

[Show pagesource](#)[Discussion](#)[Old revisions](#)[Backlinks](#)[Wiki Syntax](#)  
[Recent changes](#)  
[Index](#)  

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Username

Password

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## S I G P R O C

### Table of Contents

[SIGPROC](#)  
[Software](#)  
[Data reduction](#)

The SIGPROC is a package which holds programs written to process, reduce and convert pulsar data. SIGPROC manual and package itself can be downloaded from [here](#).

## Software

Here are some SIGPROC programs:

**bandpass** - outputs the pass band from a filterbank file

```
usage: bandpass {filename} -{options}
N.B. filename - filterbank data file (def=stdin)
options:
  -d numdumps - number of dumps to average over (def=all)
  -t dumptime - number of seconds to average over (def=all)
```

**barycentre** - refer a datafile to a frame at rest wrt the solar system barycentre

```
usage: barycentre inputfile -{options} > outputfile
options:
  -mypolyco - take user-defined polyco.bar file (def=create one)
  -verbose - write out barycentre information to stderr (def=quiet)
  inputfile - the name of the filterbank/time series file
```

**best** - displays the best suspects from **seek**

```
usage: best <INFILE> -{options}
N.B. input file may be of the ".prd", ".top" or ".frq" variety
options:
  -v - view output selectively
  -p - produce postscript file output automatically
  -i - zap integer harmonics only
  -t - trace mode... show all harmonic relationships
  -f[fold] - read a specific harmonic fold (1-5;def=all)
  -s[smin] - set signal-to-noise threshold smin (def=8)
  -l[mini] - set minimum prd/frq to consider (ms;def=0)
  -h[maxi] - set maximum prd/frq to consider (ms;def=inf)
  -L[mini] - set minimum ac/dm to consider
  -H[maxi] - set maximum ac/dm to consider
  -F[fMHz] - set centre freq for DMsmear test (optional)
  -C[fMHz] - set channel band for DMsmear test (optional)
```

**chaninfo** - time series stats of 1-bit data

```
usage: chaninfo file (nblk) (cthr) (bthr)
options:
  file - name of raw .dat file
  nblk - (optional) blocks to read (def=all)
  cthr - (optional) threshold for bad channels (def=+/-0.2)
  bthr - (optional) threshold for bad blocks (def=3 sigma)
```

**csearch** - script to do a companion search on a dedispersed time series

```
usage: csearch filestem parstem
N.B. The script requires a .tim file with the dedispersed data and an "aclist" file
which is an ASCII list of the trial ACs and ADOTs to use in the search.
```

**decimate** - reduce time and/or frequency resolution of filterbank data

```
usage: decimate {filename} -{options}
N.B. filename - filterbank data file (def=stdin)
options:
  -c numchans - number of channels to add (def=all)
  -t numsamps - number of time samples to add (def=none)
  -T numsamps - (alternative to -t) specify number of output time samples
  -n numbits - specify output number of bits (def=input)
  -headerless - do not broadcast resulting header (def=broadcast)
```

**dedisperse** - form time series from filterbank data or profile from folded data

```
usage: dedisperse {filename} -{options}
N.B. filename - full name of the raw data file to be read (def=stdin)
options:
  -d dm2ddisp - set DM value to dedisperse at (def=0.0)
  -b numbands - set output number of sub-bands (def=1)
  -B num_bits - set output number of bits (def=32)
  -o filename - output file name (def=stdout)
  -c minvalue - clip samples > minvalue*rms (def=noclip)
  -f reffreq - dedisperse relative to reffr MHz (def=topofsubband)
```

```
-F newfreq - correct header value of centre frequency to newfreq MHz (def=header value)
-n num_bins - set number of bins if input is profile (def=input)
-i filename - read list of channels to ignore from a file (def=none)
-p np1 np2 - add profile numbers np1 thru np2 if multiple WAPP dumps (def=all)
-j Jyfactor - multiply dedispersed data by Jyfactor to convert to Jy
-J Jyfl Jyf2 - multiply dedispersed data by Jyfl and Jyf2 to convert to Jy (use only for two-polar)
-wappinvert - invert WAPP channel order (when using LSB data) (def=USB)
-wappoffset - assume wapp fsky between two middle channels (for pre-52900 data ONLY)
-swapout - perform byte swapping on output data (def=none)
-nobaseline - don't subtract baseline from the data (def=subtract)
-sumifs - sum 2 IFs when creating the final profile (def=don't)
-subzero - subtract the zeroDM mean from each sample (def=don't)
-headerless - write out data without any header info
-epn - write profiles in EPN format (def=ASCII)
-asciipol - write profiles in ASCII format for polarization package
-stream - write profiles as ASCII streams with START/STOP boundaries
```

