

*AHELP for CIAO 3.4*

## acisspec

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## Synopsis

(1) Extract source and/or background ACIS imaging spectra for both point-like and extended sources; (2) coadd ACIS spectra; (3) build weighted ARFs and RMFs.

## Syntax

```
acisspec soufile1 root [bgfile1] [soufile2] [bgfile2] [souwmap1]
[bgwmap1] [souwmap2] [bgwmap2] [binwmap] [ewmap] [weight1] [weight2]
[gtype] [gspec] [bggtype] [bggspec] [pbkfile] [dafile] [clobber]
[verbose]
```

## Description

'acisspec' is a script which lets the user:

- extract ACIS PI spectra and associated WMAPs for both point-like and extended sources (and background)
- create weighted responses (WARF and WRMF)
- coadd or average two source (and background) ACIS PI spectra and associated WMAPs (and build weighted responses)
- optionally group the output spectra.

The script combines the dmextract, dmtcalc, dmimgcalc, dmcoppy, mkwarf, mkrmf, dmgroup and dmhedit CIAO tools.

The user supplies either event lists and extraction regions, or spectra for primary (and/or secondary) source and background. If spectra are supplied, they must be in PI space or the tool will exit with an error. Extraction regions have to be specified as part of the input event files, following the usual data-model syntax for filtering (see "ahelp dmsyntax"). WMAPs are also needed to create the weighted responses, and can be either supplied by the user or computed internally by the software for specified energy range and binning factor (in which case the primary and/or secondary input files must be event file).

Any combination of source and background primary and secondary event files and spectra can be input. If event files are input and WMAPs are not supplied, then acisspec will extract them (using the specified energy range and detector binning factor). If spectra are input, then WMAPs must be supplied, or the software will

exit with an error.

If secondary files are provided, then acisspec will coadd primary and secondary spectra and WMAPs and will create weighted ARFs and RMFs for the summed spectrum. Background spectra and WMAPs are weighted accounting for different exposures and extraction–region areas (according to the [HEASARC definition of the BACKSCAL keyword](#)). Additional weights can be optionally provided for the sum.

The number of files created depends on the number of input files. It ranges from a minimum of 2 (weighted RMF and ARF for the input source spectrum and WMAP), to a maximum of 8 files, namely: source and background spectra, WMAPs, WARFs and WRMFs (when both source and background event files are provided and associated WMAPs are not supplied).

## HEADER KEYWORDS FOR THE OUTPUT SPECTRA

Headers of the output spectra are edited to update a number of keywords.

- The keywords RESPFILE and ANCRFILE in the header of the source spectrum are always updated with the weighted RMF and ARF filenames. The same keywords in the output background spectra (if present) are updated with the corresponding responses filenames only if the user choose to group the background spectrum. Otherwise they are left blank.
- The keyword BACKFILE in the source spectrum is updated with the filename of the output background spectrum (if present).
- If secondary files are present, and primary and secondary files correspond to different ObsIds, the keyword EXPOSURE in the output coadded spectra is updated with the sum of the exposure times of the single ObsIds. Otherwise, the exposure time of primary and secondary files is propagated into the output spectra.
- If secondary files are present, the keyword BACKSCAL of the background coadded spectrum is updated, while the keyword BACKSCAL of the source coadded spectrum is equalized to 1.

## GROUPED OUTPUT SPECTRA

The user can choose to group the output source and background spectra. All the group–type options available with dmgroup (see "ahelp dmgroup" for details) are allowed. If the user choose to group the background output spectrum, then the keyword BACKFILE of the source spectrum is NOT updated with the background spectrum filename, while both the RESPFILE and ANCRFILE keywords of the background spectrum are updated with the filenames of the corresponding WRMF and WARF. This is useful if the user wants to fit simultaneously source and background spectra, each with its own responses. If the user wants to fit the background–subtracted source spectrum, then the output background spectrum should NOT be grouped (i.e. the bggtype and bggspec parameters should be left blank)

## CREATING RMFS

This script uses the older tool mkrmf to create the RMF files. Users who are working with CTI–corrected, –120 C data should run mkacismrf standalone to generate new RMFs after using the script to create the spectrum and ARF files. The [Creating ACIS RMFs with mkacismrf thread](#) has more details and shows how to run the tool.

Acisspec checks for CTI keywords in the input file headers and prints a warning if users should remake the RMF response with the mkacismrf tool. The warnings are printed at verbosity > 0.

## Example 1

```
acisspec soufile1="evt.fits[sky=region(sou.reg)]" root=mysource
```

Extract a source spectrum from evt.fits using the region sou.reg. Extract the source WMAP from the same region, and with default binning factor (i.e. det=8) and energy range (i.e. 300:2000 eV). Don't make a background spectrum and don't group the output. Creates source.pi, mysource.wrmf and mysource.warf.

