

fMRI Preprocessing
“RCW”
spm8Batch
methodology

What you need:

- spm8Batch system
- spm8 with at least revision 4667
- FSL 4.1.9 or FSL 5.0.2.2

spm8Batch processing tools:

Standard Directory Structure

bash commands from unix shell

launches to background

email/txt msg notification

Expected directory structure

```
/diskdrive/  
  [experiment]/  
    Subjects/  
      [subject]/  
        anatomy/  
          htloverlay.nii  
          htspgr.nii  
        func/  
          run_XX/  
            run_XX.nii  
        connect/func/  
          func/  
            run_XX/  
              run_XX.nii
```

Auxiliary Commands

- getfMRI
- UNNIFTI
- tarBET

Main Processing Commands

- [next page]

Login

Launch command

(automatically builds components goes into background)

Logout (if you wish)

Check email, check the log for any errors.

```
/diskdrive/  
  [experiment]/  
    matlabScripts/  
      spm8batch/  
        [command]/  
          YYYY_MM/  
  
warpfMRI_XXXXX_...sh  
warpfMRI_XXXXX_...log  
warpfMRI_XXXXX_...m
```

processing order



[physioCorr]
sliceTime8
realignfMRI
coregOverlay
coregHiRes
vbm8HiRes
vbm8Check
warpfMRI
smoothfMRI

all commands have built-in help

Command Options (common uses)

-A	process all runs present
-a [directory]	anatomy directory e.g. anatomy/BET
-b	also put best BET one picked
-D	super debug flag
-d	debug flag
-E [# #]	erosion parameters
-e [ext]	extension override for smoothfMRI
-F [TR]	fMRI TR
-f [directory]	functional directory e.g. connect/func
-G [STC info]	information for sliceTime/sliceTime8
-g [gradient]	gradient value to pass to 'bet'
-H	calculate bias field only from vbm8HiRes
-h [name]	high resolution image
-i [run number]	include this run number
-L	when to do erosion
-M [directory]	master subject directory
-m ["options"]	mcflirt options
-N [#]	recon run number start
-n [name]	name prepend

-O [name]	other object to drag into process or sliceTime8 slice acq order
-o [name]	overlay image name
-R	reslice flag set to 2
-r	reslice flag set to 1
-S [#]	standard volume number for mcflirt
-s [directory]	sub-directory name to search for images
-T [name]	template image name
-t	test flag
-U [unique]	user email name/txt msg address
-v [name]	volume to use for coregistration
-w [directory]	coregistration output directory
-z [#]	voxel reslice size
-# [#-#]	inclusive run list

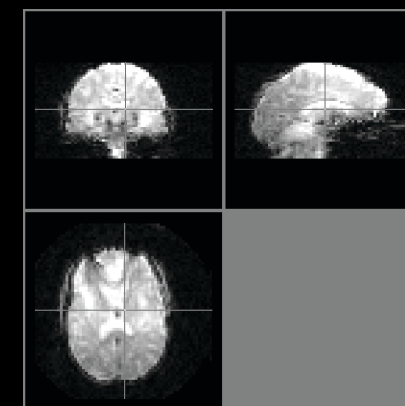
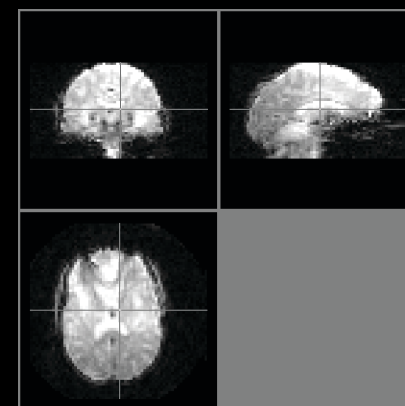
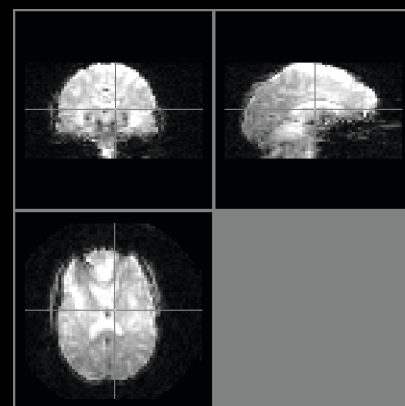
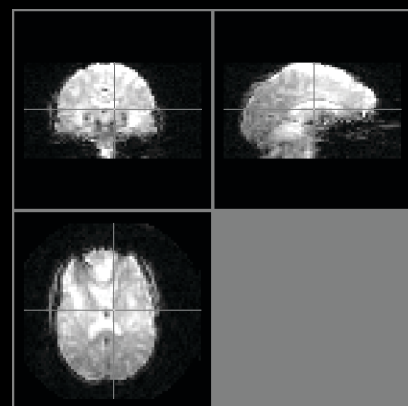
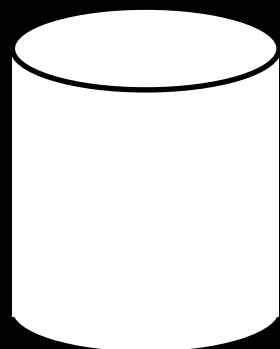
Expected data:

overlay image in the same rough space as
the functional data

hi resolution image needed for warping

time-series data

Pre-processing done at fMRI Lab



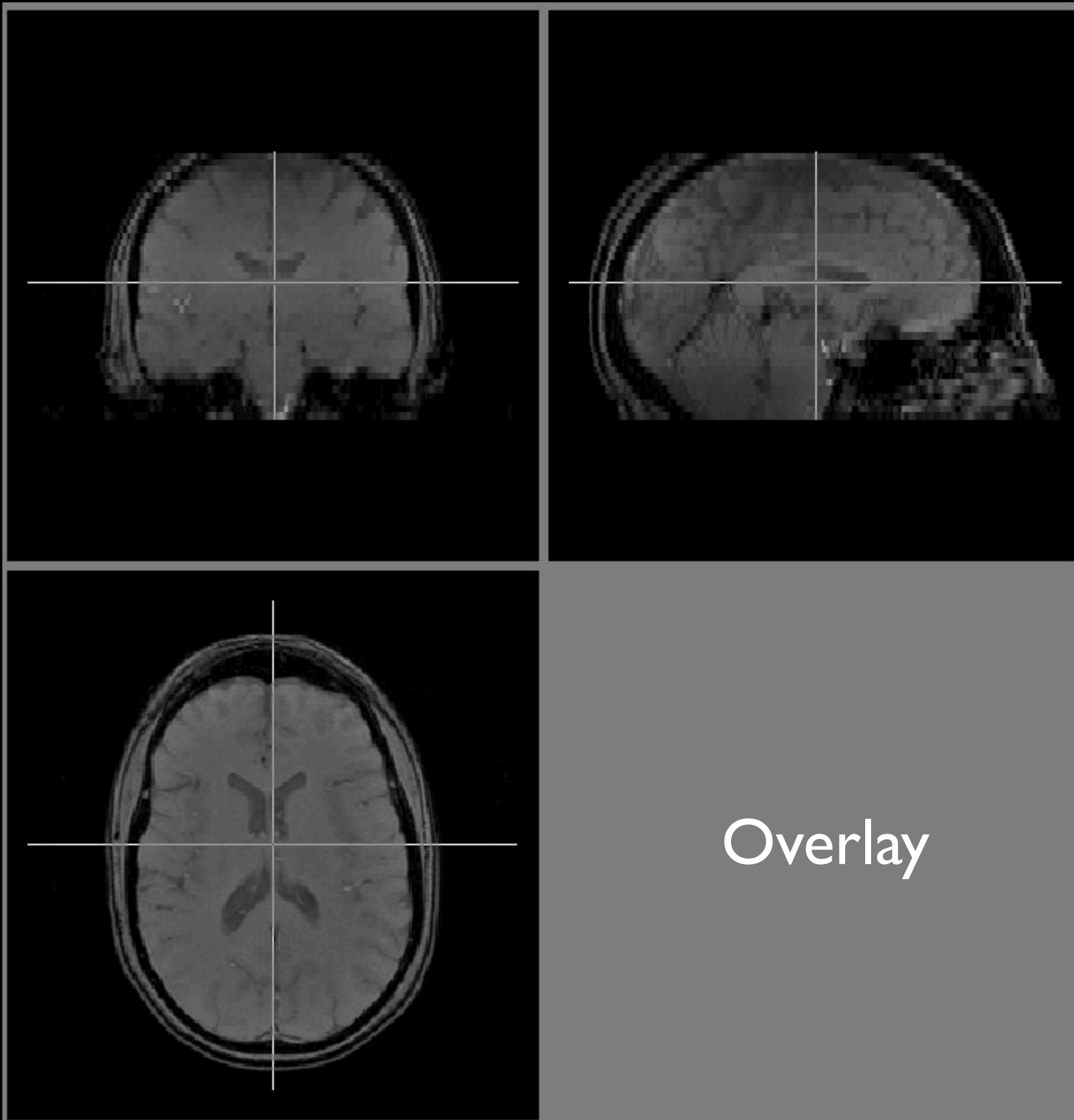
p-file
(k-space)

