



# CIAO 2.2 Highlights

[cxc.harvard.edu/ciao/intro\\_releasenotes.html](http://cxc.harvard.edu/ciao/intro_releasenotes.html)

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## Extended Source Analysis

The major focus of CIAO 2.2 is the addition of new tools and improvement of existing tools to accommodate extended source analysis.

### **mkwarf & mkrmf**

Users can now create weighted responses (ARFs and RMFs) using detector WMAPs. **mkwarf** creates a weighted ARF file based on an input weight map. It also produces a set of weights that are used by the newly upgraded **mkrmf** to create the associated weighted RMF.

### **reproject\_events**

Using the available blank-sky event files, users can create background datasets appropriate for their observation. **reproject\_events** now replicates the functionality of Maxim's `make_acisbg` tool (applying the aspect solution of an observation to blank-sky datasets).

### **dmfilth**

Tired of those annoying point sources? Fill them in! **dmfilth** removes sources from an image and replaces them with one of several methods, including bilinear interpolation, polynomial fit, and Poisson distributed data.

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## New Tools

### **acisreadcorr**

Flag and relocate out-of-time CCD events from a bright source. **acisreadcorr** removes the readout streak from the image (for cosmetic reasons) and retains the streak photons (for accurate timing information unaffected by pile-up).

### **asphist**

Essentially an entirely new tool, **asphist** now works directly on the aspect solution (`asol`) files. The SIM aspect corrections, previously applied with **asp\_apply\_sim**, are now taken into account by **asphist** as well.

### **dmimgthresh**

Set low exposure regions of an image to a constant value. With strongly variable exposure across an image, you can get spurious results from smoothing or source detection algorithms. Using **dmimgthresh** to blank out regions of an image improves the accuracy of the other tools.

### **dmjoin**

Join two files whose sampling is different. **dmjoin** allows you, for example, to generate an aspect solution with one record per photon, interpolated to the times of a given set of photon events.

### **mkgrmf**

Create grating RMFs instead of using the off-the-shelf versions! **mkgrmf** generates an OGIP-style RMF appropriate for spectral analysis of grating observations. The gRMF is a representation of how the incident source photons are redistributed onto the detector.

### **rmfimg**

Turn an RMF into a 2D image that can be easily viewed with ds9. The ARF can also be included, either independently or multiplied by the RMF to give an image of the total response.

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## ***Sherpa***

There are many enhancements to the CIAO modeling and fitting program, *Sherpa*:

### **Generalized use of background**

Input source and background do not need to be the same size.  
Generalized filtering for source and background data sets is available.

### **Background instrument models**

RMF & ARF allow for simultaneous fitting of the background and source data.

### **Exposure maps can be used in the analysis**

Entered as a GridModel, exposure maps are filtered automatically to match the source filter.

### **PSFFROMFILE**

Convolution performance has been improved.  
The function has been generalized to 1D or 2D use.

### **Filtering enhancements**

For PHA files, filtering can be done in either energy or wavelength.  
Additional filters can be specified on the command line after some have been entered from a file.

### **Models**

GridModel can be used to input the model from a file.  
Added normalized beta1d model, pile-up model; upgraded edge model.  
There is now an option to unlink the model parameters and stacks.  
Equivalent width can now become an S-Lang function.

### **Statistics**

Added statistical tests MLR and F-tests.  
Updated use of statistical and systematic errors.

## **S-Lang**

Added S-Lang functions/models.  
Sherpa\_eval() added to allow for executing sherpa commands in S-Lang scripts.  
More scripts for doing high resolution spectroscopy (GUIDE) are available.

## **Visualization**

New STORE/RESTORE with chips: the plotted data is stored with the FITS file.  
Fit images are tiled by default.  
CPLOT/SPLIT can be used on arbitrary filtered data; it can also create multiple windows plots.  
Filtered/unfiltered spaces may be visualized, as well as arbitrary model stacks.  
See data-model residuals using the NONSIGMA function.

## **WRITE**

Uses PLOTX/PLOTY settings to determine X/Y units.  
Outputs proper NxM FITS image files, as opposed to 1 x (NxM), in 2D.  
Writing to fitsbin or qpoe includes more accurate specification of column names and units.  
By default, uses ASCII for 1D and FITS for 2D.

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## ***Prism***

A number of file editing options have been incorporated into the file browser GUI:

### **Cell editing**

Perform simple cell value editing on tables and images.  
Limited range, overflow, and type checking are provided.  
An undo option exists for cell edits.

### **Column appending**

Append new columns (scalar or array) to a table extension.  
Users specify the number of elements (if an array), column name, data type, units, and description.

### **Row appending**

Append one or more rows to a table extension.

### **Recently accessed files list**

A list of up to the last 10 accessed files is maintained.  
Selecting one of the specified files reloads it into the file browser.

### **Column filtered file viewing**

View a table extension column filtered to the user's preference.  
Which columns to display (and in what order to display them) may be specified.

# Beyond CIAO 2.2

Longer term development -- including some major increases in the power of CIAO -- are in the works. We want to respond to your needs. If you email [ciaoenhancements@head-cfa.harvard.edu](mailto:ciaoenhancements@head-cfa.harvard.edu) with your suggestions for upgrades, we will fold them into our plans.

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## ISIS

The Interactive Spectral Interpretation System (**ISIS**) is designed to support the analysis and interpretation of high resolution X-ray spectra using a spectroscopy database such as APED/APEC. It is currently a stand-alone, programmable, and extensible S-Lang based system, independent of GUIDE and Sherpa, but is on an integration path for CIAO 3.0 (which will have a fully integrated S-Lang interpreter). A variety of fitting modes are provided to support simple line profile fits as well as global fits; a pileup model for CCD spectra is also included. See the ISIS web page -- <http://space.mit.edu/CXC/ISIS> -- for more information and download instructions.

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