



UCLA Brain Mapping Center

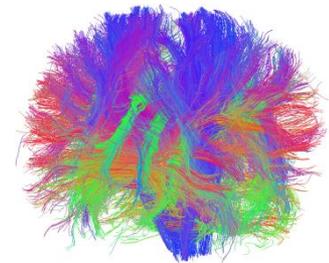
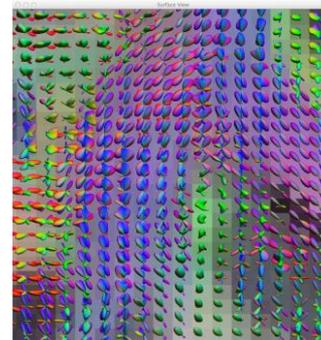
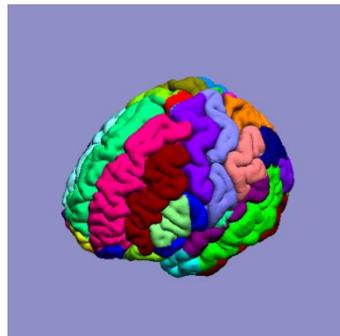
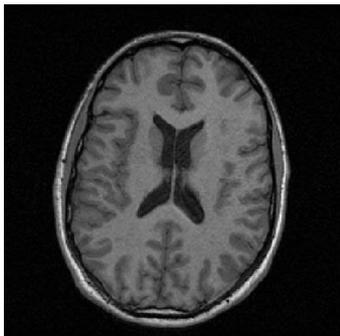
BrainSuite

Presented at the **UCLA Advanced Neuroimaging Summer Program**
14 July 2016

David Shattuck
Ahmanson-Lovelace Brain Mapping Center
Department of Neurology
David Geffen School of Medicine at UCLA
<http://shattuck.bmap.ucla.edu>

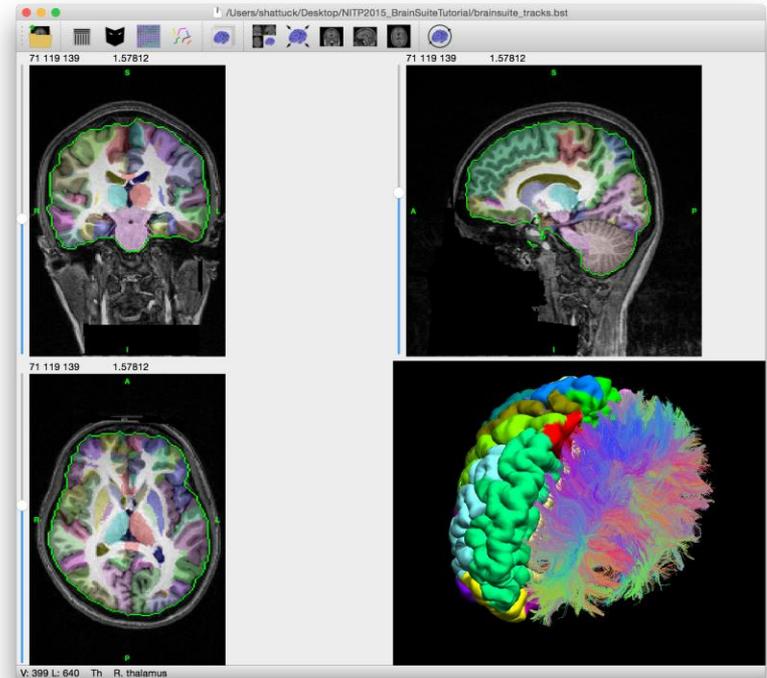
Objectives

- Introduce you to the BrainSuite software tools
- Provide an overview of the major components of the software
- Provide hands-on training with assistance from experienced users
 - Sample data sets
 - Your own data
- Provide assistance with how to integrate the software into your research approach



BrainSuite

- Collection of image analysis tools designed to process structural and diffusion MRI
 - Automated sequence to extract cortical surface models from T1-MRI
 - Tools to register surface and volume data to an atlas to define anatomical ROIs
 - Tools for processing diffusion imaging data, including coregistration to anatomical T1 image, ODF and tensor fitting, and tractography.
 - Visualization tools for exploring these data.
- Runs on Windows, Mac, and Linux

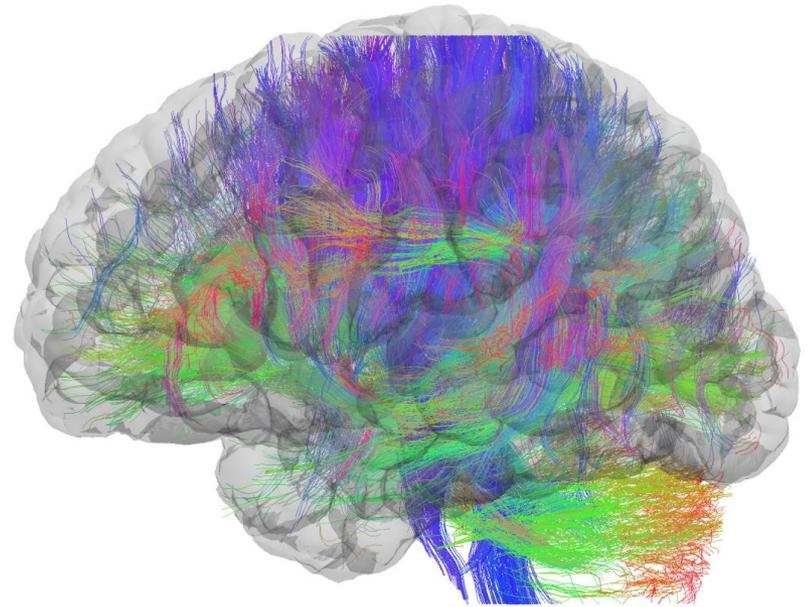


BrainSuite Contributors

- David Shattuck, PhD
- Richard Leahy, PhD
- Anand Joshi, PhD
- Chitresh Bhushan
- Divya Varadarajan
- Justin Haldar, PhD
- Shantanu Joshi, PhD
- So Young Choi
- Noor Al-Sharif
- Yeun Kim
- Jason Wong
- Jessica Wisnowski, PhD
- Hanna Damasio, MD

BrainSuite Highlights

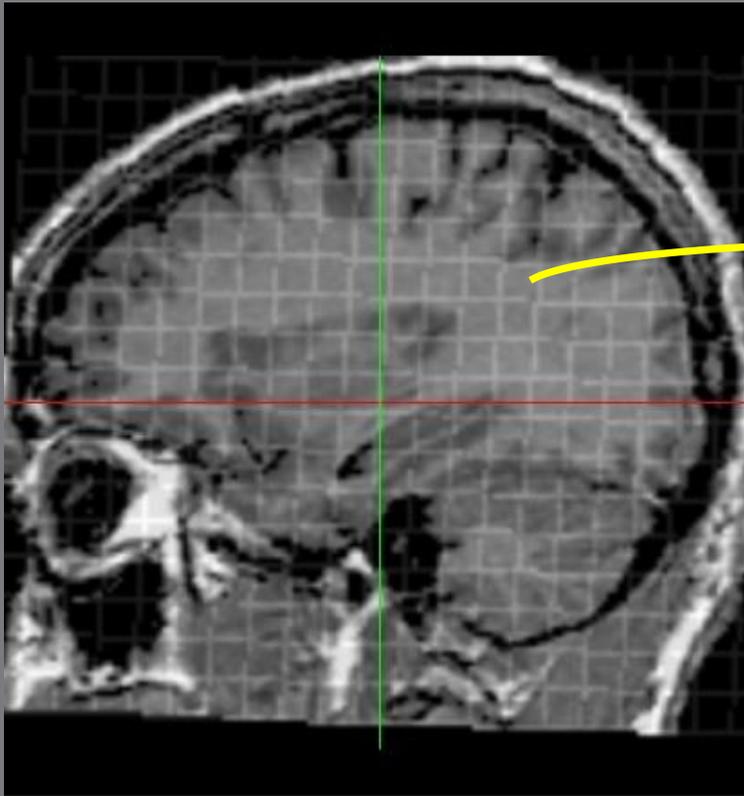
- Interactive processing
- Visualization capabilities
- Cortically-constrained volumetric registration
- New BCI-DNI brain atlas
- Customizable atlases
- Unique diffusion modeling (FRACT)
- Multiple methods for B0-distortion correction
- Atlas-based connectivity analysis
- GUI and command-line versions with cross-platform consistency
- Open Source (GPL v2 license)



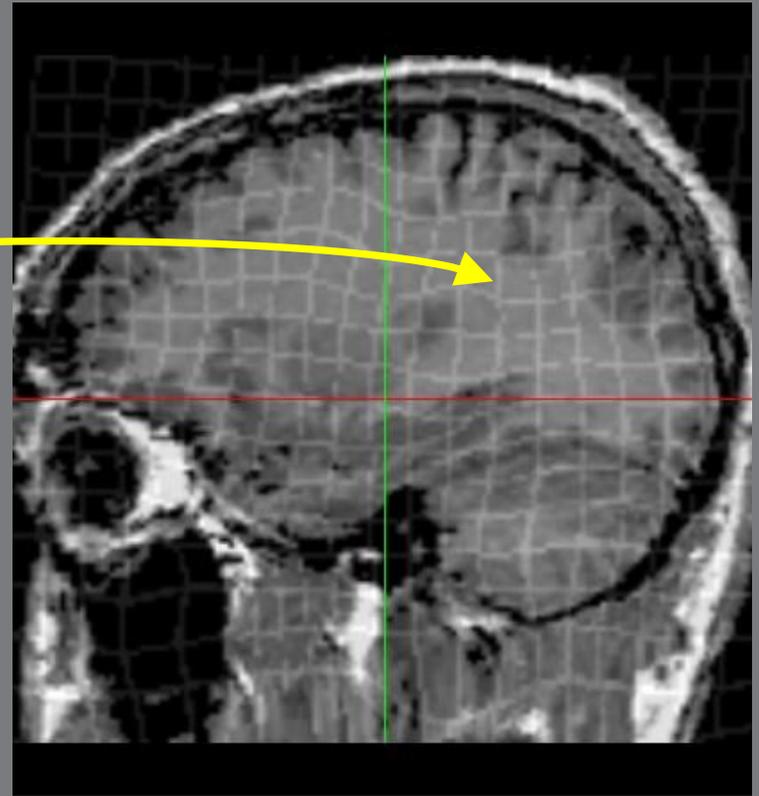
Motivation

- We are typically interested in performing comparisons across different brains or brains at different points in time.
- For these comparisons to be meaningful, we must be able to establish spatial anatomical correspondence across the data
- Once correspondence is established, we can study various neuroanatomical features in the data.
 - Size of structures, cortical thickness, cortical complexity
 - White matter architecture, connectivity relationships
 - How these change over time or in the presence of disease or trauma
- BrainSuite software goals
 - Address these challenges with automated processing where possible
 - Provide facilities to intervene when necessary
 - Provide tools to streamline the tasks of performing analysis

Image Registration



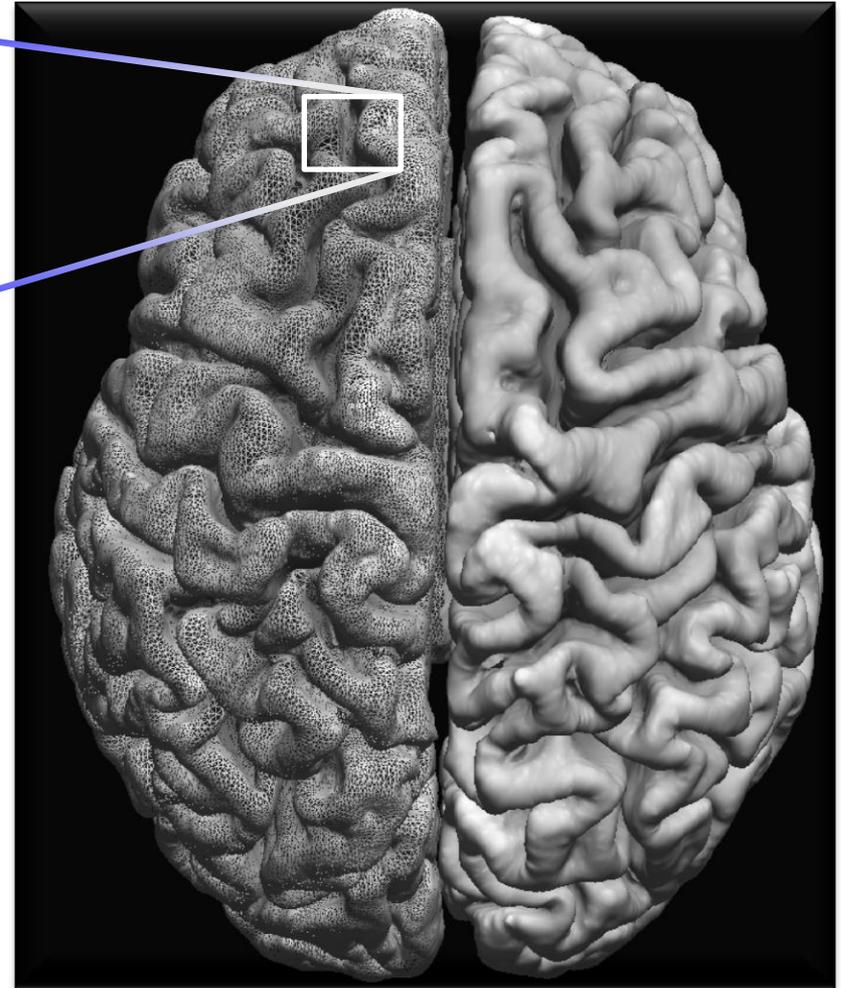
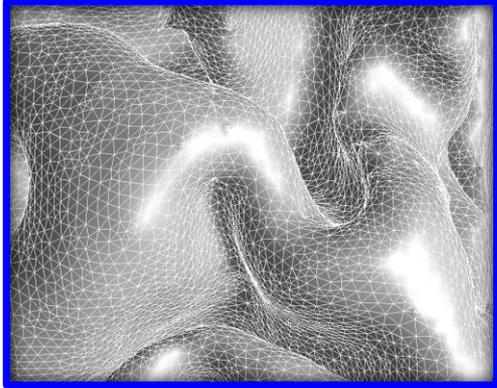
Brain image with grid overlay



Warped brain with grid overlay

- Mapping from points in a template brain image to matching points in a target brain image.

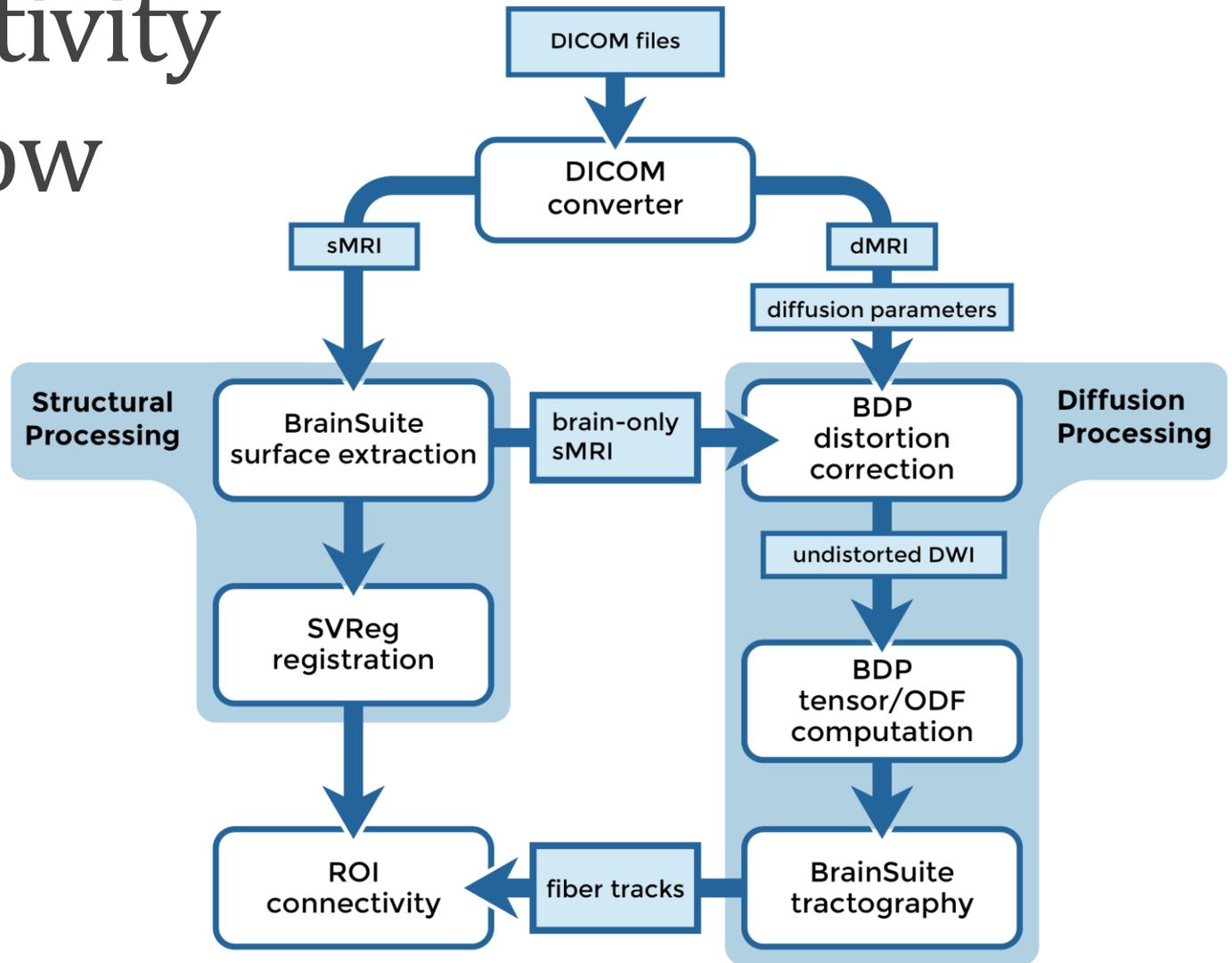
Surface Models



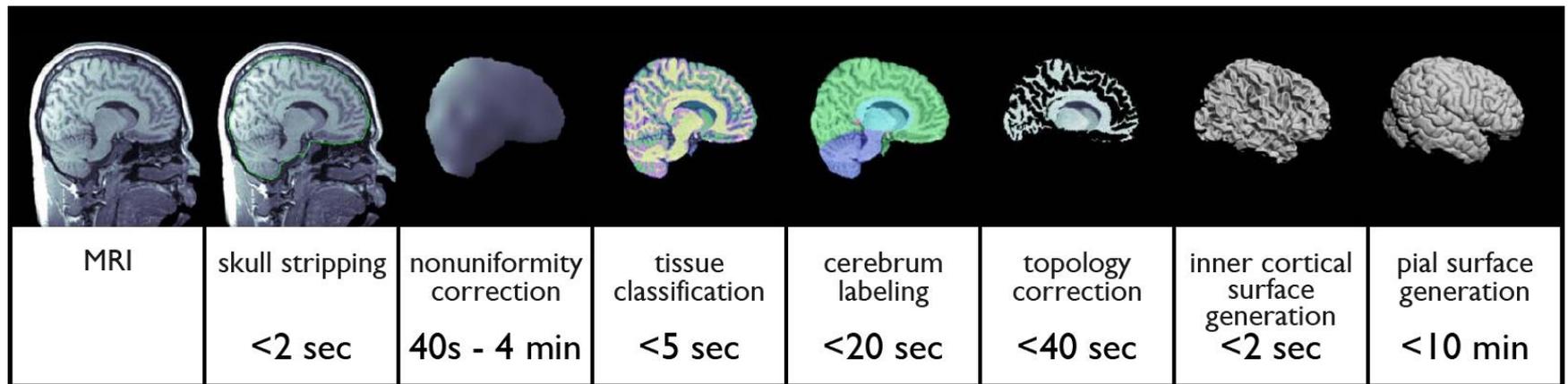
- We are often interested in functional areas in the cortex
- Surface-based features are of interest in the study of development or disease processes
- Many volumetric-based approaches do not align the cortical anatomy well
- EEG/MEG source localization: the location and orientation of the cortical surface can provide additional information
- Cortex can be represented as a high resolution triangulated mesh with $\sim 700,000$ triangles

Cortical surface mesh representation

BrainSuite Connectivity Workflow



Cortical Surface Extraction



Cortical Extraction Sequence

The screenshot displays the BrainSuite software interface for the Cortical Surface Extraction Sequence. The main window shows two axial brain slices with coordinate axes (S, A, P) and dimensions (64 128 128 1). A central panel lists the extraction stages, and a right-hand panel provides configuration options for the skull stripping step.

