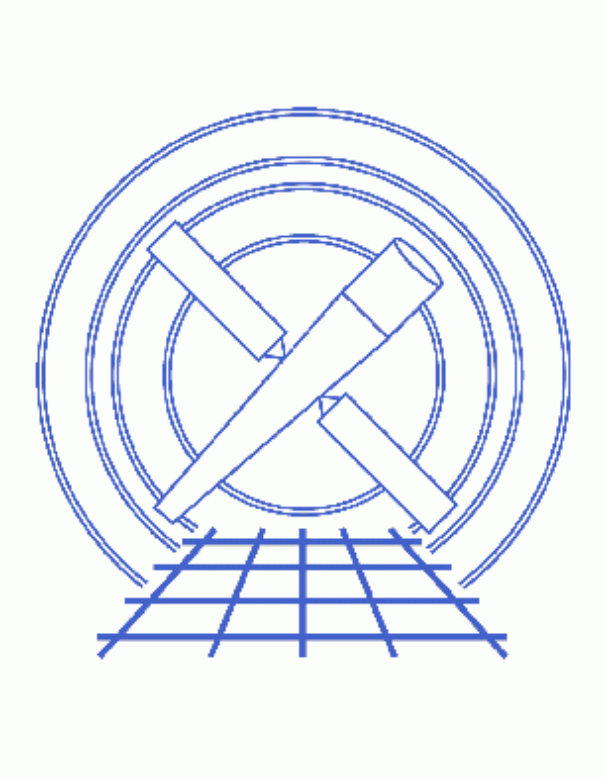
Create Grating RMFs for HRC Observations



CIAO 3.4 Science Threads

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Create Grating RMFs for HRC Observations

CIAO 3.4 Science Threads

Overview

Last Update: 1 Dec 2006 − reviewed for CIAO 3.4: no changes

Synopsis:

`mkgrmf` generates a grating RMF (gRMF) appropriate for spectral analysis of grating observations. The tool can be used either to create a standard gRMF with the most up−to−date calibration or to calculate a gRMF using non−standard grids.

Purpose:

To create observation−specific gRMFs.

Read this thread if:

you are working with HRC grating data and would like to create a grating RMF file. Get Started discusses the available calibration.

Related Links:

- Analysis Guide for Chandra High Resolution Spectroscopy: an in−depth discussion of grating analysis.
- The Formal Underpinnings of the Response Functions used in X−Ray Spectral Analysis (PS, 22pp)

Proceed to the HTML or hardcopy (PDF: A4 | letter) version of the thread.

Get Started

Sample ObsID used: 460 (LETG/HRC−S, 3C 273)

File types needed: pha2

Make sure that you have set up ardlib to use the bad pixel file for your observation before following this thread.

About the calibration files

The calibration files used by `mkgrmf` (`LSFPARM` files) are labeled as +/− 1 order:

```
unix% cd $CALDB/data/chandra/tel/grating/letg/cpf/lsf/
unix% ls −1 hrcsleg*
hrcsleg−1D1999−07−22lsfparmN0003.fits
hrcsleg1D1999−07−22lsfparmN0002.fits
hrcsleg1D1999−07−22lsfparmN0003.fits
```

The 1st order LSF scales nicely at higher orders, however, allowing `mkgrmf` to build higher order gRMFs based on 1st order model. If you request a higher order response file, a message of this form will be printed:

```
WARNING: Unable to find a row with TG_M=2 −−− rescaling TG_M=1 region
```

The tool looks for a 2nd−order calibration file and, failing to find one, chooses the 1st order LSF and builds the gRMF based on it.

Randomized vs. unrandomized data

In CIAO 3.1 (and DS 7.3.0), the value of the `rand_pix_size` parameter in `tg_resolve_events` was changed from 0.5 to 0.0. This means that, by default, randomization is not applied to the chip pixel coordinates before diffraction coordinates are derived. `mkgrmf` uses the value of the `RAND_TG` header keyword to determine whether or not the input data (`obsfile` parameter) was randomized and to select the correct calibration file; `RAND_TG=0` indicates that the data is not randomized.

It is recommended that users remove the pixel randomization from their data before running this thread. To do so, re−run `tg_resolve_events` − as shown in the Obtain Grating Spectra for LETG/HRC−S Data thread − and extract a new PHA2 file.

If your analysis requires that you use randomized data, please read the responses for randomized HRC−S data caveat.

Run mkgrmf

Here we create a +1 order gRMF with standard grids:

```
unix% punlearn mkgrmf
unix% pset mkgrmf order=1
unix% pset mkgrmf grating_arm=LEG
unix% pset mkgrmf outfile=leg_p1.rmf
unix% pset mkgrmf obsfile="hrcf00460N004_pha2.fits[SPECTRUM]"
unix% pset mkgrmf regionfile=hrcf00460N004_pha2.fits
unix% pset mkgrmf detsubsys=HRC−S2
unix% pset mkgrmf wvgrid_arf=compute
unix% pset mkgrmf wvgrid_chan=compute
unix% pset mkgrmf clobber=no
unix% mkgrmf
Output File Name (leg_p1.rmf):
Enter ARF side wavelegth grid [angstroms] (compute):
Enter channel−side wavelegth grid [angstroms] (compute):
Enter Grating order (1):
```

```
Name of fits file with obs info (hrcf00460N004_pha2.fits[SPECTRUM]):
File containing extraction region (hrcf00460N004_pha2.fits):
SrcID (1):
Enter RMF threshold (1e−06):
Verbosity (0:5) (0):
Detector Name (e.g., ACIS−S3) (HRC−S2):
Enter Grating Arm (HEG|MEG|LEG|NONE) (LEG):
```

There are a few details to note:

- The `detsubsys` parameter is set to the chip on which the 0th order falls. For most observations, this will be HRC−S2.
- Specifying `compute` as the grid value is the same as using the default gridding. The default grids for the `wvgrid arf` parameter, suitable for most analysis, are listed in the help file. In general, `wvgrid chan` is set to be the same as the arf grid.

