

*AHELP for CIAO 3.4*

## add\_grating\_spectra

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## Synopsis

Add two, source and background, grating PHA spectra, averages the corresponding ARFs, and group the coadded spectrum.

## Syntax

```
add_grating_spectra pha1 pha2 garf1 garf2 root [gtype] [gspec]
[clobber] [verbose]
```

## Description

### WHAT THE TOOL DOES

'add\_grating\_spectra' is a script which lets the user add up two grating (PHA) spectra and average their associated ARF. Optionally the output spectrum can be grouped. Only combinations of PHA files and ARFs belonging to the same instrumental configuration (i.e. ACIS–HETG–HEG, ACIS–HETG–MEG, ACIS–LETG–LEG, or HRC–LETG–LEG), and diffraction order, are allowed. The script combines a series of "dmtcalc" and "dmpaste" commands, performing math operations between columns of temporary files, and then merging the final columns into the output PHA and ARF files. The CIAO tool "dmgroup" is then eventually run, and some header keywords of the output files are edited using "dmhedit".

### WHAT THE USER SHOULD SUPPLY

The user supplies input PHA grating spectra and ARFs, and, optionally, the grouping type and specifications (see "ahelp dmgroup").

### OUTPUT SOURCE SPECTRUM

Source counts from the two input spectra are simply added together, and written out in the output file. A new column is written with the statistical errors, calculated according to the formula:  $STAT\_ERR = (1 + \sqrt{COUNTS + 0.75})$ .

## OUTPUT AVERAGED EFFECTIVE AREA

The two effective areas are weighted by the relative exposure,  $f1 = (\text{exp1}/\text{exp})$ ;  $f2 = (\text{exp2}/\text{exp})$  [where  $\text{exp} = (\text{exp1} + \text{exp2})$ ], and added together.

## OUTPUT BACKGROUND SPECTRA

Background spectra are weighted by their relative (exposure-weighted) extraction area, according to the formula:  $\text{BGD\_UP} = \text{BACKSCUP} * [(\text{BGD1}/\text{BACKSCUP1}) + (\text{BGD2}/\text{BACKSCUP2})]$  (and the analogous for the  $\text{BGD\_DN}$ ). In this formula,  $\text{BACKSCUP1}$  and  $\text{BACKSCUP2}$  are taken from the headers of the two input pha files, and are the ratios between the width of the background extraction region and the width of the source extraction region (typically 4.5 for default extraction ACIS-HETG or LETG spectra, and 5.0 for HRC-LETG spectra).  $\text{BACKSCUP}$  (and  $\text{BACKSCDN}$ ) is propagated into the header of the output spectrum according to the formula:  $\text{BACKSCUP} = 1/(f1/\text{BACKSCUP1} + f2/\text{BACKSCUP2})$ .

## GROUPING THE OUTPUT SPECTRUM

Optionally the output spectrum is grouped, according to the given grouping type and specifications (see the parameters description, below). Currently, the following `dmgroup` group-type options are available: `BIN`, `NONE`, `SNR`, `NUM_BINS`, `NUM_CTS`, and `ADAPTIVE` (see "ahelp dmgroup" for details). However, the `dmgroup` parameters "xcolumn" and "ycolumn" are hard-coded and fixed to "channel" and "counts", respectively, as appropriate for standard PHA files.

## HEADER KEYWORDS IN THE OUTPUT FILES

A number of keywords in the header of both the output PHA and ARF, are edited. Namely: (a) the keyword `EXPOSURE`, is given the value  $\text{exp} = (\text{exp1} + \text{exp2})$ ; (b) the keyword `BACKSCUP` and `BACKSCDN` are edited according to the above formula (see section on "OUTPUT BACKGROUND SPECTRA"); (c) the keyword `ANCRFILE` in the header of the output PHA file, is edited and given the output ARF filename; (d) the keywords `INSTRUMEN`, `GRATING` and `TG_PART` and `TG_M` (if any) are just copied from the headers of the input files into the headers of the output files.

### Example 1

```
add_grating_spectra pha1=spec1.pha pha2=spec2.pha garf1=eff_area_1.arf
garf2=eff_area_2.arf root=test1 gtype=NONE gspec verbose=2
```

Add together source and background spectra in `spec1.pha` and `spec2.pha`, and the corresponding ARFs in `eff_area_1.arf` and `eff_area_2.arf`. The output spectrum is not grouped. Output spectrum and ARF are named `test1_<configuration>_<order>_NONE.pha` and `test1_<configuration>_<order>.arf`.

