Shifting your images

Tiina Liimets (tiina.liimets@asu.cas.cz Office nr 209)

Research workshop on evolved stars 02.09.2022

To shift or not to shift?



- Any shifting is interpolation of pixel values. You will see that shifted images are slightly different. The peak and FWHM values have changed perhaps a bit more than you feel comfortable, but the integrated flux values are the same within 1%.
- This is a trade-off. You will have to decide yourself if this is acceptable for your science.

Primitive shifting

- We use pixel coordinates, which is enough for your current work.
 Simple IRAF tasks are used (display, imexam, imshift), which are combined into a self-made task. We use also a short python program to calculate the shifts.
- In the future, you might want to start using the WCS (astrometry), then shifting is not needed.

IRAF task align

- This is self-made IRAF task (similar to Mauricio). It is in a file align.cl
- Copy align.cl into the directory where you have the images you want to align.
- Copy to the same directory the little python program pre_shifts2.py which is calculating the shifts.
 - pre_shfits2.py uses python2.7! It is available in the virtual box. Later pythons may not work.
 - In virtual box before starting IRAF, in terminal type: conda activate iraf27
- You have to let IRAF know that you have your own task. In IRAF terminal: task align=align.cl

THIS HAS TO BE DONE EVERY TIME YOU OPEN IRAF!!!

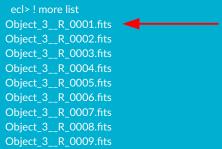
If you do not do it, you get the following error:

ecl> align

ERROR: task 'align' not found

Preparation

Create a list of your images. The name of the list has to be "list", otherwise the script will not work!!!

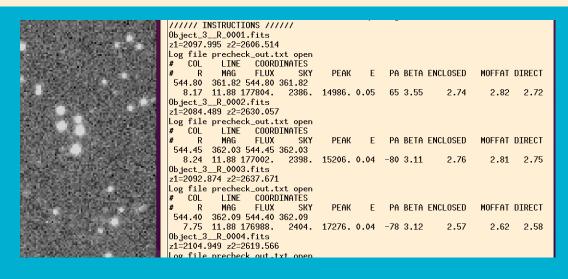


- The first image of the list is the reference image. All other images will be aligned with this frame.
- If you have a long list of images (> ~50), I recommend splitting the list into smaller portions because the task requires manual clicking on a star on each image. If you make a mistake, you will have to start from the beginning.
 Keep the reference frame the same!!! The first image of each list has to be the same.
- Ds9 has to be open.

align in action

 In IRAF terminal type: align list and follow the instructions on the screen

```
ecl> align list
///// INSTRUCTIONS /////
In the ds9 window, on top of your reference star
click 'a' to measure the star and click 'q' to go to the next frame
///// INSTRUCTIONS /////
Object_3__R_0001.fits
z1=2097.995 z2=2606.514
Log file precheck_out.txt open
```



align: outputs

- Shifted images: fits files which have "s.fits" in the end. ecl> cat listout

Object_3__R_0001s.fits Object_3__R_0002s.fits

•••

Check what you got!
 In ds9 display and blink few frames (e.g. first, middle, last)

align: additional outputs (just for information)

- Files that are created during the process:

precheck_out.txt (imexam output (text) file with the information about the clicked stars)

<u>pre_shifts.txt</u> (text file with the shifts to be applied to the frames. This is the output from the python program pre_shifts2.py)

listout (text file with the filenames that will be shifted)