selfreqavg, selfreqcomb

1 Introduction

selfreqavg and **selfreqcomb** are programs for computing the amplitude and phase of the hemodynamic response at a certain frequency. This is typically done in retinotopic (or phase encoding) studies. These programs are meant to replace **analyse** and **combine** for phase encoding studies. The paradigm consists of a periodically varying stimulus (eg, a rotating spoke or expanding/contracting ring). The stimulus is characterized by its fundamental frequency, direction, and type. The the amplitude and phase of hemodynamic response at the stimulation frequency are measured by computing the FFT of the bold signal. The significance of the effect is assesed with an F-test in the following way. An F-ratio is computed as the ratio of the signal power to the noise power. The signal power is the power at the fundamental. The noise power is sum of the remaining spectrum excluding the following components: harmonics of the stimulus, components within one frequency bin of the fundamental and harmonics, and the first three bins.

   selfreqavg computes the amplitude, phase, and noise directly from the raw MR signal. **selfreqcomb** combines the results from several invokations of **selfreqavg** into a single average. This is done by separately averaging the real and imaginary components of the fundamental as well as averaging the noise power. The average real and imaginary components are used to recompute the power at the fundamental which is then used to perform the F-test as described above. The software appropriately handles the case where the inputs may have different degrees-of-freedom (eg, different number of time points).

2 Questions, Comments, and Bug Reports

The software authors are interested in your questions, comments, and bug reports. However, since the software is free, our responsiveness to your needs may be limitted. To get the most out of an interaction with us, please follow these suggestions: (1) read the documentation thoroughly to make sure you are not asking about something for which there is already an answer, (2) ask someone else in your lab, (3) send COMPLETE information about the problem (ie, operating system, machine type, user name, version number, log files, etc). Send questions, comments, and bug reports to analysis-bugsnmr.mgh.harvard.edu.

3 Usage

Typing **selfreqavg** at the command-line without any options will give the following message:

```
USAGE: selfreqavg
   -i instem  ...    : input stem(s)
   -TR TR            : temporal resolution (sec)
   -o outstem        : output stem
   -parname name     : parfile, same in each instem directory
   -stimtype  type   : eccen or polar (see also parname)
   -ncycles ncycles  : number of stimulation cycles (see also parname)
   -direction string : pos or neg (see also parname)
```

```
    -delay   delay    : global delay (in seconds)
    -sdf     file     : slice delay file
    -nskip nskip      : skip the first nskip TRs
    -rescale target   : rescale so global mean equals target
    -firstslice fs    : first anatomical slice
    -nslices    ns    : number of anatomical slices
    -monly mfile      : just create a matlab file
    -umask umask      : set unix file permission mask
    -version          : print version and exit
```

Typing **selfreqcomb** at the command-line without any options will give the following message:

```
USAGE: selfreqcomb
    -i instem  ...    : input stem(s)
    -o outstem        : output stem
    -firstslice fs    : first anatomical slice
    -nslices    ns    : number of anatomical slices
    -monly mfile      : just create a matlab file
    -umask umask      : set unix file permission mask
    -version          : print version and exit
```

4   Command-line Arguments

Note that command-line arguments can also be specified inside of a configuration file (see the -cfg argument).

-i instem: stem of the input volume for a single run. It is assumed that the data are stored in *bfile format*. If multiple runs are to be analyzed, each input stem must be preceded by a *-i* flag.

-parname parname: name of file in which the stimulus characteristics are stored. The format is

```
stimtype  eccen
direction pos
ncycles   8
```

where *stimtype* is the type of stimulus, *direction* is the direction of the stimulus (either *pos* or *neg*), and *ncycles* is the number of cycles in the run. These are redundant with other command-line arguments to **selfreqavg**. If both are specified, presidence will be given to the command-line arguments. If the parname option is specified, there must be a file with the specified name in each of the input directories (ie, parname is only specified once).

-o outstem: this is the stem of the output volume (in bfile format) to be generated. This will have 12 planes:

1. $\pm||log10(sig)||$ - sign based on the sign of the imaginary component

2. $||log10(sig)||sin(\phi)$

3. $||log10(sig)||cos(\phi)$

4. F

5. $\sqrt{(F)}sin(\phi)$

6. $\sqrt{(F)}cos(\phi)$

7. Standard deviation of the noise.

8. Real part of the signal at the fundamental.

9. Imaginary part of the signal at the fundamental.

10. Phase (ϕ) in radians.

11. Mean Image.

12. Trend Image.

13. Magnitude (sum of squares of real and imag parts).

14. Phase masked by $p < 0.01$

Note: when using the *paint* command to render the results on the cortical surface, make sure to set the *-offset* option to one less than the plane number.
-TR float: temporal sampling resolution (ie, time between scans in seconds).

-delay float: specify the hemodynamic delay (in seconds) to apply to all voxels.

-sdf filename: specify a slice delay file (SDF). The SDF has two columns. The first is the slice number, and the second is acquisition delay (in seconds) of the slice with respect to the start of the TR.

-detrend: instruct selfreqavg to fit and remove any trend from the raw fMRI data that is linearly related to time. This is done on a run-by-run basis.

-rescale target: used in conjunction with **inorm**. **inorm**, the global intensity normalization program, will produce a file called *instem.meanval* in which the global mean value (after segmentation) is stored. When the -rescale option is specified, selfreqavg will read the meanval file and the target value and rescale the entire input volume so that it's new global mean is target.

-nskip nSkip: specify the number of *functional* slices to skip at the beginning of each run. This applies to all runs and all anatomical slices. Note: this can severely affect the FFT computations.

