



# FreeSurfer Tools

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# Resources

- Make sure you sign-in!
- Tutorial Slides \*currently\* available:
  - <http://rcs.bu.edu/examples/imaging>
  - Will be uploaded to standard rcs tutorial page too!
- Questions, Problems, Need Help?
  - [help@scc.bu.edu](mailto:help@scc.bu.edu)
  - [mhorn@bu.edu](mailto:mhorn@bu.edu)

# Notable FreeSurfer 7+ Features

- 7.0 (July 2020)
  - 20-25% faster
  - Better hires features ( $\geq 7T$ )
  - bias-field correction uses ANTS N4 instead of MNI N3
  - **fspalm** interface (FSL parametric analysis)
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/FsPalm>
  - **run\_samseg** whole-head segmentation (deep learning)
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/Samseg>

# Notable FreeSurfer 7+ Features

- 7.2 (July 2021)
  - TRACULA new 42-WM pathway
  - TRACULA auto-configure to BIDS
  - `mri_segment_hypothalamic_subunits`
    - GPU compatible
    - deep learning
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/HypothalamicSubunits>

# Notable FreeSurfer 7+ Features

- 7.3 (August 2022)
  - `dcmunpack` can now use `dcm2niix`
  - `MiDeFace`
    - image defacing pipeline
  - `mri_gradunwarp`
    - correct for image distortion (typical in high-field 7T)
  - `segment_subregions` (BETA)
    - thalamus, hippo-amygdala, brainstem,
    - deep learning
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/SubregionSegmentation>
  - `mri_synthstrip`
    - brain extraction tool for any image type
    - deep learning
    - <https://surfer.nmr.mgh.harvard.edu/docs/synthstrip/>
  - `mri_sclimbic_seg`
    - another tool to segmentation hypothalamic subunits
    - deep learning
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/ScLimbic>
  - `mri_synthseg`
    - contrast **INDEPENDENT** whole brain segmentation AND parcellation
    - neural network, GPU compatible
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/SynthSeg>

# Notable FreeSurfer 7+ Features

- 7.4 (May 2023)
  - recon-all-clinical
    - bundles mri\_synthseg, mri\_synthsr, mri\_synthdist
    - any modality, any contrast, any resolution (results vary...)
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all-clinical>
  - mri\_easyreg
    - new registration tool
    - more evolved version of mri\_synthmorph
    - deep learning
    - <https://surfer.nmr.mgh.harvard.edu/fswiki/EasyReg>

# Outline

- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- Freeview
- Registration Tools
- fMRI

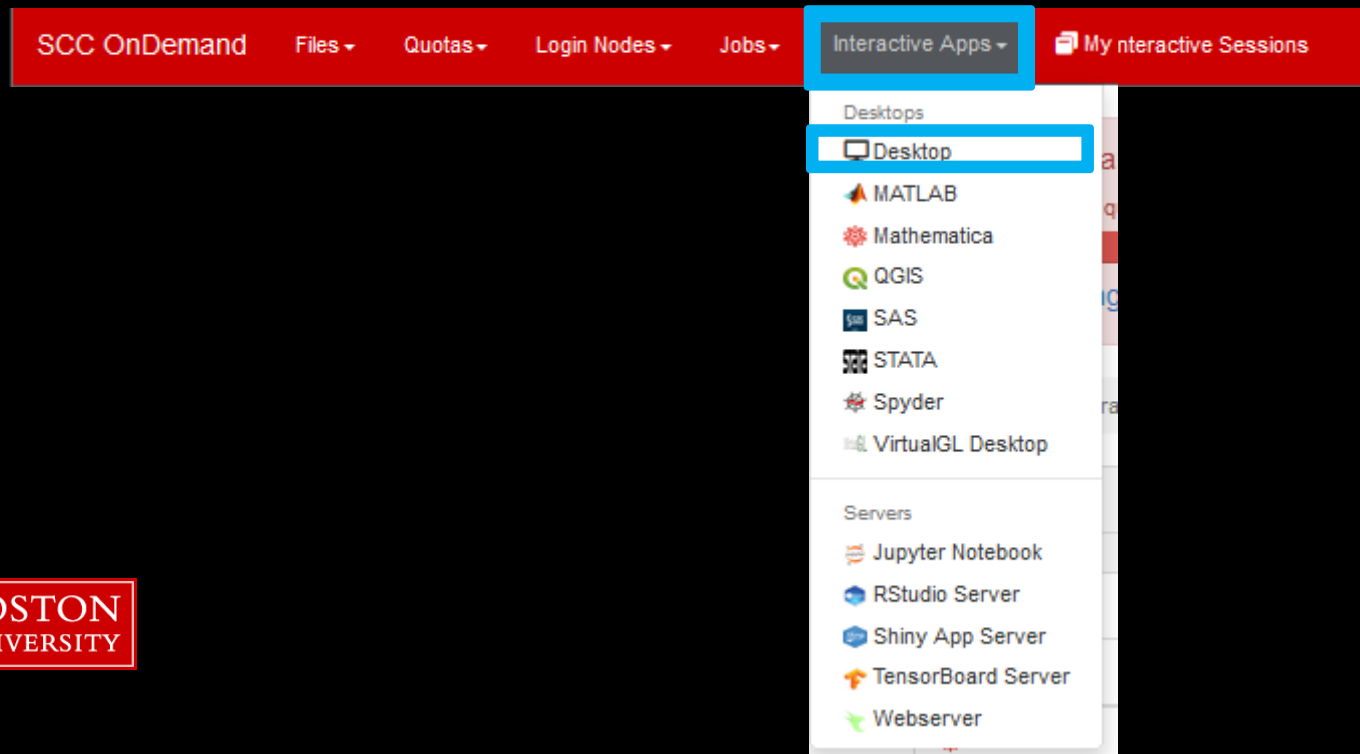
# Outline

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- Refresher
- Stats Tools
- Freeview
- Registration Tools
- fMRI



# Open an OnDemand session

1. Go to: [scc-ondemand.bu.edu](https://scc-ondemand.bu.edu)
2. Interactive Apps
3. Desktop



# Anybody Without an SCC Account?

- [scc-ondemand-tutorial.bu.edu](https://scc-ondemand-tutorial.bu.edu)
- username: tuta#
- password:

# Open an OnDemand session

**Desktop**  
This app will launch an interactive desktop on a compute node.

**List of modules to load (space separated)**  
 Select Modules

**Working Directory**  
 Select Directory  
The directory to start in. (Defaults to home directory.)

**Initial command to run**

**Number of hours**

**Number of cores**

**Number of gpus**

**Project**

**Extra qsub options**

I would like to receive an email when the session starts

\* The Desktop session data for this session can be accessed under the data root directory.

12 hours

4 core

project-ID

click launch!

11

# Open an OnDemand session

Desktop (6994379) 1 core | Running

Host: [>\\_scc-bb3](#) Delete

Created at: 2022-08-29 11:12:24 EDT

Time Remaining: 19 hours and 53 minutes

Session ID: [afff80fb-ca1f-44fd-a440-0637da849e84](#)

Compression Image Quality

0 (low) to 9 (high) 0 (low) to 9 (high)

[Connect to Desktop](#) View Only (Share-able Link)

**click Connect to Desktop!**

# Tutorial Setup

```
[t0@scc-1~]$ module load sublime
```

```
[t0@scc-1~]$ sublime /project/scv/examples/imaging/tut_fs2_scc/notes.txt
```

# Tutorial Setup

1. Copy the tutorial data to your local project space.

a. To see the SCC projects you're a part of:

```
[ ]$ groups
```

b. Copy the tutorial .zip file to your project directory:

```
[ ]$ cd /projectnb/YOUR_PROJECT/
```

```
[ ]$ cp /project/scv/examples/imaging/tut_fs2_scc/fs2.zip .
```

```
[ ]$ unzip fs2.zip
```

c. Set the SUBJECTS\_DIR path to our new directory:

```
[ ]$ cd fs2
```

```
[ ]$ module load freesurfer/6.0
```

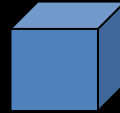
```
[ ]$ export SUBJECTS_DIR=$PWD
```

# Outline

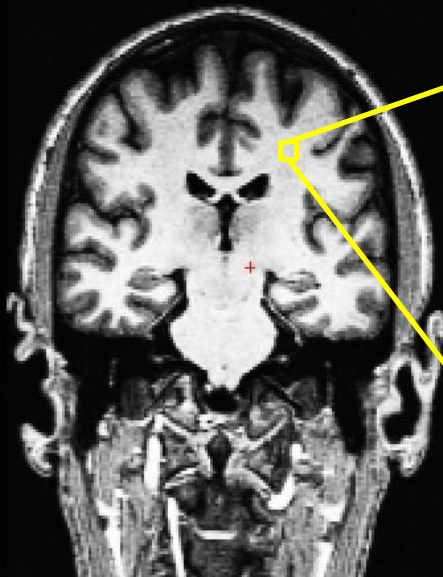
- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- Freeview
- Registration Tools
- fMRI

# Voxel

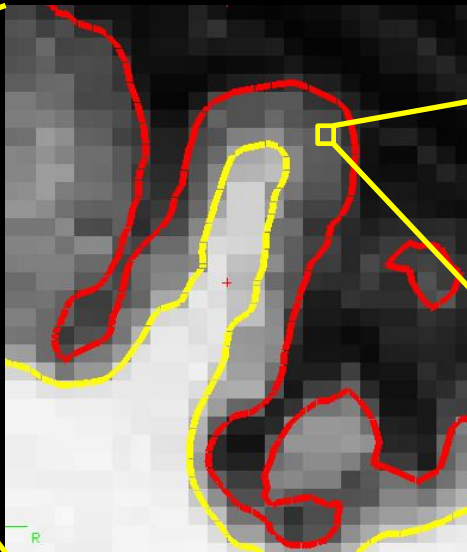
(volume element)



