

Initializing spm8 Batch

A command line command to drive batch processing to warp the fMRI time series to the standard template using normalization derived during the 'warpHiRes' phase +.

The 'warpfMRI' command builds a script in the directory:

matlabScripts/spm8Batch/warpfMRI/YYYY_MM directory

directly below the current directory and will launch this script in background. The names of the matlab and shell scripts will be in the format of :

warpfMRI_yymmdd_HH_MM_[USER]_[COMPUTER].m and
warpfMRI_yymmdd_HH_MM_[USER]_[COMPUTER].sh

where yymmdd is the date and HH_MM is the time.

This script is expecting to find the necessary components in the directory structure of :

```
yymmddLF/                                (subject directory)
  anatomy/
  func/
  coReg/
  run_XX/
```

Usage:

warpfMRI [OPTIONS] [subject_1] [subject_2] ... [subject_N]

Options

Key Parameter	Description
-d	enable debug flag.
-D	enable super debug flag.
-f sub-directory	set relative path functional directory, default=func
-h HiResName	name of high resolution file, default is 'ehtlspgr'
-M SUBJECTMASTER	set the directory to scan for subjects, default is Subjects/
-n PrependName	name to add to output file name, default is none.
-t	enable testing flag, script will be built but not run.
-U user-email	set the user name for email notification, default is "rcwelsh" of present shell.
-v volume-wild	set the volume name wild-card, default "raprun".
-w sub-directory	set coregistration path under func, default=coReg
-z VOXELSIZE	set the voxel size for resampling, default is spm default.

e.g.

To warp fmri using the 'hetlspgr':

```
warpfMRI -w func/MSIT 050126zz
```

*NOTE: This code will actually hunt out rapruns's (or those specified in the -v fl
+tag The code does not actually care where the files live and will attempt to wa
+rp any and all volumes using the specified SPGR (or default) volume. However y
+ou can narrow the search by supplying the '-s subdir' option which will then r
+require that 'subdir' is a string contained in the list of directories returned for
+ warping.
If this DOES NOT make sense to you please contact Robert before proceeding.

Current command default configuration is:

```
directory to coreg      : func//coReg//  
name of the high res   : ehtlspgr  
template image dir/name : /net/dysthymia//spm8/templates//T1.nii  
prepending name        : w  
Voxel dimension (0=spm) : 0  
volumeWILD             : raprun  
functional sub-dir     :  
  
functional images path : func/  
Subject directory      : Subjects/  
  
spm8 is located in     : /net/dysthymia//spm8  
spm8Batch is located in : /net/dysthymia//spm8Batch  
spm8 patch is located in : /net/dysthymia//spm8Batch/matlabScripts  
auxillary matlab path  : /net/dysthymia//spm8Batch/spm8_patch  
  
User                   : rcwelsh  
MATLAB                 : /net/misc/matlab2007b/bin/matlab  
  
SANDBOXHOST            : dysthymia  
SANDBOX                : /dysthymia/sandbox/  
SANDBOXPID             :
```

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