-firstslice int: first *anatomical* slice to process (usually 0). If unspecified, the first slice will be autodetected. It is highly recommended that the first slice number be 0.

-nslices int: total number of *anatomical* slices to process. If unspecified, the number of slices will be autodetected.

-monly: only generate the matlab file which would accomplish the analysis but do not actually execute it. This is mainly good for debugging purposes.

5 Interfacing with FreeSurfer and Paint

For phase encoding studies, FreeSurfer expects the surface data to conform to a certain naming convention. Specifically, FreeSurfer expects three surface files for each hemisphere. For example, for the left hemisphere these files are: sigf-lh.w, sig2-lh.w, and sig3-lh.w. These correspond to the first three planes in the output of **selfreqavg**. These .w files are created by paint. For an output stem of *sfaout*, paint would be invoked in the following way:

```
paint sfaout_%03d.bfloat lh orig sigf-lh.w -nslices 16 -imageoffset 0
paint sfaout_%03d.bfloat lh orig sig2-lh.w -nslices 16 -imageoffset 1
paint sfaout_%03d.bfloat lh orig sig3-lh.w -nslices 16 -imageoffset 2
```

Note that before paint can be invoked, the subject must have been anatomically reconstructed using the FreeSurfer tools, and the functional run must have been registered with the anatomical run.

6 Example

Consider a set of raw data consisting of 6 runs. Runs 1, 3, and 5 use a polar stimulus, where as runs 2, 4, and 6 use an eccentricity stimulus. All have 8 cycles per run in the same (positive) direction. The TR is 2 seconds, and 16 slices were collected. The data are in bshort format with stem *f* in the following directories: 001, 002, 003, 004, 005, 006. To process the data, cd to the directory just above the run directories, and run:

```
selfreqavg -i 001/f -i 003/f -i 005/f -o polar/sfaout \
    -TR 2 -ncycles 8 -stimtype polar -direction pos

selfreqavg -i 002/f -i 004/f -i 006/f -o eccen/sfaout \
    -TR 2 -ncycles 8 -stimtype eccen -direction pos
```

These will create two new directories: *polar* and *eccen* with bfloat volumes with stem *sfaout*.
    To paint this data, again cd to the directory just above the run directories, and type

```
paint polar/sfaout_%03d.bfloat lh orig polar/sigf-lh.w -nslices 16 -imageoffset 0
paint polar/sfaout_%03d.bfloat lh orig polar/sig2-lh.w -nslices 16 -imageoffset 1
paint polar/sfaout_%03d.bfloat lh orig polar/sig3-lh.w -nslices 16 -imageoffset 2

paint eccen/sfaout_%03d.bfloat lh orig eccen/sigf-lh.w -nslices 16 -imageoffset 0
paint eccen/sfaout_%03d.bfloat lh orig eccen/sig2-lh.w -nslices 16 -imageoffset 1
paint eccen/sfaout_%03d.bfloat lh orig eccen/sig3-lh.w -nslices 16 -imageoffset 2
```

Note that before paint can be invoked, the subject must have been anatomically reconstructed using the FreeSurfer tools, and the functional run must have been registered with the anatomical run.
    To view the results on the surface, create and execute a surfing script with the following content:

```
#!/bin/csh -f
set name = subject  # put the subject's name here
set hemi = lh
setenv eccendir eccen
setenv polardir polar
```

```
#setenv patch occip.patch.flat
setenv revpolarflag 1
setenv rgbname eccenthinmot
setenv fthresh 0.4
setenv fslope 1.3
setenv fmid 0.8
setenv angle_offset 0.77
setenv noexit
tksurfer -$name $hemi 1000a -tcl eccen-flat.tcl
```

7 mri_glmfit and selfreq

Testing multiple regressors across subjects is challenging in that there are multiple measures per subject (usually there is only one). One could test a magnitude, but then that does not have 0 mean. Another is to estimate the real and imaginary components across subject separately and then perform an multivariate (F) test on those. This assumes that there is no correlation between the real/imag within a subject. This is what is described below.

```
# Get real components
foreach session
  mri_convert h-lh.bhdr h-lh-real.mgh --frame 7 # grab real component
end
mri_concat allssessions/h-lh-real.mgh --o allsession.h-lh-real.mgh

# Get imaginary components
foreach session
  mri_convert h-lh.bhdr h-lh-imag.mgh --frame 8 # grab imaginary component
end
mri_concat allsessions/h-lh-imag.mgh --o allsession.h-lh-imag.mgh

# Now concat the real and imag
mri_concat allsession.h-lh-real.mgh allsession.h-lh-imag.mgh
  --o allsession.h-lh-complex.mgh
```

Create an fsgd file with your subjects divided into two groups, one for real and one for imaginary. If you already have groups/classes, then you will need to divide those into two. Take your normal fsgd file with each subject listed once and concatenate the subject list (ie, the Input lines). Put the first half in the real group and the second half in the imaginary group. If you have variables (covariates), then those stay the same for each subject. In the case where you have only one group (dividied into real and imag), then the first regressor will be the mean real part and the second will be the mean imaginary part. Create the following contrast matrix (adding 0s if you have covariates):

```
1 0
0 1
```

This will test the magnitude=0.

If you have two groups (say Male and Female), then you'd create four classes, eg:

```
Class RealMale
Class RealFemale
Class ImagMale
Class ImagFemale
```

You would then create the following contrast matrix:

```
1 1 0 0
0 0 1 1
```