slice



75 voxels

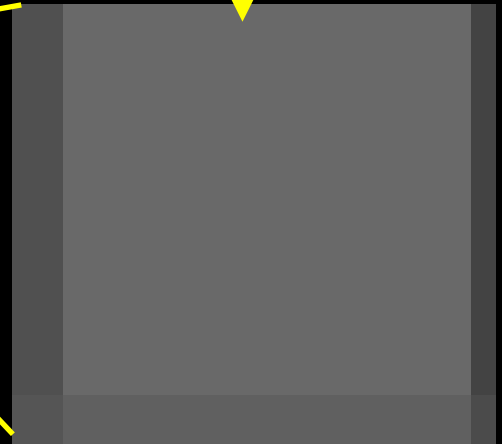


75 voxels

voxel



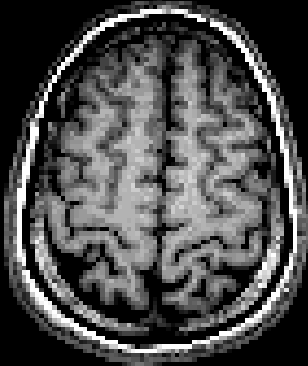
1 voxel



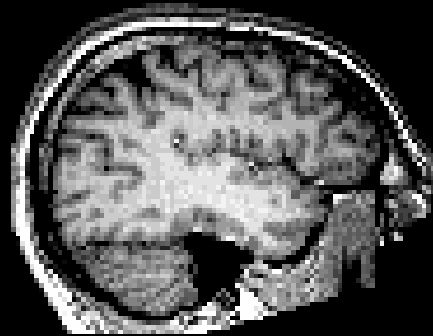
1 voxel



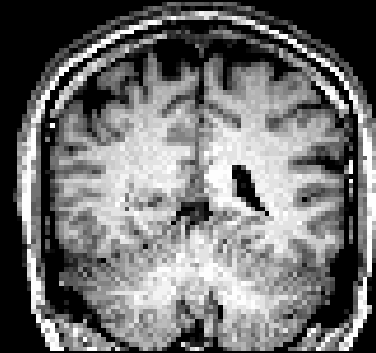
# Volumes



axial

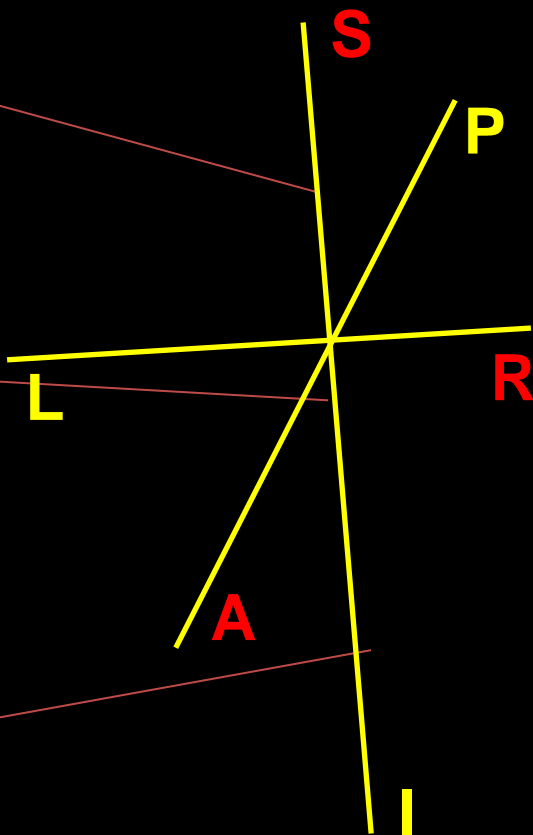
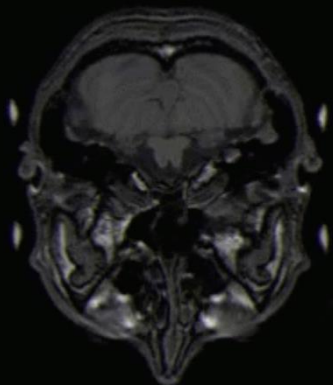
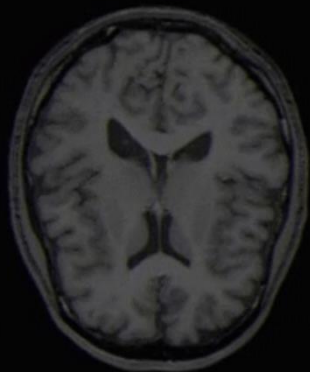
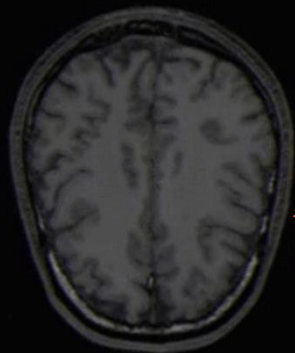


sagittal

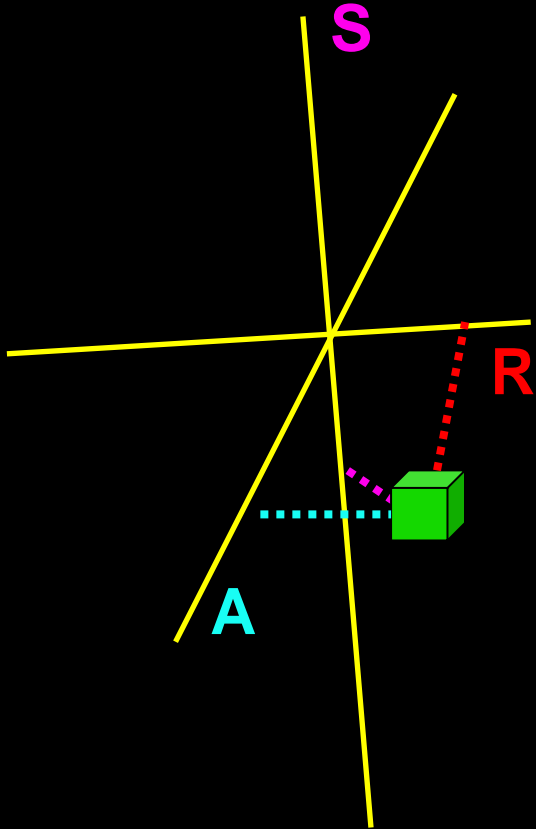


coronal

# Volumes

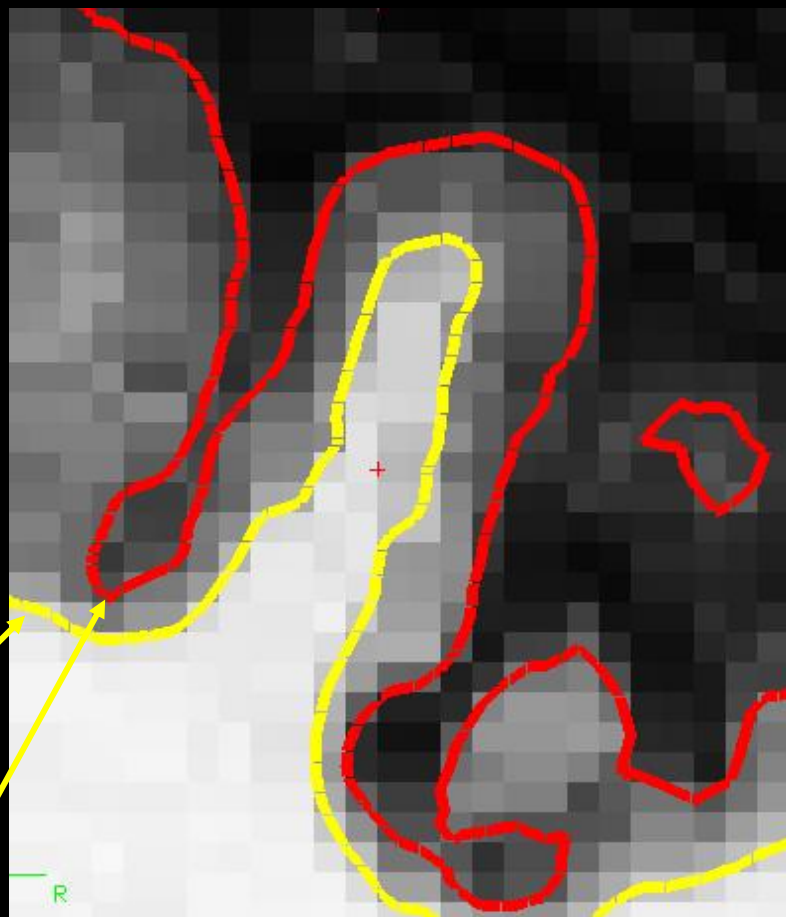
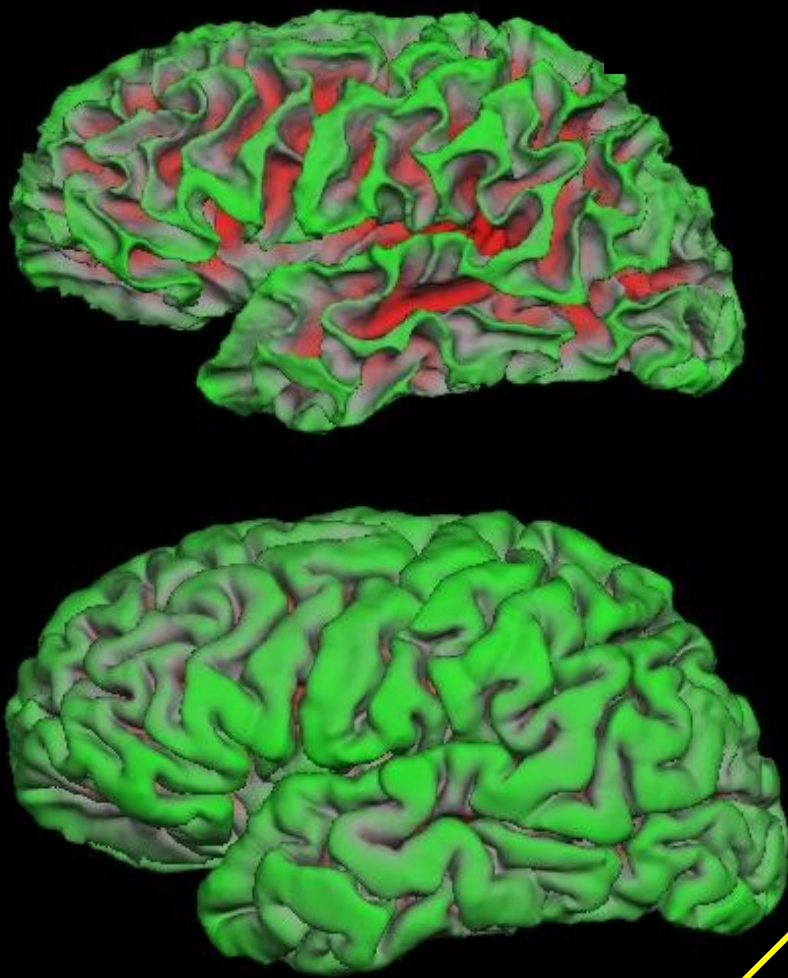


# Coordinate System



R	A	S
10.163	66.405	-29.582

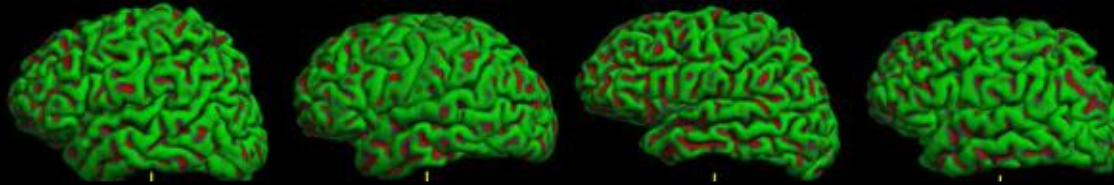
# Surface



surface

# Why FreeSurfer is Unique

Using a surface-based registration in a common space: 2001



- subject surfaces

- subject spheres

- fsaverage sphere

- fsROIs in subject surface

# Freeview

FreeView (/scratch/129142.1.ood/Fall\_2022/sub-2022/mri/T1.mgz)

File Edit View Layer Action Tools Help

**Volumes**

- T1

File name: /Fall\_2022/sub-2022/mri/T1.mgz

Mask: None

Opacity: 1.00

Smooth display

Color map: Grayscale

Window: 273.53

Level: 138.81

Min: 2.04

Max: 275.57

Use percentile

Clear background

Cursor		Mouse	
RAS	1.00, 0.00, 1.00	RAS	432.41, 122.19, 1.00
TkReg RAS (T1)	1.00, 0.00, 1.00	TkReg RAS (T1)	432.41, 122.19, 1.00
MNI305 (T1)	1.39, 0.16, 14.73	MNI305 (T1)	477.95, 137.22, -73.55
T1	23 [127, 127, 128]	T1	0 [-304, 127, 250]

# SUBJECTS\_DIR

- This is FreeSurfer variable path
- FreeSurfer commands default to this directory for inputs and outputs
- You will find yourself defining and redefining this path variable

