

afni_proc.py
is your *friend*
or it will be soon

Example scripts from

AFNI_data6/FT_analysis

Also see <https://arxiv.org/abs/1709.07471>

Appendix has processing scripts

What the hell is afni_proc.py?

- It is a Python program that
 - Takes as input a series of “options” describing processing steps to use to analyze datasets *from one subject*
 - Produces as output a Unix tcsh script file that runs all the **AFNI** programs to do the processing
- Reasons to use afni_proc.py
 - It is flexible and compact, to produce a long script
 - The output script not only does the data analysis, but also saves various diagnostic tools and files
 - All intermediate output datasets are saved to help diagnose things when results are confusing or just plain wrong
 - You can get help from us on the **AFNI** message board

Where do afni_proc.py command lines/scripts come from?

- **Method #1:**
 - take an existing script (from yourself or a friend), and modify it to meet your needs
- **Method #2:**
 - find an approximate fit to what you want in examples, or from afni_proc.py's help, and modify to meet your needs
- **Method # $\sqrt{-1}$:**
 - use GUI uber_subject.py
- **Method #666:**
 - beg for help on the **AFNI** message board

Starting Simple - 1

```
afni_proc.py -subj_id FT \
  -dsets FT/FT_epi_r?+orig.HEAD \
  -copy_anat FT/FT_anat+orig \
  -tcats_remove_first_trs 2 \
  -regress_stim_times FT/AV*.txt \
  -regress_stim_labels Vrel Arel \
  -regress_basis 'BLOCK(20,1)' \
  -regress_est_blur_errts \
  -regress_opts_3dD \
  -gltsym 'SYM: Vrel -Arel' \
  -glt_label 1 V-A
```

Script file
s01.ap.simple

Starting Simple - 2

`afni_proc.py` `-subj_id FT`

ID will label
output files

```
-dsets FT/FT_epi_r?+orig.HEAD \
-copy_anat FT/FT_anat+orig \
-tcat_remove_first_trs 2 \
-regress_stim_times FT/AV*.txt \
-regress_stim_labels Vrel Arel \
-regress_basis 'BLOCK(20,1)' \
-regress_est_blur_errts \
-regress_opts_3dD \
      -gltsym 'SYM: Vrel -Arel' \
      -glt_label 1 V-A
```

Script file
s01.ap.simple

Starting Simple - 3

```
afni_proc.py -subj_id FT
```

EPI time
series
datasets
to analyze

```
-dsets FT/FT_epi_r?+orig.HEAD
```

```
-copy_anat FT/FT_anat+orig
```

```
-tcat_remove_first_trs 2
```

```
-regress_stim_times FT/AV*.txt
```

```
-regress_stim_labels Vrel Arel
```

```
-regress_basis 'BLOCK(20,1)'
```

```
-regress_est_blur_errts
```

```
-regress_opts_3dD
```

```
    -gltsym 'SYM: Vrel -Arel'
```

```
    -glt_label 1 V-A
```

Script file
s01.ap.simple

Starting Simple - 4

```
afni_proc.py -subj_id FT \
  -dsets FT/FT_epi_r?+orig.HEAD \
  -copy_anat FT/FT_anat+orig \
  -tcats_remove_first_trs 2 \
  -regress_stim_times FT/AV*.txt \
  -regress_stim_labels Vrel Arel \
  -regress_basis 'BLOCK(20,1)' \
  -regress_est_blur_errts \
  -regress_opts_3dD \
  -gltsym 'SYM: Vrel -Arel' \
  -glt_label 1 V-A
```

T1-weighted
anatomical
dataset for
alignment to
EPI datasets

Script file
s01.ap.simple

Starting Simple - 5

```
afni_proc.py -subj_id FT \
  -dsets FT/FT_epi_r?+orig.HEAD \
  -copy_anat FT/FT_anat+orig \
  -tcat_remove_first_trs 2 \
  -regress_stim_times FT/AV*.txt \
  -regress_stim_labels Vrel Arel \
  -regress_basis 'BLOCK(20,1)' \
  -regress_est_blur_errts \
  -regress_opts_3dD \
  -gltsym 'SYM: Vrel -Arel' \
  -glt_label 1 V-A
```

Stimulus
timing files,
labels, and
HRF model;
Note: timing
files have
start times
for each
task iteration

