BADRS Commands Guide

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Abstract

The pointed-observing mode of SHARC, using the `CHOP_SLEWY` command, produces a data file which cannot be read by either the CLASS or CAMERA packages, the other two CSO standard data reduction packages. With this in mind, we have developed BADRS, the Bolometer Array Data Reduction Software, specifically optimized for reducing pointed observing data in the hopes of detecting sources far too weak to be mapped. This brief guide summarizes the commands as they exist in May of 1998. These descriptions are also available via the `HELP` command from within BADRS. Those familiar with CLASS will find that there is a striking and not coincidental similarity between the structure of the two; BADRS is designed with the intent of making it intuitive to CLASS users.

BADRS: BADRS is the CSO SHARC Bolometer Array Data Reduction Software. It is used to analyze and reduce the scans produced by `CHOP_SLEWY`, which are used to integrate on a line $2' \times 10''$ with 24 bolometer pixels. BADRS is pronounced BAD-RISS, and is currently in version 2.0β (98/5/19) For more information, contact Dominic Benford (dbenford@tacos.caltech.edu).

BASE: Removes a linear fit from the current scan. BASE 0 removes a 0-th order baseline, BASE 1 a 1st order. The fit only looks at good pixels excluding the window (SET WINDOW).
ALL Removes a linear fit from the each scan in the list of found scans.

CALIBRATE: This will run through the list of currently selected scans, applying a multiplicative correction factor $\exp(-\tau \times (airmass - airmassref))$. Then each scan is correctly calibrated for coadding. TAU /TAU=1.5 will set the in-band tau value to 1.5; otherwise it is set to $25 \times \tau_{225\mathrm{GHz}}$.
AIRMASS /AIRMASS=0 will correct the flux to above the atmosphere. By default, it is 1.

CLASS: Generates an ASCII file listing of each scan in the specified data file (preceeded by header variables) suitble to be read into CLASS.

COMMENT: Can be abbreviated C or even ! if you like that sort of thing. This is a robust 3-D N-body Simulated Annealing commenting routine. Use it with care.

DEBUG: This is a switch which turns debugging mode off and on. It prints BADRS internal variables. Watch out if you open a file with this turned on.

DESPIKE: Runs a simple despiking algorithm, removing all spikes greater than some multiple of the scan sigma. I.E. DESPIKE 3 will remove any spike greater than 3 sigma. This is applied to all scans in the found list; use NEW to undo. Minimum DESPIKE is 2sigma. The algorithm uses the nearest neighbors to determine the new value.

DEVICE: Creates a graphics output. If you do not specify a graphics device, it will ask you. Typical ones are /X11 (XWindows), /VT125, and /GF.

DIRECTORY: Typing DIRECTORY will give you a listing of the current directory. DIRECTORY 'directory' gives you a listing of the directory pointed to by 'directory'.

DRAW: Used to add items to the graphics display.
IDENTITY Puts a little ID string on the plot with your name and the date.
TEXT Allows you to draw text on the plot. DRAW TEXT

xpos ypos text angle
CLEAR Clears the plot
FONT DRAW FONT 'font' changes the font. Options are SIMPLEX and DUPLEX.
SIZE DRAW SIZE 'size' changes to new size. 0.65 is default.
COLOR Changes the pen color.
`LINE_STYLE` Changes the line style between solid and dots.
WIDTH Changes the line width. Default is 1.

DROP: Allows you to drop a single scan from the list of found scans (see FIND). Example: DROP 17 will drop scan #17. Using FIND will bring it back.

EXIT: EXITs the program, returning you to the DCL command prompt.

FILE: FILE is used to input or output files to the disk. BADRS can read only SHARC `CHOP_SLEWY` data files, so don't bother trying to reduce anything else. The output file format is also `CHOP_SLEWY` data, so you can read files back in. If you want a (slightly) more portable format, use PRINT or CLASS.
IN Used for input: FILE IN filename This command loads into memory the desired filename. Therefore it removes any file currently in memory.
OUT This opens an output file for writing. FILE OUT will always create a new file, writing the file header to it and closing. To add scans to the file, use the WRITE command.

Special thanks to Todd Hunter for developing the SHARC scan writing routines!

FIND: Performs a search on the current input file, extracting the scans you specify by SET NUMBER. This enables you to work with a subset of the whole data file.
/ALL Finds everything, regardless of specifications.

FLIP: Multiplies all found scans by -1. Used if you accidentally observed in the negative beam. Because one rarely swaps beams, this command cannot be used on the current scan in memory.

GAUSS: Fits a gaussian to the current scan. It is a pretty robust method, so it doesn't need any input parameters. Use PLOT/GAUSS to view.

GET: Get a scan number from the file into current scan memory. Use GET i to get scan number i; use GET NEXT to get $i+1$. Use GET FIRST to get the first scan in the index, and GET LAST to get the last scan in the index.

HELP: Typing HELP yields the standard HELP screen. HELP 'command' will give you help on the specified command. It's pretty straight forward.

HEADER: Lists information about the current scan in memory.
/FULL Lists everything, including parameters you probably don't care about.
/FILE Lists the file header information only.
/SCAN Lists the header for the indicated scan.

IGNORE: Like DROP, IGNORE removes a scan number from the current found list. Unlike DROP, FIND won't bring it back, but FIND/ALL will.

INTERPOLATE: The current scan will be fit by a `CURRENT_PIXELS/2` polynomial, and any bad pixels will be filled in by the interpolated values. After this, use SET BAD NONE to turn on all pixels. Actually, this lovely polynomial method has problems. For the time being, INTERPOLATE is just going to use the nearest neighbors.

