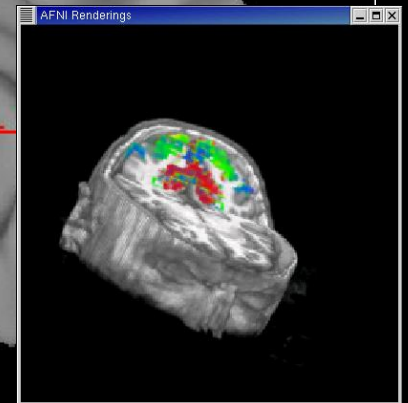
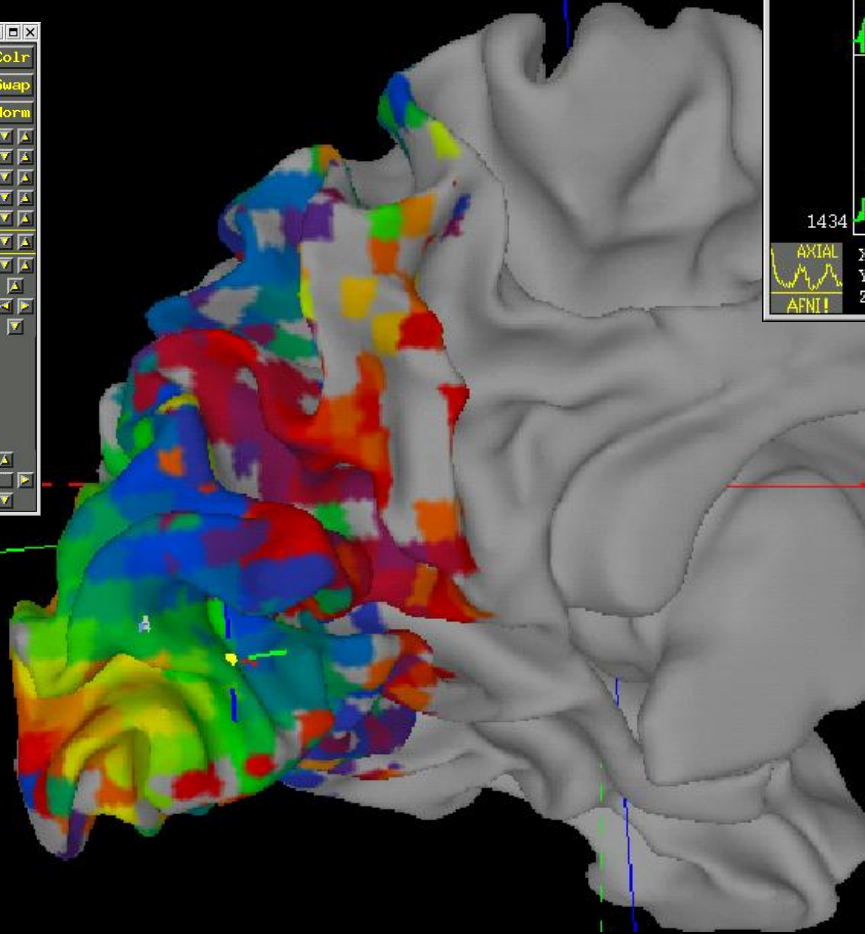
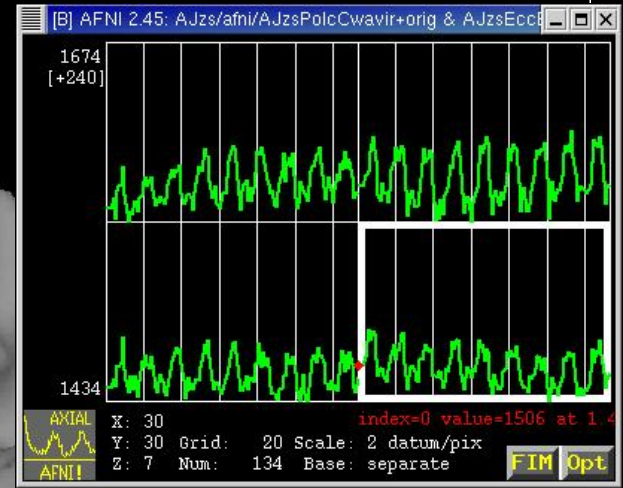
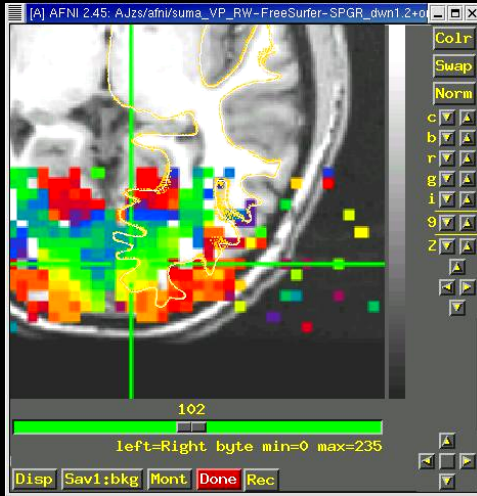
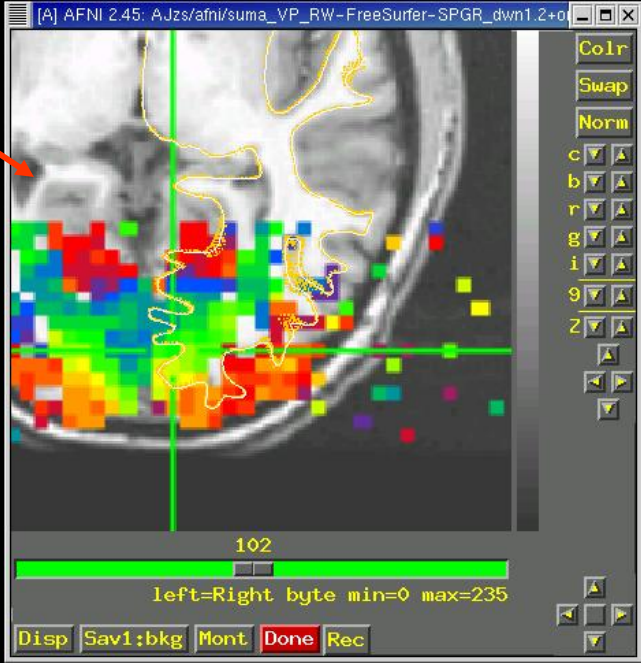


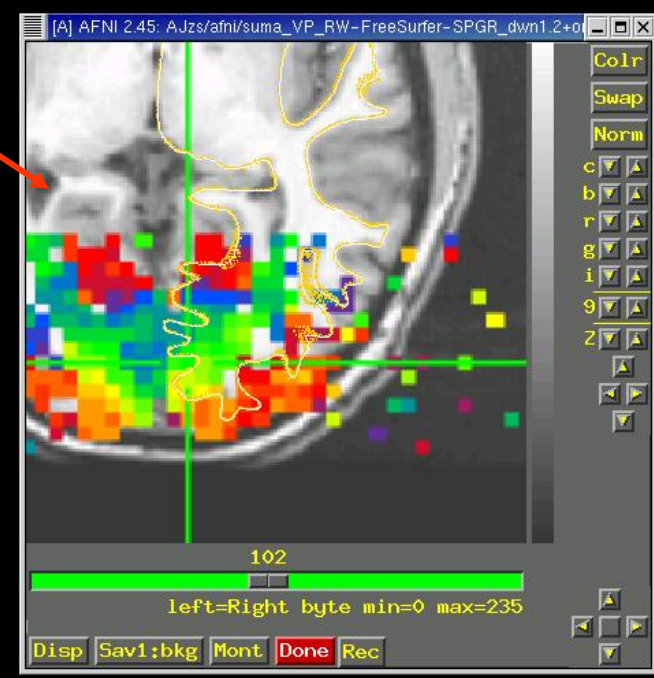
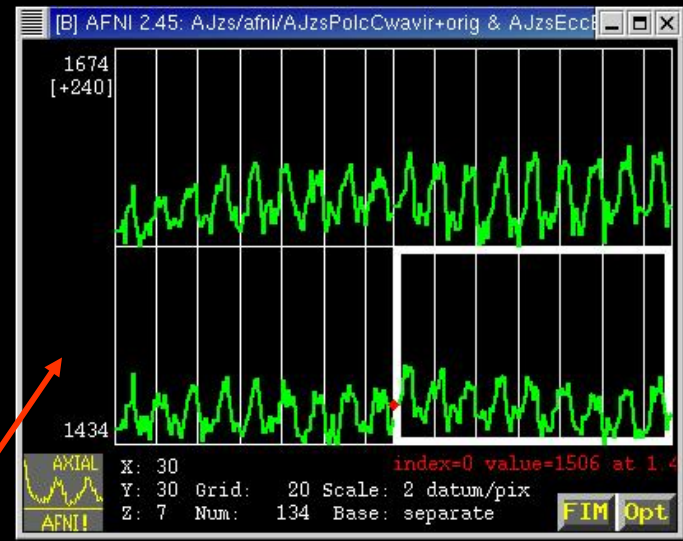
SUMA

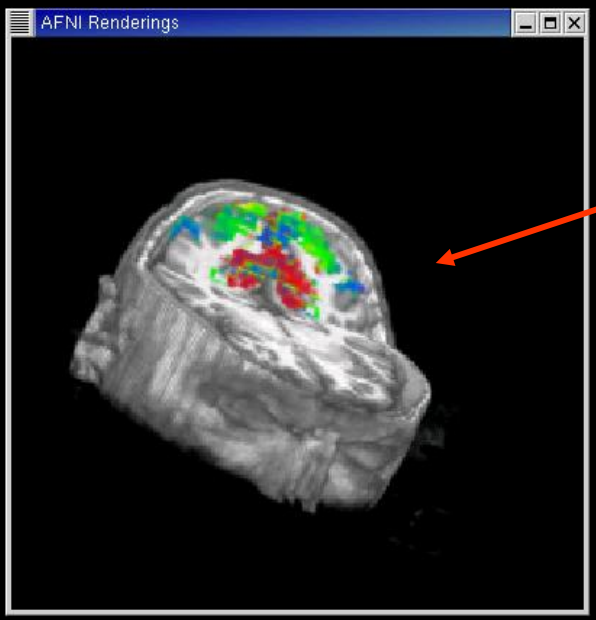
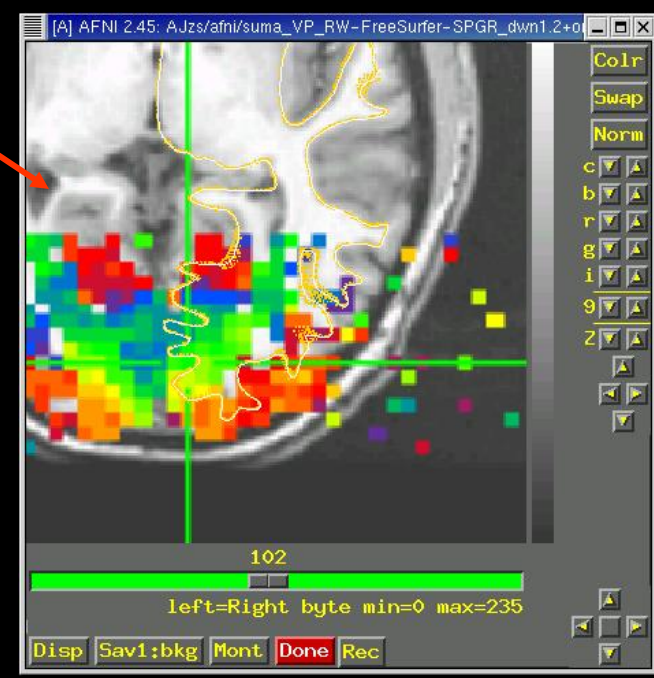
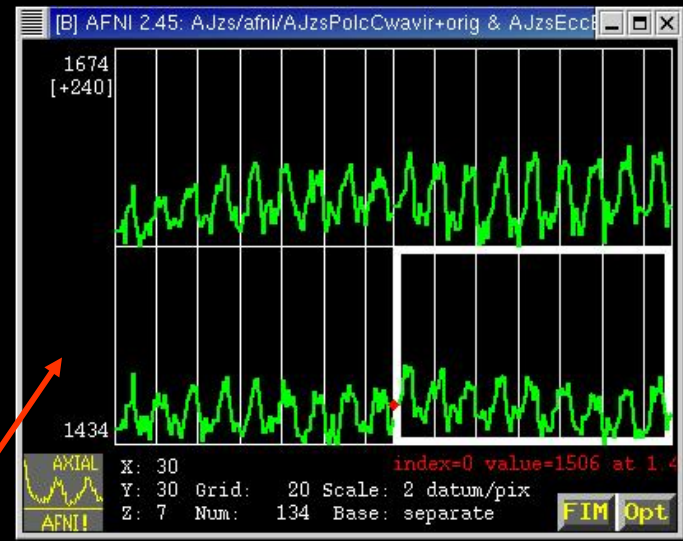


Statistical & Scientific Computing Core



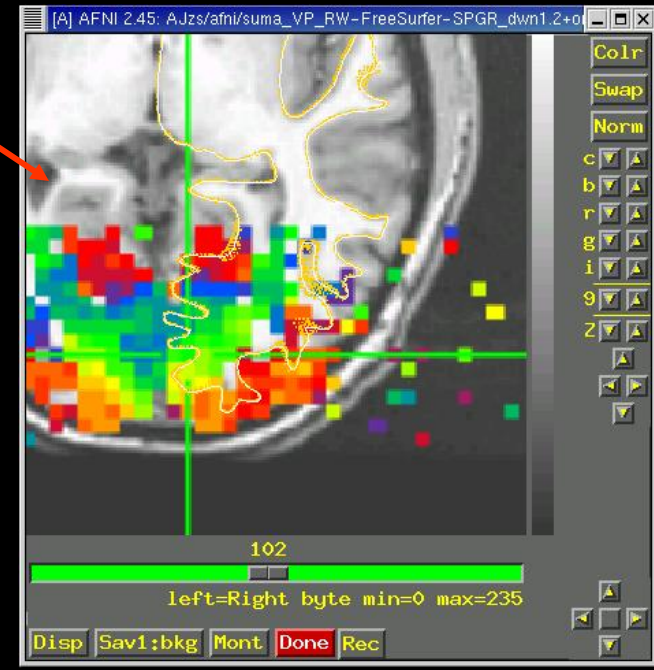
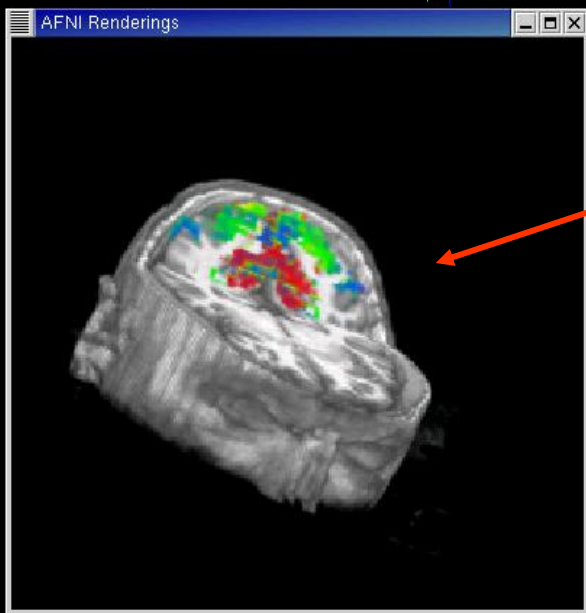
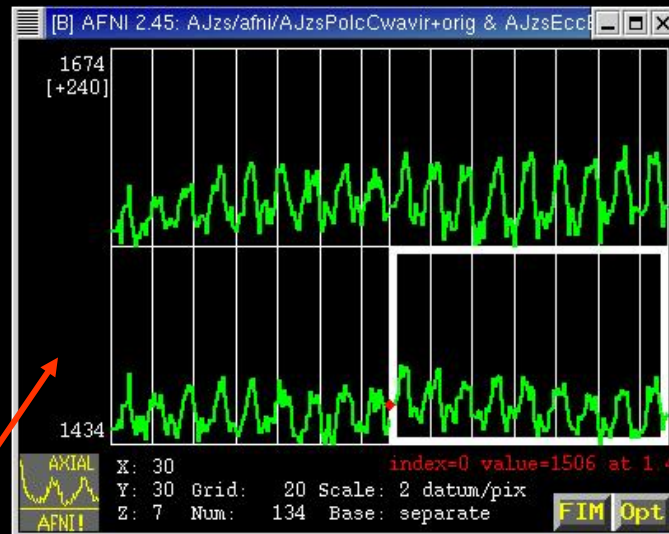
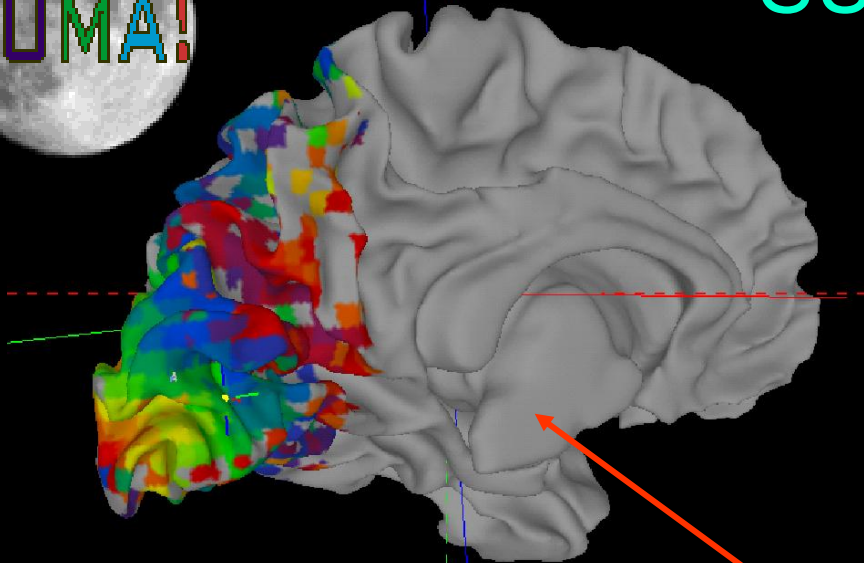






SUMA!