Script file
s01.ap.simple

Starting Simple - 6

```
afni_proc.py -subj_id FT \
  -dsets FT/FT_epi_r?+orig.HEAD \
  -copy_anat FT/FT_anat+orig \
  -tcats_remove_first_trs 2 \
  -regress_stim_times FT/AV*.txt \
  -regress_stim_labels Vrel Arel \
  -regress_basis 'BLOCK(20,1)' \
  -regress_est_blur_errts \
  -regress_opts_3dD \
  -gltsym 'SYM: Vrel -Arel' \
  -glt_label 1 V-A
```

Estimate
smoothness
of EPI noise
for group
analysis

Script file
s01.ap.simple

Starting Simple - 7

```
afni_proc.py -subj_id FT \
  -dsets FT/FT_epi_r?+orig.HEAD \
  -copy_anat FT/FT_anat+orig \
  -tcat_remove_first_trs 2 \
  -regress_stim_times FT/AV*.txt \
  -regress_stim_labels Vrel Arel \
  -regress_basis 'BLOCK(20,1)' \
  -regress_est_blur_errts \
  -regress_opts_3dD \
  -gltsym 'SYM: Vrel -Arel' \
  -glt_label 1 V-A \
```

Set up
General
Linear
Test
between 2
conditions

Script file
s01.ap.simple

A Real Case - 1

```
#!/usr/bin/env tcsh
```

```
# creation date: Thu Sep 10 14:27:59 2015
```

```
# set data directories
```

```
set top_dir      = FT
```

```
# set subject and group identifiers
```

```
set subj         = FT
```

```
set group_id     = horses
```

Not actually
used here

Code subject level information
into shell variables:

Makes it easier to re-use this afni_proc.py command

A Real Case - 2

Script file
s05.ap.uber

```
afni_proc.py -subj_id $subj \
  -script proc.$subj -scr_overwrite \
  -blocks tshift align tlrc volreg blur mask scale regress \
  -copy_anat $top_dir/FT_anat+orig \
  -dsets \
    $top_dir/FT_epi_r1+orig.HEAD \
    $top_dir/FT_epi_r2+orig.HEAD \
    $top_dir/FT_epi_r3+orig.HEAD \
  -volreg_align_to MIN_OUTLIER \
  -volreg_align_e2a \
  -volreg_tlrc_warp \
  -blur_size 4.0 \
  -tcat_remove_first_trs 2 \
  -regress_stim_times \
    $top_dir/AV1_vis.txt \
    $top_dir/AV2_aud.txt \
  -regress_stim_labels \
    vis aud \
  -regress_basis 'BLOCK(20,1)' \
  -regress_censor_motion 0.3 \
  -regress_opts_3dD \
    -jobs 2 \
    -gltsym 'SYM: vis -aud' -glt_label 1 V-A \
    -gltsym 'SYM: 0.5*vis +0.5*aud' -glt_label 2 mean.VA \
  -regress_compute_fitts \
  -regress_make_ideal_sum sum_ideal.1D \
  -regress_est_blur_epits \
  -regress_est_blur_errts \
  -regress_run_clustsim yes \
  -execute
```

The entire afni_proc.py
command:
Font size will be bigger
on following slides!

A Real Case – 3a

Script file
s05.ap.uber

```
afni_proc.py -subj_id $subj  
-script proc.$subj -scr_overwrite  
-blocks tshift align tlrc volreg blur mask scale regress  
-copy_anat $top_dir/FT_anat+orig  
-dsets  
    $top_dir/FT_epi_r1+orig.HEAD  
    $top_dir/FT_epi_r2+orig.HEAD  
    $top_dir/FT_epi_r3+orig.HEAD  
-volreg_align_to MIN_OUTLIER  
-volreg_align_e2a  
-volreg_tlrc_warp  
-blur_size 4.0
```

Set up which
processing
"blocks"
will be run

\
\
\
\
\
\
\
\
\
\
\
\

A Real Case – 3b

Script file
s05.ap.uber

```
afni_proc.py -subj_id $subj \
  -script proc.$subj -scr_overwrite \
  -blocks tshift align tlrc volreg blur mask scale regress \
  -copy_anat $top_dir/FT_anat+orig \
  -dsets \
    $top_dir/FT_epi_r1+orig.HEAD \
    $top_dir/FT_epi_r2+orig.HEAD \
    $top_dir/FT_epi_r3+orig.HEAD \
  -volreg_align_to MIN_OUTLIER \
  -volreg_align_e2a \
  -volreg_tlrc_warp \
  -blur_size 4.0 \
```

