Advanced normalization tools (ANTs) show-and-tell

Outline

- Intro & scripts…
- How to build your own study-specific template
- Examples
- Pushing data into and out of template space
- Examples
- Normalization to standard space (e.g. MNI)

Intro

- Package of .sh and binaries
- Handles common image formats:

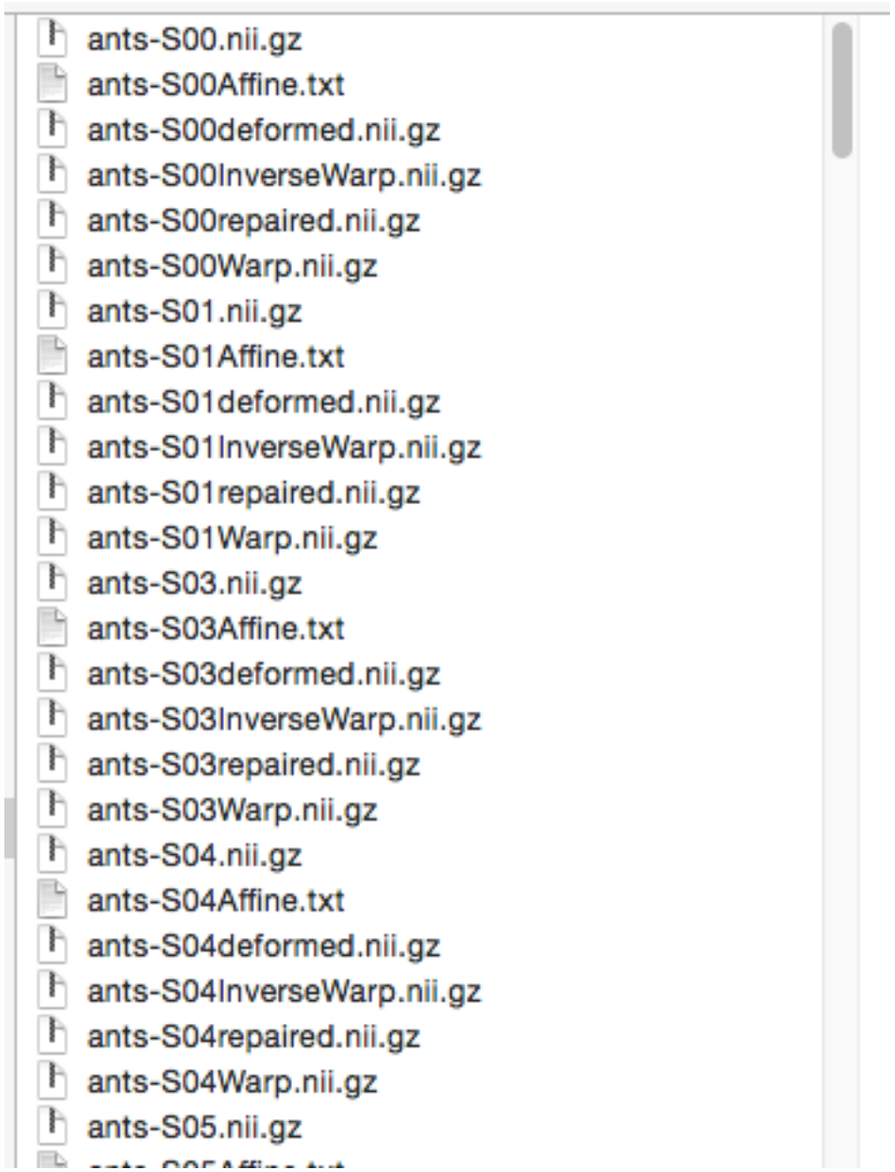
  .nii, .nii.gz, .img/.hdr, .img.gz, .jpg!