Extraction Stages

- Skull stripping
- Skull and scalp
- Nonuniformity correction
- Tissue classification
- Cerebrum labeling
- Inner cortical mask
- Scrub mask
- Topology correction
- Wisp removal
- Inner cortical surface
- Pial surface
- Split hemispheres
- Register and label brain

Skull Stripping
next step: anisotropic diffusion filter

Skull Stripping

- Diffusion Iterations: 3
- Diffusion Constant: 30
- Edge Constant: 0.8
- Erosion Size: 1
- dilate final mask
- trim spinal cord/brain stem

Automatically Save Results

- save output of each stage automatically

[Suggest Prefix and Directory](#)

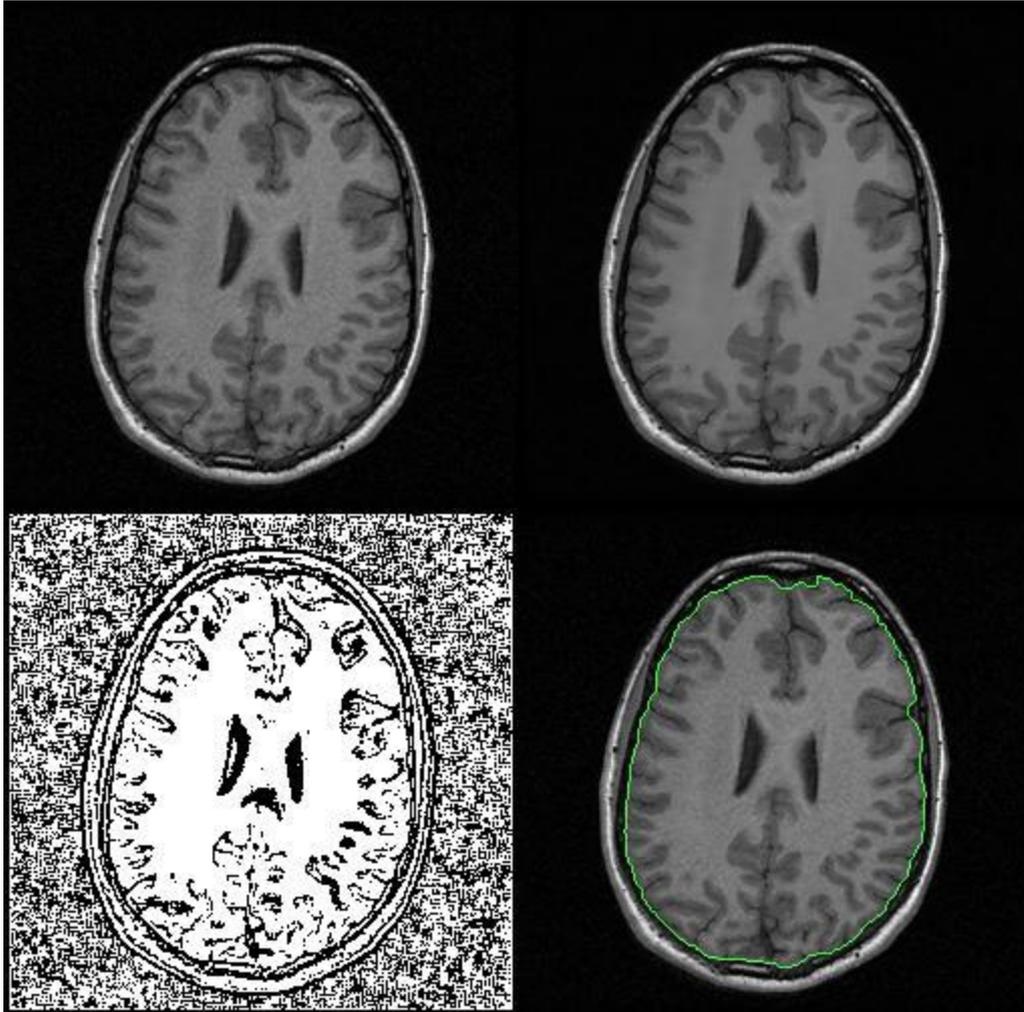
Extraction results will be saved to
/Users/shattuck/Desktop/NITP2015_BrainSuiteTutorial/extraction/2523412.*

Filename Prefix: 2523412
Working Directory: rs/shattuck/Desktop/NITP2015_BrainSuiteTutorial/extraction

Skull Stripping

MRI

Filtered MRI



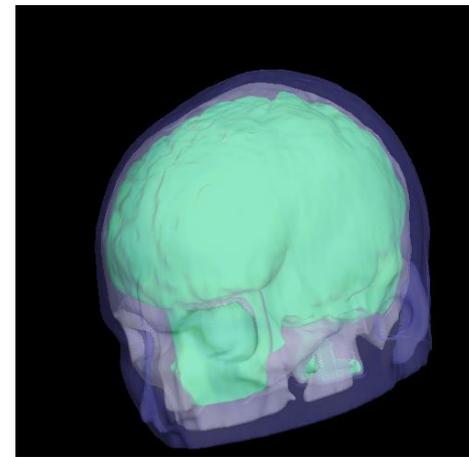
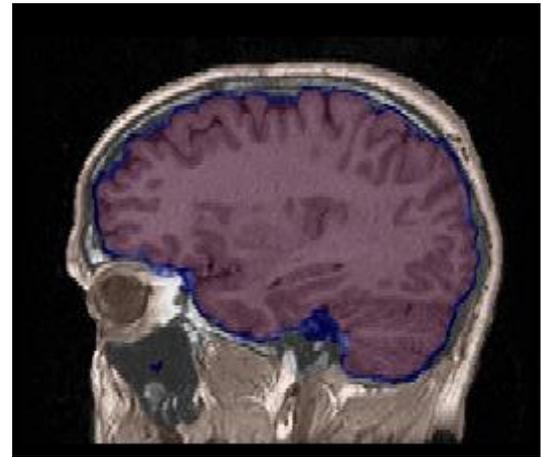
Edge Mask

Brain Boundary (green)

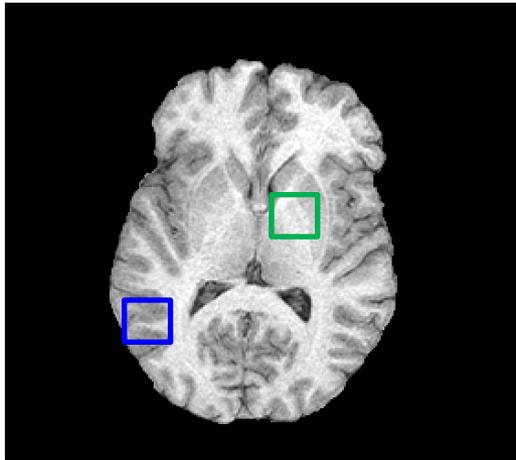
- Brain Surface Extractor (BSE) extracts the brain from non-brain tissue using a combination of:
 - anisotropic diffusion filtering
 - edge detection
 - mathematical morphological operators
- This method can rapidly identify the brain within the MRI

Skull and Scalp Modeling

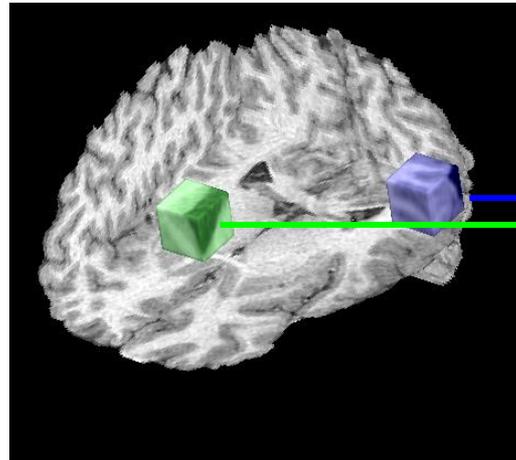
- We can apply thresholding, mathematical morphology, and connected component labeling to MRI to identify skull and scalp regions.
- The method builds upon the BSE skull stripping result.
- The volumes produced by this algorithm will not intersect.
- We can produce surface meshes from the label volume.
- The results are suitable for use in MEG/EEG source localization.



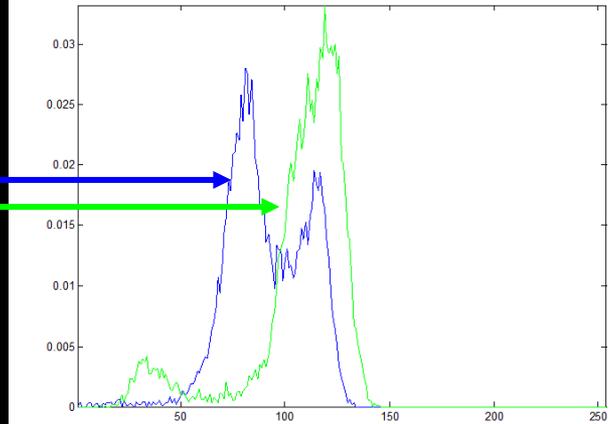
Nonuniformity Correction



Two cubic regions ROIs



3D rendering of the ROIs

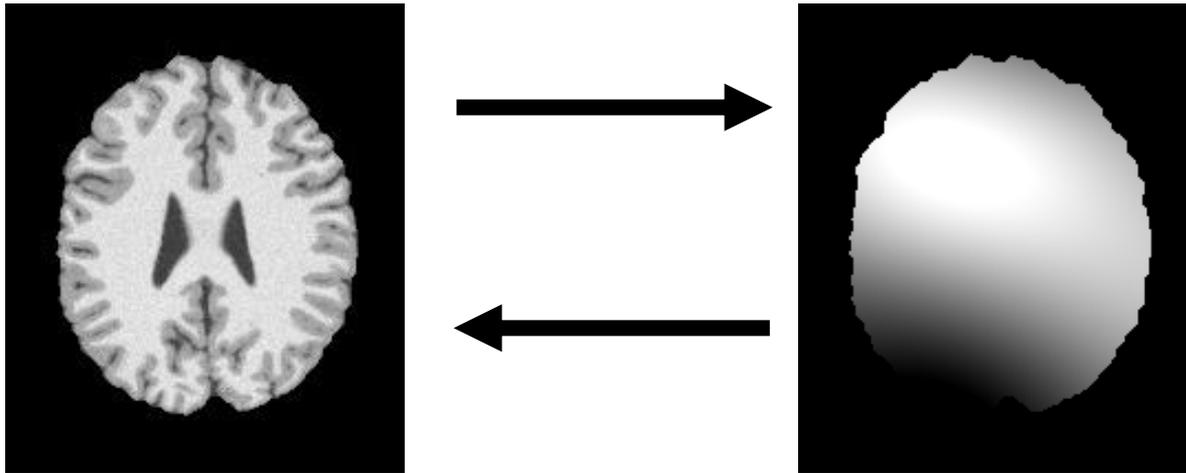


Histograms of the two ROIs

- Nonuniform signal gain can confound tissue classification techniques
- Bias Field Corrector (BFC) performs nonuniformity correction by analyzing the intensity profiles of regions of interest (ROIs)
- We can fit a histogram model to these ROIs and estimate the local gain variation

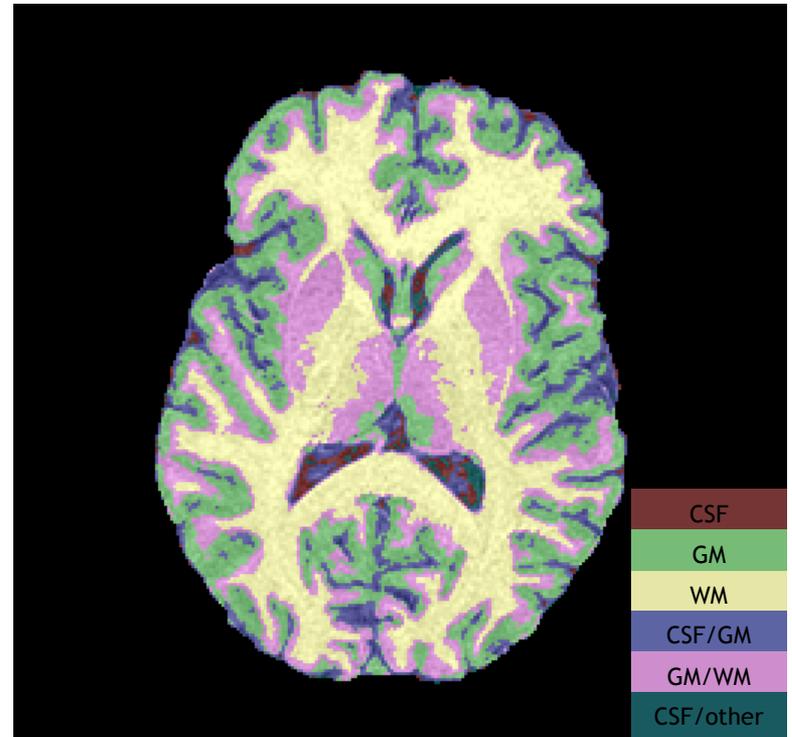
Nonuniformity Correction

- Estimate bias parameter at several points throughout the image.
- Remove outliers from our collection of estimates.
- Fit a tri-cubic B-spline to the estimate points.
- Divide the image by the B-spline to make the correction.



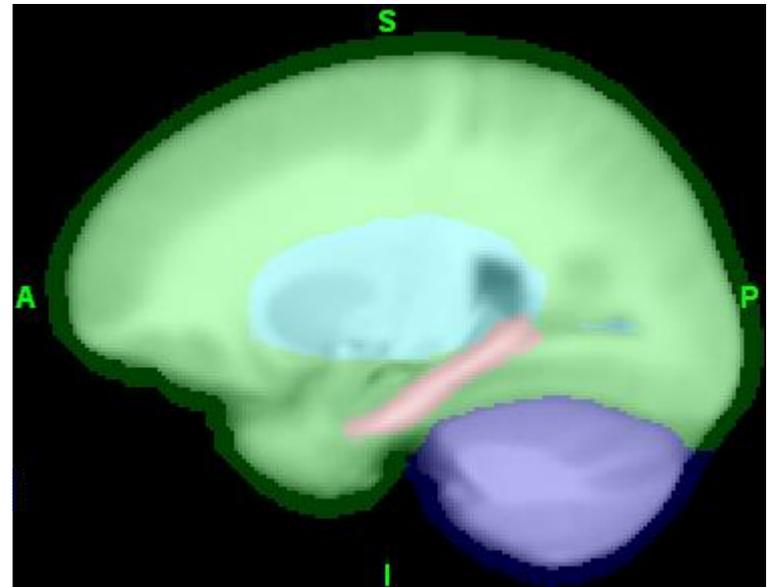
Tissue Classification

- We use a statistical tissue classifier to label each voxel according to tissue type.
 - Initialize with a maximum likelihood classification
 - Refine with a maximum a posteriori (MAP) classifier that produces more contiguous regions of tissue
- Tissue categories are
 - Pure: GM, WM, CSF
 - Mixed: GM/CSF, GM/WM, CSF/Other
- Also estimate tissue fractions at each voxel

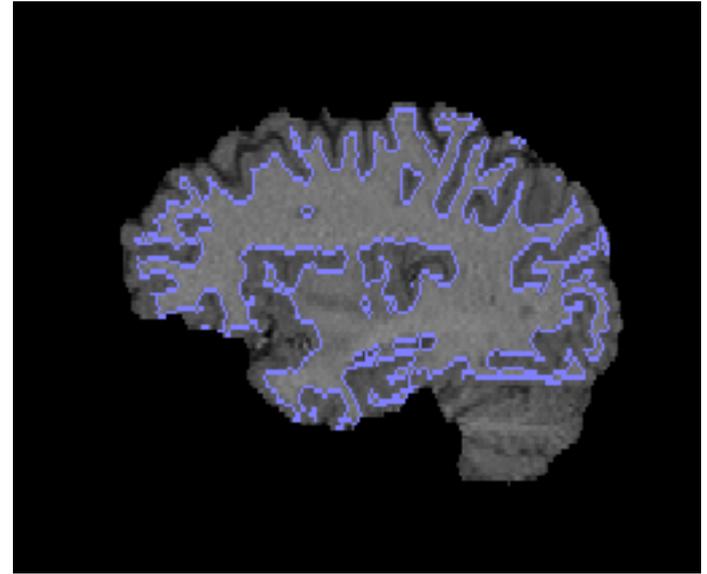
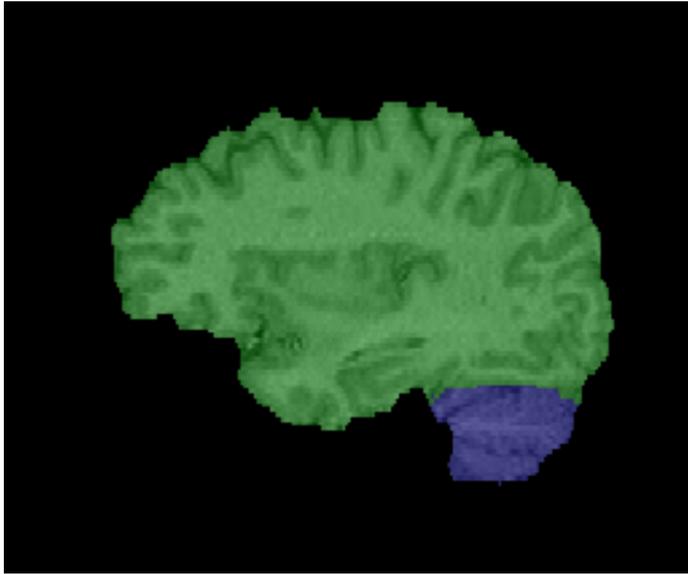


Cerebrum Labeling

- For the cortical surface, we are interested in the cerebrum, which we separate from the rest of the brain.
- We achieve this by registering a multi-subject average brain (ICBM452) to the individual brain using AIR (R. Woods)
- We have labeled this atlas:
 - cerebrum / cerebellum
 - subcortical regions
 - left / right hemispheres



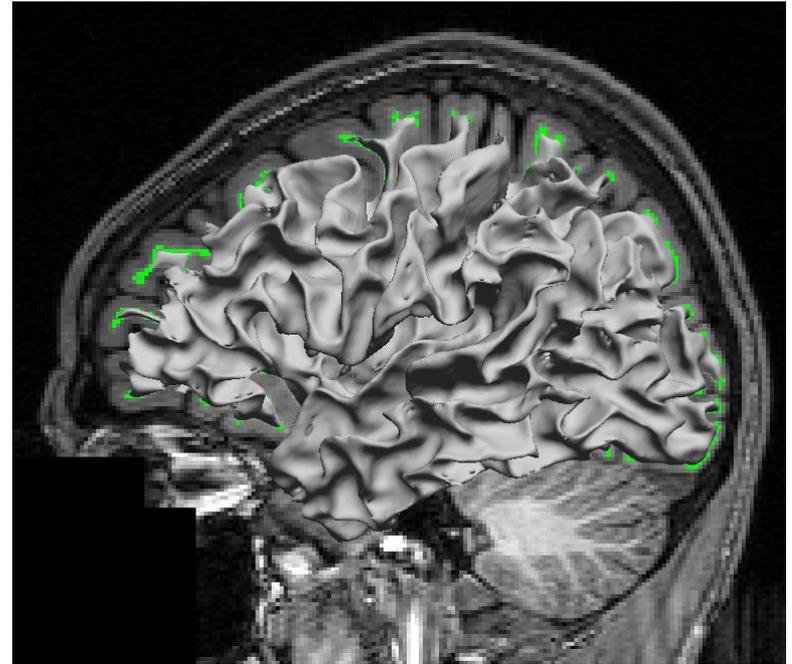
Inner Cortical Mask



- We combine our registered brain atlas with our tissue map
 - Retain subcortical structures, including nuclei
 - Identify the inner boundary of the cerebral cortex

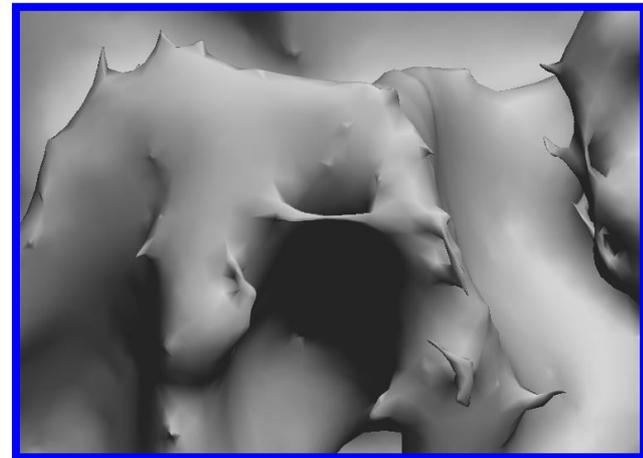
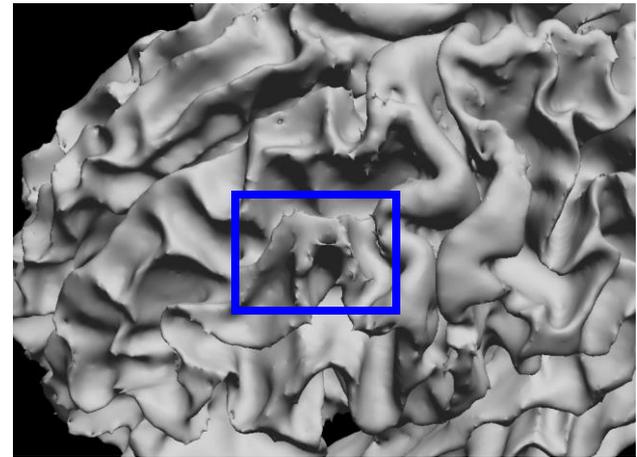
Surface Generation

By applying a tessellation algorithm, we can generate a surface mesh from a 3D volume.

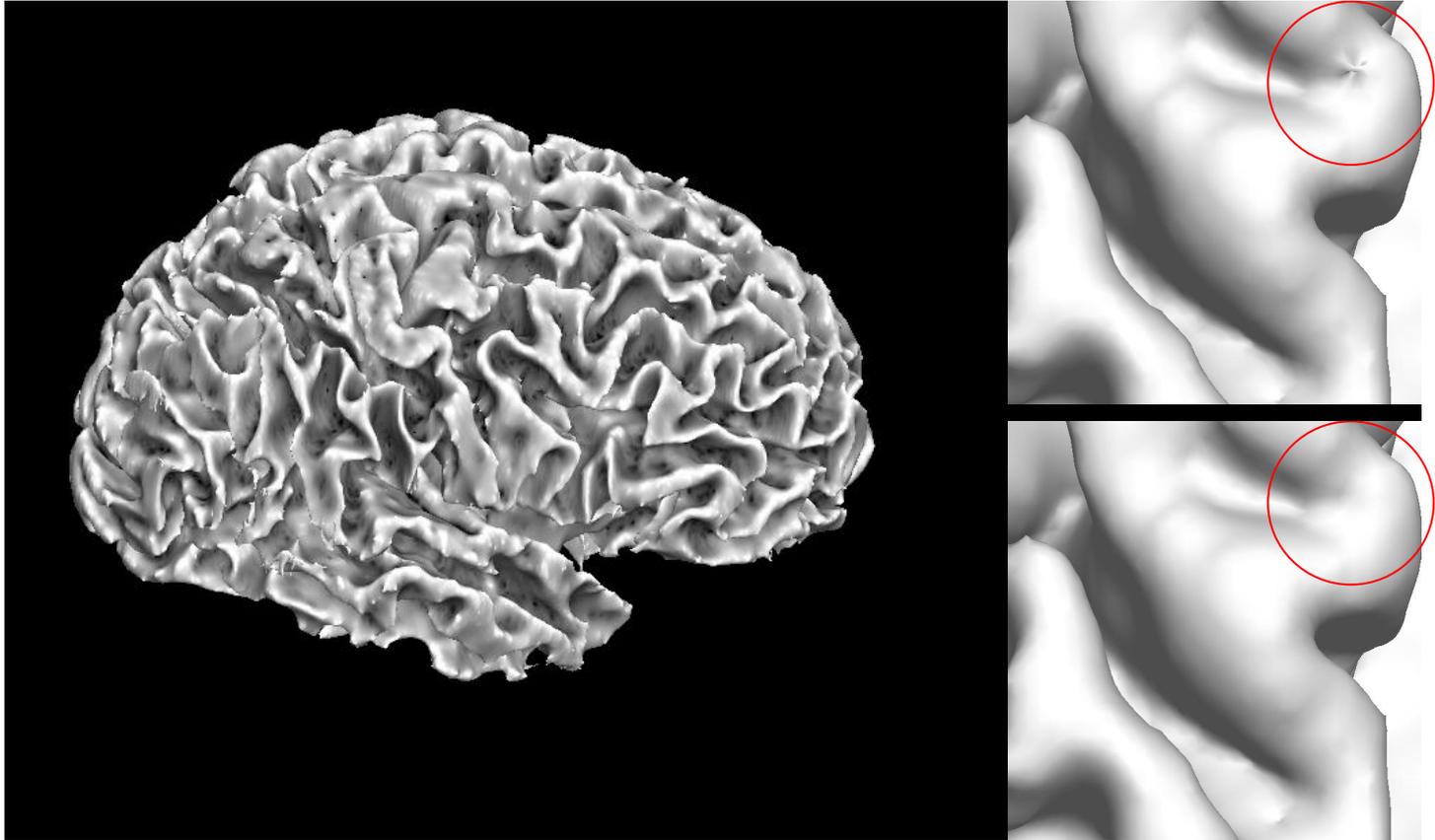


Topological Errors

- In normal human brains, the cortical surface can be considered as a single sheet of grey matter.
- Closing this sheet at the brainstem, we can assume that the topology of the cortical surface is equivalent to a sphere, i.e., it should have no holes or handles.
- This allows us to represent the cortical surface using a 2D coordinate system.
- Unfortunately, our segmentation result will produce a surface with many topological defects.