Select input
datasets
(anat and EPI)

A Real Case – 3c

Script file
s05.ap.uber

```
afni_proc.py -subj_id $subj \
  -script proc.$subj -scr_overwrite \
  -blocks tshift align tlrc volreg blur mask scale regress \
  -copy_anat $top_dir/FT_anat+orig \
  -dsets \
    $top_dir/FT_epi_r1+orig.HEAD \
    $top_dir/FT_epi_r2+orig.HEAD \
    $top_dir/FT_epi_r3+orig.HEAD \
  -volreg_align_to MIN_OUTLIER \
  -volreg_align_e2a \
  -volreg_tlrc_warp \
  -blur_size 4.0
```

Specify how
“volreg” step
will operate

A Real Case – 3d

Script file
s05.ap.uber

```
afni_proc.py -subj_id $subj \
  -script proc.$subj -scr_overwrite \
  -blocks tshift align tlrc volreg blur mask scale regress \
  -copy_anat $top_dir/FT_anat+orig \
  -dsets \
    $top_dir/FT_epi_r1+orig.HEAD \
    $top_dir/FT_epi_r2+orig.HEAD \
    $top_dir/FT_epi_r3+orig.HEAD \
  -volreg_align_to MIN_OUTLIER \
  -volreg_align_e2a \
  -volreg_tlrc_warp \
  -blur_size 4.0 \
```

Specify how
much spatial
blurring will
be used
(FWHM mm)

A Real Case – 4b

Script file
s05.ap.uber

```
-tcat_remove_first_trs 2
-regress_stim_times
    $stop_dir/AV1_vis.txt
    $stop_dir/AV2_aud.txt
-regress_stim_labels
    vis aud
-regress_basis 'BLOCK(20,1)'
-regress_censor_motion 0.3
-regress_opts_3dD
    -jobs 2
    -gltsym 'SYM: vis -aud' -glt_label 1 V-A
    -gltsym 'SYM: 0.5*vis +0.5*aud' -glt_label 2 mean.VA
-regress_compute_fitts
-regress_make_ideal_sum sum_ideal.1D
-regress_est_blur_epits
-regress_est_blur_errts
-regress_run_clustsim yes
-execute
```

Maximum motion
(in mm) to accept
between
successive TRs

A Real Case – 4d

Script file
s05.ap.uber

```
-tcat_remove_first_trs 2
-regress_stim_times
    $stop_dir/AV1_vis.txt
    $stop_dir/AV2_aud.txt
-regress_stim_labels
    vis aud
-regress_basis 'BLOCK(20,1)'
-regress_censor_motion 0.3
-regress_opts_3dD
    -jobs 2
    -gltsym 'SYM: vis -aud' -glt_label 1 V-A
    -gltsym 'SYM: 0.5*vis +0.5*aud' -glt_label 2 mean.VA
-regress_compute_fitts
-regress_make_ideal_sum sum_ideal.1D
-regress_est_blur_epits
-regress_est_blur_errts
-regress_run_clustsim yes
-execute
```

Other regression options:
Compute fitted model
(best fit to data);
Create sum of task ideal
response time series
(for display purposes)

A Real Case – 4e

Script file
s05.ap.uber

```
-tcat_remove_first_trs 2
-regress_stim_times
    $stop_dir/AV1_vis.txt
    $stop_dir/AV2_aud.txt
-regress_stim_labels
    vis aud
-regress_basis 'BLOCK(20,1)'
-regress_censor_motion 0.3
-regress_opts_3dD
    -jobs 2
    -gltsym 'SYM: vis -aud' -glt_label 1 V-A
    -gltsym 'SYM: 0.5*vis +0.5*aud' -glt_label 2 mean.VA
-regress_compute_fitts
-regress_make_ideal_sum sum_ideal.1D
-regress_est_blur_epits
-regress_est_blur_errts
-regress_run_clustsim yes
-execute
```

Estimate smoothness
of *noise* in the data:
From the dataset itself,
From the *residuals*
(=data-model fit).

