Using IRAF in Swain West 246

About IRAF:

The IRAF software package (Image Reduction and Analysis Facility) was developed at the National Optical Astronomy Observatories for use with astronomical data in the early 1980s, and has become the primary software used by astronomers for handling data. IRAF was adopted by the Space Telescope Science Institute for use with HST data, and is also used for data from several other NASA missions and facilities. It is distributed for free, and runs on Linux, Unix, and OS X platforms, among others. We will be using IRAF on the Macintosh computers in SW246. This computers use the OSX operating system.

IRAF contains many routines or *tasks* designed to do specific data reduction or analysis jobs. The tasks are organized into *packages* related to specific types of data or functions. Examples of packages include **dataio** (reading and writing data), **ccdred** (reducing CCD data), **image** (for image analysis), and **onedspec** (for processing spectra). Specific tasks in the **dataio** package include *rfits* (to read fits images), *wfits* (to write fits images), etc.

Getting Started:

Because IRAF uses interactive graphics, it runs from a particular window called an "xgterm" window. Before starting IRAF, you must open an xgterm window by clicking the IRAF button on the dock. Select one of the buttons in the window that pops up to open an xgterm window and the **ds9** image display window. The xgterm window will open with IRAF already running. Other terminal windows can be used for computer commands outside of IRAF.

To quit an IRAF session, type "**logout**" in the xgterm window.

Once IRAF is started, you can load the particular packages with the tasks you need by typing the names of the packages. To unload a package, type "**bye**" in the xgterm window. (You do not need to unload packages before logging out of IRAF.)

To execute a task, simply type the name of the task (e.g. typing "**rfits**" will execute the task **rfits**).

Type "**help** *packagename*" to find out what tasks a package contains and "**help** *taskname*" to find out what a particular task does (and how it works).

The delete key: An annoying quirk of IRAF in the xgterm window is that the backspace key may not work. Use the delete key instead.

The login.cl File:

When you start IRAF, the file *login.cl* is used to set the defaults for how IRAF operates. These include the definition of where your IRAF home directory is, where the data pixels are stored, which editor you use, which printer plots are sent to, etc. The file is already present in your home directory on the computer and it has been edited to match our local environment. You may want to look at the file once you are familiar with IRAF and make further changes to match your own style.

If you are using IRAF on another computer, you will need to execute the command **mkiraf** to set up the necessary directories and files for IRAF to run from your account. Once you have run **mkiraf** you will not need to so again. **mkiraf** will create a login.cl file in your directory, and you can edit the file to change the defaults to suit your own needs. The "cl" command in the xgterm window starts IRAF running (on our Macs, this is already done for you).

Parameter Files:

Each IRAF task has a parameter file that specifies the values of the parameters needed to run that task. To find out what the parameters (and their values) are for a particular task, type

> **lpar** *taskname* (for example, type *lpar display* at the prompt)

Some parameters are enclosed in parenthesis. The task assumes the values given in the parameter set for these parameters (called "hidden" parameters) whenever the task is run. The values of all other parameters must be specified either on the command line each time a task is executed, or interactively during the execution of a task.

To edit a parameter file, type e.g.

> **epar** *taskname* (for example, type *epar display* at the prompt)

Use the arrow keys (right side of keyboard) to navigate. Enter the new parameter value and the enter key to change it. To exit the parameter set editor and save the new values, type

> **:q** (or CNTL-d)

To exit and execute the command with the new parameter values, type

> **:go**

The parameter values are saved and will be used whenever the task is executed unless you edit the parameter file again, or specify otherwise on the command line. To reset the task parameters to their original, default values, type

> **unlearn** *taskname*

Alternatively, you can execute a command without modifying the parameter file by including the parameter settings on the command line. In that case, the parameter file is not changed. Note that there are short and long ways to do this. You need only to type enough characters that the procedure/parameter is uniquely identified:

>**imhead** *imagename* **long=yes** (for example, try typing *imhead dev$pix* or *imhead dev$pix long=yes*)

is equivalent to:

>**imhead** *imagename* **l+**

Image Formats:

Most images used in IRAF are in one of two formats: "FITS" images or "IRAF" images. Most data begin as FITS (with the ".fits" suffix) images. FITS stands for Flexible Images Transport System, and is a standardized format used by most observatories for astronomical images. While most IRAF tasks work well with either format, some work only with the IRAF image format. The tasks *rfits* and *wfits* are used to convert images back and forth between the two formats.

