



AHELP for CIAO 3.4

grpBinFile

Context: group

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Synopsis

Group an array using the grouping applied to another dataset.

Syntax

```
grpBinFile( Array_Type axisArray, Array_Type fAxisSize, Array_Type
fGroupingCol, Array_Type fQualCol )
grpBinFile( Array_Type axisArray, Array_Type fAxisSize, Array_Type
fGroupingCol, Array_Type fQualCo, Array_Type tabStops )
```

```
Returns: ( Array_Type grouping, Array_Type quality )
```

Description

This function allows you to calculate the grouping information needed to group the input data (the axisArray array) to match the grouping of another dataset (the fAxisSize, fGroupingCol, and fQualCol arrays which can be read from a file). Often you can apply the grouping information directly – i.e. call

```
grpGetGroupSum( axisArray, fGroupingCol )
```

rather than grpBinFile() – unless the two datasets do not have the same set of axis values. An example of this is when different binning factors are used to create spectra, e.g. calling dmextract with

```
[bin pha=1:4096:4]
```

and

```
[bin pha=1:4096:1]
```

To apply the grouping calculated from one of these spectra to the other one requires the use of grpBinFile().

This function provides the same functionality as the BIN_FILE option of dmgroup.

Example

```
chips> pha1 = readbintab( "spec1.pi" )
chips> pha2 = readbintab( "spec2.pi" )
chips> ( grp, qual ) = grpBinFile( pha2.PI, pha1.PI, pha1.GROUPING,
pha1.QUALITY )
```

In this example we read in the data from two spectra which were binned on the PI channel. The `grpBinFile()` routine is used to calculate the grouping and quality arrays for `spec2.pi` that match the grouping applied to `spec1.pi`.

Note that `readbintab()` was used to read in both files; `readpha()` should not be used since this automatically applies the grouping information when reading in the data, and the resulting data can not be used in `grpBinFile()` since information has been lost.

Bugs

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

See Also

group

[grpadaptive](#), [grpadaptivesnr](#), [grpbin](#), [grpbinfile](#), [grpbinwidth](#), [grpgetchanspergroup](#), [grpgetgroupsum](#), [grpgetgrpnum](#), [grpmaxslope](#), [grpminslope](#), [grpnumbins](#), [grpnumcounts](#), [grpsnr](#)

modules

[group](#)

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URL:
<http://cxc.harvard.edu/ciao3.4/grpbinfile.html>
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