# spm8Batch

A unix shell command interface to SPM8 to facilitate data pre-processing for spatial normalization to MNI space

There are philosophies behind the design of spm8Batch:

- minimize user script writing
- automatic and extensive logging/tracking of all processing
- •interaction with SPM/MATLAB from simple shell command line
- •allowing for quality control (check reg) between steps
- •ensuring analysis pieces (data) exist prior to execution
- •allowing for large scale data throughput
- uniformity of pre-processing (with allowing for flexibility)
- notification when process is complete
- •truly running in background to be less sensitive to glitches
- •"job" files are essentially archives of processing
- •commands all have "built-in" help

Assuming data are from an imaging center that provides for *slicetiming* and *realignment* corrections the remaining steps to get functionals into MNI space prior to statistical analysis are:

- coregistration of overlay to functional
- coregistation of high-resolution to overlay
- •MNI normalization of high-resolution image (VBM8 or SPM8)
- •MNI normalization of functional data
- •smoothing of functional data

Preprocessing Workflow

coregoverlay

coregHiRes

vbm8HiRes

warpfMRI

smoothfMRI

To facilitate data integrity, operations such as coregistration and MNI normalization of high-resolution image takes place in new coReg directory.

MNI normalization and smoothing of functional data take place in the run directories.

When a process is run, the command will automatically configure a "job" by writing a shell-script file and as needed a matlab script file. These files will be created in a directory specified by the name of the command being issued and then further segregated by the year and month. The "job" files have names that are based on the command issued, the date/time, the user and the computer node. Once the command completes building the process it will launch into the background for execution, releasing the interactive terminal.

A log file is also produced.

Example:

matlabScripts

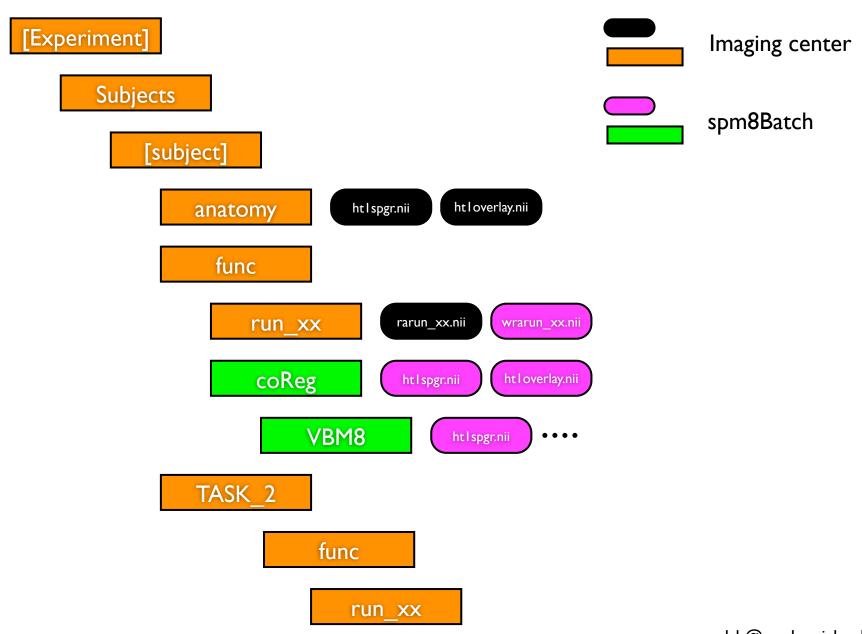
spm8Batch

coregOverlay

2012\_03

coregOverlay\_120313\_09\_37\_18\_rcwelsh\_gaviero.sh coregOverlay\_120313\_09\_37\_18\_rcwelsh\_gaviero.m coregOverlay\_120313\_09\_37\_18\_rcwelsh\_gaviero.log

#### **Expected Data Structure**



rcwelsh@med.umich.edu 2012-03-13

#### Example Preprocessing Workflow

coregOverlay

coregOverlay -o htloverlay -v rar -w coREG FINAL -M ./ 080430rf

coregHiRes

coregHiRes -o htloverlay -h htlspgr -w coREG\_FINAL -M ./ 080430rf

vbm8HiRes

vbm8HiRes -h ht1spgr -a func/coreg\_FINAL \
 -w func/coreg\_FINAL/VBM8 \
 -I r3mm avg152T1 -n w3mm -M ./ 080430rf

warpfMRI

warpfMRI -h ht I spgr -w coREG\_FINAL/VBM8 -I r3mm\_avg I 52T I \
-n w3mm\_ -M ./ 080430rf -v rar -W

smoothfMRI

smoothfMRI -v w3mm rar -M ./ 080430rf