**depolyco** - resample a time series to either barycentric or pulsarcentric frames

```
usage: depolyco {timfile} {polycofile} -{options}
N.B. no polyco file implies barycentric correction to be applied
options:
  timfile - the name of the time series to be read
  polycofile - the name of the polyco file for the pulsarcentric case
  -singlebyte - write output as unsigned characters (def=floats)
  -raj - use different RA (J2000; hh:mm:ss.s) than header
  -decj - use different DEC (J2000; dd:mm:ss.s) than header
  -verbose - write out TEMPO information to stderr (def=quiet)
```

**fake** - produce fake filterbank format data for testing downstream code

```
usage: fake -{options}
options:
  -period p - period of fake pulsar in ms (def=random)
  -width w - pulse width in percent (def=4)
  -snrpeak s - signal-to-noise ratio of single pulse (def=1.0)
  -dm d - dispersion measure of fake pulsar (def=random)
  -nbits b - number of bits per sample (def=4)
  -nchans n - number of filterbank channels (def=128)
  -tsamp t - sampling time in us (def=80)
  -tobs t - observation time in s (def=10)
  -tstart t - MJD time stamp of first sample (def=50000.0)
  -nifs n - number of IFs (def=1)
  -fchl f - frequency of channel 1 in MHz (def=433.968)
  -foff f - channel bandwidth in MHz (def=0.062)
  -seed s - seed for Numerical Recipes ran1 (def=seconds since midnight)
  -nosmear - do not add in dispersion/sampling smearing (def=add)
  -swapout - perform byte swapping on output data (def=none)
  -evenodd - even channels=1 odd channels=0 (def=noise+signal)
  -headerless - do not write header info at start of file (def=header)
binary options:
  -binary - create binary system
  -bper - orbital period in hours (def=10.0)
  -becc - eccentricity (def=0.0, circular)
  -binc - inclination in degrees (def=90.0)
  -bomega - longitude of periastron in degrees (def= 0.0)
  -bphase - starting orbital phase (number between 0 and 1, def=0.0)
  -bpmass - pulsar mass in solar units (def=1.4)
  -bcmass - companion mass in solar units (def=5.0)
```

**filterbank** - convert raw pulsar-machine data to filterbank format

```
usage: filterbank <rawdatafile1> .... <rawdatafileN> -{options}
N.B. rawdatafile - raw data file (recognized machines: WAPP, PSPM, OOTY)
options:
  -o filename - output file containing filterbank data (def=stdout)
  -s skiptime - skip the first skiptime (s) of data (def=0.0)
  -r readtime - read readtime (s) of data (def=all)
  -i IFstream - write IFstream (IFstream=1,2,3,4)
  -n nbits - write n-bit numbers (def=input format)
  -c minvalue - clip DM=0 samples > mean+minvalue*sigma (def=noclip)
  -swapout - perform byte swapping on output data (def=none)
  -floats - write floating-point numbers (equal to -n 32)
  -sumifs - sum IFs 1+2 to form total-power data
  -headerfile - write header parameters to an ASCII file (head)
  -headeronly - write ONLY binary header parameters
options for correlator (currently WAPP) data:
  -hammingv - apply Hamming window before FFT (def=nowindow)
  -hanning - apply Hanning window before FFT (def=nowindow)
  -novanvleck - don't do van Vleck correction before FFT (def=doit)
  -invert - invert the band after FFT (def=noinversion)
  -zerolag - write just the zero-lag value for each IF
  -rawcfs - write raw correlation functions (novanvleck)
  -corcfs - write corrected correlation functions (vanvleck)
```