# SUBJECTS\_DIR

sub-001/

sub-002/

sub-003/

sub-004/

sub-005/

sub-006/

sub-007/

sub-008/

sub-009/



# SUBJECTS\_DIR

sub-001/ → outputs

sub-002/

sub-003/

sub-004/

sub-005/

sub-006/

sub-007/

sub-008/

sub-009/

# Outputs

sub-001/

└─ label/

└─ mri/

└─ scripts/

└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/

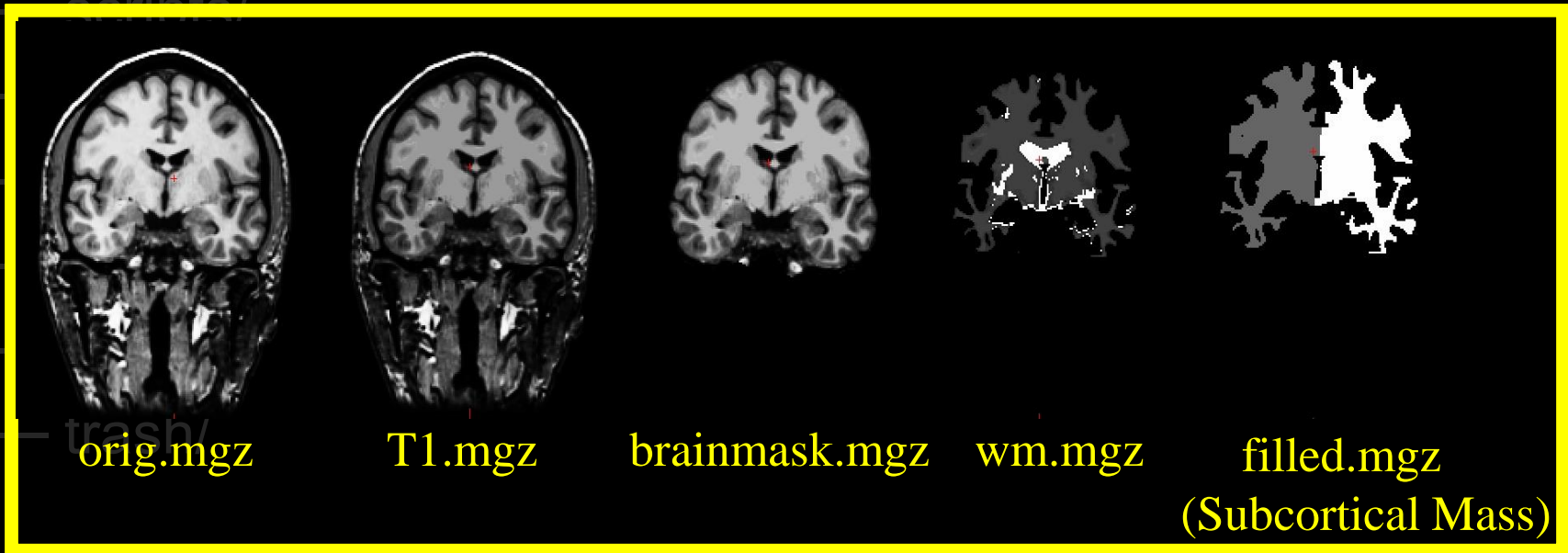
# Outputs

sub-001/

└─ label/

└─ mri/ ───────────────────▶

3D files (nifti)



# Outputs

sub-001/

└─ label/

└─ mri/transforms ────────────> transform files

└─ scripts/

└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/

- .lta Linear Transform Array
- .dat “legacy” transform file type
- .xfm “new” transform file type

# Outputs

sub-001/

└─ label/

└─ mri/

└─ **scripts/** → **Log files**

└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/

# Outputs

sub-001/

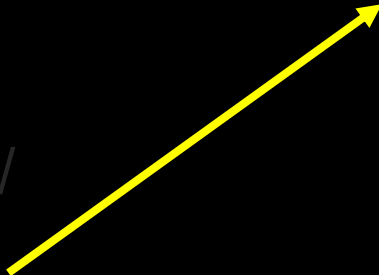
└─ label/

└─ mri/

└─ scripts/

└─ stats/

Output statistics



- aseg.stats – subcortical volumetric stats
- wmparc.stats – white matter segmentation volumetric stats
- lh.aparc.stats – left hemi Desikan/Killiany surface stats
- rh.aparc.stats – right hemi Desikan/Killiany surface stats
- lh.aparc.a2009.stats – left hemi Destrieux
- rh.aparc.a2009.stats – right hemi Destrieux

# Outputs

sub-001/

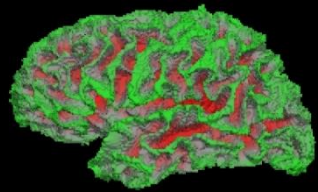
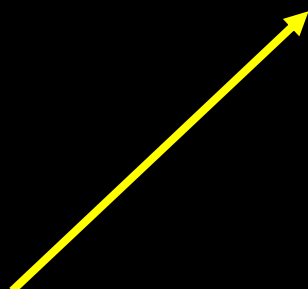
└─ label/

└─ mri/

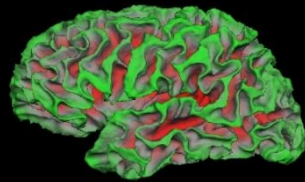
└─ scripts/

└─ stats/

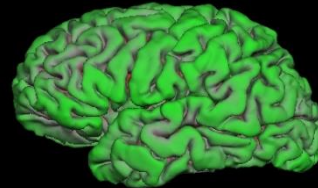
2D surface files



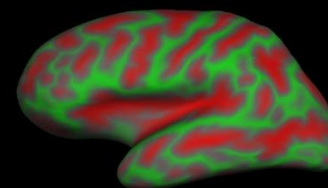
lh.orig



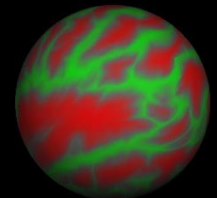
lh.white



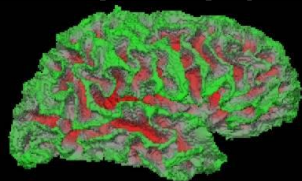
lh.pial



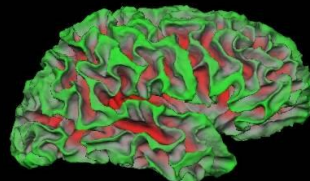
lh.inflated



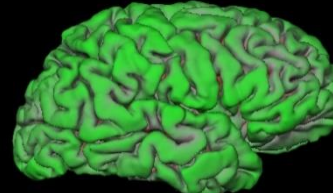
lh.sphere.reg



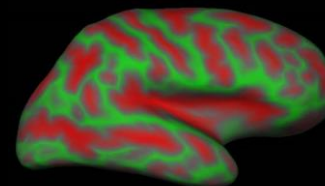
rh.orig



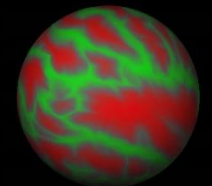
rh.white



rh.pial



rh.inflated



rh.sphere.reg

# Outputs

sub-001/

└─ label/

└─ mri/

└─ scripts/

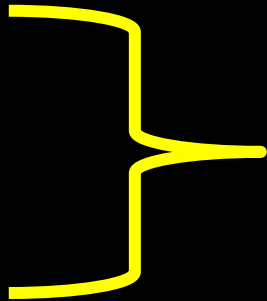
└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/



Temporary files, deleted, etc.



# Outputs

sub-001/

└─ label/ →

files for identifying ROIs for surfaces and volumes

└─ mri/

└─ scripts/

└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/

- labels
- color lookup tables
- annotations
- overlays

# Outputs

sub-001/

└─ label/ →

files for identifying ROIs for surfaces and volumes

└─ mri/

└─ scripts/

└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/

- **labels**
- color lookup tables
- annotations
- overlays

# Outputs

sub-001/

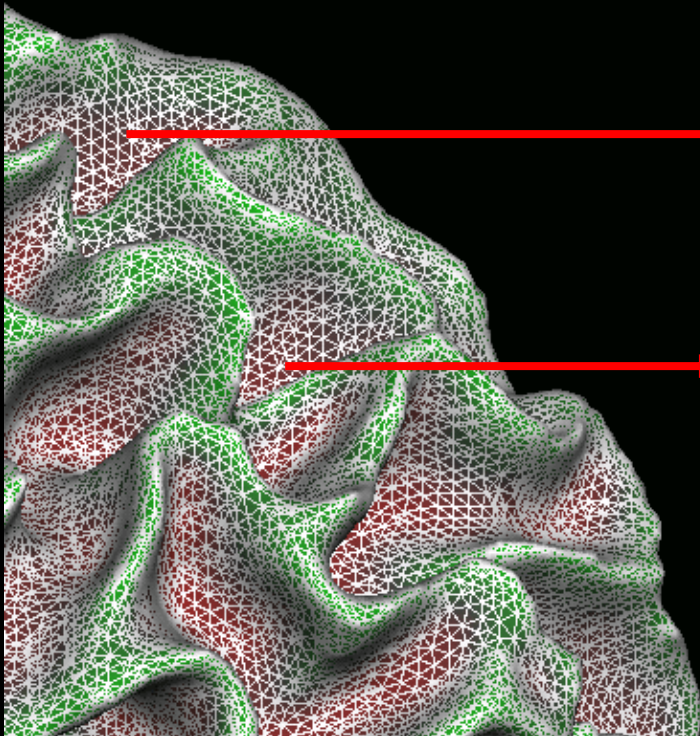
└─ label/ → • What's a label?

# Outputs

sub-001/

└─ label/ Example Label File: **lh.cortex.label**

surface



Vertex #

	R	A	S	
1	-22.796	-66.405	-29.582	0.00

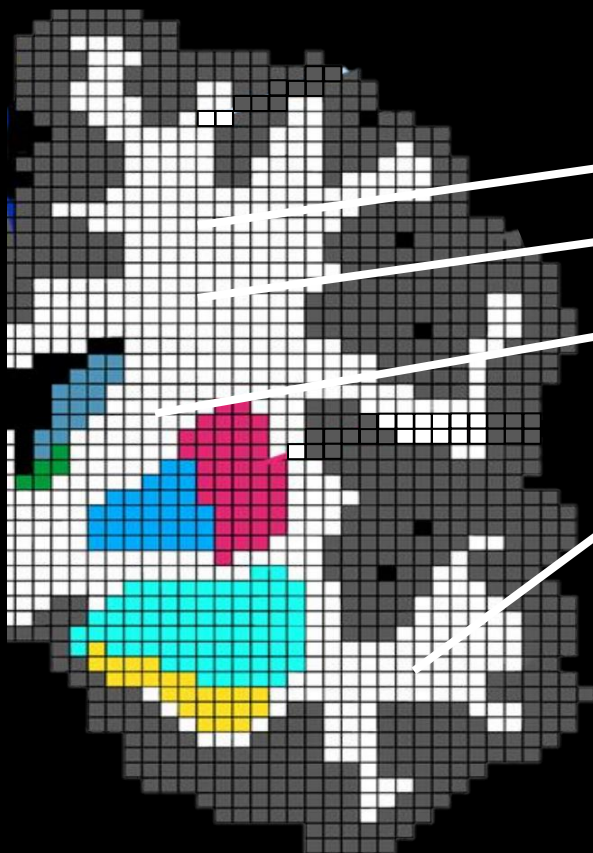
# Outputs

sub-001/

└─ label/

Example *Custom* Label File: **wm.label**

volume



Voxel #

R

A

S

4

-22.796

-66.405

-29.582

0.00

# Outputs

sub-001/

└─ label/ →

files for identifying ROIs for surfaces and volumes

└─ mri/

└─ scripts/

└─ stats/

└─ surf/

└─ tmp/

└─ touch/

└─ trash/

- labels
- **color lookup tables**
- annotations
- overlays

# Outputs

sub-001/

└─ label/ → • What's a color lookup table?