SUMA





SURface MAPPING with AFNI



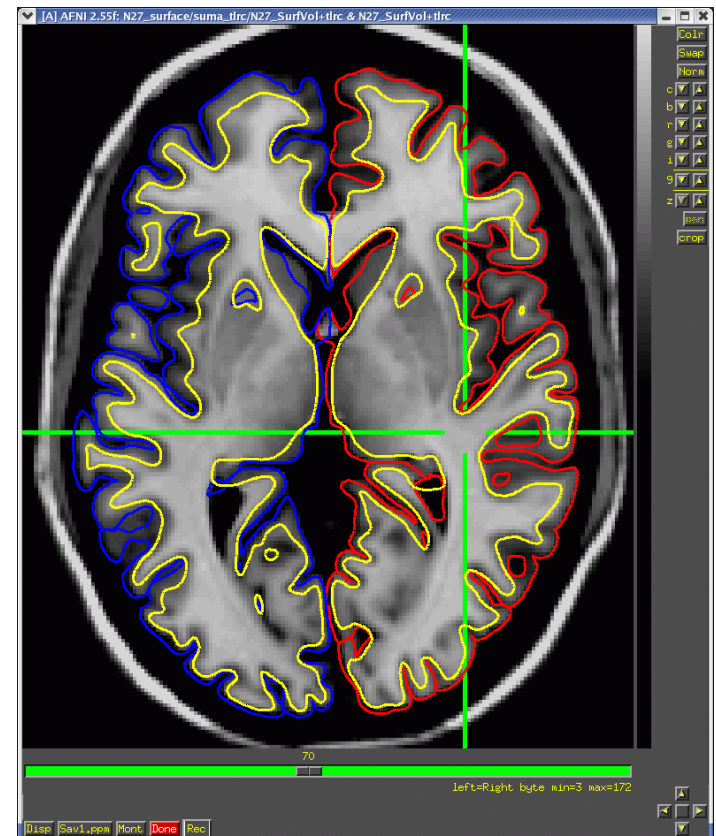
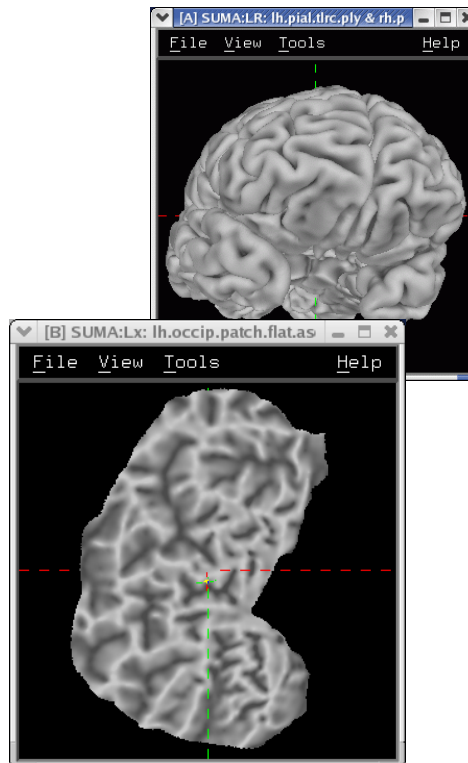
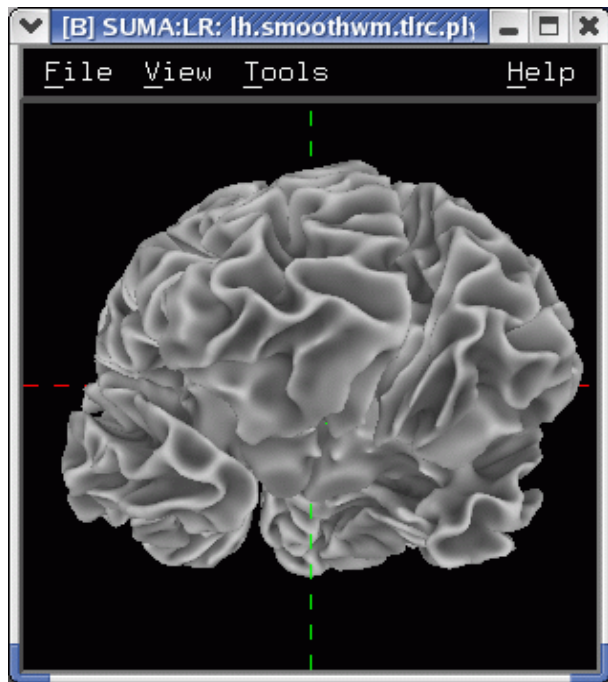
- Surface mapping & viewing program tightly linked to interactive AFNI — but SUMA is a separate program
- Complements AFNI's slice and volume rendering modes
 - AFNI works with data defined over volumes
 - SUMA works with data defined over surfaces
- Provides a framework for fast and user-customizable surface-based analysis
- Supports surface models created by:
 - FreeSurfer <http://surfer.nmr.mgh.harvard.edu>
 - SureFit/Caret <http://stp.wustl.edu/resources/display.html>
 - BrainVoyager <http://www.brainvoyager.com>
- Allows representation of 2D and 3D objects in projection frame or surface coordinate space.

The Process of Using SUMA

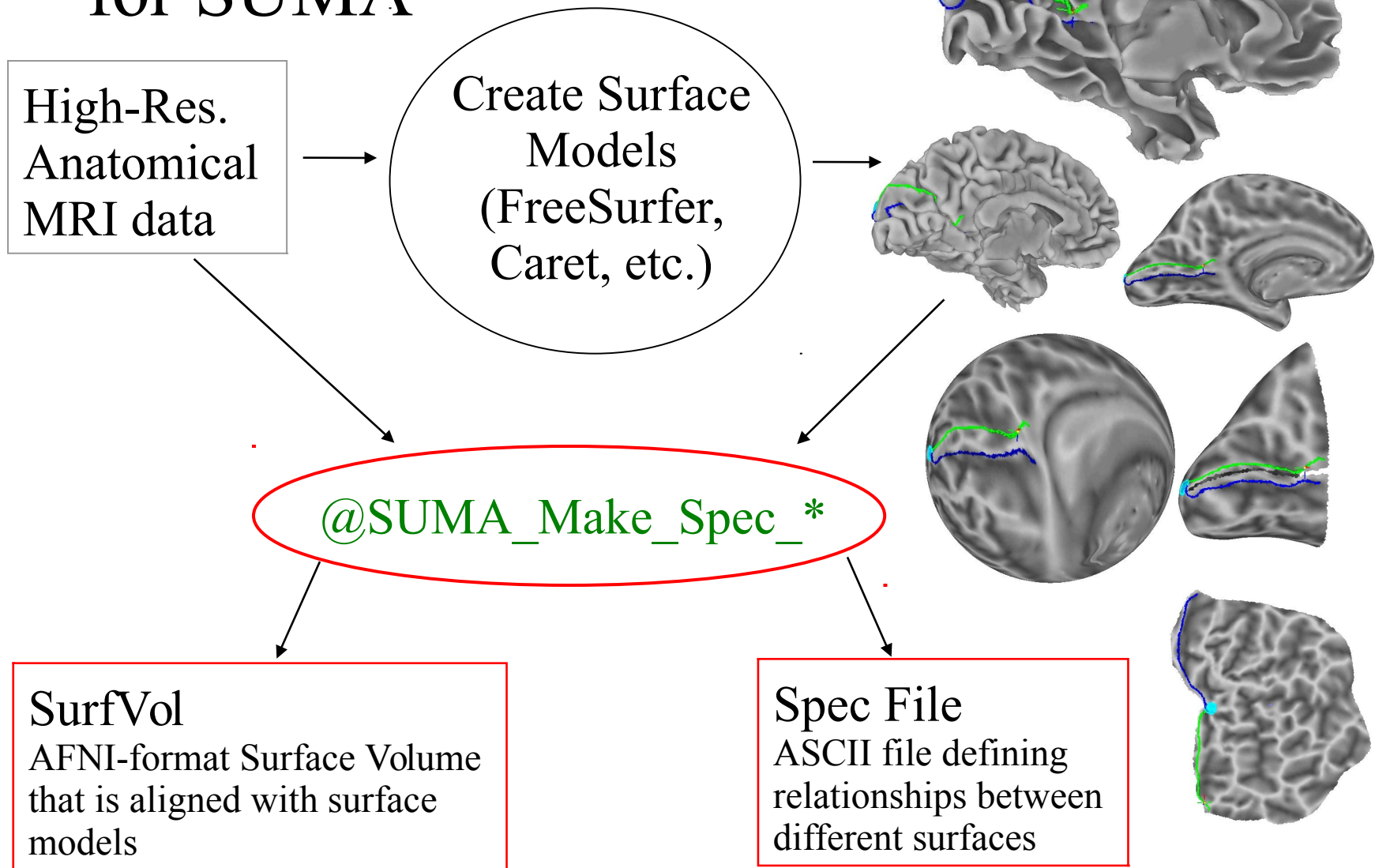
- **PreSUMA** (setup phase):
 - Collect, align, and average high-quality, high-resolution anatomical data
 - Typically, having 1-3 MPRAGE datasets is good, depending on analysis
 - Can correct image non-uniformity
 - Using AFNI's **3dUnifize** or the N3 normalization tool [J.G. Sled et al. 98]
 - Create and correct surfaces
 - Using FreeSurfer, SureFit, or BrainVoyager
- **CircumSUMA**:
 - Create standard-mesh version of surface models
 - Align surface with experimental data
 - Using **@SUMA_AlignToExperiment**
 - Map experimental volumetric data to surface
 - Using AFNI and SUMA (interactively or with command line program)
 - Time series analysis on datasets defined over surface domain
 - Smoothing, statistics, clustering, group analysis.

The Simpler and Lesser Process

- For display (mostly) of Talairach or MNI data:
 - Use the Talairach (http://afni.nimh.nih.gov/pub/dist/tgz/suma_TT_N27.tgz) or MNI (http://afni.nimh.nih.gov/pub/dist/tgz/suma_MNI_N27.tgz) surfaces created from the N27 brain dataset using FreeSurfer.
 - Ready to use, no surface creation or alignment needed (but match to your subject's anatomy will not be very good)



A: Preparing surface models for SUMA



@SUMA_Make_Spec_* scripts

- These scripts prepare surfaces and volumes for use with SUMA:
 - ★ @SUMA_Make_Spec_FS for FreeSurfer surfaces
 - ★ @SUMA_Make_Spec_SF for SureFit surfaces
 - ★ @SUMA_Make_Spec_Caret for Caret surfaces
- Output of these scripts include:
 - ★ Surface Volume: SurfVol
 - ★ AFNI dataset created from anatomical MRI, used to create the surfaces
 - ★ AFNI volumes of cortical and subcortical segmentations (FreeSurfer)
 - ★ ASCII versions of all surfaces (FreeSurfer)
 - ★ Surface specifications file: (*.spec)
 - ★ ASCII file defining relationships between family of surfaces.

A note using FreeSurfer

- + When acquiring an anatomical volume to run with FreeSurfer (or at least when running *recon-all*), it appears to be **very** important to have:
 - isotropic voxels (i.e., equal voxel edge lengths)
 - an even number of slices in **all** planes (all matrix dimensions even)
 - preferably 1 mm voxel edge lengths (for default *recon-all*)
 - for higher resolution dsets, there is a “-hires” option for *recon-all*, apparently down to about 0.5 mm voxel edges (according to FS website, but check with FS experts if scanning in this range!).
- + Otherwise, the output surfaces are noticeably different.
- + FS v6 allows for multiple CPUs to be used for *recon-all* processing, so considering adding a “-openmp **Ncpu**” option to use up to *Ncpu* CPUs-- save yourself some time!
- + When converting FS results to AFNI+SUMA, include the “-NIFTI” option in *@SUMA_Make_Spec_FS* for best registration results.

Viewing Surfaces with SUMA

After `@SUMA_Make_Spec_*` scripts are run, surface models should be in excellent alignment with SurfVol

- + Use SUMA to verify alignment
- + Scroll through the volume to make sure surfaces are accurate
 - Check especially for inferior temporal and occipital areas

Demo using FreeSurfer surfaces:

- + `cd ~/AFNI_data6/FT_analysis/FT/SUMA`
 - This is where the output of `@SUMA_Make_Spec_FS` resides
- + `afni -niml &`
 - launches AFNI to allow the viewing of `DemoSubj_lh.spec`
 - the `-niml` option tells AFNI to listen to connections from SUMA
- + `tcsh run.suma.00.both.141`
 - just one command to open surface viewer with desired dsets

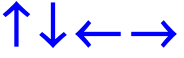
Check for proper alignment and defects

- With both SUMA and AFNI running
 - ★ Press 't' in the suma window to 'talk' to AFNI
 - ★ This sends anatomically correct surface(s) to AFNI
 - ★ Switch AFNI **Underlay** to **DemoSubj_SurfVol+orig**
 - ★ Contours are the intersection of the surface with the slice.
 - ⇒ You could also see boxes representing the nodes that are within $\pm 1/2$ slice from the center of the slice in view.
 - ⇒ Colors and node box visibility can be changed to suit your desires from the **Control Surface** button in AFNI.
 - ★ Navigate through the volume in AFNI
 - ➔ make sure you have an excellent alignment between volume and surface
 - ➔ make sure surface adequately represents areas of the brain that are difficult to segment
 - ⇒ occipital cortex
 - ⇒ inferior frontal and inferior temporal regions
 - ⇒ Surface may *look* good in SUMA, but may not match anatomy in some places — this is why you check surfaces in AFNI display

Check for proper alignment and defects

- The Surface Volume and the surfaces must be in nearly perfect alignment.
 - ★ If you have an improper alignment, it should be addressed here and now
 - ↳ This should not happen for FreeSurfer and SureFit surfaces created in the standard fashion.
 - ★ Watch for error messages and warnings that come up in the shell as the surfaces are read in. These messages should be examined once per subject, since they do not change unless the surface's geometry or topology is changed.
 - ★ Viewed without the volume underlay, it is extremely difficult to tell if surface models with no topological defects accurately represent the cortical surface.

Basic SUMA viewer functions

- Rotating the surface:
 - ★ **Mouse button-1**: keep it down while moving the mouse left to right.
This rotates the surface about the screen's Y-axis (dotted green). Let go of button-1 (usually the left button).
 - ★ Repeat with up and down motion for rotation about X-axis and motion in various directions for rotations mimicking those of a trackball interface.
 - ★ Also try up/down/left/right  arrow keys.
 - ➔ Arrow keys rotate by increments specified by the Unix environment variable: **SUMA_ArrowRotAngle** (degrees).
 - ➔ You can set SUMA environment variables in file **~/.sumarc**

Basic SUMA viewer functions

- Prying & Z rotating the hemispheres:
 - ★ **Mouse ctrl+button-1**: Moving the mouse horizontally while button 1 is pressed and ctrl is down will pry hemispheres apart for better visualization. The prying behavior is different for spherical and flattened surfaces. Better try it than read about it.
 - ★ Ctrl+button 1 doubleclick: Undo prying.
 - ★ **Mouse shift+button-1**: Rotate surfaces about screen's Z-axis. This option is useful for positioning flat surfaces when displayed one at a time. In most other circumstances it leads to confusion.
 - ★ Shift+button 1 doubleclick: Undo Z rotation

Basic SUMA viewer functions

- Translating the surface:
 - ★ **Mouse button-2**: keep it down while moving the mouse to translate surface along screen X and Y axes or any combinations of the two.
 - ★ Also try **Shift+arrow** keys.
- Zooming in/out:
 - ★ **Both buttons 1&2 or Shift+button 2**: while pressing buttons, move mouse down or up to zoom in and out, respectively.
 - ★ Also try keyboard buttons '**Z**' and '**z**' for zooming in and out, respectively.

Basic SUMA viewer functions

- Picking a Node or Facet:
 - ★ **Mouse button 3**: press over a location on a surface to pick the closest facet and node to the location of the pointer.
 - ➔ The closest node is highlighted with a blue sphere
 - ➔ The closest facet is highlighted with a gray triangle
 - ★ Note the information written to the shell regarding the properties of the picked Node and Facet.
 - ★ When connected to AFNI (after having pressed **'t'**), watch the AFNI crosshair jump to the corresponding location in the volume.
 - ★ Conversely, position the crosshair in AFNI (**left click**) at a position close to the surface and watch the crosshair relocate in SUMA.
- You can swap button 1 & 3's functions using the environment variable: **SUMA_SwapButtons_1_3**

Basic SUMA viewer functions

- Cardinal views (along coordinate directions):
 - ★ **ctrl + Left/Right**: Views along LR axis
 - ★ **ctrl + Up/Down**: Views along SI axis
 - ★ **ctrl + shift + Up/down**: Views along AP axis
- Resetting the view point:
 - ★ Press **Home (fn+left arrow macs)** to get back to the original vantage point.
- Using momentum feature:
 - ★ Press '**m**' to toggle momentum on. Click the **left mouse** button and release the button as you are dragging the mouse.
- Lots more:
 - ★ Function keys modify various aspects of the display
 - ★ Those may be usurped by OS X, see Keyboard setup
 - ★ **ctrl+h** opens a help window for all interactive options.

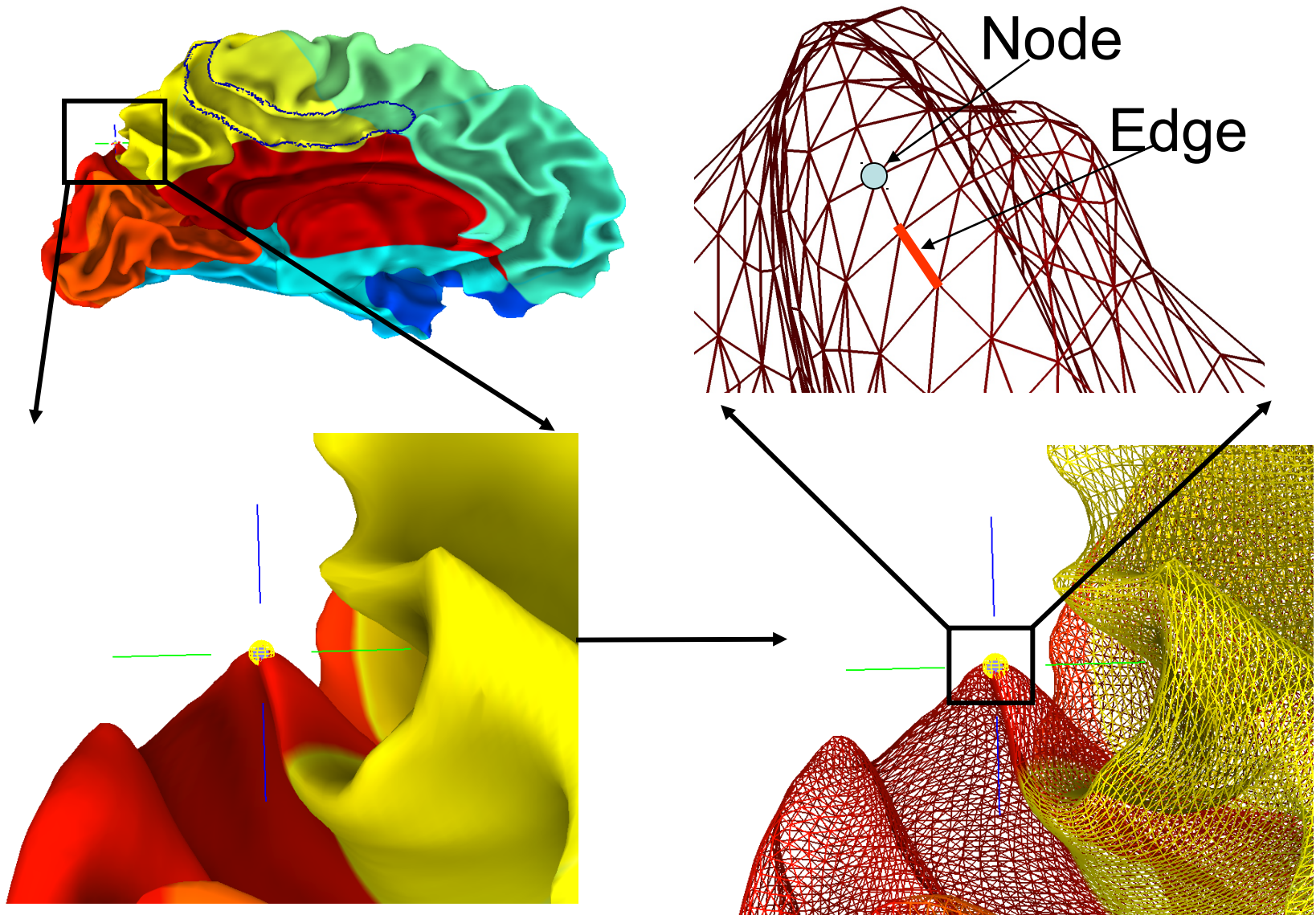
Recording your beautiful SUMA images

- Using 'r' in SUMA to record the current scene (a single image).
- Using 'r' on the colorbar creates an image of the colorbar.
- Using 'R' to record continuously the rendered scene, as you change it.
- Images are captured by an AFNI-esque image viewer.
 - ★ Identical consecutive images are rejected
 - ★ Images caused by window expose events are ignored
 - ★ Images can be saved in all ways allowed by AFNI, including MPEG and animated GIF movies
 - ★ If you let the recorder run continuously with very large images, you might quickly run out of memory on your computer!
- Using 'ctrl+r' in SUMA to record current image directly to disk (see 'ctrl+h' for details)
- You can save/load viewer setting used to create a figure
 - ★ Use **File**→**Save View** and **File**→**Load View**

world ↔ AFNI ↔ SUMA ↔ world

- AFNI and SUMA are independent programs and communicate using NIML formatted data elements (a subset of XML)
 - ★ Via shared memory or TCP/IP network sockets
 - ★ Both AFNI and SUMA can also communicate with other programs
- NIML: NeuroImaging Markup Language (developed by RW Cox)
 - ★ NIML is the main format for SUMA's data storage
- NIML API library for packing/unpacking data is available
- Protocol allows independent program to communicate with AFNI
- Advantages include:
 - ★ Programs execute on separate machines
 - ★ Fast development (programming with NIML is pretty easy)
 - ★ Screen real-estate (more displays)
- Blemishes include:
 - ★ Only one AFNI can be listening for connections
 - ★ Only one SUMA can connect to AFNI

What's a surface made of?

