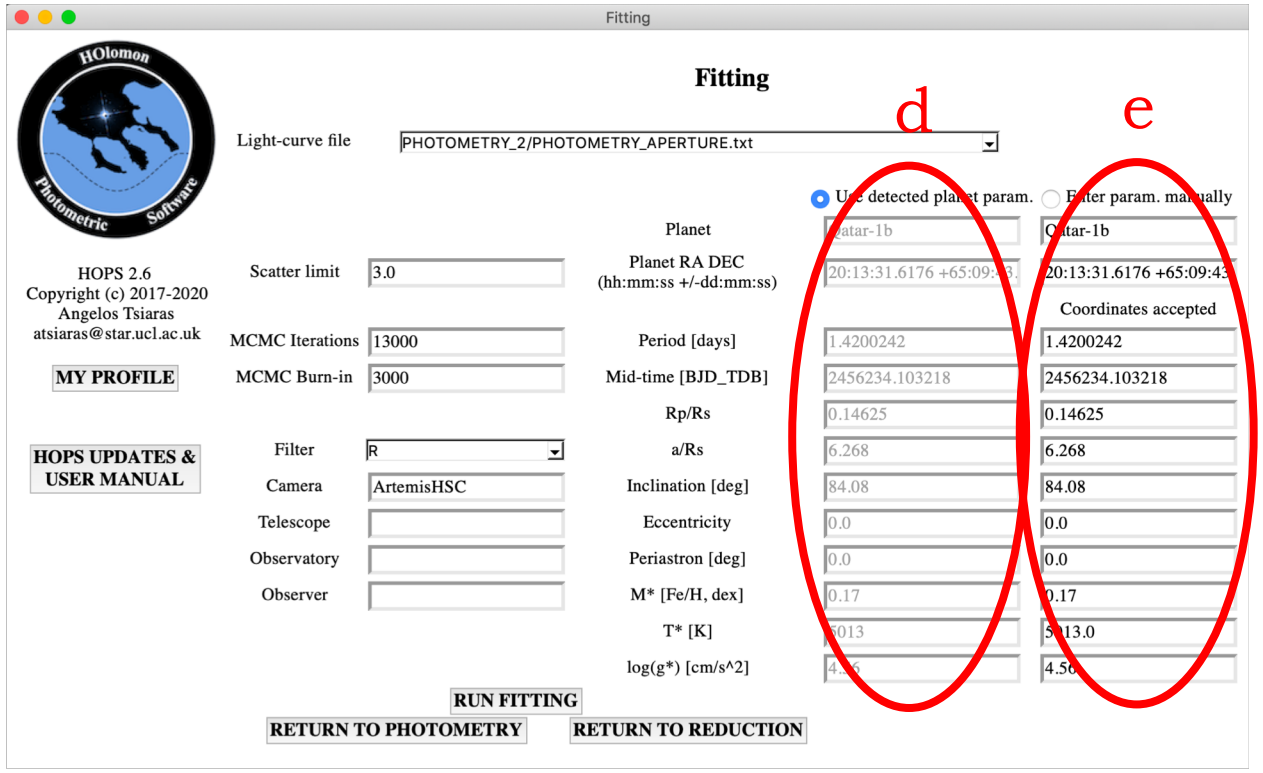


Set your target parameters

d. The exoplanet that is closer to your coordinates will be chosen from a built-in catalogue, at this stage the fitting preview should appear on the secondary window.