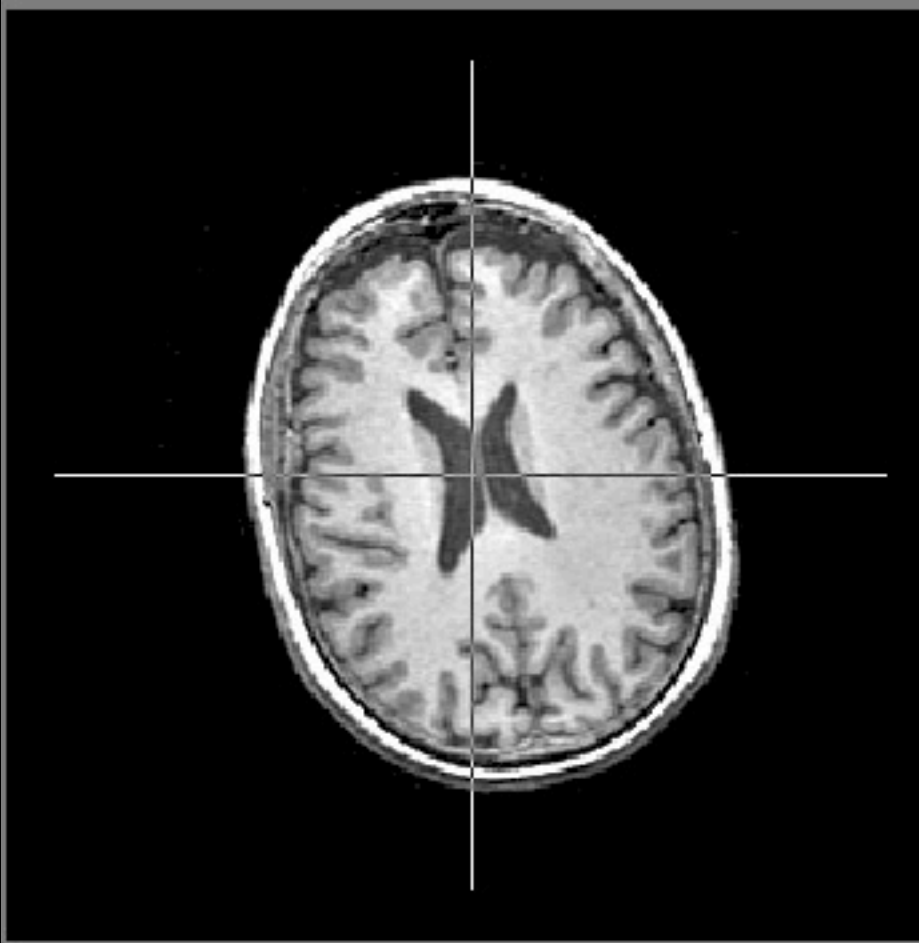
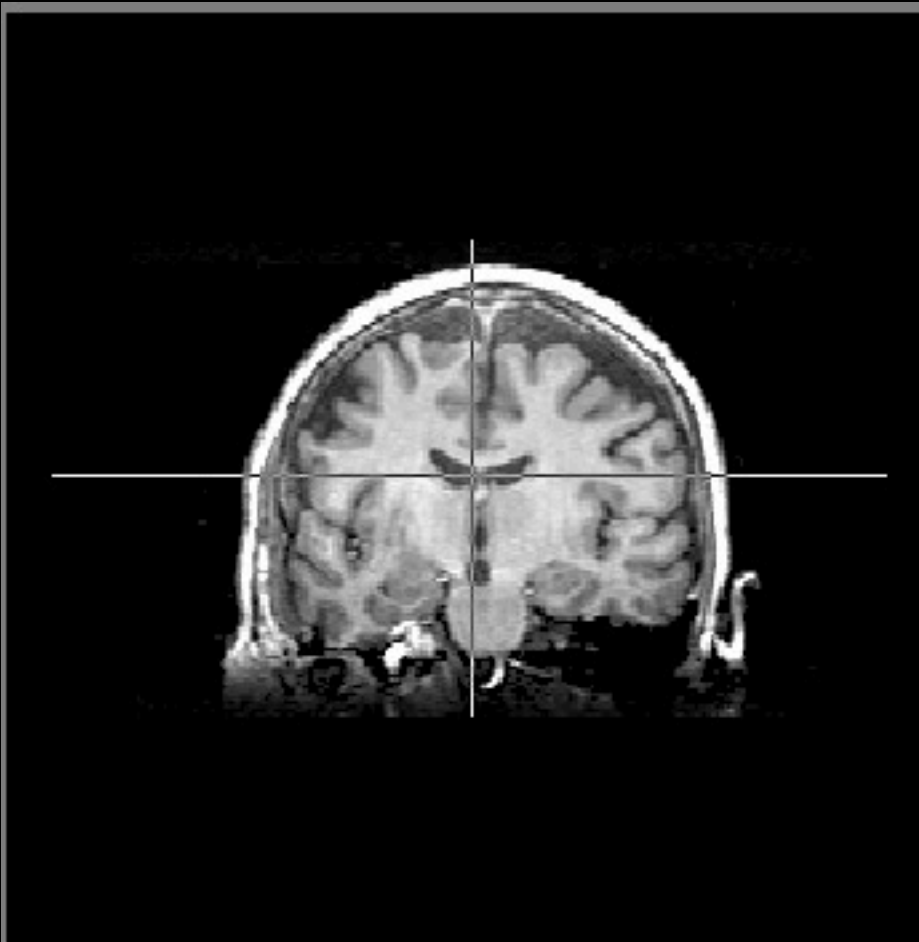
run

prun

aprun

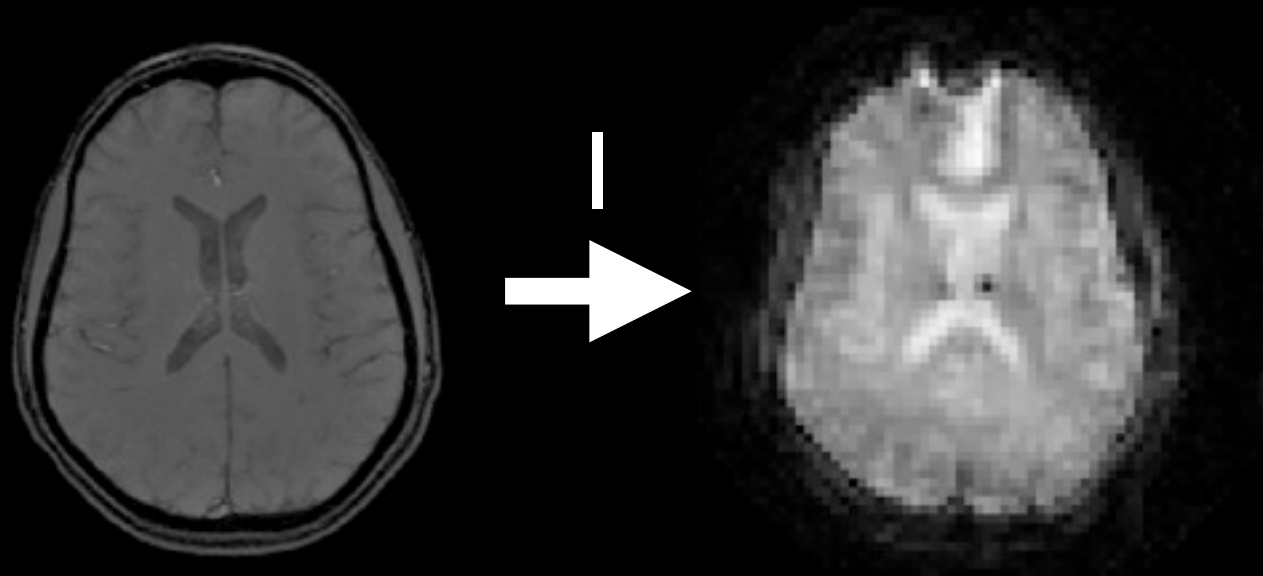
raprun





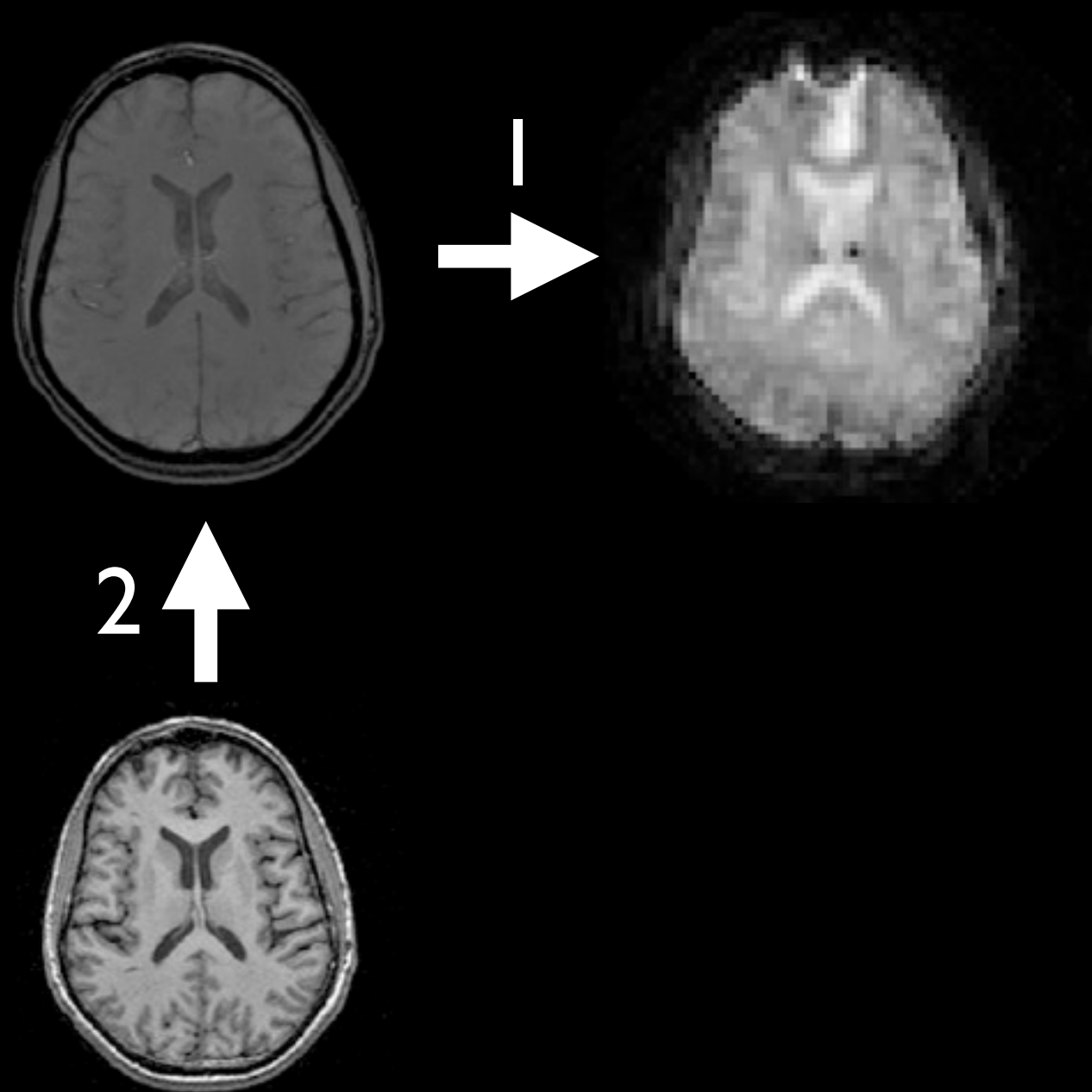
Hi Resolution

Strategy for normalization of functionals



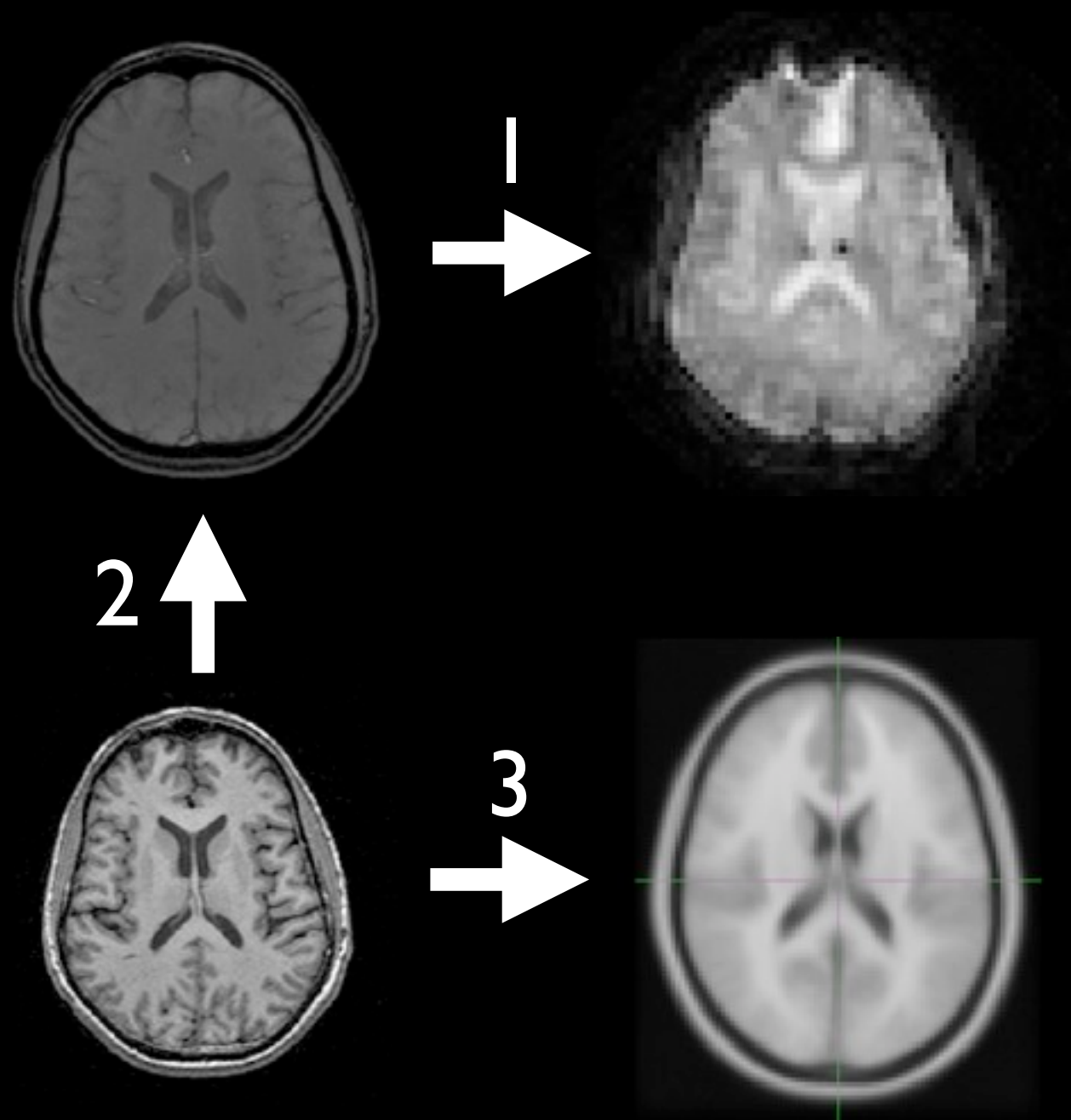
- 1 - coregOverlay
- 2 - coregHiRes
- 3 - warpHiRes
- 4 - warpfMRI