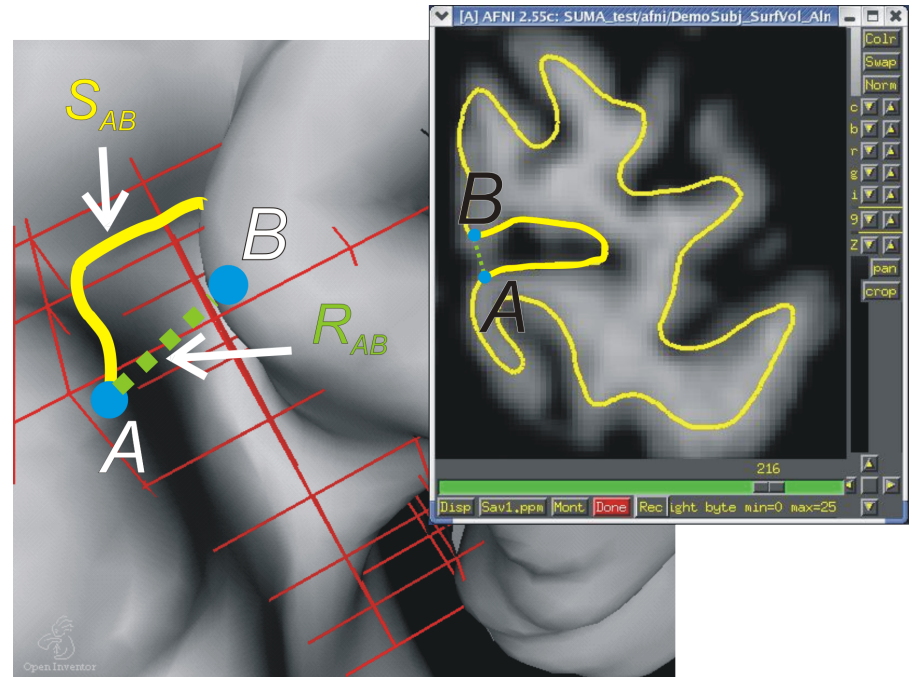


Relationships between surface models

- Surface Geometry:
 - ★ refers to the spatial coordinates of nodes forming a surface model
- Surface Topology:
 - ★ refers to the connectivity between nodes forming a surface model
- A family of surfaces with different geometry but similar topology is created for each surface model.
 - ★ white/grey, pial, inflated, spherical, flattened, etc.
- Some models' geometries are anatomically correct
 - ★ Pial and/or white matter surfaces can be used for relating to volume data.
 - ★ Inflated, flattened and spherical cannot be directly linked to volume data. The link is done via their corresponding anatomically-correct surfaces.
- Those relationships are encoded in the Spec file.

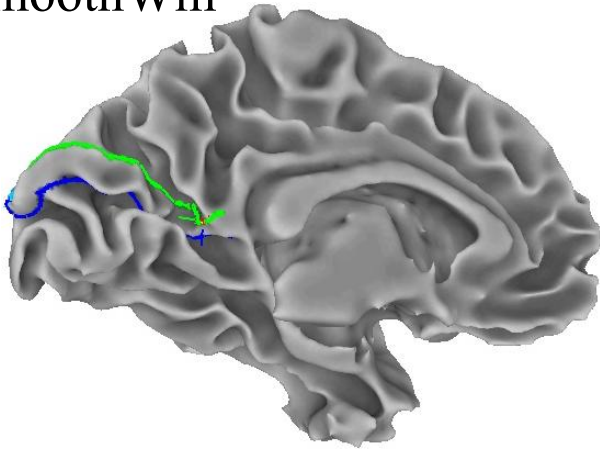
Geometry and Topology

- Geometry: Spatial location
 - ★ X,Y,Z coordinates of brain structures
- Topology: Spatial connectivity
 - ★ Relative positions of brain structures along the surface

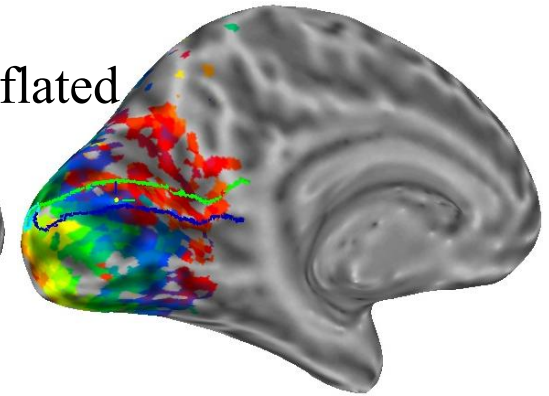
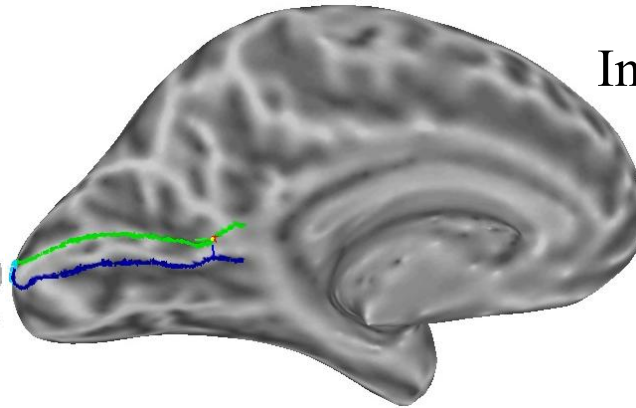


- Geometric proximity does not imply topological proximity
 - If you care about the topology of activation, you should transfer FMRI data onto the surface before spatial manipulations of the data

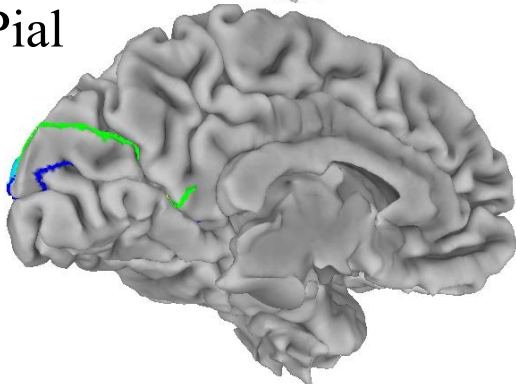
SmoothWm



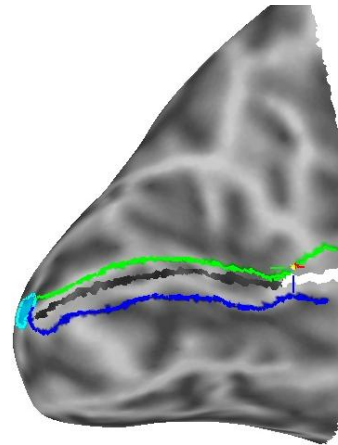
Inflated



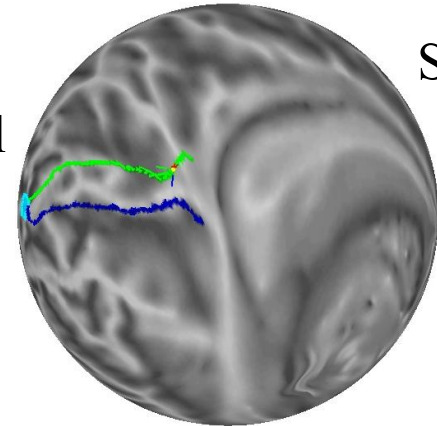
Pial



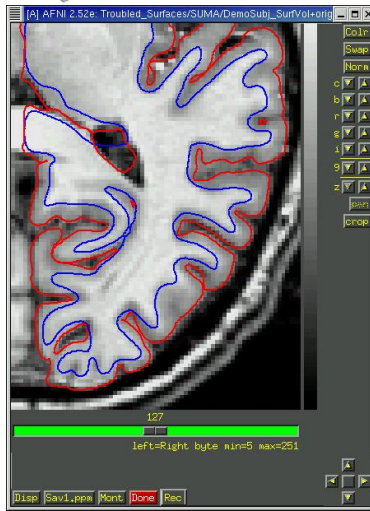
Inflated,
Occipital
cut



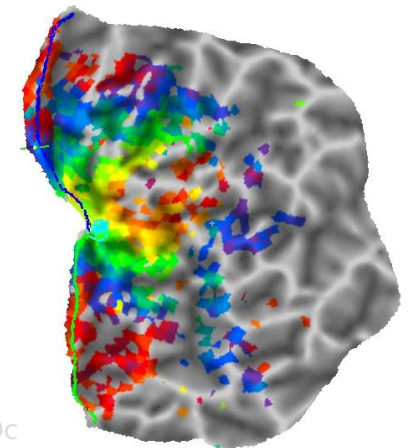
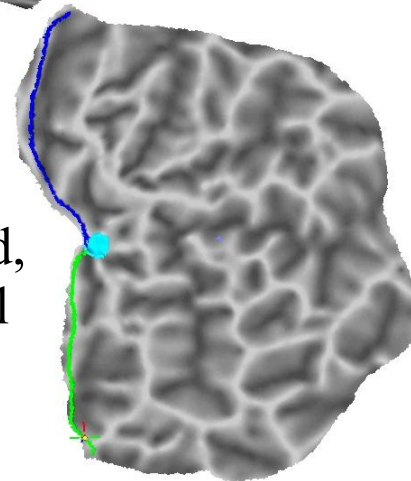
Spherical



Overlay of anatomically correct Pial and SmoothWm surfaces over anatomical volume



Flattened,
Occipital
cut



Viewing the group of surfaces

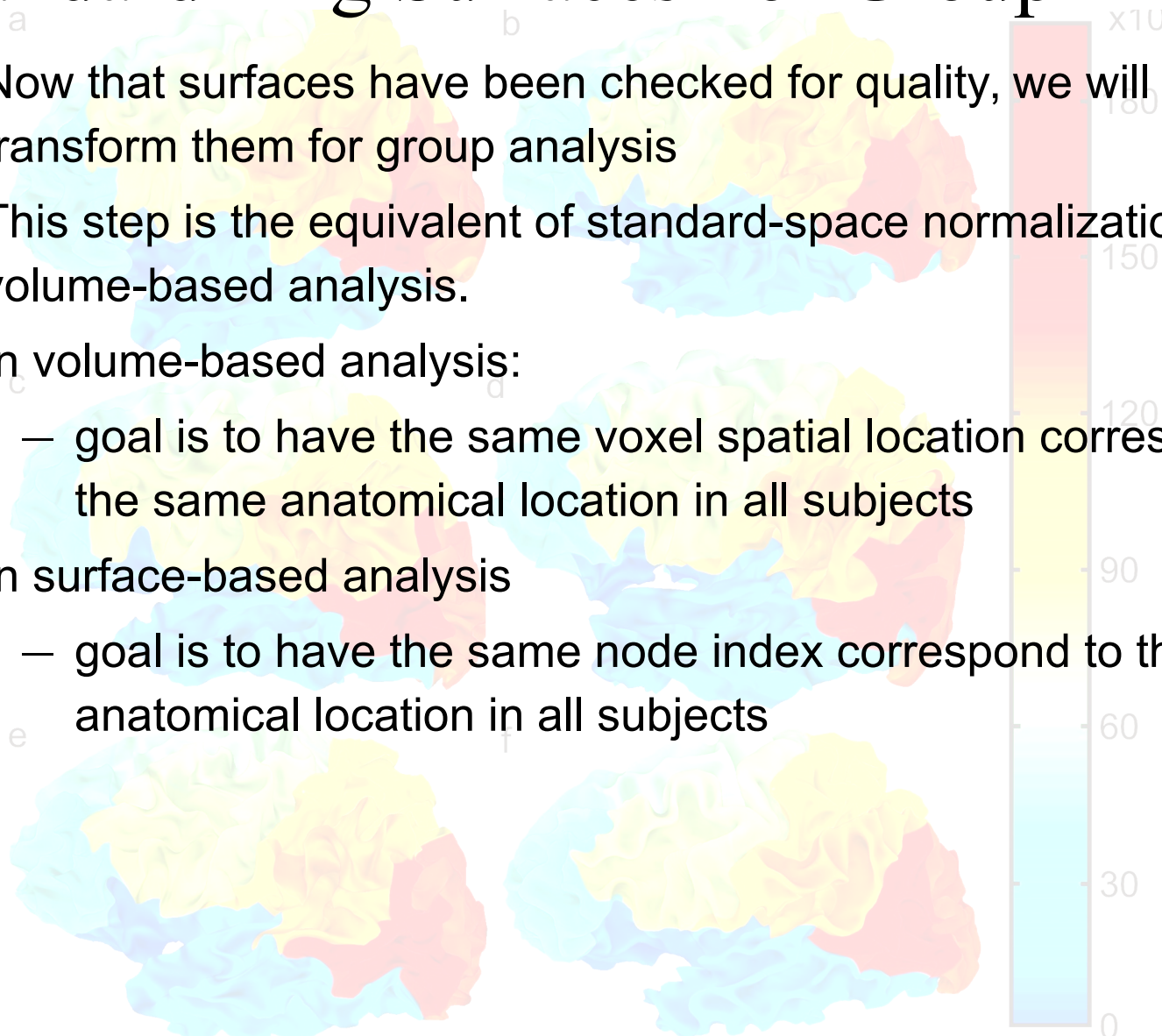
- Switch Viewing States:
 - ★ '.' (period) switches to next viewing state (pial then inflated, ...)
 - ★ ',' (comma) switches to previous viewing state
 - ★ Navigate on any of the surfaces and watch AFNI's crosshair track surface
 - ★ **SPACE** toggles between current state and Mapping Reference state
- Viewing multiple states concurrently:
 - ★ **ctrl+n** opens a new SUMA controller (up to 6 allowed, more possible but ridiculous)
 - ★ switch states in any of the viewers
 - ★ all viewers are still connected to AFNI (if any are)

Viewing the group of surfaces

- Controlling link between viewers:
 - ★ Open SUMA controller with **ctrl+u** or **View->SUMA Controller**
 - ★ SUMA controller crosshair locking options:
 - ↳ **'-'**: no locking
 - ↳ **'i'**: node index locking (i.e., topology based)
 - ↳ **'c'**: node coordinate locking (i.e., geometry based)
 - ★ SUMA controller view point locking
 - ↳ **'v'**: depress toggle button to link view point across viewers.
 - ↳ Surface rotation and translation in one viewer is reflected in all linked viewers

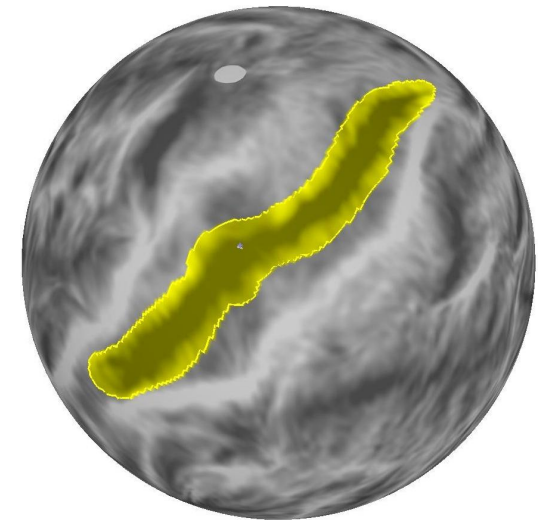
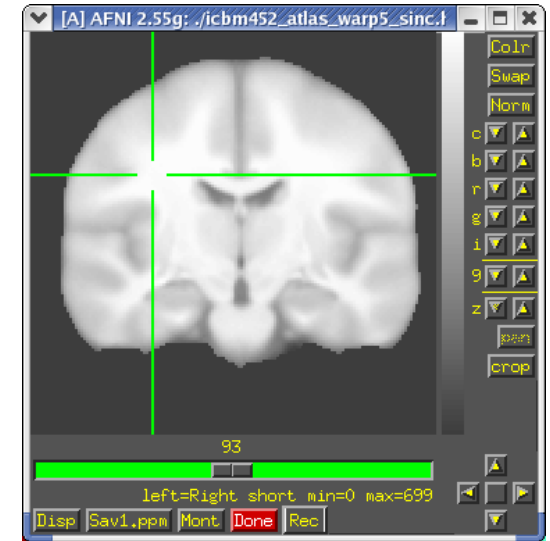
Standardizing Surfaces For Group Analysis

- Now that surfaces have been checked for quality, we will transform them for group analysis
- This step is the equivalent of standard-space normalization for volume-based analysis.
- In volume-based analysis:
 - goal is to have the same voxel spatial location correspond to the same anatomical location in all subjects
- In surface-based analysis
 - goal is to have the same node index correspond to the same anatomical location in all subjects



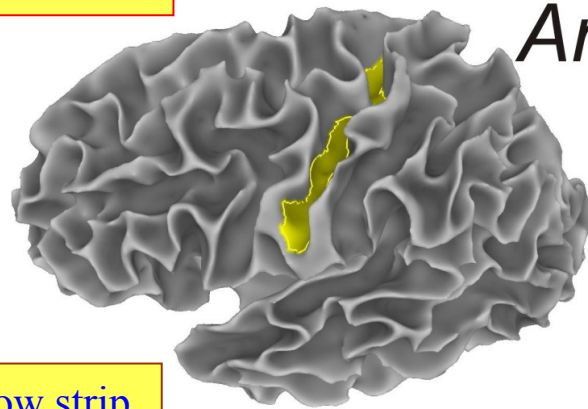
Group analysis

- Group analysis requires data defined over a spatial domain common to all subjects
 - ★ Talairach space for volume-based analysis
 - ★ With low order registration
 - + Small amount of geometric distortion
 - No respect for topology of activation
 - ★ With high order registration
 - + Preserves the topology of action
 - Considerable geometric distortion
 - ★ Spherical coordinate system for surface-based analysis
 - + Preserves the topology of activation
 - Considerable geometric distortion
- Preserving the topology of activation is Good in general and crucial for
 - ★ Retinotopy
 - ★ Plasticity
 - ★ High-resolution Mapping



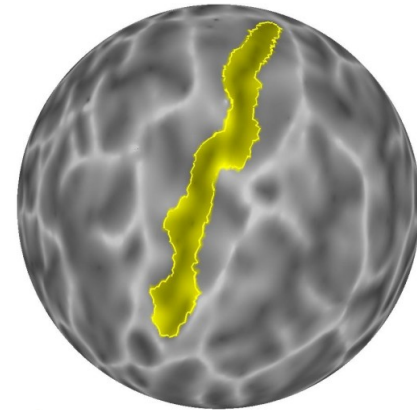
Spherical Warping

Subject data



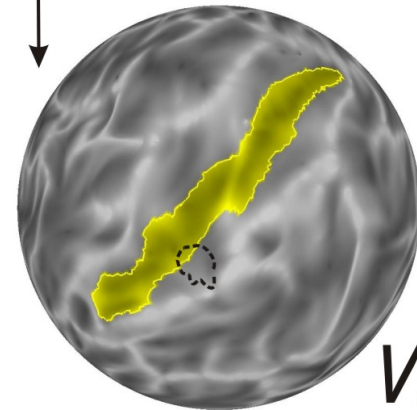
Anat

Inflate



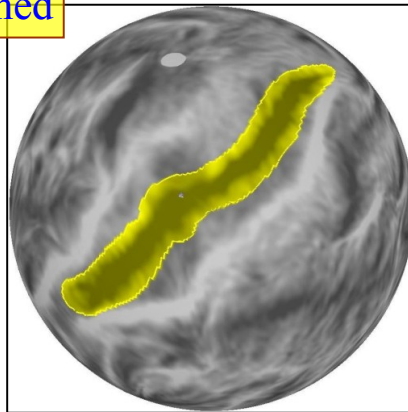
Sph

Warp to Match
Template



Warp

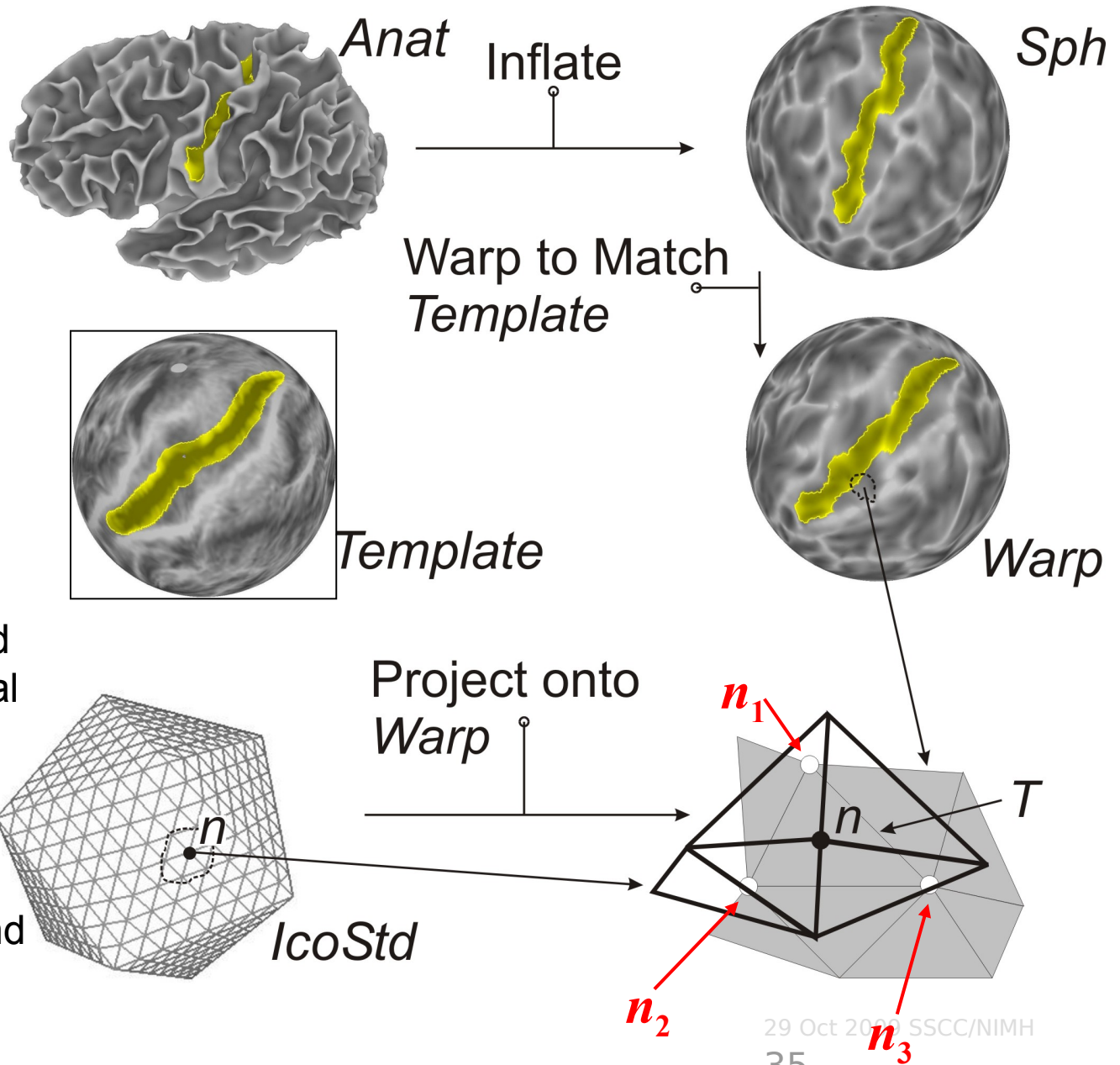
Yellow strip
is one sulcus
being matched



Template

Surface-based warping (based on matching geometrical features like sulci and gyri) is more accurate than the more common low order Talairach volume-based analysis because it preserves the topology of the cortical sheet *and* uses more landmarks for the warping

Mapping data



Problem is that surfaces from different subjects are not topologically isomorphic (different meshes).