- http://stnava.github.io/ANTs/
- pdf of ‘documentation’: https://github.com/stnava/ANTsDoc/blob/master/ants2.pdf
- Install: Download precompiled binaries, compile yourself, already on neuro cluster (be careful about version)

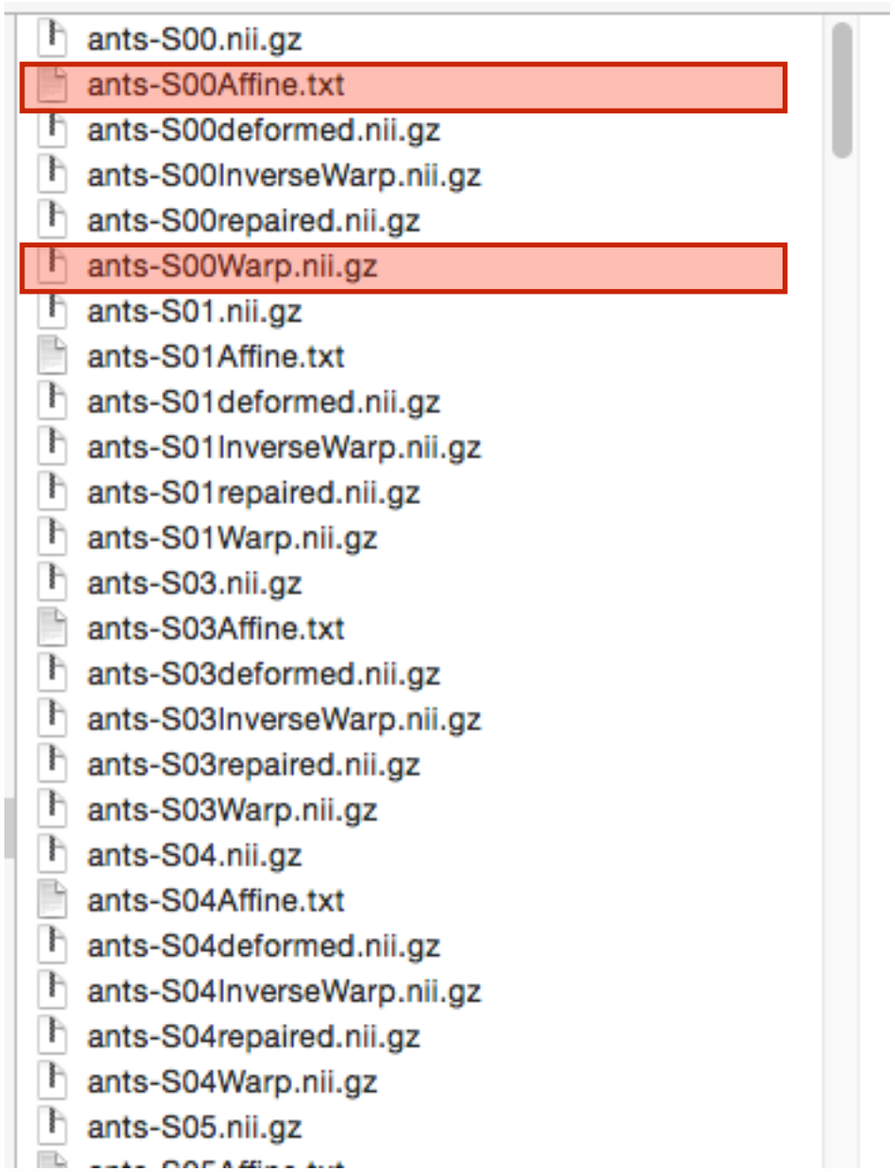
Building a template

- Before: skull strip
- great resource: http://miykael.github.io/nipype-beginner-s-guide/ANTS.html