## FreeSurferColorLUT.txt

#No.	Label Name:	R	G	B	A
0	Unknown	0	0	0	0
1	Left-Cerebral-Exterior	205	62	78	0
2	Left-Cerebral-WM	245	245	245	0
3	Left-Cerebral-Cortex	205	62	78	0
...					

# Outputs

sub-001/

└─ label/ → • What's a color lookup table?

## FreeSurferColorLUT.txt

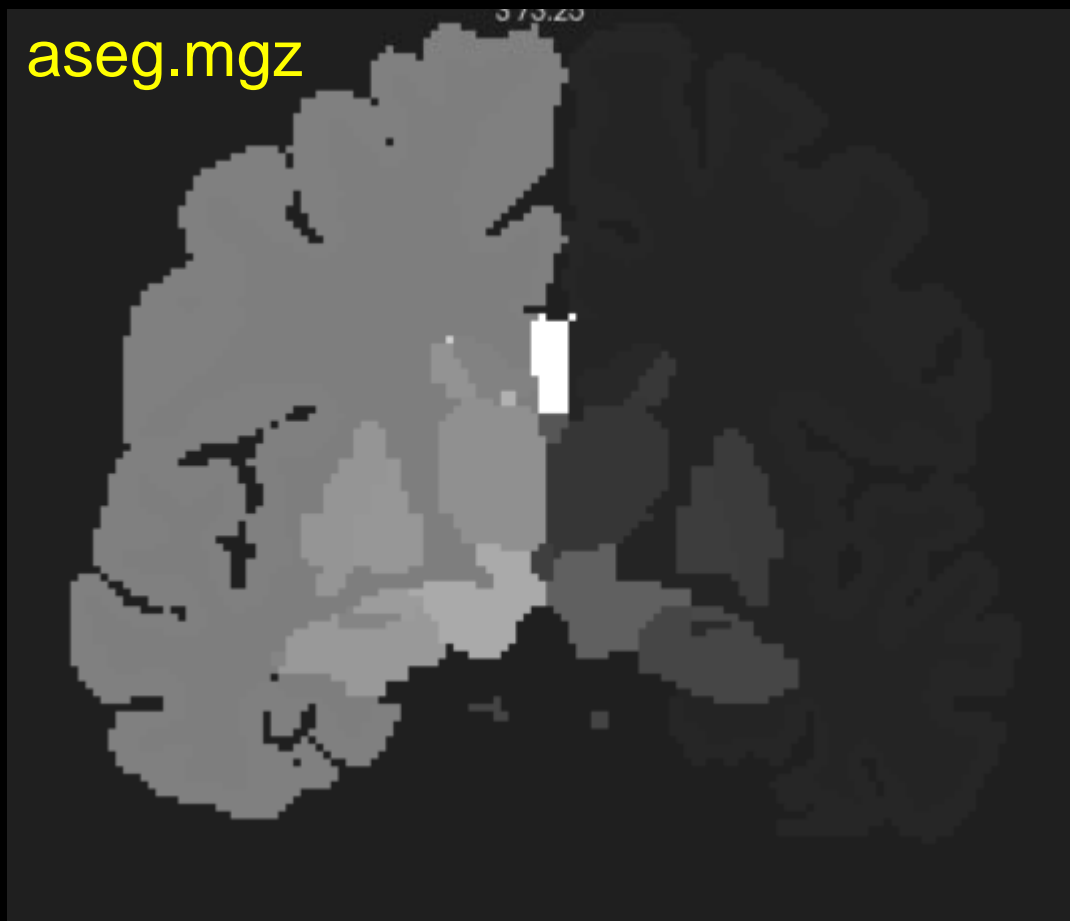
#No.	Label Name:	R	G	B	A
0	Unknown	0	0	0	0
1	Left-Cerebral-Exterior	205	62	78	0
2	Left-Cerebral-WM	245	245	245	0
3	Left-Cerebral-Cortex	205	62	78	0
...					



# Outputs

sub-001/

└─ label/ ──→ color lookup table



# Outputs

sub-001/

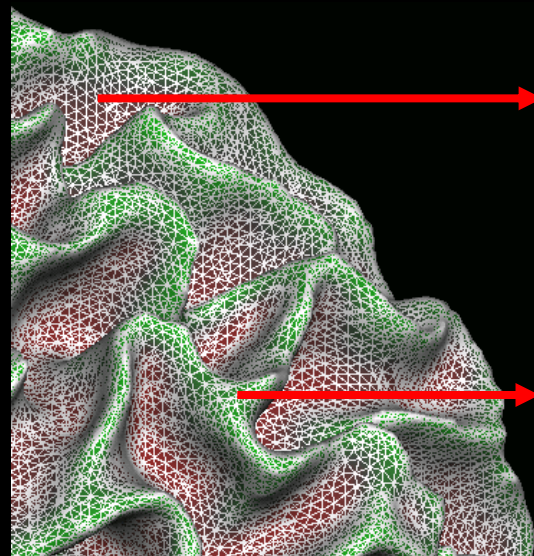
└─ label/ → • What's an annotation file?

# Outputs

sub-001/

└─ label/

surface

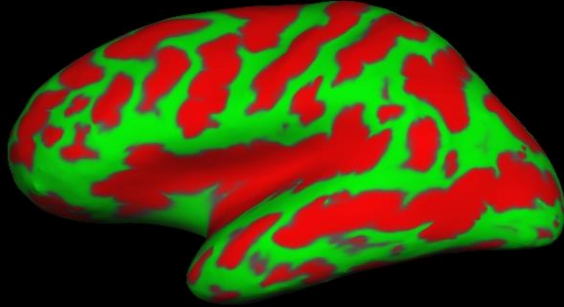


*Vertex*  
*Structure*

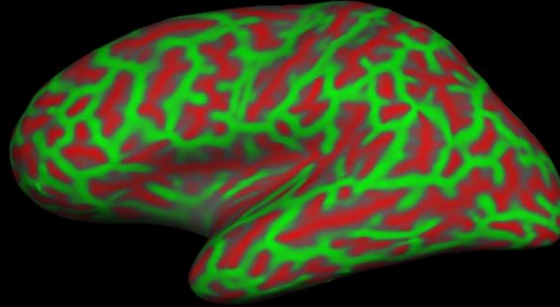
		R	A	S	R	G	B
1	Sulci	-22.796	-66.405	-29.582	255	0	0
2	Sulci	-22.273	-43.219	-26.134	255	0	0
...							
138	Gyri	-10.875	-28.201	-23.108	0	255	0
202	Gyri	-14.139	-11.422	-24.372	0	255	0
...							

# Outputs

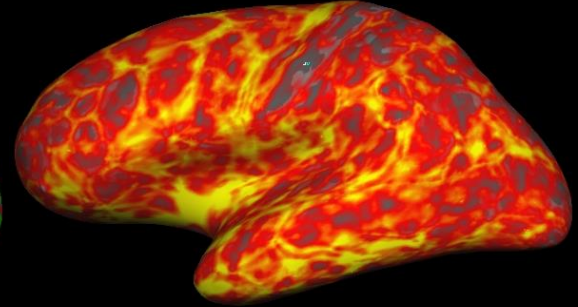
lh.sulc on inflated



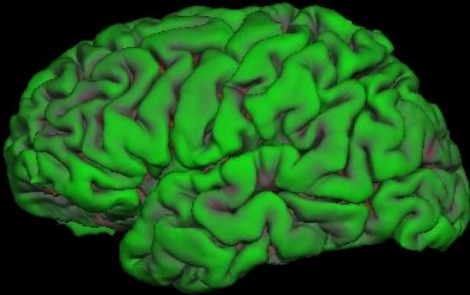
lh.curv on inflated



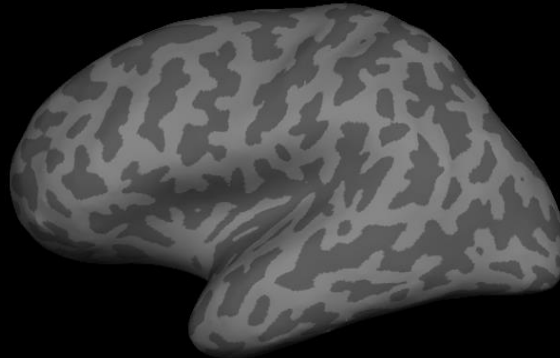
lh.thickness on inflated



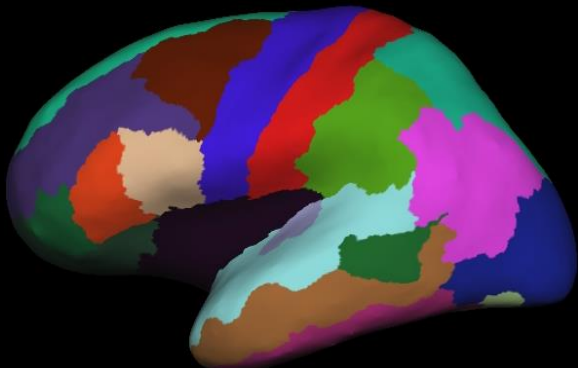
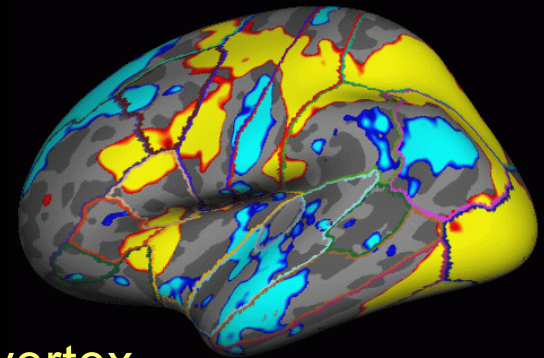
lh.sulc on pial



lh.curv on inflated



fMRI on inflated



lh.aparc.annot on inflated

- Value for each vertex
- Color indicates value
- Color: gray, red/green, heat, color table
- Rendered on any surface
- fMRI/Stat Maps too

# Outline

- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- Freeview
- Registration Tools
- fMRI