Topology Correction

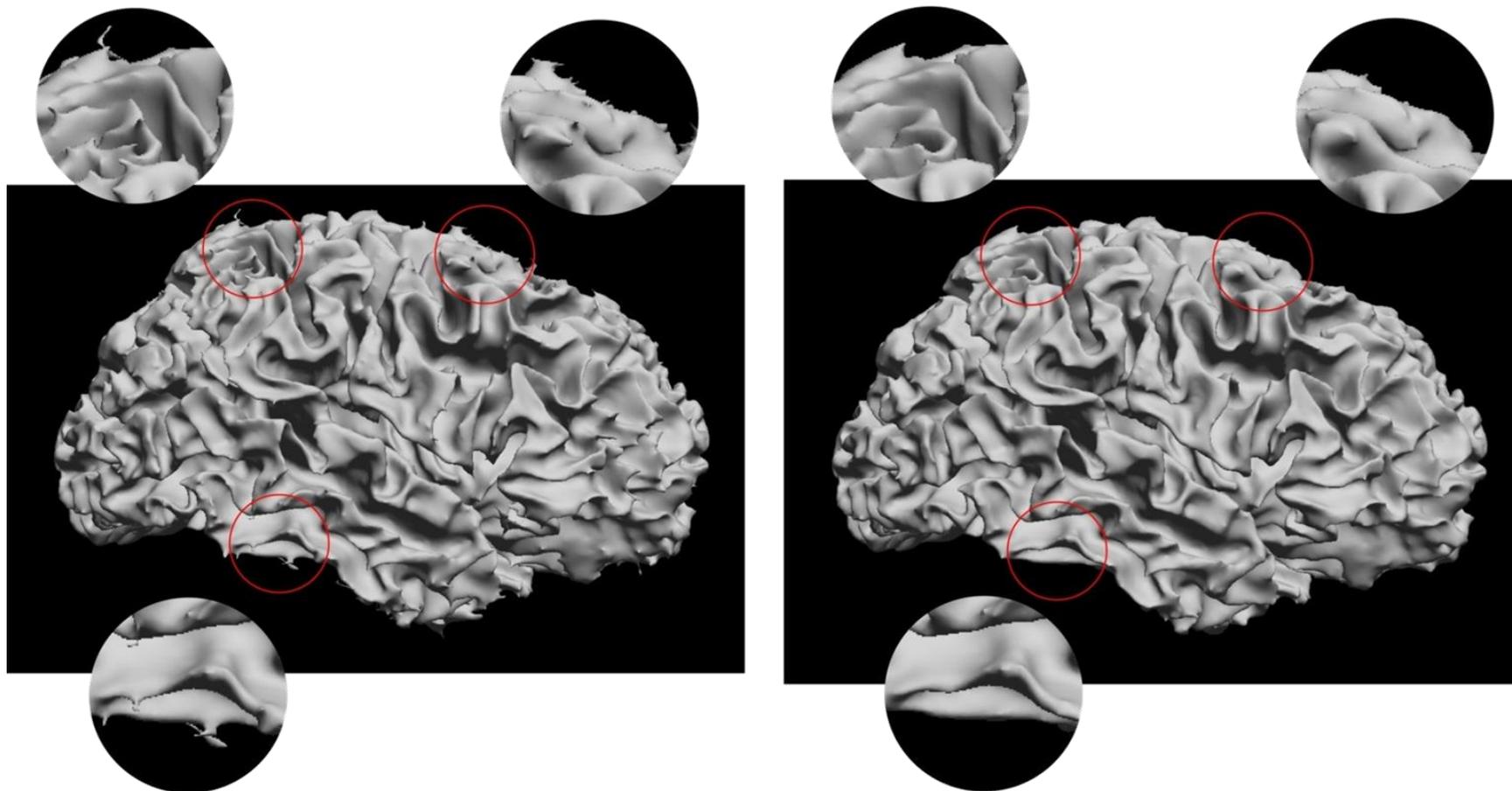


(left) cortical surface model produced from binary masks

(top right) close-up view of a handle on the surface generated from the volume before topological correction

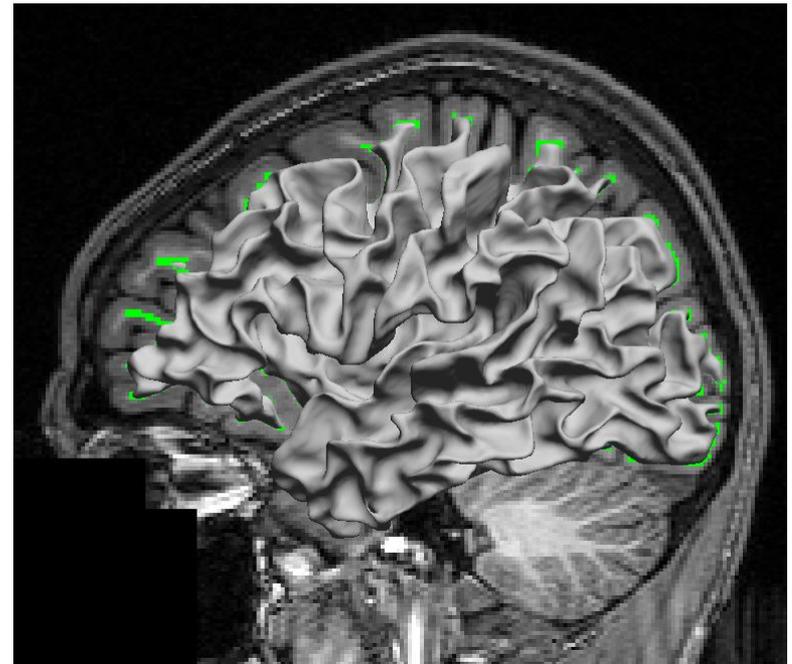
(bottom right) close-up view of the same region on the surface generated from the same volume after topology correction.

Wisp Removal



Inner Cortical Surface

After applying the topology correction and dewisp filters, we apply marching cubes to generate a representation of the inner cortical boundary.

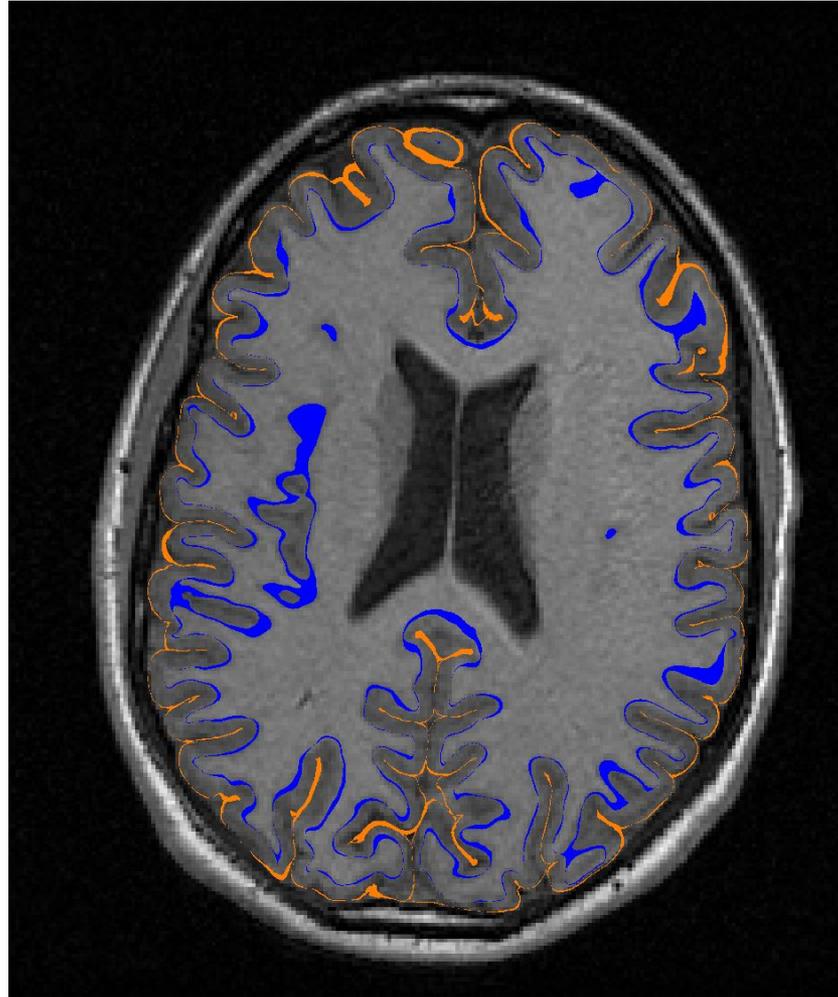


Pial Surface

- Expand inner cortex to outer boundary
- Produces a surface with 1-1 vertex correspondence from GM/WM to GM/CSF
 - Preserves the surface topology
 - Provides direct thickness computation
 - Data from each surface maps directly to the other



Pial Surface

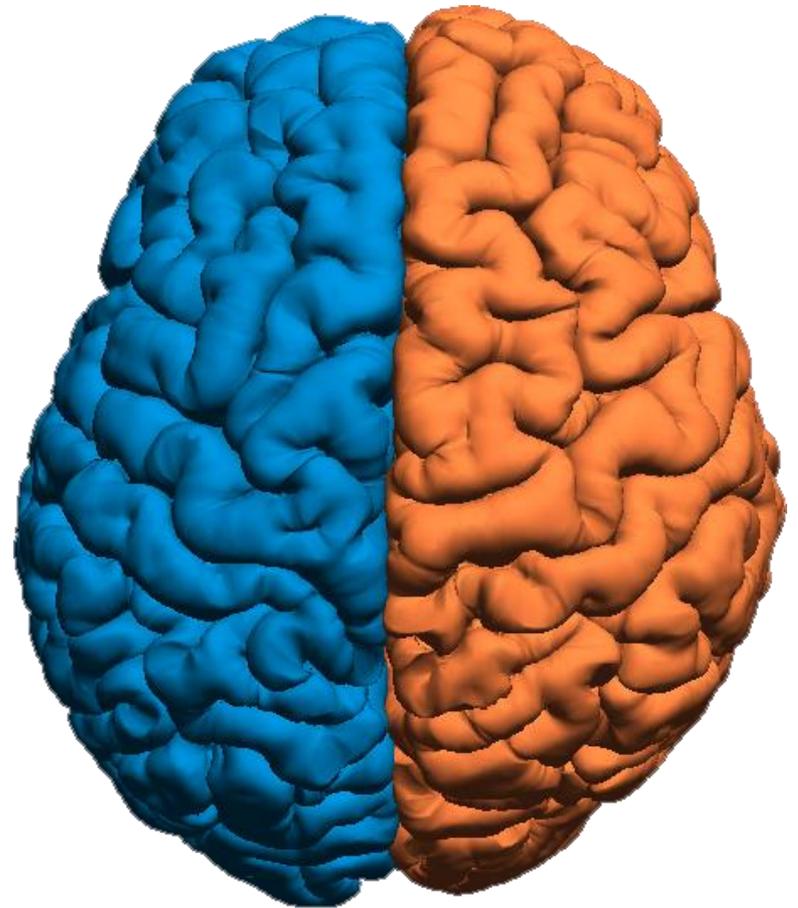


Contour view showing the inner (blue) and outer (orange) boundaries of the cortex.

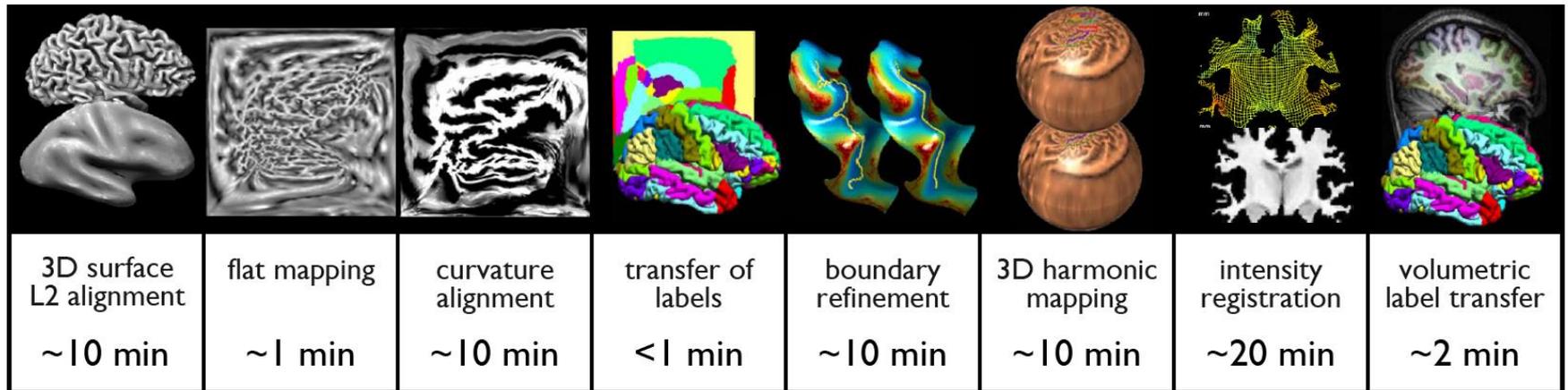
Split Hemispheres

We can separate the meshes into left and right hemispheres based on hour cerebrum labeling

These surface models are then used by the surface/volume registration and labeling routine (SVReg)

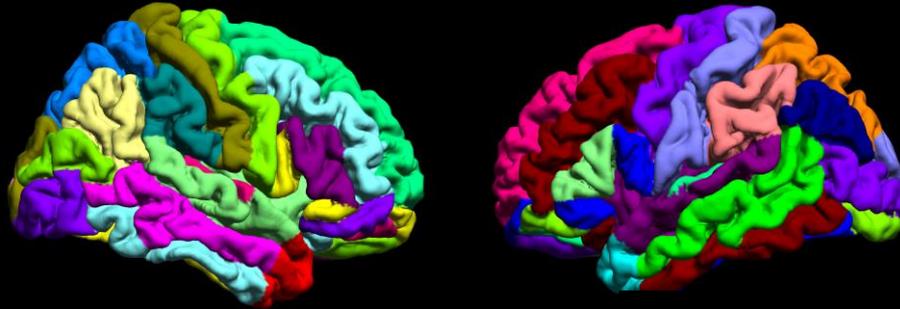
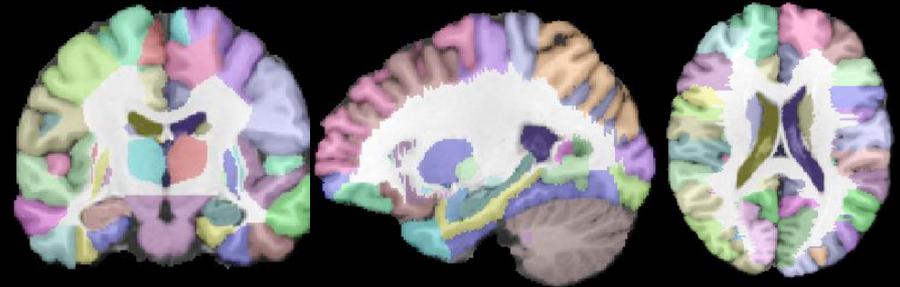


Surface-constrained Volumetric Registration



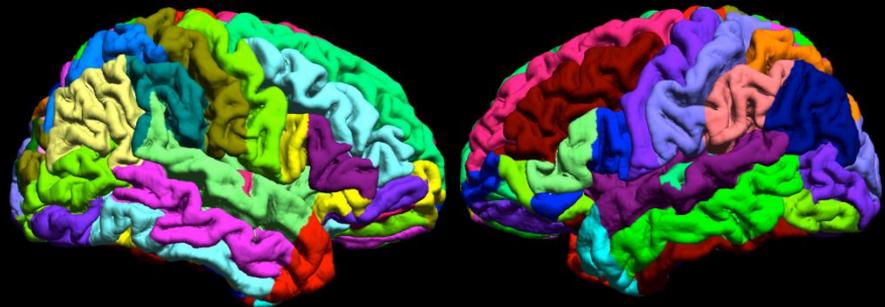
BrainSuite Atlas1

- Single subject atlas labeled at USC by an expert neuroanatomist
- 26 sulcal curves per hemisphere
- 98 volumetric regions of interest (ROIs), 35*2=70 cortical ROIs



BCI-DNI Atlas

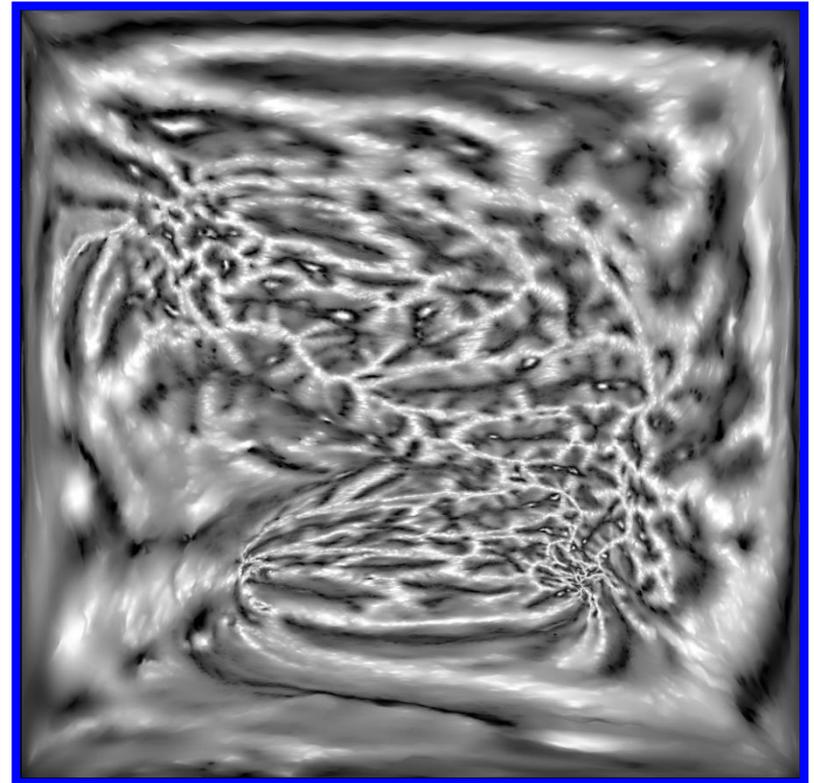
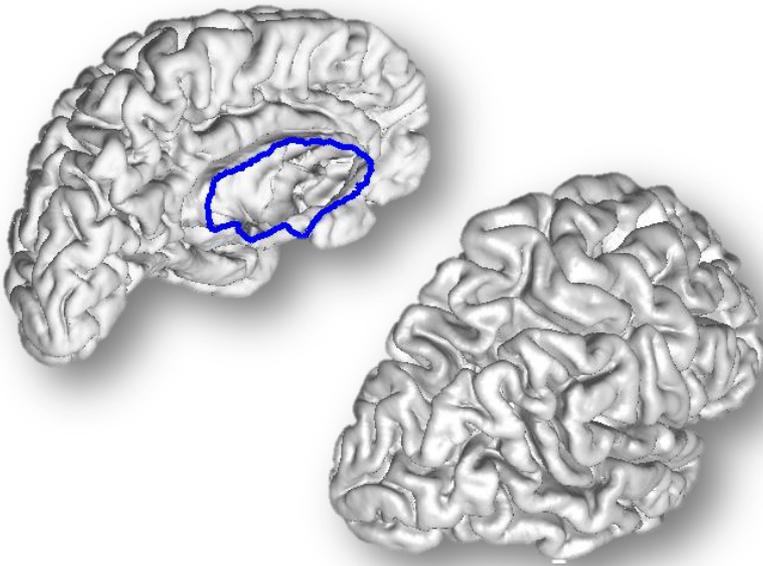
- Single subject atlas labeled at USC by an expert neuroanatomist
- high-resolution (0.5 mm × 0.5 mm × 0.8 mm) 3D MPRAGE, 3T scan
- 26 sulcal curves per hemisphere
- 95 volumetric regions of interest (ROIs), 33*2=66 cortical ROIs



Flat Mapping

Cortical Surface Parameterization

Corpus callosum



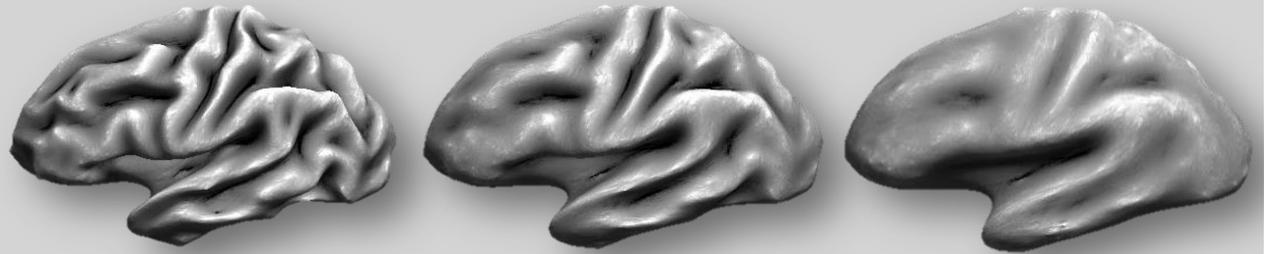
Flat-map color coded by curvature

Curvature Alignment

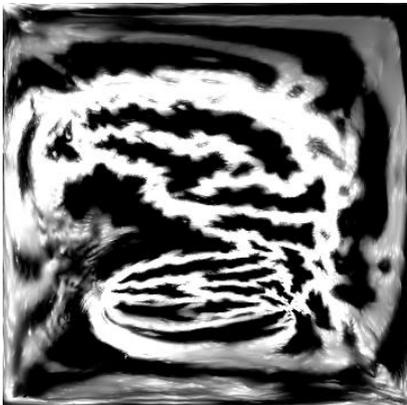
Input mid surface



Smoothed surfaces



Cumulative curvature computation for multiresolution representation



atlas



subject



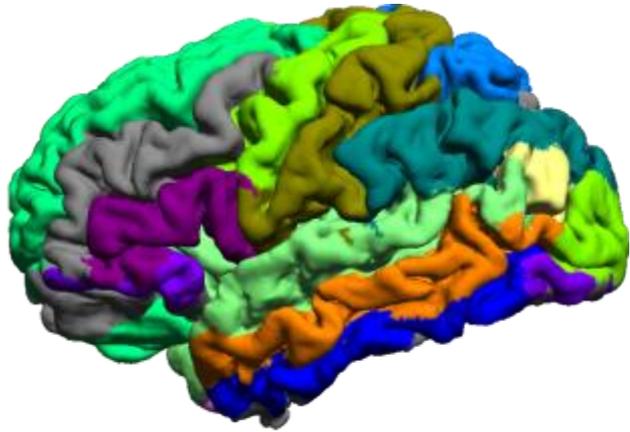
warped subject



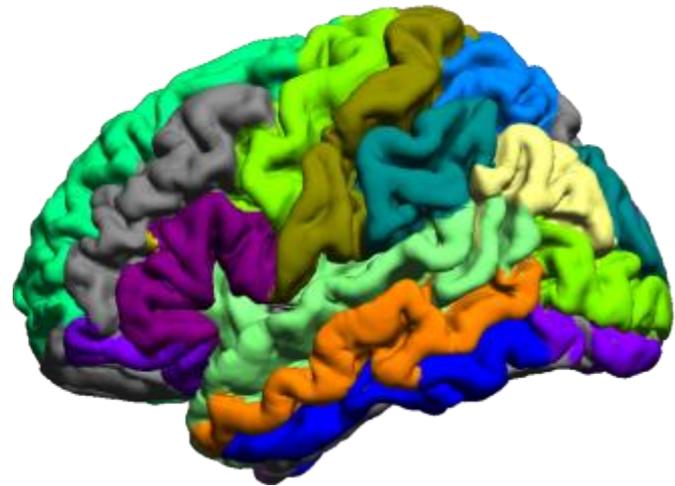
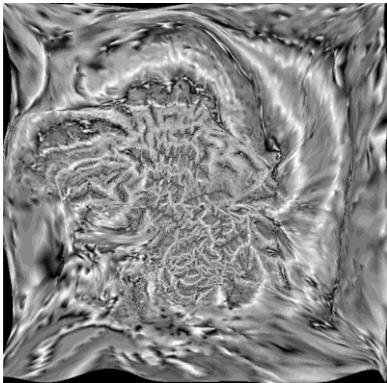
color-coded labels

Elastic matching for atlas and subject flat maps

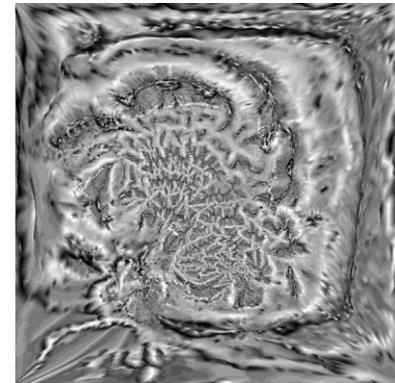
Transfer of Labels



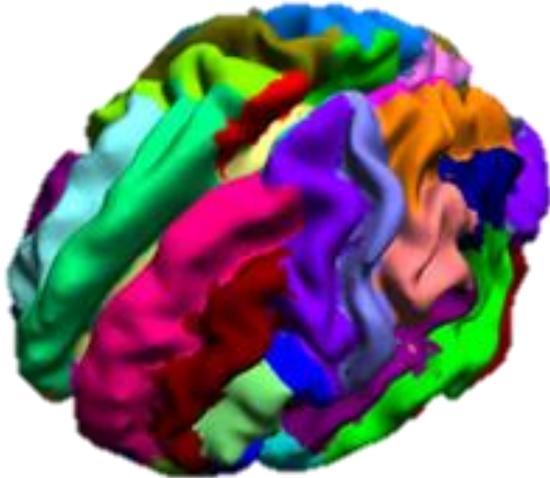
subject



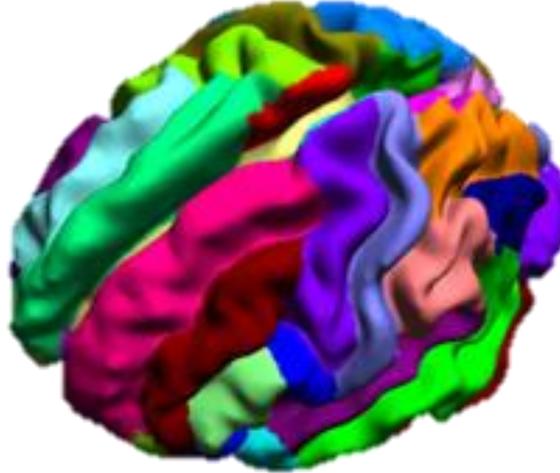
atlas



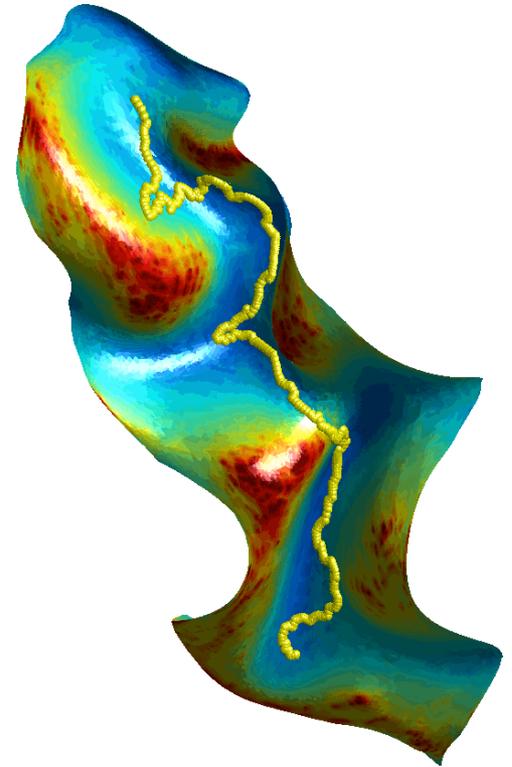
Boundary Refinement



Original labels plotted on a smoothed representation of a cortical surface.

