

BLDPFF User's Guide

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1.0 Introduction

BLDPFF is an interactive processor designed to manipulate data contained in one or more Portable File Format (PFF) files. These manipulations allow selected data from files to be copied from one file to another. The selection of datasets can be via dataset number, string-matching in the datasets' comment field, or by sorting of the datasets' comment field. BLDPFF also provides commands to open PFF files and to display a directory of each open file's contents.

PFF is a file format developed at Sandia National Laboratories to allow codes to write compact, binary data files. These files are easily read by applications on a wide variety of computers, without any need for translation from one machine to another. The compactness of PFF files is a result of converting floating point arrays to arrays of 2-byte integers, based on the assumption that 16 bit precision (1 part in 64,000) is more than adequate for most post-processing needs. PFF is described in detail in the PFF User's Guide. To use BLDPFF, it is sufficient to know that a PFF file is built up of datasets that can be accessed randomly. A PFF dataset contains all information required to describe a given set of data.

In addition to its own features, BLDPFF gains further functionality from the TIOLIB I/O library. TIOLIB provides the user interface to BLDPFF. It processes interactive commands with a case-insensitive free-format input processor. It also allows the user to define and manipulate symbols, run nested command files, execute loops, and much more.

2.0 Using BLDPFF

BLDPFF is used through a command-line interface. Although designed to be used interactively, it can also be used in a non-interactive batch mode. The details of invoking BLDPFF is described in section 2. 1.

BLDPFF provides tools to perform extensive manipulation of the datasets in one or more PFF files. These commands are described in section 2. 2.

In addition to its own set of commands, BLDPFF gains further functionality from the TIOLIB I/O library. TIOLIB provides the user interface to BLDPFF. It processes interactive commands with a case-insensitive, free-format input processor. It also allows the user to define and manipulate symbols, run nested command files, execute loops, and much more. For complete documentation of TIOLIB commands and functionality, see the TIOLIB User's Guide or enter the command "**^help**" from the BLDPFF command line.

2.1 Command-line options

BLDPFF is invoked from the command line, and its behavior and initial state can be modified with provided command-line options and arguments. The syntax for BLDPFF is as follows:

```
bldpff [ -D tio_var[=value] ... ] [ [ -B] -c cmd_file ] [ -b|-a output_file ] [ [ -o] input_file ... ]  
bldpff -h
```

-D <i>tio_var</i> [= <i>value</i>]	Predefine TIO global symbol <i>tio_var</i> with <i>value</i> . If <i>value</i> is not supplied, the value of <i>tio_var</i> is set to 1 (the numeral "one").
-c <i>file</i>	Process input commands from <i>file</i>
-B	Exit after processing command file. This option is only valid when used in conjunction with the -c option.
-a <i>file</i>	Open <i>file</i> in append mode
-b <i>file</i>	Open <i>file</i> in build mode
-o <i>file</i>	Open <i>file</i> in read mode
-h	Usage help

BLDPFF allows only one output file to be open at a time, so the **-a** and **-b** options cannot be used together. However, multiple files in read mode are allowed. Consequently, multiple "read-only" files can be specified with the **-o** option. In addition, any command-line arguments supplied after these command-line options are also opened in "read-only" mode. The last "read-only" file specified is considered to be the active input file.

2.2 Summary of Interactive commands

This section contains an alphabetically-ordered list of all BLDPFF commands. The syntax for each command is shown, as well as a complete description of each command and all its arguments. As previously mentioned, BLDPFF also supports a wide variety of general-purpose commands through the TIOLIB I/O interface. To access these commands from

BLDPFF, simply preface TIOLIB command with the carat (^) prefix character.

APPEND

Open an existing PFF file for output. The file will become the active output file. Any datasets copied to this file will be appended to those datasets already present in the file. Note that the output file will be in multiple pieces if the maximum PFF file size is exceeded – see the MULTI_OUTPUT command.

format: **app[*end*] [*filespec*]**

where:

filespec - Name of file to be opened in append mode. If not supplied, user will be prompted.

BUILD

Open a new PFF file for output. The file will become the active output file. Note that the output file will be in multiple pieces if the maximum PFF file size is exceeded – see the MULTI_OUTPUT command.

format: **b[*uild*] [*filespec*]**

where:

filespec - Name of file to be opened for output. If not supplied, user will be prompted.

CLOSE

Close a PFF file.

format: **cl[*ose*] [*filespec*]**

where:

filespec - Close the specified file: *file_spec* can either be a file number, or the character strings 'i[nput]' or 'o[utput]'. If not supplied, user will be prompted.