And estimate cluster-
size thresholds from
smoothness estimates

A Real Case – 4f

Script file
s05.ap.uber

```
-tcat_remove_first_trs 2
-regress_stim_times
    $stop_dir/AV1_vis.txt
    $stop_dir/AV2_aud.txt
-regress_stim_labels
    vis aud
-regress_basis 'BLOCK(20,1)'
-regress_censor_motion 0.3
-regress_opts_3dD
    -jobs 2
    -gltsym 'SYM: vis -aud' -glt_label 1 V-A
    -gltsym 'SYM: 0.5*vis +0.5*aud' -glt_label 2 mean.VA
-regress_compute_fitts
-regress_make_ideal_sum sum_ideal.1D
-regress_est_blur_epits
-regress_est_blur_errts
-regress_run_clustsim yes
-execute
```

Run script after
it is created

Summarizing Results

- Each afni_proc.py **results** directory has a file with a name like **out.ss_review.SUBJECT-ID.txt**
 - Each line give some information about the data and the processing results, such as number of time points censored
- A command like this will generate a table with all these summary results from all subjects:

```
gen_ss_review_table.py  
-infile data_orig/sub*/*.results/out.ss_review.*.txt  
-tablefile UCLA.xls
```

- Next slide: what part of this output looks like in Excel
 - On Linux, you can use LibreOffice <http://www.libreoffice.org/>

Excel Snapshot Image of UCLA.xls

num TRs per run (censored)

O	P	Q	R	S	T	U	V
max censored	outlier limit	average outlier	num TRs above	num runs found	num TRs per	num TRs per	num TRs per
value_1	value_1	value_1	value_1	value_1	value_1	value_1	value_1
1.86277	0.02	0.0015669	3	1	242	222	20
0.542716	0.02	0.00133806	5	1	242	236	6
1.01995	0.02	0.00101045	2	1	242	231	11
0.970727	0.02	0.00113016	2	1	242	239	3
1.2554	0.02	0.00493115	17	1	242	220	22

Number of TRs with too many outlier values for each subject

Number of TRs found for each subject

Number of TRs censored for each subject

Another Valuable Summary: TSNR

TSNR average
value_1
183.74
218.72
190.983
223.144
194.404

- Measures magnitude of EPI signal strength divided by standard deviation of noise
- For 3 Tesla data, TSNR values near 180-200 are usual – with “standard” scanning parameters (TR 2-3s, voxel size 2-3mm)
- If some subject’s TSNR is much lower than others, examine the data to find the problem!

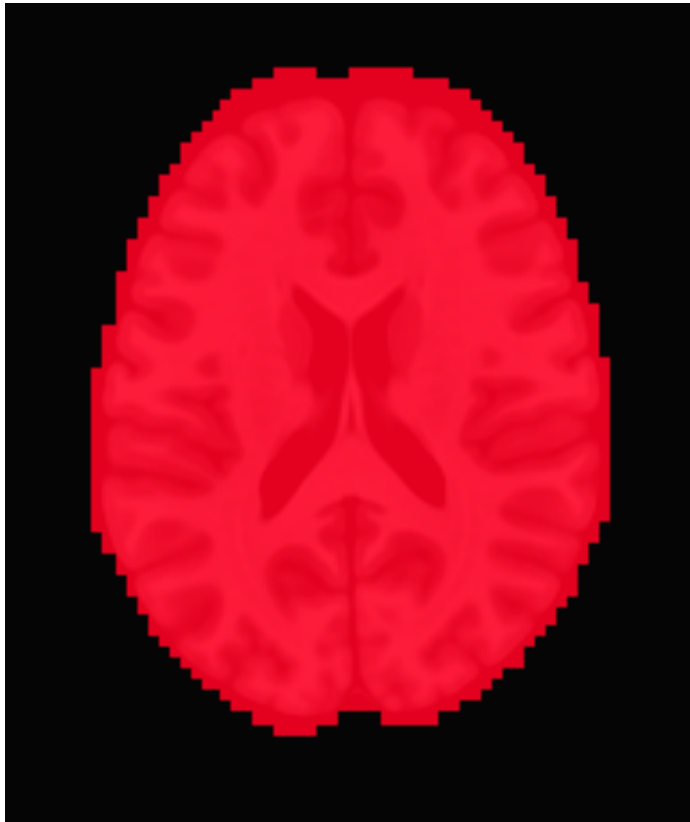
Masking for Group Analysis

- In each **results** directory, the output dataset **mask_epi_anat.SUBJECT-ID+tlrc.HEAD** is the 0-1 brain mask of the EPI dataset in the template space
- Combine all these masks into one mask dataset:

