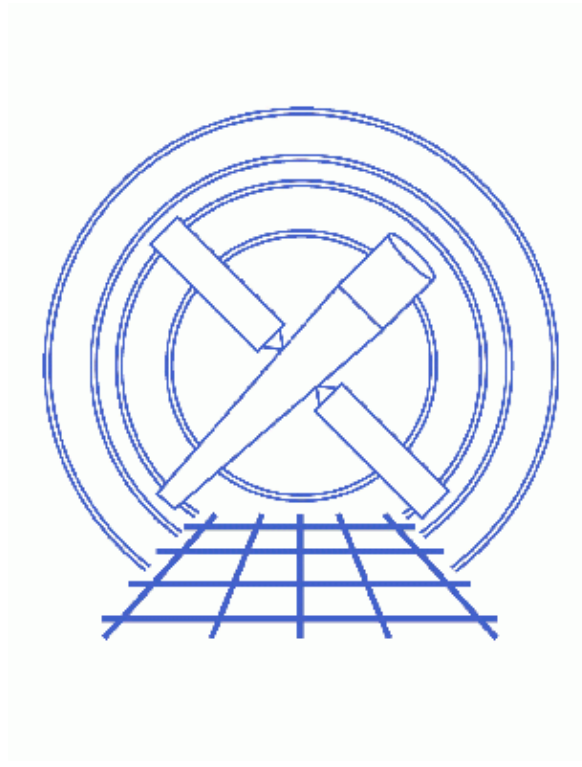


Introduction to Plotting Using ChIPS



CIAO 3.4 Science Threads

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Introduction to Plotting Using ChIPS

CIAO 3.4 Science Threads

Overview

Last Update: 1 Dec 2006 – updated for CIAO 3.4: *ChIPS* version

Synopsis:

The Chandra Imaging and Plotting System (*ChIPS*) is the visualization interface which can receive commands from any application within CIAO. *ChIPS* is designed so that plots can be built up interactively in small steps and can easily be refined, saved, printed, and restored. It is particularly flexible at creating plots from tables, but also allows users to generate plots of selected columns from an image or event file.

Related Links:

- Full details on *ChIPS* commands can be found in the [ChIPS Reference Manual](#).
- [chips help page](#): information on how to use S-Lang within *ChIPS*.

Proceed to the [HTML](#) or [hardcopy \(PDF: \[A4\]\(#\) / \[letter\]\(#\)\)](#) version of the thread.

Getting Started

If you haven't obtained it yet, the data used in this thread is available as [chips.tar.gz](#) (SHIFT-click to download the file). Use the `tar xvf chips.tar` command to unpack the unzipped file.

Move to that directory and start a *ChIPS* session:

```
unix% chips

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chips> ls
data1.pha      data2b.dat    data4.tab     plot.chp
data2a.dat    data3.tab     data5.dat
```

Within *ChIPS*, Unix commands must be preceded by a dollar sign (`$`), except for `cd`, `pwd`, and `ls`. For example, to view the contents of the ASCII data `data2a.dat`:

```
chips> $more data2a.dat
40535      31.24      0.69
40872      29.67      0.36
41006      30.18      1.33
41285      30.5       0.3
41713      29.5       0.4
43556      26.2       0.1
```


```
.
. (etc.)
.
```

Also, *ChIPS* commands are *case insensitive*; they may be used in either upper or lower case.

Creating Simple Plots


To begin, we create a plot from the file `data1.pha`:

```
chips> plot data1.pha
The inferred file type is PHA type I.
```

As seen in [Figure 1](#) , `x` is plotted from the first column of the file, `y` from the second.

This can also be specified explicitly, e.g. for an ASCII file:

```
chips> clear
chips> plot data2a.dat x 1 y 2
```

This selects column 1 as `x` and column 2 as `y`; see [Figure 2](#) . The `clear` command is used to remove all previous plotting objects and create a new blank drawing area.


If the file contains error data, they can be included:

```
chips> clear
chips> plot data2a.dat 1 2 3
```

This command plots `x` and `y` from columns 1 and 2, respectively, as shown in [Figure 3](#) . Data from column 3 is used to plot symmetrical error bars in `y`.

If the file contains data for nonsymmetrical error bars:

```
chips> clear
chips> plot data3.tab x 1 y 2 yup 3 ydown 9
```

This command plots `x` and `y` from columns 1 and 2 respectively, as shown in [Figure 4](#) ; data from column 3 is used to plot the positive error bars in `y` and data from column 9 is used to plot the negative error bars in `y`.