CONFIRM

Set the confirm mode for dataset copying. If option (ON, OFF, or ?) is not specified, ON is assumed.

format: **con[*firm*] [*on/off[f]/?*]**

where:

on - Sets confirm mode ON. (default if not supplied)
off - Sets confirm mode OFF. (default state on program entry)
? - Displays current confirm mode on terminal

CP

Copy datasets from active input file to active output file.

format: **cp** [*ib* [*ie* [*iskip*]]]

where:

- ib* - Number of the first dataset to be copied. *ib* must be positive. If not specified, user will be prompted for entire do-list.
- ie* - Number of the last dataset to be copied. A value less than or equal to 0 indicates the last dataset in file. If not specified, *ie* = *ib*.
- iskip* - Skip factor between copied datasets. *iskip* must be positive. If not specified, *iskip* = 1.

END

If command input mode is interactive, the END command exits the BLDPFF utility. All open PFF files are closed before exiting. If input commands are currently being read from a file (via the RUN command), command control is returned to the command level that originally initiated the command file.

format: **end**

synonyms: **quit**

EXACT

Set the case-sensitivity for string searches. If option (ON, OFF, or ?) is not specified, ON is assumed.

format: **ex[act]** [on/off[f]/?]

where:

- on - Forces string searches to be case-sensitive. (default if not supplied)
- off - Forces string searches to be case-insensitive.
- ? - Displays current case-sensitivity setting on terminal

FILE

List open files. The pointers 'I>' and 'O>' indicate the active input and output files, respectively. If option is not supplied, center point of last display will be used.

format: **f[ile]** [*ifile*] or **f[ile]** [u/d] or **f[ile]**]

where:

- ifile* - Number of file about which listing is to be centered. If not supplied, center point of last display will be used.
- u - Scrolls the file list up one screen from last display.

- d - Scrolls the file list down one screen from last display.
-] - Scrolls the file list to the end of file.

HELP

Provide documentation for BLDPFF and all its commands. If the environment variable "BLDPFFhelp" is defined and specifies an existing file, it will be used as the help file. If this is not the case, BLDPFF then looks for the file "\$HERMES_ROOT/doc/Bldpff.pdf", which will be used as the help file. The help file is opened by spawning a new process with the command "acoread", unless the environment variable "TIO_help_reader" is used to define an alternate command for reading the help file. If the help file is not located by either of these methods, a list of available BLDPFF commands will be provided. Additionally, the "^help" command can be used to access the help for the commands provided by the TIO library, as previously described.

format: **h[elp]**

IDIR

List Dataset directory of active input file. If option is not supplied, center point of last display will be used.

format: **id[ir] [ids] or id[ir] [u/d] or id[ir]]**

where:

- ids* - Number of dataset about which directory list is to be centered. If not supplied, center point of last display will be used.
- u* - Scrolls the directory list up one screen from last display.
- d* - Scrolls the directory list down one screen from last display.
-]* - Scrolls the directory list to the last dataset in file.

INPUT

Select the active input file. The file must be open in READ mode.

format: **in[put] [ifile]**

where:

- ifile* - Number of file to be selected as active input file. If not supplied, user will be prompted.

LOG

Set the log mode for dataset copying. If option (ON, OFF, or ?) is not specified, ON is assumed.

format: **lo[g] [on/of[f]/?]**

where:

- on - Sets log mode ON. (default if not supplied)
- off - Sets log mode OFF. (default state on program entry)
- ? - Displays current log mode on terminal

MULTI_OUTPUT

Provide user control over building the 'output file' in multiple pieces: out.pff, out_2.pff, out_3.pff, etc. Even when this command is not specified, this is the default behavior when the output file exceeds the maximum allowable PFF file size (as might occur when building a single output file concatenating datasets from multiple input files).

format: **mu**[*lti_output*] **max_bytes** ['MB'/'GB'] [*nchsuf*]

where:

- max_bytes* - Maximum number of bytes in each individual output file: initialized to $0.75 * \text{max_possible_bytes}$ at startup, where *max_possible_bytes* is either $2^{31}-1$ for 4-byte file pointers, and $\sim 2^{42}$ for 8-byte file pointers. The optional string 'MB' or 'GB' specify that *max_bytes* is the number of megabytes or gigabytes respectively. One of these is required if the file size exceeds $2^{31}-1$, since the TIOLIB input processor unconditionally loads *max_bytes* into a signed 4-byte integer.
- nchsuf* - Number of characters in the suffix for extra files: initialized to 1 at startup; default if not specified here is to leave it unchanged. Suffixes are written out in an 'iN.N' format, where $N = \text{nchsuf}$. For example with *nchsuf*=3, suffixes are '_002', '_003', etc.