One Solution: Data from each subject are mapped onto the icosahedral surface for group analysis

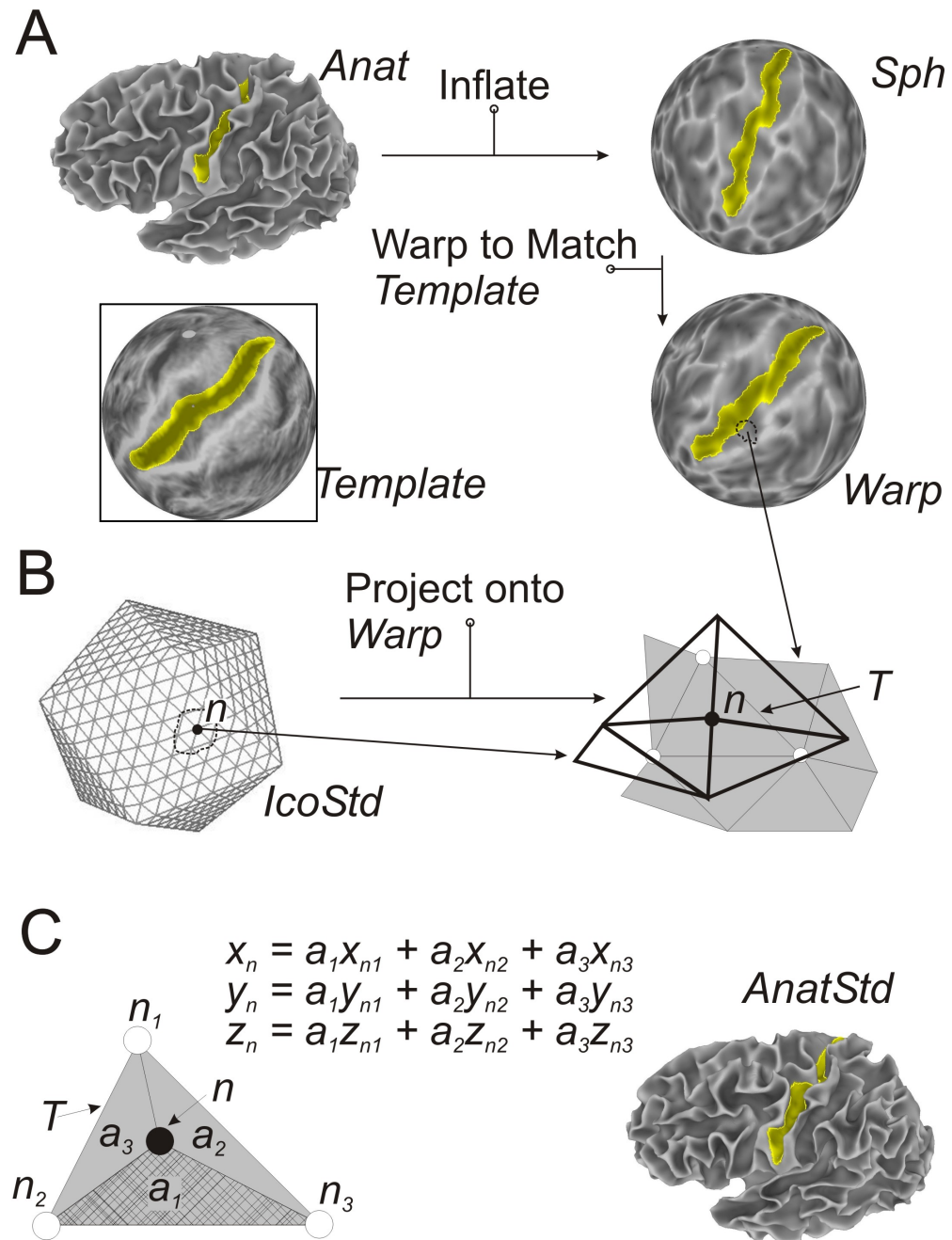
Cumbersome and unnecessary second interpolation

Our Way

Instead of interpolating data values to the icosahedral nodes, interpolate using the coordinates of the original surface's node.

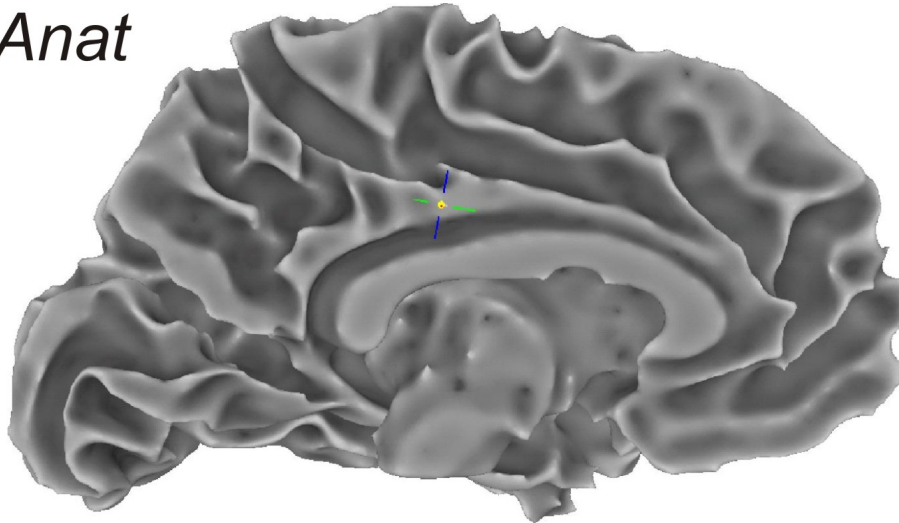
This results in a new surface that is virtually identical in geometry to the original surface **but** with the mesh of the icosahedron - the same mesh for each subject.

Cross-subject surface based analysis is thus reduced to node-based analysis

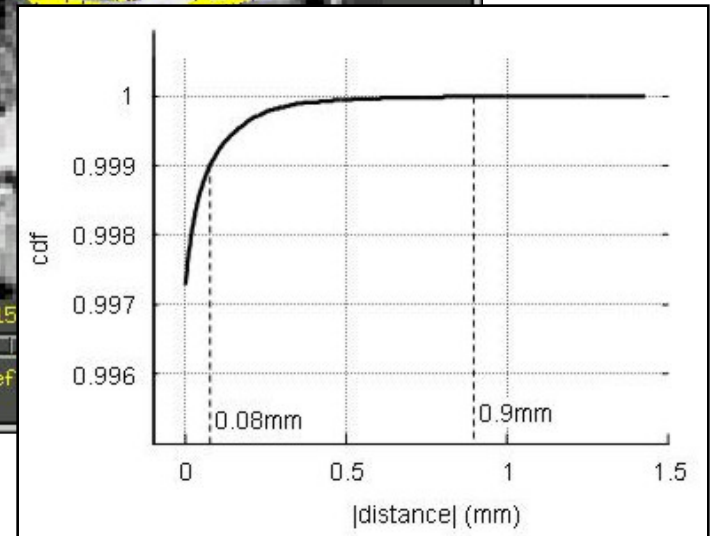
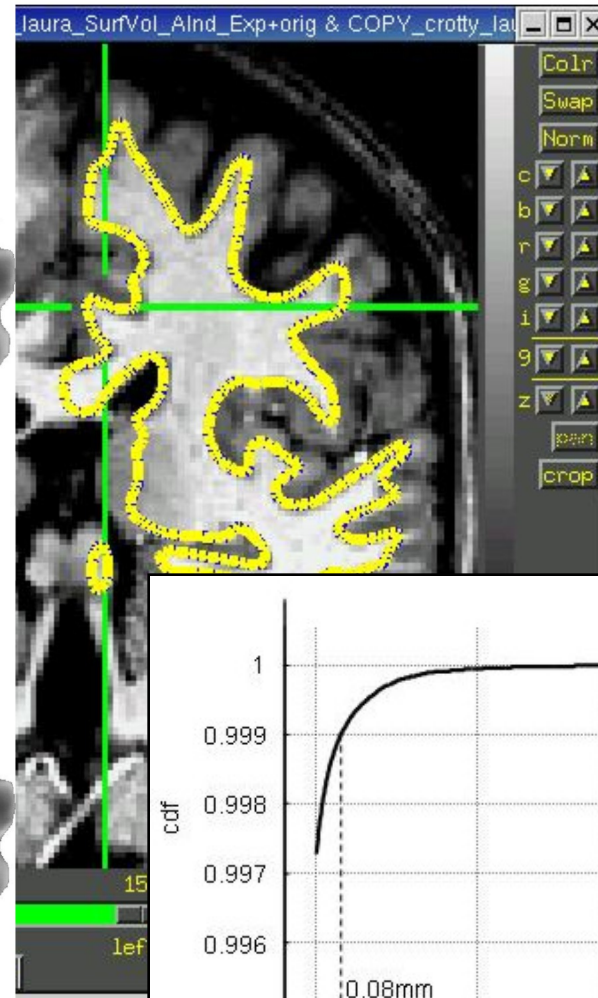
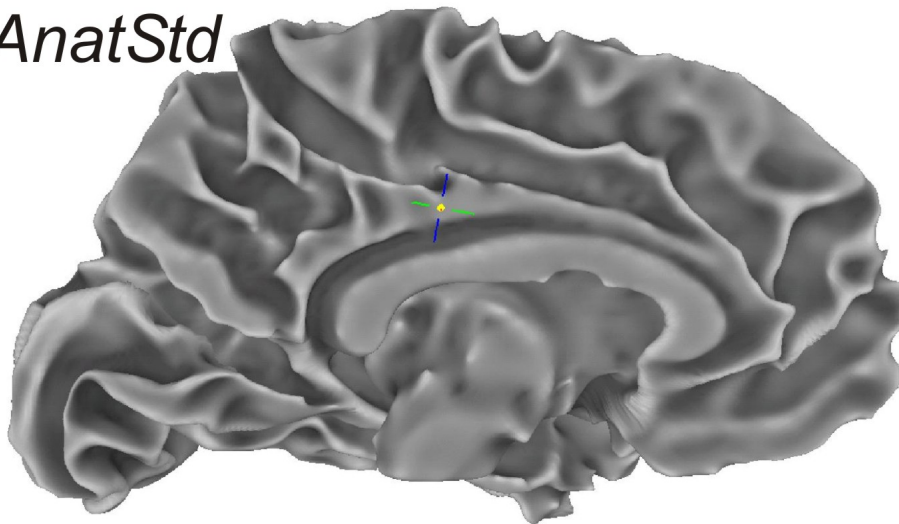


Compare surfaces: Original and Standard

Anat



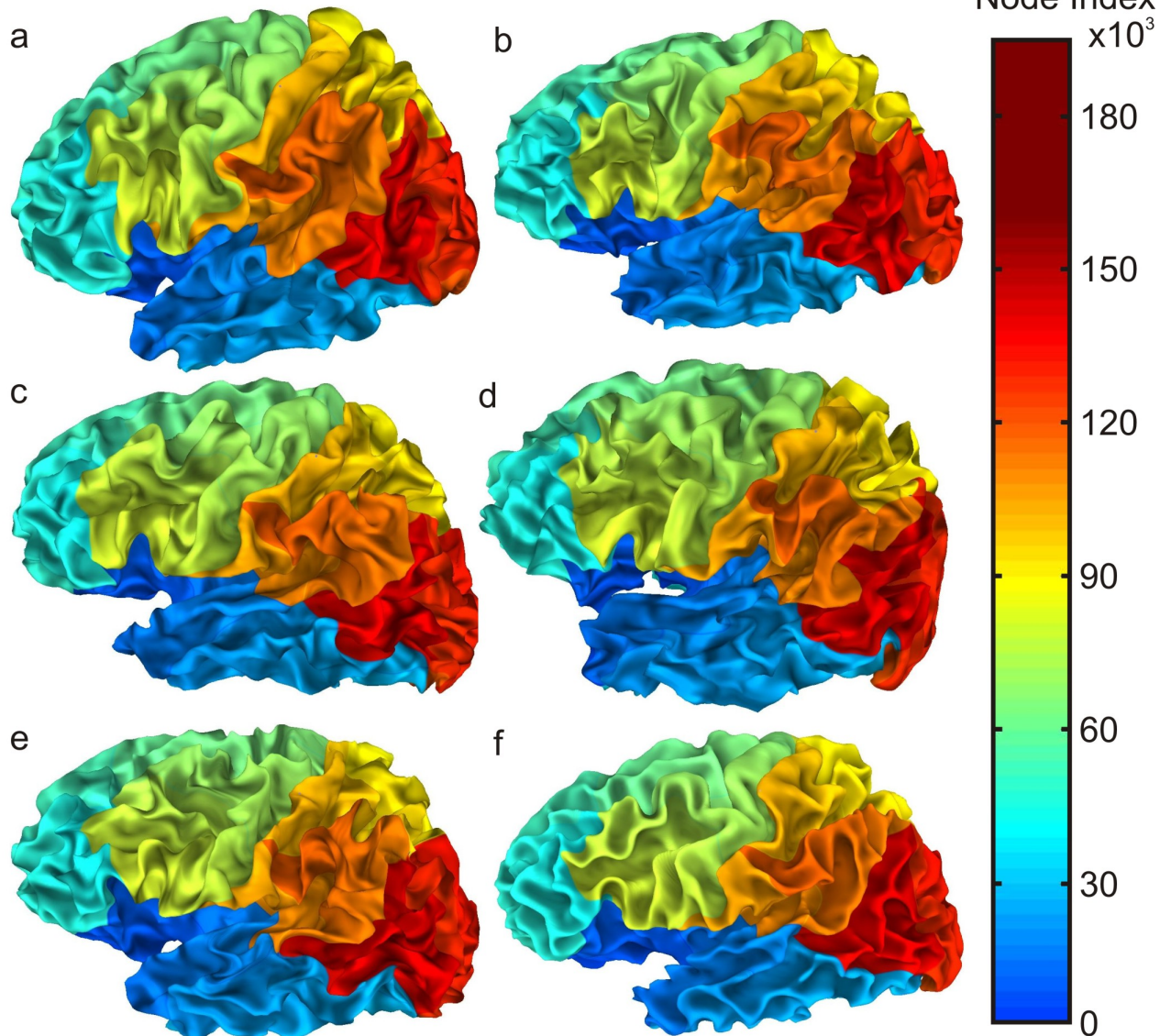
AnatStd



Standard meshes for 6 subjects

A- Standard Meshes

- 6 standard-mesh surface models from different subjects.
- Node colors encode for node index n on the standard mesh.
- Nodes with similar indices correspond to comparable sulcal landmarks despite anatomical variability across subjects.