Customizing the Plot

Labels and titles may be added to a plot:

```
chips> clear
chips> plot data1.pha
chips> title "Test Plot"
chips> ylabel "Count Rate"
chips> xlabel "Channel"
```

In addition, the characteristics of the labels and title may be modified:

```
chips> xlabel blue
chips> xlabel size 1.5
chips> ylabel blue
chips> ylabel size 1.5
chips> title red
```

The plot now appears as shown in [Figure 5](#) .

See the appropriate [ahelp](#) files for other commands that may be used to customize the appearance of the plot:

- [axes](#): specify the bounding box surrounding a drawing area.
- [curve](#): change curve attributes.
- [errs](#): specify the appearance of errorbars.
- [grids](#): add grid lines or change grid attributes.
- [limits](#): set the ranges to be displayed in the axes.
- [line](#): add a line or change line attributes.
- [symbol](#): change or remove symbols from a curve.
- [ticks](#): specify the spacing of tick marks.
- [tickvals](#): control the numerical tick mark labels.

Plotting Two Datasets Together

An important *ChIPS* concept is the "plotting object". Plotting objects are curves, labels, lines, titles, etc. When multiple plotting objects of the same type exist in a single plot, each is assigned a unique reference number.

To plot two datasets in the same drawing area, the first curve is plotted:

```
chips> clear
chips> plot data3.tab 1 2 3
chips> symbol circle
chips> limits 1982.0 1999.0 0.0 3.0
```


then the second curve is added:

```
chips> plot data4.tab 1 2 3
chips> c\_2 symbol square
```

When the symbol type for the second curve is changed, "[c_2](#)" specifies the curve on which you wish to operate.

Labels are then added to the drawing area:

```
chips> xlabel "Time (years)"
chips> ylabel "Flux (2-10keV)"
chips> xlabel size 1.5
chips> ylabel size 1.5
```

[Figure 6](#)  shows the resulting plot.

It may also be useful to overlay one dataset on another; here we plot a dataset overlaid by the fit:

```
chips> clear
chips> plot data2a.dat 1 2 3
chips> plot data2b.dat
chips> c\_2 simpleline
chips> c\_2 symbol none
chips> c\_2 red

chips> xlabel "Time (JD-2,400,000)"
chips> ylabel Velocity
```

[Figure 7](#)  shows the resulting plot.

Plotting Two Datasets Separately

Similar to curves, multiple drawing areas may be created and referenced by a number.

Two drawing areas are created and a gap between them is defined:

```
chips> clear
chips> split 2
chips> split gap 0.05
```


A curve is added to each drawing area:

```
chips> d_1 plot data3.tab 1 2 3
chips> d_2 plot data3.tab x 1 y 4 yup 5 ydown 6
```

Note that the "d #" portion of these commands specifies the drawing area.


Various modifications are made to the two drawing areas and their curves:

```
chips> d 1,2 symbol circle
chips> d 1 tickvals x off
chips> d 1 ylabel "Flux (2-10keV)"
chips> d 2 xlabel "Time (years)"
chips> d 2 ylabel "N_H (/10^{23} cm)"
chips> d 2 xlabel size 1.5
chips> d all ylabel size 1.5
```

Both drawing areas are changed at the same time by using the "d 1,2" or "d all" syntax. [Figure 8](#)  shows the resulting plot.

Add another curve to each of the drawing areas:

```
chips> d 1 plot data4.tab 1 2 3
chips> d 1 c 2 symbol square
chips> d 2 plot data4.tab X 1 Y 4 yup 5 ydown 6
chips> d 2 c 2 symbol square
chips> d 1 limits 1982.0 1999.0 0.5 3.5
chips> d 2 limits 1982.0 1999.0 0.0 4.5
```

Now it is necessary to give both the drawing area number (d #) and the curve number (c #) to change a curve attribute. [Figure 9](#)  shows the resulting plot.

Saving and Printing a Plot

The `print` command may be used to save a plot in postscript format or send it directly to the system printer:

```
chips> print postfile plot.ps
chips> ls *ps
plot.ps

chips> print
```

The commands `pagesize` and `colorsys` are used to control the appearance of the hardcopy.

The `store` command may be used to save a plot for future use in another *ChIPS* session:

```
chips> store plot.chp
```

```
chips> exit

unix% chips

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chips> restore plot.chp
chips> exit
```

Getting More Help

There are several ways to get help on *ChIPS*:

- A complete discussion of each command can be brought up by typing ahelp from within *ChIPS* (e.g. "ahelp curve"). Use "q" to exit from the help page.
- This information is also available from the *ChIPS* Reference Manual.
- The chips help page contains information on how to use S-Lang within *ChIPS*.

