ecl>

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This is the EXPORT version of IRAF V2.16 supporting PC systems.									
Welcome to IRAF. To list the available commands, type ? or ??. To get detailed information about a command, type 'help <command/> '. To run a command or load a package, type its name. Type 'bye' to exit a package, or 'logout' to get out of the CL. Type 'news' to find out what is new in the version of the system you are using. Visit http://iraf.net if you have questions or to report problems. The following commands or packages are currently defined:									
(Updated on 2013-12-13)									
ctio.	finder. fitsutil. gemini.	lists. mem0. mscdb.	noao.	sqiid. stecf. stsdas. system. tables.	utilities. vo. ×dimsum.				

# **Using IRAF for the first time**

- To start IRAF: open an **xgterm** terminal in the normal terminal and type cl.
- Likely this will issue a warning: *no login.cl found in login directory*.
- The file login.cl contains the default configuration for IRAF; you should create it before using it for the first time.
- Exit IRAF by typing logout, and then create the login.cl by typing mkiraf; choose terminal type xgterm.
- Edit the file login.cl according to your preferences, mainly:

set editor = emacs set stdimage = imt4096

set imextn = "oif:imh fxf:fit,fits ..."

- Now start iraf again.
- In our case it is much simpler, just type <code>\$iraf</code> when you are in your home directory /home/workshop/

- IRAF is divided in different packages including different tasks for doing photometry or spectroscopy, as well as data analysis
  - You can import the different packages by typing their name
  - You can get a list of the tasks of the package you are in by typing '?' or '??'
  - To remove the packages again, type **bye**

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    adccdrom.
                deitab.
                            images.
                                        mtools.
                                                    softools.
                                                                upsaiid.
    cfh12k.
                esowfi.
                                                                utilities.
                            kepler.
                                        nfextern.
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    cirred.
                finder.
                            language.
                                        noao.
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    ctio.
                fitsutil.
                            lists.
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                                                                xray.
    dataio.
                gmisc.
                            mscdb.
                                        proto.
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                guiapps.
                                                    ucsclris.
    dbms.
                            mscred.
                                        rvsao.
```

#### Some basic commands:

- epar [task]  $\rightarrow$  edit task parameters.
- :wq  $\rightarrow$  write the parameters and exit.
- : go  $\rightarrow$  execute the task.

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#### Some more basic commands:

- help task, to get some help on your task
- ? to get commands in the plot window and available commands in epar
- If you want to know, which package your task belongs to: which task
- To plot a spectrum: splot spectrum.fits
- To check the fits header: imhead spec.fit l+ | page
- To select some fields from the header:

hselect spec.fit\$I,obj-name,exptime yes

• Check stats of image or spectrum: imstat image.fits

Commands in the plot window:

- Type q to exit plot window
- To zoom in window press w and then

e (cursor lower left corner) e (cursor upper right corner)

- With w and a you can zoom out again
- With w and r you can move right
- With w and l you can move left
- With w and u you can move up
- With w and d you can move down

• If you want to know the commands in the specific plot window, type '?'

- A really useful tool is the task imexamine, which allows to analyse fits images.
- It can be used as a quick-look tool during observing runs.
- To use it, you will need to display the images in ds9. To open it, type:

!ds9 &

• To plot an image: display image.fits

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lds9 &

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Tells IRAF this is an external command.

You can run any terminal command like this Sends it to background so you can still use command lines.

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- To display an image, do display [image name]
- Run imexamine (just type imexam on terminal).
- You will notice the cursor turns into a circle in ds9 this means imexamine is activated.
- Some basic imexamine commands:

l – plot the counts on the selected line c - plot the counts on the selected column r - display radial profile a - show counts, sky, FWHM, etc. on screen e - display contours