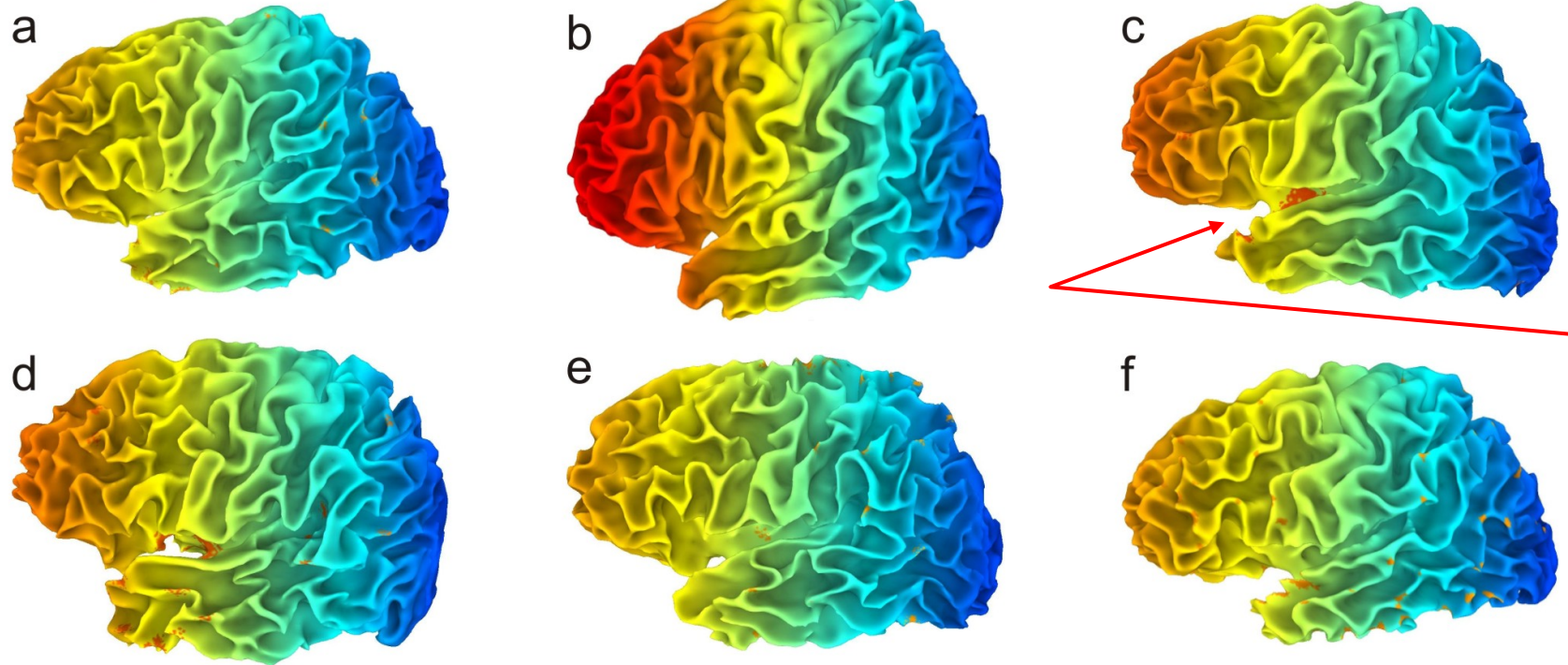


Reproduce figure from http://afni.nimh.nih.gov/pub/dist/edu/data/std_meshes.tgz

with: `tsh run_stdmesh_demo`

29 Oct 2009 SSCC/NIMH

B- Original Meshes



- Original-mesh versions of standard-mesh surfaces with same coloration scheme
- Surfaces have differing numbers of nodes, some colors may not be represented
- Nodes with similar indices no longer correspond to comparable anatomical areas
- Small clusters of **red color** show new nodes later added to correct topological errors

Creating Standard-Mesh Surfaces

- Required Data:
 - Original Surface models
 - Warped Spherical surface
 - Spec file of the surfaces above (i.e. DemoSubj_lh.spec)
- Creating the standard-mesh versions of the original surfaces

```
MapIcosahedron      -spec Demo_Subj_lh.spec    \   Written by B. Argall
                    -ld 141                                     \
                    -prefix ld141
```

-spec SpecFile: option specifying spec file with original surfaces

-ld n : number of subdivisions for each edge of the icosahedron.

$$Nv = 2 + 10n^2 \quad (198812 \text{ vertices})$$

$$Nt = 20n^2 \quad (397620 \text{ triangles})$$

$$Ne = 30n^2 \quad (596430 \text{ edges})$$

-prefix: prefix assigned to standard mesh surfaces

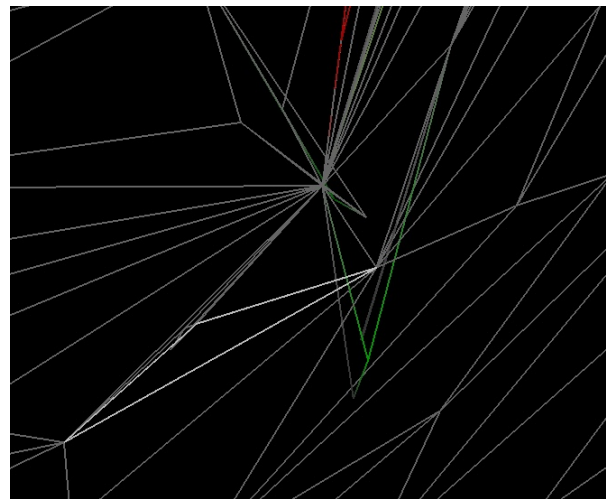
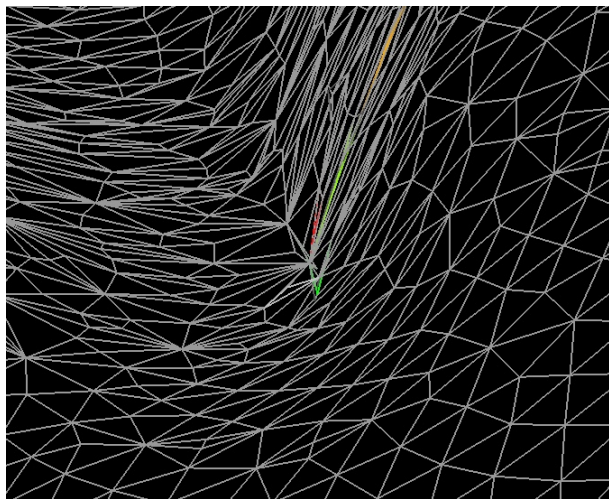
- **@SUMA_Make_Spec_FS** now generates standard-mesh surfaces by default. See **@SUMA_Make_Spec_FS -help** for details.
- Script *run_stdmeshes* was used to generate standard-mesh surfaces for the hands-on material

Using Standard-Mesh Surfaces

- Subsequent analysis will use standard-mesh surfaces, not originals
 - ★ Map single-subject data to corresponding standard-mesh surfaces.
 - ★ Use any of AFNI's **3dXXX** voxel-based statistical tools to perform within- and cross-subject analysis in the surface domain
 - ★ **3dXXX** programs can read/write NIML-formatted datasets defined over surface domains as well as true 3D volume files
- Creating standard-mesh surfaces takes a couple of minutes per subject
- You can compare original and standard surfaces using:
 - SUMA
 - create a spec file containing both original and standard-mesh surfaces.
 - open two views, one showing original surface and one showing standard-mesh surfaces
 - link viewers by coordinates (not by node index) from the SUMA controller (**ctrl+u**)
 - **CompareSurfaces** Written by Shruti Japee
 - a program that calculates the distance from each node on surface 1 along its normal to surface 2
 - **SurfaceMetrics**
 - a program that calculates metrics of the mesh like edge lengths, triangle areas, curvature, etc.

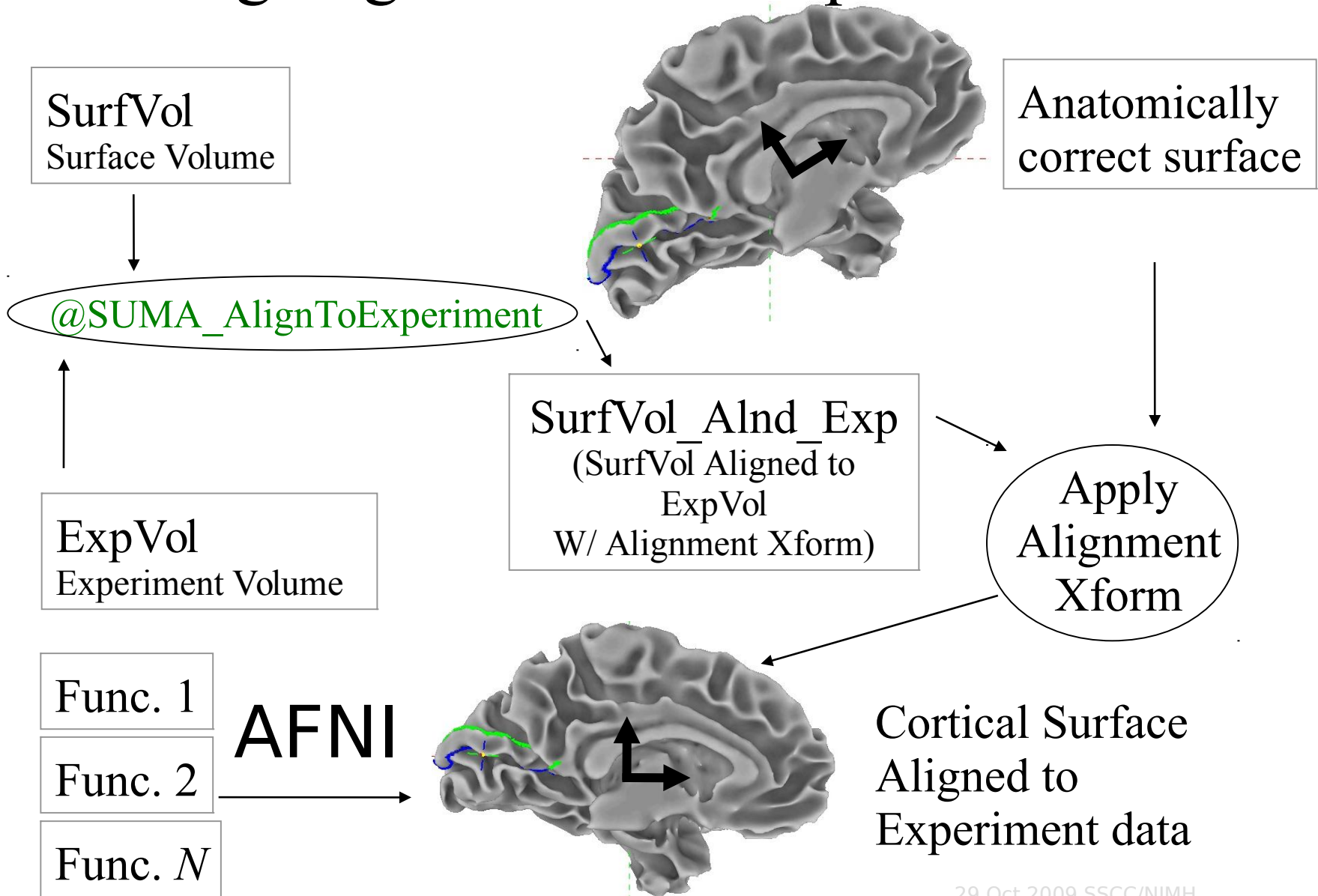
Artifacts with standard meshes

- In the past, there have been localized distortions between the standard-mesh surface and the original surface.
- These had **all** been caused by topological errors in the original spherical surfaces.
- **SurfQual** was written to highlight these errors
 - ★ if causing distortions, errors must be fixed with the program used to generate them.
 - ★ These topological errors can be ignored if they do not cause any visible distortions in the standard-mesh surfaces.



- Distortions in triangle sizes are the dual of compression/stretching on the registered sphere. If distortions are extreme, revisit regularization parameters of the registration procedure.

B: Aligning Surface w/ Experiment Data



B: Aligning Surface w/ Experiment Data

- Functional data are assumed to be in register with experiment's anatomical
 - ★ Align Anatomical to EPI using: [align_epi_anat.py](#).
- Surface Volume is aligned to experiment's anatomical volume with rigid-body or affine transformation
 - ★ The script [@SUMA_AlignToExperiment](#) simplifies this step and rarely fails. If it does, you could try manual registration with [3dTagalign](#)
 - ★ Brain coverage and image types should be comparable, not necessarily identical
- Functional data are not interpolated

B: Aligning Surface w/ Experiment Data

- Demo: (close previous SUMA and AFNI sessions)
 - ★ `cd suma_demo/afni`
 - ➔ `DemoSubj_spgrax+orig` (experiment's high-res. anatomical scan)
 - ➔ `DemoSubj_EccExpavir+orig` & `DemoSubj_EccExpavir.DEL+orig` (EPI timeseries and function.)

- ★ To perform the alignment we ran the SUMA package script:

```
@SUMA_AlignToExperiment \
    -exp_anat DemoSubj_spgrsa+orig \
    -surf_anat ../SurfData/SUMA/DemoSubj_SurfVol+orig
```

- ➔ This script uses `3dvolreg` or `3dAllineate` to align the experiment's anatomical volume to the Surface Volume.
- ➔ The script takes care of resampling (with `3dresample`) the experiment's anatomical volume to match the Surface Volume if need be.
- ➔ The output volume is named with the prefix of the Surface Volume with the suffix `_AInd_Exp` (read "Aligned to Experiment").
- ➔ Use `-wd` option if `exp_anat` has been non-rigidly aligned to the epi

B: Aligning Surface w/ Experiment Data

- Launch AFNI to check that volumes aligned well:
 - *afni -niml &*
 - Switch **Underlay** to *DemoSubj_SurfVol_AIInd_Exp+orig*
 - Switch **Overlay** to *DemoSubj_spgrsa+orig*
 - Visually check the alignment:
 - For example, with pointer in slice viewing window:
 - press 'o' on the keyboard to turn off the overlay
 - press 'u' repeatedly to toggle between displaying the two volumes

★ Launch SUMA to check alignment of surface with volumes

```
suma -spec ../SurfData/SUMA/std.DemoSubj_lh.spec \  
-sv DemoSubj_SurfVol_AIInd_Exp+orig &
```

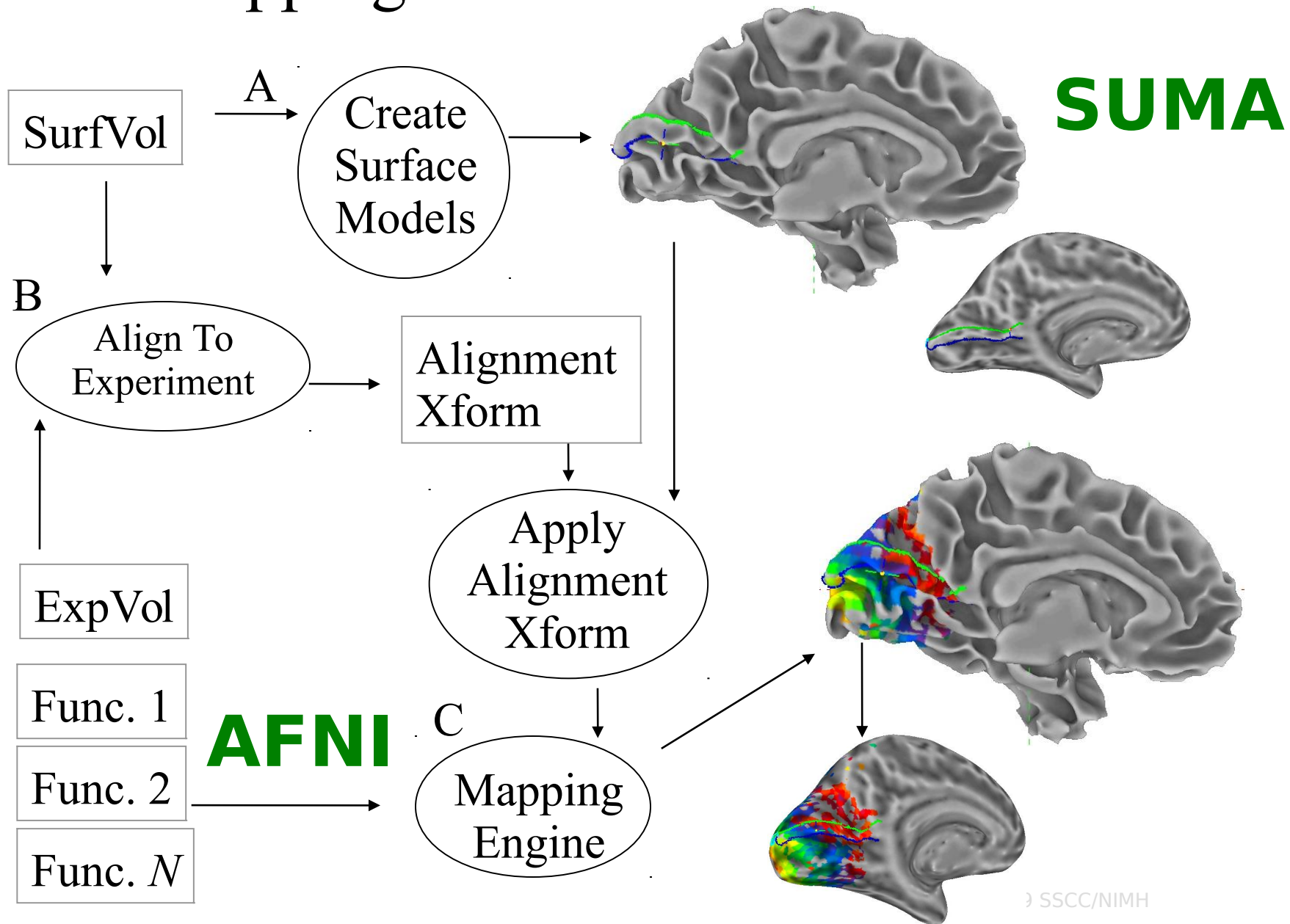
➡ or execute the script: *tcsch run_suma*

Press 't' to talk to AFNI

➡ You should see a surface overlaid onto *DemoSubj_SurfVol_AIInd_Exp+orig*

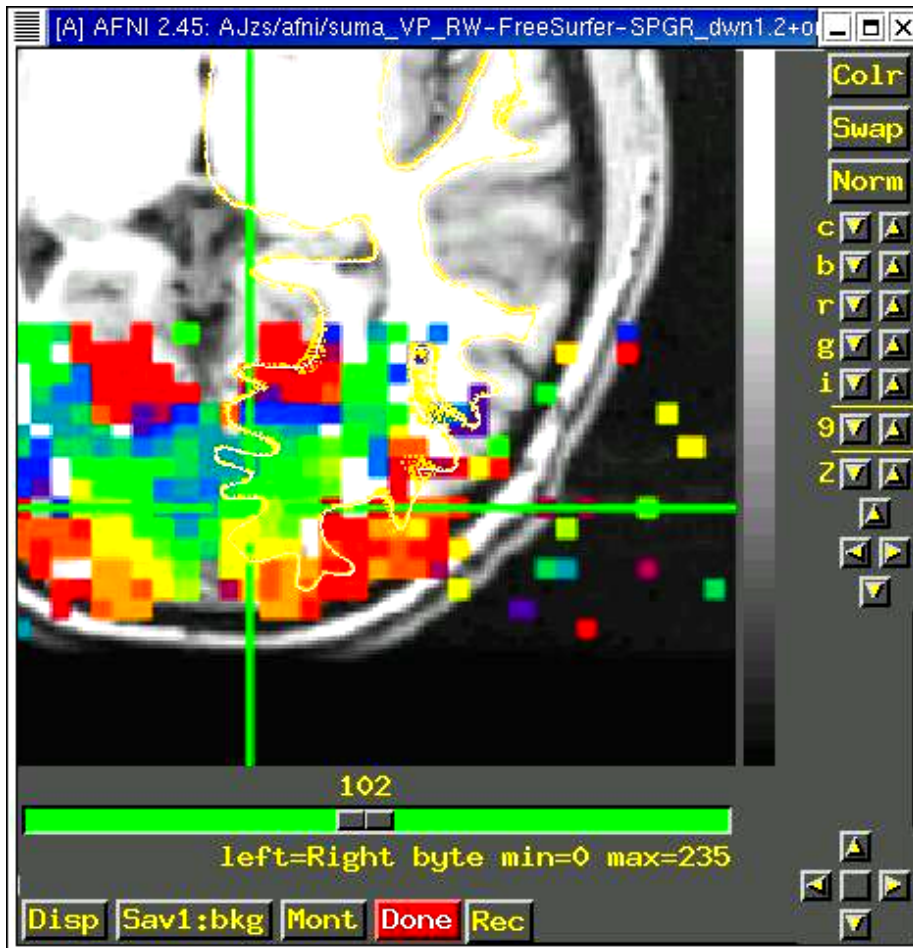
➡ Alignment should be proper, otherwise you have a problem.