# Outline

- [mri\\_robust\\_template](#)
- [mri\\_nu\\_correct.mni](#)
- [talairach](#)
- [mri\\_normalize](#)
- [mri\\_watershed](#)
- [mri\\_em\\_register](#)
- [mri\\_ca\\_normalize](#)
- [mri\\_ca\\_register](#)
- [mri\\_remove\\_neck](#)
- [mri\\_ca\\_label](#)
- [mri\\_segstats](#)
- [mri\\_mask](#)
- [mri\\_segment](#)
- [mri\\_edit\\_wm\\_with\\_aseg](#)
- [mri\\_preteess](#)
- [mri\\_fill](#)
- [mri\\_tessellate](#)
- [mris\\_smooth](#)
- [mris\\_inflate](#)
- [mris\\_sphere](#)
- [mris\\_fix\\_topology](#)
- [mris\\_make\\_surfaces](#)
- [mris\\_surf2vol](#)
- [mris\\_register](#)
- [mrisp\\_paint](#)
- [mris\\_ca\\_label](#)
- [mris\\_anatomical\\_stats](#)
- [mri\\_aparc2aseg](#)
- [mri\\_convert](#)
- [brik2bfloat](#)
- [minc\\_to\\_bshort](#)
- [mri\\_annotation2label](#)
- [mri\\_convert\\_mdh](#)
- [mri\\_vol2label](#)
- [mri\\_label2label](#)
- [mri\\_label2vol](#)
- [mri\\_surf2surf](#)
- [mri\\_surf2vol](#)
- [mri\\_vol2roi](#)
- [mri\\_vol2surf](#)
- [mri\\_volcluster](#)
- [spm2bfloat](#)
- [mri\\_robust\\_template](#)
- [mri\\_motion\\_correct](#)
- [talairach](#)
- [talairach\\_mgh](#)
- [mri\\_normalize](#)
- [mri\\_watershed](#)
- [mri\\_segment](#)
- [mkxsubjreg](#)
- [mri\\_add\\_xform\\_to\\_header](#)
- [mri\\_average](#)
- [mri\\_ca\\_label](#)
- [mri\\_ca\\_normalize](#)
- [mri\\_ca\\_train](#)
- [mri\\_diff](#)
- [mri\\_em\\_register](#)
- [mri\\_fill](#)
- [mri\\_gdfglm](#)
- [mri\\_head](#)
- [mri\\_info](#)
- [mri\\_label\\_volume](#)
- [mri\\_make\\_register](#)
- [mri\\_make\\_template](#)
- [mri\\_matrix\\_multiply](#)
- [mri\\_ms\\_fitparms](#)
- [mri\\_parse\\_sdcmdir](#)
- [mri\\_partial\\_ribbon](#)
- [mri\\_probedicom](#)
- [mri\\_probe\\_ima](#)
- [mri\\_relabel\\_hypointensities](#)
- [mri\\_seghead](#)
- [mri\\_strip\\_skull](#)
- [mri\\_surfcluster](#)
- [mri\\_synthesize](#)
- [mri\\_tessellate](#)
- [mri\\_volsynth](#)
- [mri\\_wmfilter](#)
- [mri\\_xvolavg](#)
- [mri\\_tessellate](#)
- [mris\\_smooth](#)
- [mris\\_inflate](#)
- [mris\\_sphere](#)
- [mris\\_register](#)
- [mris\\_make\\_surfaces](#)
- [mris\\_sample\\_parcs](#)
- [mris\\_ca\\_label](#)
- [mris\\_ca\\_train](#)
- [mris\\_flatten](#)
- [mris2rgb](#)
- [mris\\_anatomical\\_stats](#)
- [mris\\_average\\_curvature](#)
- [mris\\_convert](#)
- [mris\\_curvature](#)
- [mris\\_euler\\_number](#)
- [mris\\_find\\_flat\\_regions](#)
- [mris\\_glm](#)
- [mris\\_make\\_average\\_surface](#)
- [mris\\_make\\_template](#)
- [mris\\_spherical\\_average](#)
- [mris\\_thickness](#)
- [mris\\_twoclass](#)
- [mrisp\\_paint](#)
- [nmovie](#)
- [optseq2](#)
- [paint](#)
- [stat\\_normalize](#)
- [vss-dump](#)

# Outline

```
[t0@scc-1~]$ mri_convert --help
```



**insert any command!**

<https://surfer.nmr.mgh.harvard.edu/fswiki>

# Outline

- Tutorial Setup (Hands-On)
- Refresher
- **Stats Tools**
- Freeview
- Registration Tools
- fMRI



# Stats Files

2. Move into the /stats directory and view some statistical outputs.

```
[ ]$ cd sub-001/stats  
[ ]$ less aseg.stats
```

ctrl+z

```
# TableCol 9 Units MR  
# TableCol 10 ColHeader normRange  
# TableCol 10 FieldName Intensity normRange  
# TableCol 10 Units MR  
# NRows 45  
# NTableCols 10  
# ColHeaders Index SegId NVoxels Volume_mm3 StructName normMean normStdDev normMin normMax normRange  
1 4 7021 7361.1 Left-Lateral-Ventricle 37.2639 12.2284 18.0000 89.0000 71.0000  
2 5 147 207.7 Left-Inf-Lat-Vent 52.7959 7.6945 31.0000 73.0000 42.0000  
3 7 14980 15503.3 Left-Cerebellum-White-Matter 87.1084 5.5066 38.0000 103.0000 65.0000
```

# Stats Files

3. Create a stats file for an individual Brodmann Area (BA) label:

```
[ ]$ mris_anatomical_stats -l lh.BA1_exvivo.label -f stats/lh.BA1_exvivo.stats sub-001 lh
[ ]$ less lh.BA1_exvivo.stats
```

ctrl+z

```
# TableCol 8 FieldName Integrated Rectified Gaussian Curvature
# TableCol 8 Units mm^-2
# TableCol 9 ColHeader FoldInd
# TableCol 9 FieldName Folding Index
# TableCol 9 Units unitless
# TableCol 10 ColHeader CurvInd
# TableCol 10 FieldName Intrinsic Curvature Index
# TableCol 10 Units unitless
# ColHeaders StructName NumVert SurfArea GrayVol ThickAvg ThickStd MeanCurv GausCurv FoldInd CurvInd
lh.BA1_exvivo.label 2964 1705 4717 2.246 0.614 0.103 0.029 25 3.1
```

# Stats Files

## 4. Parse statistics from multiple subjects:

```
[ ]$ cd $SUBJECTS_DIR
[ ]$ asegstats2table --subjects sub-001 sub-002 sub-003 --segno 11 17 18 --tablefile
aseg.vol.table
[ ]$ less aseg.vol.table
```

ctrl+z

Measure:volume	Left-Caudate	Left-Hippocampus	Left-Amygdala	BrainSegVol	BrainSegVolNotVent	lhCortexVol			
rhCortexVol	CortexVol	lhCerebralWhiteMatterVol	rhCerebralWhiteMatterVol	CerebralWhiteMatterVol	SubCortGrayVol	TotalGrayVol			
SupraTentorialVol	SupraTentorialVolNotVent	MaskVol	BrainSegVol-to-eTIV	M	askVol-to-eTIV	lhSurfaceHoles	rhSurfaceHoles	SurfaceHoles	EstimatedTotalIntraCranialVol
sub-001	3007.1	4486.1	1583.1	1211627.0	1192714.0	243655.171745	243146.507849	486801.679594	245090.0
	244506.0	489596.0	61235.0	674279.679594	1055109.0	1036196.0	1789539.0	0.770218	
	1.13759	18.0	20.0	38.0	1573097.115382				
sub-002	3007.1	4486.1	1583.1	1211627.0	1192714.0	243655.171745	243146.507849	486801.679594	245090.0
	244506.0	489596.0	61235.0	674279.679594	1055109.0	1036196.0	1789539.0	0.770218	
	1.13759	18.0	20.0	38.0	1573097.115382				
sub-003	3007.1	4486.1	1583.1	1211627.0	1192714.0	243655.171745	243146.507849	486801.679594	245090.0
	244506.0	489596.0	61235.0	674279.679594	1055109.0	1036196.0	1789539.0	0.770218	
	1.13759	18.0	20.0	38.0	1573097.115382				

# Stats Files

5. Use Linux's version of Excel to view stats:  
[)]\$ libreoffice --calc aseq.vol.table

	A	B	
1	Measure:volume	Left-Caudate	Left
2	sub-001	3007.1	
3	sub-002	3007.1	
4	sub-003	3007.1	
5			

Text Import - [stats.xlsx]

**Import**

Character set: Western Europe (ISO-8859-1)

Language: Default - English (USA)

From row: 1

**Separator Options**

Fixed width  Separated by

Tab  Comma  Semicolon  Space  Other

Merge delimiters

Text delimiter: "

**Other Options**

Quoted field as text  Detect special numbers

**Fields**

Column type:

	Standard	Standard	Standard	Standard
1	Measure:volume	Left-Lateral-Ventricle	Left-Inf-Lat-Vent	Left-Cer
2	sub-2022	17687.4	852.6	12917.3

Help OK Cancel

F	G	H
<u>SegVolNotVent</u>	<u>lhCortexVol</u>	<u>rhCortexVol</u>
1192714	243655.171745	243146.507849
1192714	243655.171745	243146.507849
1192714	243655.171745	243146.507849

# Stats Files

6. Parse white matter segmentation statistics (for region 3007 & 3021) from multiple subjects:

```
[ ]$ asegstats2table --subjects sub-001 sub-002 sub-003 --segno 3007 3021 --stats
wmparc.stats --tablefile wmparc.vol.table
[ ]$ libreoffice --calc wmparc.vol.table
```

A	B	C	D	E	F	G	H
Measure:volume	wm-lh-fusiform	wm-lh-pericalcarine	lhCerebralWhiteMatterVol	rhCerebralWhiteMatterVol	CerebralWhiteMatterVol	MaskVol	EstimatedTotalIntraCranialVol
sub-001	6709.8	3135.1	245090	244506	489596	1789539	1573097.115382
sub-002	6709.8	3135.1	245090	244506	489596	1789539	1573097.115382
sub-003	6709.8	3135.1	245090	244506	489596	1789539	1573097.115382

# FreeSurfer Color Lookup Table

7. View the FreeSurfer Color Lookup Table:

```
[ ]$ libreoffice $FREESURFER_HOME/FreeSurferColorLUT.txt  
  
exit
```

#No.	Label Name:	R	G	B	A
0	Unknown	0	0	0	0
1	Left-Cerebral-Exterior	70	130	180	0
2	Left-Cerebral-White-Matter	245	245	245	0
3	Left-Cerebral-Cortex	205	62	78	0
4	Left-Lateral-Ventricle	120	18	134	0
5	Left-Inf-Lat-Vent	196	58	250	0

# aparctats2table

```
[t0@scc-1 ~]$ aparctats2table --help
```

**REQUIRED: --hemi=lh OR --hemi=rh**

# Outline

- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- **Freeview**
- Registration Tools
- fMRI



# Freeview

8. Open a volume in Freeview with predefined colormap and opacity:

```
[ ]$ cd $SUBJECTS_DIR/sub-001
```

```
[ ]$ freeview mri/aseg.mgz mri/aseg.mgz:colormap=heat mri/aseg.mgz:colormap=jet:opacity=0.2
```