Strategy for normalization of functionals



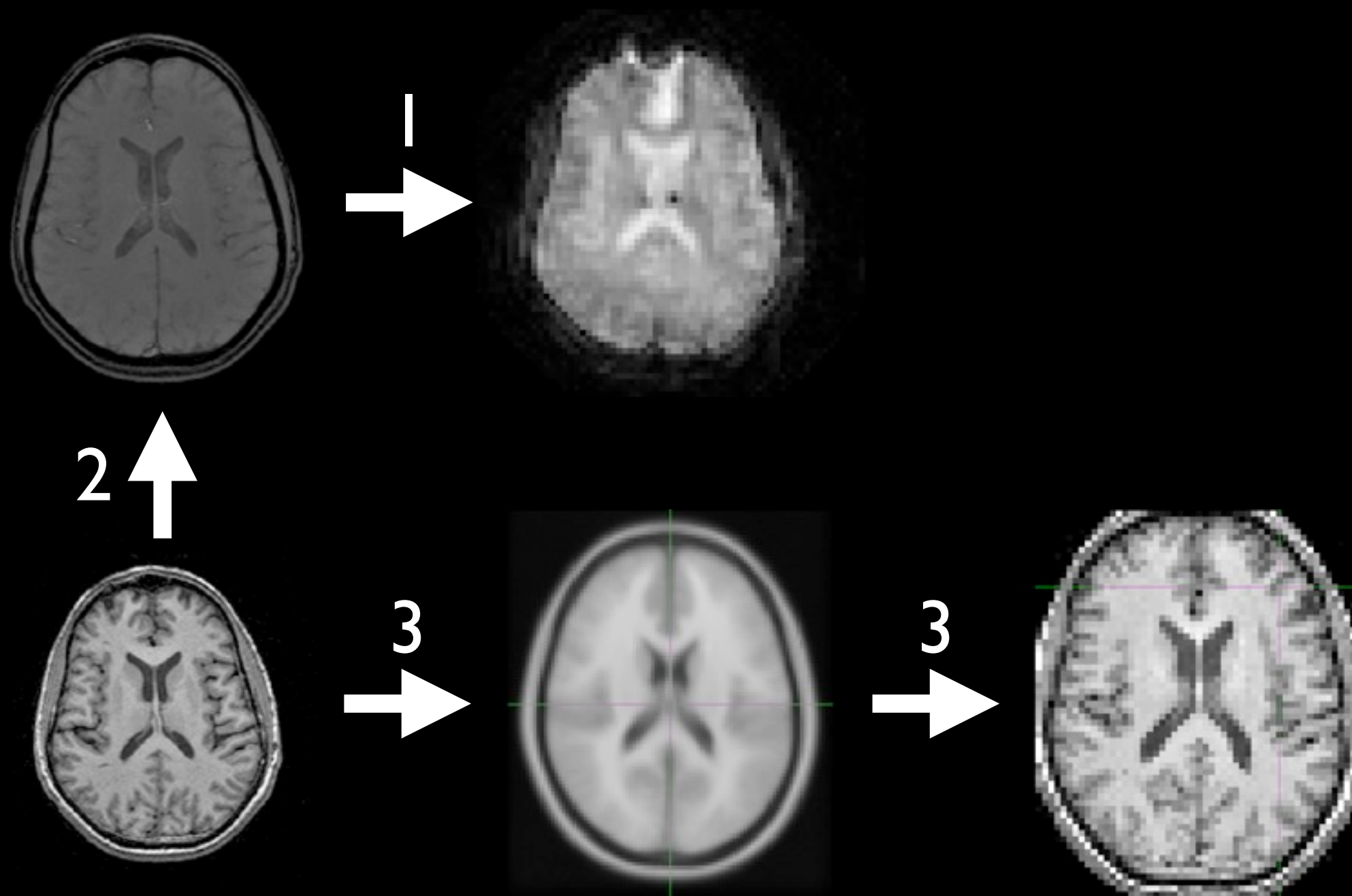
- 1 - coregOverlay
- 2 - coregHiRes
- 3 - warpHiRes
- 4 - warpfMRI

Strategy for normalization of functionals



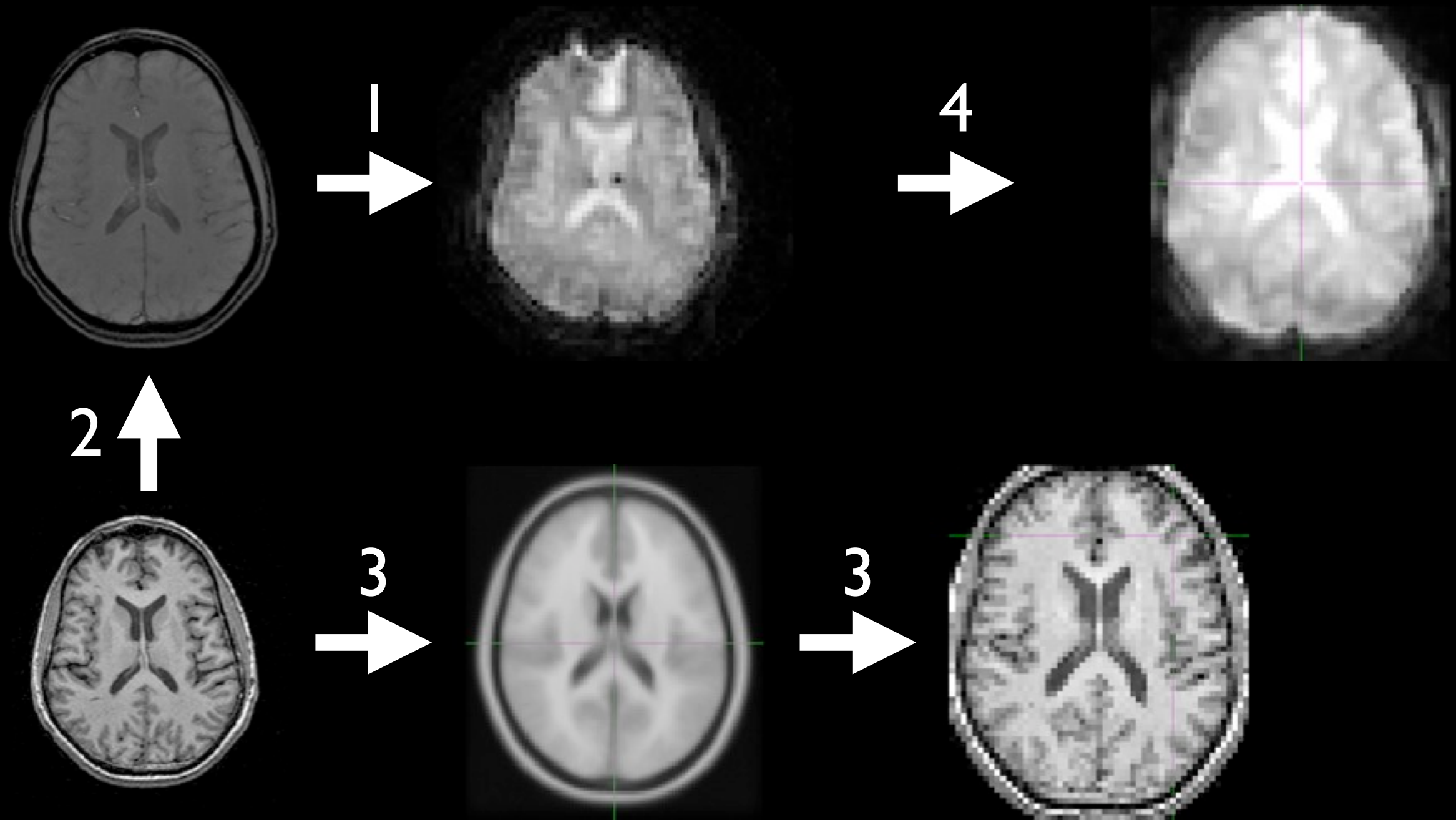
- 1 - coregOverlay
- 2 - coregHiRes
- 3 - warpHiRes
- 4 - warpfMRI