C: Mapping FMRI Data Onto Surface

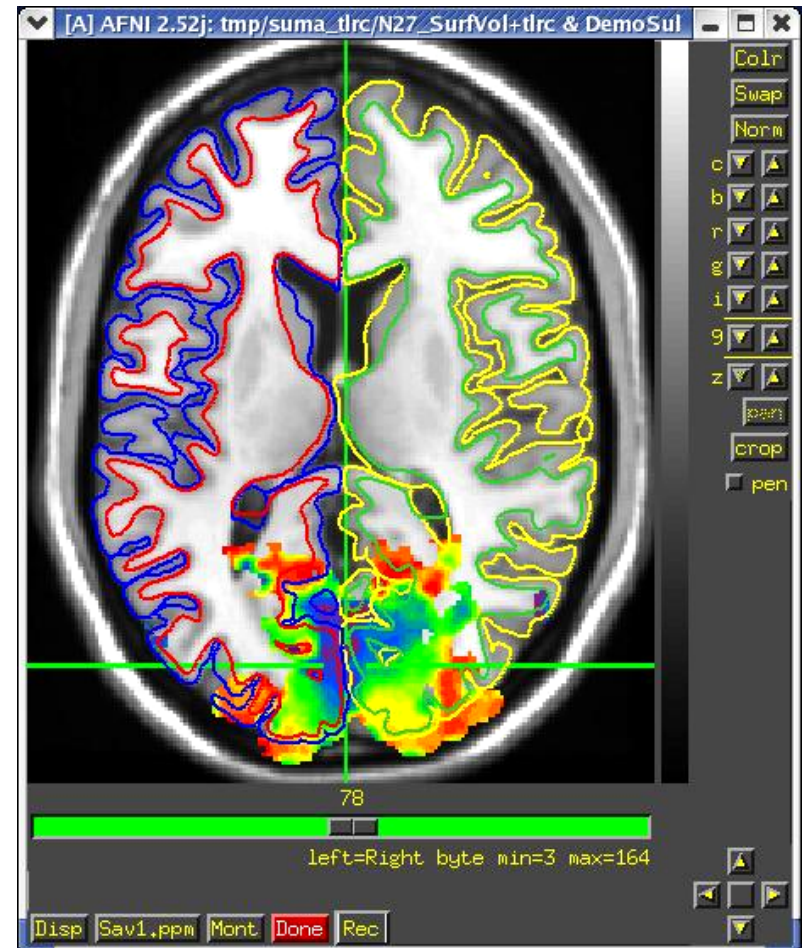


Mapping Options

- Surface/volume Intersection



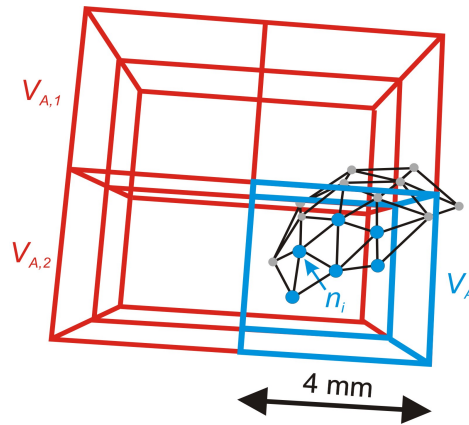
- Shell/volume Intersection



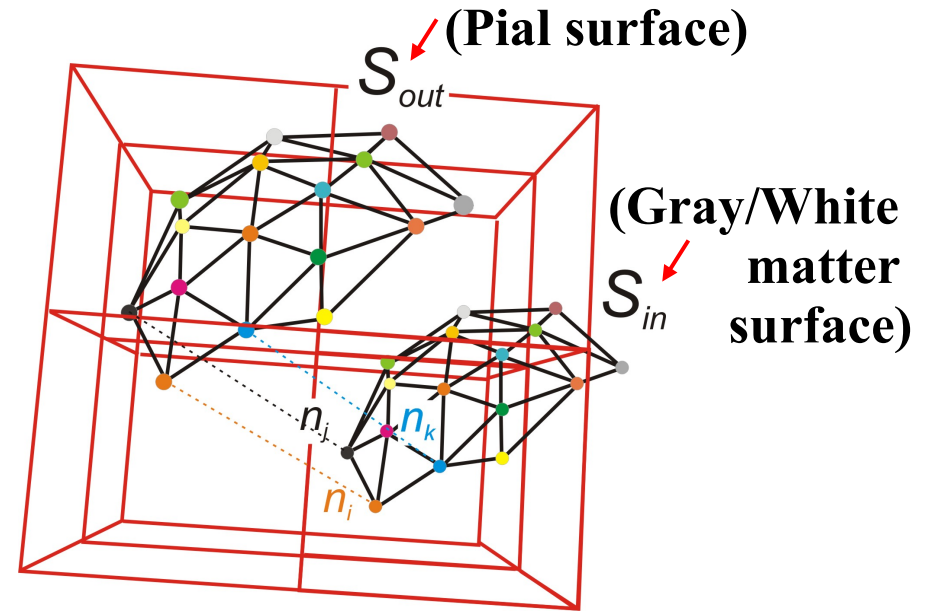
Mapping options

- Surface/volume Intersection
 - ★ One voxel per node

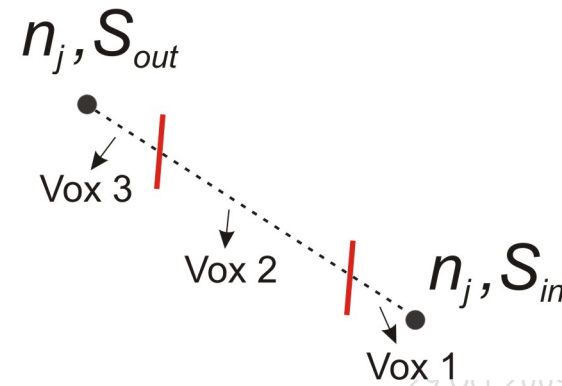
(whatever voxel that node lies inside of)



- Shell/volume Intersection
 - Multiple voxels possible per node



Node segment intersecting 3 voxels



Mapping Habits

- When mapping data from volume to surface domains
 - ★ If mapping assigns multiple voxels to one node
 - ➔ How do you deal with functional datasets?
 - ⇨ Do you average statistics?
 - ⇨ Do you apply a threshold before or after averaging?
 - » What if some of the voxels are active and some are not?
 - ➔ These problems are best avoided by:
 - ⇨ Mapping the time series data onto the surface
 - ⇨ Performing statistical analysis directly in the surface domain using **3dXXX** AFNI programs
- When combining surface data across subjects
 - ★ Same concerns as with volumetric group analysis
- You can also create volumetric data from surface-based data
 - ★ use **3dSurf2Vol**, the inverse of **3dVol2Surf**

Interactive Mapping Onto Surface

- Interactive mapping is controlled by AFNI's **Vol2Surf plugin**
 - ★ Mapping is done using anatomically correct surfaces sent to AFNI with the overlay data volume.
 - ➔ See plugin's help for details.
 - ★ Only colors (not data values) are sent from AFNI to SUMA.
- Demo (*Continued*): To map data from volume to surface interactively:
 - ★ Execute `tcsh run_3dVol2Surf`, to ensure you have demo sets.
 - ★ Switch **Overlay** to DemoSubj_EccExpavir.DEL
 - ★ **Define Overlay** with:
 - ➔ **Olay**: Delay
 - ➔ **Thr**: Corr. Coef.
 - ➔ **Pos**. color mapping
 - ➔ **#20** color map
 - ➔ **See Function**
 - ◇ You should see the function on the surface model in SUMA.
 - ◇ The colors are applied to all topologically related surfaces
 - ◇ NOTE: Only AFNI controller **A** sends function back to SUMA
 - ➔ Change threshold in AFNI and watch change in SUMA

Command-line Mapping

- **3dVol2Surf** maps data from a 3D volume dataset directly onto the cortical surface, creating a new dataset defined over a surface

3dVol2Surf

```
-spec          ../SurfData/SUMA/std.DemoSubj_lh.spec |
-surf_A       lh.smoothwm.asc                       |
-surf_B       lh.pial.asc                           |
-sv           DemoSubj_SurfVol_AInd_Exp+orig        |
-grid_parent  DemoSubj_EccExpavir.DEL+orig         |
-map_func     ave                                   |
-f_steps      10                                    |
-f_index      nodes                                |
-out_niml     v2s.lh.DEL.niml.dset
```

Written by Rick Reynolds

(see output of *3dVol2Surf -help* for details.)

- Execute script *tcsh run_3dVol2Surf* to map various types of data onto the surfaces

Options for 3dVol2Surf example

- ★ Basic Parameters:

- spec: SUMA spec file containing surface(s) to be used in mapping.

- surf_A (-surf_B): Surface(s) to be used in the mapping.

- sv: Surface Volume used to align surface to data

- grid_parent: AFNI volume containing data to be mapped.

- map_func: Method for handling voxels to node mapping

- out_niml: Output dataset file in NIML format

- ★ Optional parameters (just a few of them):

- cmask: Option for masking data in DataVol on the fly..

- oom_value V0 : Assign V0 to nodes in masked voxels

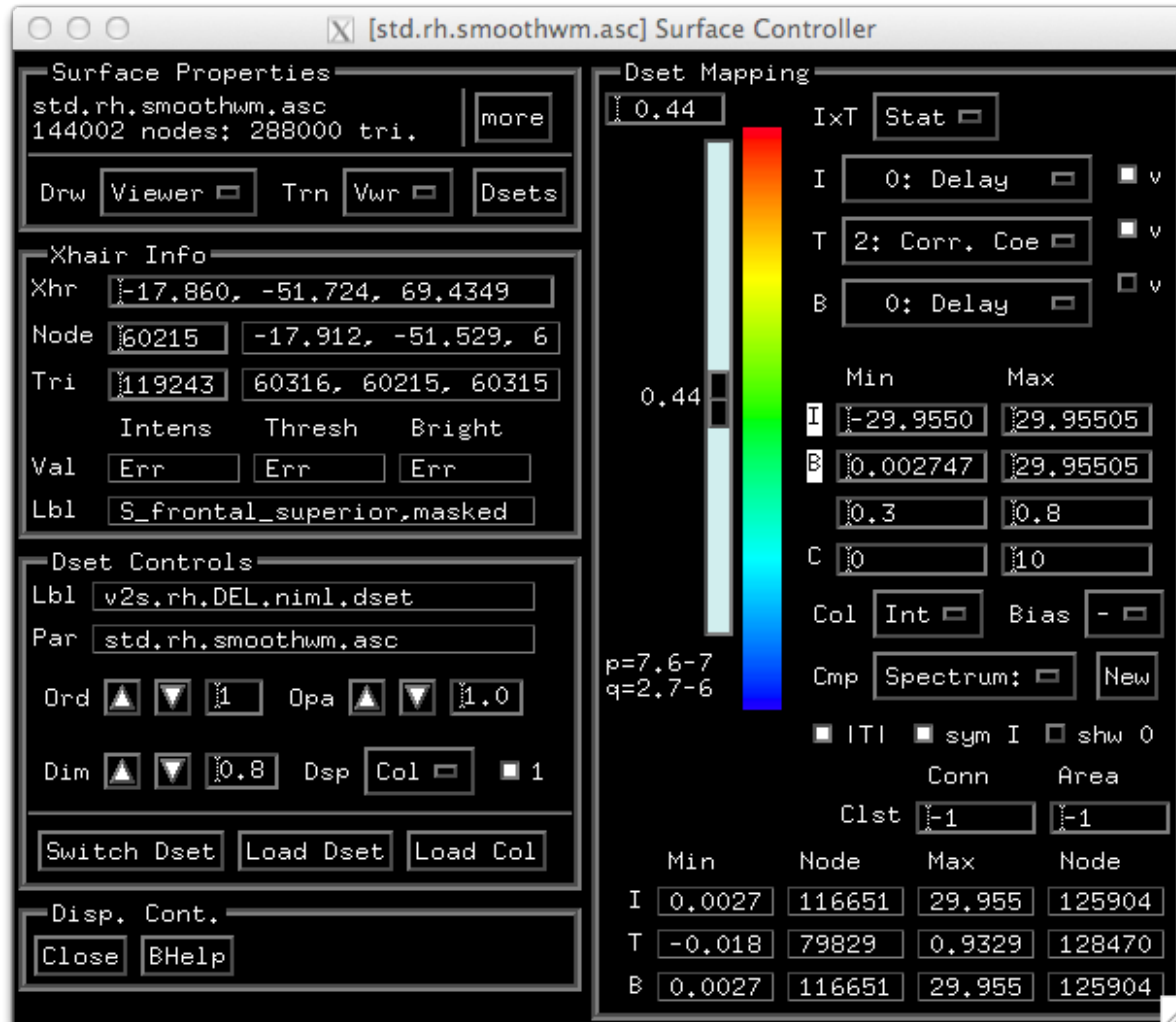
- oob_value V1: Assign V1 to nodes that are not covered by any voxels

- oom_value and -oob_value are useful for creating 'full' datasets.

Format of surface-based datasets

- The output dataset can be thought of as a table of numbers.
 - Each column represents data from one sub-brick in the volume
 - Each row represents the values mapped to a node
 - By default, a surface dataset is 'sparse'; containing only rows for the nodes that had data mapped onto them
 - When combining surface-based datasets, it is safest to work with 'full' datasets which contain a row for each node
 - **ConvertDset** can turn 'sparse' datasets into 'full' ones.
- Useful tools for manipulating datasets:
 - **3dinfo** (Information as viewed by AFNI's **3dXXX** programs)
 - **SurfDsetInfo** (Information as viewed by SUMA)
 - **ConvertDset** (A tool to convert between formats)
- Selection qualifiers to dataset names
 - [SEL]** to select certain columns (sub-bricks)
 - {SEL}** to select certain rows
 - #SEL#** to select certain nodes
 - The format of SEL is the same as in AFNI, see section 'INPUT DATASET NAMES' in **3dcalc -help** for details.
 - [i]** to select the node index column (NIML dsets only)

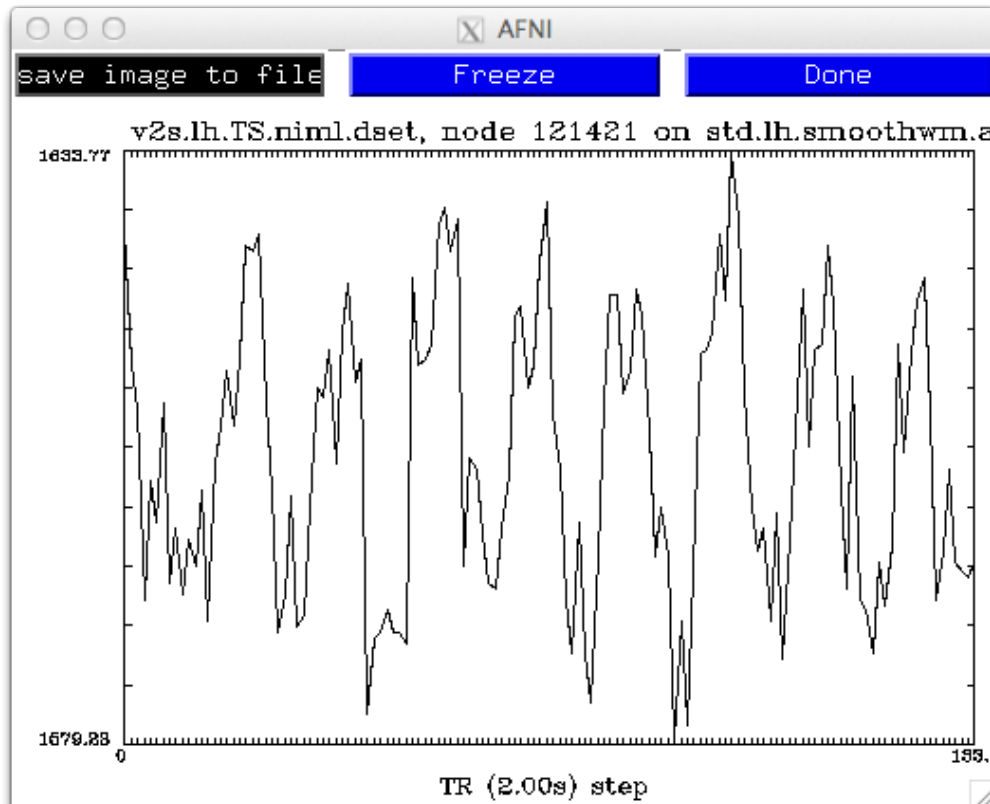
Colorizing Results Interactively



- Demo (continued):
 - ★ In SUMA, press 'ctrl+s' to open Object Controller.
 - ➔ Use View→Object Controller if you were born after 1981.

Graphing Time Series

- Demo (*continued*):
 - ★ Press “**Load Dset**” and read in “**v2s.lh.TS.niml.dset**”
 - ★ Contralateral dataset, if sanely named, gets automatically loaded too
 - ➔ In SUMA, press ‘**g**’ to graph data points at the selected node
 - ➔ Select other nodes (or **right-click+drag**) to see data at other nodes
 - ➔ Press ‘**Freeze**’ on graph window to preserve current graph
 - ➔ Clicking on other nodes will start a new graph



Hands-On

Colorizing results interactively

- Demo (*continued*):

- ★ Press “[Load Dset](#)” and read in “[v2s.lh.DEL.niml.dset](#)”

- SUMA will colorize the loaded Dset (create a color plane for Dset) and display it on the top of pre-existing color planes.

- We begin by describing the right side block “[Dset Mapping](#)” which is used to colorize a Dset. Many of the options mimic those in AFNI’s “[Define OverLay](#)” controls.

- Many features are not mentioned here. See online docs. and BHelp.

- ★ From the Dset Mapping block (right side of interface)

- Select column [Corr. Coef.](#) for Threshold (T)

- ↳ Press ‘[v](#)’ button to apply thresholding

- ↳ Use scale to set the threshold. Nodes whose cross correlation value does not pass the threshold will not get colored

- ↳ Note p (uncorrected), and q values (FDR) below the slider

- ↳ FDR values are per-hemisphere

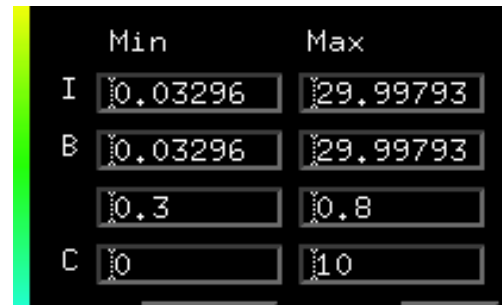


- ↳ Note:

- ↳ For simplicity, we mapped a statistical dataset onto the surface. This resulted in statistical parameters being averaged without being normalized

- ↳ A better approach would be to map the time series, and then perform the statistical computation. See script [./run_3dVol2Surf](#) for examples.

Dset Mapping block



	Min	Max
I	0.03296	29.99793
B	0.03296	29.99793
	0.3	0.8
C	0	10

- Demo (*continued*):
- **Mapping Parameters Table:**
 - ➔ Used for setting the clipping ranges.
 - ➔ Clipping is only done for color mapping. Actual data values do not change.
- ★ Column **Min**:
 - ➔ Minimum clip value. Clips values (v) in the Dset less than Minimum (min): **if $v < \text{min}$ then $v = \text{min}$**
- ★ Column **Max**:
 - ➔ Maximum clip value. Clips values (v) in the Dset larger than Maximum (max): **if $v > \text{max}$ then $v = \text{max}$**
- ★ Row **I**
 - ➔ Intensity clipping range. Values in the intensity data that are less than Min are colored by the first (bottom) color of the colormap. Values larger than Max are mapped to the top color.
- ★ **Left click** on the **I** locks ranges from automatic resetting when you choose a different dataset column for **I**
- ★ **Right click** on the **I** resets values to full range in data

Dset Mapping block

- Demo (*continued*):

- **Col:**

- Switch between color mapping modes.

- *Int*: Interpolate linearly between colors in colormap

- *NN* : Use the nearest color in the colormap.

- *Dir*: Use intensity values as indices into the colormap. In *Dir* mode, the intensity clipping range is of no use.

- **Cmp:**

- Switch between available color maps. If the number of colormaps is too large for the menu button, right click over the '**Cmp**' label and a chooser with a slider bar will appear.

- Alternately, as with many of SUMA's menus, detach the menu by selecting the dashed line at the top of the menu list. Once detached, the menu window can be resized so you can access all elements in very long lists.

- More help is available via **ctrl+h** while mouse is over the colormap

- **Bias**: This is mostly for fun — shifts node coordinates by the data value



Dset Mapping block



- Demo (*continued*):
- **The Colormap:**
 - The colormap is actually a display surface in disguise and shares some of the functions of SUMA's viewers:
 - **Keyboard Controls** while mouse cursor is over colormap:
 - **r** : record image of colormap
 - **Ctrl+h** : a help message for the Dset Mapping block
 - **z** : Zoom in on colormap
 - Maximum zoom shows 2 colors in the map
 - **Z** : Zoom out on colormap
 - Minimum zoom shows all colors in the map
 - **Up/Down arrows** : rotate colormap up/down.
 - **Home** : Reset zoom and translation parameters
 - **Mouse Controls**
 - None yet, some maybe coming someday

Dset Mapping block

- Demo (*continued*):

- **|T|** :

- ★ Toggle Absolute thresholding.

- ➔ **OFF**: Hide node color for nodes 'n' that have:

- $T(n) < T_{scale}$

- ➔ **ON**: Hide node color for nodes that have:

- $|T(n)| < T_{scale}$

where: T_{scale} is the value set by the threshold scale.

$T(n)$ is the value in the selected threshold column (**T**).

- **sym I** :

- ★ Toggle Intensity range symmetry about 0.

- ➔ **ON** : Intensity clipping range is forced to go from -val to val . This allows you to mimic AFNI's color ranging mode.

- ➔ **OFF**: Intensity clipping range can be changed to your liking.

- **shw 0** :

- ★ Toggle color hiding of nodes with intensity = 0

- ➔ **ON** : 0 intensities are mapped to the colormap as any other values.

- ➔ **OFF**: 0 intensities are hidden, a là AFNI



Dset Mapping block

- Demo (*continued*):



- **Interactive Clustering:**

- ★ Left click on 'Clst' to activate/deactivate. Cluster table is output to shell. Clicking on a node shows its cluster label in the viewer.
- ★ Conn: Minimum distance between nodes in the same cluster
 - ↳ Default is in *mm* (units of the surface coords). Negative values specify distance in number of edges between nodes.
- ★ Area: Minimum area () criterion for accepting a cluster.
 - ↳ Default area units are in *mm*². Negative numbers indicate masking by node number rather than area.

