

*AHELP for CIAO 3.4*

## store

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## Synopsis

Saves a plot with all attributes.

## Syntax

```
chips> STORE <filename>
```

## Description

The STORE command creates an ASCII file which contains all the commands needed to re-create the current plot display. The <filename> is the name of the file to be created and may contain a directory path. This file can then be read into another ChIPS session using the RESTORE command.

This allows you to create a plot – perhaps in Sherpa – and save it so it can be re-created or modified at a later date.

When storing plots created using the ChIPS CURVE command, the store file will reference the data file by name – including the full path. If the plots were created without an associated data file – for instance a Sherpa plot or data plotted using the the S-Lang curve() function – then the plot data will be written to a FITS file called "<filename>.fits". The one exception to this is for contour plots, when the data for that plot is stored in the /tmp/ directory as an ASCII file.

## Example 1

```
chips> cd /work
chips> SPLIT 2
chips> D 1 CURVE data/data.dat
chips> D 1 CURVE data/fit.dat
chips> D 2 CURVE data/residuals.dat
chips> D 1 C 2 SYMBOL NONE
chips> D 1 C 2 SIMPLELINE
chips> D 1,2 LIMITS 0.0 11.0
chips> D 2 SYMBOL CIRCLE
chips> D 2 SYMBOL SIZE 1
```

```

chips> D 1 LIMITS Y 1.0 4.5
chips> D 2 LIMITS Y 0.0 4.5
chips> XLABEL "Off-Axis (arcmin)"
chips> D 1,2 YLABEL "SNR"
chips> TITLE "HRC-I 100ks"
chips> TITLE CYAN
chips> XLABEL CYAN
chips> D 1,2 YLABEL CYAN
chips> SPLIT GAP y 0.04
chips> D 1 TICKVALS X OFF
chips> D 1,2 TICKVALS y "%1.1f"
chips> STORE myplot.chp

```

After plotting some data and customizing the look of the plot, it is stored to the file myplot.chp in the current directory. This is an ASCII file that references the plotted data using full path specifications; it may be restored from any location, as long as the data has not been moved.

```

chips> $more myplot.chp
#This is a ChIPS state file.
#ChIPS_Version: 2.20

redraw off

#####
# Start of a new drawing area.
#####
drawarea 0.15 0.9 0.52 0.9

#####
# Start of a new curve.
skip 0
curve "/work/data/data.dat"

#####
# Start of a new curve.
skip 0
curve "/work/data/fit.dat"
symbol none
symbol 0 0
simpleline

(etc.)

```

## Example 2

```

chips> x = [0:10:0.02]
chips> y = tan(x)
chips> chips.curvestyle = _chips->simpleline
chips> chips.symbolstyle = _chips->none
chips> () = curve(x,y)
chips> limits y -10 10
chips> store tanplot.chp

```

Here we use S-Lang commands to create and plot the curve  $y=\tan(x)$ . As well as creating the file tanplot.chp, the STORE command also creates the file tanplot.chp.fits which contains the data that was plotted.

Note that the store file does not record the contents of the ChIPS State object. So, when the plot is re-created via a call to RESTORE, it will be drawn with no symbols and with a line connecting the points but the

chips.curvestyle and chips.symbolstyle fields will not be set to `_chips->simpleline` and `_chips->none` respectively.

## Example 3

```

sherpa> READ DATA 1 data/example1.dat
sherpa> PARAMPROMPT OFF
Model parameter prompting is off
sherpa> POLY[modela]
sherpa> SOURCE 1 = modela
sherpa> THAW modela.2 modela.3
sherpa> FIT
sherpa> LPLOT FIT
sherpa> STORE myplotfromsherpa.chp
sherpa> ls myplotfromsherpa.chp*
myplotfromsherpa.chp
myplotfromsherpa.chp.fits
    
```

Here the STORE command is used from within Sherpa to save a plot generated using the Sherpa command LPLOT. Two files have been generated: the ASCII file with the plot commands and a FITS file that contains the data. The data for each curve is stored in a separate FITS extension:

```

chips> list myplotfromsherpa.chp.fits blocks
-----
Dataset: myplotfromsherpa.chp.fits
-----

```

Block Name	Type	Dimensions
Block 1: PRIMARY	Null	
Block 2: curve0	Table	6 cols x 12
Block 3: curve1	Table	2 cols x 12

The [curve0] extension contains the input data and the [curve1] extension contains the fit.

## CHANGES IN CIAO 3.0

The format of the store file has changed slightly, in that the first two lines now start with the "#" character. This means that you can now use them as ChIPS command files – so if you did "STORE plot.chp" you can now say

```
unix% chips plot.chp
```

The old format store files will still work in ChIPS.

## Bugs

See the [bugs page for ChIPS](#) on the CIAO website for an up-to-date listing of known bugs.

## See Also

*chips*

[colorsys](#), [pagesize](#), [print](#), [restore](#), [skip](#)

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URL:  
<http://cxc.harvard.edu/ciao3.4/store.html>  
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