



 AHELP for CIAO 3.4

rmfimg

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Synopsis

Create a simple image of an RMF or ARF file

Syntax

```
rmfimg infile outfile [arf] [arfout] [product] [verbose] [clobber]
[mode]
```

Description

A response matrix file (RMF) encapsulates the mapping between the physical properties of incoming photons (such as their energy) and their detected properties (such as detector pulse heights or PHA) for a given detector. For X-ray spectral analysis, the RMF encodes the probability $R(E,p)$ that a detected photon of energy E will be assigned to a given channel value (PHA or PI) of p . The standard Legacy format (see the GSFC HEASARC journal Legacy, issue no. 2) for the RMF uses a binary table in which each row contains $R(E,p)$ for a single value of E as a function of p . Non-zero sequences of elements of $R(E,p)$ are encoded using a set of variable length array columns. This format is compact but hard to manipulate and understand. The `rmfimg` program converts this format to a simple 2-dimensional image of $R(E,p)$ versus E and p , allowing one to visualize the response of the instrument.

An ancillary response file (ARF) contains the effective area $A(E)$ including the probability that a photon of energy E will be detected at all. The total 'response' is $A(E)R(E,p)$. The Legacy format for ARF is a binary table of $A(E)$ versus E . To make it easy to visualize $A(E)$ together with $R(E,p)$, `rmfimg` optionally allows you to create a two-dimensional 'ARF image' $A(E,p)$, which just replicates $A(E)$ for each value of p . (To simply see the 1-dimensional function, you can use `prism` directly on the ARF, or use `dmlist` to dump it to an ascii file and use `ChIPS` to view it). Optionally, the output RMF image will be multiplied by the ARF to give an image of the total response.

Example 1

```
(1) rmfimg rmf.fits rmf.img
```

Makes an image from a Legacy RMF file.

Example 2

```
(2) rmfimg rmf.fits rmf.img arf=arf.fits arfout=arf.img product=no
```

As above, but also makes an ARF image from arf.fits.

Example 3

```
(3) rmfimg rmf.fits rsp.img arf=arf.fits arfout=arf.img product=yes
```

Makes response image rsp.img containing $A(E)*R(E,p)$ (since product=yes) from rmf.fits and arf.fits. Also makes ARF image.

Example 4

```
(4) rmfimg "rmf.fits[bin energy=8,pi=2]" bin_rmf.img
```

Makes image from rmf.fits, binning axes by the given factor. Only the names "ENERGY", "PHA", and "PI" are recognized, and only a single value representing the binning factor may be given; full DM rebinning syntax of the form start:stop:step is NOT supported. This functionality allows you to make a reasonable size image from a large RMF file.

Parameters

name	type	ftype	def	min	max	reqd
<u>infile</u>	file	input				yes
<u>outfile</u>	file	output				yes
<u>arf</u>	file	input				
<u>arfout</u>	file	output				
<u>product</u>	boolean		no			
<u>verbose</u>	integer		0	0	5	
<u>clobber</u>	boolean		no			

Detailed Parameter Descriptions

Parameter=infile (file required filetype=input)

Input Legacy RMF FITS file, possibly with binning expression.

Input RMF file.

Parameter=outfile (file required filetype=output)

Output RMF or response image.

Parameter=arf (file filetype=input)

Input ARF file, optional.

Parameter=arfout (file filetype=output)

Output ARF image, if input ARF file is supplied.

Parameter=product (boolean default=no)

If product is yes, the main output is a response image containing the product of RMF and ARF.

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

Controls screen output information, value is 0 (no info) to 5 (most info).

Parameter=clobber (boolean default=no)

Clobber output if it exists? (yes/no)

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](#)

tools

[acis_bkgrnd_lookup](#), [acis_fef_lookup](#), [acis_set_ardlib](#), [acispec](#), [add_grating_orders](#),
[add_grating_spectra](#), [asphist](#), [dither_region](#), [dmarfadd](#), [dmfilth](#), [dmregrid](#), [fullgarf](#), [mkacisrmf](#), [mkarf](#),
[mkexpmap](#), [mkgarf](#), [mkgrmf](#), [mkinstmap](#), [mkpsf](#), [mkrmf](#), [mkwarf](#), [psextract](#), [psf_project_ray](#),
[specextract](#)

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