

OGIP Calibration Memo CAL/SW/93-010

# GRPPHA

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## SUMMARY

GRPPHA is a task within the HEASARC sub-package of FTOOLS to define the channel grouping card, quality flags and fractional systematic errors associated with a FITS PHA file conforming to an OGIP standard format. Here we describe in detail the required user inputs, currently available commands & limitations of the task. A number of examples are also provided for illustration.

**LOG OF SIGNIFICANT CHANGES**

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## 1 INTRODUCTION

GRPPHA is an interactive command driven task to define (or redefine) and/or display the grouping (binning) & quality flags, and the fractional systematic errors associated with channels in a FITS PHA file. A new FITS PHA file can be written at any time which includes the latest setting of the above along with a copy of any other extensions in the original file. The various commands and their syntax are described in the command summary below.

On entry, the task displays the values of the keywords mandatory for FITS PHA extension conforming to an OGIP standard format (see Arnaud, George & Tennant 1992; George & Arnaud 1993). The user is then repeatedly prompted for commands until they exit (or quit) the task.

**It should be noted that unlike its predecessor CHANPHA, none of the commands available within GRPPHA change the actual PHA dataset itself (ie the observed counts vs channel histogram) in any way. Instead the necessary grouping, quality & systematic error information for each channel is written alongside the PHA dataset to be picked up by downstream software (eg. XSPEC).**

## 2 INPUT PARAMETERS FOR GRPPHA

The following parameters are currently used:

- **infile** [file name]  
The input filename containing the PHA data in OGIP standard, as a BINTABLE FITS extension
- **outfile** [output file]  
The name of the output file to be created (in OGIP standard format).
- **comm** [command string]  
The command string (see Section 3)
- **chatter** [integer] (hidden)  
The value of the chatter flag, useful for reassurance & diagnostics purposes. The default value is chatter=9, with chatter  $\leq 5$  being very quiet and chatter  $\geq 20$  very verbose.

There are also a number of other hidden parameters which are used internally by the task, and which should not be changed by users.

### 3 COMMAND SUMMARY

There are 8 "families" of command strings currently implemented:

1. group - to define the channel grouping
2. bad - to set channels to bad quality (can be ignored by XSPEC etc)
3. good - to (re)set channels to good quality
4. systematics - to set the fractional systematic error of the data
5. show - to display the current settings to the terminal
6. reset - to remove any current settings
7. chkey - to change keyword value
8. dump - to write an ASCII file of various current values

along with the following straightforward utilities:

- help - interactive help on the task, its commands and their syntax
- write - to write a new PHA file with the current settings
- exit - to exit the task (writing a new file)
- quit - to quit the task

Several commands can be specified on the command line by separating them with an ampersand "&", see example 4 in Section 5.

The various capabilities, limitations & syntax of each of the above are as follows:

#### 3.1 HELP

An interactive help which lists the available commands

*Example:* `grppha> help`

displays the top-level help. The commands

`grppha> commands`

`grppha> ?`

will give the same information.

Interactive help on a particular command (and the syntax), can be obtained using

```
grppha> help COMMAND
```

where COMMAND is one the commands listed above.

*Example:* grppha> help group

gives help upon the commands available to set the grouping flags.

## 3.2 GROUP

Sets the grouping flags such that the PHA dataset can be rebinned by downstream software. It is stressed that the group command does **NOT** change the observed counts vs PHA channel dataset in any way. Rather this command fills the GROUPING column with appropriate flags to delineate which channels start each new group or 'bin' (value = +1), and which are part of a continuing bin (-1). Thus the number of channels (and the channel numbering-scheme itself) in any PHA written by GRPPHA will be the same as that for the input file. (See also Section 3.7.1.)

There are 3 methods by which the grouping can be set:

### 3.2.1 grppha>GROUP MINCHAN MAXCHAN NCHAN

The data is grouped from MINCHAN to MAXCHAN (inclusive) with NCHAN channels in each group. Any 'spare' channels (at the high end of the specified channel range when  $(MAXCHAN - MINCHAN + 1)/NCHAN$  is not an integer) will be left ungrouped and the user informed. Any grouping requested which partially overlaps a pre-existing grouping will be ignored and the user informed. A maximum of 6 sets of groupings is allowed on the command line.