## Example 2

```
acisspec soufile1="evt.fits[time=1000:2000][sky=region(sou.reg)]"
bgfile1="evt.fits[time=1000:2000][sky=region(bgd.reg)]"
soufile2=sou2.pi bgfile2=bgd2.pi souwmap2=sou2.wmap bgwmap2=bgd2.wmap
root=mysource gtype="NUM_CTS" gspec=20 clobber=yes
```

Extract primary source and background spectra and WMAPs from the same event file with different extraction regions. Coadd these spectra and WMAPs with the provided secondary spectra and WMAPs for source and background. Group the coadded source spectrum to contain a minimum of 20 counts in the grouped channels; do not group the coadded background spectrum.

## Parameters

name	type	ftype	def	reqd
<u>soufile1</u>	file	input		yes
<u>root</u>	string	output		yes
<u>bgfile1</u>	file	input		no
<u>soufile2</u>	file	input		no
<u>bgfile2</u>	file	input		no
<u>souwmap1</u>	file	input		no
<u>bgwmap1</u>	file	input		no
<u>souwmap2</u>	file	input		no
<u>bgwmap2</u>	file	input		no
<u>binwmap</u>	string		det=8	no
<u>ewmap</u>	string		300:2000	no
<u>weight1</u>	real		1	no
<u>weight2</u>	real		1	no
<u>gtype</u>	string			no
<u>gspec</u>	string			no
<u>bggtype</u>	string			no
<u>bggspec</u>	string			no
<u>pbkfile</u>	string	input	NONE	
<u>dafile</u>	string	input	NONE	
<u>clobber</u>	boolean		no	
<u>verbose</u>	integer		0	

## Detailed Parameter Descriptions

**Parameter=soufile1 (file required filetype=input)**

*Primary source file*

The input may be either an event file or a spectrum.

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

*Root name for the output files*

**Parameter=bgfile1 (file not required filetype=input)**

*Primary background file*

The input may be either an event file or a spectrum.

**Parameter=soufile2 (file not required filetype=input)**

*Secondary background file*

The input may be either an event file or a spectrum.

**Parameter=bgfile2 (file not required filetype=input)**

*Secondary background file*

The input may be either an event file or a spectrum.

**Parameter=souwmap1 (file not required filetype=input)**

*Primary source WMAP*

**Parameter=bgwmap1 (file not required filetype=input)**

*Primary background WMAP*

**Parameter=souwmap2 (file not required filetype=input)**

*Secondary source WMAP*

**Parameter=bgwmap2 (file not required filetype=input)**

*Secondary background WMAP*

**Parameter=binwmap (string not required default=det=8)**

*Binning factor of the output WMAPs*

Must be given in detector coordinates. See "ahelp dmextract", or "ahelp mkwarf" for details.

**Parameter=ewmap (string not required default=300:2000)**

*Energy range for WMAP extraction*

See "ahelp dmextract", or "ahelp mkwarf" for details.

**Parameter=weight1 (real not required default=1)**

*Weight for the primary inputs*

This weight is used for the primary source spectrum, background spectrum, and WMAPs to be coadded with the secondary source and background spectra.

Setting the value to "1" (or "1.0") creates unweighted output.

**Parameter=weight2 (real not required default=1)**

*Weight for the secondary inputs*

This weight is used for the secondary source spectrum, background spectrum, and WMAPs to be coadded with the primary source and background spectra.

Setting the value to "1" (or "1.0") creates unweighted output.

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

*Source grouping type*

Allowable values are NONE, BIN, SNR, NUM\_BINS, NUM\_CTS, and ADAPTIVE.

- NONE: The data are grouped using maximum resolution.
- BIN: Explicitly state the binning boundaries, e.g. "10:40:5".
- SNR: Data are grouped until the square root of the number of counts in each group exceeds the given signal-to-noise value.
- NUM\_BINS: Data are grouped into a number of equal-width groups.
- NUM\_CTS: Data are grouped until the number of counts in each group exceeds the minimum number of counts specified.
- ADAPTIVE: Keeps bright features ungrouped, while grouping low SNR regions.

More information on grouping is available from "ahelp dmgroup".

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

*Source grouping specification*

A numerical value used for the grouping method. The format of the grouping specification depends on what is chosen for the gtype parameter. Here are some example gspec values for each gtype option:

- gtype=NONE, gspec=NONE (no grouping)
- gtype=BIN, gspec="10:40:5" (start:stop:stepsize)
- gtype=SNR, gspec=30 (signal-to-noise value)
- gtype=NUM\_BINS, gspec=10 (number of bins)

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- `gtype=NUM_CTS`, `gspec=30` (minimum number of counts per group)
- `gtype=ADAPTIVE`, `gspec=100` (counts value for low SNR regions)

More information on grouping is available from "ahelp dmgroup".