Build template output

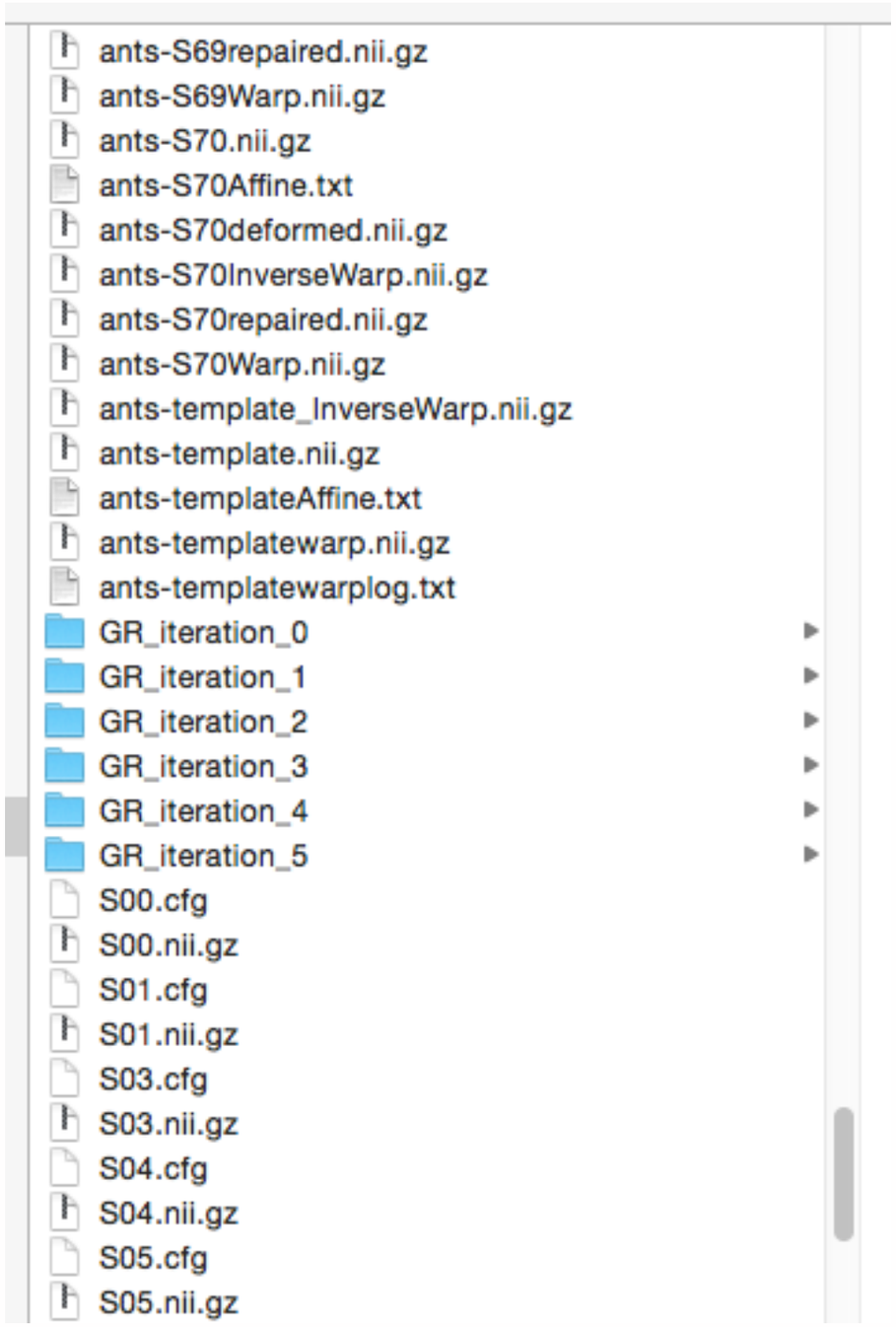


Build template output

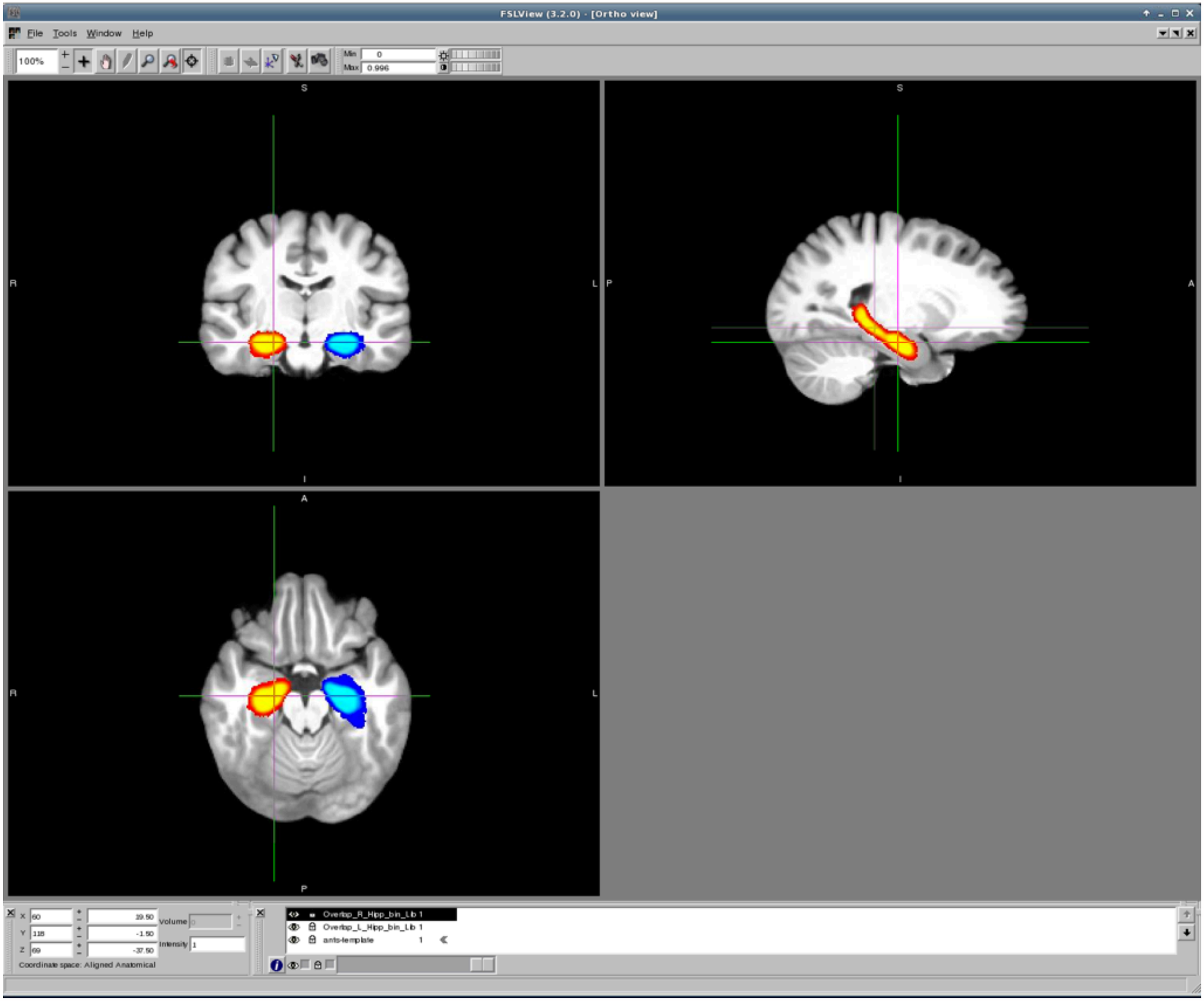


Build template output

Build template output



Example templates


FSLView (3.2.0) - [Ortho view]
File Tools Window Help
100%
Min 0
Max 0.996
S
R
L
I
P
A
Volume
Intensity 1
Coordinate space: Aligned Anatomical
Overlap_R_Hipp_bin_Lib 1
Overlap_L_Hipp_bin_Lib 1
ants-template 1

FSLView (3.2.0) - [Ortho view]
File Tools Window Help
100%
Min 0.7
Max 0.995
S
R
L
I
S
P
A
I
A
R
L
P
x 59 20.50
Y 118 -1.50
Z 68 -36.50
Volume 0
Intensity 0
Coordinate space: Aligned Anatomical
Overlap_R_Hipp_bin_Lib 1
Overlap_L_Hipp_bin_Lib 1
ants-template 1

Pushing data

- WarpImageMultiTransform!

ants_warp.sh

UNREGISTERED

ants_warp.sh | ants_inverse_warp.sh | encode_singlesubject_make_RvsK_vmps.m

```
#!/bin/bash

#example usage: source ~/scripts/ants_warp.sh orig_file output_file ants_directory ants_prefix ants_suffix ss


antspath=$HOME/antsbin
input_img=$1
output_img=$2
ants_dir=$3
ants_prefix=$4
suffix=$5
iss=$6

cmd="$antspath/WarpImageMultiTransform 3 $input_img $output_img \
-R $ants_dir/$ants_prefix"template.nii.gz" \
$ants_dir/$ants_prefix$iss$suffix"Warp.nii.gz" \
$ants_dir/$ants_prefix$iss$suffix"Affine.txt""

eval $cmd