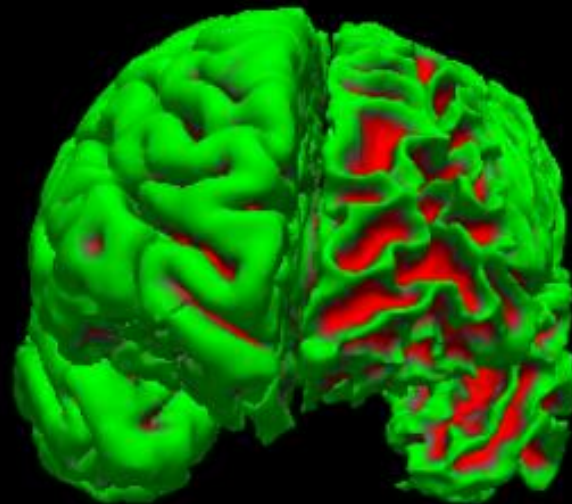
```
|  
ctrl+c
```



# Freeview

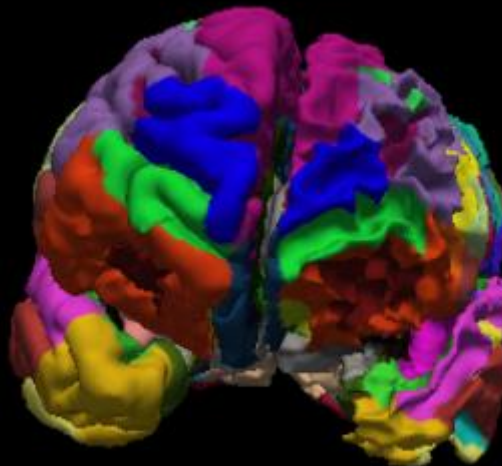
9. Open surfaces for left hemisphere white matter and right hemisphere gray matter:  
[]\$ freeview -f surf/lh.white surf/rh.pial --viewport 3d

ctrl+c



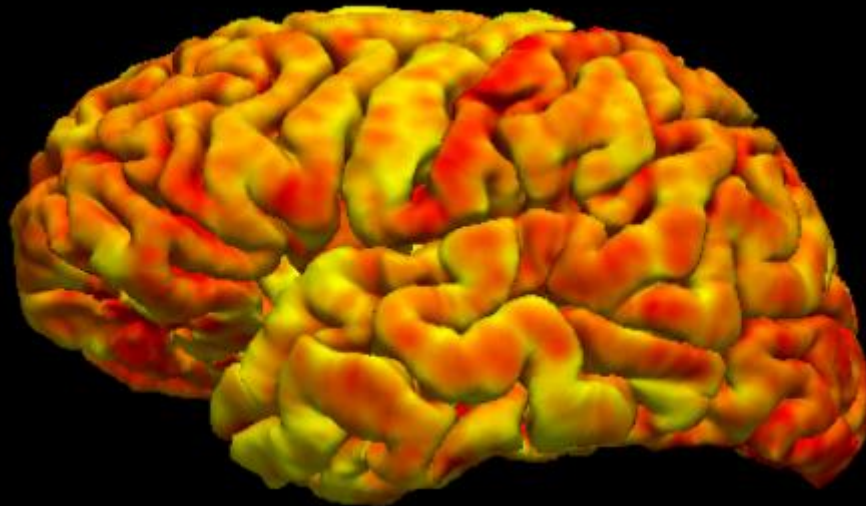
# Freeview

10. Open the same surfaces with the aparc.a2009s annotation file:  
[]\$ freeview -f surf/lh.white:annot=aparc.a2009s.annot surf/rh.pial:annot=aparc.a2009s.annot --viewport 3d  
ctrl+c



# Freeview

```
11. Open the a surfaces with the overlay of cortical thickness with a defined threshold:  
[]$ freeview -f surf/lh.pial:overlay=lh.thickness:overlay_threshold=0,4 --viewport 3d  
ctrl+c
```



# Freeview

12. Create a gif of the 3D surface.

a. Create a directory to save our freeview frames into:

```
[ ]$ mkdir gif
```

b. Open our freesurfer surface with aparc:

```
[ ]$ freeview -f surf/lh.white:annot=aparc.a2009s.annot --viewport 3d
```

c. Save movie frames to our directory:

```
File > Save Movie Frames...
```

```
Output Location > Select Folder Icon > gif
```

```
Fly through > Angle
```

```
Step size > 10.00 |
```

```
Write
```

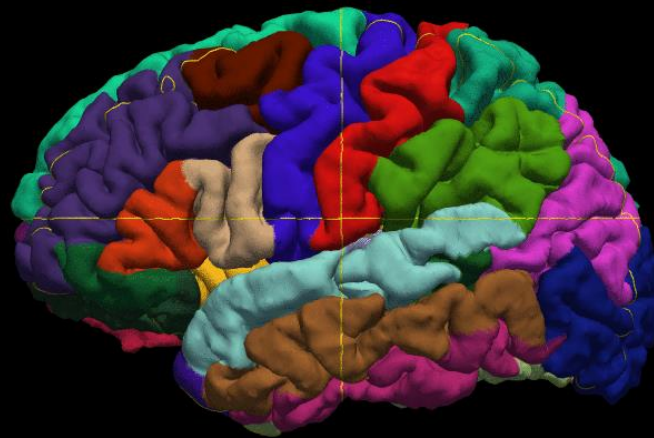
d. Use imagemagick package to convert frames to a gif:

```
[ ]$ convert -delay 0.05 gif/*.png aparc_lh.gif
```

e. View our gif:

```
[ ]$ firefox aparc_lh.gif
```

# Freeview

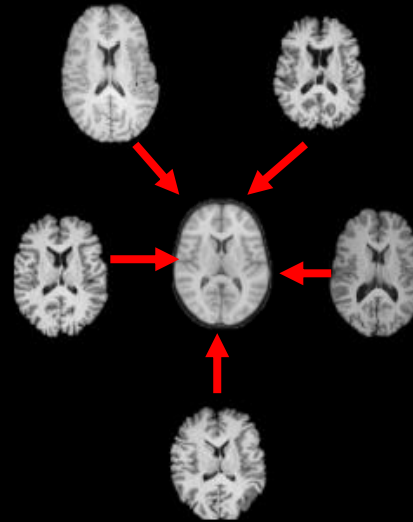


# Outline

- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- Freeview
- **Registration Tools**
- fMRI

# Registration

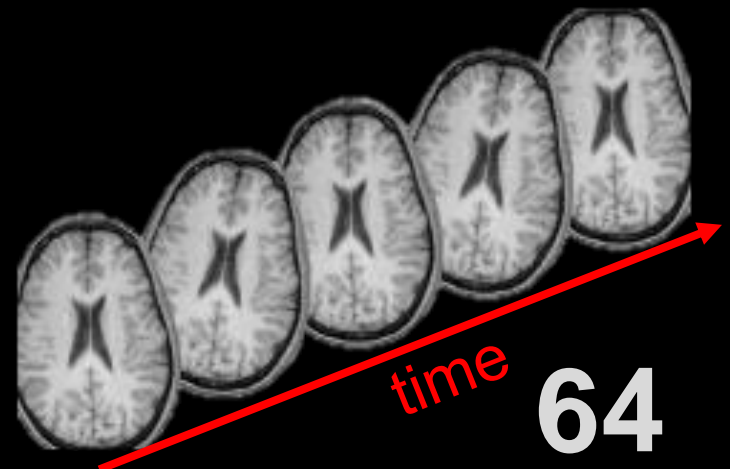
- combining across individual in a group study



- quantify structural changes



- correct for motion



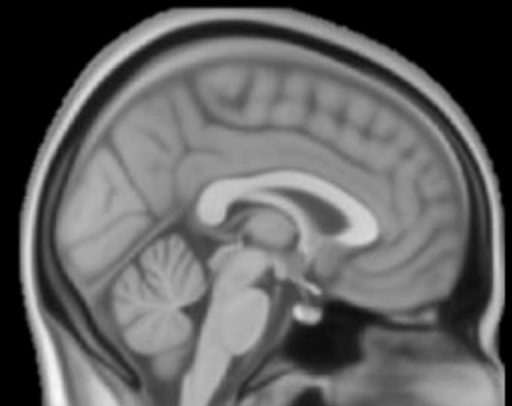
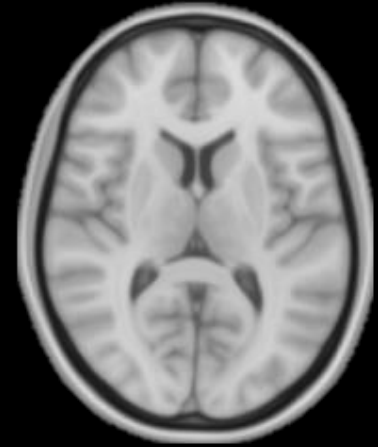


# Registration – Core Concepts

- image “spaces”
- spatial transformations
- cost functions
- interpolation

# Registration – image “spaces”

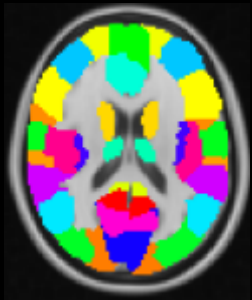
- image “spaces”
  - common reference coordinate system
  - register individuals for group study
  - original space was Talairach based on post-mortem brain
  - now used group average brains (MNI152)



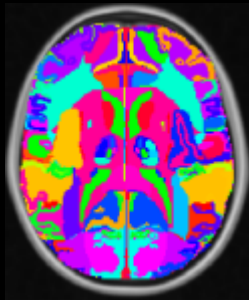
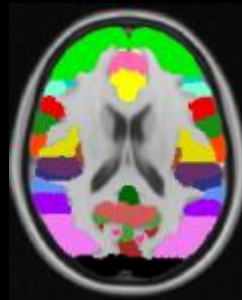
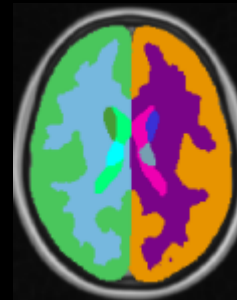
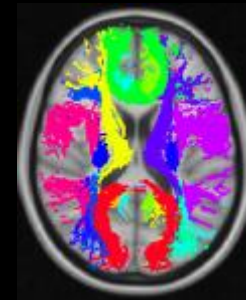
# Registration – image “spaces”

- atlases are in standard space
  - most common is MNI152
  - can alter the resolution (voxel size)
  - useful for group studies in standard space

AAL

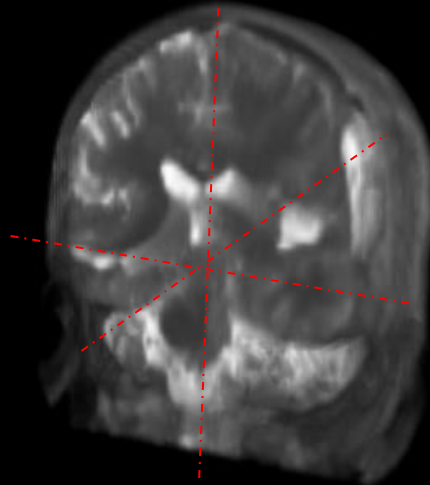


Talairach

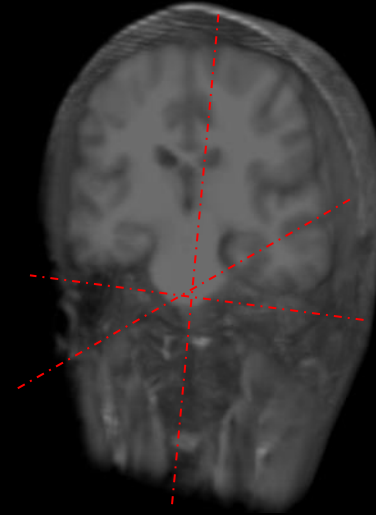
Harvard-Oxford  
CorticalHarvard-Oxford  
Sub-CorticalJHU White-Matter  
Tractography

