



 AHELP for CIAO 3.4

dmarfadd

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Synopsis

Add multiple ARF files together, weighting by exposure.

Syntax

```
dmarfadd infile outfile [clobber] [kernel] [verbose]
```

Description

`dmarfadd' will add several Auxiliary Response Files (ARF) together to create a single output ARF file. In the Chandra case, there is a separate ARF for each detector element (ACIS CCD or HRC MCP). The user can use `dmarfadd' to combine these files to create an ARF that covers the region (spatial or spectral) of interest. Each CCD generally has different good-time intervals (GTI), and hence, a different EXPOSURE. `dmarfadd' weights the ARF by the exposure time and derives a mean EXPOSURE. For grating spectra, where aspect dither causes different chips to overlap the same spectral region, this produces the correct ARF.

Although 'dmarfadd' was designed to add ARFs for grating observations, it can also work on imaging ARFs. When adding imaging ARFs for point sources, it is assumed that the same RMF applies to every ARF. If the RMFs are significantly different, it is advised to NOT combine the ARFs using dmarfadd, but to analyse these data separately.

In addition to the effective area column (SPECRESP), 'dmarfadd' also averages the 'FRACEXPO' column, which is primarily needed for grating pileup modeling. FRACEXPO is a value between zero and one, which indicates the fractional time that region was exposed by a detector (e.g., it is 1.0 on chip, and drops in chip gaps).

NOTE: (1) The energy grids across the files to be combined must be the same. (2) For grating observations, the keywords, GRATING, (HETG or LETG), TG_PART (which indicates HEG or MEG grating types for HETG), and TG_SCRID must match across the files. (3) The keyword EXPOSURE must exist in all input files. (4) For gratings, TG_M must match in absolute value (that is, orders -1 and +1 may be added, but not 1 and 2). For imaging-mode (GRATING='NONE'), the grating keywords are ignored.

Example 1

```
ls acis*MEG_-1.fits > data.lis
dmarfadd @data.lis acis_MEG_-1_garf.fits
```

Make a list of grating ARF components for MEG order -1 in file data.lis. Open the file "data.lis" and combine the files listed in the file to the output file, acis_MEG_-1.fits

Example 2

```
dmarfadd "m1_arf.fits,m2_arf.fits" output.fits
```

This will combine the files m1_arf.fits and m2_arf.fits and place the results in output.fits.

Parameters

name	type	ftype	def	min	max	reqd	stacks
<u>infile</u>	file	input				yes	yes
<u>outfile</u>	file	output				yes	
<u>kernel</u>	string		default				
<u>clobber</u>	boolean		no				
<u>verbose</u>	integer		0	0	5		

Detailed Parameter Descriptions

Parameter=infile (file required filetype=input default= stacks=yes)

Input list of files.

The input list of files to be combined into one output file.

Parameter=outfile (file required filetype=output default=)

Output dataset name

This is the resultant combined ARF. All input files are combined into this output.

Parameter=kernel (string default=default)

options=FITS/default

Output Kernel

This is the output file kernel. The default is to use the same kernel as the input file.

Parameter=clobber (boolean default=no)

If "yes", then overwrite any existing output file. If a file exists and clobber is set to "no", the tool will exit with an error message.

Parameter=verbose (integer default=0 min=0 max=5)

Control the amount of diagnostic output to file from none (0) to a maximum (5).

CHANGES IN CIAO 3.0

The FRACEXPO column written by mkgarf is also weighted and summed in the same way as SPECRESP. This is in support of grating pileup modeling.

Bugs

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

See Also

calibration

[ardlib](#)

dm

[dmcols](#), [dmfiltering](#), [dmopt](#)

tools

[acis bkgnd lookup](#), [acis fef lookup](#), [acis set ardlb](#), [acisspec](#), [add grating orders](#), [add grating spectra](#), [asphist](#), [dither region](#), [dmappend](#), [dmfilth](#), [dmgroup](#), [dmgti](#), [dmjoin](#), [dmmerge](#), [dmpaste](#), [dmregrid](#), [dmsort](#), [dmtcalc](#), [dmtype2split](#), [fullgarf](#), [mkacisrmf](#), [mkarf](#), [mkexpmap](#), [mkgarf](#), [mkgrmf](#), [mkinstmap](#), [mkpsf](#), [mkrmf](#), [mkwarf](#), [psextract](#), [psf project ray](#), [rmfimg](#), [specextract](#)



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