Strategy for normalization of functionals



- 1 - coregOverlay
- 2 - coregHiRes
- 3 - warpHiRes
- 4 - warpfMRI

Strategy for normalization of functionals



- 1 - coregOverlay
- 2 - coregHiRes
- 3 - warpHiRes
- 4 - warpfMRI

physioCorr [subject]
run_XX.nii \longrightarrow *prun_XX.nii*

sliceTime8 [subject]
prun_XX.nii \longrightarrow *aprun_XX.nii*

realignfMRI [subject]
aprun_XX.nii \longrightarrow *raprun_XX.nii*

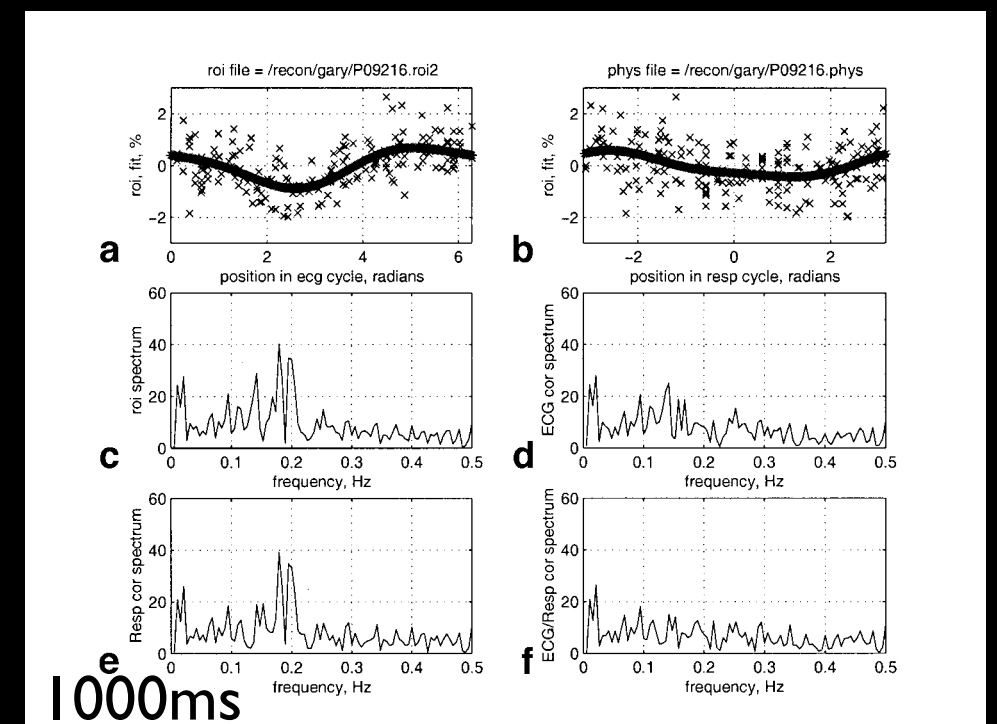
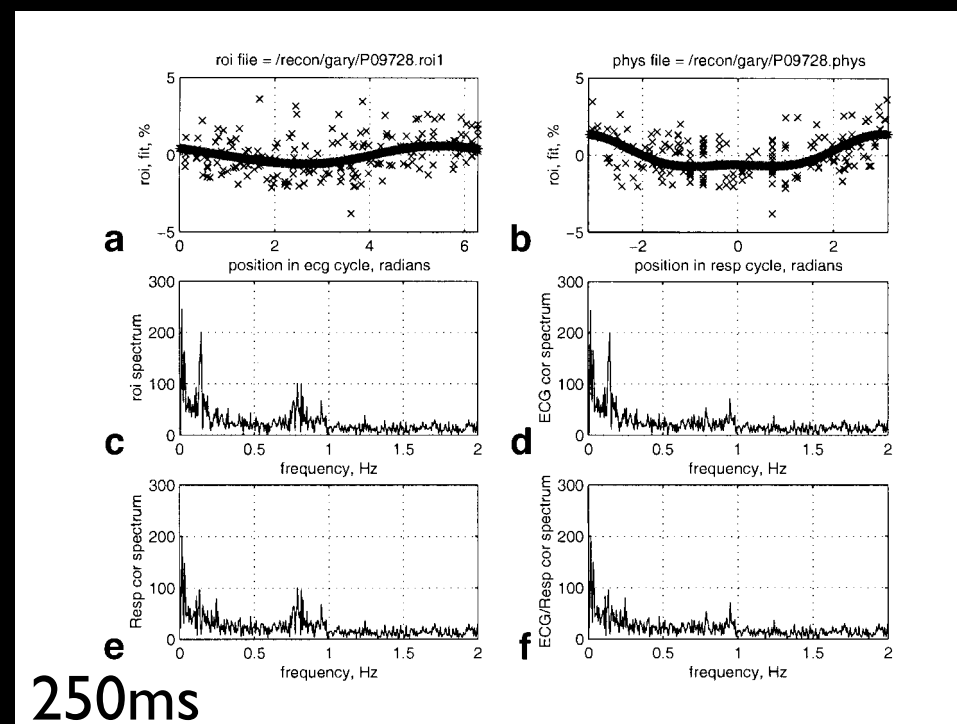
physioCorr [subject]

physiological correction:

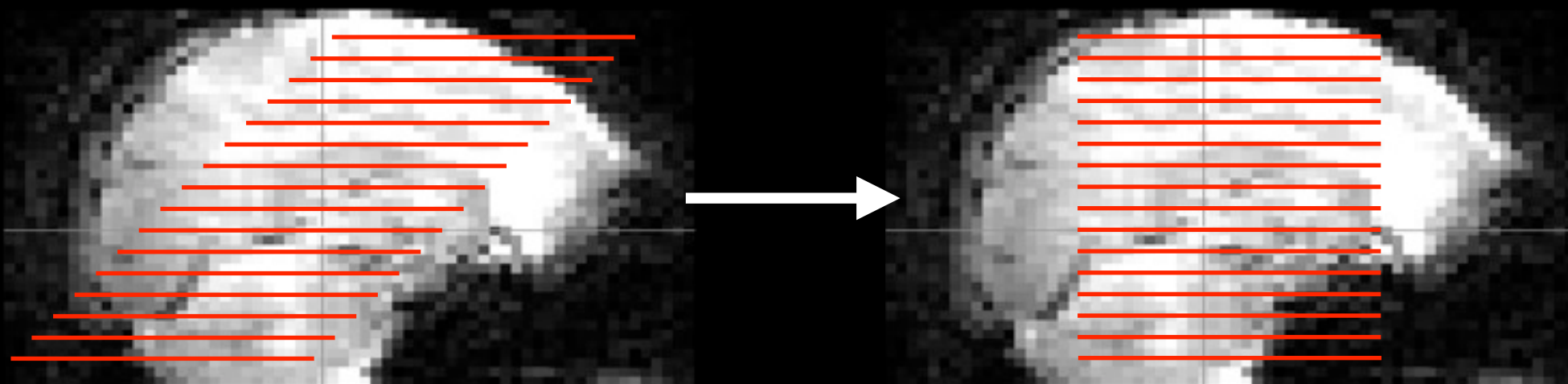
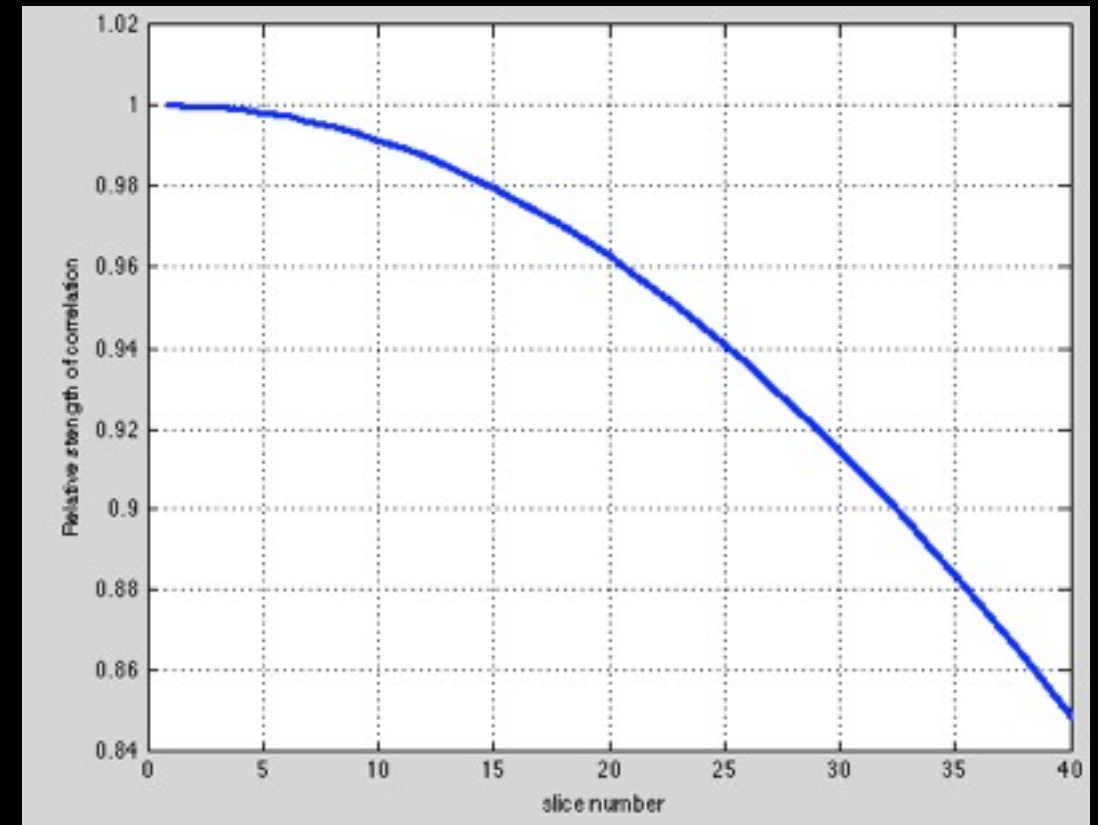
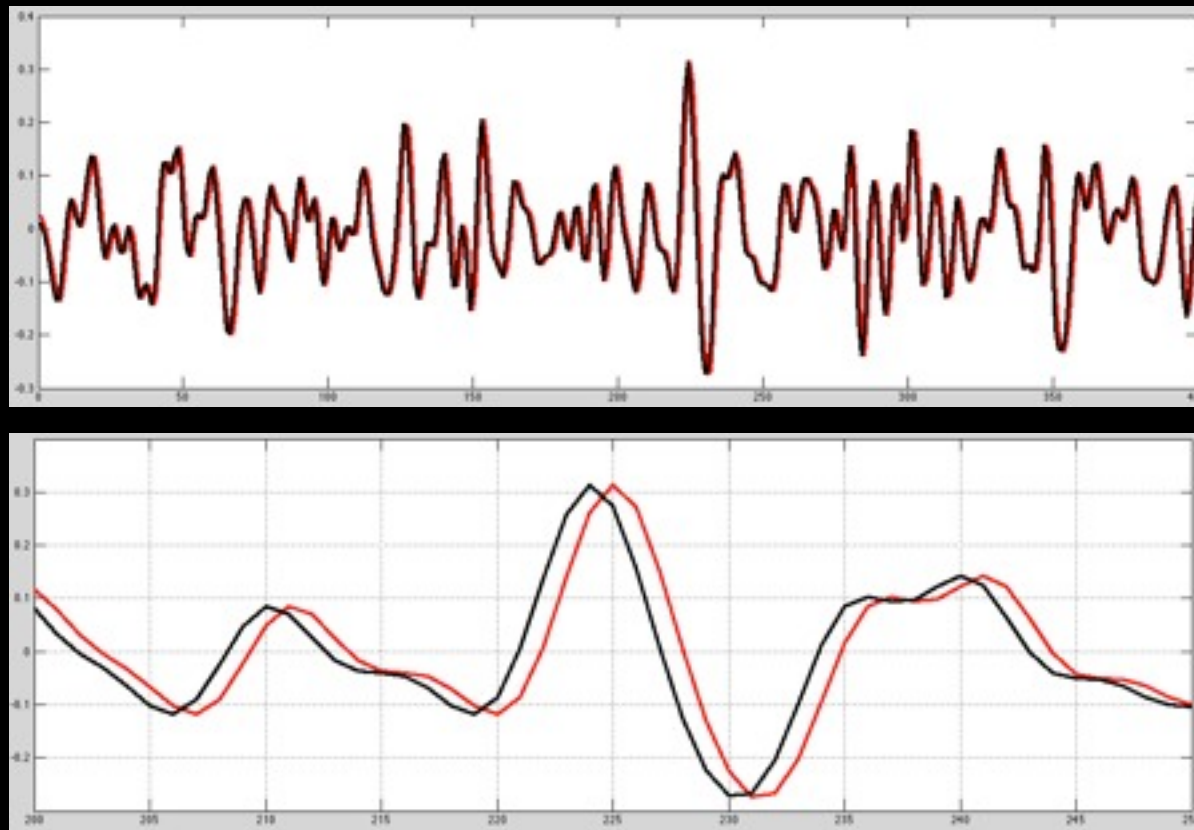
In the current paper, we have shown that the NVR model composed of a comprehensive set of nuisance regressors substantially reduces the structured noise in fMRI residuals. The NVR model is based on a number of effects which are known to contribute to the non-white noise in fMRI (hardware drift, residual movement artefacts, respiration and cardiac pulsation). In fact, the proposed NVR model is only new in the sense that we for the first time have used a combination of several already published models in the same analysis.