# Registration – “spaces”

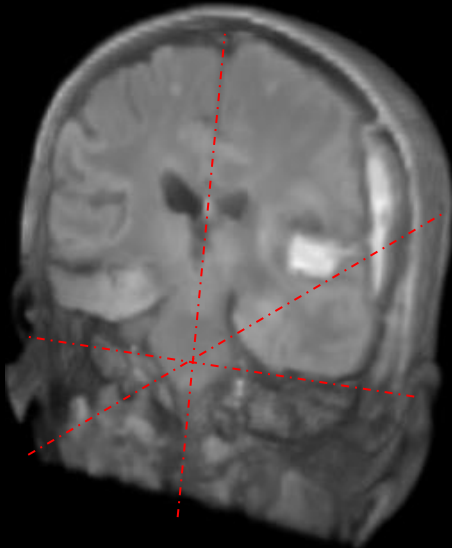
T2w



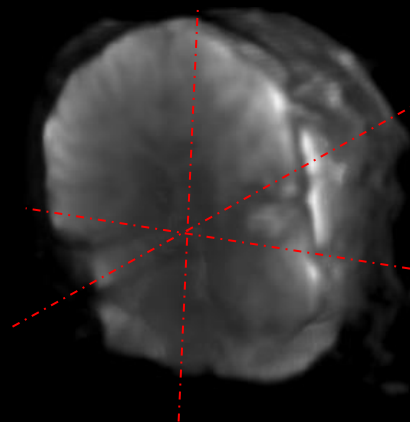
T1w



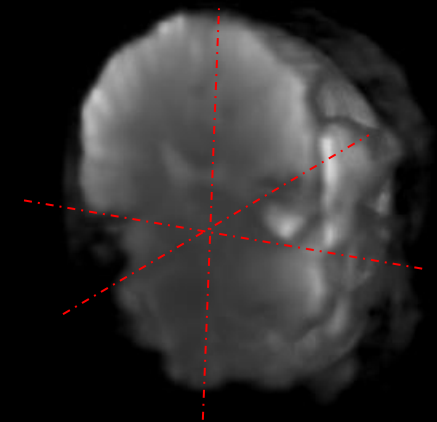
flair



dwi



bold

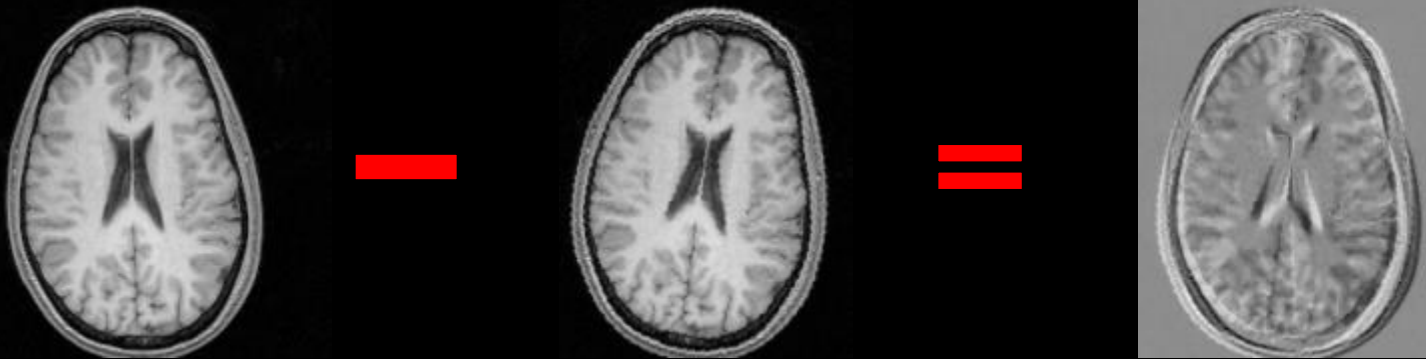


# Registration – spatial xfms

- spatial transformations
  - degrees of freed (DOF) describe nature of xfm
  - rigid body (6 DOF): 3 rotation + 3 translation
    - linear transform
    - good for within-subject
  - affine (12 DOF): 3 rotation + 3 translation + 3 scaling + 3 skew/shear
    - linear transform
    - good for initializing non-linear methods and biased images
  - non-linear (12 – millions DOF)
    - non-linear transform
    - good for between-subject and across modalities (both imaging and MRI)
    - *not the focus of the tools we will be using*
- more is not always better!

# Registration – cost functions

- cost functions
  - measures the “goodness” of alignment
  - seek the minimal value
  - several types of cost functions to choose from



# Registration – cost functions

- Linear Cost Functions

Least Squares	Same Modality (exact same sequence)
Normalized Correlation	Same Modality (different contrasts okay)
Correlation Ratio	Any MR Modalities
Mutual Information	Any Imaging Modalities (CT, PET, MRI, etc.)
Normalized Mutual Information	Any Imaging Modalities (CT, PET, MRI, etc.)
Boundary Based Registration	Within-subject EPI to structural

# Registration Tools

mri\_robust\_register

mri\_coreg

bbregister

easyreg



# mri\_robust\_register

- **ideal: within subject & MRI modality (e.g., longitudinal)**
  - can register part to whole hemispheres (histology, etc.)
  - can register to “half-way” space template
  - has optional standard cost function registration
    - can do within subject cross MRI-modality

## General Usage:

```
mri_robust_register --mov mov.nii --dst dst.nii --lta .lta
```

# mri\_robust\_register

13. Simple full head registration; same modality (T1w) and across timepoints:

```
[ ]$ cd $SUBJECTS_DIR/registration  
[ ]$ mri_robust_register --mov timepoint2.nii.gz --dst timepoint1.nii.gz --lta 2to1.lta --mapmov  
2to1.nii.gz --iscale --satit  
[ ]$ freeview timepoint2.nii.gz timepoint1.nii.gz 2to1.nii.gz:colormap=heat:opacity=0.3
```

# mri\_robust\_register (optional)

14. Standard cross modality registration (T2w to T1w):

```
[ ]$ mri_robust_register --mov T2.nii --dst T1.nii --mapmov T2toT1.nii --lta T2toT1.lta --cost NMI  
[ ]$ freeview T2toT1.nii:colormap=heat T1.nii
```

# mri\_coreg

- **ideal: within subject & across imaging modalities (e.g., PET → MRI)**
  - wrapper of SPM's `spm_coreg`
  - uses NMI cost-function
  - has capability for multi-core processing!

## General Usage:

```
mri_coreg --mov mov.nii --ref dst.nii --reg .lta --threads N
```

# mri\_coreg

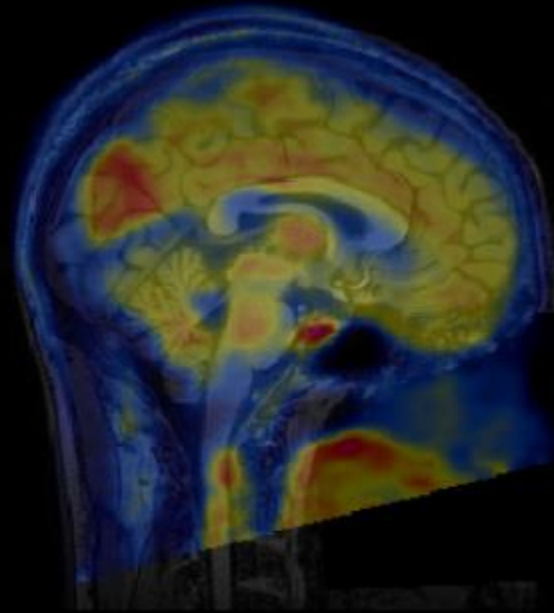
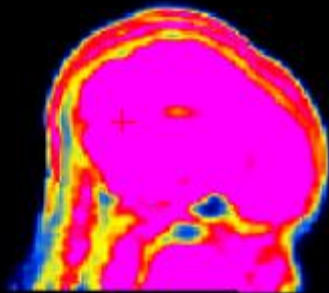
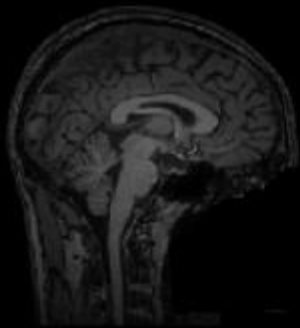
15. Use `mri_coreg` on 4 cpu's to register our PET average dynamic (template) to T1w:

```
[ ]$ mri_coreg --mov sub-dummy_PET.avg.nii.gz --ref sub-dummy_T1w.nii.gz --reg PETtoT1w.lta --threads 4
```

# this may take 2-3 minutes

```
[ ]$ mri_vol2vol --mov sub-dummy_PET.avg.nii.gz --lta PETtoT1w.lta --targ sub-dummy_T1w.nii.gz --o sub-dummy_PET-T1w.nii.gz
```

```
[ ]$ freeview sub-dummy_T1w.nii.gz sub-dummy_PET.avg.nii.gz:colormap=pet sub-dummy_PET-T1w.nii.gz:colormap=pet:opacity=0.3
```



# bbregister

- **ideal: within subject & across MRI modalities (e.g., EPI → T1w)**
  - bread & butter of FreeSurfer registrations
  - important to choose proper initialization method
  - use WM boundaries
    - need good structural processed in FreeSurfer
    - more robust to pathology and artifacts in EPI

## General Usage:

```
bbregister --mov template.nii --bold --s sub-001 --lta register.lta
```

# bbregister

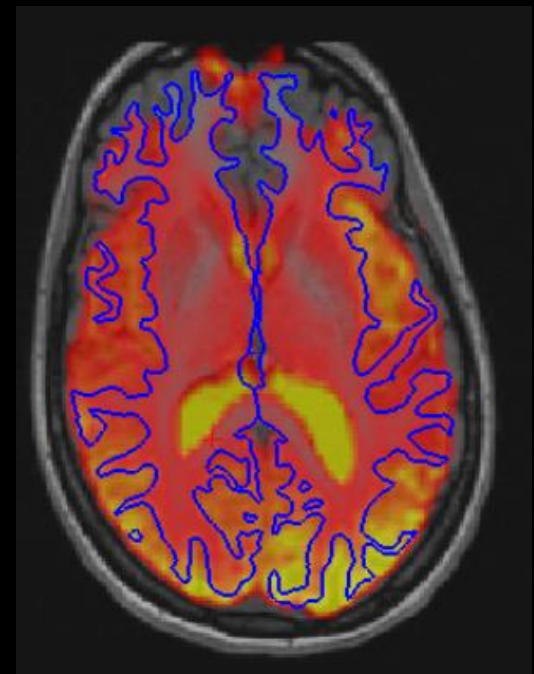
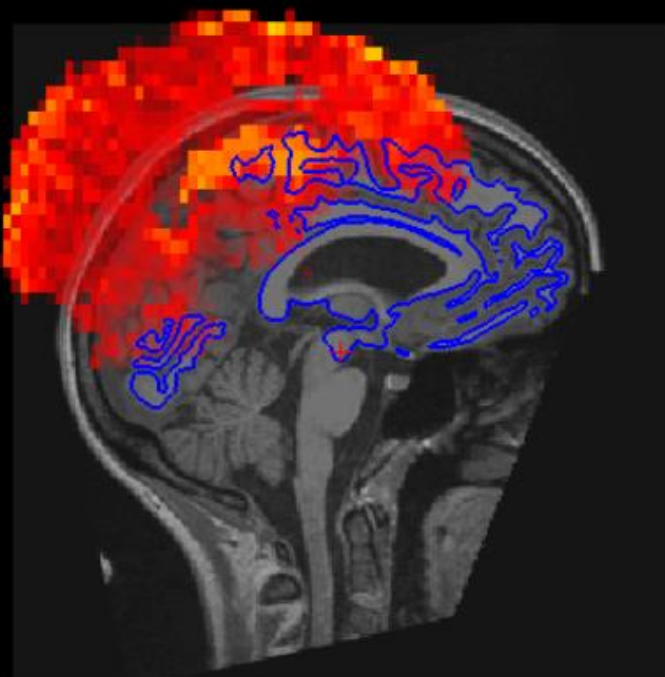
16. Use bbregister to register EPI (bold) template to the subject's T1w (using their recon output):

```
[ ]$ bbregister --mov sub-004_boldtemp.nii.gz --bold --s sub-004 --lta bold2t1w.lta --o sub-004_bold-t1w.nii.gz
```

# this may take 2-3 minutes

```
[ ]$ freeview sub-004_T1w.nii.gz sub-004_boldtemp.nii.gz:colormap=heat
```

```
sub-004_bold-t1w.nii.gz:colormap=heat:opacity=0.3:visible=0 -f rh.white:edgecolor=blue lh.white:edgecolor=blue
```