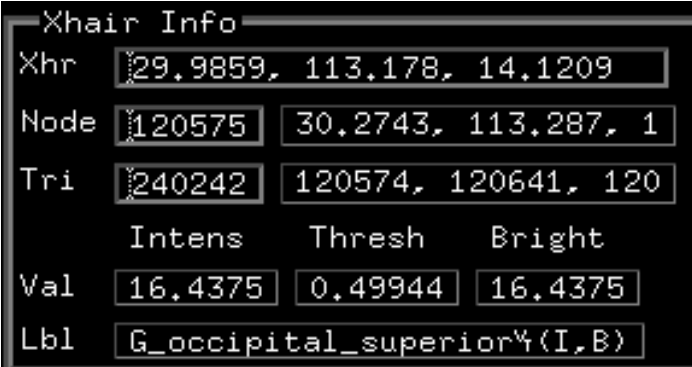
- **Data Range Table:**

- ★ Full range of values in Dset.
 - ↳ Right click in "Node" columns to have crosshairs jump to that node.
 - ↳ You might have to move the surface around to see it.

	Min	Node	Max	Node
I	0.0329	80378	29.997	109447
T	-0.024	115153	0.9420	111286
B	0.0329	80378	29.997	109447

Xhair Info block

- Demo (*continued*):
- **Xhr:**
 - ★ Crosshair coordinates on this controller's surface. Entering new coordinates makes the crosshair jump to that location (like 'ctrl+j').
 - ➔ Use 'alt+l' (that's a lower-case 'ell') to center crosshairs in your viewer.
- **Node:**
 - ★ Node index of node in focus on this controller's surface. Nodes in focus are highlighted by the blue sphere in the crosshair. Entering a new node's index will put that node in focus and send the crosshair to its location (like 'j').
- **Node Values Table:**
 - ★ Data Values at node in focus
 - ➔ Column **Intens**: Intensity (I) value
 - ➔ Column **Thresh**: Threshold (T) value
 - ➔ Column **Bright**: Brightness modulation (B)
 - ➔ Row **Val**: Data Values at node in focus
- **Node Label Table:**
 - ★ Row **Lbl**:
 - ➔ Labels available at the node in focus. Labels include FreeSurfer's parcellations, intensity, threshold, and brightness values, cluster membership, etc. You're better off reading the label from the viewer.

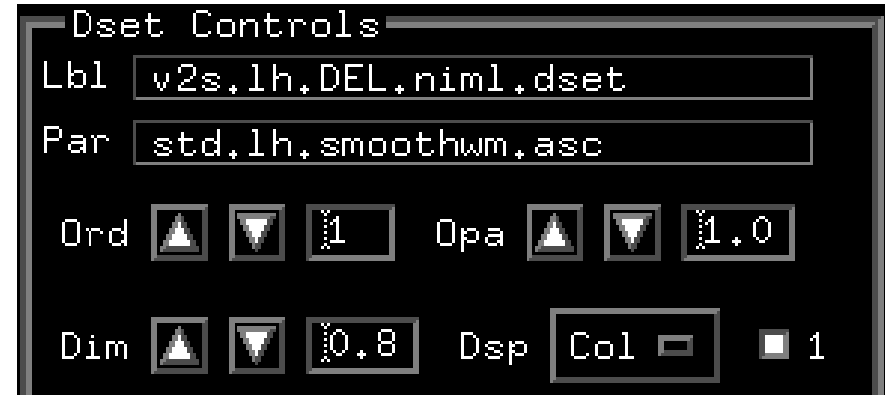


Xhair Info

Xhr	29.9859, 113.178, 14.1209		
Node	120575	30.2743, 113.287, 1	
Tri	240242	120574, 120641, 120	
	Intens	Thresh	Bright
Val	16.4375	0.49944	16.4375
Lbl	G_occipital_superior%(I,B)		

Dset Controls block

- Demo (*Continued*):
- **Dset Info Table:**
 - ★ Row **Lbl**: Label of Dset.
 - ★ Row **Par**: Parent surface of Dset.



- **Ord**:
 - ★ Order of Dset's colorplane. Dset with highest number is on top of the stack. Separate stacks exists for foreground (fg:) and background planes (bg:).
- **Opa**:
 - ★ Opacity of Dset's colorplane. Opaque planes have an opacity of 1, transparent planes have an opacity of 0. Opacities are used when mixing planes within the same stack foreground (fg:) or background (bg:).
 - ★ Opacity values are not applied to the first plane in a group. Consequently, if you have just one plane to work with, opacity value is meaningless.
 - ★ Color mixing can be done in two ways, use **F7** to toggle between mixing modes.

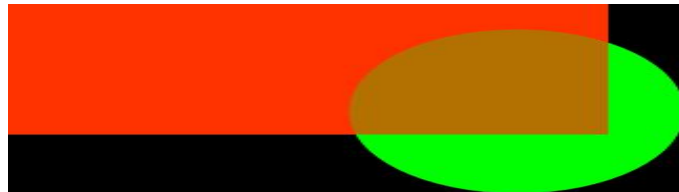
Dset Controls block

- Demo (*Continued*):
- **Dim:**
 - ★ Dimming factor to apply to colormap before mapping the intensity (**I**) data. The colormap, if displayed on the right, is not visibly affected by **Dim** but the colors mapped onto the surface are.
 - ★ For RGB Dsets (.col files), **Dim** is applied to the RGB colors directly.
- **Dsp:**
 - ★ How to display node color values. Options include pseudocoloring, contouring (at discrete color levels), both, or none.
- **1: (for 1 only)**
 - ★ If **ON**, view only the selected Dset's colors. No mixing of colors in the foreground stack is done.
 - ★ If **OFF**, mix the color planes in the foreground stack.
 - ★ This option makes it easy to view one Dset's colors at a time without having to worry about color mixing, opacity, and stacking order.
 - ★ Needless to say, options such as '**Ord:**' and '**Opa:**' in this panel are of little use when this button is **ON**.

Color overlay planes

- Colorized Dsets are organized into layered color planes
 - ★ 2 commonly used planes are:
 - ↳ Surface Convexity (usually in gray scale)
 - ↳ AFNI Function (usually in color)
 - ★ Planes are assigned to two groups
 - ↳ Background planes (like Convexity)
 - ↳ Foreground planes (like AFNI Function)
 - ★ Many other planes can be added to either group.
- Color planes of the same group are mixed together:
 - ★ Planes are stacked based on their order and opacity.
 - ★ Opacity of 1st plane in a group does not affect color mixing.
 - ★ There are 2 modes for mixing colors. See **F7** key in SUMA.

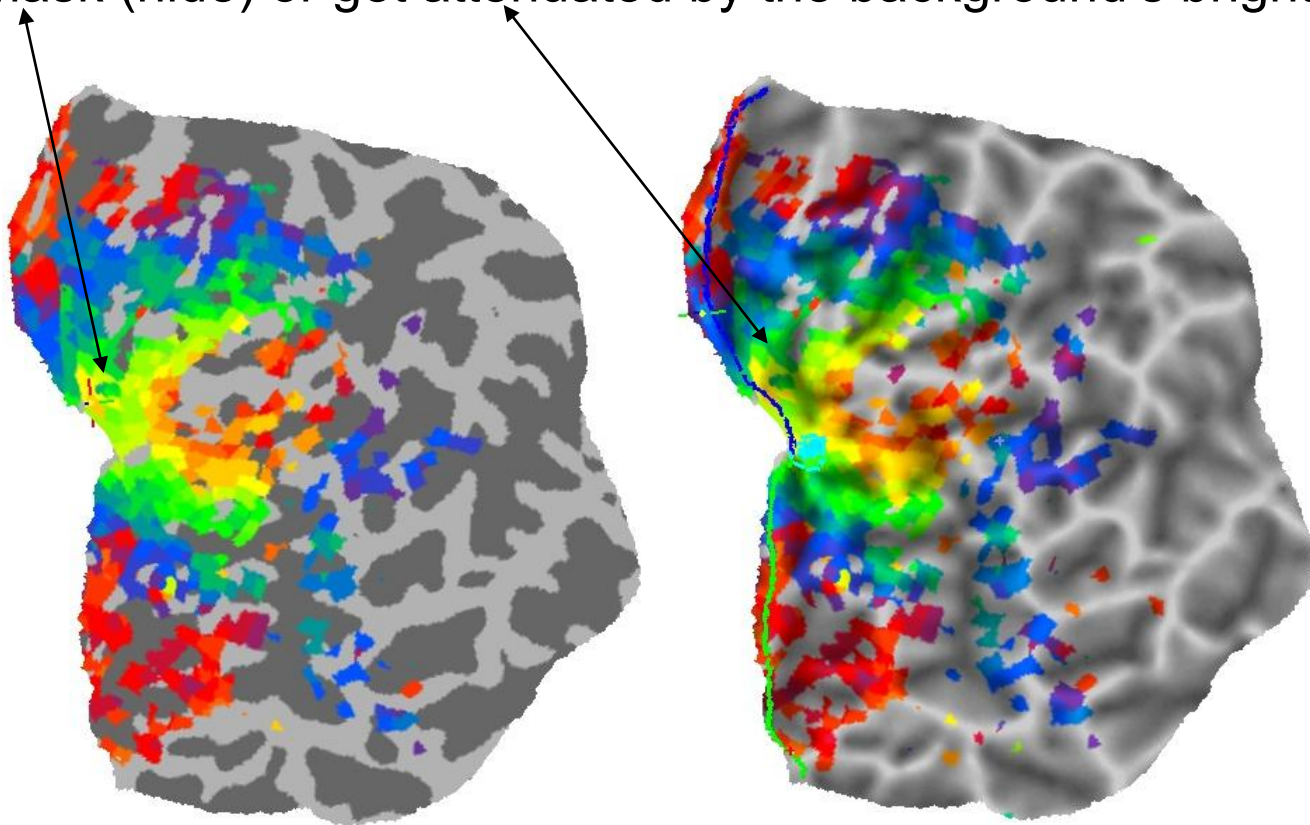
Plane 1: 80% opacity



Plane 2: 30% opacity

Color overlay planes

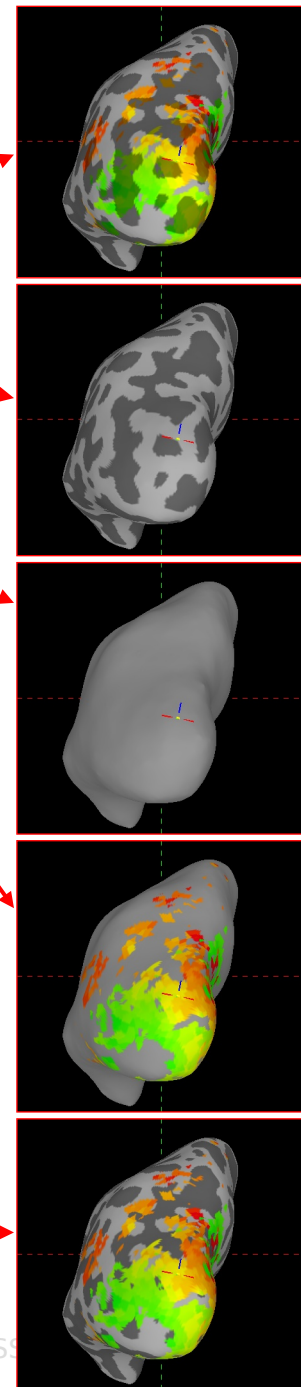
- Node colors displayed on surface are obtained by:
 - ★ 1st: mixing background planes
 - ★ 2nd: mixing foreground planes
 - ★ 3rd: layering mixed foreground atop mixed background plane
 - ➔ When foreground colors overlap background colors, they either mask (hide) or get attenuated by the background's brightness.



Layering fore- & background planes

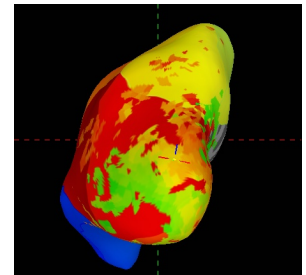
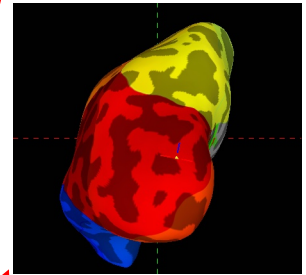
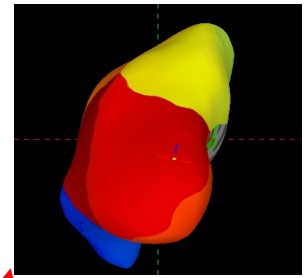
- Demo (*continued*):

- ★ View an inflated surface with function from AFNI
- ★ Turn foreground plane(s) off by pressing '**f**' once
 - ➔ Now all you see is the background plane(s)
- ★ Turn background planes off by pressing '**b**' once
 - ➔ Now all you see is “No Color” color on all nodes
- ★ Turn foreground plane(s) back on with '**f**'
 - ➔ Now you have foreground without background
- ★ Turn background plane(s) back on with '**b**'
 - ➔ Now you have foreground atop background
 - ➔ You can still see the background underneath the foreground—this is due to the background brightness attenuation of the foreground colors.
- ★ Toggle background intensity attenuation off and on with '**a**' and see the effect on the resultant maps.



Playing with color plane opacity

- Demo (continue from inflated view with function)
 - ★ 'ctrl+s' or View→Object Controller to open surface controller
 - Turn OFF '1 Only'
 - ★ Load in color plane lh.1D.col with 'Load Col' or 'c'
 - This is an RGB Dset, color mapping controls are hidden
 - Plane is placed atop of the foreground group
 - Its opacity is 1 so it will obscure the functional data
 - Background attenuation is not affected by plane's opacity.
 - ⇒ try turning it on and off again with 'a'
 - Now lower the opacity of lh.1D.col with Opa: and watch the colors from the planes below start to show through



Playing with color plane order

- Demo (continue from inflated view with function)
 - ★ You could put `lh.1D.col` below the function
 - ➔ **Switch Dset** to get a list of available planes
 - ➔ Prefixes `fg:` and `bg:` denote plane's group membership
 - ➔ Select `lh.1D.col` and lower its order with the **Ord:** button
 - ➔ Select `FuncAfni_0` and play with its opacity
 - ➔ Note: You can't make a plane change its group membership, yet.
 - ★ You can't delete a loaded color plane yet, but you can hide it.
 - ★ Turn '1' ON if you just want to see the selected plane.
 - ★ The one whose label is shown in the object controller
- **Test!**
 - ★ Find a way to flip between the mapping from AFNI and the mapping done with `3dVol2Surf` before.
 - ➔ Appreciate the differences between the two mappings.



Drawing surface-based ROIs


- Demo

- ★ ‘**Ctrl+d**’ or **Tools→Draw ROI** to open ROI drawing tool

- ↳ When in Draw ROI mode (cursor turns into target circles) 

- ↳ The pick (usually third) mouse button is used for drawing

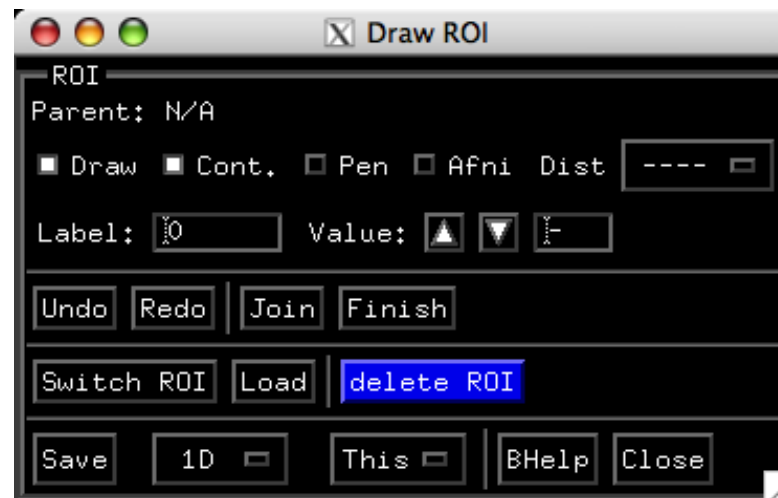
- ↳ Picking is done by combining shift key and pick button

- ↳ If pen mode is selected (cursor turns into a pen) 

- ↳ Drawing and picking (with shift) are done with the 1st mouse button and rotations are done with the third button

- ★ When you draw for the first time, a new “drawn ROI” is created.

- ↳ Note the **Parent:** field in the ROI frame gets filled when you draw



Drawing surface-based ROIs

- Demo
 - ★ Move the mouse to a new location and click again to draw a line from the location of the first click to a new one.
 - ★ Or click while dragging the mouse to create a smoother line.
 - ★ Both drawing methods might fail if you are drawing over very rough terrain.
 - ➔ When that happens, you continue from where the drawing stopped.
 - ➔ Drawing in 3D looks easy but it isn't.
 - ★ Use [Undo](#) and [Redo](#) when you get your drawings messed up.
 - ★ To close a loop you can press '[Join](#)' button or [double click](#)

Drawing surface-based ROIs

- Demo (*Continued*)
 - ★ To fill a closed loop, click inside the loop.
 - ➔ Note: If you have patterns that make a figure 8 jealous you might have to do multiple fills.
 - ★ Press **Finish** when you are done drawing and have set the drawing label and value to your liking.
 - ★ Now you can draw another ROI, and another and another.
 - ★ Drawing can be started/continued on any of the related surfaces
 - ➔ When you hit '**Join**', the loop is closed using the surface where the ROI was created
 - ★ **Switch ROI** to switch between ROIs and delete/modify them.
 - ★ **Load** to load ROIs from file
 - ★ **Save** to save ROIs to file
 - ➔ **1D** or **NIML** = Format of ROI file
 - ➔ **This** or **All** = which ROI to save into the file

Surface ROI → Volume ROI

- ROIs files should be transformed to dataset files (Dset).
 - ★ A dataset file has an equal number of values for each node
 - ★ You can draw two ROIs, such that some nodes belong to more than one ROI (i.e., they have more than one value)
- The program **ROI2dataset** is used to change ROIs to datasets
- Execute: *tcsh run_ROI2dataset*

```
ROI2dataset -label_dset lh.OccROIs.niml.dset \  
-input lh.OccROIs.niml.roi
```

- Note the warning:

```
Warning SUMA_ROIv2dataset:  
155/2536 nodes had duplicate entries.  
(ie same node part of more than 1 ROI)  
Duplicate entries were eliminated.
```

- ★ At the moment, duplicate entries are ignored, 1st come, 1st adopted. More options could be added if truly necessary.