It was furthermore found that our approach, in general, was superior to the covariance estimation currently implemented in SPM2. In particular, we found the global AR(1) model of SPM to be inadequate near larger arteries which is not surprising given the inability of a first-order AR model to account for oscillatory noise. -- Lund, Neuroimage 29, 2006

RETROICOR - implemented at fMRI BIRB

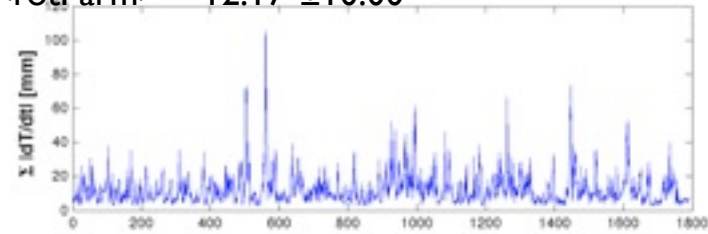


sliceTime8 [subject]

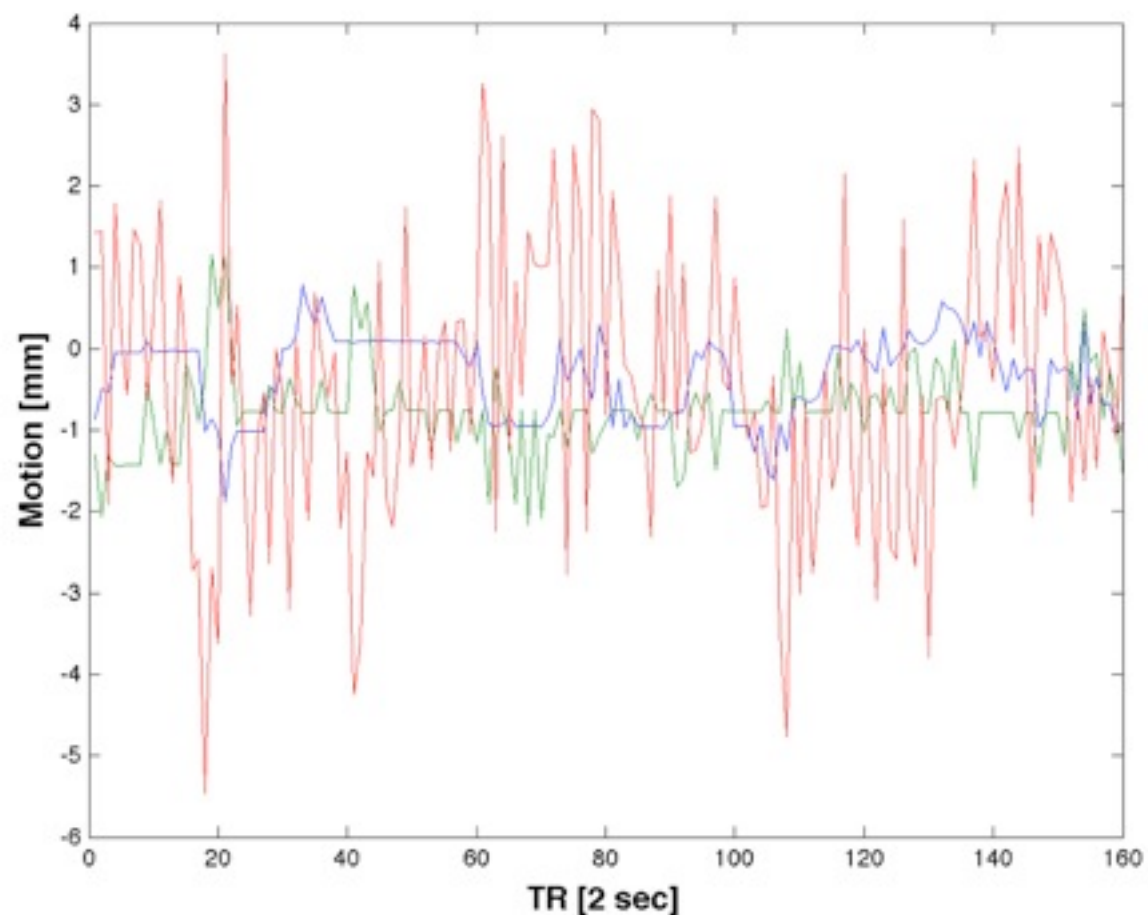
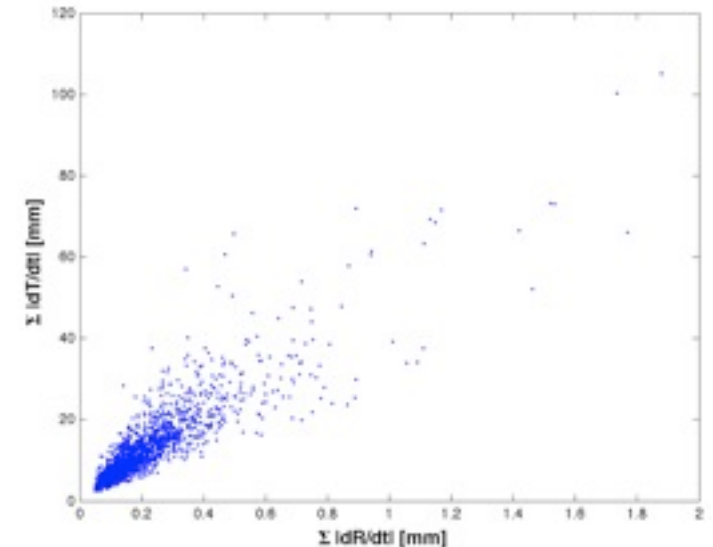
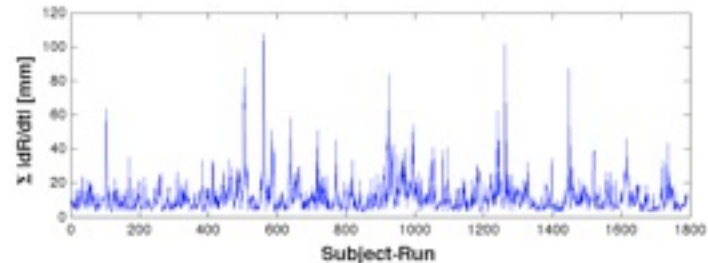
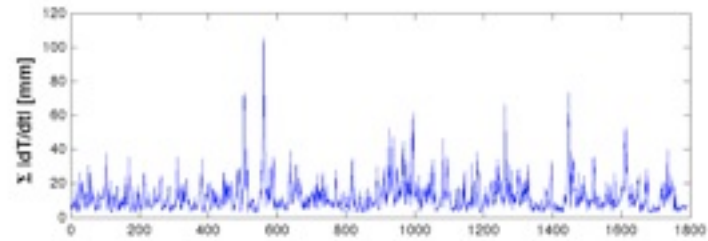
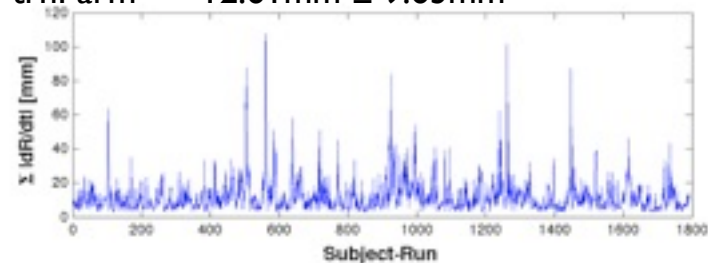


realignfMRI [subject]

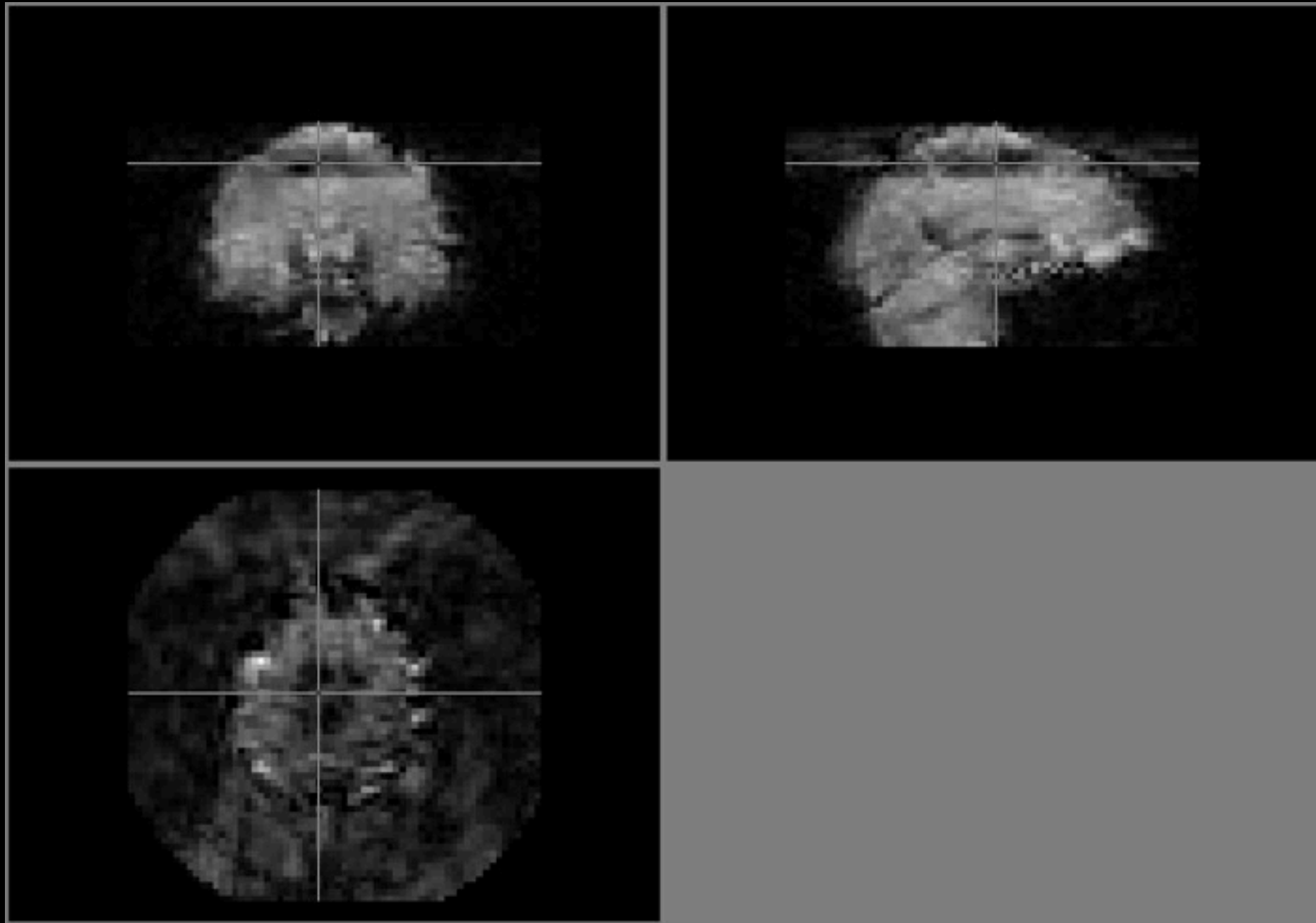
$\langle \text{rotParm} \rangle = 12.17^\circ \pm 10.00^\circ$



$\langle \text{trnParm} \rangle = 12.61\text{mm} \pm 9.63\text{mm}$



Always check for bad data. Arduous task
but critical.



coregOverlay [subject]