### **Parameter=bggtype (string not required)**

#### *Background grouping type*

Allowable values are NONE, BIN, SNR, NUM\_BINS, NUM\_CTS, and ADAPTIVE; see the "gtype" parameter description for details. More information on grouping is available from "ahelp dmgroup".

### **Parameter=bggspec (string not required)**

#### *Background grouping specification*

A numerical value used for the background grouping method. The format of the grouping specification depends on what is chosen for the bggtype parameter; see the "gtype" parameter description for details. More information on grouping is available from "ahelp dmgroup".

### **Parameter=pbkfile (string filetype=input default=NONE)**

The parameter block file, which defines ACIS pixel clocking parameters, is used in conjunction with the "dafile" parameter to apply the ACIS dead area correction. The correction is off by default in CIAO 3.4.

Note that acisspec applies the same pbkfile to the source and background datasets. If this is not appropriate for your analysis, you will have to run mkwarf independently to create an ARF with the dead area correction.

In addition, it is not appropriate to apply the dead area correction when coadding files with acisspec. Since the coadded data is provided as input to mkwarf, there is not an accurate single file to provide for the pbkfile parameter.

This is a standard product of pipeline processing and is available for every observation. Parameter block files have names of the form, "acisf146860615N001\_pbk0.fits". The long string of digits refers to the time of observation (seconds since reference date).

See "ahelp mkwarf" for more information on this parameter.

### **Parameter=dafile (string filetype=input default=NONE)**

ACIS "dead area" coefficients file, which may have the values "NONE" (no dead area computation), CALDB (for automatic lookup), or an explicit file reference to an ACIS "dead area" coefficients FITS table. The correction is off by default in CIAO 3.4.

The parameter block file is required to scale the coefficients in the dafile. If dafile=NONE, then pbkfile=NONE is assumed.

See "ahelp mkwarf" for more information on this parameter.

**Parameter=clobber (boolean default=no)**

*Overwrite existing output files?*

**Parameter=verbose (integer default=0)**

*Controls amount of information printed to the screen.*

The verbose parameter provides debugging information.

## CHANGES IN ACISSPEC 4.0

### New Parameters: pbkfile and dafile

New parameters added to the acisspec.par file: pbkfile and dafile; see the parameter descriptions for details. These values are used to apply the ACIS dead area correction in the mkwarf step. The correction is off by default in CIAO 3.4.

Note that acisspec applies the same pbkfile to the source and background datasets. If this is not appropriate for your analysis, you will have to run mkwarf independently to create an ARF with the dead area correction.

In addition, it is not appropriate to apply the dead area correction when coadding files with acisspec. Since the coadded data is provided as input to mkwarf, there is not an accurate single file to provide for the pbkfile parameter.

### Using mkacisrmf

Acisspec checks for CTI keywords in the input file headers and prints a warning if users should remake the RMF response with the mkacisrmf tool. The warnings are printed at verbosity > 0.

### Error and warning messages

The script name has been added to error and warning messages.

## CHANGES IN CIAO 3.4/ACISSPEC 3.7

Two new hidden parameters have been added to mkwarf – a tool called by acisspec – to allow the ACIS dead area correction to be taken into account: "pbkfile" and "dafile". By default, the correction is "off", i.e. both parameters are set to "NONE". See the parameter descriptions in "ahelp mkwarf" for more information.

To apply this correction when running acisspec, set the mkwarf parameters BEFORE executing the script:

```
unix% pset mkwarf pbkfile=acisf063875928N002_pbk0.fits dafile=CALDB
unix% acisspec
```

There is also a new mkwarf "asolfile" parameter which may be set before acisspec is run. Read the mkwarf help file for information on when you may want to do this.

These changes required that a "punlearn mkwarf" be removed from v3.7 of acisspec.

## CHANGES IN CIAO 3.2

acisspec may be used to create response files for the 0th-order of a grating observation. Support has been added to mkwarf for 0th-order grating spectra. The grating efficiencies are taken into account, correctly

Parameter=clobber (boolean default=no)

determining the number of photons detected. The mkwarf tool gets the grating information from the file header.

## 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](#)

*concept*

[subspace](#)

*dm*

[dm](#), [dmcols](#), [dmfiltering](#), [dmimages](#), [dmimfiltering](#), [dmintro](#), [dmopt](#), [dmsyntax](#)

*tools*

[acis bkgrnd lookup](#), [acis fef lookup](#), [acis set ardlib](#), [add grating orders](#), [add grating spectra](#), [asphist](#), [dither region](#), [dmarfadd](#), [dmcoppy](#), [dmextract](#), [dmfilth](#), [dmlist](#), [dmregrid](#), [fullgarf](#), [mkacisrmf](#), [mkarf](#), [mkexpmap](#), [mkgarf](#), [mkgrmf](#), [mkinstmap](#), [mkpsf](#), [mkrmf](#), [mkwarf](#), [psextract](#), [psf project ray](#), [rmfimg](#), [specextract](#)

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