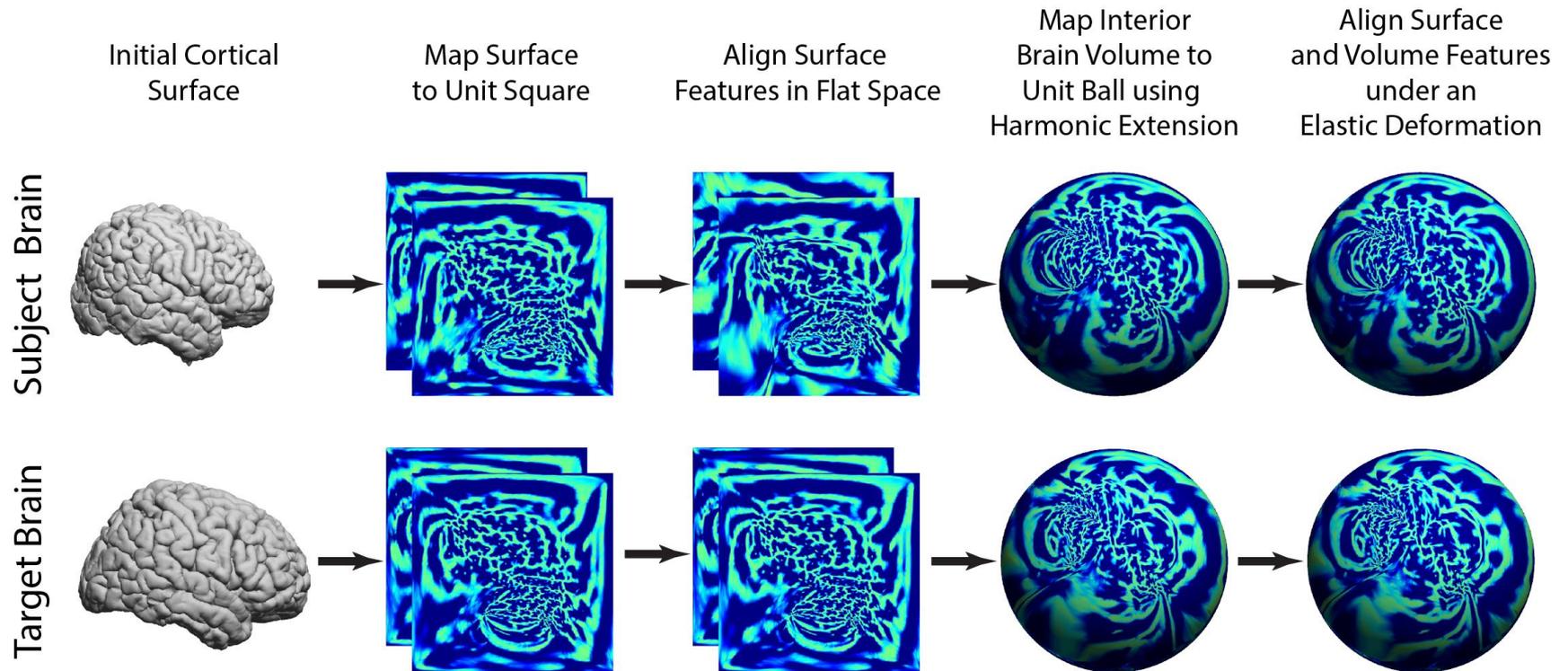


Labels after geodesic curvature flow plotted on a smoothed representation of a cortical surface.



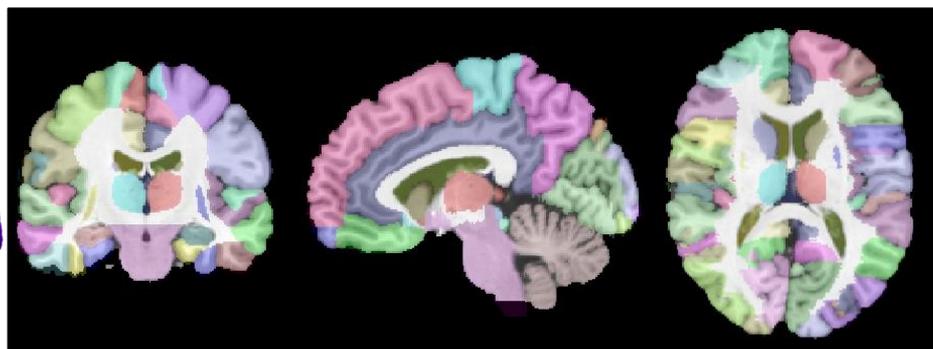
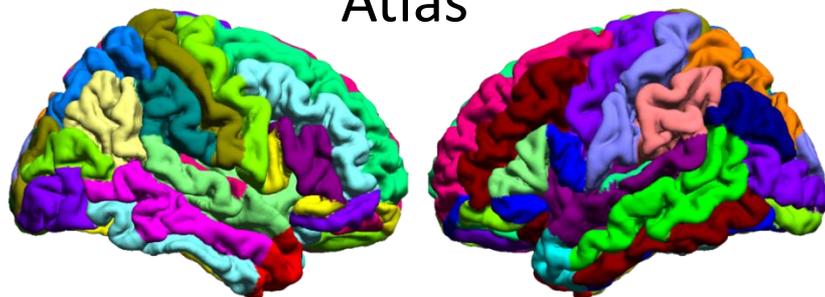
Animation of the geodesic curvature flow for sulcal refinement.

3D Harmonic Mapping & Intensity Registration



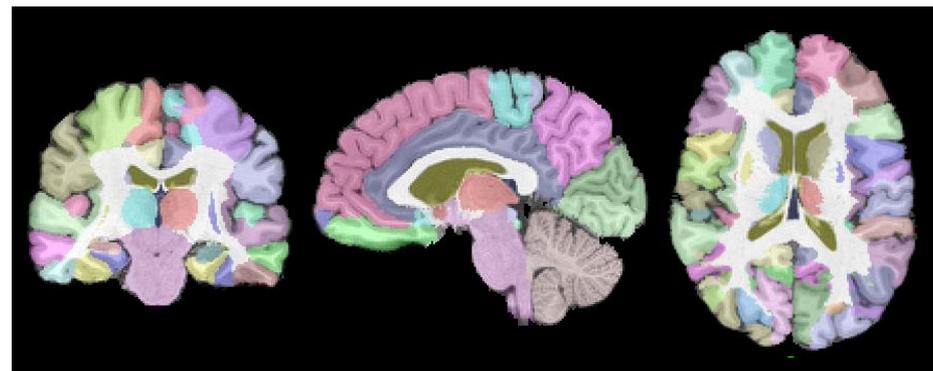
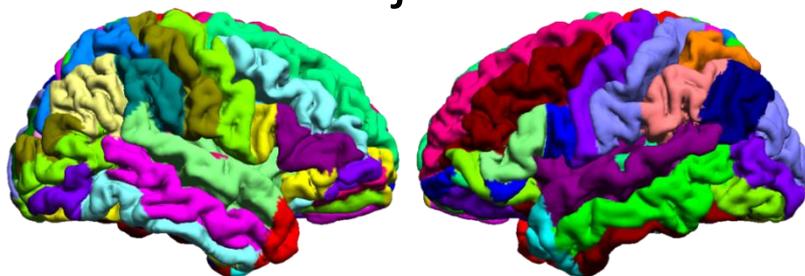
Volumetric Label Transfer

Atlas



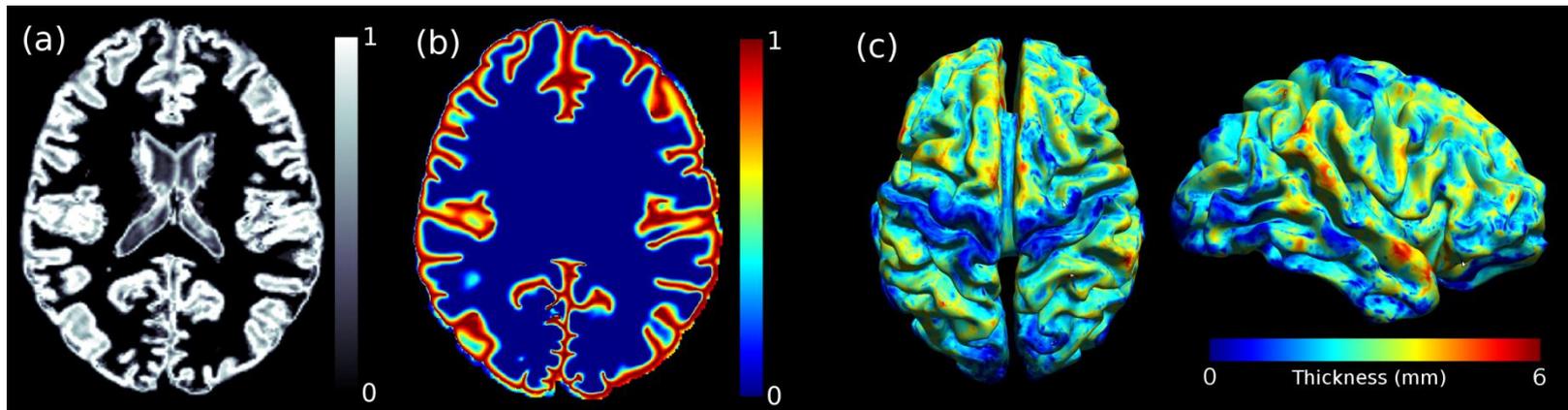
Views of the BrainSuite anatomical atlas, delineated into anatomical ROIs.

Subject



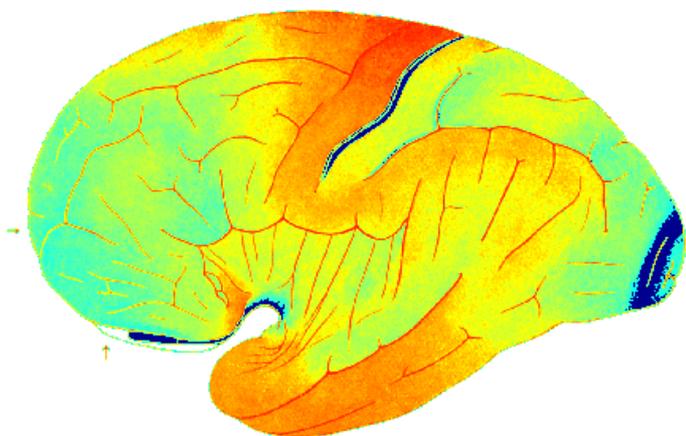
Similar views of an automatically labeled subject dataset.

Cortical Thickness using Partial Tissue Fraction Estimates

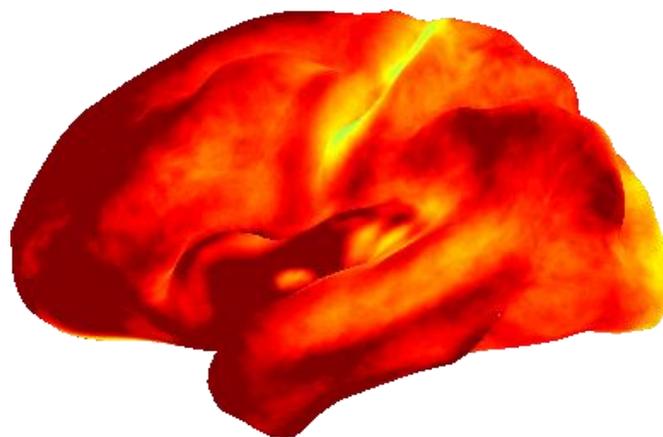


- (a) Gray-matter fraction estimated using a partial volume model;
- (b) Temperature map obtained using the proposed ALE method; and
- (c) Thickness estimate using the ALE method shown on the estimated mid-cortical surface.

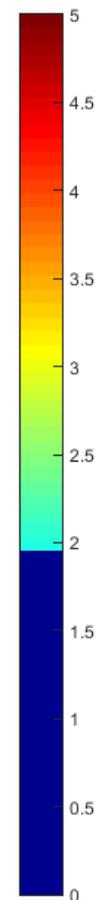
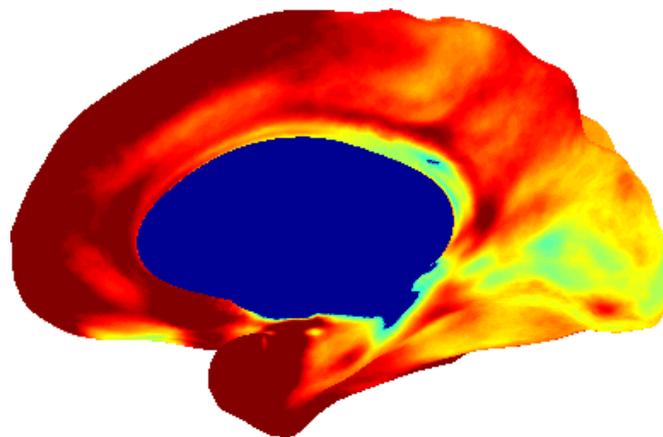
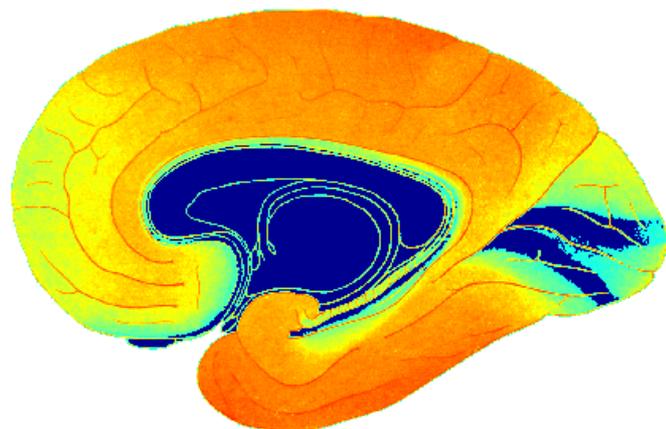
Cortical Thickness Comparisons



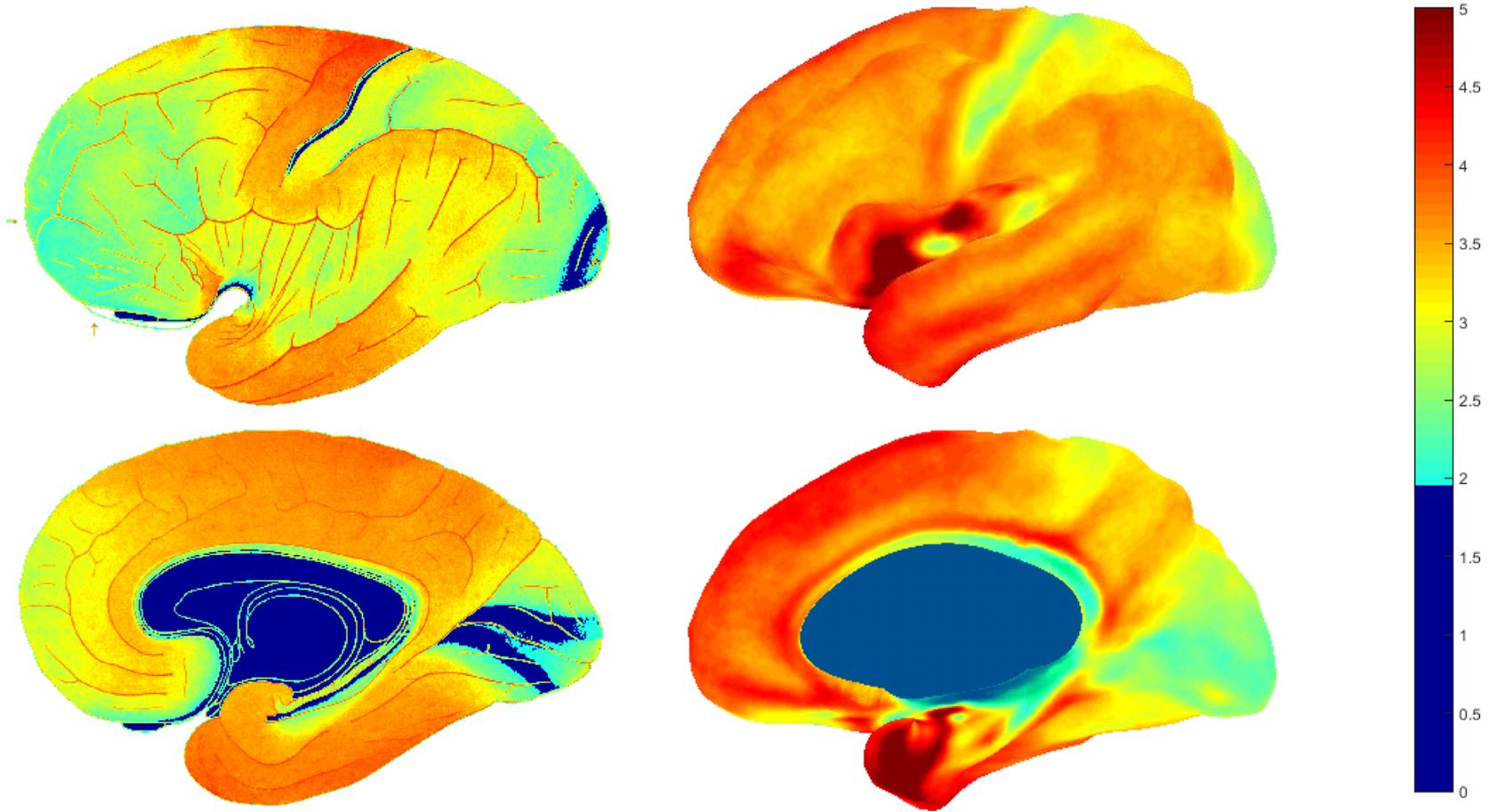
Von Economo and Koskinas (1925)



From MRI using linked distance
(averaged over 186 subjects)



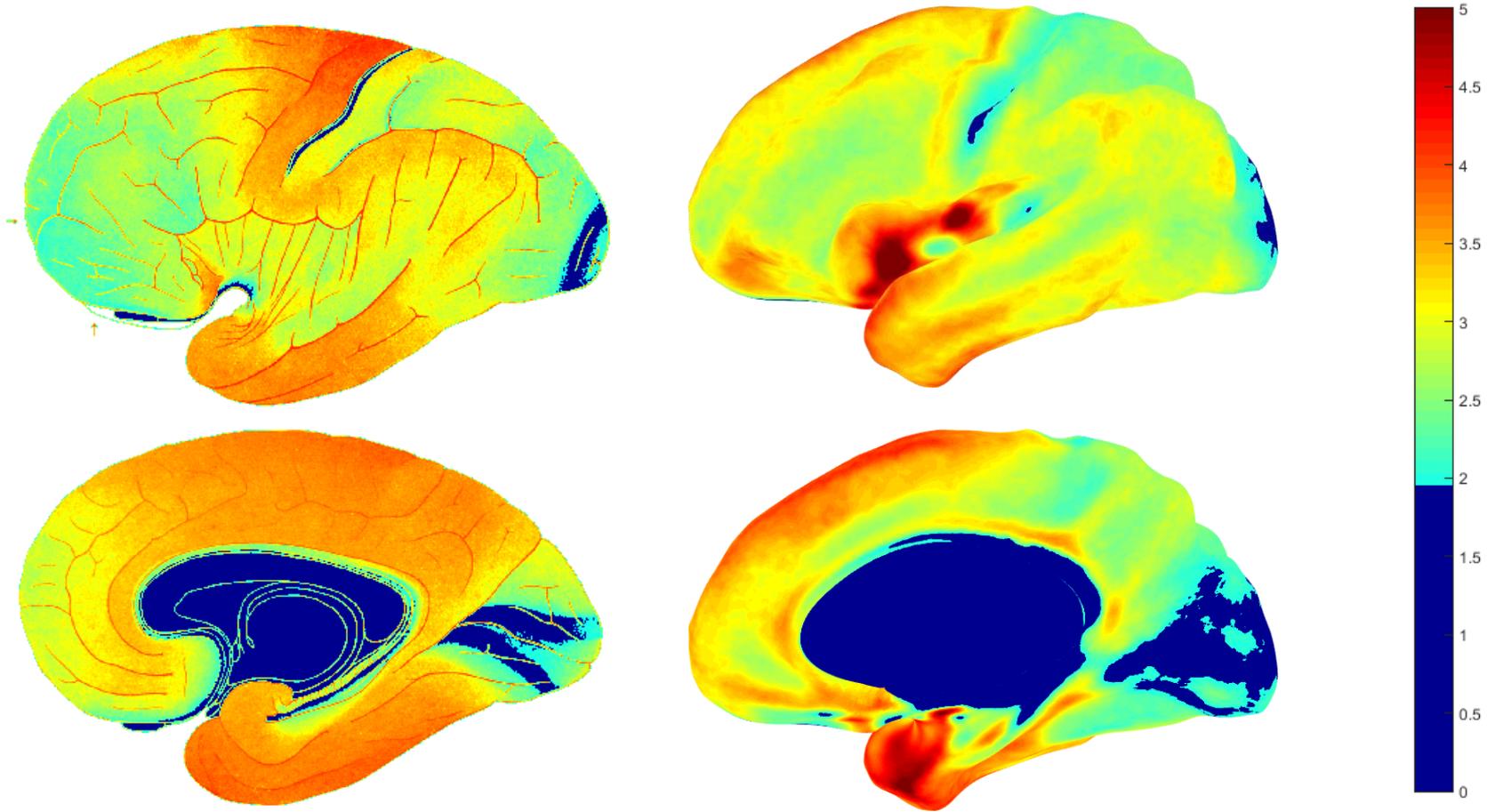
Cortical Thickness Comparisons



Von Economo and Koskinas (1925)