Prior

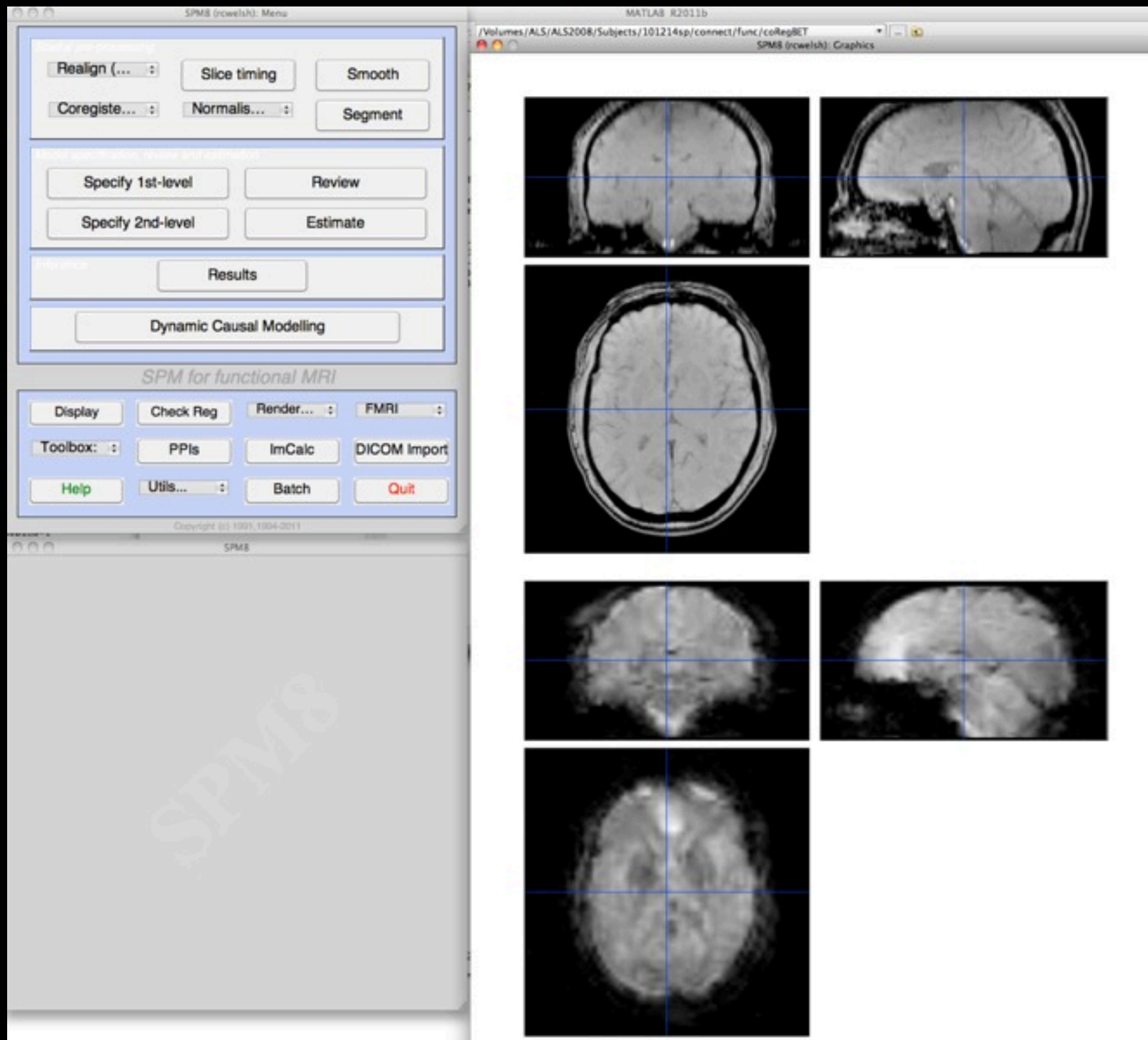


After

```
[subject]/  
  anatomy/  
    ht1overlay.nii  
    htspgr.nii  
func/  
  run_XX/  
    run_XX.nii  
    raprun_XX.nii
```

```
[subject]/  
  anatomy/  
    ht1overlay.nii  
    htspgr.nii  
func/  
  run_XX/  
    run_XX.nii  
    raprun_XX.nii  
coReg/  
  ht1overlay.nii
```


Check registration : overlay & fMRI



coregHiRes [subject]

Prior



After

```
[subject]/  
  anatomy/  
    htlooverlay.nii  
    htspgr.nii  
    BET/  
      best_BET_hiRes.nii  
func/  
  run_XX/  
    run_XX.nii  
    raprun_XX.nii
```

```
[subject]/  
  anatomy/  
    htlooverlay.nii  
    htspgr.nii  
func/  
  run_XX/  
    run_XX.nii  
    raprun_XX.nii  
coReg/  
  htlooverlay.nii
```

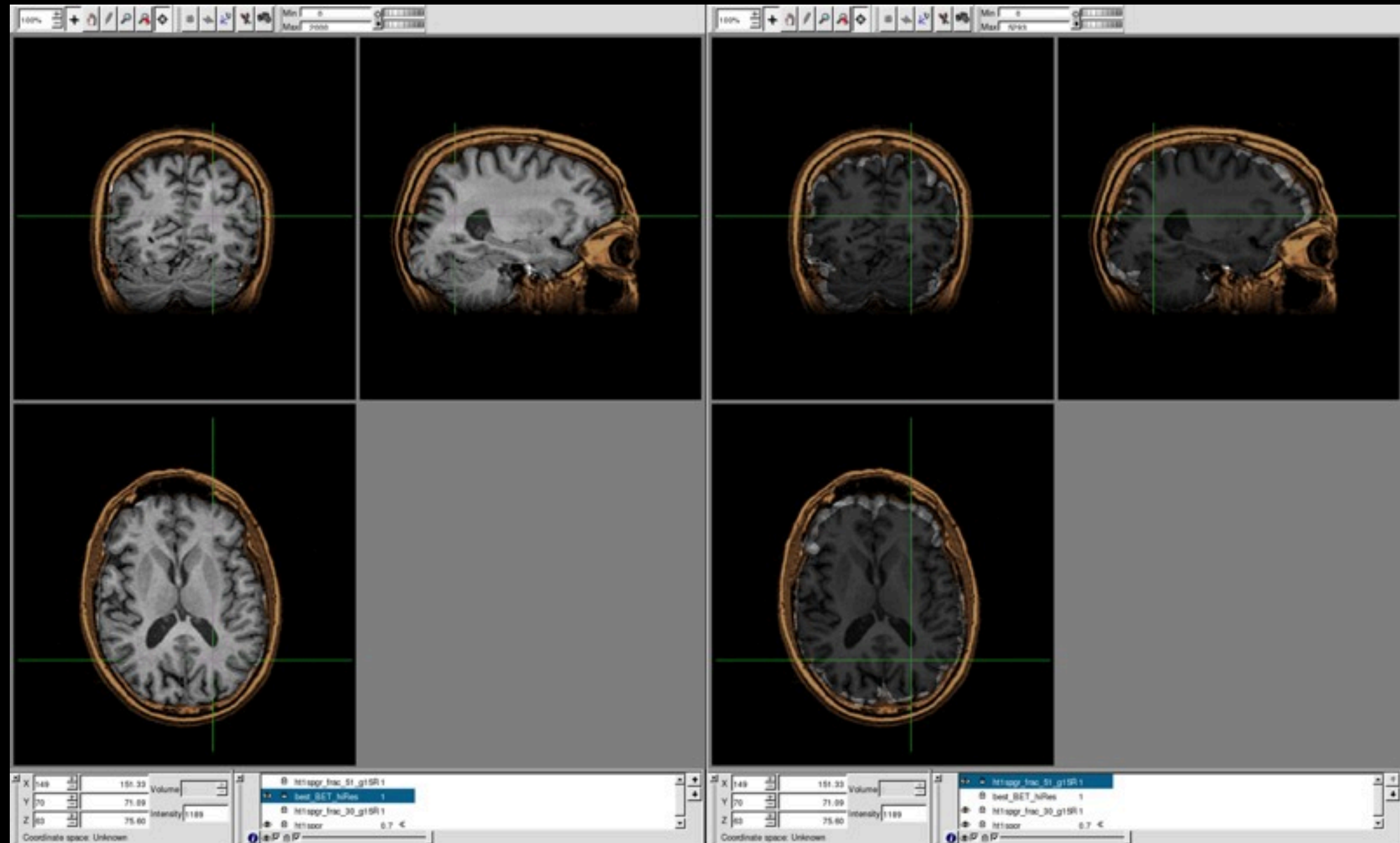
Spatial Normalization with VBM8

vbm8HiRes [subject]

ht1spgr.nii → *w3mm_vbm8_ht1spgr.nii*

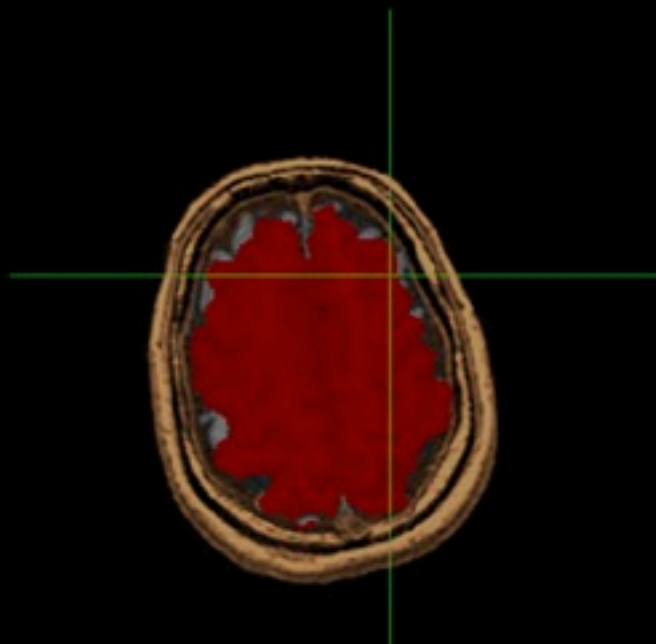
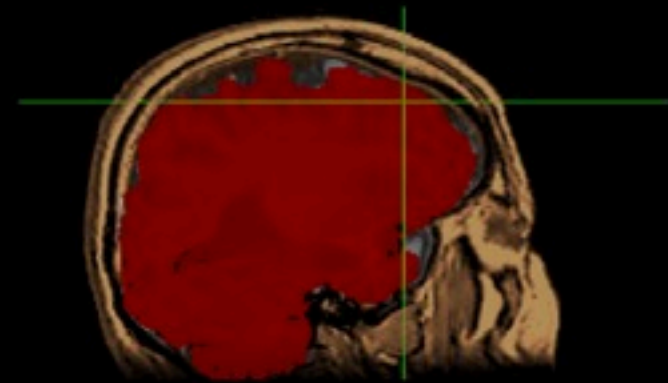
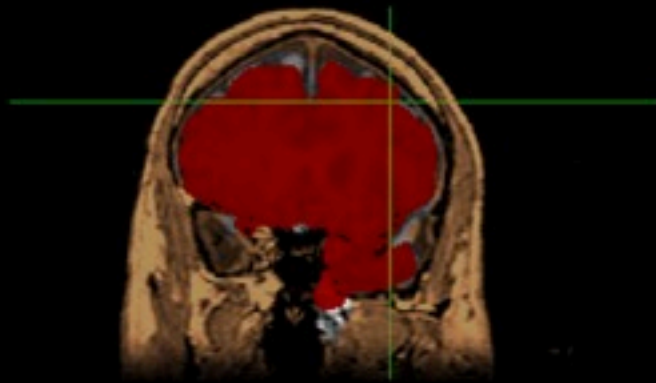
vbm8Check [subject]