History

14 Dec 2004 reviewed for CIAO 3.2: no changes
01 Dec 2005 updated for CIAO 3.3: *ChIPS* version number
01 Dec 2006 updated for CIAO 3.4: *ChIPS* version

URL: http://cxc.harvard.edu/ciao/threads/chips_intro/

Last modified: 1 Dec 2006

Image 1: Plotting the first 2 columns of a PHA file

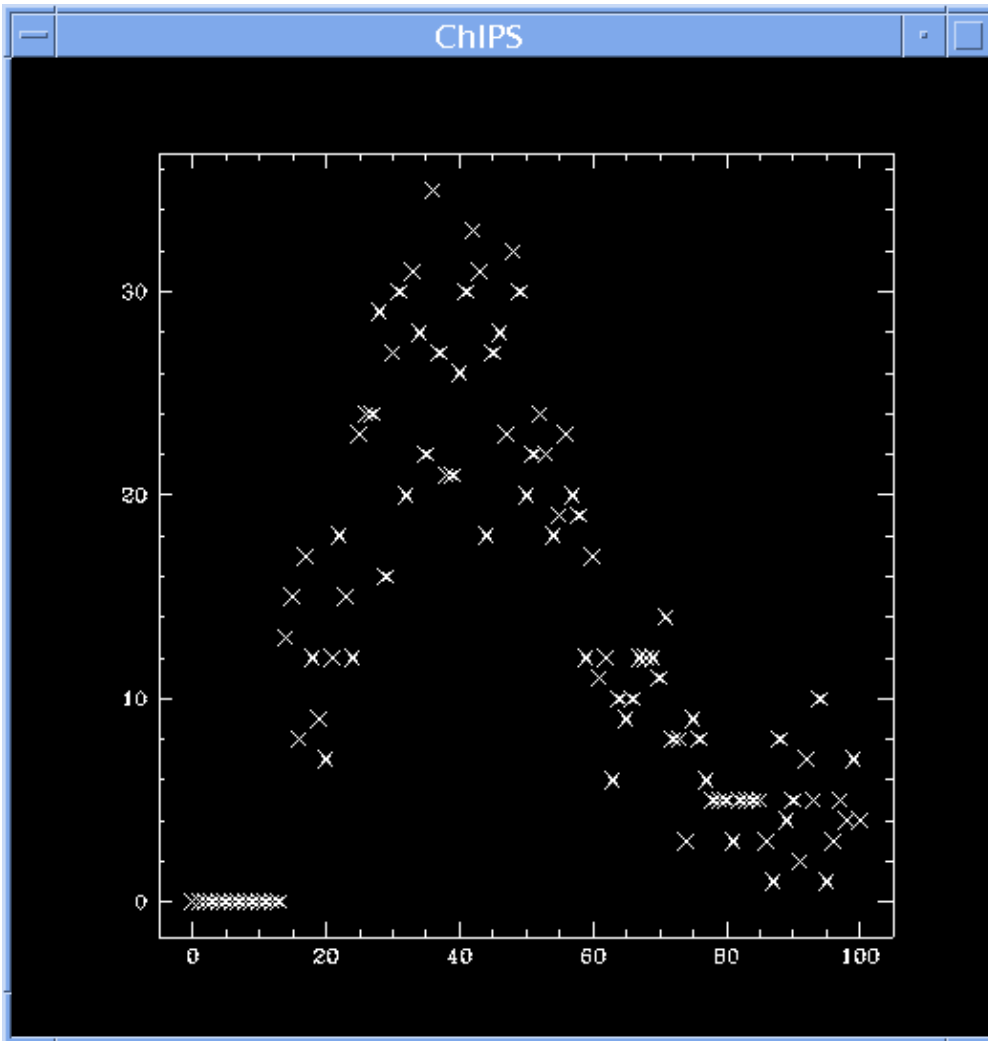