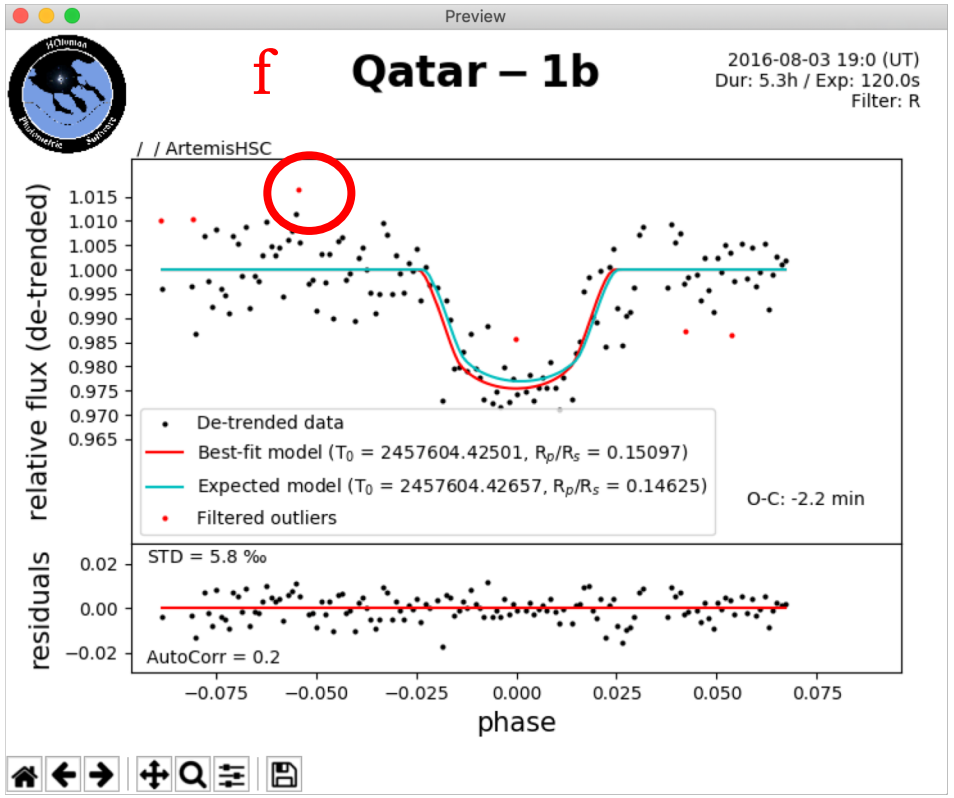
e. This catalogue contains about 500 exoplanets but not all of them. If this is not your target or if you want to change the default values.