vbm8Check



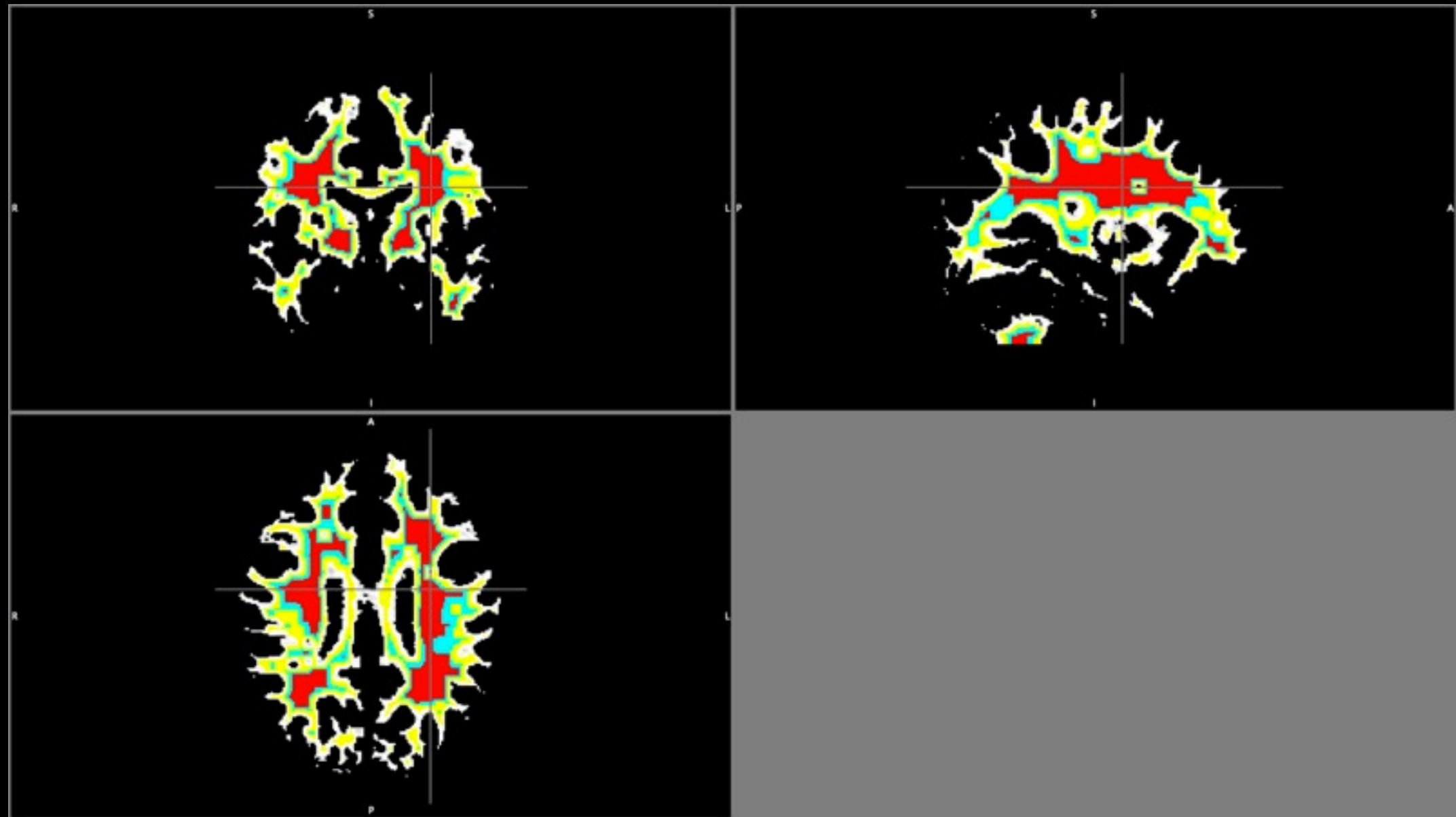
Example of different thresholds.

Red is not great.

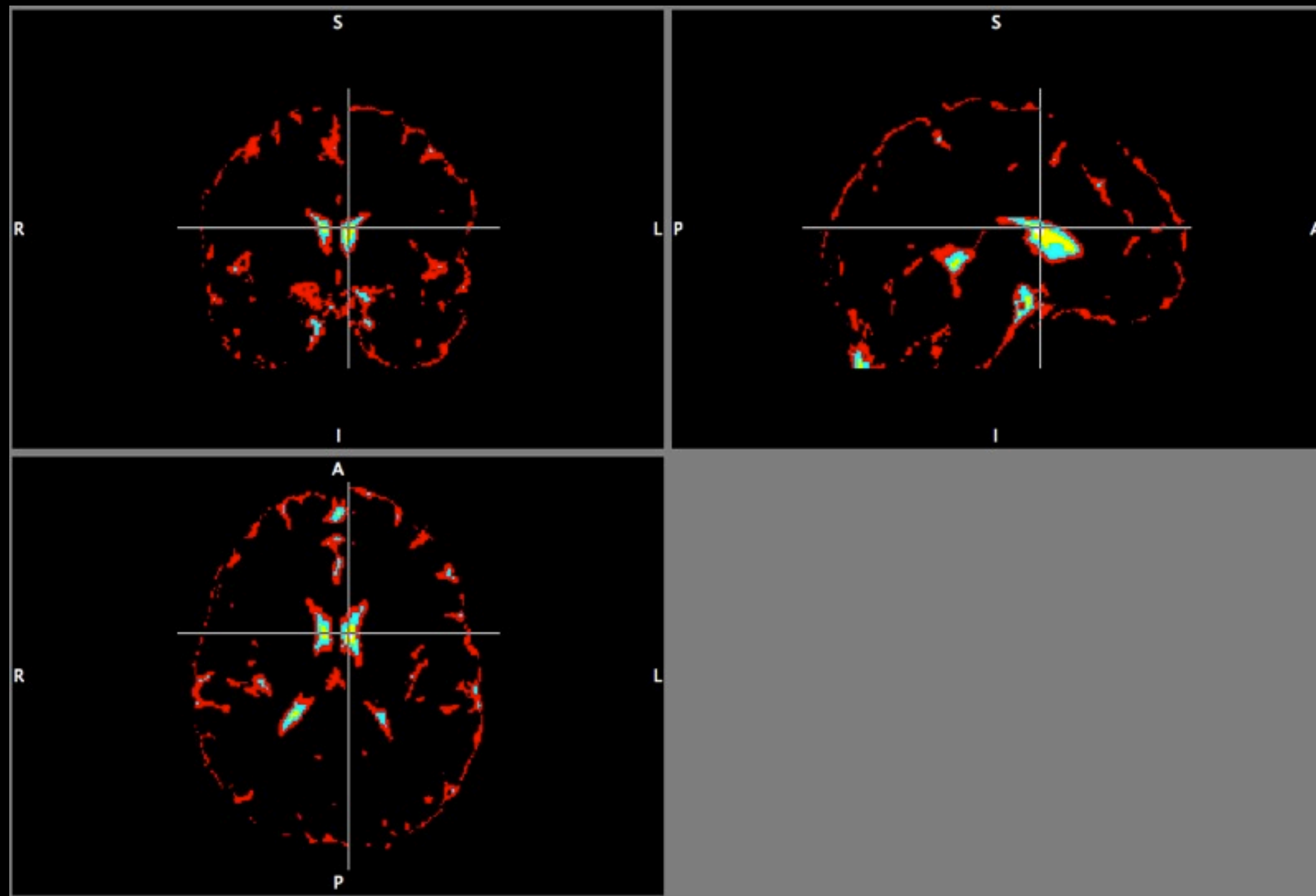


As part of vbm8HiRes, different tissue segments are created. vbm8HiRes will also automatically erode these for you. See the built-in help for vbm8HiRes

White matter segment with various erosions.



CSF segment with various erosions.

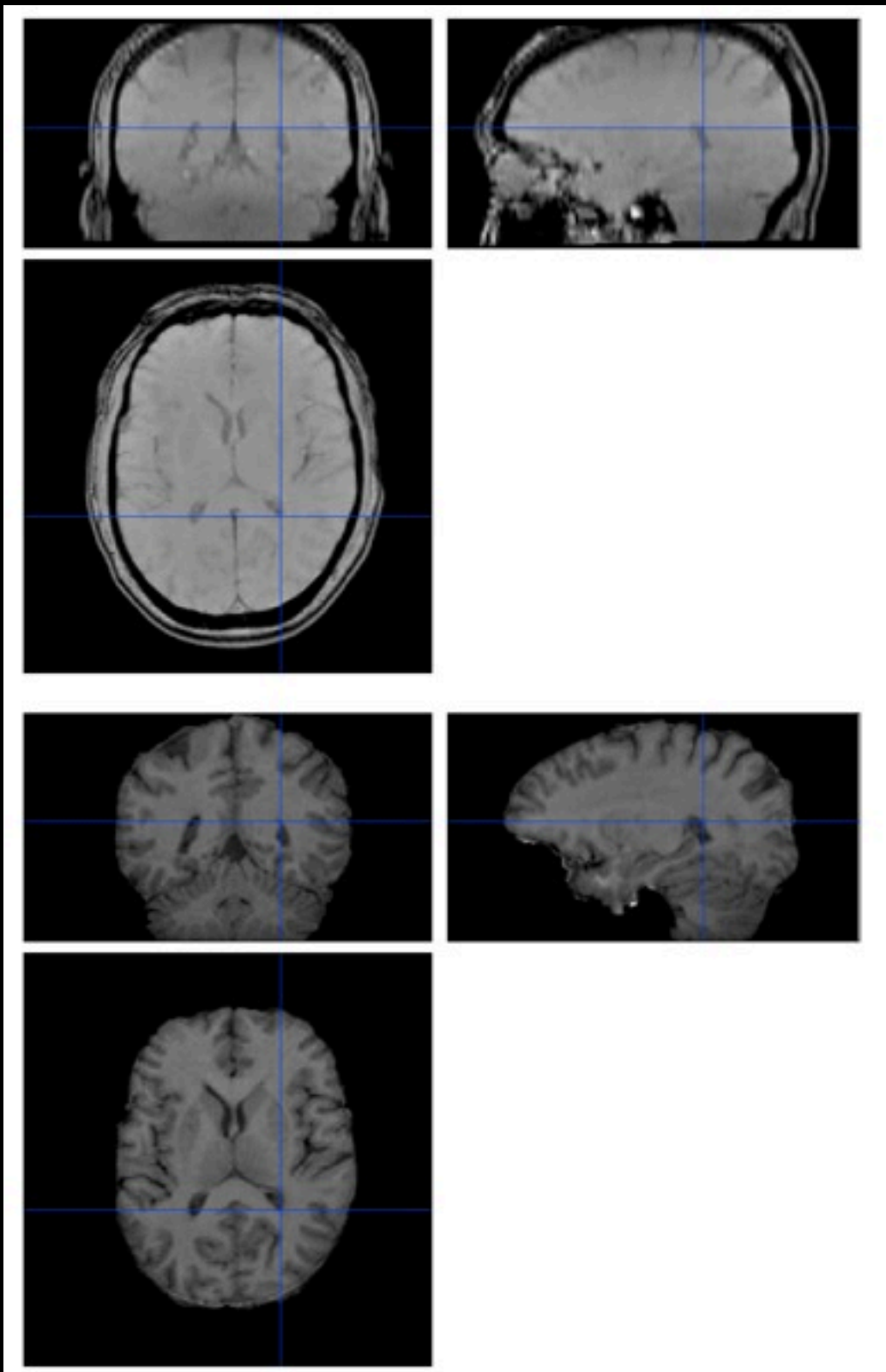


vbm8HiRes [subject]