Image 2: Plotting the first 2 columns of an ASCII file

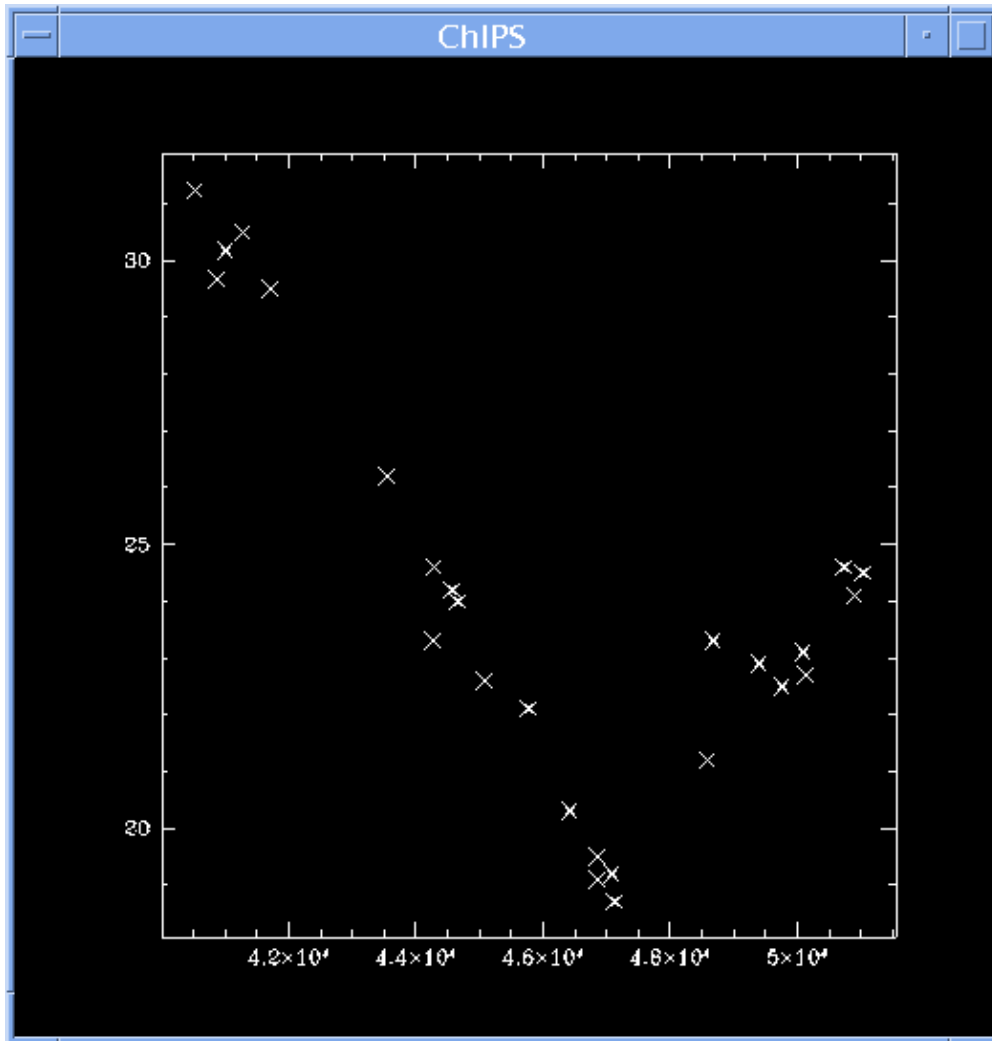


Image 3: Including error bars