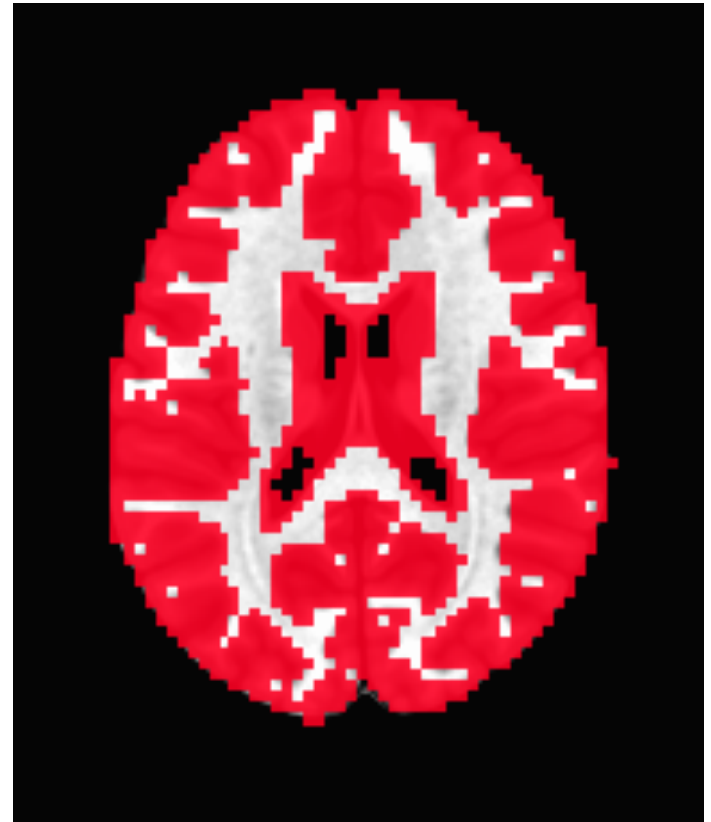
```
3dmask_tool -input  
  data_orig/sub-*/*.results/mask_epi_anat.*.HEAD  
  -prefix mask_all.nii -frac 0.8
```
- Another way: use a gray matter plus CSF mask from MNI template (*if* you have used nonlinear alignment to that template):

```
3dresample -master mask_all.nii -prefix mask_GC.nii  
  -rmode NN  
  -input ~/abin/MNI152_2009_template.nii.gz'[4]'
```