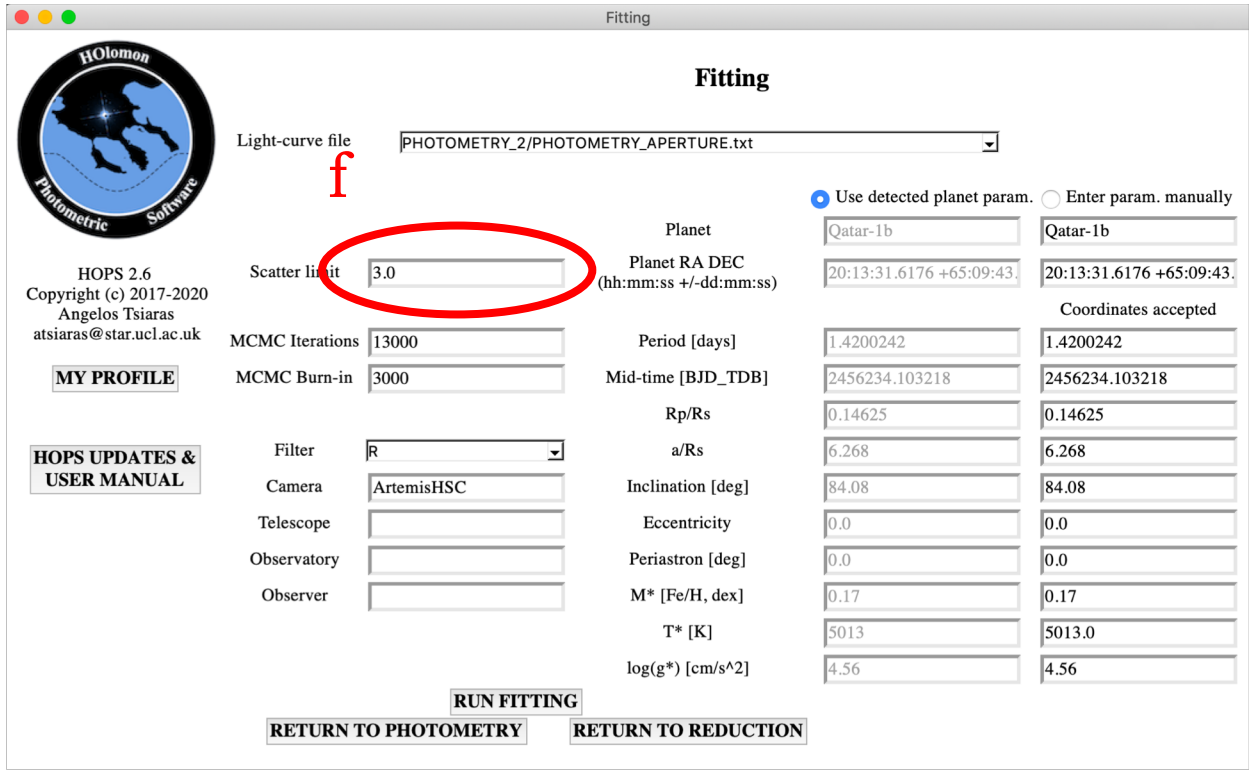




Clear outliers

f. The scatter limit is a parameter for excluding outliers, the lower the value the more sensitive the filtering process is (i.e. more point will be excluded). Reasonable values are above 3, otherwise to many point will be excluded. The excluded points appear red in the preview.