LIST: Lists the contents of the file currently in memory. By default, provides a short listing of the scans in the current found list.
/ALL Lists all scans, not just those in the found list.
/FULL Lists the contents in a longer format - this can take a while.
/SCAN Lists everything stored in a single scan. You must supply the scan number: LIST /SCAN=2

MULTIPLY: This allows you to multiply the current scan by a number (for instance, the Jy/mV conversion factor). This is useful for writing out the scan to a new file, since you'll want to retain correct calibration for each scan in the new (reduced) data file, even if they have different conversion factors themselves.

NEW: Reopens the file, getting any new scans. All modifications made to the file (BASE, FLIP, DESPIKE, etc.) will be undone! Note that for data files being written to (i.e. in the process of observing into them), the most recent scan will probably be junk.

PLOT: Displays a scan on the graphics output. If no number is specified, it will plot the scan in current scan memory. Otherwise, PLOT number will plot that scan number. By default, the PLOT command only prints the in_phase data.
number This number is the counter, usually 1 to n, of the data set. This is NOT the "scan number" written by Poliahu. Why? Because it is theoretically possible to have a file with 100 scans, all with the same "scan number". The BADRS counter is therefore used, because it is guaranteed to be unique. By the way, PLOT 1 just *displays* scan 1, it doesn't GET 1 first. This means that you cannot do PLOT 1/GAUSS, because you won't have found a Gaussian fit to a scan you haven't GOT.
/HARD Sends a hardcopy to the printer.
/SPEC Prints only the spectrum, not the box.
/`GOOD_ONLY` Leaves off the bad channels.
/TITLE Prints a title on: PLOT /TITLE="Scan name".
/`TOTAL_POWER` Plots total power as opposed to in_phase.
/QUADRATURE Plots the quadrature (out of phase) data as opposed to the in_phase.
/`IN_PHASE` Plots the `in_phase` data. This is the default.
/`GAUSS_FIT` Displays the gaussian fit found using GAUSS.
/ARCSECONDS Displays the X axis in units of arcseconds (default is in pixel number).
/`BLANK_BAD` By default, dots are placed to mark where the bad pixels' values would be. Blanking them removes this, which

is probably better for presentation quality plots. As though anyone will ever present this stuff.

PRINT: Prints an ascii table of the current scan. Prompts for an output filename if one is not supplied on the command line.
/ALL Prints each scan in the current index (i.e. those found by the most recent FIND command) into separate files including header information and the scan data averages. The file names take on the following format: `CURRENT_INFILE.SCAN`n. This feature is useful for porting the data to other packages such as CLASS.

`WRITE_SCAN:` Writes the CURRENT scan in memory to the file on disk specified by the FILE OUT command. Note that summed scans don't yet have meaningful on/off data, only the final averages. The on/off data is blank, and there is only one scan. Because SUM adds together averages, only the averages are written.

SET: This command is used to set a BADRS parameter.
NUMBER Sets the number range for selection using FIND. Format is SET NUMBER low_endhigh_end. Using an asterisk (*) as a wildcard allows you to choose variable ranges. I.E. SET NUMBER 10 * will select everything from 10 on up; SET NUMBER * * takes everything.
WEIGHT Sets the weighting for summation. Can be TIME (longer scans get more weight) or SIGMA (noisier scans get less weight). SIGMA uses the scan sigma, not the channel sigma (see SET SIGMA for more information).
CALIBRATION Set the conversion factor for mV to Jy, as determined by SET UNIT. This is not a permanent feature of a scan - when you write out a scan, MULTIPLY it by the calibration factor first.
UNIT Determines whether the unit is mV or Jy. BADRS automatically converts into mJy or microV when the source is sufficiently weak.
WINDOW This specifies an area of pixels to avoid including in BASE fits or in the calculation of sigma. It is inclusive, so

SET WINDOW 10 14 ignores all 5 pixels between 10 and 14.
SOURCE This specifies a source name to be found when using FIND.
BAD Allows you to flag bad pixels. It works as a switch. SET BAD 11 will first turn off pixel 11 (assuming it was good to begin with), then SET BAD 11 a second time will turn it back on. SET BAD NONE turns on all pixels, SET BAD ALL turns 'em all off.
MATCH This allows you to turn on and off (NOMATCH) position matching for SUM. What this actually does is track the rotation of the array on the sky (well, really just the PA of the source- assuming no dewar rotation) and checks to see if the outlying pixels are overlapping. It will SET BAD all those pixels that have slewed away from themselved due to sky rotation.
SIGMA Not to be confused with SET WEIGHT, this switch determines how sigma is measured. The usual way is to measure the sigma in the scan (i.e. 24 pixels are used to determine the RMS in the 24 pixels). This is SET SIGMA SCAN. The other way is SET SIGMA CHANNEL. This will calculate, during a SUM, the RMS in each channel from the set of scans used to build up the sum.

SHIFT: Allows you to move the scan to the left or right by 1 pixel, thereby taking out some amount of pointing/ref_pixel drifts. Use the required parameter LEFT or RIGHT to indicate direction.

SHOW: Shows the value of a BADRS parameter. See SET.

SPAWN: Use this to send a command to DCL. If you do not specify a command, a subprocess is spawned. An easy way to do things is to put a command in quotes, i.e. SPAWN "DELETE /NOCONFIRM JUNK.TXT;*"

SUM: Adds the current scan list (created by FIND). The weighting for summation is derived from SET WEIGHT TIME (in which those scans with more time are given more weight) or from SET WEIGHT SIGMA (in which those scans with the lowest sigma are more heavily weighted). The sigma used here is always the scan sigma, not the channel sigma (see SET SIGMA for more help).