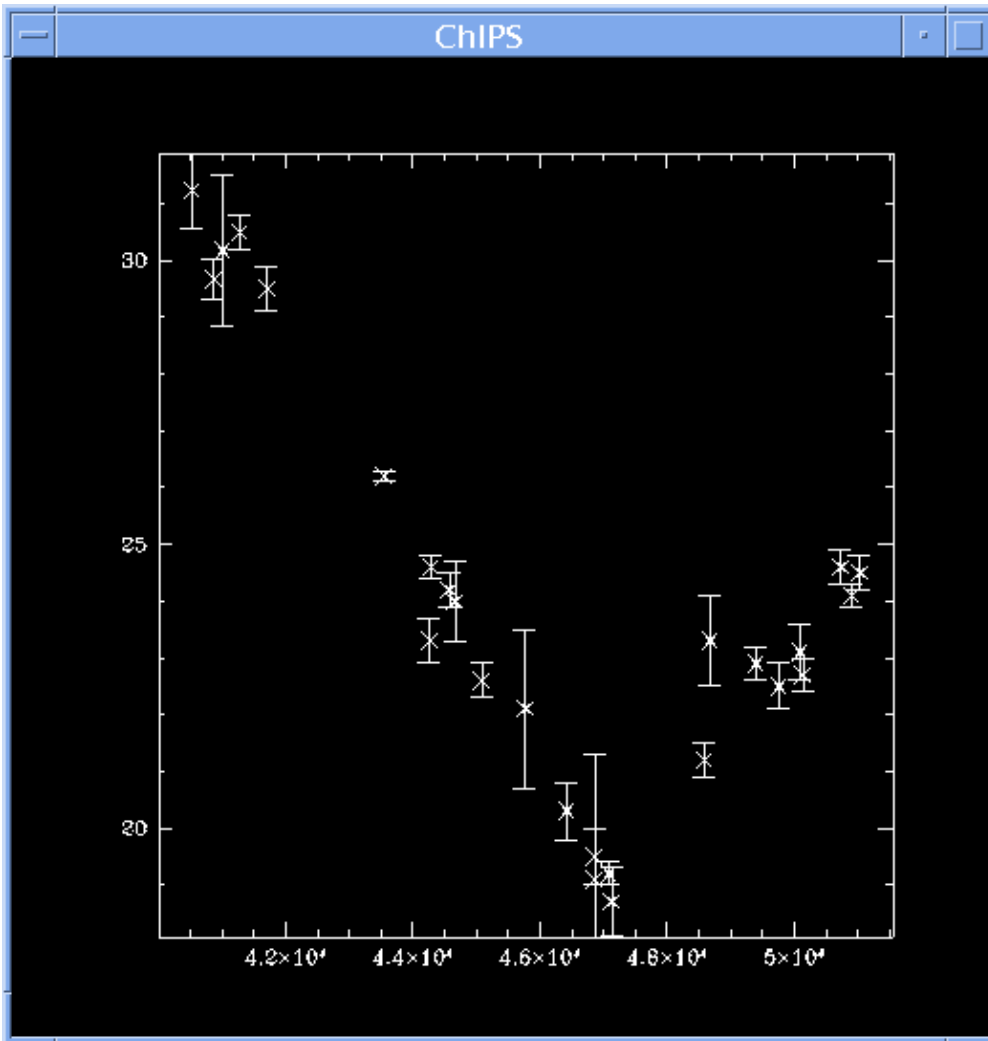


Image 4: Including asymmetric error bars

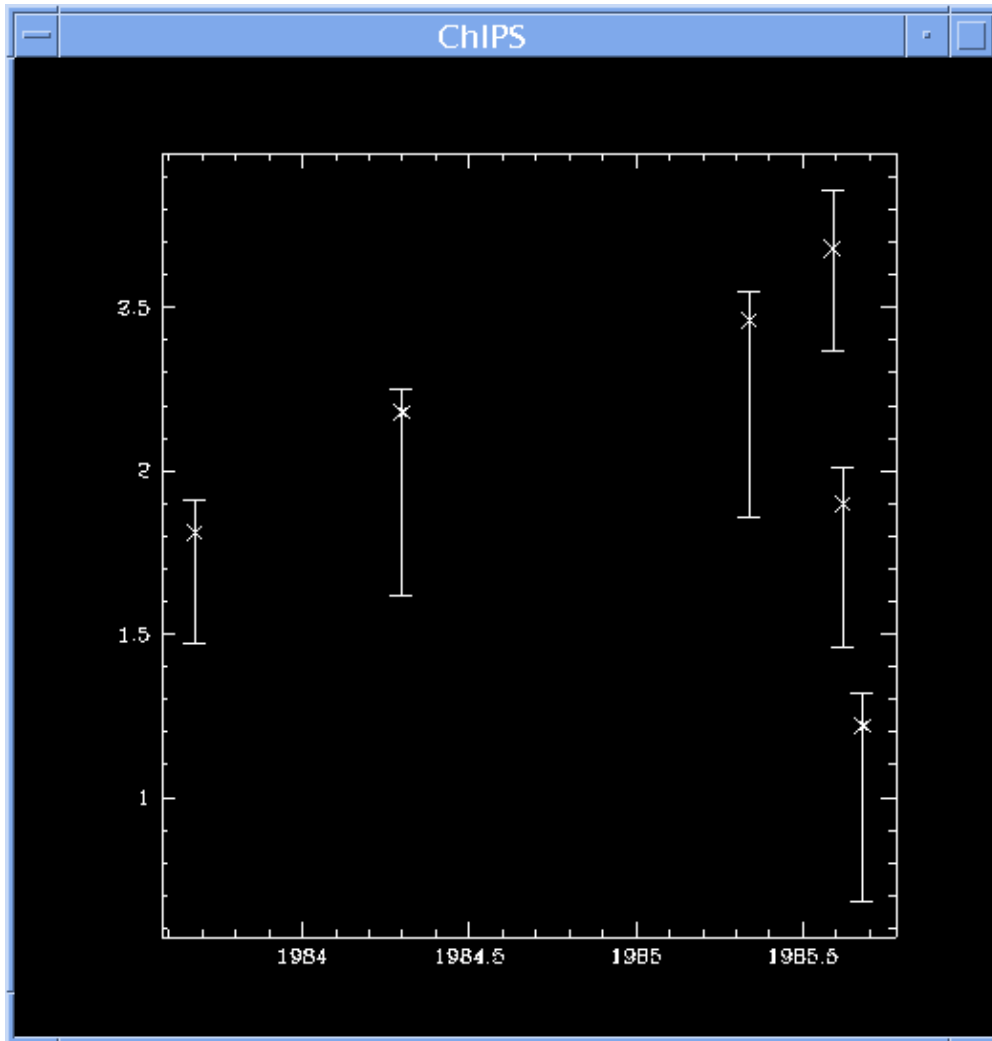


Image 5: Customizing a plot