**flux** - TBD

**fold** - fold filterbank channels/time series data

```
usage: fold {filename} -{options}
N.B. filename - full name of the raw data file to be read (def=stdin)
options:
-o out_file - output file for pulse profile data (def=stdout)
-p fold_prd - period to fold (ms) or polyco file (def=polyco.dat)
-a accelern - fold using constant acceleration (def=0 m/s/s)
-f p_factor - multiply the period by p_factor (def=1.0)
-m m_factor - output multiple profiles (STREAM only; def=1)
-n num_bins - number of bins in folded profile(s) (def=window/tsamp)
-d time/num - dump profiles every time s or num pulses (def=nodumps)
-t samptime - hard-wire the sampling time (us) (def=header)
-l phaseval - phase value (turns) of left edge of pulse (def=0.0)
-r phaseval - phase value (turns) of right edge of pulse (def=1.0)
-j Jyfactor - multiply all profiles by Jyfactor to convert to Jy
-b baseline - subtract baseline from all profiles (def=autobase)
-dt timeoff - add a time offset in seconds to tstart (def=0.0)
-sk skiptim - skip the first skiptim s before folding (def=0.0)
-re readtim - read and fold only readtim s of data (def=ALL)
-ascii - write profiles as ASCII numbers (this is the default)
-epn - write profiles in EPN format (def=ASCII)
-acc - write out accumulated profiles (def=subints)
-bin - write profiles in SIGPROC binary format (def=ASCII)
-sub subint - shorthand for -nobaseline -stream -d subint.0
-psrfits - write profiles in PSRFITS format (def=ASCII)
-totalpower - sum polarizations 1+2 before writing (def=nosumming)
-asciipol - write profiles in JMCs ASCII format for polarization
-stream - write profiles as ASCII streams with START/STOP bounds
-nobaseline - don't subtract baseline from profiles (def=subtract)
```

**foldsignals** - script to dedisperse and fold signals from SEEK

```
usage: foldsignals stem -{options}
options:
-nbands n - number of sub-bands in output plot (def=8)
-ntrials n - number of trial periods to try (def=64)
-nsubints n - number of sub-integrations in output plot (def=8)
-srmin s - minimum signal-to-noise ratio (def=8)
-nbins n - number of bins in output profile (def=P/tsamp)
-ncand n - process only candidate number n (def=all)
-listonly - just list the candidates from best
```

**getpulse** - make and/or plot a time series from dedispersed file

```
usage: getpulse {filename} -{options}
N.B. filename - dedispersed data file
options:
-t time - time (in seconds) on which to center time series (REQUIRED)
-w width - width (in seconds) of time series to plot (def=1)
-c fchan - to only output frequency channel fchan (def=all)
-i ifchan - to only output IF channel ifchan (def=all)
-p pgdev - pgplot device (def=/xs)
-numerate - to precede each dump with sample number (def=time)
-noindex - do not precede each dump with time/number
-plot - PGPLOT the results
```

**grey** - program to greyplot EPN data

```
usage: plotg [filename] <options>
N.B. Input file must be in EPN format!
options:
-r - set start record number (def=1)
-s - set min=0 & max=n*rms (def=autoscale)
-c - centres profile to first record (optional)
```

**header** - program to display header information

```
usage: header {filename} -{options}
N.B. filename - filterbank data file (def=stdin)
options:
-telescope - return telescope name
-machine - return datataking machine name
-source_name - return source name
-fchl - return frequency of channel 1 in MHz
-off - return channel bandwidth in MHz
-nchans - return number of channels
-tstart - return time stamp of first sample (MJD)
-tsamp - return sample time (us)
-nbits - return number of bits per sample
-nifs - return number of IF channels
-headersize - return header size in bytes
-datasize - return data size in bytes if known
-nsamples - return number of samples if known
-tobs - return length of observation if known (s)
```

**hunt** - script to dedisperse and search data using seek over a given DM range

```
usage: hunt filestem (option)
N.B. The script requires a filterbank file with the raw data and a "dmlist" file
```

which is an ASCII list of the trial DMs to use in the search.

