

## ctools - Change request #2404

### csphagen output fits file missing OGIP standard headers

03/08/2018 04:02 PM - Moore Chris

|   |                    |                        |            |
|---|--------------------|------------------------|------------|
| <b>Status:</b>  | Closed             | <b>Start date:</b>     | 03/08/2018 |
| <b>Priority:</b>  | Normal             | <b>Due date:</b>       |            |
| <b>Assigned To:</b>   | Knödlseider Jürgen | <b>% Done:</b>         | 80%        |
| <b>Category:</b>  |                    | <b>Estimated time:</b> | 0.00 hour  |
| <b>Target version:</b>  | 1.6.0              |                        |            |
| <b>Description</b>  |                    |                        |            |
| <p>I have recently tested the compatibility of ctools and CTA data with xspec using csphagen to create on, off, arf and rmf fits files.</p> <p>However, I discovered that the files were missing several jey headers required to conform to OGIP standards, and so they did not work in xspec.</p> <p>Manually inputting these headers allowed the data to work in xspec.</p> <p>Missing headers for each file (with descriptions from the documentation and example inputs that worked for me):-</p> <p><b>For the onoff_on and onoff_off files:</b></p> <p>-The following must be added to the SPECTRUM index:</p> <p>TELESCOP = 'CTA' / telescope (mission) name</p> <p>INSTRUME = 'CTA' / instrument name</p> <p>FILTER = 'NONE' / filter</p> <p>BACKFILE = 'none' / associated background filename</p> <p>CORRFILE = 'none' / associated correction filename</p> <p>CORRSCAL = 1 / correction file scaling factor</p> <p>RESPFILE = 'none' / associated redistribution matrix filename</p> <p>ANCRFILE = 'none' / associated ancillary response filename</p> <p>HDUCLASS = 'OGIP' / format conforms to OGIP standard</p> <p>HDUCLAS1 = 'SPECTRUM' / PHA dataset</p> <p>HDUVERS = '1.2.0' / version of the file format (I took a guess for this)</p> <p>POISSERR = T / poissonian errors to be assumed</p> <p>CHANTYPE = 'PI' / channel type (PHA, PI etc)</p> <p>DETHANS = 120 / total number of possible channels</p> <p><b>For the onoff_arf file:</b></p> <p>-The following must be added to the SPECRESP index:</p> <p>TELESCOP = 'CTA' / telescope (mission) name</p> <p>INSTRUME = 'CTA' / instrument name</p> <p>FILTER = 'NONE' / filter</p> <p>HDUCLASS = 'OGIP' / format conforms to OGIP standard</p> <p>HDUCLAS1 = 'RESPONSE' / extension contains response data</p> <p>HDUCLAS2 = 'SPECRESP' / extension contains an arf</p> <p>HDUVERS = '1.2.0' / version of the file format (guess)</p> <p><b>For the onoff_rmf file:</b></p> <p>- The following must be added to the EBOUNDS index:</p> <p>TELESCOP = 'CTA' / telescope (mission) name</p> <p>INSTRUME = 'CTA' / instrument name</p> <p>FILTER = 'NONE' / filter</p> <p>CHANTYPE = 'PI' / channel type (PHA, PI etc)</p> <p>DETHANS = 120 / total number of possible channels</p> <p>HDUCLASS = 'OGIP' / format conforms to OGIP standard</p> <p>HDUCLAS1 = 'RESPONSE' / extension contains response data</p> <p>HDUCLAS2 = 'EBOUNDS' / extension contains EBOUNDS</p> <p>HDUVERS = '1.2.0' / version of the file format (guess)</p> <p>- The following must also be added to the MATRIX index:</p> <p>TELESCOP = 'CTA' / telescope (mission) name</p> <p>INSTRUME = 'CTA' / instrument name</p> <p>FILTER = 'NONE' / filter</p> <p>CHANTYPE = 'PI' / channel type (PHA, PI etc)</p> <p>DETHANS = 120 / total number of possible channels</p> |                    |                        |            |

HDUCLASS = 'OGIP' / format conforms to OGIP standard  
HDUCLAS1 = 'RESPONSE' / dataset relates to the spectral response  
HDUCLAS2 = 'RSP\_MATRIX' / dataset is a spectral response matrix  
HDUVERS = '1.2.0' / version of the file format (guess)  
TLMIN4 = 0 / the minimum value allowed in column 4 (number corresponds to the number of the F\_CHAN column)

The above are the minimum requirement for OGIP conformation, however there are other non-essential headers that may be of use. Full details of the above and non-essential headers can be found here for the PHA files:  
[https://heasarc.gsfc.nasa.gov/docs/heasarc/ofwg/docs/spectra/ogip\\_92\\_007/node6.html](https://heasarc.gsfc.nasa.gov/docs/heasarc/ofwg/docs/spectra/ogip_92_007/node6.html).

For the arf and rmf files, full details can be found here (page 8 and 14 for the rmf extensions and page 17 for the arf extensions):  
[ftp://legacy.gsfc.nasa.gov/caldb/docs/memos/cal\\_gen\\_92\\_002/cal\\_gen\\_92\\_002.pdf](ftp://legacy.gsfc.nasa.gov/caldb/docs/memos/cal_gen_92_002/cal_gen_92_002.pdf).

I hope this helps.

- Chris Moore

## History

### #1 - 06/12/2018 04:09 PM - Knödlseider Jürgen

- Status changed from New to In Progress
- Assigned To set to Knödlseider Jürgen
- Target version set to 1.6.0
- % Done changed from 0 to 80

I implemented the changes. It seems to me that the keywords for the EBOUNDS in the RMF file are not required for Xspec.

I installed Xspec and did some testing. Looks good. Results are similar to results obtained with ctlike.

I wrote a tutorial about how to do an Xspec analysis.

The merging of the code into the trunk is in progress.

### #2 - 06/12/2018 11:02 PM - Knödlseider Jürgen

- Status changed from In Progress to Closed

Here is a link to the tutorial: [http://cta.irap.omp.eu/ctools-devel/users/tutorials/howto/howto\\_xspec.html](http://cta.irap.omp.eu/ctools-devel/users/tutorials/howto/howto_xspec.html)

The code has been merged into devel.