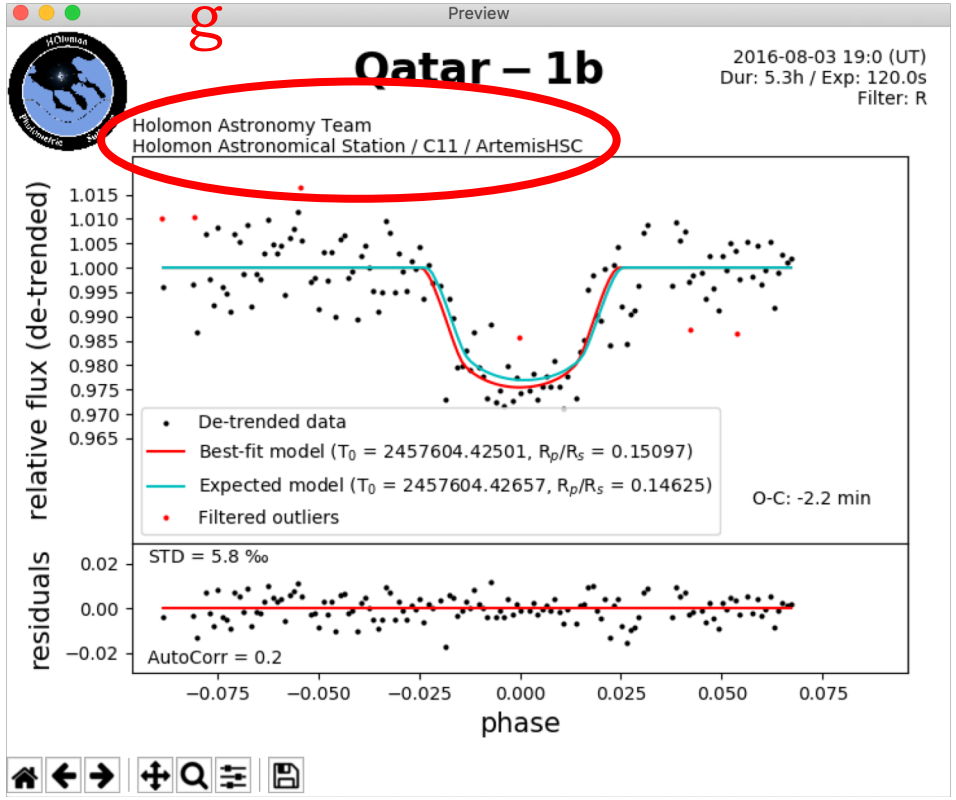


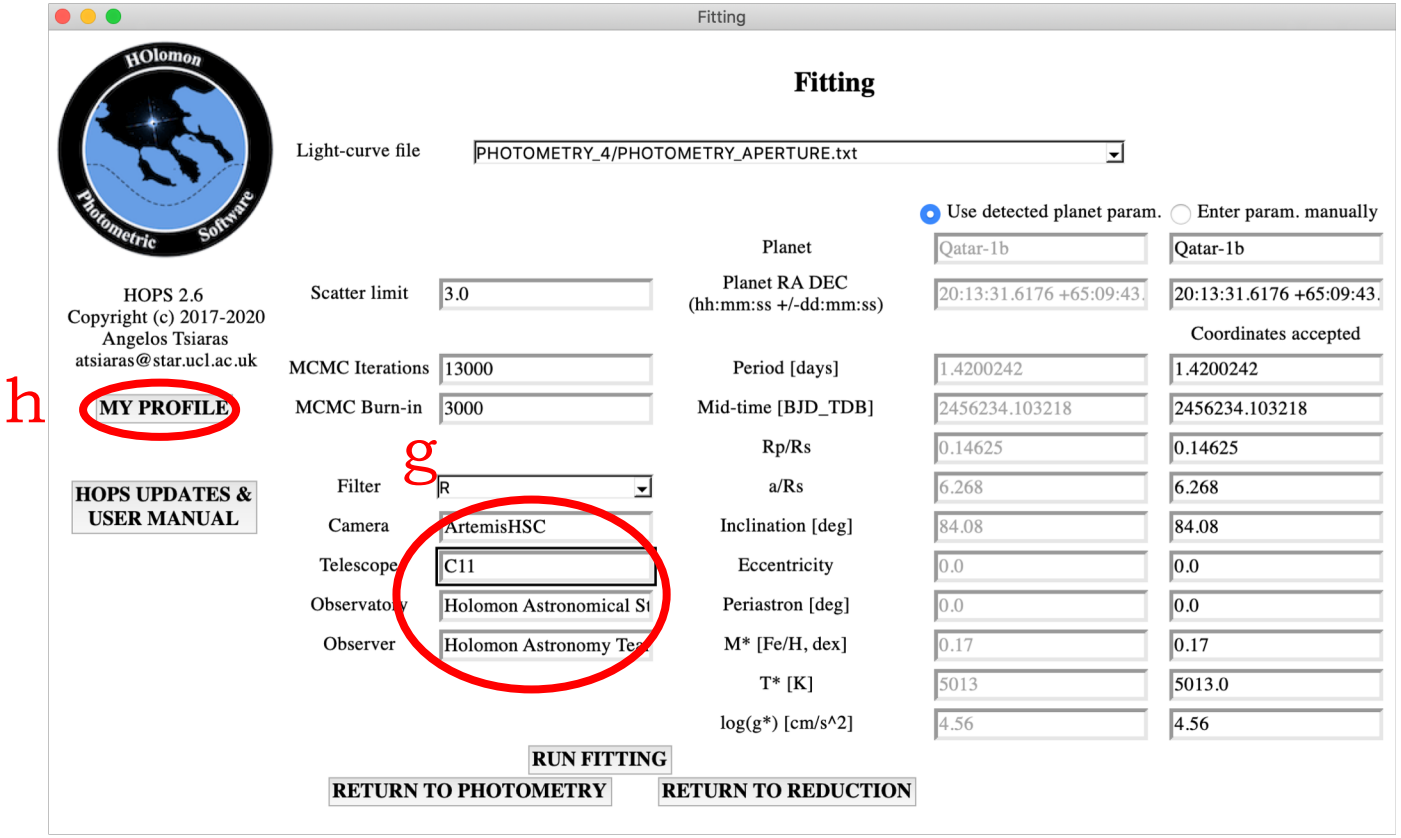


Add your personal details

g. You can add information about your Camera, Telescope and Observer, to appear in your final plot.

h. If his information is saved in the files header you can set it up in MY PROFILE for the future.