**makedmlist** - program

```
usage: makedmlist name_of_filterbank_file
N.B. DM minimum and maximum ranges are optional (0-100 is default).
options:
  -dmmin - minimum value of DM
  -dmmax - maximum value of DM
```

**mask** - produces a spectral mask for use by **seek**

```
usage: mask <SPECTRUM_FILE> -{options}
N.B. The spectrum file is produced by running find -s
This program is usually run on fold1.spc
Options given as: mask fold1.spc -t10
options:
  -f - write the spectral mask to file "mask.out"
  -l[f_hz] - lowest frequency to consider (def=0)
  -h[f_hz] - highest frequency to consider (def=Nyqst)
  -t[ampl] - amplitude threshold to mask
```

**monitor** - Tcl/Tk widget to check and display log output from programs

**pgplotter** - simple tool to plot SIGPROC streamed output with PGPLOT

**plotpulses** - PGPLOT results of single pulse search

```
usage: plotpulses filestem1 .... filestemn -{options}
options:
  -minsn s1 - minimum s/n to display (def=5)
  -maxsn s2 - maximum s/n to display (def=all)
  -pgdev - pgplot device (def=/xs)
  -wmin w1 - minimum width (in ms) to display (def=all)
  -wmax w2 - maximum width (in ms) to display (def=all)
  -dmmin d1 - minimum DM (def=all)
  -dmmax d2 - maximum DM (def=all)
  -tmin t1 - minimum time (seconds) to display (def=all)
  -tmax t2 - maximum time (seconds) to display (def=all)
  -dmplot d - 1 to plot DM and 2 to plot DM channel (def=1)
  -nmax n - maximum number of events to plot per DM channel (def=all)
  -allbeams - will do a DM-t stack for all beams in the current directory
```

**polyco** - a script to run TEMPO to generate a polyco.dat file

```
usage: polyco psrname -{options}
N.B. psrname - name of the pulsar as it appears in tztot.dat
options:
  -freq f - frequency in MHz (def=1410 MHz)
  -nspan n - span of each polyco set in minutes (def=15 min)
  -ncoeff n - number of coefficients in each polyco set (def=9)
  -maxha h - maximum hour angle (def=2 hours)
  -mjd m - mjd to calculate for (def=today)
  -mjds s - starting mjd (def=today)
  -mjdf f - finishing mjd (def=today)
  -par p - specify parfile (def=tzpar area)
  -site s - specify site code or alias (def=Arecibo)
```

**polyco2period** - returns period (sec) given mjd and polyco file

```
usage: polyco2period mjd -{options}
options:
  mjd - MJD date
  -p polyco file name
```

**postproc** - TBD

**profile** - produce ASCII or pseudo grey-scale displays of folded data

```
usage: profile {filename} -{options}
N.B. filename - profile file (def=stdin)
options:
  -p fraction - set max value to fraction of peak (def=1.0)
  -frequency - label grey-scale profiles in frequency (def=time)
```

**quicklook** - script to examine the data

```
usage: quicklook <filename> -{options}
options:
  -read time - read and process only time (s) of data
  -skip time - skip the first time (s) of data
  -addc nchans - add nchans chans together before dedispersion (def=none)
  -addt nsamps - add nsamps samples together before dedispersion (def=none)
  -nsints n - specify number of time sub-integrations (def=8)
  -nbands n - specify number of frequency sub-bands (def=8)
  -period p - fold data at constant period (ms) (def=polyco)
  -dm dmvalue - dedisperse using dmvalue (pc cm-3) (def=polyco)
  -clip value - clip samples that deviate more than value*rms (def=noclippping)
```

```
-nbins n      - fold data using n bins (def=128)
-left phase   - specify left-hand phase window (def=0.0)
-right phase  - specify right-hand phase window (def=0.0)
-singlepulse  - set number of subints to be the number of pulses
-psr name     - fix source name for running TEMPO (def=filestem)
-mypolyco     - use an existing polyco file (def=make one)
-fakescale    - plot channels/bands using fake grey scale (def=real)
-clean        - remove large files before and after (def=keep them)
-wipe         - remove large files beforehand (def=keep them)
-ext string   - add a file extension string to output files (def=none)
```

**reader** - look at filterbank data in ASCII format

```
usage: reader {filename} -{options}
N.B. filename - filterbank data file (def=stdin)
options:
-c          - output only frequency channel c (1...nchans) (def=all)
-i          - output only IF channel i (1...nifs) (def=all)
-numerate  - precede each dump with sample number (def=time)
-noindex   - do not precede each dump with number/time
-stream    - produce a stream of numbers with START/STOP boundaries
```