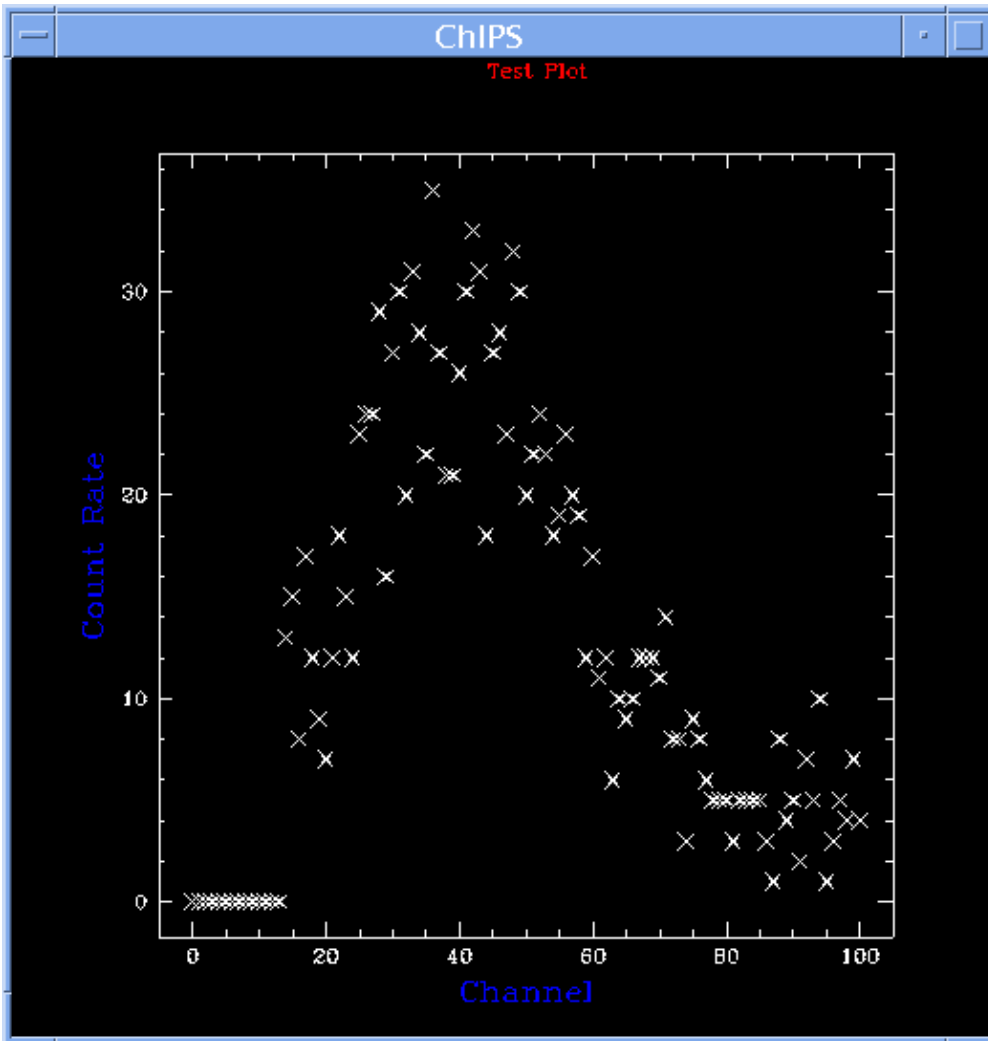


Image 6: Combining two datasets

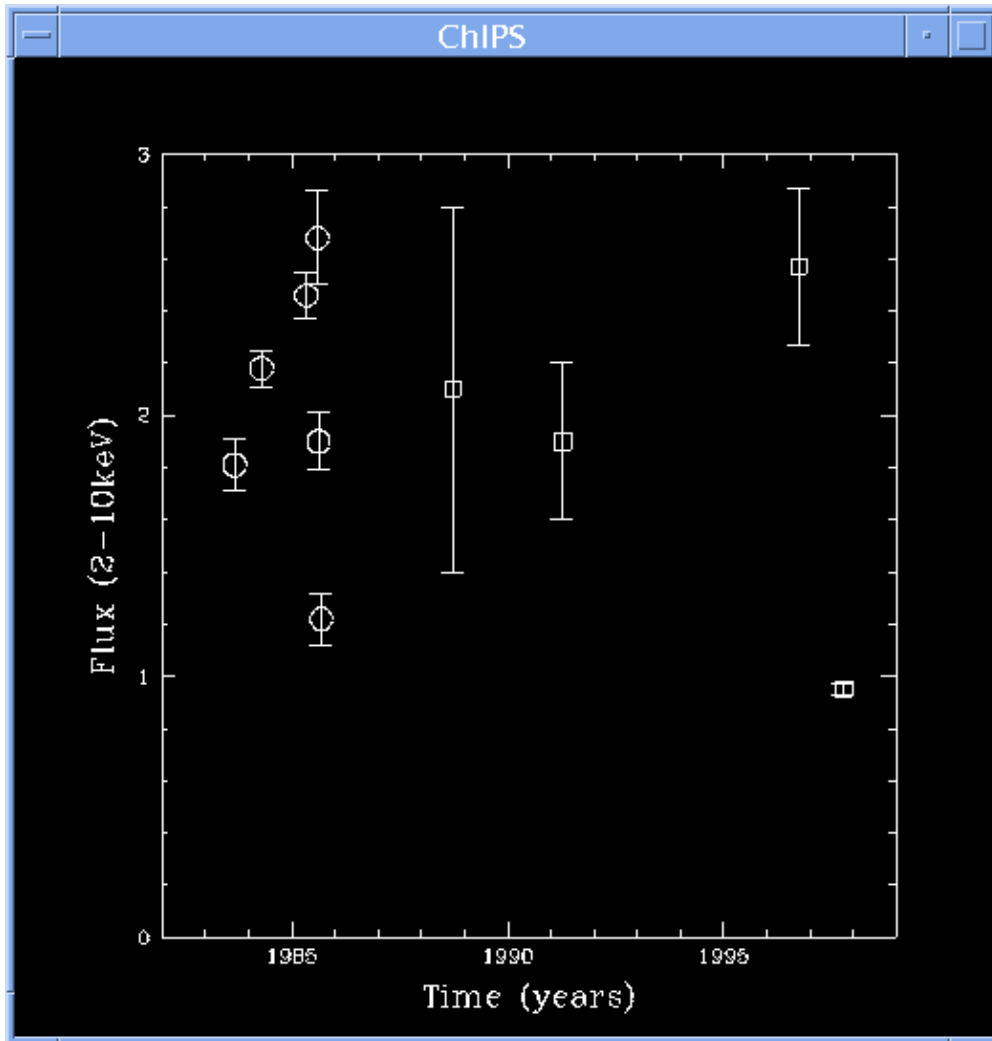


Image 7: Plotting a dataset as a curve