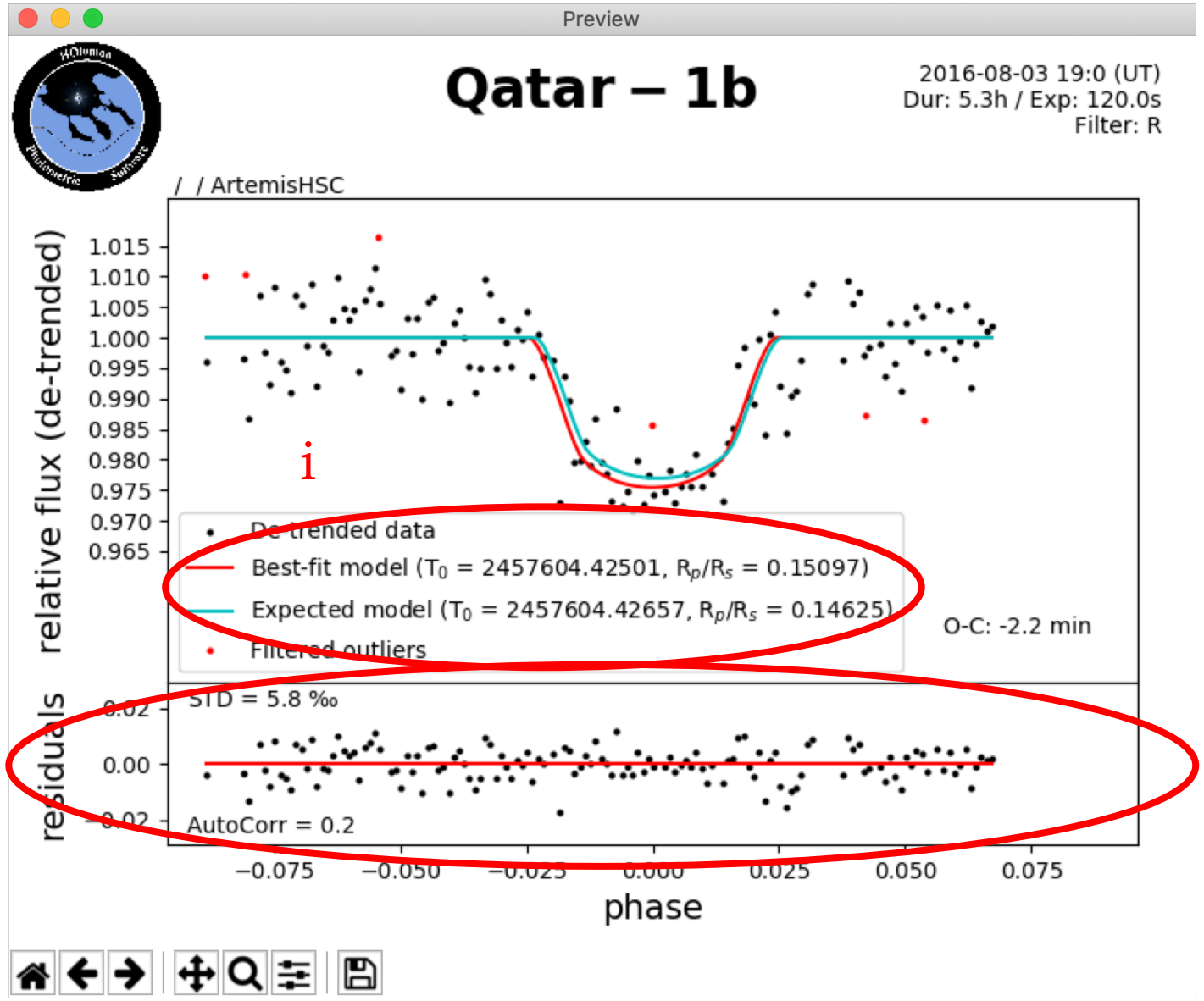


Evaluate your fitting preview

Checking the fitting preview is an important part of the process. It will tell you if your data are good to a level that results can be extracted.