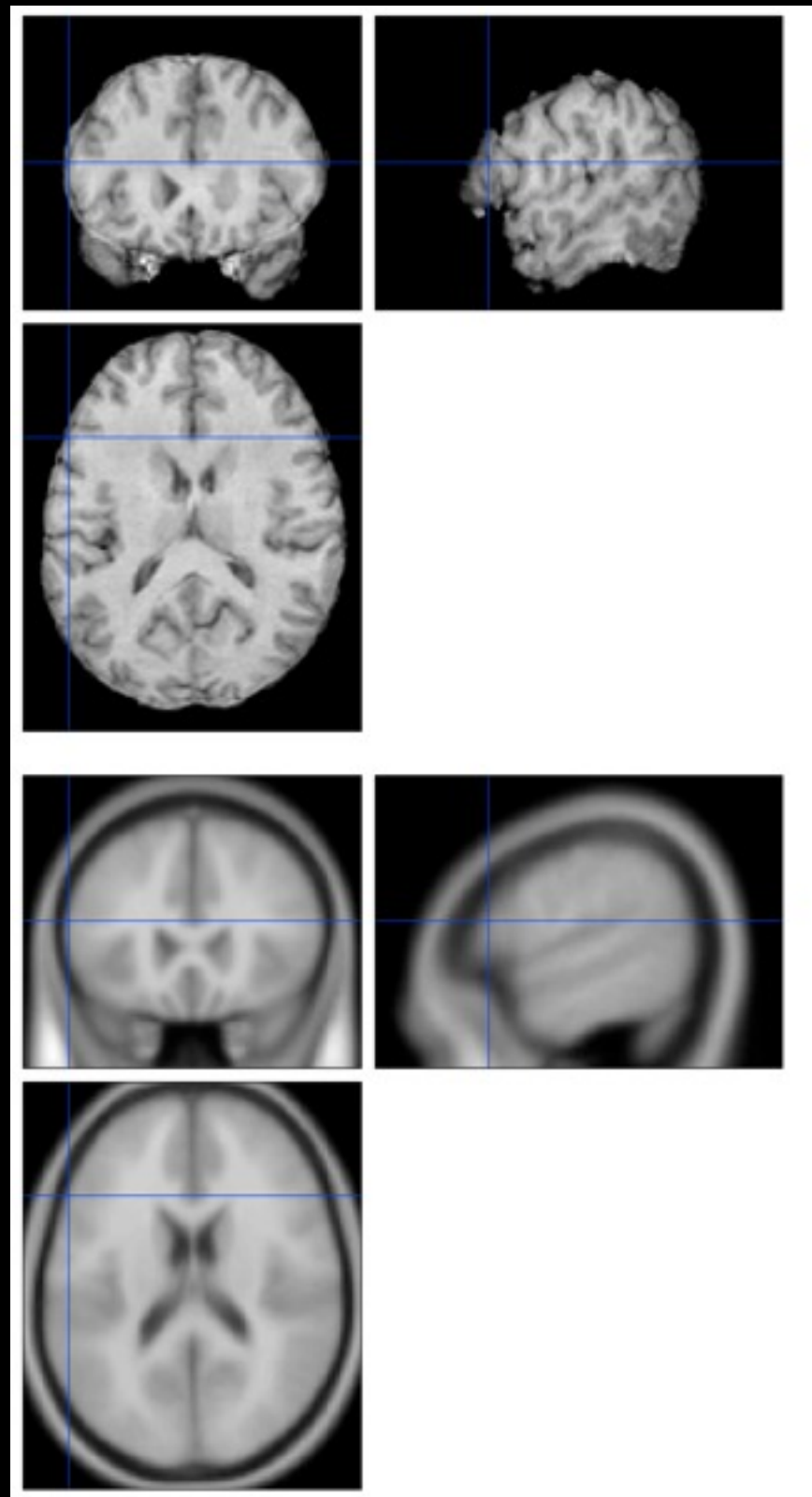
After

```
[subject]/  
  anatomy/  
    ...  
  func/  
    run_XX/  
      ...  
    coReg/  
      VBM8/  
        [many files]
```


Overlay to hires



Warped HiRes



warpfMRI [subject] [-W to use VBM8]

Prior



After

[subject]/
anatomy/
 htloverlay.nii
 htspgr.nii
func/
 run_XX/
 run_XX.nii
 raprun_XX.nii

[subject]/
anatomy/
 htloverlay.nii
 htspgr.nii
func/
 run_XX/
 run_XX.nii
 raprun_XX.nii
 w3mm_raprun_XX.nii

smoothfMRI [subject]

Prior

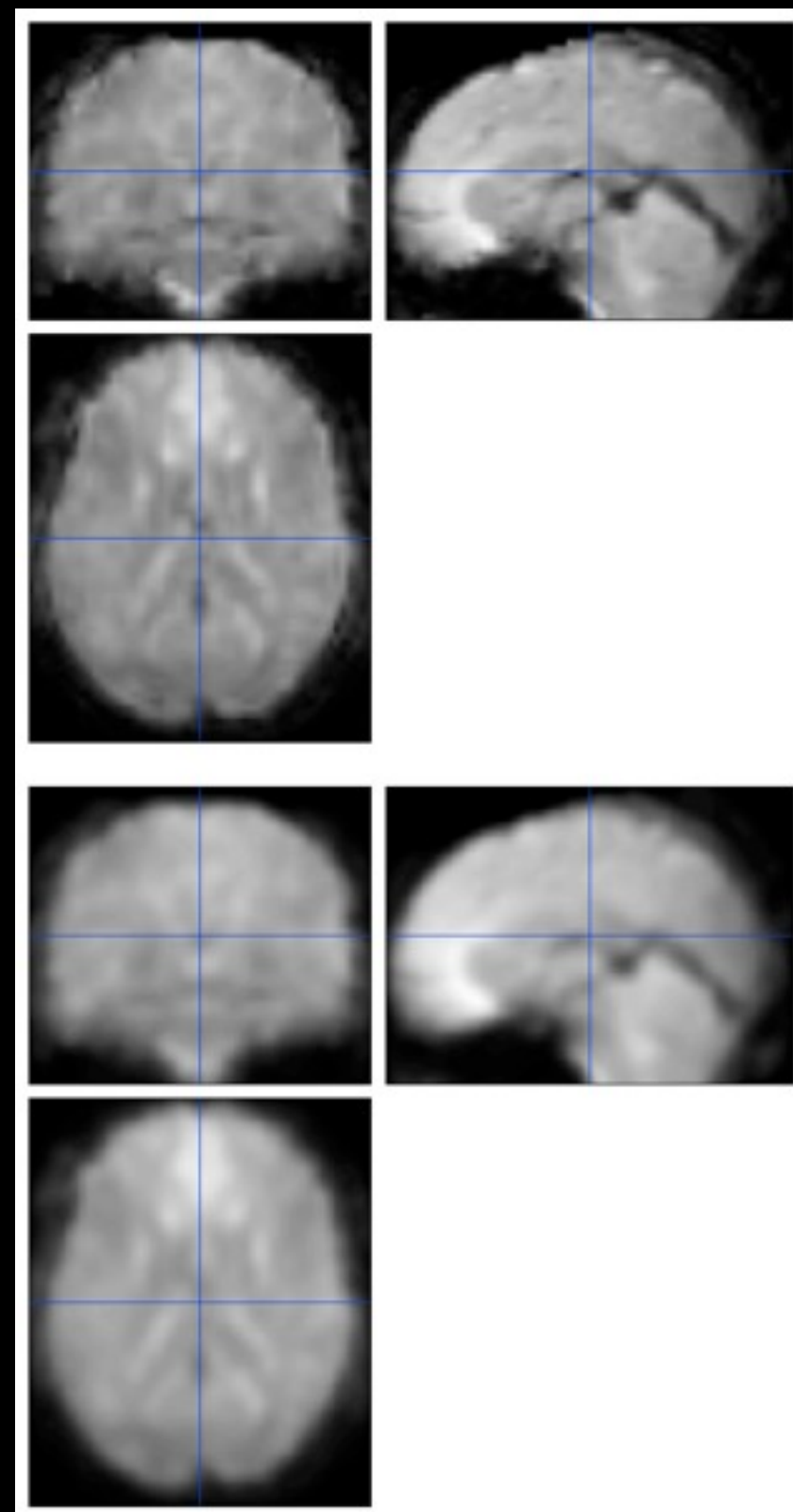
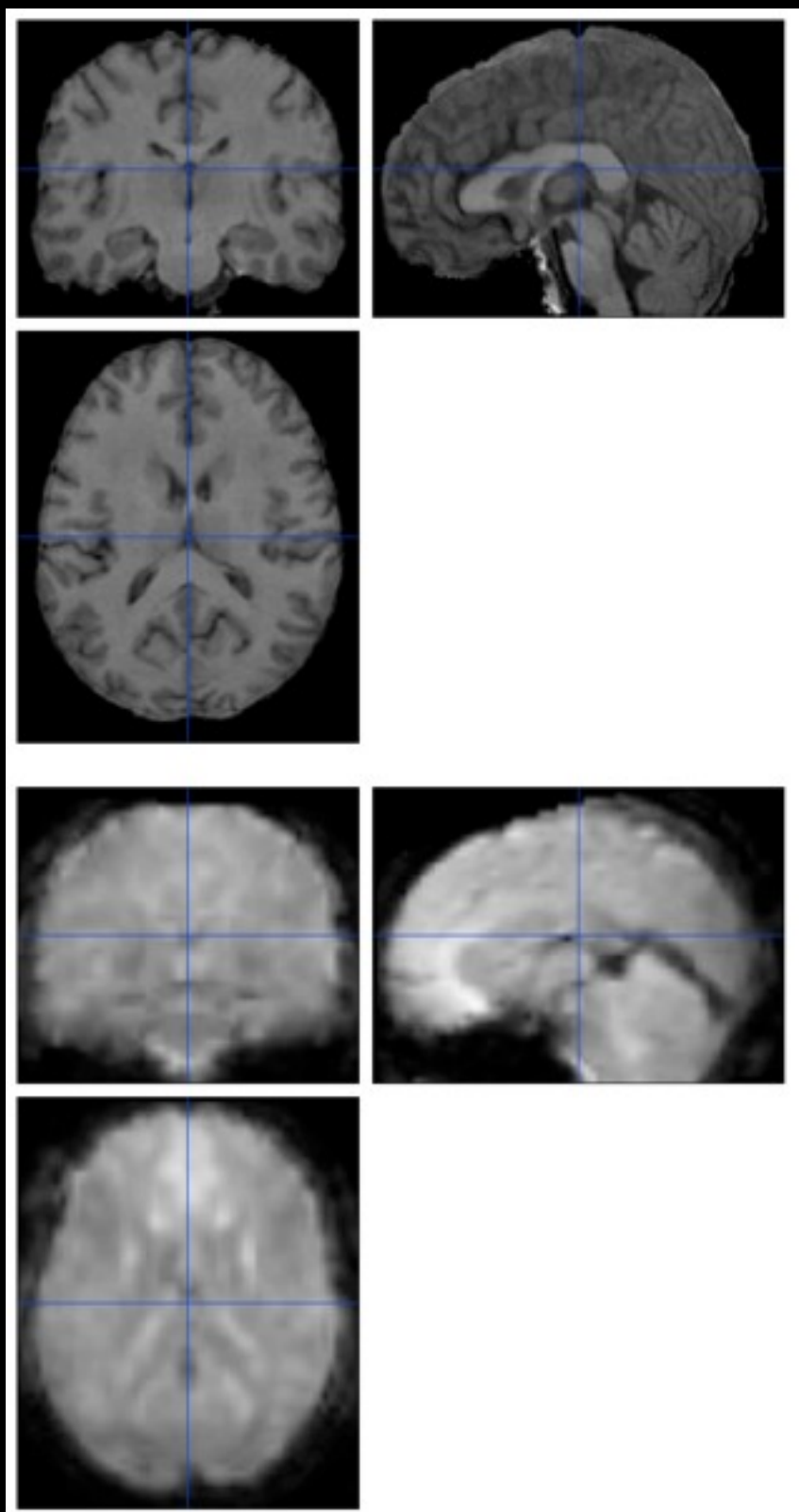


After

```
[subject]/  
  anatomy/  
    htloverlay.nii  
    htspgr.nii  
  func/  
    run_XX/  
      run_XX.nii  
      raprun_XX.nii
```

```
[subject]/  
  anatomy/  
    htloverlay.nii  
    htspgr.nii  
  func/  
    run_XX/  
      run_XX.nii  
      raprun_XX.nii  
      w3mm_raprun_XX.nii  
      s5mm_w3mm_raprun_XX.nii
```

Warped functionals Smoothed functionals



Any questions you may email
MethodsCoreHelp@umich.edu

And if you are presently in Psychiatry
your email will be answered.