From MRI: isotropic heat equations
(averaged over 186 subjects)

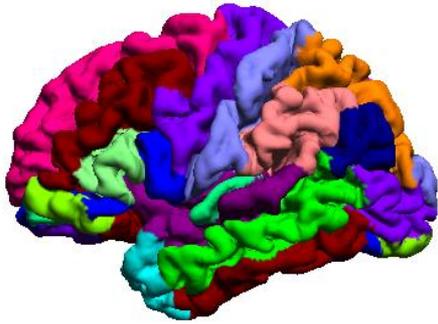
Cortical Thickness Comparisons



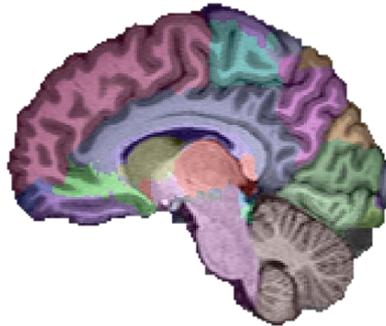
Von Economo and Koskinas (1925)

From MRI: anisotropic heat equation
(averaged over 186 subjects)

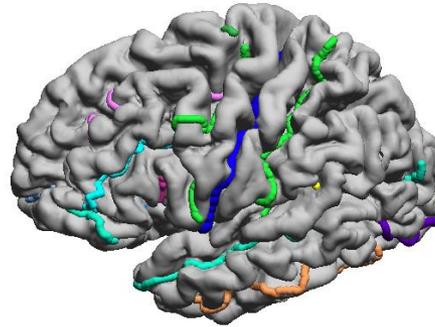
SVReg Outputs



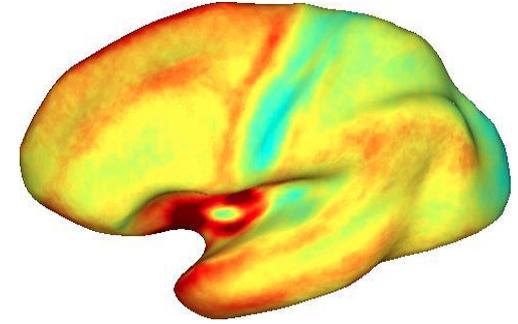
Labeled Surfaces



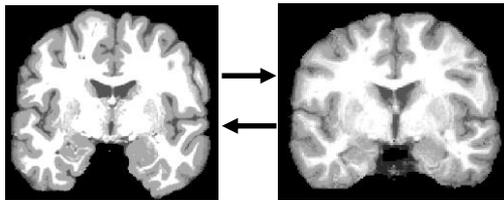
Labeled Volumes



Sulcal Curves



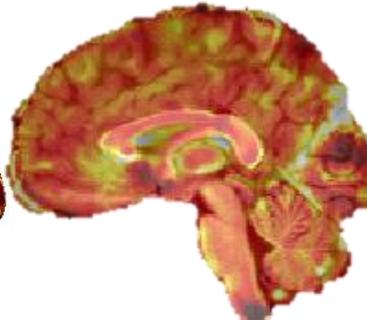
Cortical Thickness Maps



Subject to Atlas and Inverse Maps



Surface Jacobian Maps



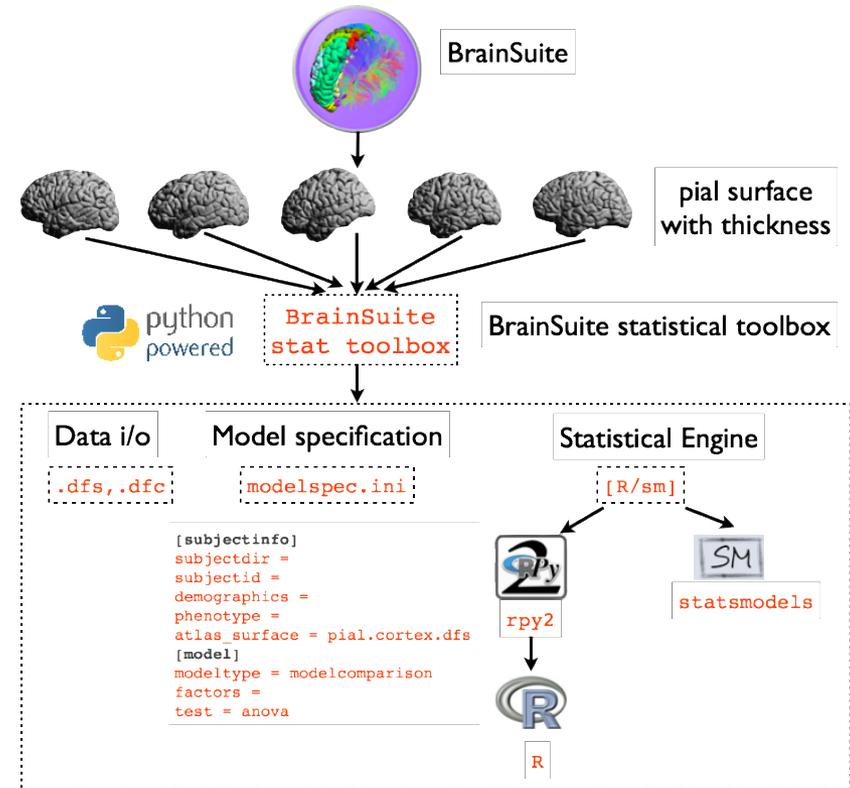
Volumetric Jacobian Maps

| ROI_ID | Mean_Thickness(mm) | GM_Volume(mm ³) | CSF_Volume(mm ³) | WM_Volume(mm ³) | Total_Volume(GM+WM)(mm ³) | Cortical_Area_mid(mm ²) | Cortical_Area_inner(mm ²) | Cortical_Area_giul(mm ²) |
|--------|--------------------|-----------------------------|------------------------------|-----------------------------|---------------------------------------|-------------------------------------|---------------------------------------|--------------------------------------|
| 120 | 4.17 | 2681.92 | 853.40 | 1327.41 | 4029.32 | 7489.67 | 6302.70 | 960.68 |
| 121 | 4.16 | 2498.02 | 6942.24 | 3050.49 | 9459.11 | 6921.69 | 5610.89 | 9599.10 |
| 130 | 3.66 | 14879.67 | 9927.32 | 6188.33 | 21180.00 | 4232.24 | 3684.07 | 6176.11 |
| 131 | 3.66 | 14473.87 | 3296.06 | 6945.39 | 21419.26 | 4360.15 | 3765.01 | 5000.23 |
| 142 | 3.92 | 3175.93 | 681.30 | 1814.73 | 4959.67 | 954.50 | 897.32 | 1140.99 |
| 143 | 3.41 | 4251.05 | 722.28 | 2765.81 | 7016.86 | 1398.41 | 1267.27 | 1738.68 |
| 144 | 4.50 | 5664.89 | 1900.69 | 2302.25 | 7955.14 | 1598.78 | 1236.32 | 2238.94 |
| 145 | 3.78 | 4709.39 | 1344.84 | 2924.60 | 6771.80 | 1495.04 | 1248.98 | 1991.26 |
| 146 | 4.28 | 2172.41 | 836.33 | 580.41 | 2552.82 | 664.11 | 429.33 | 1056.60 |
| 147 | 3.52 | 1287.09 | 440.38 | 316.83 | 1603.92 | 387.87 | 311.46 | 521.19 |
| 150 | 3.20 | 1302.17 | 3289.72 | 9672.45 | 20894.62 | 4644.47 | 4330.26 | 5407.39 |
| 151 | 3.16 | 1808.26 | 2915.41 | 7775.53 | 17619.59 | 3693.95 | 3389.52 | 4325.96 |
| 162 | 4.00 | 2591.45 | 1128.97 | 657.39 | 3259.84 | 737.81 | 602.61 | 996.03 |
| 163 | 4.52 | 2111.90 | 897.99 | 646.71 | 2756.61 | 589.98 | 458.15 | 817.60 |
| 164 | 3.92 | 3352.98 | 738.26 | 911.17 | 4264.16 | 1006.01 | 735.43 | 1432.99 |
| 165 | 3.50 | 3705.59 | 795.91 | 1170.46 | 4876.05 | 1202.79 | 910.13 | 1671.79 |
| 166 | 3.91 | 2104.74 | 211.41 | 346.74 | 2659.49 | 786.11 | 415.03 | 481.24 |
| 167 | 3.47 | 2488.29 | 894.36 | 1308.20 | 3796.49 | 979.53 | 860.75 | 1231.51 |
| 168 | 4.39 | 1423.17 | 343.20 | 493.27 | 1916.44 | 411.44 | 370.42 | 516.09 |
| 169 | 4.67 | 1996.07 | 602.77 | 723.31 | 2719.39 | 562.33 | 508.64 | 747.14 |

ROI Morphometric Measures

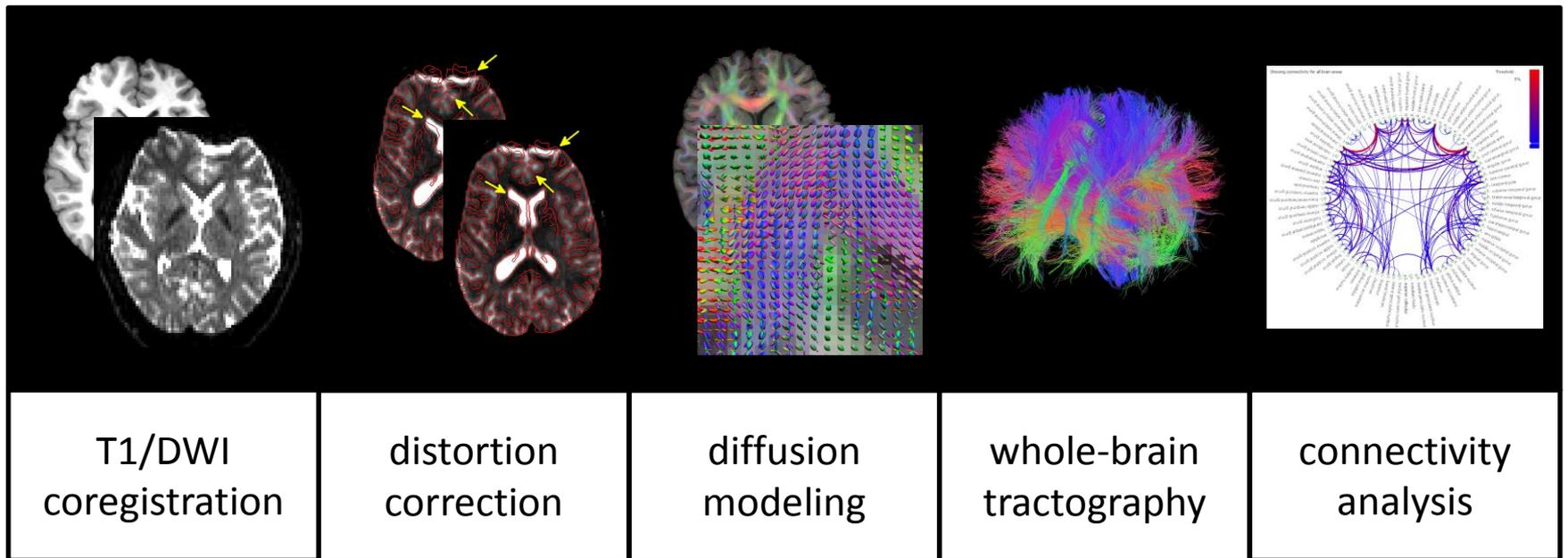
BrainSuite Statistical Toolbox

- Performs group analysis for surface and volume data
 - surface-based cortical morphometry
 - volumetric comparisons
 - tensor-based morphometry (TBM)
- Implemented in Python with rpy2.
- Offers statistical methods:
 - ANOVA, GLM, correlation
 - T-tests – paired/unpaired
 - Provision for multiple testing - FDR
- Integration with jupyter notebooks
- Uses R data.table to efficiently vectorize operations
- Cross-platform: Win, Mac, Linux
- Open source (GPL v2)

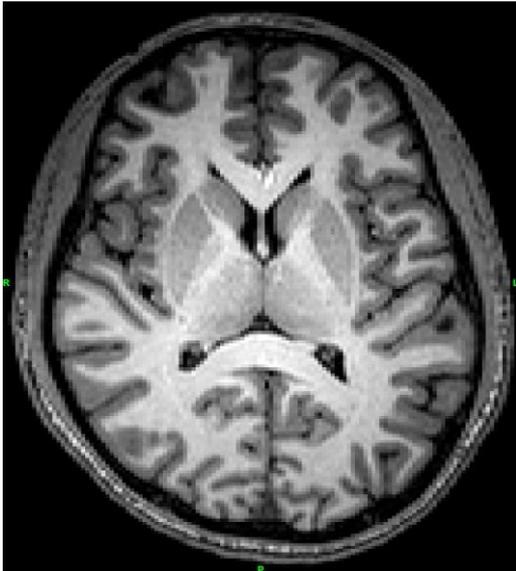


Available at <http://brainsuite.org/bss>

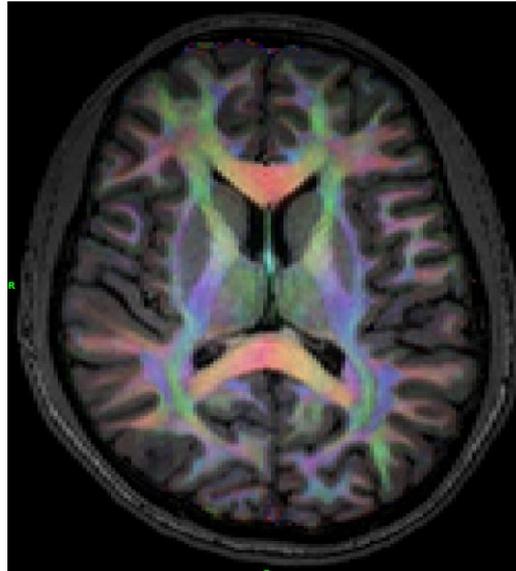
BrainSuite Diffusion Pipeline



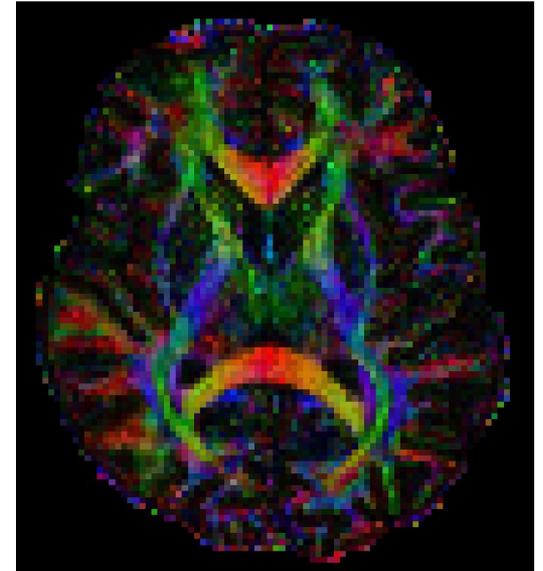
T1 / Diffusion Registration



T1 Coordinates
(Surfaces, Labels)



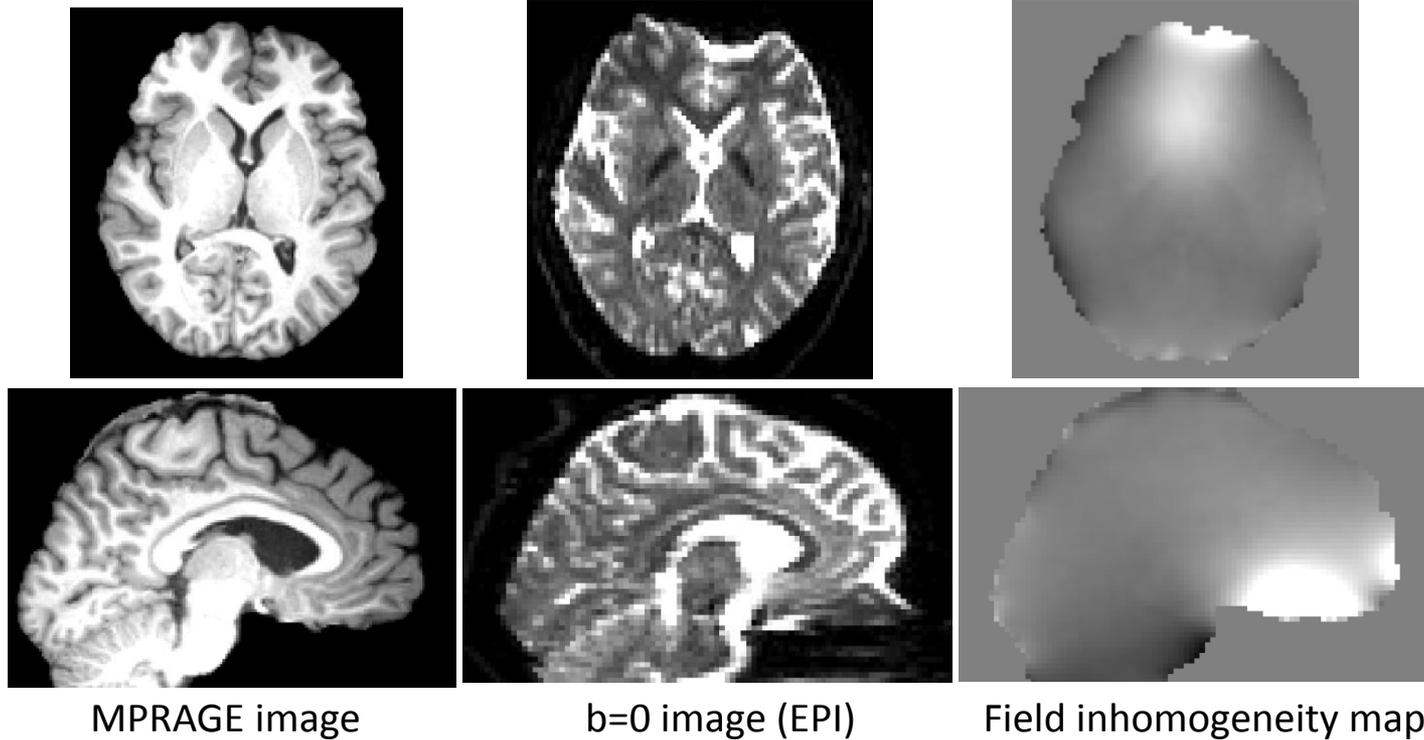
T1/Color-FA
Overlay



Diffusion Coordinates

- If we want to fuse information from diffusion and structural MRI, we need to co-register them.
- However, rigid registration is not enough.

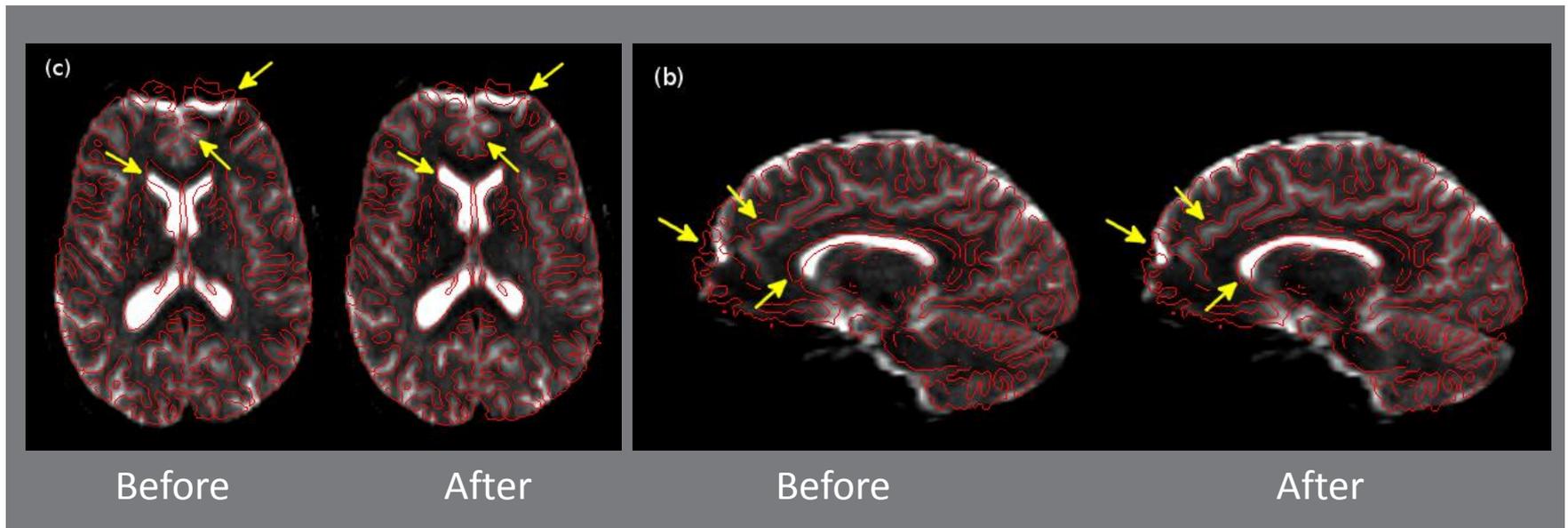
EPI Distortion



- Diffusion MRI uses fast acquisition – echo planar imaging (EPI)
- Susceptibility differences → magnetic field (B0) inhomogeneity
- EPI is sensitive to B0 inhomogeneity → localized geometric distortion

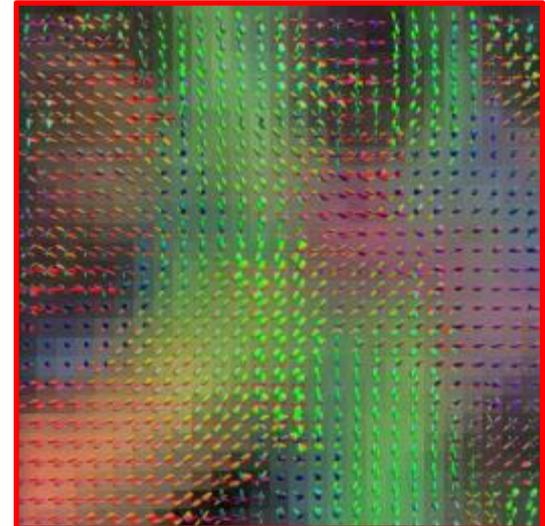
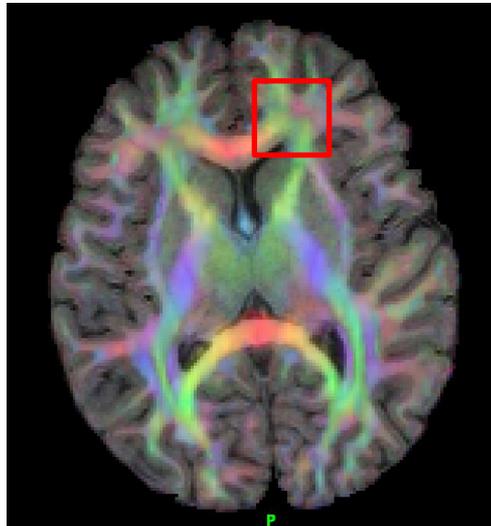
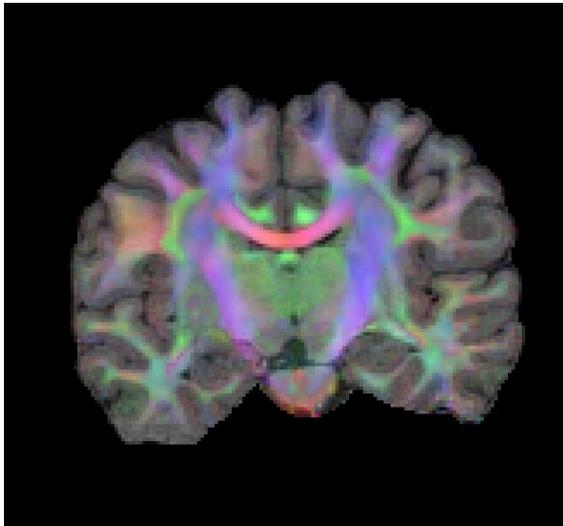
Registration-based Correction