Whole Brain and GM+CSF Masks



73517 voxels



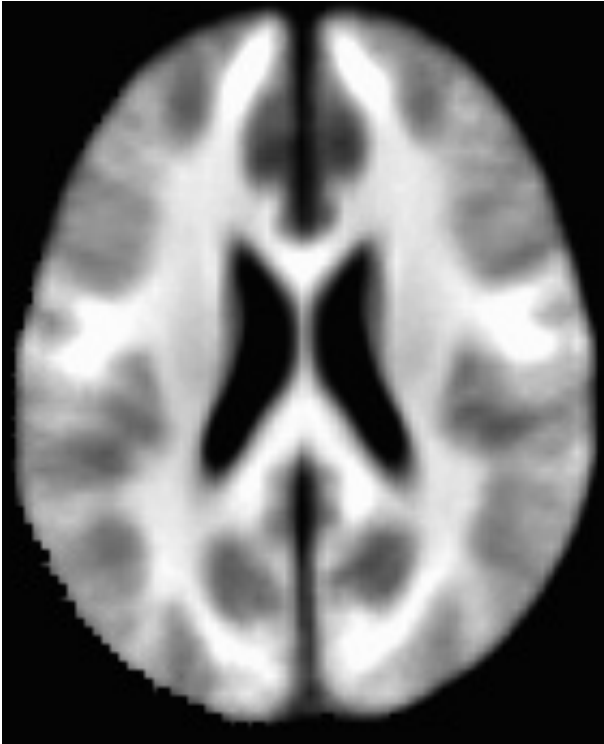
3 mm³ voxels

53104 voxels

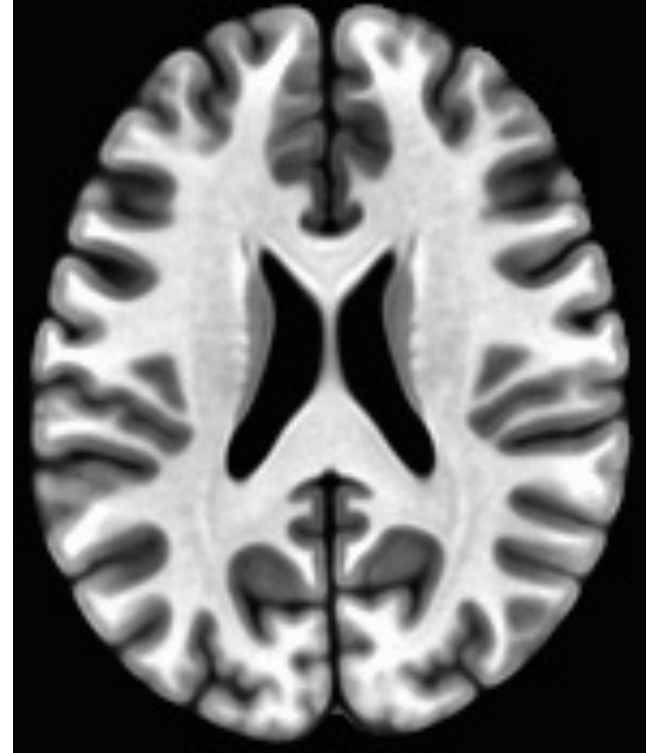
Nonlinear Warping to MNI Template

- afni_proc.py *can* do the nonlinear warping for you
 - But, nonlinear warping is slow (in fact, slowly slow)
 - If you need to re-rerun subject analysis, nonlinear warping will slow the re-run script down *a lot*
- Solution: do the nonlinear warping *before* using afni_proc.py, then supply the warping results so that afni_proc.py will skip doing the warping itself
- Mechanism: the **@SSwarper** script (tcsh)
 - Does Skull Stripping ("SS") and nonlinear warping
 - Base dataset is **MNI152_2009_template_SSW.nii.gz**
 - Nonlinearly warped, not too blurry

Two MNI Templates



MNI152_1mm_uni+tlrc
Affine alignments

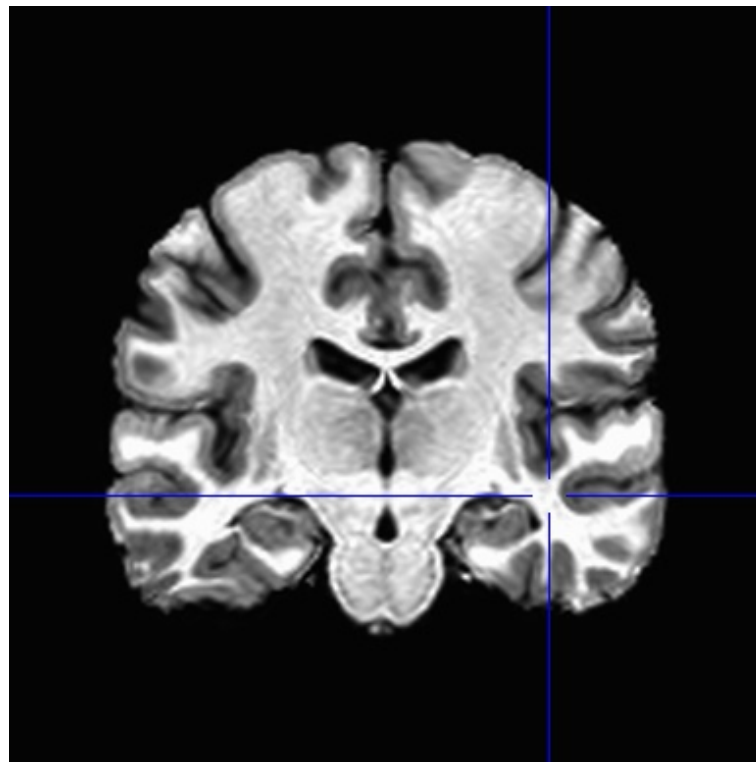
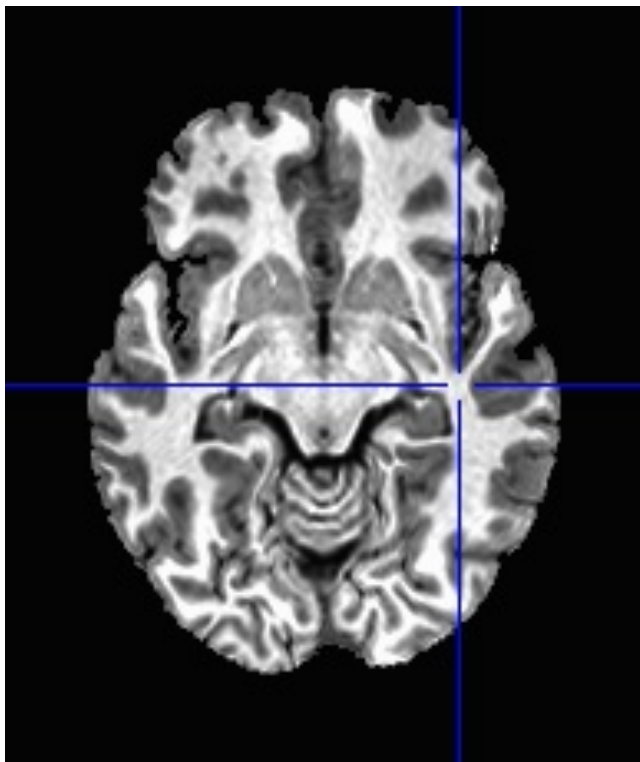