*Example:* grppha> group 10 20 2 21 30 10

will set the grouping flag such that from channel 10 to channel 19 the data can be binned up by a factor 2, channel 20 is "spare" and left unbinned, and channels 21 to 30 can form a single bin.

### 3.2.2 grppha>GROUP GRP\_FILE.DAT

The grouping information is read (free-format) from the data file "GRP\_FILE.DAT". This file is in ASCII format and can consist of up to 100 lines (sets of groupings, one per line) with the syntax MINCHAN MAXCHAN NCHAN, where these have the same meanings as above. The rules regarding spare and overlapping groupings are as above. (See also the grppha> dump group command described in Section 3.9.1.)



### 3.2.3 grppha>GROUP MIN RCNTS

The grouping is set such that each new grouping contains a minimum of RCNTS counts in each bin. Channels that are defined as BAD are not included. Any ‘spare’ channels at the high channel end of the dataset (which when added together have less than RCNTS counts) are defined BAD by software (Quality=2).

## 3.3 BAD

Sets the quality flags such that the specified channels can be ignored by certain subsequent commands (such as GROUP MIN RCNTS described in Section 3.2.3) and downstream software (*eg* XSPEC). The quality flags of unspecified channels are unchanged. All channels set bad within GRPPHA will have a quality flag of either 2 or 5 (indicating a ‘spare’ and ‘bad’ channel respectively). XSPEC can be told to ignore channels with Quality≠0 by issuing the `xspec>ignore bad` command. (See also Section 3.7.2.)

There are 2 methods whereby channels can be set bad:

### 3.3.1 grppha>BAD MINCHAN-MAXCHAN

Channels between MINCHAN and MAXCHAN (inclusive) are set bad (Quality = 5). All other channels will retain their previous quality flag. The hyphen in the above command should be noted - should this not be present, the task will set MINCHAN and MAXCHAN (only) to bad, leaving all channels in between with their previous quality flags. A maximum of 6 sets of channels are allowed on the command line.

*Example:* `grppha> bad 1 5-20 29`

will set the quality flag such that channel 1, channels 5 through 20, and channel 29 are defined to be bad.

### 3.3.2 grppha>BAD BADFILE.DAT

The quality information is read (free-format) from the data file "BADFILE.DAT". This file is in ASCII format and can consist of up to 100 lines (sets of channel ranges, one per line) with the syntax MINCHAN MAXCHAN where these have the same meanings as above. Note that unlike when the command is entered on the command line, dashes are illegal syntax in the file, and single channels which are to be set bad must be specified by explicitly setting MAXCHAN to be equal to MINCHAN. (See also the `grppha> dump quality` command described in Section 3.9.3.)

### 3.4 GOOD

Sets the quality flags such that the specified channels are considered good (Quality = 0) and hence will be used by certain subsequent commands (such as GROUP MIN RCNTS described in Section 3.2.3) and downstream software (*eg* XSPEC). The quality flags of unspecified channels are unchanged. (See also Section 3.7.2.)

There are 2 methods whereby channels can be set good:

#### 3.4.1 grppha>GOOD MINCHAN-MAXCHAN

Channels between MINCHAN and MAXCHAN (inclusive) are set good should they not be so already. As in the case of the BAD command, note the use of the hyphen - should this not be present, the task will set MINCHAN and MAXCHAN (only) to good, leaving all channels in between with their previous quality flag. A maximum of 6 sets of channels are allowed on the command line.

*Example:* grppha> good 2 6-18 99

will set the quality flag such that channel 2, channels 6 through 18 and channel 99 are defined to be good.

#### 3.4.2 grppha>GOOD GOODFILE.DAT

The quality information is read (free-format) from the data file "GOODFILE.DAT". This file is in ASCII format and can consist of up to 100 lines (sets of channel ranges, one per line) with the syntax MINCHAN MAXCHAN where these have the same meanings as above. Note that unlike the command is entered on the command line, dashes are illegal syntax in the file, and single channels which are to be set good must be specified by explicitly setting MAXCHAN to be equal to MINCHAN. (See also the grppha> dump quality command described in Section 3.9.3.)

### 3.5 SYSTEMATICS

Sets the fractional systematic error for each PHA channel, which should be combined with the corresponding statistical error on the data, to define the true (total) error on the data. It is stressed that this command obviously does **NOT** change the observed (statistical) error associated with the PHA data. Rather SYS\_ERR column is filled with the appropriate values, and the command is therefore reversible. (See also Section 3.7.3.)