- Corrects the distortion in diffusion (EPI) images using non-rigid registration
- No fieldmap is required
- Similar performance to fieldmap method

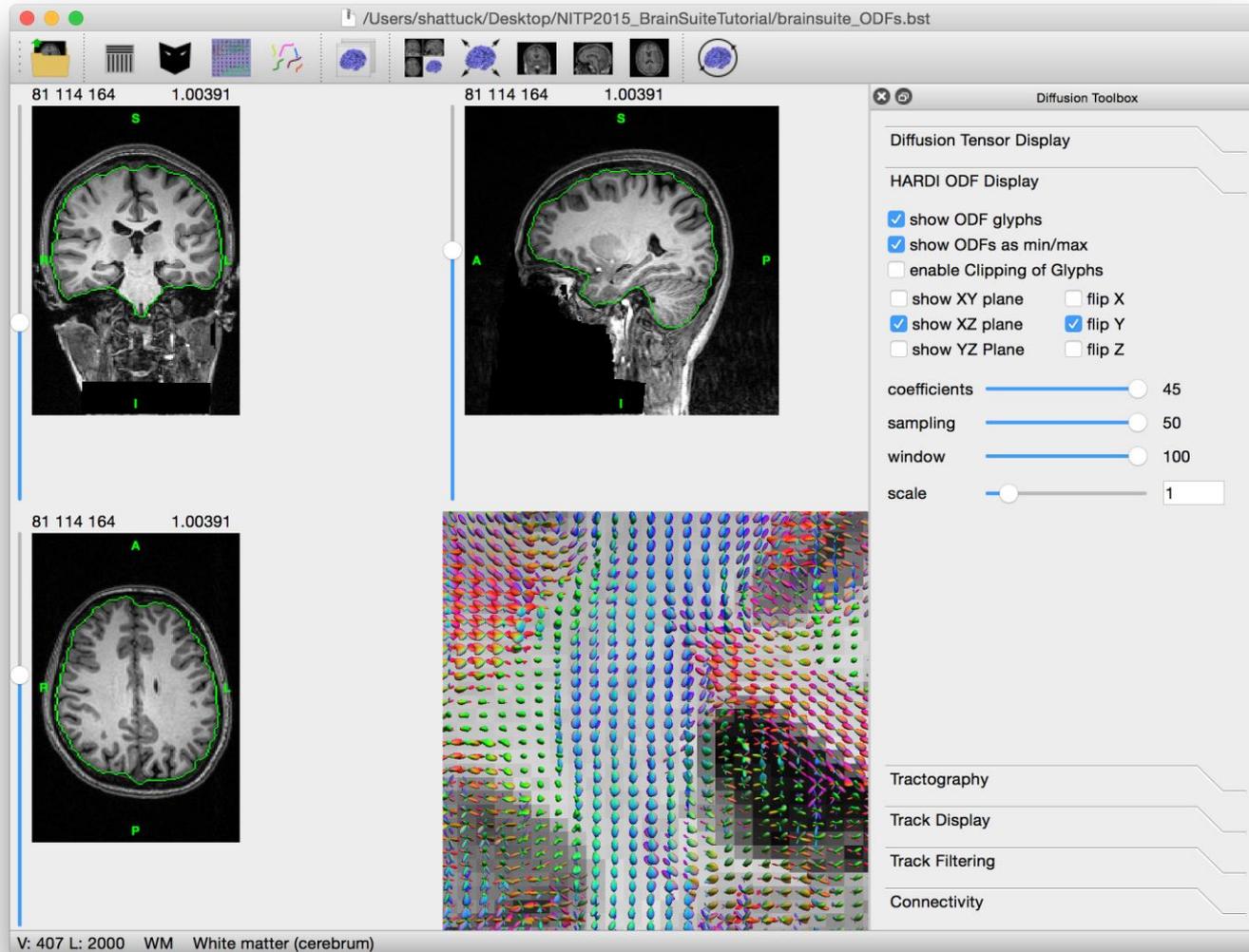


Tensor and ODF Estimation

- Estimate diffusion tensors
 - FA, MD, color-FA
- Axial, Radial diffusivity
- ODFs using FRT (Tuch, 2004)
- ODFs using FRACT (Haldar and Leahy, 2013)
 - improved accuracy
 - higher angular resolution

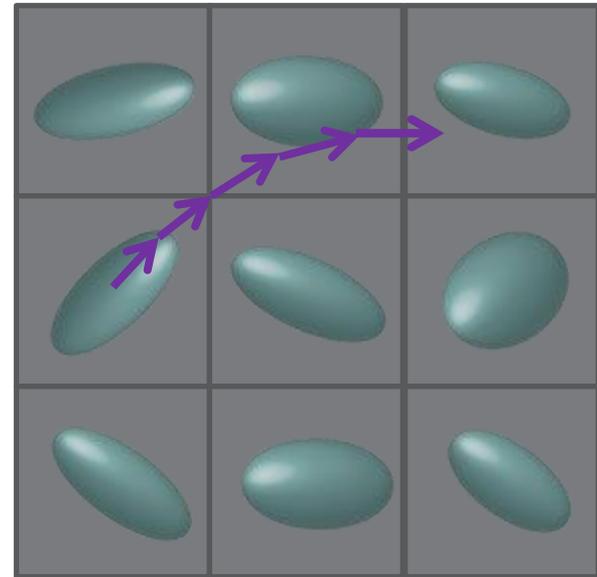


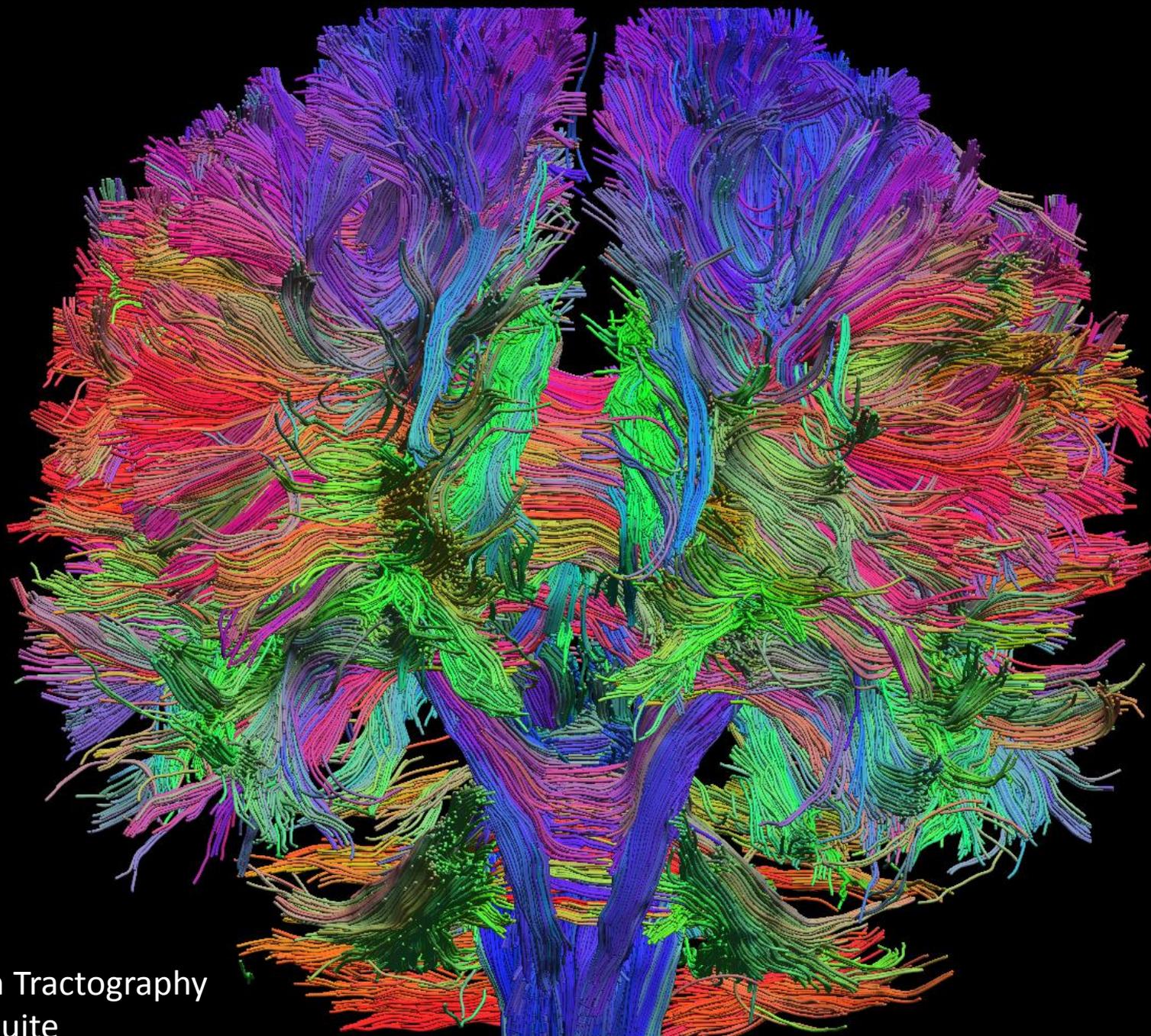
Visualization of Diffusion Data



Fiber Tracking

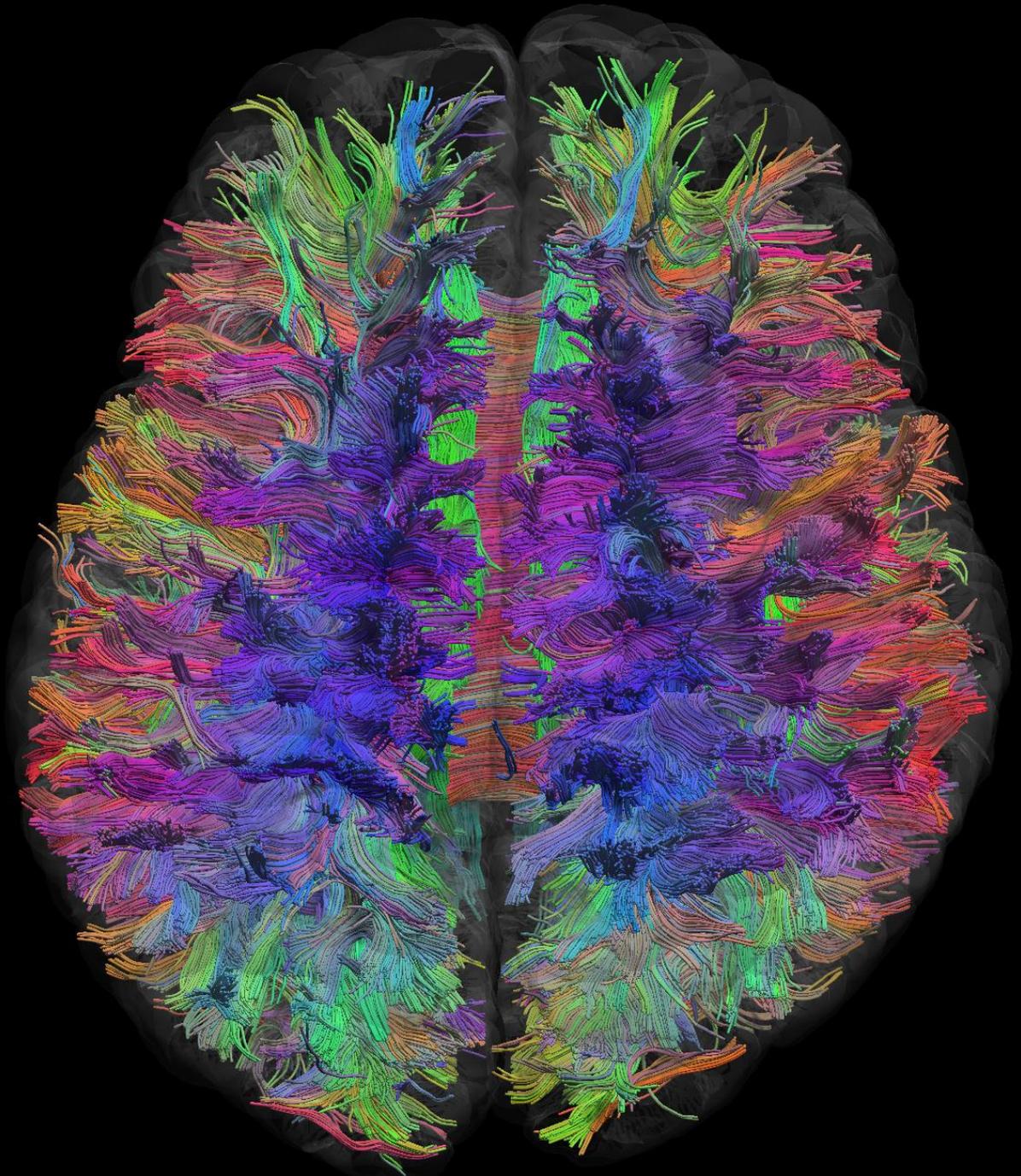
- We can trace out fiber tracks in the data using direction vectors determined from DTI ellipses or by analyzing ODFs.
- Essentially, we step through each voxel, reorienting the direction based on the estimated diffusion pattern.
- Various criteria can be used to determine when to start or stop the tracking.
- We can seed at numerous points throughout the image to get a picture of whole brain tractography.





Diffusion Tractography
in BrainSuite

Axial View of Fiber Tracking



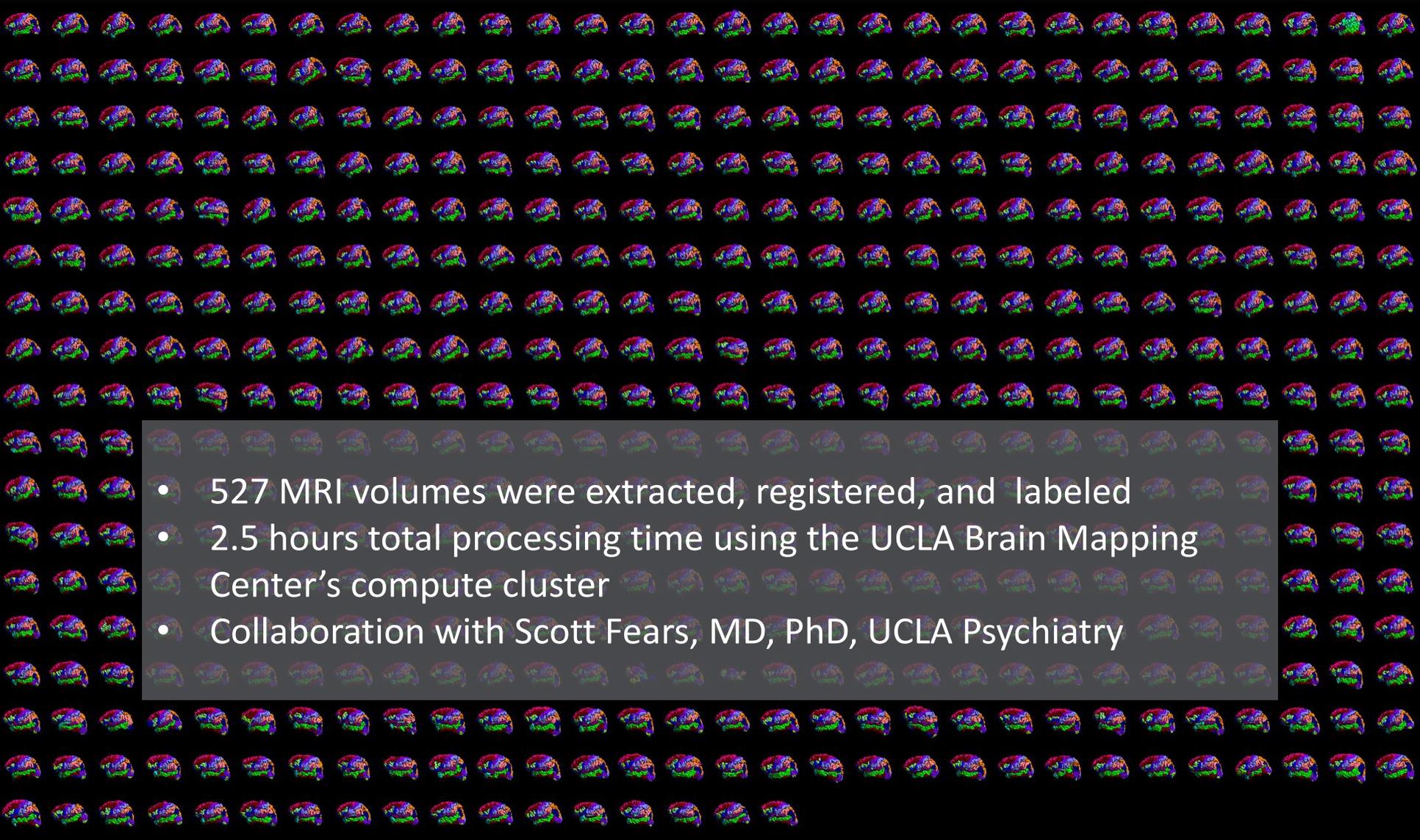
Diffusion Tractography
in BrainSuite

Applications and Ongoing Work

Large Scale Brain Mapping

- The UCLA Brain Mapping Center's data center houses a 408-node cluster with 3,264 cores attached to a 1.3 petabyte high performance storage array.

Large Scale Brain Mapping

- 
- 527 MRI volumes were extracted, registered, and labeled
 - 2.5 hours total processing time using the UCLA Brain Mapping Center's compute cluster
 - Collaboration with Scott Fears, MD, PhD, UCLA Psychiatry

Quality Control

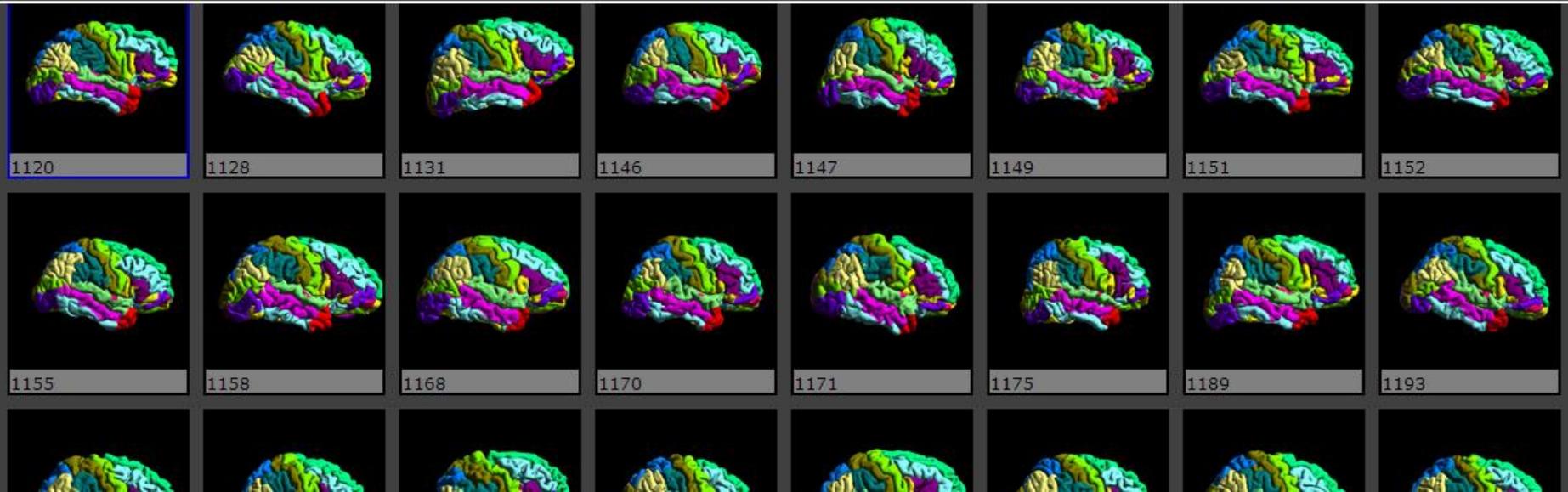
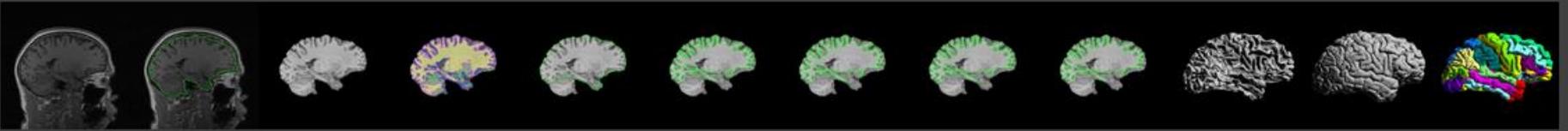
loaded subject list

showing subjects 1-100 of 100 subjects after surface labeling at size 128

thumbnail size
first subject
number of subjects
show stage

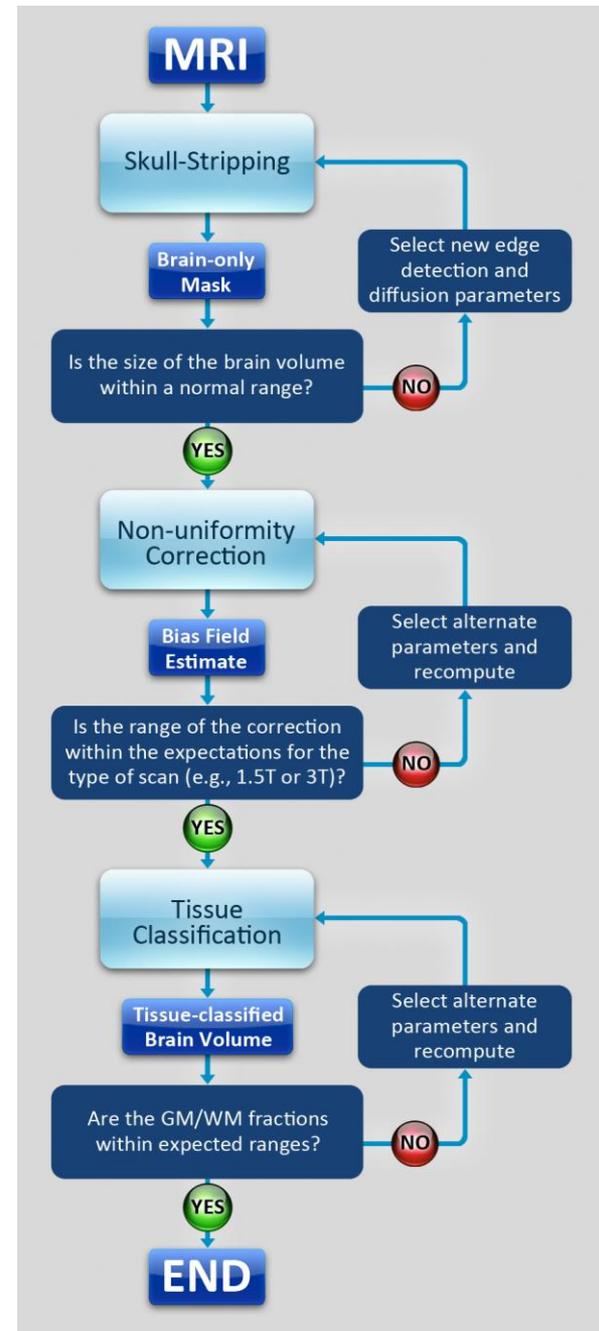


showing subject 33 (1120)



Error Detection

- We plan to develop interfaces that facilitate identification of errors in the processing chain.
 - Web-based reports
 - Software interfaces that allow errors to be corrected and the processing continued
- Quality assurance
 - Automatically identify potential failures based on measures.
 - For example, is the total brain volume within a normal range?