MNI152_2009_template_SSW.nii.gz
Nonlinear alignments

What @SSwarper Reads and Writes

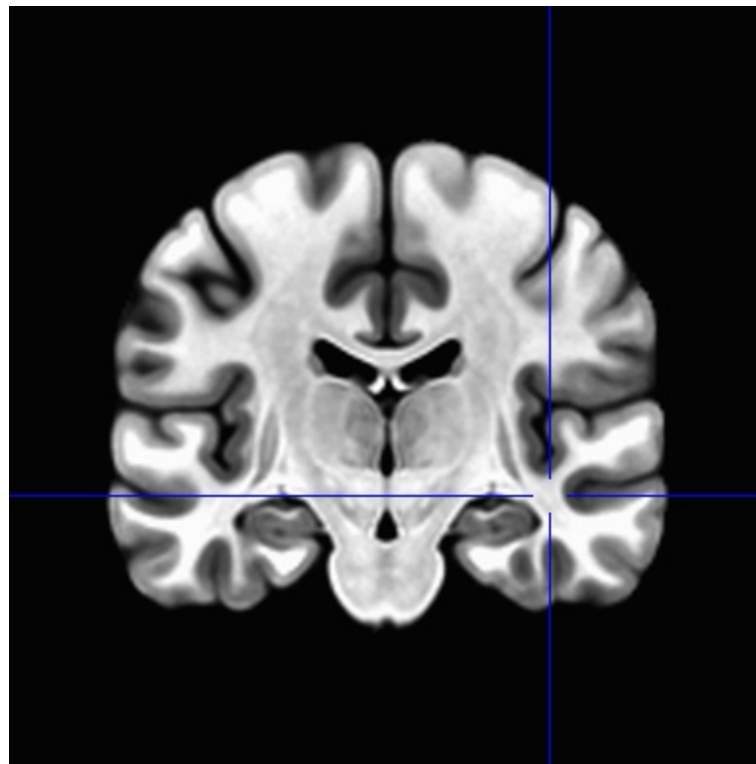
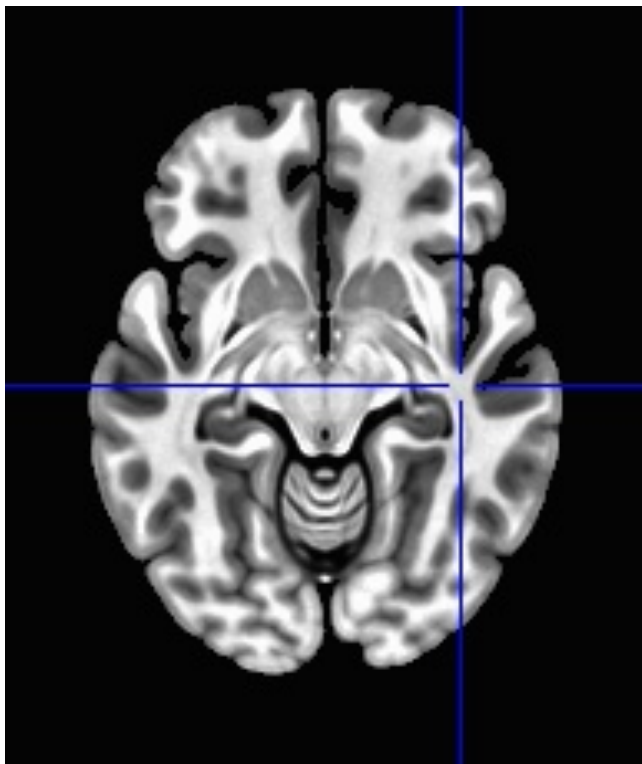
- Inputs:
 - T1-weighted anatomical image of subject (skull-on)
 - Subject ID code, for names of output files
- Outputs (subject ID = **sub007**):
 - **anatSS.sub007.nii**
 - skull-stripped dataset in original coordinates
 - **anatQQ.sub007.nii**
 - skull-stripped dataset, nonlinearly warped to MNI template
 - **anatQQ.sub007.aff12.1D**
 - affine matrix to transform original dataset to MNI template
 - **anatQQ.sub007_WARP.nii**
 - incremental warp from affine transformation to nonlinearly aligned dataset
- These files are needed for later use in `afni_proc.py`