ODIR

List Dataset directory of output file. If option is not supplied, center point of last display will be used.

format: **od**[*ir*] [*ids*] or **od**[*ir*] [*u/d*] or **od**[*ir*]]

where:

- ids* - Number of dataset about which directory list is to be centered. If not supplied, center point of last display will be used.
- u* - Scrolls the directory list up one screen from last display.
- d* - Scrolls the directory list down one screen from last display.
-]* - Scrolls the directory list to the last dataset in file.

OPEN

Open an input file. Opened file becomes the active input file.

format: **op**[*en*] [*filespec*]

where:

filespec - Name of file to be opened for input. If not supplied, user will be prompted.

OUTPUT

Select the active output file. The file must be open in WRITE mode.

format: **out[put] [ifile]**

where:

ifile - Number of file to be selected as active output file. If not supplied, user will be prompted.

PACK

Open and pack a PFF file. File is closed upon completion. ONLY files whose datasets are positioned in ascending order can be packed via this option. ANY file can be copied to another file in a packed fashion using the CP command.

format: **pack [filespec]**

where:

filespec - Name of file to be packed. If not supplied, user will be prompted.

PIDIR

Print Dataset directory of active input file to a user-specified output file.

format: **pid[ir] [filespec]**

where:

filespec - Name of file to which the active input directory listing is written.

PODIR

Print Dataset directory of active output file to a user-specified output file.

format: **pod[ir] [filespec]**

where:

filespec - Name of file to which the active output directory listing is written.

QUIT

Exit BLDPFF utility. All open PFF files are closed before exiting.

format: **q[uit]**

synonyms: **end**

REPAIR

Repair a PFF file that has been improperly closed. It opens the file and attempts to load its directory. Failing this, it attempts to rebuild the directory from the header info in each dataset, one dataset at a time. If it cannot reconstruct the entire directory, it truncates the file after the last dataset for which a directory entry was successfully loaded. It then closes the file, rewriting the directory if necessary.

format: **rep[air] [filespec]**

where:

filespec - Name of file to be repaired. If not supplied, user will be prompted.

REWIND

Rewind a PFF file. The only real use for this command is to convert a WRITE_ONLY file (created with the BUILD command) to a READ/WRITE file. This in turn allows the file to be selected as the active input file via the INPUT command.

format: **rew[ind] [ifile]**

where:

ifile - Number of file to be rewound. If not supplied, user will be prompted.

SCP

Copy datasets from active input file to active output file. Datasets are selected by matching a user-supplied string within a substring of the dataset title. The substring range is set via the SUB command. If a do-list is supplied, only those datasets that meet the do-list criteria will be tested for a string match.

format: **scp ['string'] [ib [ie [iskip]]]**

where:

string - An apostrophe-delimited string. If a user-specified substring of a dataset's title field contains '*string*', then the dataset is copied. Note that leading and trailing blanks in '*string*' are SIGNIFICANT.

ib - Number of the first dataset to be copied. *ib* must be positive. If not specified, all datasets in file are tested for a string match.

ie - Number of the last dataset to be copied. A value less than or equal to 0 indicates the last dataset in file. If not specified (and *ib* is specified), *ie* = *ib*.

iskip - Skip factor between copied datasets. *iskip* must be positive. If not specified, *iskip* = 1.

SORT

Sort the do-list-specified datasets in the active input file, and copy them in that order to the active output file. Files are sorted so that all datasets whose title substrings are identical are contiguous in the output file. Otherwise, original dataset order is preserved. The title substring range used for the match is specified via the SUB command.

format: **sort** [*ib ie [iskip]*]

where:

- ib* - Number of the first dataset to be copied. *ib* must be positive. If not specified, all datasets in input file are sorted.
- ie* - Number of the last dataset to be copied. A value less than or equal to 0 indicates the last dataset in file. If not specified (and *ib* is specified), sort command is rejected.
- iskip* - Skip factor between sorted datasets. *iskip* must be positive. If not specified, *iskip* = 1

SUBSTRING

Select dataset title substring range. This is used in conjunction with the SCR and SORT commands. If a substring is not specified, current and default values for the substring range are listed.

format: **sub**

format: **sub**[string] [*r1*]:[*r2*]

where:

- r1* - Lower substring range index. If not supplied, *r1* is set to its default value.
- r2* - Upper substring range index. If not supplied, *r2* is set to its default value.

do-list

FORTTRAN-like do-list specifying which input datasets are copied. It has the form:

format: **ib ie iskip**

where *ib* is the number of the first dataset, *ie* is the number of the last dataset, and *iskip* is the skip factor between datasets. *ib* and *iskip* must be positive. A value of *ie* that is less than or equal to 0 indicates the last dataset in file.