BrainSuite & Nipype



Nipype:
Neuroimaging in Python
Pipelines and Interfaces

- BrainSuite command line tools now work with Nipype.
 - An interface for BrainSuite's cortical surface extraction sequence is in the Nipype public github repository.
 - We have also developed Nipype interfaces for BDP and SVReg.
- We have also developed workflows for the BrainSuite processing streams that can be performed with nipype.
 - Can be run on a local machine or through Amazon Web Services
 - Workflows can be run in parallel
- Makes it easier to operate with other software packages.

<http://brainsuite.org/nipype>

Nipype / BrainSuite Tutorial



JUPYTER

FAQ



Nipype Tutorial: Cortical Surface Extraction, BDP, SVReg in Parallel

Welcome to our interactive Nipype tutorial. Below you will find a mix of code and explanatory text. If you are viewing this from an active Jupyter Notebook server, you can execute our code as you read through our tutorial. If you are unfamiliar with Jupyter Notebook, you can learn the basics [here](#).

Or, from the toolbar, go to `Help | User | Interface Tour`.

Here are some essentials:

- The current cell is surrounded by a colored border
- Runnable code is contained in a greyed box, denoted by `In [#] :` next to the cell
 - To execute the code in the current cell, use `Shift+Enter`
 - `!` denotes a bash command that will be executed. All bash commands have been commented out, so you may choose whether or not to execute them. We advise that you read each bash command before choosing to execute them. To execute the commands, uncomment the command, then use `Shift+Enter` to run the bash command.
- Pressing `Shift+Enter` on a text cell simply moves you to the cell below

Overview of Workflow

Nipype includes features that allow you to run multiple processes in parallel, in a single Nipype workflow. In a workflow that runs through BrainSuite's CSE, BDP, and SVReg, parallel processing is especially useful, and can help reduce processing time. In particular, once BFC has finished running, BDP and the rest of CSE can be run in parallel. Finally, when CSE is complete, SVReg can be started, regardless of whether BDP has finished.

Below, we will walk through our example code, which is downloadable [here](#). The code creates a workflow, `brainsuite_workflow`, that uses through CSE, BDP and SVReg, and is run using Python's multiprocessing library by calling [Nipype's MultiProc plugin](#). Finally, `ThicknessPVC` is run after `brainsuite_workflow` has finished executing.

<http://nbviewer.jupyter.org/url/brainsuite.org/code/BrainSuiteNipypeParallel.ipynb>

Nipype / BrainSuite Tutorial

Checking your installation

First, we'll check that all of BrainSuite's executables have been added to your system's path variable.

If you have not done so already, first install BrainSuite, by following the instructions on our [installation page](#). Be sure to follow the instructions for installing the required MATLAB Compiler Runtime, which is required for SVReg, BDP and ThicknessPVC.

The following python code will ensure that your system's path variable has been set up properly. In particular, the following paths must be added (replace `your_path` with the path to your BrainSuite directory):

- `/your_path/BrainSuite15c/bin/`
- `/your_path/BrainSuite15c/svreg/bin/`
- `/your_path/BrainSuite15c/bdp/`

Run the cell below and follow the instructions printed out.

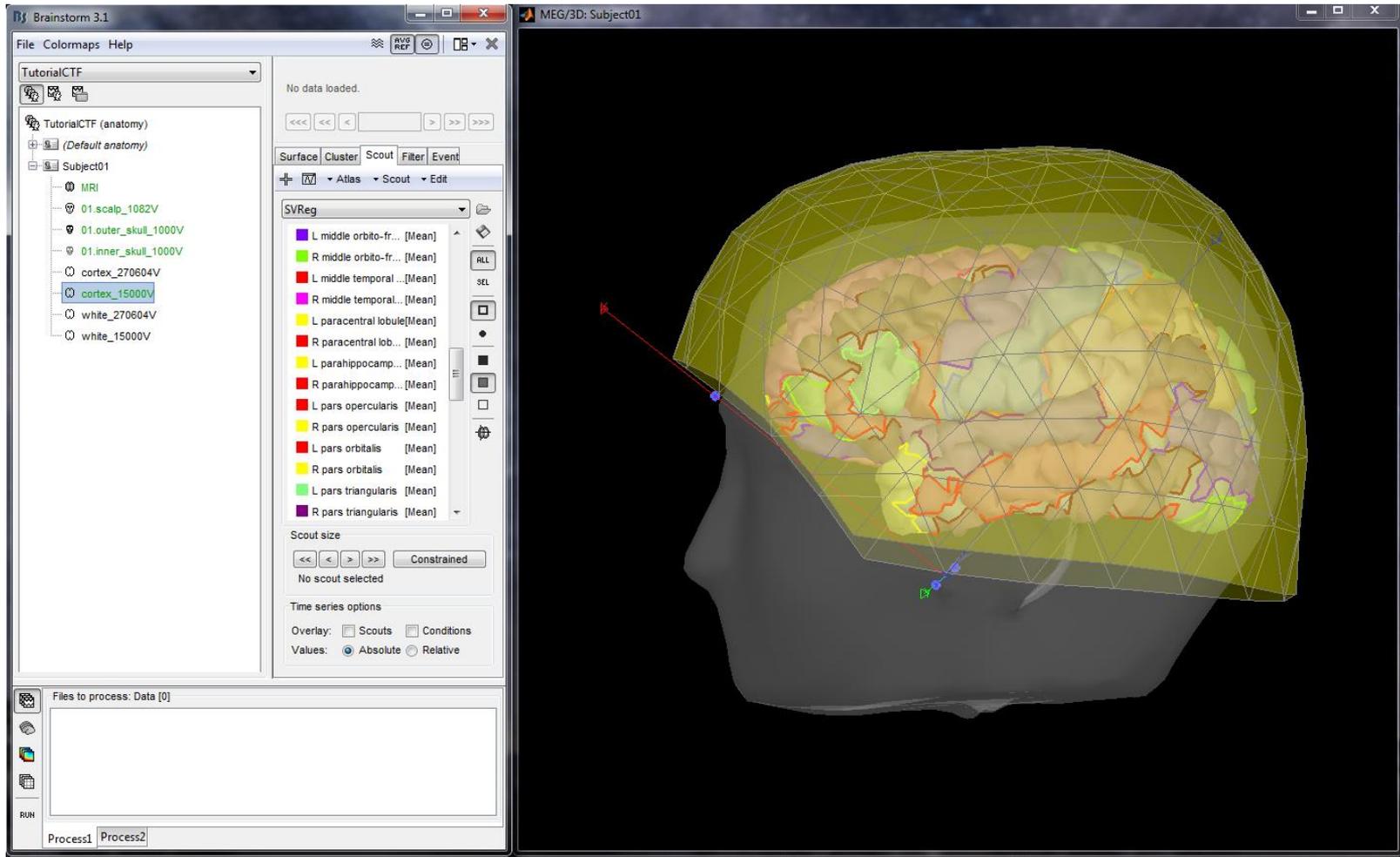
(Note that bse is just one of many steps in CSE. Since the rest of CSE is contained in the same folder as bse, it is sufficient to ensure that bse can be called properly)

```
In [1]: from distutils.spawn import find_executable
print 'Message to user:'
if(find_executable('bse') and find_executable('svreg.sh') and find_executable('bdp.sh')):
    print 'Your system path has been set up correctly. Continue on with the tutorial.'
else:
    print 'Your system path has not been set up correctly.'
    print 'Please add the above paths to your system path variable and restart the kernel for this tutorial.'
    print 'Edit your ~/.bashrc file, and add the following line, replacing your_path with the path to BrainSuite15c:\n'
    print 'export PATH=$PATH:/your_path/BrainSuite15c/svreg/bin:/your_path/BrainSuite15c/bdp:/your_path/BrainSuite15c/bin'
```

You must also have Nipype and its dependencies installed. See [Nipype's installation page](#) for more information. Another good resource for Nipype installation is the [Nipype Beginner's Guide](#).

<http://nbviewer.jupyter.org/url/brainsuite.org/code/BrainSuiteNipypeParallel.ipynb>

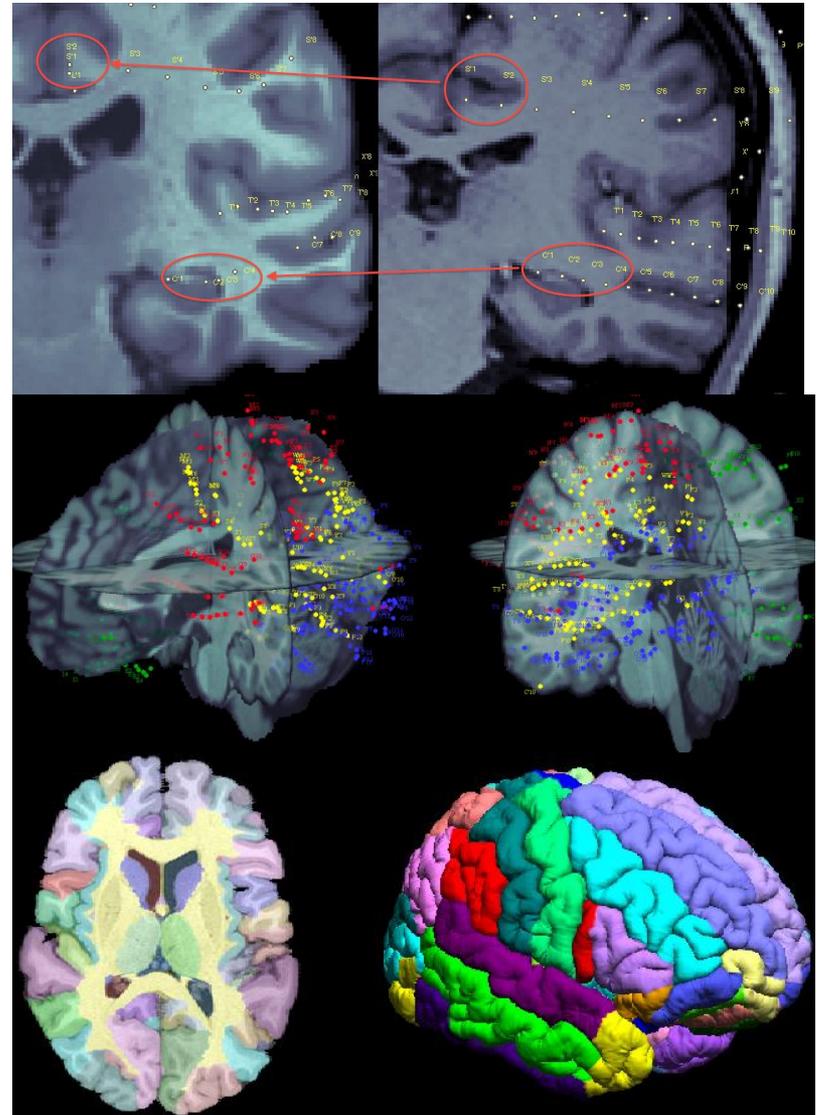
Integration with BrainStorm



BrainSuite Cortical Surface Model with ROIs Labeling imported into BrainStorm. The BrainSuite parcellation can be directly imported into BrainStorm, where the ROIs are useful for interpreting current sources.

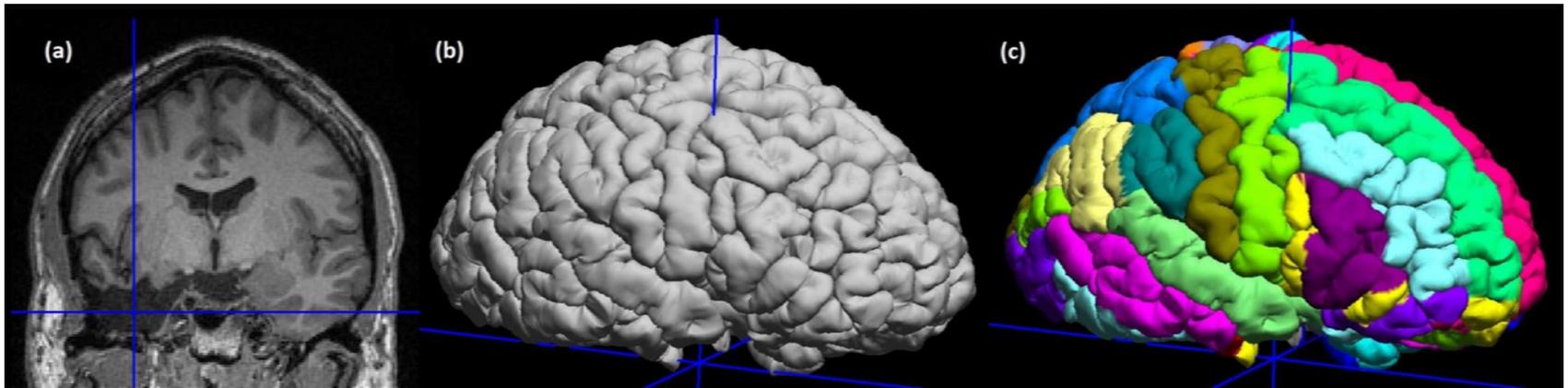
SEEG Mapping

- Stereo-electroencephalography (SEEG) are implanted to localize the source of epilepsy
- Goal: use SVREG to map SEEG electrode data into a common space
- SEEG electrode positions are deformed by the registration



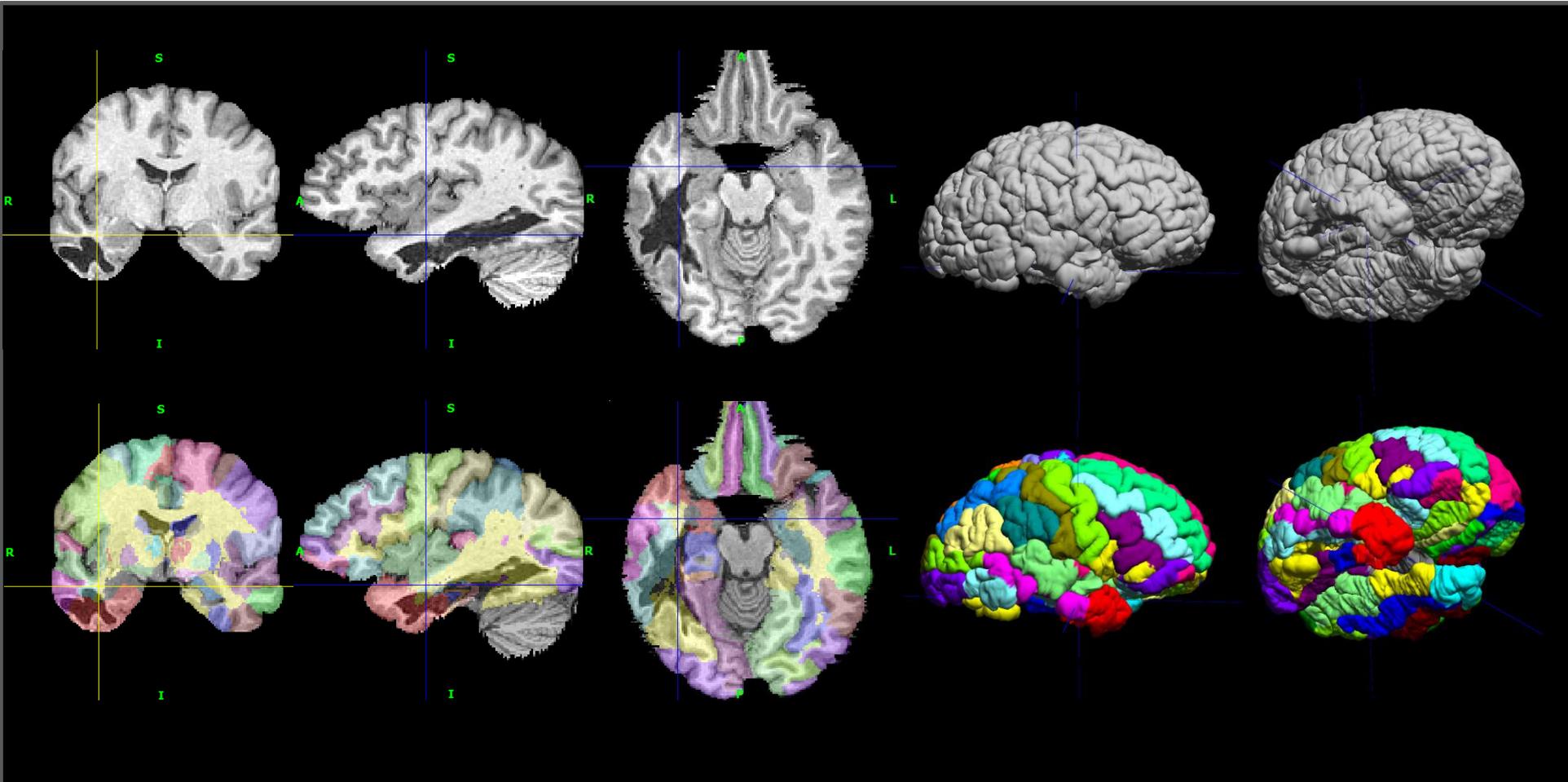
Mapping of SEEG electrodes to atlas space (J. Mosher, A. Joshi, and R. Leahy, unpublished work)

Segmentation & Labeling of Abnormal Data



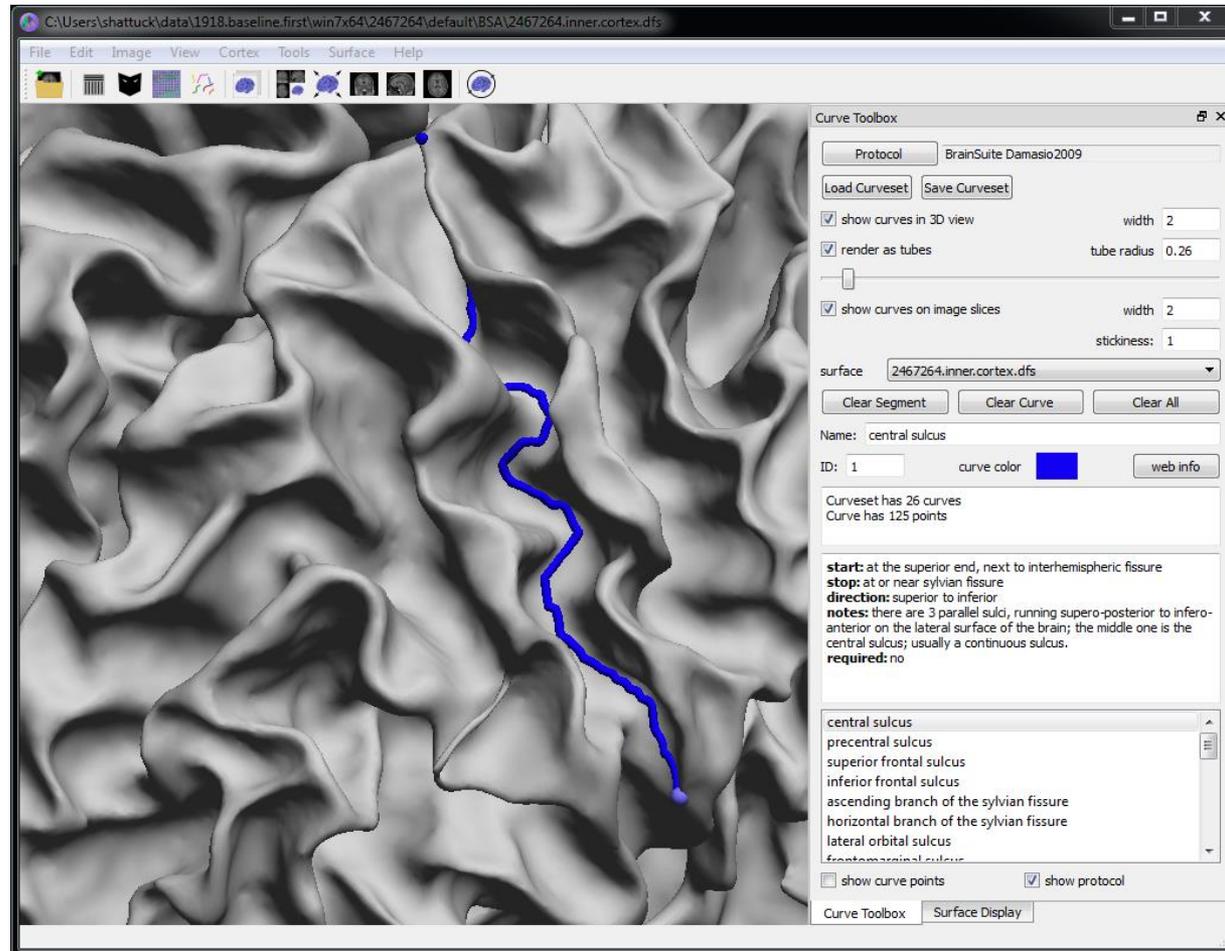
- Develop methodologies to handle lesions, resections, and other pathology
- Manual identification tools
- Segmentation, registration, and labeling tools
- Lesion detection software

Lesion Data



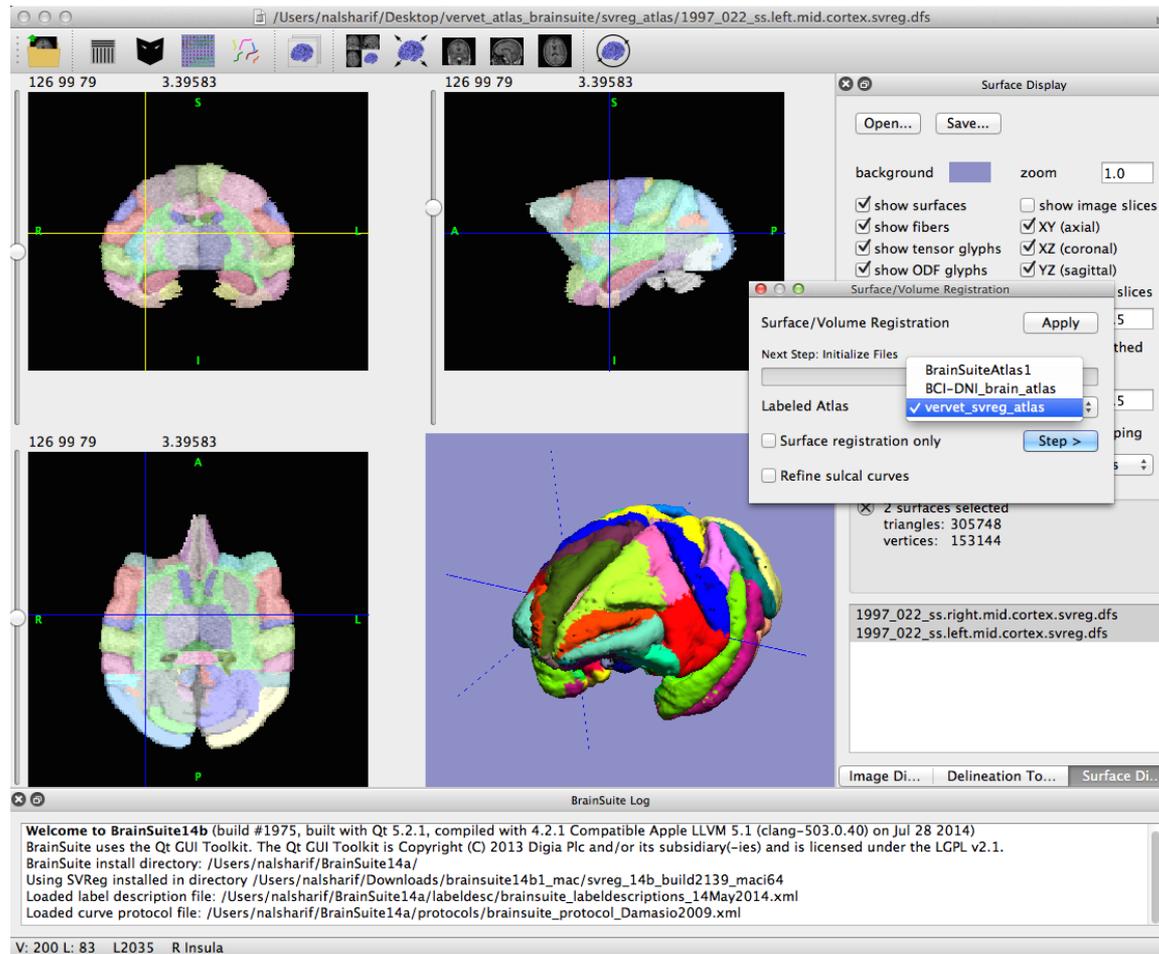
Choi S, Bhushan C, Joshi AA, Raphel K, Tranel D, Shattuck D, Haldar J, Leahy RM, Damasio H, Wisnowski J (2013) Altered orbitofrontal tissue microstructure in patients with chronic anterior temporal lobe lesions, 19th Annual Meeting of the Organization for Human Brain Mapping, Seattle, WA, June 2013.