```

Line 16, Column 1 | Tab Size: 4 | Shell Script (Bash)

ants_inverse_warp.sh — UNREGISTERED

ants_warp.sh | ants_inverse_warp.sh | encode_singlesubject_make_RvsK_vmps.m

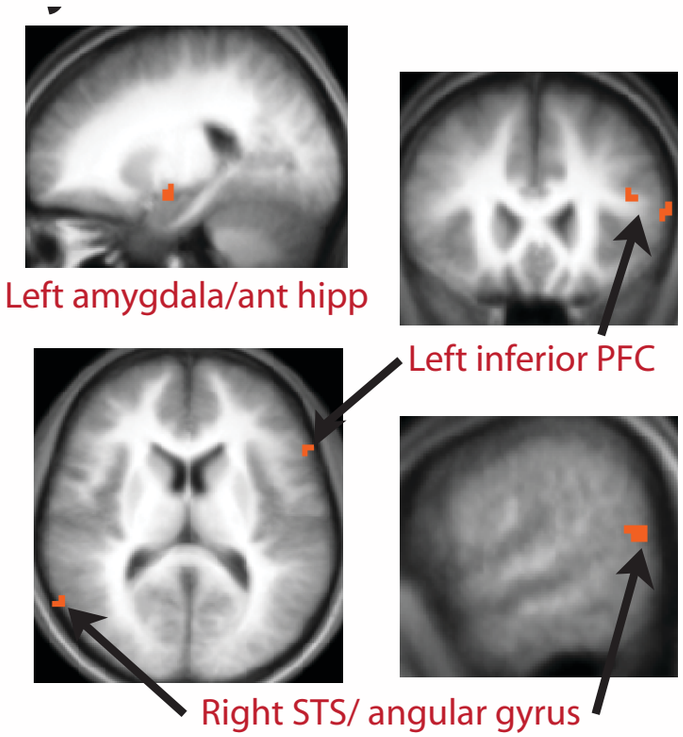
```
#!/bin/bash

#example usage: source ~/scripts/ants_inverse_warp.sh orig_file output_file ants_directory ants_prefix ants_suffix ss


antspath=$HOME/antsbin
input_img=$1
output_img=$2
ants_dir=$3
ants_prefix=$4
suffix=$5
iss=$6

cmd="$antspath/WarpImageMultiTransform 3 $input_img $output_img \
-R $ants_dir/$ants_prefix$iss$suffix".nii.gz" \
-i $ants_dir/$ants_prefix$iss$suffix"Affine.txt" \
$ants_dir/$ants_prefix$iss$suffix"InverseWarp.nii.gz""

eval $cmd

```

Line 16, Column 1 | Tab Size: 4 | Shell Script (Bash)