i. 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 comparisons 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.**
j. The residuals are the difference between your data and the best model. STD and AutoCorr are the standard deviation and autocorrelation of the residuals. The smaller these numbers, the better the fitting.

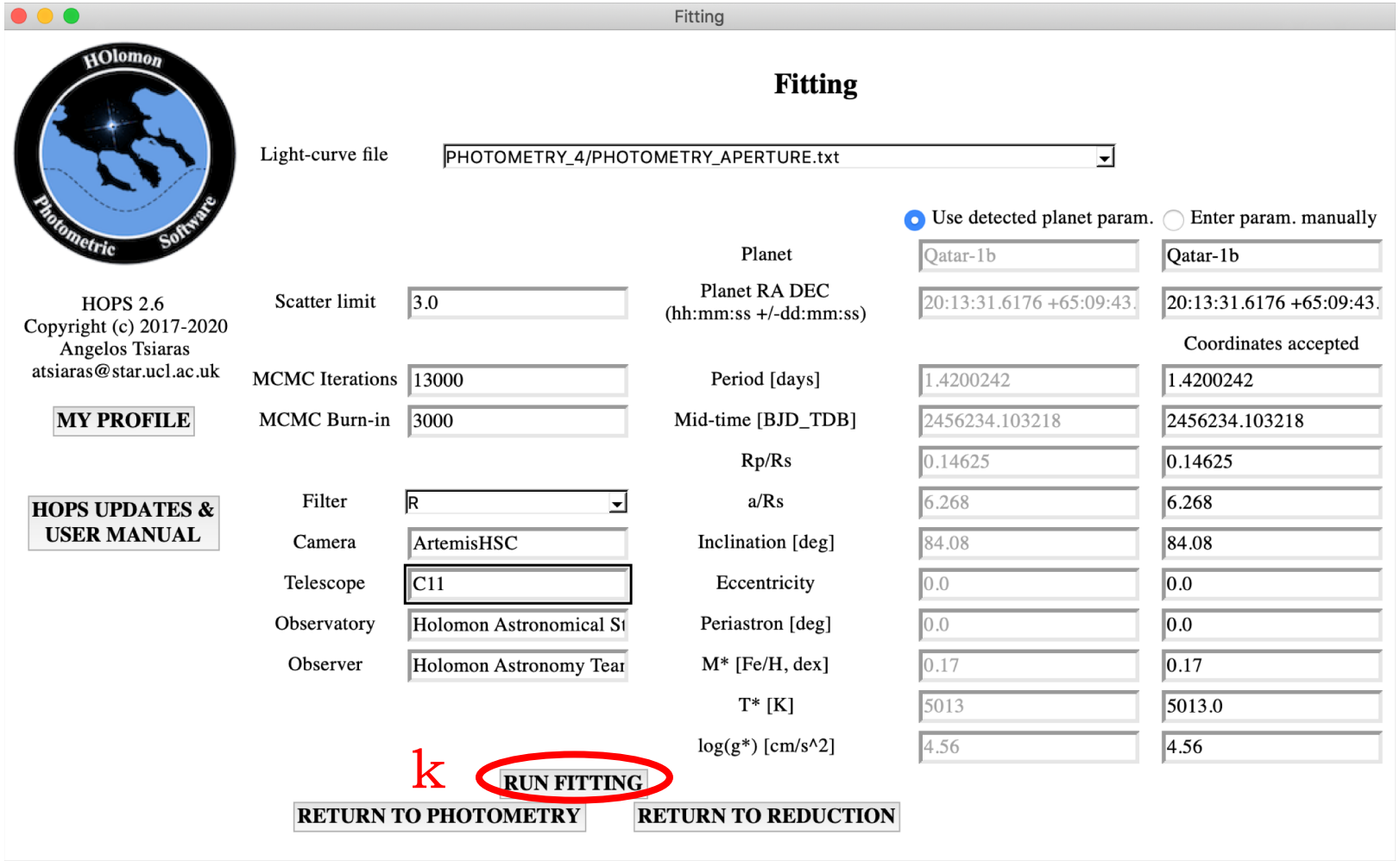
Evaluate your fitting preview



j

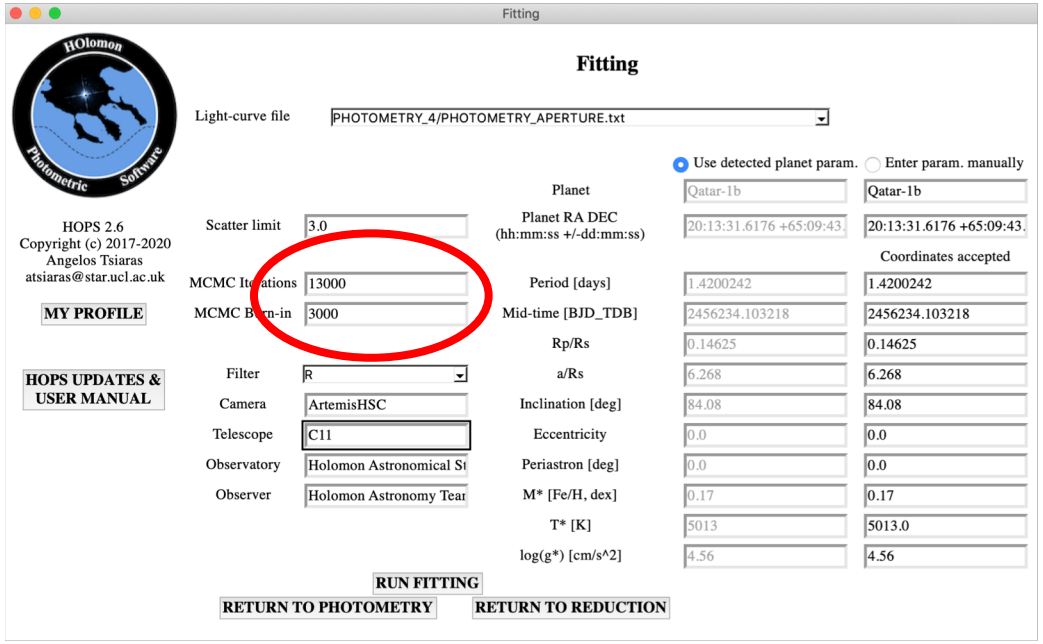
Run fitting

k. If you are satisfied with the fitting preview, click on RUN FITTING to continue.