Delineation Tools



BrainSuite provides tools for labeling and identifying volumetric and surface-based landmarks.

Custom Atlases



- BrainSuite provides capability to build custom atlases
- Example shown is a vervet atlas

CLARITY Technique for Neuroimaging: Hippocampus

Thy1-GFP endogenous
expression

Imaged with confocal
microscopy

Visualized in Vaa3D

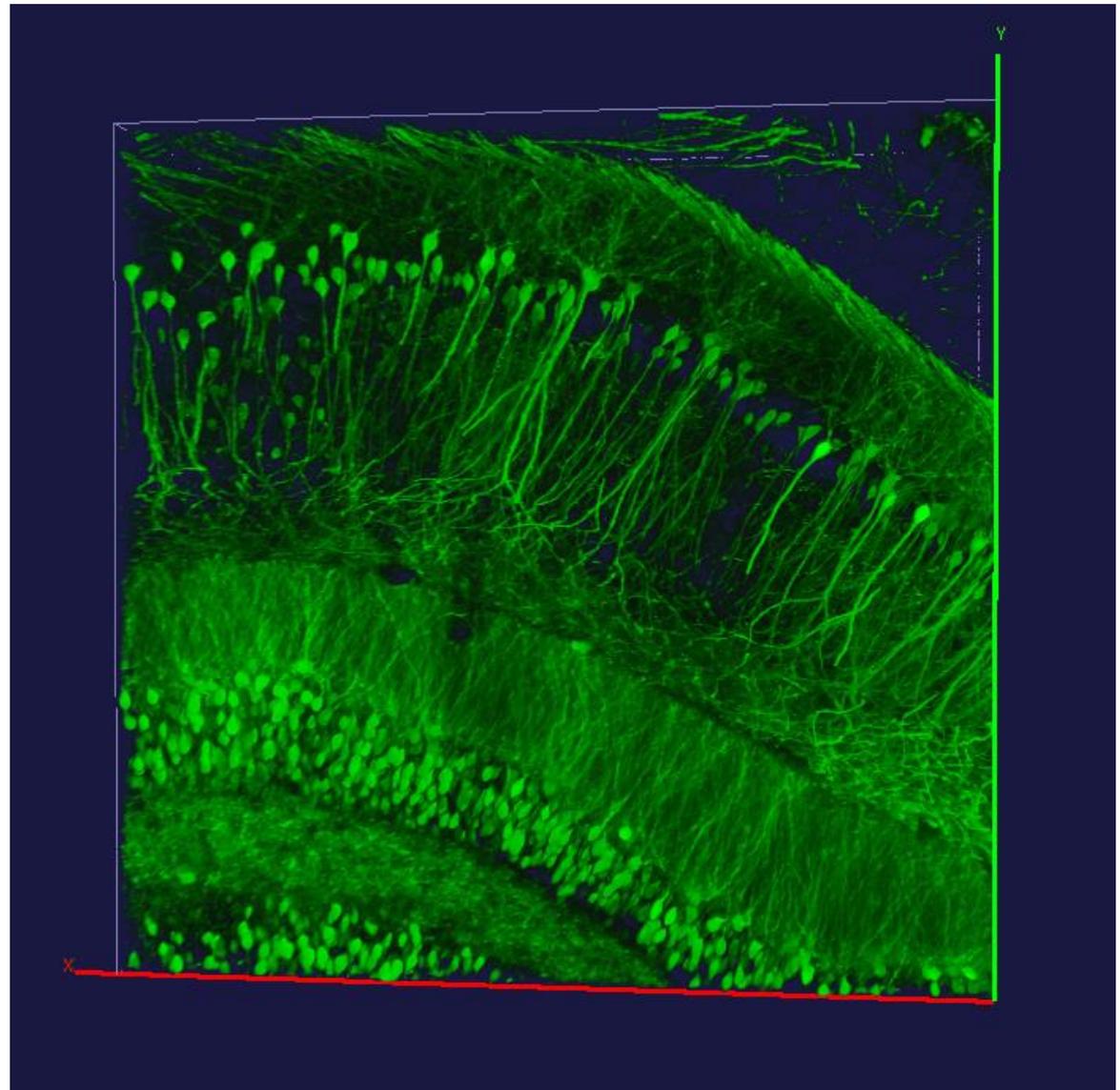


Image provided by Luis de la Torre-Ubieta, PhD, Jason Stein, PhD, and Daniel Geschwind, MD, PhD (UCLA).

CLARITY Technique for Neuroimaging: Cortex

Thy1-GFP mouse cortex

Endogenous GFP (red) and GFP
immunostaining (green)

Prepared from 1mm thick
coronal slices

Imaged with confocal
microscopy

Visualized in Vaa3D

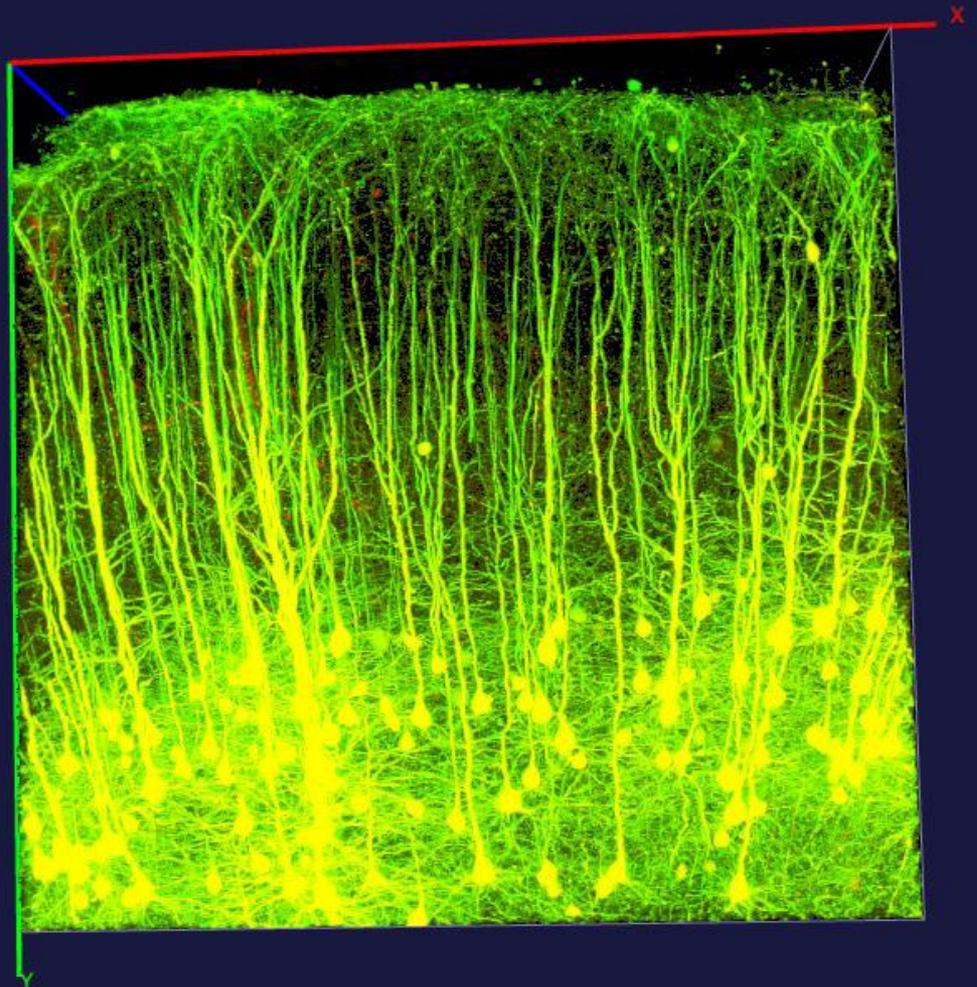
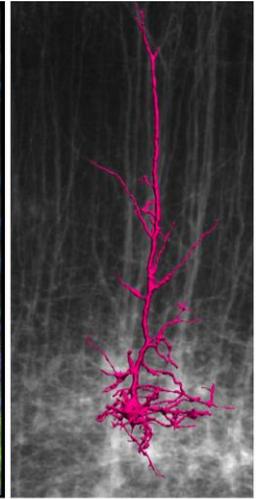
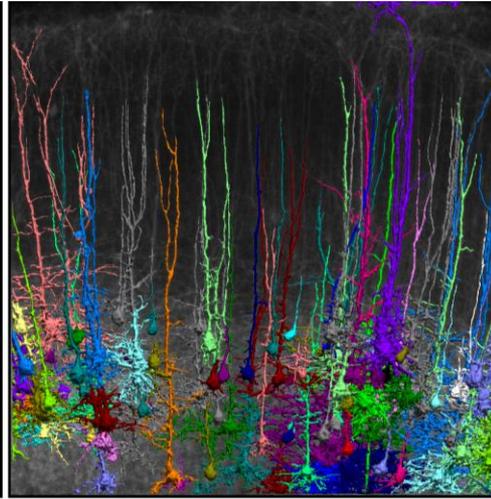
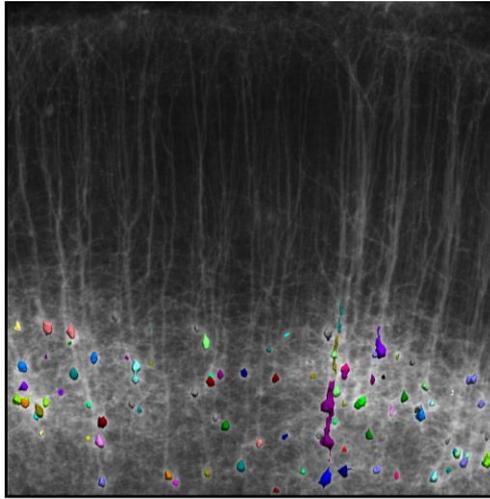
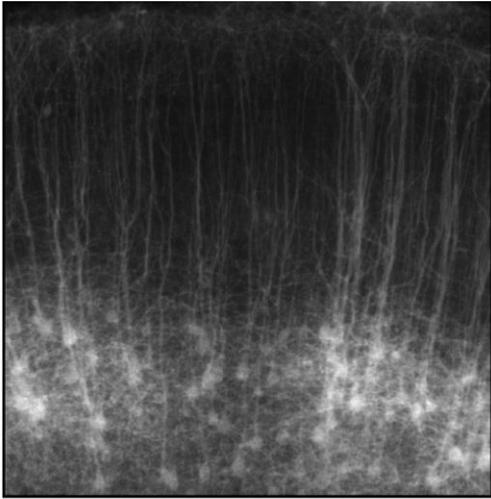


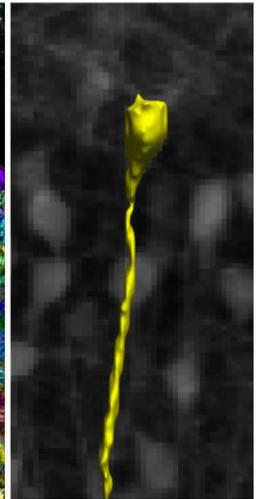
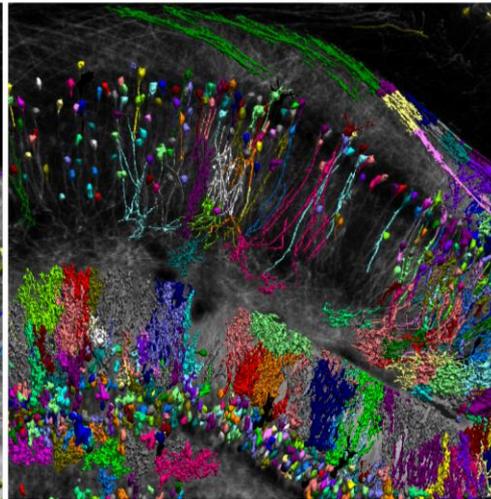
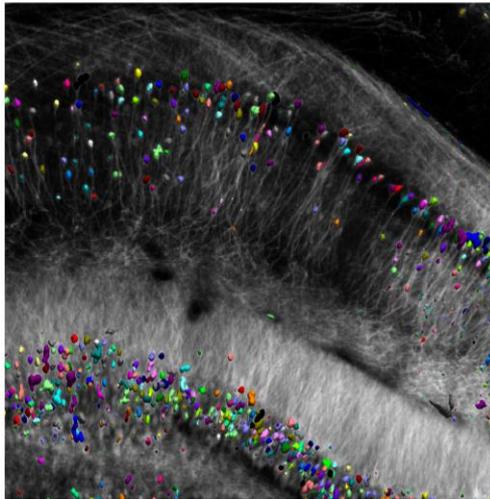
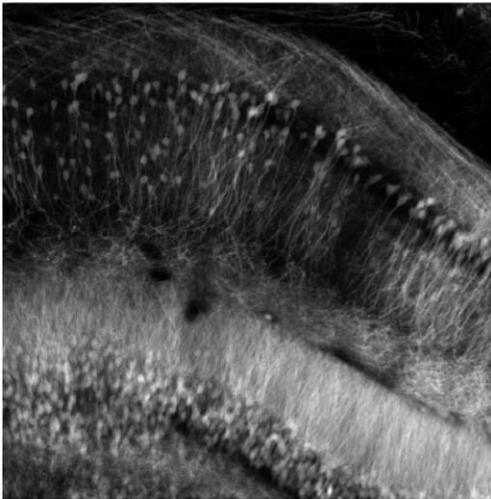
Image provided by Luis de la Torre-Ubieta, PhD, Jason Stein, PhD, and Daniel Geschwind, MD, PhD (UCLA).

CLARITY Image Analysis

Cortex



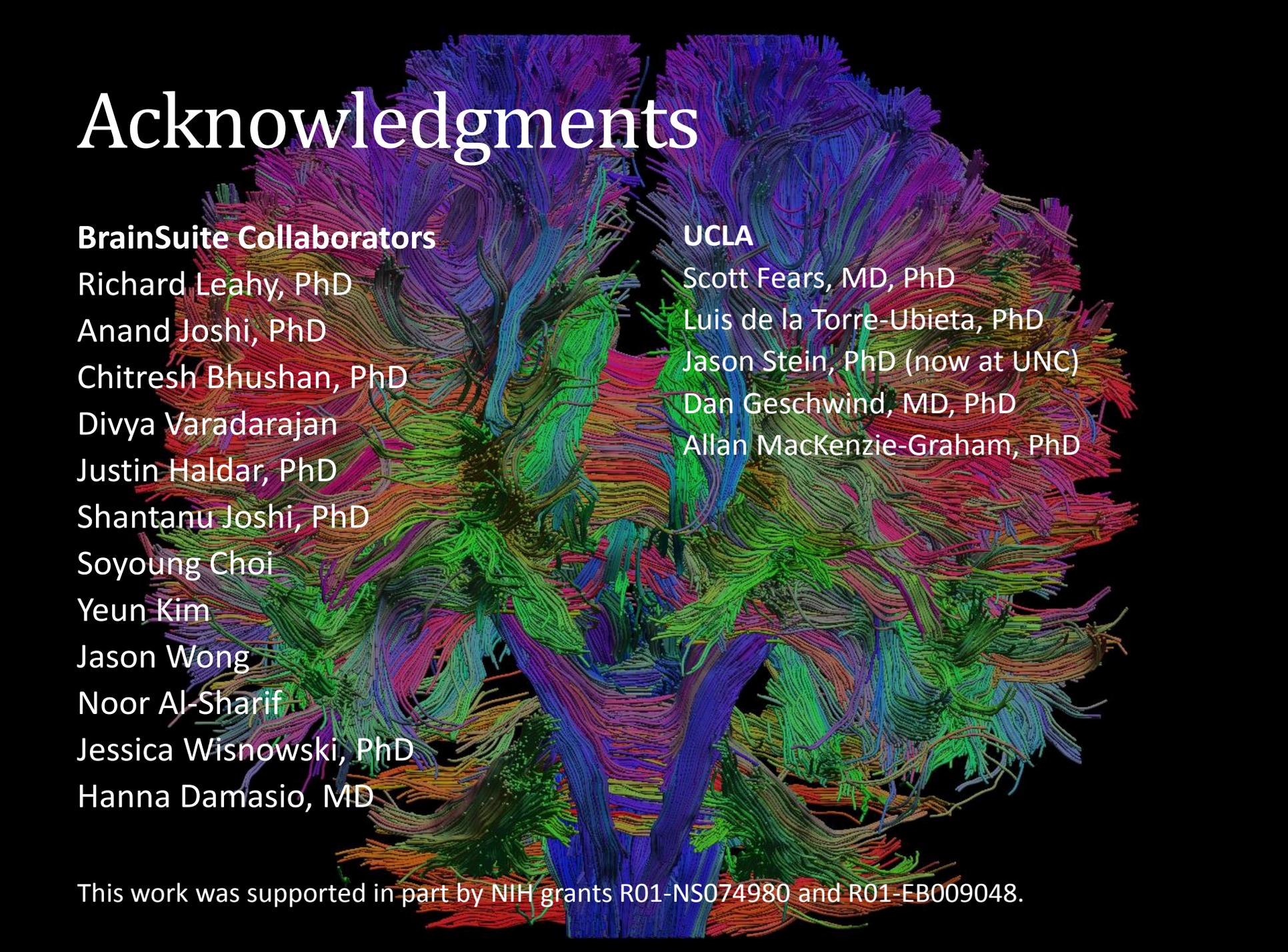
Hippocampus



Conclusions

- BrainSuite software provides a collection of flexible, open-source software tools for analyzing brain imaging data:
 - Fast tools for image segmentation and surface extraction
 - Unique method for cortically-constrained volumetric registration
 - Methods for performing diffusion coregistration, distortion correction, and tracking.
 - Tools for performing group analysis (point-wise analysis of cortical thickness, other mapped data, regional volume analysis, TBM)
 - Tools for visualizing various types of imaging and surface data
 - Tools for interactive delineation
- We are actively continuing its development and welcome feedback from interested users!
 - E-mail: support@brainsuite.org
 - Forum: <http://forums.brainsuite.org>

Acknowledgments



BrainSuite Collaborators

Richard Leahy, PhD

Anand Joshi, PhD

Chitresh Bhushan, PhD

Divya Varadarajan

Justin Haldar, PhD

Shantanu Joshi, PhD

Soyoung Choi

Yeun Kim

Jason Wong

Noor Al-Sharif

Jessica Wisnowski, PhD

Hanna Damasio, MD

UCLA

Scott Fears, MD, PhD

Luis de la Torre-Ubieta, PhD

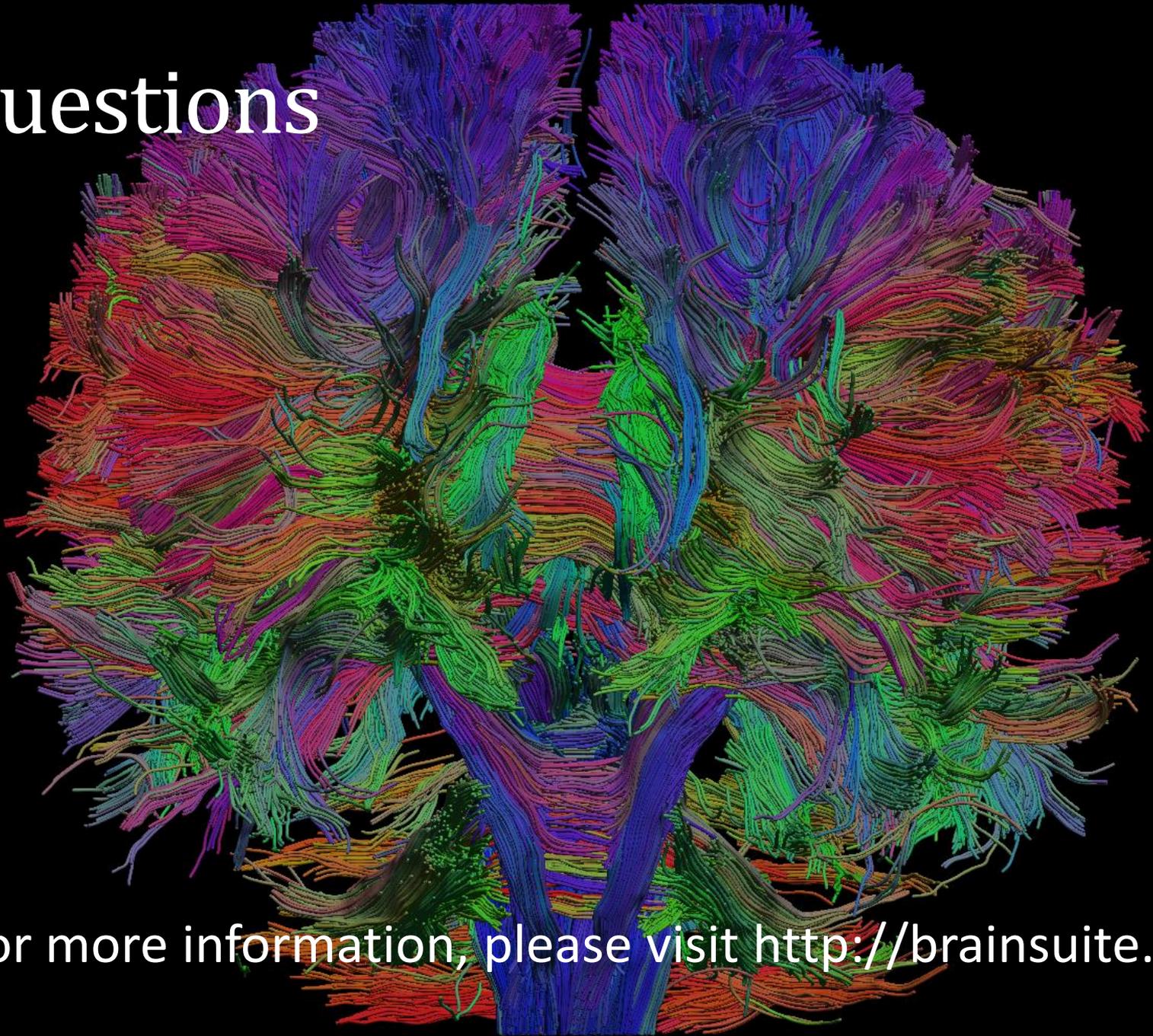
Jason Stein, PhD (now at UNC)

Dan Geschwind, MD, PhD

Allan MacKenzie-Graham, PhD

This work was supported in part by NIH grants R01-NS074980 and R01-EB009048.

Questions



For more information, please visit <http://brainsuite.org>