### Example 2

```
add_grating_spectra pha1=spec1.pha pha2=spec2.pha garf1=eff_area_1.arf
garf2=eff_area_2.arf root=test2 gtype=BIN gspec=10 verbose=2
```

Add together source and background spectra in `spec1.pha` and `spec2.pha`, and the corresponding ARFs in

eff\_area\_1.arf and eff\_are\_2.arf. The output spectrum is grouped by a factor of 10. Output spectrum and ARF are named test2\_<configuration>\_<order>\_BIN10.pha and test2\_<configuration>\_<order>.arf.

## Example 3

```
add_grating_spectra pha1=spec1.pha pha2=spec2.pha garf1=eff_area_1.arf
garf2=eff_area_2.arf root=test3 gtype=NUM_CTS gspec=20 verbose=2
```

Add together source and background spectra in spec1.pha and spec2.pha, and the corresponding ARFs in eff\_area\_1.arf and eff\_are\_2.arf. The output spectrum is grouped, allowing a minimum of 20 source counts per new bin. Output spectrum and ARF are named test3\_<configuration>\_<order>\_NUM\_CTS10.pha and test3\_<configuration>\_<order>.arf.

## Parameters

name	type	ftype	reqd
<u>pha1</u>	string	input	yes
<u>pha2</u>	string	input	yes
<u>garf1</u>	string	input	yes
<u>garf2</u>	string	input	yes
<u>root</u>	string	output	yes
<u>gtype</u>	string		no
<u>gspec</u>	string		no
<u>clobber</u>	boolean		no
<u>verbose</u>	integer		no

## Detailed Parameter Descriptions

**Parameter=pha1 (string required filetype=input)**

*First input PHA spectrum.*

**Parameter=pha2 (string required filetype=input)**

*Second input PHA spectrum.*

**Parameter=garf1 (string required filetype=input)**

*Effective Area associated to the first input PHA spectrum, pha1.*

**Parameter=garf2 (string required filetype=input)**

*Effective Area associated to the second input PHA spectrum, pha2.*

**Parameter=root (string required filetype=output)**

*Root name for the output files root\_<configuration>\_<order>\_<gtype+gspec>.pha and root\_<configuration>\_<order>.arf.*

**Parameter=gtype (string not required)**

*The grouping type (NONE, BIN, SNR, NUM\_BINS, NUM\_CTS, or ADAPTIVE). See "ahelp dmgroup" for details.*

**Parameter=gspec (string not required)**

*The grouping specification; form depends on GTYPE. See "ahelp dmgroup" for details. Note that for the BIN grouping type, gspec corresponds to the step size of the binning. The min and max of the binning specification are hard-coded (1:8192 for ACIS, 1:16384 for HRC). Thus, '10' is a valid gspec, but '1:8192:10' is not and will produce errors.*

**Parameter=clobber (boolean not required)**

*Clobber existing output files?*

Specifies if existing output files should be overwritten.

**Parameter=verbose (integer not required)**

*Controls amount of information to print (0–5).*

The verbose parameter provides debugging information; verbose = 0 is usually fine.

## **CHANGES IN ADD\_GRATING\_SPECTRA 3.4**

The dmkeypar tool is used in place of Unix "tail".

## **CHANGES IN ADD\_GRATING\_SPECTRA 3.3**

The "kernel" parameter was removed from dmtcalc and dmpaste in CIAO 4.0.

## **NOTES**

This script is not an official part of the CIAO release but is made available as "contributed" software via the [CIAO scripts page](#). Please see the [installation instructions page](#) for help on installing the package.

## **Bugs**

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

## **See Also**

*calibration*

[ardlib](#)

## Ahelp: add\_grating\_spectra – CIAO 3.4

*tools*

[acis\\_bkgrnd\\_lookup](#), [acis\\_fef\\_lookup](#), [acis\\_set\\_ardlib](#), [acisspec](#), [add\\_grating\\_orders](#), [asphist](#),  
[dither\\_region](#), [dmarfadd](#), [dmfilth](#), [dmregrid](#), [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/add\\_grating\\_spectra.html](http://cxc.harvard.edu/ciao3.4/add_grating_spectra.html)  
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