isxavg-re

1   Introduction

isxavg-re is a program for intersubject averaging using a *random-effects model* (see isxavg-fe for fixed effects model). It actually performs statistical analysis as well. It works by computing one number for each subject (at each voxel) based on the contrast matrix. This yields a set of numbers (at each voxel), one for each subject. The average and standard deviation of the set are computed and used to compute a t-statistic the siginficance of $H_0 : t = 0$ is computed using $N - 1$ degrees of freedom where N is the number of subjects. When *jackknifing* is turned on, a new set of N numbers is computed by successively averaging $N - 1$ subjects while excluding a different subject each time. This reduces the effects of small sample sizes on the correctness of the siginficance levels. Jackknifing does increase the time to process data. It is highly recommended and the default in isxavg-re. Note that isxavg-re can be run on any data set, not just the output of *selxavg*.

2   Usage

Typing isxavg-re at the command-line without any options will give the following message:

```
USAGE: isxavg-re [-options] -cmtx cmtxfile -i instem1 -i instem2 -o outstem
   cmtxfile - contrast matrix file generated by mkcontrast
   instem   - prefix of .bfloat selxavg files
   outstem  - prefix of .bfloat output files
Options:
   -voltype            : <auto>, selxavg, selavg, bvolume
   -firstslice <int>   : first slice to process <0>
   -nslices <int>      : number of slices to process <auto>
   -format string      : <log10>, ln, raw
   -nojackknife        : turn off jackknifing <on>
   -invert             : compute 1-p
   -monly  mfile       : dont run, just create a matlab file
   -version            : print version and exit
```

3   Command-line Arguments

-o cmtxfile: contrast matrix file created by calling *mkcontrast*. The contrast matrix determines which statistical test will be run.

-i instem1: stem of the volume in which the results of the selective averaging for the first subject have been stored (see selxavg). There must be at least two input volumes, each preceded by a *-i* flag.

-o outstem: stem of the output volume. The format will be the same as the input volumes, and isxavg-re will also produce appropriate dof, dat, and hdr files.

-voltype: This is the format of the type of data that will be averaged together.

-firstslice int: first *anatomical* slice to process (usually 0). This should not be confused with the first *functional* slice.

-nslices int: total number of *anatomical* slices to process.

-format: transformation to apply to the significances stored in the output file. Options: ln (natural log), log10, and raw. The default is log10.

-nojackknife: do not jackknife the averages.

-invert: report one minus the signficance value instead of the signficance value.

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