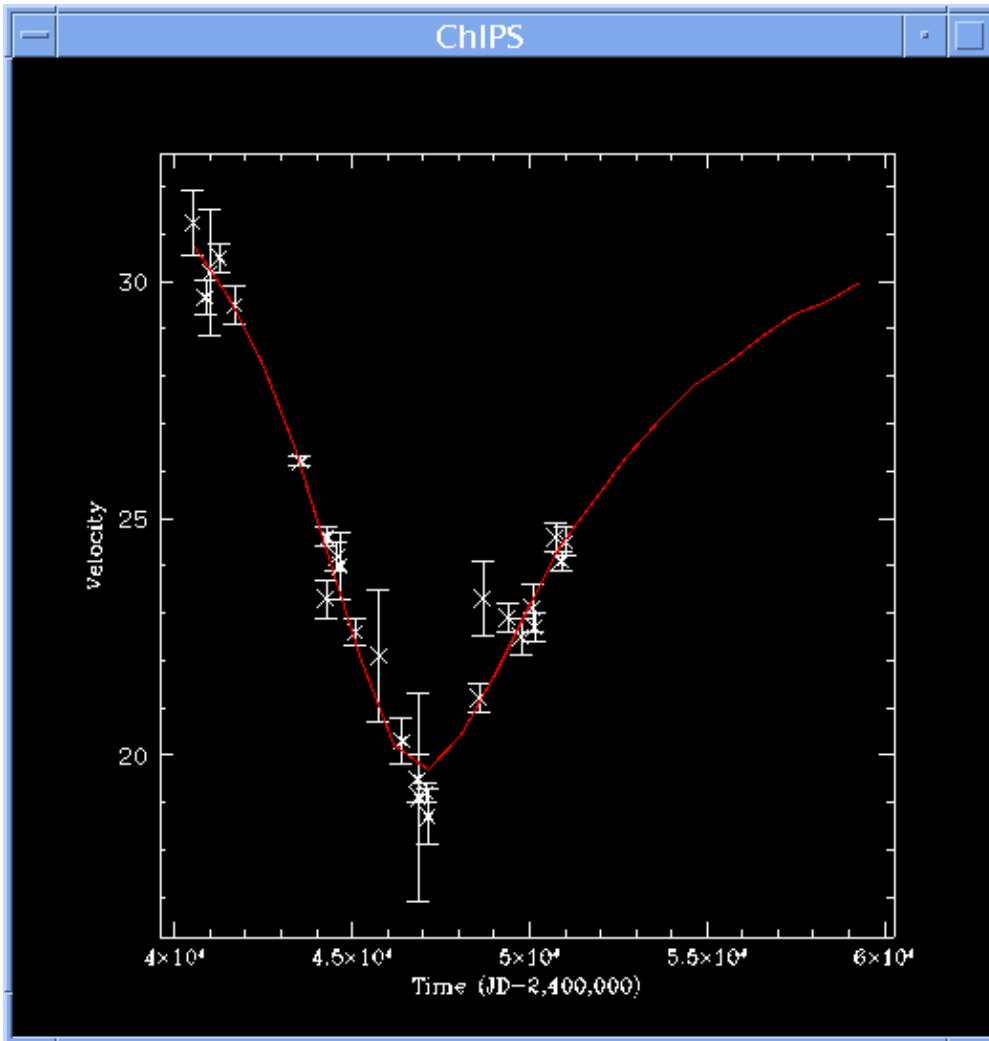


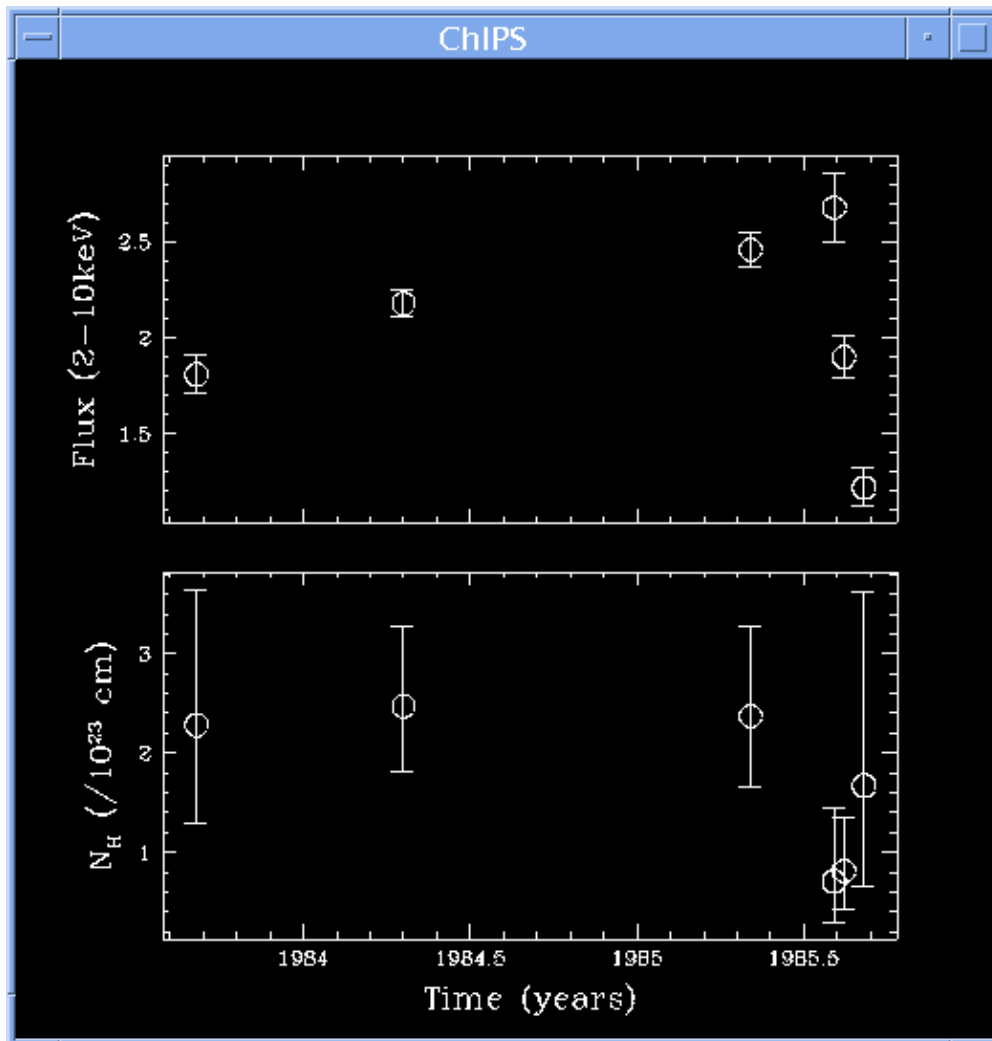
Image 8: Plotting using multiple drawing areas

Image 9: Combining multiple plots and drawing areas