@SSwarper Results



sub00440 from Beijing-Zang
in the FCON-1000 collection

MNI Template Slices



For comparison

Nonlinear Registration Script

- What follows is a script for doing nonlinear warping (registration) of *one* anatomical dataset to an MNI template
- In a real study, this script is run once for each subject
- Takes a long time, so the script should be submitted to a multi-node cluster

Nonlinear Registration - 1

```
#!/bin/tcsh
### This script nonlinear warps one anatomical dataset,
### taken from the anat_orig directory, to the MNI 2009
### nonlinear template (supplied with AFNI binaries), and
### puts the resulting files into anat_warped directory.
### The only command line argument is the subject ID
```

```
set subj = $argv[1]
```

```
set tempdir = .
```

```
# don't log AFNI programs in ~/.afni.log
```

```
# don't try any version checks
```

```
# don't auto-compress output files
```

```
setenv AFNI_DONT_LOGFILE YES
```

```
setenv AFNI_VERSION_CHECK NO
```

```
setenv AFNI_COMPRESSOR NONE
```

Nonlinear Registration - 2

```
### go to data directory
```

```
# topdir = directory above this Scripts directory
```

```
set topdir = `dirname $cwd`
```

```
cd $topdir/anat_orig
```

```
### create final output directories
```

```
mkdir -p $topdir/anat_warped
```

```
mkdir -p $topdir/anat_warped/snapshots
```

```
### create temp directory to hold work, and copy anat there
```

```
mkdir -p temp_$subj
```

```
cp anat_$subj.nii.gz temp_$subj
```

```
cd temp_$subj
```

Nonlinear Registration - 3

```
### process the anat dataset, using the AFNI script  
### that does the warping and skull-stripping
```

```
@SSwarper -input anat_${subj}.nii.gz -subid $subj \  
          -base MNI152_2009_template_SSW.nii.gz
```

```
# compress the output datasets
```

```
gzip -lv *.nii
```

```
### move the results to where they belong
```

```
# skull-stripped original, Q-warped dataset, and the warps
```

```
\mv -f anatSS.${subj}.nii.gz anatQQ.${subj}.nii.gz \  
    anatQQ.${subj}.aff12.1D anatQQ.${subj}_WARP.nii.gz \  
    $topdir/anat_warped
```

```
# snapshots for visual inspection
```

```
\mv -f *.jpg $topdir/anat_warped/snapshots
```

```
# delete the temporary directory
```

```
cd ..
```

```
\rm -rf temp_${subj}
```

```
exit 0
```

Nonlinear Registration - 4

Add these lines above `afni_proc.py` command:

```
set basedset = MNI152_2009_template_SSW.nii.gz
set tpath = `@FindAfnIDsetPath $basedset`
if( "$tpath" == '' ) then
    echo "***** @SSwarper -- Failed to find $basedset :("
    exit 1
endif
set basedset = $tpath/$basedset
```

Add these options to `afni_proc.py` command:

```
-copy_anat anat_warped/anatSS.${subj}.nii \
-tlrc_base $basedset \
-tlrc_NL_warp \
-tlrc_NL_warped_dsets \
$warpdir/anatQQ.${subj}.nii.gz \
$warpdir/anatQQ.${subj}.aff12.1D \
$warpdir/anatQQ.${subj}_WARP.nii.gz \
```