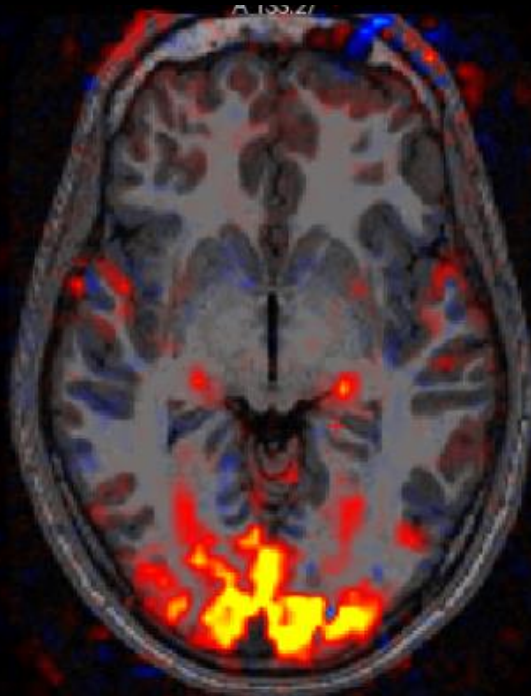
# Outline

- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- Freeview
- Registration Tools
- **fMRI**



# fMRI Viewing - Volumetric

```
17. Apply bbregister transform to our fMRI correlation score (significance) map to move to subject's T1w space:  
[]$ cd $SUBJECTS_DIR/fmri  
[]$ mri_vol2vol --mov sub-005_sig.nii.gz --lta sub-005_bold2t1.lta --targ sub-005_t1w.nii.gz --o sub-005_sig-t1w.nii.gz  
  
# this may take 1-2 minutes  
  
[]$ freeview sub-005_t1w.nii.gz sub-005_sig-t1w.nii.gz:colormap=heat:heatscale=0,10,20
```



# fMRI Viewing - Surface

What do we want to do?

View our fMRI results on the surface

How can we resample our votes to the surface?

`mri_vol2surf`

General Usage:

```
mri_vol2surf --mov in.nii --reg .lta --projfrac 0.5 --interp nearest --hemi lh  
--o output
```

# fMRI Viewing - Surface

What do we want to do?

View our fMRI results on the surface

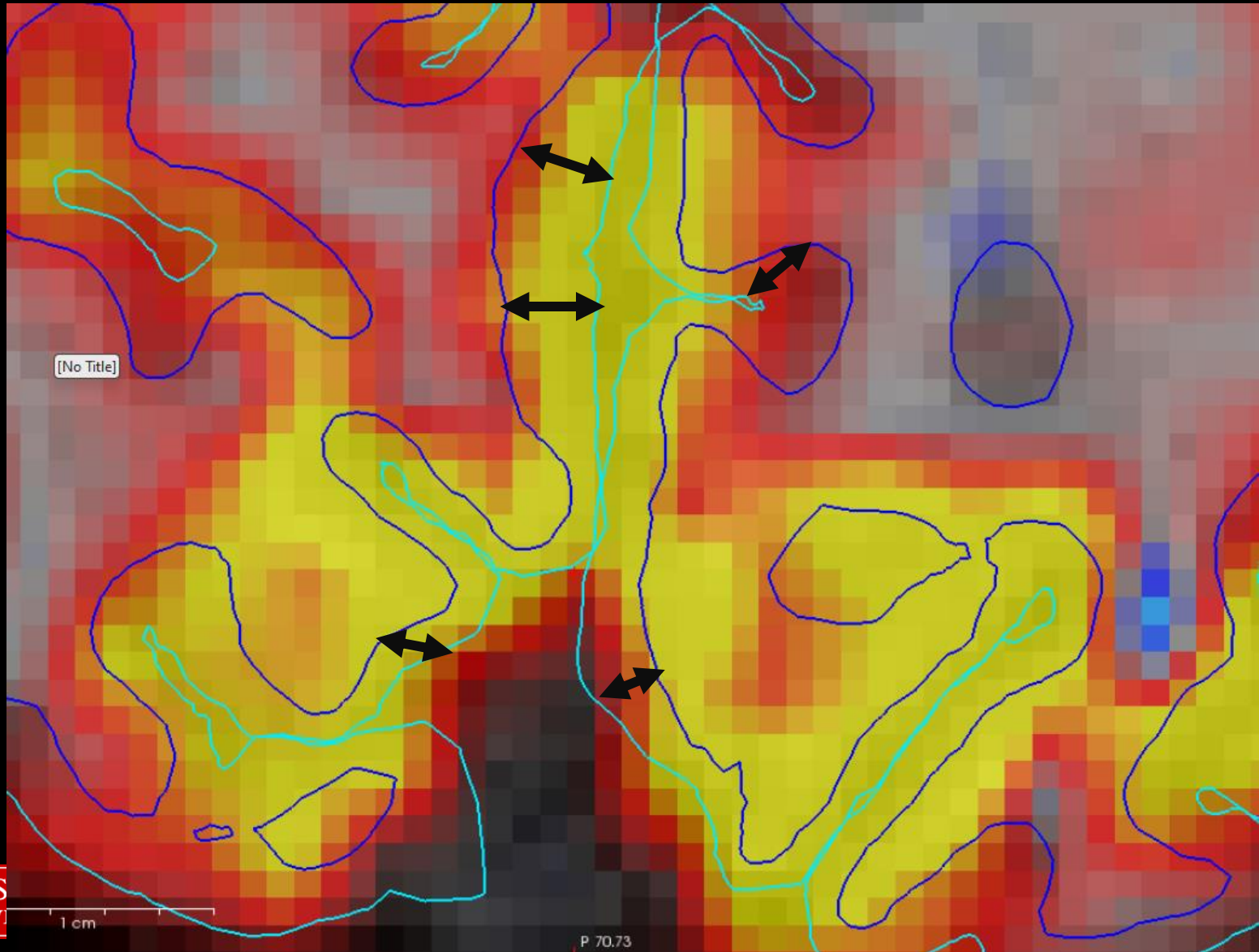
How can we resample our votes to the surface?

`mri_vol2surf`

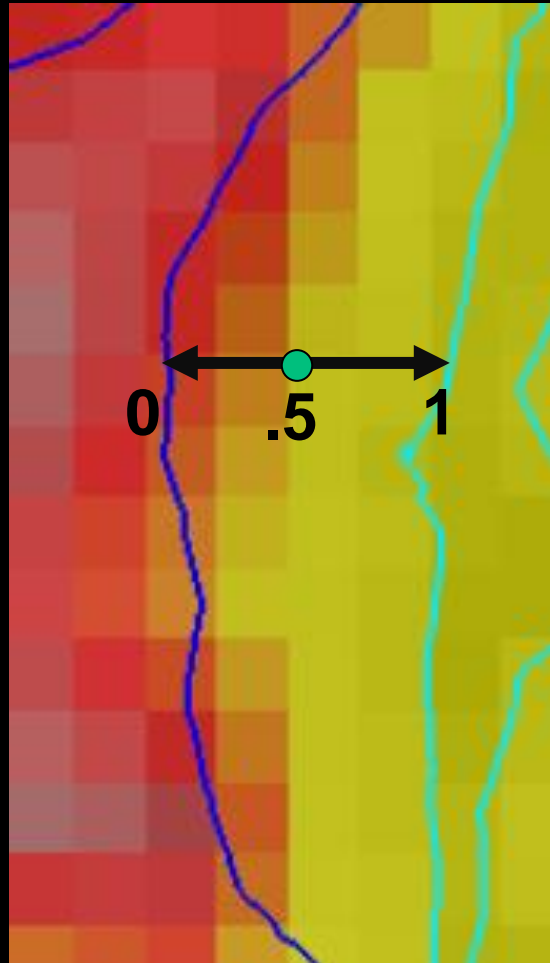
General Usage:

```
mri_vol2surf --mov in.nii --reg .lta --projfrac 0.5 --interp nearest --hemi lh  
--o output
```

# fMRI Viewing - Surface



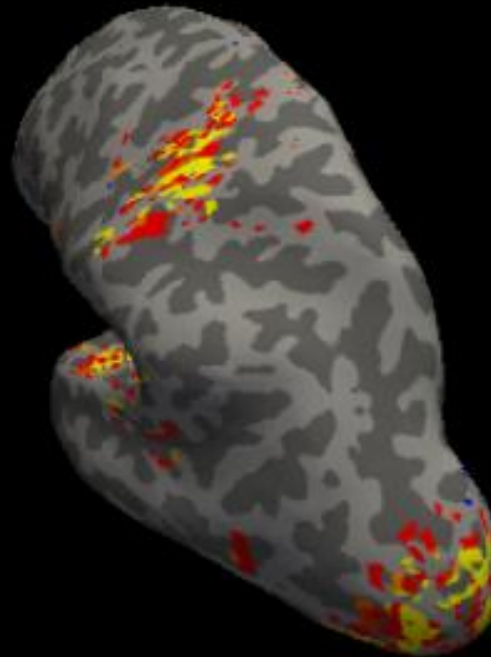
# fMRI Viewing - Surface



# fMRI Viewing - Surface

18. Apply `mri_vol2surf` to move our fMRI significance map to move to subject's surface:

```
[]$ mri_vol2surf --mov sub-005_sig.nii.gz --reg sub-005_bold2t1.lta --projfrac 0.5 --interp nearest --hemi lh --o sub-005.lh.sig.nii  
[]$ freeview -f $SUBJECTS_DIR/sub-005/surf/lh.inflated:overlay=sub-005.lh.sig.nii:overlay_threshold=10,20 -viewport 3d
```



# fMRI Viewing - Surface

Opacity  1.00

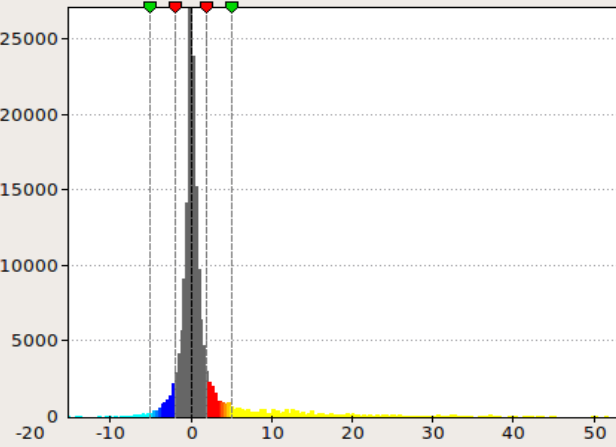
Smooth  Enable 1 steps

Color Scale

Heat  Color Wheel  Custom

Truncate  Inverse

Threshold



Min 2 Mid 3.5 Max 5

Offset 0

Use percentile




Method

Linear  Linear Opaque  Piecewise

Apply changes to all overlay layers

Automatically apply changes

Or you must click "Apply" to apply changes to the overlay.

 Help  Apply  Close

# Outline

- Tutorial Setup (Hands-On)
- Refresher
- Stats Tools
- Freeview
- Registration Tools
- fMRI



# Additional BU RCS Web Resources

- Research Computing Support Pages  
<http://www.bu.edu/tech/support/research/>
- Technical Summary of SCC Resources  
<http://www.bu.edu/tech/support/research/computing-resources/tech-summary/>
- SCC Updates – Latest SCC News  
<http://www.bu.edu/tech/support/research/whats-happening/updates/>
- Code Examples for Popular Software Packages  
<http://scv.bu.edu/examples/>

1. Please open a web browser and:
2. Google “rsc tutorial evaluation”
3. Click 1<sup>st</sup> link  
[http://scv.bu.edu/survey/tutorial\\_evaluation.html](http://scv.bu.edu/survey/tutorial_evaluation.html)
4. Fill out the survey!