**seek** - searches for periodic and/or transient signals in a noisy time series

```
usage: seek <INFILE> -{options}
N.B. The input file may be a time series, or a set of Fourier coefficients.
     The file extension MUST, however, be either ".tim" ".ser" ".dis" or ".fft"
     In the latter case, the FFT stage is skipped.
options:
-A          - append output ASCII files
-s          - dump spectra to ".spc" files
-q          - quiet mode - all messages > INFILE.log
-pmzap     - calls the PM survey routine pm_zapbrd
-rmmzap    - calls the PM survey routine mm_zapbrd
-pulse     - calls Maura single pulse search
-pzero     - pads out data with zeros (def=Gaussian)
-maxfft    - report max length of Fourier transform
-nofft     - turns off FFT search
-fftw      - uses FFTW instead of SINGLETON routine
-hsums     - show harmonic summing used
-recon     - calculate and report reconstructed S/N
-submn     - mean subtraction (old method) to whiten spectrum
-submd     - median subtraction to whiten spectrum
-head      - adds header info to output .prd files
-m[file]   - mask birdies from file (def="mask")
-z[file]   - zap birdies from file (def="birdies")
-b[freq]   - zap 10-sig+ spikes < freq (def=100 Hz)
-c[cfac]   - add every cfac samples before FFT
-a[accn]   - re-sample at constant accn (m/s/s)
-d[adot]   - re-sample at constant adot (cm/s/s/s)
-D[dmvl]   - change header DM to be dmvl
-t[tlen]   - fix transform length to 2**tlen
-i[tsec]   - ignore tsec seconds of data on reading
-p[pmax]   - set maximum period of seach (def=9.999s)
-T[spth]   - set single-pulse search threshold (sigma)
-n[nmax]   - maximum number of single-pulse candidates per DM channel
-w[smax]   - number of times to smooth time series for single-pulse search
```

**spec** - displays spectrum files produces by **find**

```
usage: spec <SPECTRUM FILE> -{options}
N.B. The spectrum file is produced by running find -s
     This program is usually run on fold1.spc
options:
-s          - run stats mode
-d          - dump ASCII version of spectrum to file "dump"
-P          - plot powers (def=amplitudes)
-l[f_hz]   - lowest frequency to consider (def=0)
-h[f_hz]   - highest frequency to consider (def=Nyqst)
-f[fold]   - give fold number instead of filename
-n[nbin]   - number of bins (histograms) in stats mode
-F[f_hz]   - mark frequency and harmonics on plot
```

**splice** - joins multiple filterbank files

```
usage: splice filename1...filenameN > splice.fil
N.B. filename - filterbank data file (def=stdin)
```

**splice timeseries** - joins multiple timeseries files

```
usage: splice_timeseries filename1...filenameN > splice.tim
N.B. filename - timeseries data file (def=stdin)
```

**step** - TBD


**tune** - fine tune a period in a time series by stacking sub-integration

```
usage: tune {filename} -{options}
```

```
N.B. filename - full name of the raw data file to be read (def=stdin)
options:
-p fold_prd - center period to fold (ms) or polyco file (def=polyco.dat)
-a accelern - center acceleration to fold (def=0 m/s/s)
-f p_factor - multiply the period by p_factor (def=1.0)
-n num_bins - max number of bins in folded profile(s) (def=64)
-t samptime - hard-wire the sampling time (us) (def=header)
-sub subint - Number of subints to use (def=128)
-quickgray - plot data using pdm-style quickgray code (def=pggray)
-useaccn - Do an acceleration search *Experimental* (def=don't)
-usejerk - Do an acceleration search *Experimental* (def=don't)
-pf pfactor - divide the period search range by this number (def=1)
-af afactor - divide the accel search range by this number (def=1)
-jf jfactor - divide the jerk search range by this number (def=1)
-format fmt - set the output format, standard PGPLOT formats (def=/xserv)
-jreaper f - write out ascii based output to file f (def=don't)
-bestfile f - read the 'best' summery file for candidate info (def=don't)
```

## Data reduction

Here is the example how from time series file, fold and convert the data into an **epn** file.

First the TOA file for the pulsar (polyco.dat) should be generated using  **TEMPO** package. You can do it by running command:

```
tempo -z pulsar_name.tz -f pulsar_name.par
```

This will generate a polyco.dat file which will be used (unless you specify otherwise) to fold the data.

To fold the data and write it to epn format with **fold** program, you can use command like this:

```
fold -d 1 -p 3.0 filename -epn > filename.epn
```

