

sactool package to manage large amounts of sac data

Release 0.1 (initial release)

Components of the package

libmbsac.a && libmbsac.so

- sachinfo
 - Extract informations from sac headers, create tables of information
- sacchhdr
 - Change header values (delta, npts, leven and nvhdr is denied)
- sacrgap
 - Remove extreme gaps values from sac files created by GCF2SAC (Guralp to sac converter)
- sacrename
 - Renames sac files based on the header content
- more to come the library is ready !!

Features

- Capacity to read only the header when needed, improving speed.
- Can handle infinite amount of data in one command line, search thru directories.
- Independent of any library, libmbsac has anything needed.
- Capacity to copy or (when available) only rename files.
- Two methods for gap removal (mean and linear trend).

Common options

-d Directory to search for files

```
$ sacrename -d /data/bdfb/
```

-e File ending when search for files in directory

```
$ sacrename -e .1.sac -d /data/bdfb/
```

-v Show version information

```
$ sacrename -v
```

-h Show help

```
$ sacrename -v
```

sachinf options

Synthax

```
sachinfo  
  [-h] [-v]  
  [-e <string>]  
  <-d <dir> <vars >|<file> <vars>
```

- Create a table with A marks:

```
$ sachinfo -e .z.sac -d /data/ nzyear nzjday nzhour nzmin nzsec nzmsec  
KA A
```

- List the sample rate from a specific file:

```
$ sachinfo file-bdfb.sac delta
```

- Or even show all available variables:

```
$ sachinfo -h
```

sacchhdr options

Sacchhdr

Synthax

```
[-h] [-v] [-oz] [-on] [-oe]  
[-e <file ending string>] [-f <file> | -d <dir>]  
-- <var0> <value0> [<var1> <value1> ... ]
```

- Change station name to “bdfb” and kcmpnm to “BHZ”:

```
$ sacchhdr -d /data/bdfb -kstnm bdfb kcmpnm BHZ
```

- Set cmpaz, cmpinc and kcmpnm at the same time for all .z.sac files in dir /data/bdfb

```
$ sacchhdr -e .z.sac -d /data/bdfb -oz
```

The sacchhdr program reads and writes only the header part of the files making it extremely fast for dealing with large amount of data.

sacrgap

- The GCF2SAC (Guralp to sac) converter when encounter a gap in data (alowed in gcf files) fill the values with the number -2147483647 creating very large steps that make impossible to analise such files. This program, detects this gaps and fill them with much resonable values with two different algorithms:
 - Mean, the mean between the last and first sampled around the gap.
 - Trend, a linear trend betwen the samples.

sacrgap options

Synthax

```
sacrgap  
  [-h] [-g <gap value>] [-m <0|1>] [-v]  
  [-e <file ending string>]  
  <-d <dir>|-f <file1> ... <fileN>>
```

- Remove gaps from all file in bdfb dir:

```
$ sacrgap -d /data/bdfb
```

- Remove gaps from all file in bdfb dir with mean:

```
$ sacrgap -m 0 -f data-bdfb.z.sac
```

- Remove gaps from all file in bdfb dir with trend (default):

```
$ sacrgap -m 1 -f data-bdfb.z.sac
```


sacrename

- Try to rename files using the header information. The format for output is:

YYYY.JJJ.HH.MM.SS.<station>.C.sac

or if changing tree mode is enabled (-m)

YYYY/JJJ/YYYY.JJJ.HH.MM.SS.<station>.C.sac

YYYY – Year with 4 digits
JJJ – Julian day with 3 digits
HH – Hour with 2 digits
MM – Minutes with 2 digits
SS – Seconds with 2 digits
C – Component (Z,N,E or u for undefined)
<station> is station name (kstnm header value).

sacrename options

sacrename

Synthax

[-h] [-v]

[--luke] [--showme] [-c]

[-e <fileend>] [-m <dir base>]

<-d <dir>|-f <file 1> ... <file N>>

- With -c the files are copied and not renamed
- Using -m the -c is also implied (it's impossible to rename files across filesystems)
- If some error is found you must use --luke to proceed.
- To see a resume of what should be done use --showme
- -e, -d, -f, -h and -v as usual

Comments & Improvements

All these codes are released in GPL and should be kept this way. Feel free to use and redistribute it, but you are not allowed to change the licence.

One time GPL forever GPL.

Don't hesitate to contact me at:

www.foo4fun.net

with any suggestion or improvements !!