

*AHELP for CIAO 3.4*

dmjoin

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Synopsis

Join two files whose sampling is different.

Syntax

```
dmjoin infile joinfile outfile join [interpolate] [verbose] [clobber]
```

Description

The dmjoin program allows you to perform interpolations on tables which have a common column.

Suppose you have a file asol.fits which gives the aspect solution as a function of time, sampled on a specific time interval, and a set of photon events whose times are arbitrary. dmjoin allows you to generate a version of the aspect solution with one record per photon, interpolated to the times of those photons.

Another example would be a table linking photometric color BV_COL to stellar effective temperature TE, together with a star catalog containing values of BV_COL for each star. The program will generate the corresponding TE values for each star.

NB: Interpolating has been generalized to offer more options than a simple linear interpolation. These other options are selected by setting the parameter 'interpolate' to a non-default value (see the parameter section).

Example 1

```
dmjoin evt.fits "asol.fits[cols ra,dec,roll,time]" evt_join.fits
join=time
```

The column "time" is present in both evt.fits and the virtual file "asol.fits[cols ra,dec,roll,time]". In the latter, time is monotonic, so we can interpolate. The output file evt_join.fits will be a copy of evt.fits with the columns ra,dec,roll added to it. The values of ra,dec,roll in the output file will be determined by using the value of time in evt.fits and interpolating in the asol.fits file to calculate the values of ra,dec and roll.

Example 2

```
dmjoin "evt.fits[cols time]" asol.fits asol_join.fits join=TIME
```

Makes a version of the aspect file evaluated only at the times of photons in the event file. Since the (virtual) event file has only one column, time, and this is the join column, the output has exactly the same column structure as the `asol.fits` file – except that the `TIME` column will be the first one in the file.

Example 3

```
dmjoin "catalog.fits" "color_table.fits[cols BV_COL,TE]" join=BV_COL
outfile=catalog_with_te.fits
```

Make a version of the catalog with a derived column `TE` generated from the lookup table `color_table.fits` which gives the function `TE(BV_COL)`.

Parameters

name	type	ftype	def	min	max	reqd
<u>infile</u>	file	input				yes
<u>joinfile</u>	file	input				
<u>outfile</u>	file	output				yes
<u>join</u>	string					
<u>interpolate</u>	string		linear			
<u>verbose</u>	integer		0	0	5	
<u>clobber</u>	boolean		no			

Detailed Parameter Descriptions

Parameter=infile (file required filetype=input)

Input virtual file

Input virtual file used as a basis for the output file. Must contain the join column; need not be sorted.

Parameter=joinfile (file filetype=input)

Input virtual join file.

Must contain the join column and at least one other column. Must be monotonically sorted on the join column.

Parameter=outfile (file required filetype=output)

The output file, with the interpolated column. The output file is a copy of the input virtual file, but with the columns from the join file appended and interpolated.

Parameter=join (string)

Name of join column.

The name of the common column in the join file and input file.

Parameter=interpolate (string default=linear)

Interpolation method

There are several methods of selecting values of the entries in the new column(s), based on the relevant values in the join column.

- linear – a simple linear interpolation
- first – pick values from the first of the two rows bracketing the input value of the join column.
- last – pick values from the second of the two rows
- closest – pick values from the row closest to the input value of the join column.
- furthest – pick values from the row furthest from the input value of the join column.
- minimum – pick the smaller value of the two which bracket the input value of the join column.
- maximum – pick the larger value

Parameter=verbose (integer default=0 min=0 max=5)

Controls screen output information, value is 0 (no info) to 5 (most info).

Parameter=clobber (boolean default=no)

Clobber output if it exists? (yes/no)

CHANGES IN CIAO 3.0

In addition to the original linear interpolation for choosing values within an interval of the join column, several other options are now available. These are controlled by the new parameter, "interpolate" (whose default is the original linear interpolation). These other options are described in the parameter section of this file.

Bugs

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

See Also

dm

[dmcols](#), [dmfiltering](#), [dmopt](#)

tools

[dmappend](#), [dmarfadd](#), [dmgroup](#), [dmgti](#), [dmmerge](#), [dmpaste](#), [dmsort](#), [dmtcalc](#), [dmtype2split](#)



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