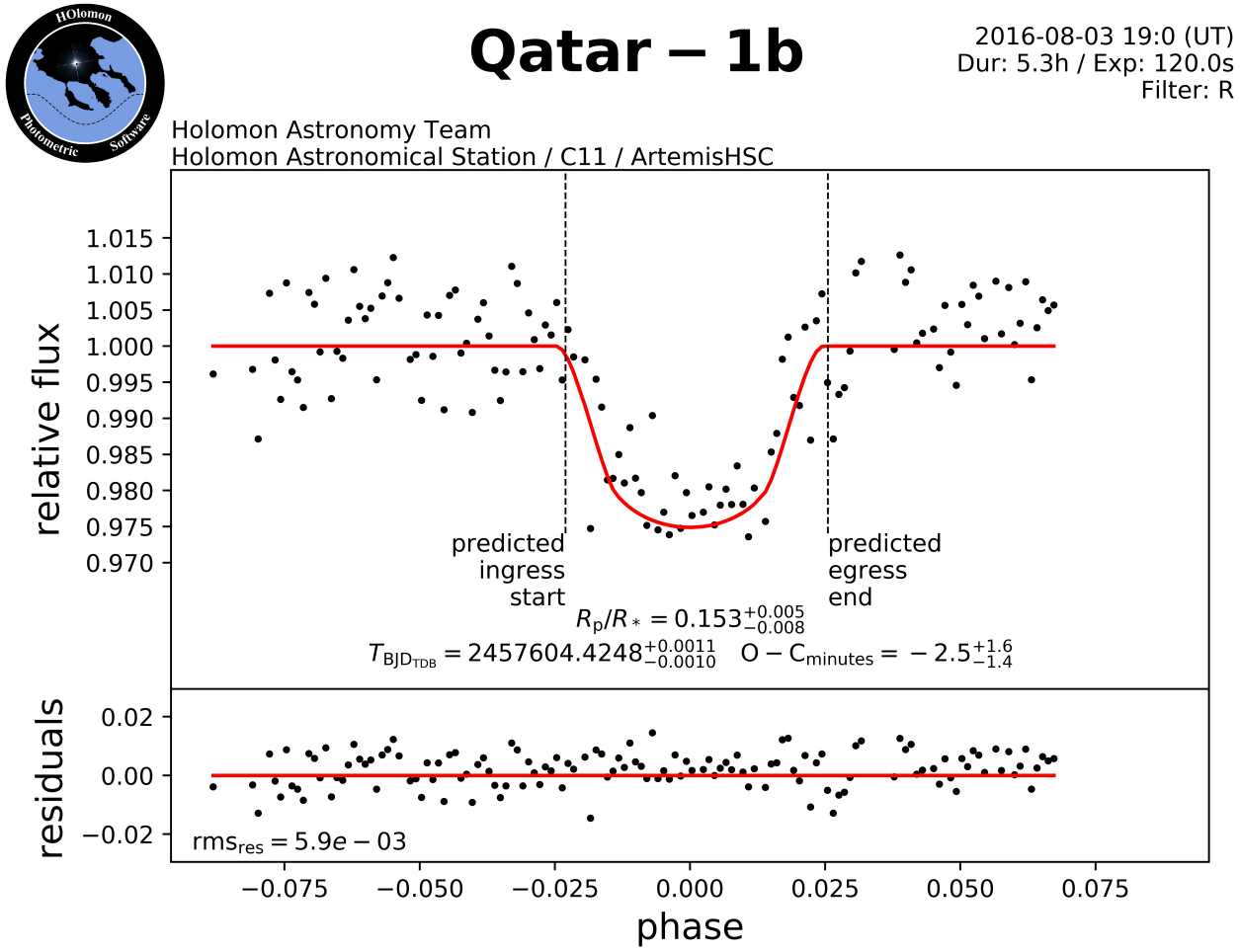
Run fitting

HOPS uses MCMC fitting, which is a process that tries to reach the best result by approaching it in small steps. The numbers of steps is indicated by the MCMC iterations. The default value of 130000 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 (because in the beginning the algorithm is trying to "find its way towards the best solution). If you increase MCMC iterations, increase MCMC burn-in accordingly.



Final graph

After a couple of minutes the final graph will pop up. This is the same as the preview but with the MCMC fitting results displayed instead of the quick fitting results.



Output files

File structure

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

- log.yaml - supporting file with all the information (DO NOT DELETE THIS FILE!)
- all_stars.pickle - supporting file with information on alignment (DO NOT DELETE THIS FILE!)
- 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
- FITTING – folder that contains the fitting results, one for each time you run fitting
- Inside the PHOTOMETRY and the FITTING folders you will find more detailed descriptions of the output files inside them.