There are 2 methods whereby the systematic errors can be set:

### 3.5.1 grppha>SYSTEMATICS MINCHAN-MAXCHAN ERR

Channels between MINCHAN and MAXCHAN (inclusive) will have a fractional systematic error of ERR defined (ERR = 0.03 corresponds to a systematic error of 3% of the observed PHA counts or count rate for that channel). A maximum of 6 errors are permitted on the command line.

*Example:* grppha> systematics 20 0.02 30-40 0.01

will set channel 20 to have a systematic error of 2%, and channels 30 through 40 have a systematic error of 1%.

### 3.5.2 grppha>SYSTEMATICS SYSFILE.DAT

The information regarding the fractional systematic errors is read (free-format) from the data file "SYSFILE.DAT". This file is in ASCII format and can consist of up to 100 lines (sets of channel ranges, one per line) with the syntax MINCHAN MAXCHAN ERR where these have the same meanings as above. Note that unlike when the command is entered on the command line, dashes are illegal syntax in the file, and single channels which are to have an error applied must be specified by explicitly setting MAXCHAN to be equal to MINCHAN. (See also the grppha> dump systematics command described in Section 3.9.2.)

## 3.6 SHOW

Displays the current settings to the screen in a concise format.

### 3.6.1 grppha>SHOW GROUPING

Displays the current channel GROUPING cards to the screen.

*Example:* grppha> show group

will result in the following screen display:

```

-----
GROUPING
-----
Channel Grouping (Channel-Channel) :
-----
    4 -   5  of undefined grouping
    6 -  84  are single channels
   85 -  92  are grouped by a factor 2
   93 - 128  of undefined grouping (Channel quality=bad)
-----

```

where undefined indicates that the grouping flag is 0, for single channels the grouping flag is 1, the start of a new bin has a grouping flag of 1, and channels that are part of a continuing group have the grouping flag of -1.

### 3.6.2 grppha>SHOW QUALITY

Displays the QUALITY flags to the screen of all channels or ranges of channels which are currently defined as bad.

*Example:* `grppha> show quality`

will result in the following screen display:

```
-----
QUALITY
-----
Bad Channels (Channel - Channel) :
-----
    4 -   5  have quality 5
    91 - 128 have quality 2
-----
```

where quality=5 indicates that the channel has been set bad by the user, and quality=2 has been defined "dubious" by software. A full list of possible quality flag values and their meaning is given in Arnaud *et al* (1992). As noted above, channels set bad within GRPPHA will have a quality flag of either 2 or 5, and can be ignored within XSPEC by issuing the `xspec>ignore bad` command.

### 3.6.3 grppha>SHOW SYSTEMATICS

Displays current fractional SYSTEMATIC errors to the screen for those channels for which it is defined.

*Example:* `grppha> show systematics`

will result in the following screen display:

```
-----
SYSTEMATIC ERRORS
-----
Systematic Errors (Channel - Channel) :
-----
    13 -  23  have systematic error 0.0300
    24 -  20  have systematic error 0.0750
-----
```

indicating channels 13 to 23 (inclusive) have a systematic error of 3%, and channels 24 to 36 have a systematic error of 7.5%. All other channels have no (*ie* a 0%) systematic error defined.

### 3.6.4 grppha>SHOW ALL

Displays the current channel GROUPING cards, QUALITY flags and fractional SYSTEMATIC errors to the screen in the formats described above.

### 3.6.5 grppha>SHOW KEYWORDS

Displays all the mandatory PHA keywords, and their current values to the screen.

### 3.6.6 grppha>SHOW INFILE

Displays input filename.

### 3.6.7 grppha>SHOW CHKEYS

Displays names of keywords within the PHA file that can have their values changed within GRPPHA (via the command `grppha> chkey`, see Section 3.8).

In addition any of the CHKEY keywords can be displayed in full (even if it exceeds 80 characters). This is useful for character string keywords such as the path and name of response matrices *etc*, which can often get truncated in other standard displays available within GRPPHA.

*Example:* `grppha> show respfile`

will result in a screen display with the following format:

```
RESPFILE= /home/local/users/username/asca/gis/matrices/special/g2v3_1_1a.rmf
```

showing the current response file name.

## 3.7 RESET

Resets the current settings to 'null', **NOT** to those in the original input file.