The FITS format is a self-contained file with both the pixel values and the header information. IRAF images (images with the .imh suffix) separate the header information and the pixel values into two separate files. The large pixel files are usually stored in a separate directory (the *imdir* directory, defined in the *login.cl* file), and only the headers are kept in your working directory.

Frequently-Used Commands:

To execute an IRAF task, simply type the name of the task followed by any necessary parameters. For example, the command *imhead* allows you to examine the contents of the image header. Check out the parameter file (via "lpar") and the help file (via "help") to see the different options for running *imhead*. For example, try the following:

> **imhead** *imagename*

> **imhead** *imagename* long+

will print the full image header to the screen.

> **imhead** *imagename* long+ | page

will break the header into screen-sized portions by "*piping*" the output of the *imhead* task into the *page* task.

Other frequently used commands include:

imcopy	Copy an image
imdelete	Delete an image (similar to Linux "rm")
imrename	Rename an image (similar to Linux "mv")
imhead	Show the image header
display	Display an image
imexamine	Examine a displayed image interactively

NOTE: **NEVER EVER EVER** use the Linux commands "rm", "mv" etc. on .imh files; you must manipulate them using IRAF in order to access the .pix files at the same time.

Displaying Images:

The command "display" displays an image.

Try out "display" on one of your images, first using autoscaling:

> **display** *imagename* **1**

Practice using the mouse to adjust the contrast and learn how to manipulate the display using the SAOImage controls.

The task *imexamine* allows you to examine the image interactively, and performs such functions as displaying cuts along rows or columns, or surface plots, etc. Useful commands to get you started are:

c Plot of a column or average of columns
l Plot of a line or average of lines
r Gaussian fit to circular aperture
x Print cursor location in image coordinates
a Statistics of circular aperture at position
q Exit imexamine

See the "**help imexamine**" documentation. You'll use *imexamine* a lot, so it is worth studying the documentation and then practicing with it to see what it can do for you. To quit *imexamine*, type **q** with the cursor on the display.

What do I do if IRAF crashes?

- First, flush the process cache by typing

> **flpr** (pronounced "flipper") a couple of times if something aborts or crashes.

- If an IRAF task is hung and you don't have a cursor in the xgterm window, try typing

> **CNTL-c** (hold the control key down and type a c at the same time), and then a **flpr**.

- If things remain hung, try logging out of IRAF completely and then restarting.

- If you want to abort a task in the plot window, *shift-I* usually works.

OSX Commands:

Some OSX commands are identical to IRAF commands, e.g.

> **ls *.imh**

whereas others are not ("more" for example is "type" within IRAF). OSX commands can be run within the IRAF environment by preceding them with a "!" (pronounced "bang").

> **!lpr textfilename**

Running a command again:

IRAF stores a history of the commands you type. You can recapture a recent command via one of several methods. Type

> **history**

To show the recent commands.

> **e**

will show the most recently executed command and allow you to edit it with the arrow keys.

> ^

will execute the most recent command automatically.

More Information About IRAF

To learn more about IRAF, visit the IRAF website at iraf.noao.edu. Many manuals and documents are available to describe the software and data reduction procedures, and the IRAF tutorials can help you become more familiar with IRAF's many packages and tasks.

An excellent tutorial for IRAF is available from the Astronomy department at the University of Washington. See: www.astro.washington.edu/astro480/

Other good sources of information can be found at:

- IRAF Project Home Page (iraf.noao.edu)
- The IRAF tutorials page (iraf.noao.edu/tutorials/tutorials.html)
- IRAF Recommended Docs (iraf.noao.edu/iraf/web/docs/recommend.html)

This document is derived from one prepared by Martha Haynes at Cornell University, and is used at Indiana University to introduce undergraduate students to IRAF.