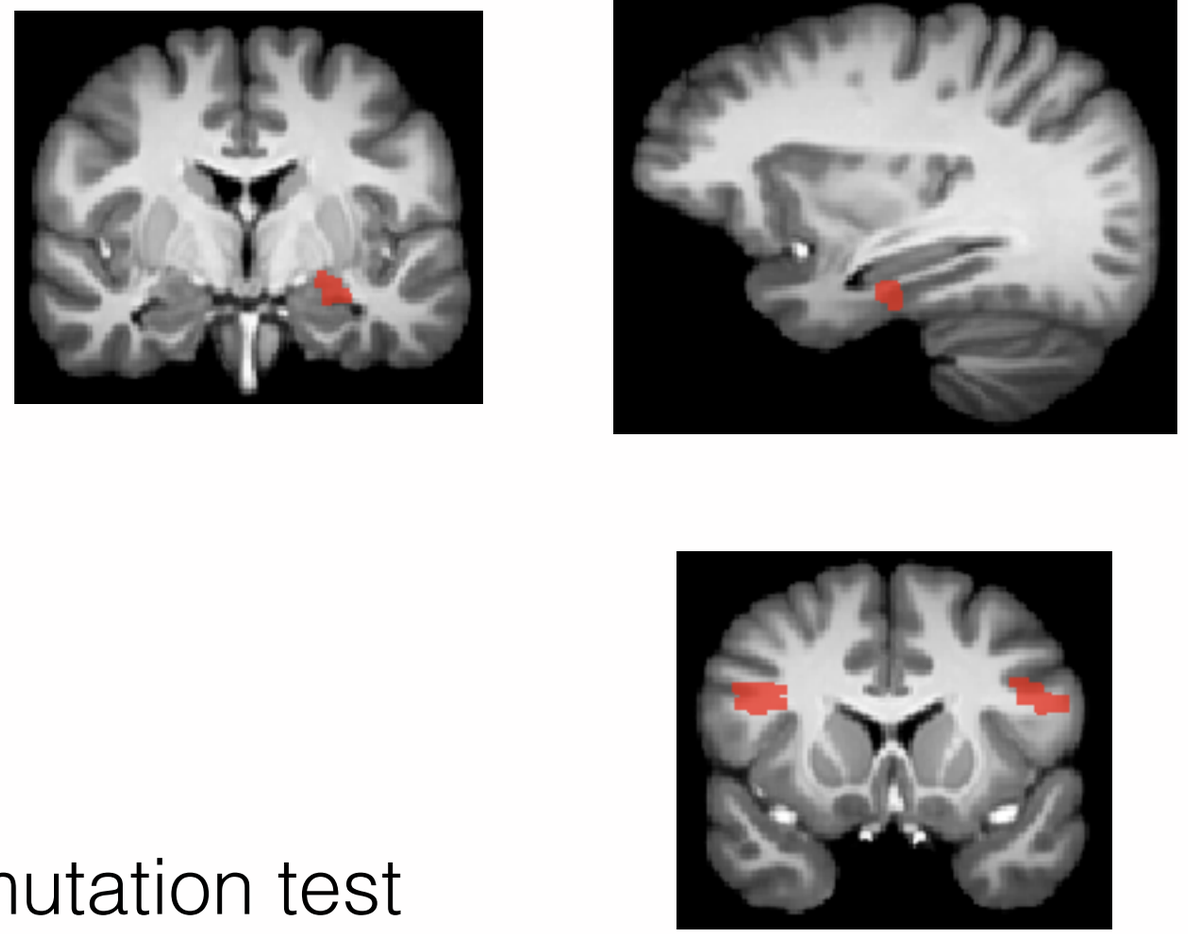
Examples

Examples

SPM



ANTs

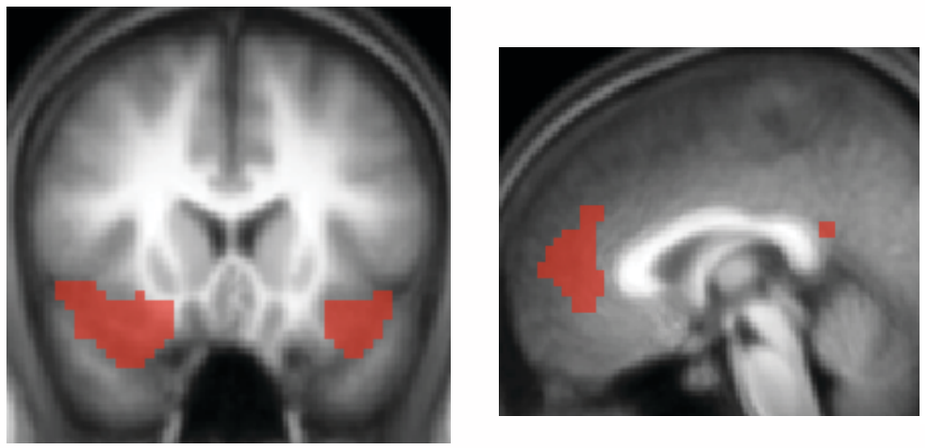


Both FWE corrected using permutation test

+4, -1 regions

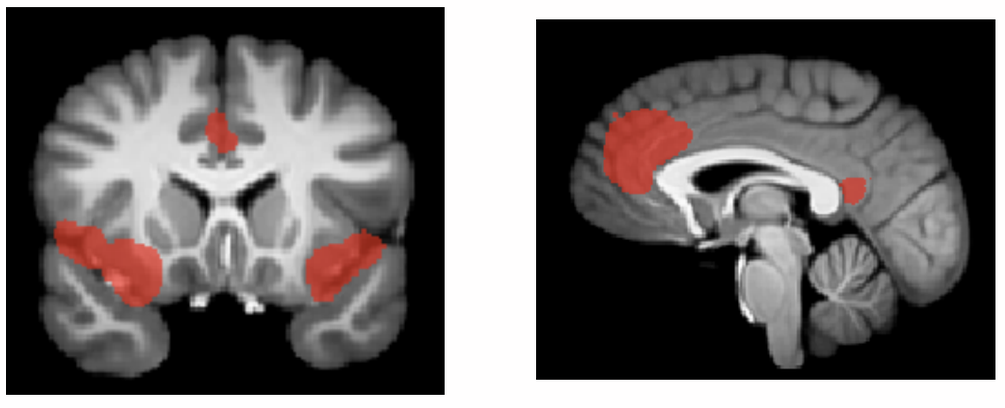
Examples

SPM



Mean correlation (z) > .25

ANTs



Mean correlation (z) > .4

Normalizing to standard space

- Can separately align study-specific template brain to standard

- Can include standard brain in study-specific template creation