### 3.7.1 grppha>RESET GROUPING

Reset all the channel GROUPING flags to 1, that is to ungrouped (**not** to those in the input file).

### 3.7.2 grppha>RESET QUALITY

Reset all the channel QUALITY flags to good (Quality = 0), regardless of the original setting.

### 3.7.3 grppha>RESET SYSTEMATICS

Reset the fractional SYSTEMATIC errors to zero, (**not** to those in the input file).

### 3.7.4 grppha>RESET ALL

Reset all the channel GROUPING card, QUALITY flags and fractional SYSTEMATIC errors, as described above.

## 3.8 CHKEY

This command allows a keyword value to be changed. Currently users are permitted to change the values of only a subset of the mandatory keywords.

### 3.8.1 grppha>CHKEY KEYWORD NEWVALUE

The value of KEYWORD is changed to NEWVALUE. It should be noted that the maximum allowed length for a number is 20 characters, and for a character string (*eg* for filenames) is 120 characters.

*Example:* grppha> CHKEY AREASCAL 1.03  
will change the value of AREASCAL keyword to 1.03.

## 3.9 DUMP

This command allows the current values of a number of quantities/settings to be written to ASCII file. These ASCII files can be read back into GRPPHA and hence the DUMP facility is useful if the

user wishes to apply the same settings in future GRPPHA runs. Currently there 3 quantities able to be DUMPed:

### 3.9.1 grppha>DUMP GROUP GRP\_FILE.DAT

The current grouping information is written to an ASCII data file "GRP\_FILE.DAT", each row of which lists the values of the MINCHAN MAXCHAN NCHAN for a given group. This grouping information can then be read into GRPPHA via the command `grppha$>$GROUP GRP_FILE.DAT` (see Section 3.2.2).

### 3.9.2 grppha>DUMP SYSTEMATICS SYSFILE.DAT

The current fractional systematic errors are written to an ASCII data file "SYSFILE.DAT", each row of which lists the values of the MINCHAN MAXCHAN ERR. These systematics can then be read into GRPPHA via the command `grppha$>$SYSTEMATICS SYSFILE.DAT` (see Section 3.5.2).

### 3.9.3 grppha>DUMP QUALITY QUALFILE.DAT

The channels which are currently flagged as **BAD** (only) are written to an ASCII data file "QUALFILE.DAT", each row of which has the format MINCHAN MAXCHAN. This quality flag information can then be read into GRPPHA via the command `grppha$>$BAD QUALFILE.DAT` (see Section 3.3.2). It should be noted that if the command `grppha$>$GROUP MIN` (see Section 3.2.3) was used to define which channels are currently flagged as bad, then the `grppha$>$DUMP QUALITY QUALFILE.DAT` does not differential between bad channels interactively defined by the user (which have a Quality flag of 5) and those set bad by the `grppha$>$GROUP MIN` command (which have a Quality flag of 2) – all channels with a non-zero quality flag are written to the output ASCII file.

## 3.10 WRITE

Writes an output PHA file with the current settings, including copies of any other extensions present within the original input PHA file.

### 3.10.1 grppha>WRITE ABCD.PHA

Writes a new PHA file called "ABCD.PHA". For the protection of users, under unix/ultrix this command will produce an error message should a file of this name already exist in the current directory. No new file will be written and thus the pre-existing file will not be lost. Under VAX/VMS a new file will be written (with a higher version number), and the user warned of the existing file. An

error message will also be returned if the requested filename is illegal under the operating system in use.

This command does not stop the task, thus settings can be altered further and subsequently written to another file if desired.

GRPPHA v.2.0.0 (and higher) allows the new PHA file to have the same name as the input PHA file (and hence allows the input file to be overwritten). This can be achieved either by:

- setting the hidden boolean parameter `clobber` to `yes` prior to entering the GRPPHA, or
- making use of the "!"-convention described in Section 3.10.2.

### 3.10.2 `grppha>WRITE !ABCD.PHA`

Writes a new PHA file called "ABCD.PHA" irrespective of whether a file of the same name already exists in the current directory. Under unix/ultrix the pre-existing file will thus be **overwritten**; under VAX/VMS the latest (most current) version of the pre-existing file will be overwritten.

## 3.11 EXIT

Exits the task, after writing an output file.