  It is also possible to run `mkgrmf` with non−standard grids for the `wvgrid arf` and `wvgrid chan` parameters, e.g.:

  ```
  unix% pset mkgrmf wvgrid_arf="1.0:205.8:0.01"
  unix% pset mkgrmf wvgrid_chan="1.0:205.8:0.01"
  ```

The contents of the parameter may be checked with plist mkgrmf.

Run the tool for every order you wish to model, changing the `order` parameter accordingly. This process can be automated with a `foreach` loop (shown here for the `tcsh` shell). After setting the `mkgrmf` parameters:

```
unix% foreach f ( −1 −2 −3 1 2 3 )
foreach? mkgrmf outfile=460_leg_{$f}.grmf order=$f mode=h
foreach? end
```

This loop creates gRMFs for the first three positive and negative orders of the spectra. The Creating Higher−order Responses for HRC−S/LETG Spectra thread provides some advice on determing the number of orders to model.

Caveats

Responses for randomized HRC−S data

For randomized data, there is only calibration available for the positive orders. This is primarily due to the fact that users are recommended to work with unrandomized data, so a higher priority is placed on making those calibration files.

Since the effect of randomization on LETG+HRC−S data is virtually zero, the randomized and unrandomized calibration is essentially identical. This means that you can use the negative−order unrandomized file to make negative−order ***randomized*** gRMFs.

In order to do so, it is necessary to set the filename in `ardlib.par`:

```
unix% pset ardlib \
      AXAF_LETG_1111_LSF_FILE="$CALDB/data/chandra/tel/grating/letg/cpf/lsf/hrcsleg−1D1999−07−22lsfp
```

This forces `mkgrmf` to use the −1 randomized file for all runs of the tool, so ***make sure*** to "`punlearn ardlib`" when finished with this analysis. Otherwise the wrong file will be selected in future sessions.

Working with LETG/HRC−I data

The calibration files used by `mkgrmf` (`LSFPARM` files) were calibrated for LETG/HRC−S data, but may be used for HRC−I data as well. The calibration would be identical, except at the very ends of the spectrum. The difference became noticeable around 0.2 keV and worsened quickly at a lower energies.

- Pixel size is not an issue, and intrinsic charge cloud−related detector broadening in HRC−I is very similar to HRC−S, and small compared with mirror broadening.
- The HRC−I plate is 90x90mm, or 127mm along the diagonal of the dispersion axis, compared to 100mm for the HRC−S central plate. The Rowland circle will deviate from the detector for HRC−I only at the extra ~8.5mm at each end. As can be seen from the LETG/HRC−S though, this effect is insignificant over the whole of the HRC−S, so will likely not get that much worse over the extra few mm in HRC−I.

Users that have questions or need further information on creating gRMFs for LETG/HRC−I should contact the Helpdesk.

Summary

This thread is now complete. You may procede to the Compute Grating ARF thread appropriate for your observation: LETG/HRC−S or LETG/HRC−I.

```
Parameters for /home/username/cxcds_param/mkgrmf.par


       outfile = leg_p1.rmf       Output File Name
    wvgrid_arf = compute          Enter ARF side wavelength grid [angstroms]
   wvgrid_chan = compute          Enter channel-side wavelength grid [angstroms]
         order = 1                Enter Grating order
       obsfile = hrcf00460N004_pha2.fits[SPECTRUM] Name of fits file with obs info
    regionfile = hrcf00460N004_pha2.fits File containing extraction region
         srcid = 1                SrcID
#
     threshold = 1e-06            Enter RMF threshold
     detsubsys = HRC-S2           Detector Name (e.g., ACIS-S3)
   grating_arm = LEG              Enter Grating Arm
#
       verbose = 0                Verbosity
  (diagonalrmf = no)              Compute diagonal RMF?
#
#
(ardlibparfile = ardlib.par)      name of ardlib parameter file
      (geompar = geom)            Parameter file for Pixlib Geometry files
#
       (mirror = HRMA)            Mirror Name
```

```
(clobber = no)              Overwrite existing files?
   (mode = ql)              Enter mode for parameter file.
```

History

20 Dec 2004	updated for CIAO 3.2: canned gRMFs are no longer available in the CALDB, users *must* run this thread
14 Jan 2005	added Working with LETG/HRC−I data caveat
08 Apr 2005	added more detail to thread overall; new section − Get Started: About the calibration files; new caveat − Responses for randomized HRC−S data
05 Dec 2005	reviewed for CIAO 3.3: no changes
06 Feb 2006	removed "Matching the grid to the PHA file" section, as it is not straightforward for HRC observations; users who set a custom bin size when running `tgextract` (e.g. ***not*** 0.0125 Å) may contact the Helpdesk for assistance.
01 Dec 2006	reviewed for CIAO 3.4: no changes

URL: http://cxc.harvard.edu/ciao/threads/mkgrmf_hrcs/ Last modified: 1 Dec 2006