### 3.11.1 `grppha>EXIT`

Exit the task, first writing a new PHA file with the name as specified by the input parameter `outfile` with the final settings, including copies of any other extensions present within the original input PHA file. The rules regarding illegal filenames given in Section 4 apply.

### 3.11.2 `grppha>EXIT !ABCD.PHA`

Exit the task, first writing a new PHA file "ABCD.PHA" irrespective of whether a file of the same name already exists in the current directory. Under unix/ultrix the pre-existing file will thus be **overwritten**; under VAX/VMS the latest (most current) version of the pre-existing file will be overwritten. The specification of the output filename in this way overrides the value given via the input parameter `outfile`.



### 3.12 QUIT

Quits the task.

*Example:* `grppha> quit`

Exits the task without writing the PHA file specified by the `outfile` parameter.

## 4 WARNINGS ON USAGE

When the grouping command `grppha> group MINCHAN MAXCHAN NCHAN` is used and an overlap occurs with channels for which the grouping has previously been defined, the grouping of the channels in the region of overlap is left unchanged and the user warned. The grouping is however set (if possible) for all channels outside the region of overlap. Users wishing to overwrite a pre-existing grouping should first use the `grppha>reset group` command.

The `grppha> group min` command will overwrite any grouping flags previously set.

When using input ASCII files with the commands, filenames containing hyphens are not permitted.

The `CHKEY` command has been updated to allow a maximum string length of 120. In order to do this a `fitsio` continuation convention is used. **NOTE:** This may cause problems if downstream software has not been appropriately modified.

## 5 EXAMPLES

1. To manipulate the PHA file "my\_file.pha", and write to "my\_file.grp" with the changes if any, and default chattiness:

```
unix> grppha my_file.pha myfile.grp
```

Now the PHA extension mandatory keywords, and values will be displayed on the screen.

The `grppha>` prompt will appear. An example command is `grppha>group MINCHAN MAXCHAN NCHAN`: the data would be rebinned from MINCHAN to MAXCHAN, with NCHAN specifying the number of bins to be grouped:

```
grppha> group 1 400 10
```

This command will group 1 to 400 with 10 bins in each group.

To show the current grouping:

```
grppha> show grouping
```

EXIT can be used to write a new file with the rebinned data.

Note that in addition to the extension containing the PHA data, all other extensions in the input file are copied:

```
grppha> exit
```

2. To use "test.pha" as input PHA file, and use the default output file, with default chattiness

(quiet):

```
unix> grppha test.pha
```

To add a 3% systematic error to channels 40 to 56:

```
grppha> systematics 40-56 0.03
```

Now to set a number of channels 'bad' (such that they can be ignored in XSPEC):

```
grppha> bad 11 20-40
```

This command sets channel 11 to bad, and channels 20 to 40 bad inclusively.

In order to see the current grouping, systematic errors, and quality settings:

```
grppha> show all
```

To exit the program without writing to a file:

```
grppha> quit
```

3. To use "bbxrt.pha" as input file, and "bbxrt.grp", as output filename, with verbose chattiness:

```
unix> grppha bbxrt.pha bbxrt.grp 20
```

To group the data with at least 30 raw counts in each bin:

```
grppha> group min 30
```

The current changes can be written to a file, without exiting grppha:

```
grppha> write bbxrt30.grp
```

The reset command can be used to set all the data as unbinned.

After this the data can be rebinned afresh. To reset:

```
grppha> reset grouping
```

To set bad channels by reading a list of such channels from a file:

```
grppha> bad badfile.dat
```

To exit, and write a new PHA file (overwriting test.pha, should it exist):

```
grppha> exit !test.pha
```

4. To use GRPPHA in a non-interactive manner with no chatter :

```
unix> grppha infile="test.pha" outfile="new.pha"  
chatter=0 comm="group 1 2048 4 & bad 1-10 & exit "
```

## 6 FUTURE ENHANCEMENTS

The following enhancements have been suggested and/or are planned in the near future (mainly to reproduce the functionality of the old XANADU task CHANPHA):

- Allow the use of 'wild' cards in the specification of channel ranges for many of the commands
- Add commands such as `grppha> group SASS` (which would only be allowed in the case of PHA files from the *ROSAT* PSPC) to explicitly set the grouping card to be equivalent to the 34 standard bins used by the SASS processing.
- `grppha>time` to change the active integration time

The authors would appreciate any comments, suggestions for additional enhancements *etc* users may have.

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