Surface ROI → Volume ROI

- `lh.OccROIs.1D.dset` (created on the previous slide) can be transformed into a volume ROI with `3dSurf2Vol`
- Execute: `source run_3dSurf2Vol`

```
3dSurf2Vol -spec../SurfData/SUMA/DemoSubj_lh.spec \
  -surf_A lh.smoothwm.asc \
  -surf_B lh.pial.asc \
  -sv DemoSubj_SurfVol_AIнд_Exp+orig \
  -grid_parent DemoSubj_SurfVol_AIнд_Exp+orig \
  -map_func max \
  -f_steps 10 \
  -f_p1_mm -0.5 -f_pn_fr 0.5 \
  -sdata lh.OccROIs.niml.dset \
  -prefix lh.OccROIs
```

`-grid_parent` specifies the output volume's geometric properties

`-f_p1_mm`, `-f_pn_fr`: Specify extensions on node pair segment, either in mm or fractions of segment length (both used simultaneously here for illustration)

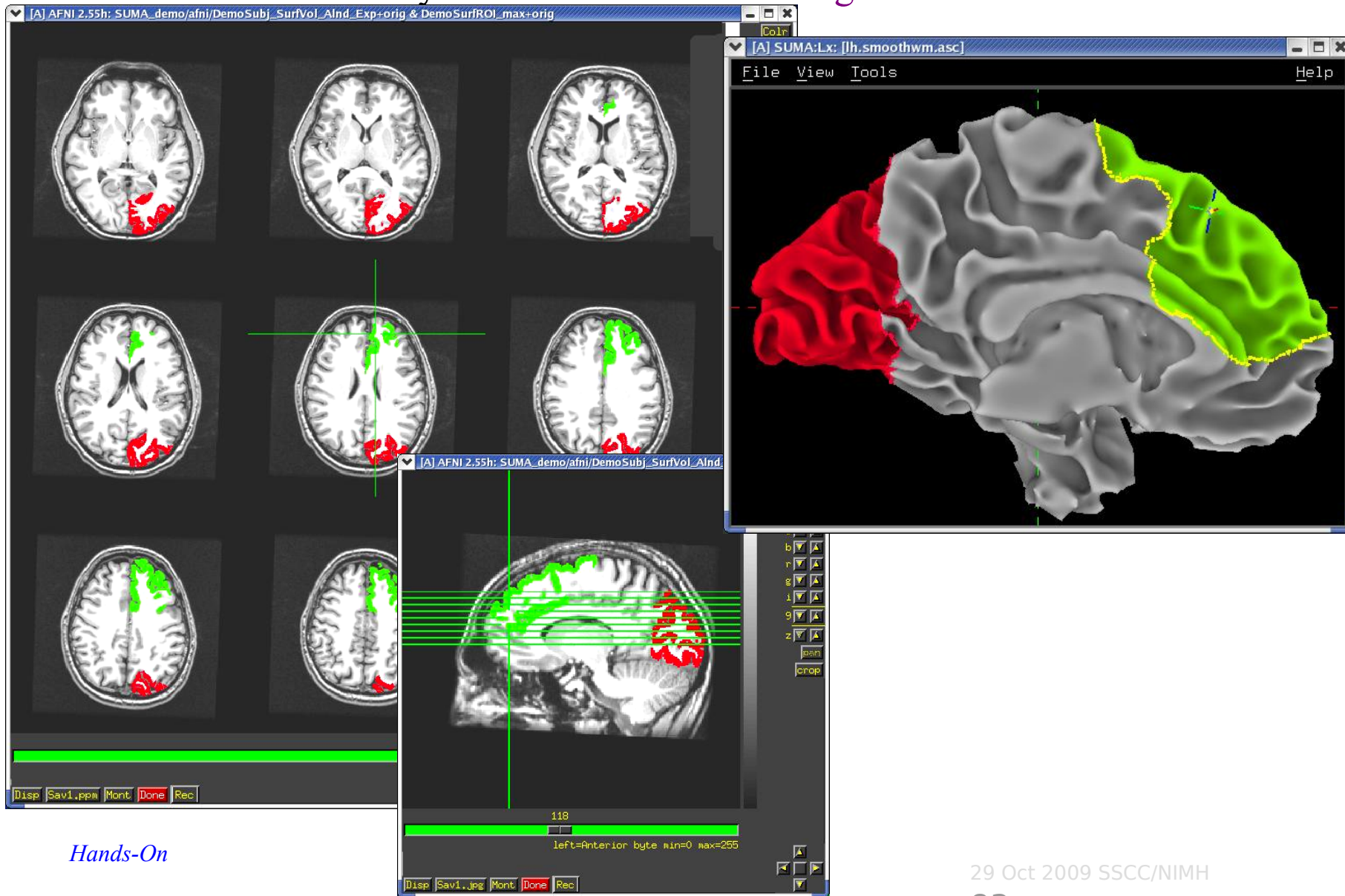
`-sdata_1D`: Specify surface data file

Surface ROI Utilities

- **SurfPatch**
 - Takes ROIs on a surface and form a new surface using the ROI nodes only
 - Compute volume of a patch/ROI if you have two bounding surfaces
- **SurfMeasures**
 - Produce surface derived measurements that are node based such as the volume attributed to a node, etc.
- **SurfaceMetrics**
 - Also produce surface derived measurements that are node based
- **ConvertSurface**
 - Surface format and coordinate transformations including projections

Surface ROI → Volume ROI

check your own *lh.OccROIs+orig* in AFNI

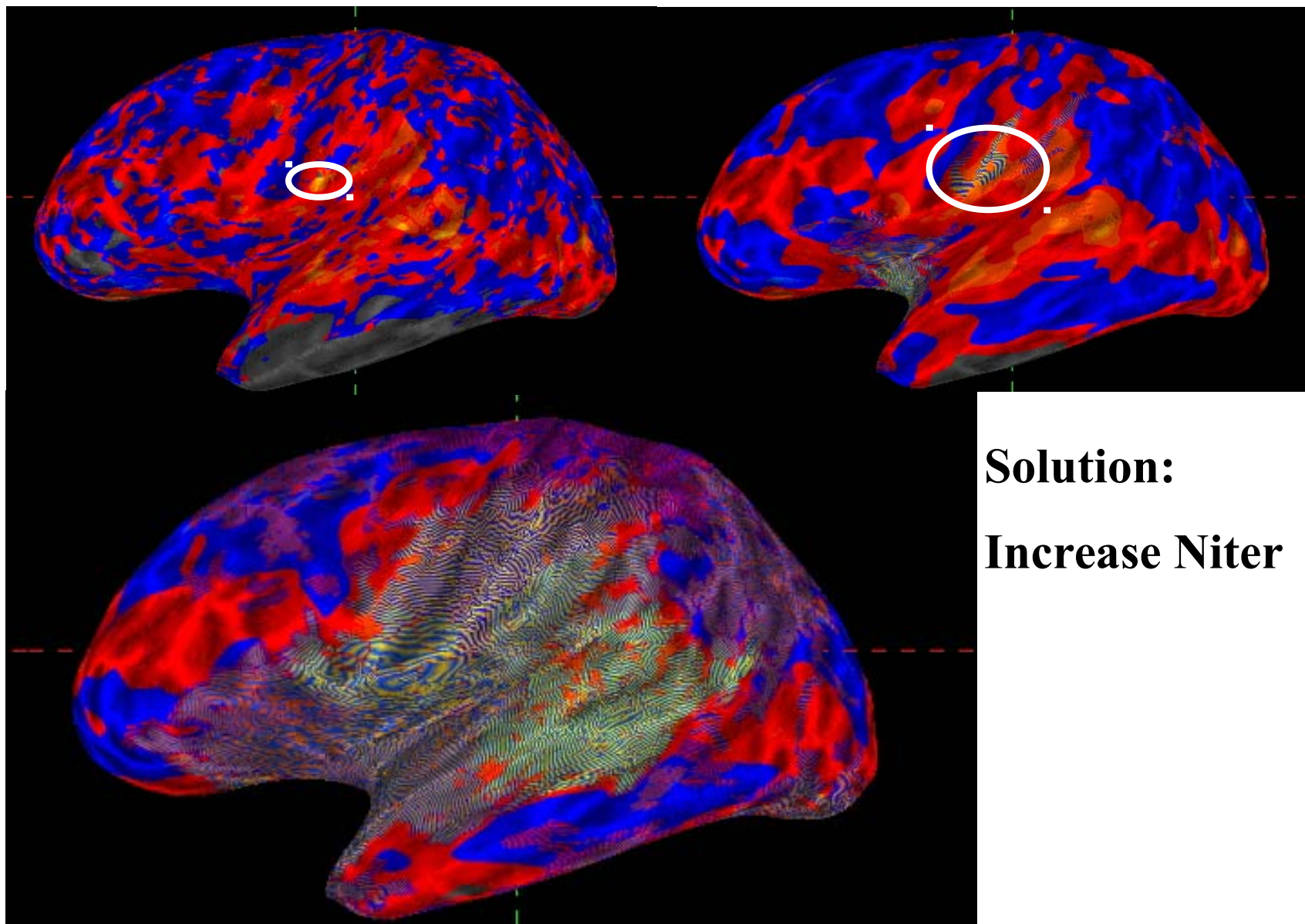


Hands-On

Smoothing data on surface models

- Data smoothing (along the surface) is done with **SurfSmooth**
 - ★ The difficulty in smoothing lies in calculating geodesic distances between node pairs.
 - ★ Smoothing can be performed by solving the diffusion equation on the surface. However effect of the kernel is somewhat poorly estimated. Number of iterations needed is a wild guess with numerical accuracy issues. Better smooth until a certain smoothness is reached.
 - ★ SurfSmooth can estimate smoothness
 - ★ until desired smoothness is reached
 - ★ or until additional smoothness is achieved
- Demo (*close SUMA and afni*)
 - ★ Execute: *tcsh run_SurfSmooth_data*
 - ➔ The script will use the output of *3dVol2Surf* in *run_3dVol2Surf* to map timeseries data onto the surfaces
 - ➔ SUMA is then launched and the script waits for you to setup the recorder ON with '**R**'
 - ➔ Hit **Enter** twice (in the shell) to launch the smoothing program
 - ➔ Watch the smoothing progress with each iteration. You can play the whole sequence at the end.

Look At Your Data!



Solution:

Increase Niter

Smoothing geometry of surface

- Surface geometry smoothing can also be done with **SurfSmooth**
 - ★ The difficulty in geometry smoothing is in preventing the surface from shrinking in size.
 - ★ **SurfSmooth** uses the smoothing algorithm by (Taubin G. 2000)
- Demo (*close SUMA and AFNI*)
 - ★ Execute: *tcsh run_SurfSmooth_geom*
 - ➔ The script will add noise to the smoothwm surface, then filter it
 - ➔ SUMA is then launched and the script waits for you to setup
 - ❏ Turn off background colors ('**b**')
 - ❏ Switch to noisy surface ('**.**')
 - ❏ Turn recorder ON ('**R**')
 - ➔ Hit **Enter** twice (in the shell) to launch the smoothing program
 - ➔ Watch the smoothing progress with each iteration. You can play the whole sequence at the end (e.g., with the '**v**' key in the image viewer window)

Talairach or MNI data display, for panache

- Without creating individualized surfaces, you can display data on a Talairach-ed or MNI-ed surface model.
 - ★ The surface models were created with FreeSurfer from the N27 dataset. (Holmes, CJ et al. JCAT 1998)
 - ★ Surfaces were created from AFNI's `TT_N27+tlrc` and `MNI_caez_N27+tlrc`, for Talairach and MNI versions, respectively.
 - Demo: (close previous SUMA and AFNI sessions)
 - ★ *If you need `suma_TT_N27/` download and unpack:*
 - `http://afni.nimh.nih.gov/pub/dist/tgz/suma_TT_N27.tgz`*
 - `tar xvzf suma_TT_N27.tgz`*
 - ★ *`cd AFNI_data6/group_results`*
 - ↳ You should find `FT_anat+tlrc` and a functional datasets in Talairach space
 - ★ *`afni -niml &`*
 - ↳ setup function as shown in the earlier slides
- ```
suma -spec ~/suma_TT_N27/TT_N27_both.spec \
-novolreg -sv FT_anat+tlrc
```
- ↳ start communication with AFNI
  - ↳ map function onto surface
  - ↳ appreciate the geometric limitations of this approach
  - ↳ ignore the limitation and make cool pictures

# Processing Pipelines

- [afni\\_proc.py](#)
  - ★ With a couple of extra options (-spec and -sv), afni\_proc.py can process single-subject data in the surface domain.
    - ★ This includes surface-based smoothing and regression analysis.
      - ★ See *example 8* in [afni\\_proc.py -help](#)
    - ★ All voxel wise programs will work with surface-based data
    - ★ Level-II (group) analysis programs are applicable to surface-based results.
      - ★ [3dcalc](#), [3dROIstats](#), [3dMEMA](#), [3dLME](#), [3dMVM](#), etc.
- [@RetinoProc](#)
  - ★ Process retinotopic data, see [@RetinoProc -help](#) for detail including test data

# Demos/Autmaginations

- @DO.examples
- @DriveSuma
- @RetinoProc
- @Install\_TSrestMovieDemo
- @Install\_AfniRetinoDemo
- @Install\_InstaCorr\_Demo
- [http://afni.nimh.nih.gov/sscc/staff/ziad/Misc\\_Download/Beauteous/ChunmaoWang.lh\\_lat\\_inflated.mpg](http://afni.nimh.nih.gov/sscc/staff/ziad/Misc_Download/Beauteous/ChunmaoWang.lh_lat_inflated.mpg)

# Auxiliary programs

- To see a list of all programs in SUMA:
  - ★ `suma -progs`
- **3dSurf2Vol** (by R. Reynolds)
  - ★ Maps data in surface domain volumetric domain
- **3dVol2Surf** (by R. Reynolds)
  - ★ Maps data in volume domain to surface domain
- **CompareSurfaces** (by S. Japee)
  - ★ calculates the distance along the normal from one surface to the next
- **ConvertSurface**
  - ★ Converts surfaces between the different formats that SUMA can read:
    - ➔ FreeSurfer
    - ➔ SureFit
    - ➔ Simple ASCII matrix format
    - ➔ PLY format
    - ➔ GIFTI (XML-based) format
  - ★ Converts surface coordinates to Talairach space
- **ConvexHull**
  - ★ Finds the convex hull of a volume or a set of points



# Auxiliary programs

- **CreaterIcosahedron** (by B. Argall)
  - ★ Creates Icosahedral meshes of varying node counts
- **inspec**
  - ★ Outputs information about a spec file
- **IsoSurface**
  - ★ Creates an isosurface from a volumetric dataset
- **MakeColorMap**
  - ★ Creates colormaps for use with AFNI
- **MapIcosahedron** (by B. Argall)
  - ★ transforms the topology of surface models to standard models without distorting the geometry (tested with FreeSurfer's spherical mapping).
  - ★ use to check for errors in topology of spherical surfaces
- **quickspec**
  - ★ Creates a spec file for one or a set of surfaces (quick and dirty)
- **ROI2dataset**
  - ★ Transforms ROI files into surface datasets

# Auxiliary programs

- **ScaleToMap**
  - ★ Transforms a set of node values to node colors based on chosen color map
- **SurfaceMetrics**
  - ★ Outputs other information about the surface such as the edge list, curvature, triangle areas (mostly for debugging use)
- **SurfClust**
  - ★ Clustering on the surface
- **SurfMeasures** (by R. Reynolds)
  - ★ Outputs node-based surface measures such as areas, volumes, thickness, surface normals, etc. etc.
- **SurfSmooth**
  - ★ a program for filtering surface data and/or surface geometry
- **SurfPatch**
  - ★ Creates surface patches from a set of nodes.
- **SurfQual**
  - ★ Locates topological errors in spherical surfaces.

# Getting Helped

- `suma -help` for SUMA's command line usage
- 'ctrl+h' opens a window with help for:
  - ★ SUMA's usage when cursor is in viewer
  - ★ SUMA's colormap usage when cursor is over colormap
- **BHelp** provides help for most buttons in the GUI interface
- AFNI's web site:
  - ★ <http://afni.nimh.nih.gov/>
  - ★ <http://afni.nimh.nih.gov/afni/community/board>
- AFNI's Message Board
- E-mail to [saadz@mail.nih.gov](mailto:saadz@mail.nih.gov)
- If you can't get help here, please get help somewhere.

# Tracts in SUMA

- Tracts are generated by AFNI's FATCAT toolbox



**FATCAT: Functional And Tractographic Connectivity Analysis Toolbox (Taylor & Saad, 2013)**

# Tracts in SUMA

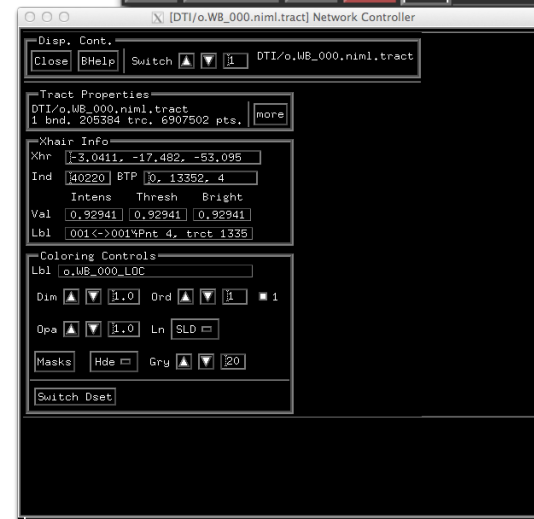
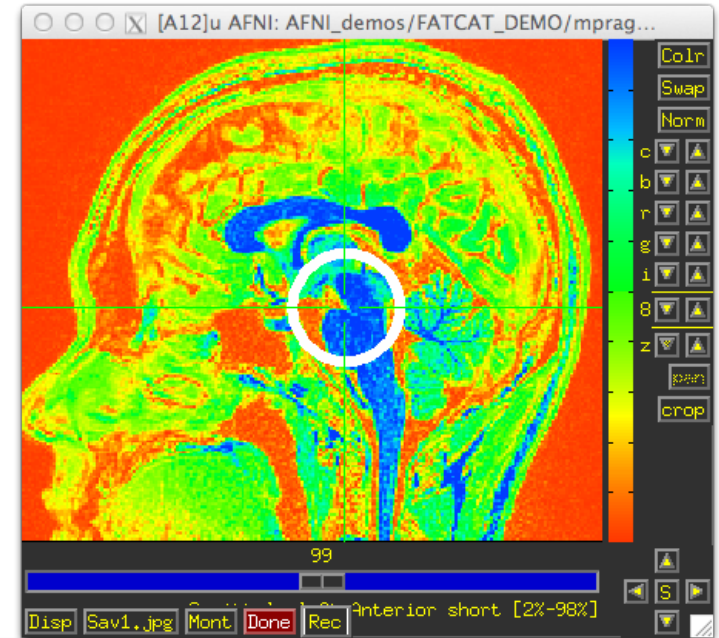
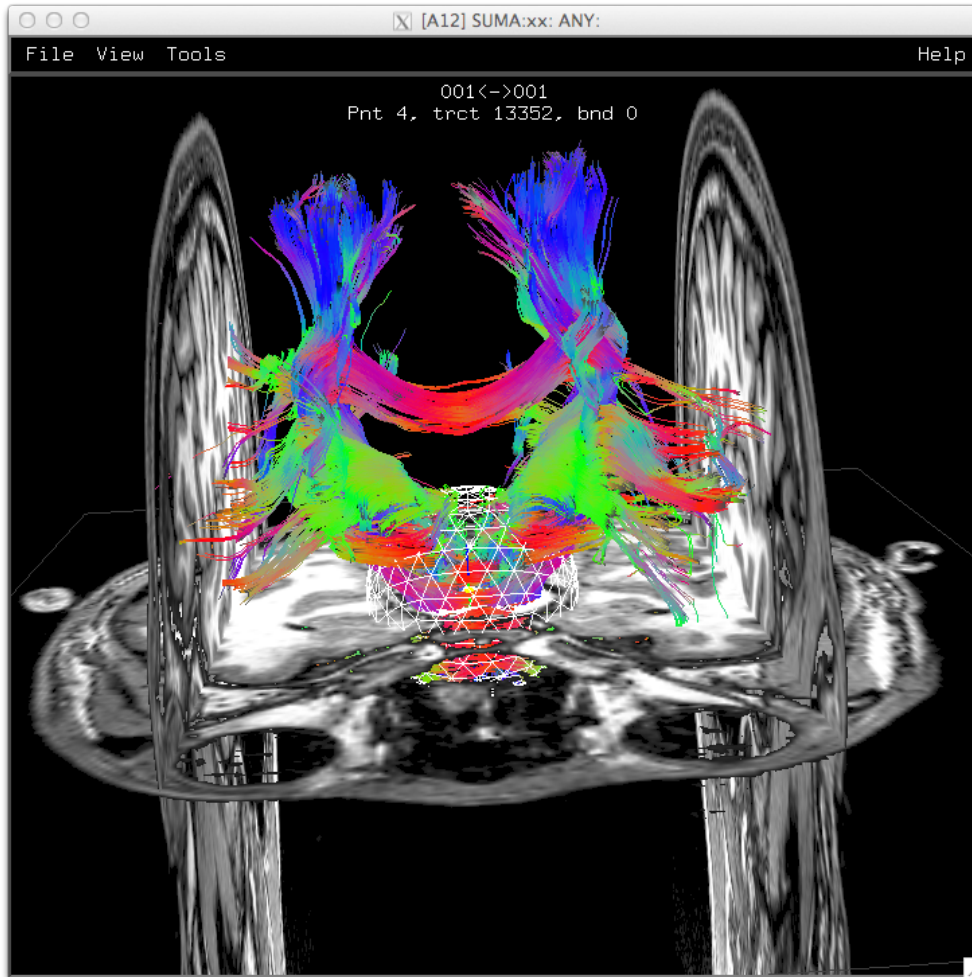


- Tracts are generated by AFNI's FATCAT toolbox
  - If using AFNI bootcamp data:
    - `cd ~/AFNI_demos/FATCAT_DEMO`
- Else
  - Run `@Install_FATCAT_DEMO` for demo data and scripts
- If you have not done so already
  - Process everything with `tcsch Do_00_PRESTO_ALL_RUNS.tcsch`
- To look at whole brain tracts
  - `tcsch Do_06_VISdti_SUMA_visual_ex1.tcsch`

**FATCAT: Functional And Tractographic Connectivity Analysis Toolbox** (Taylor & Saad, 2013)

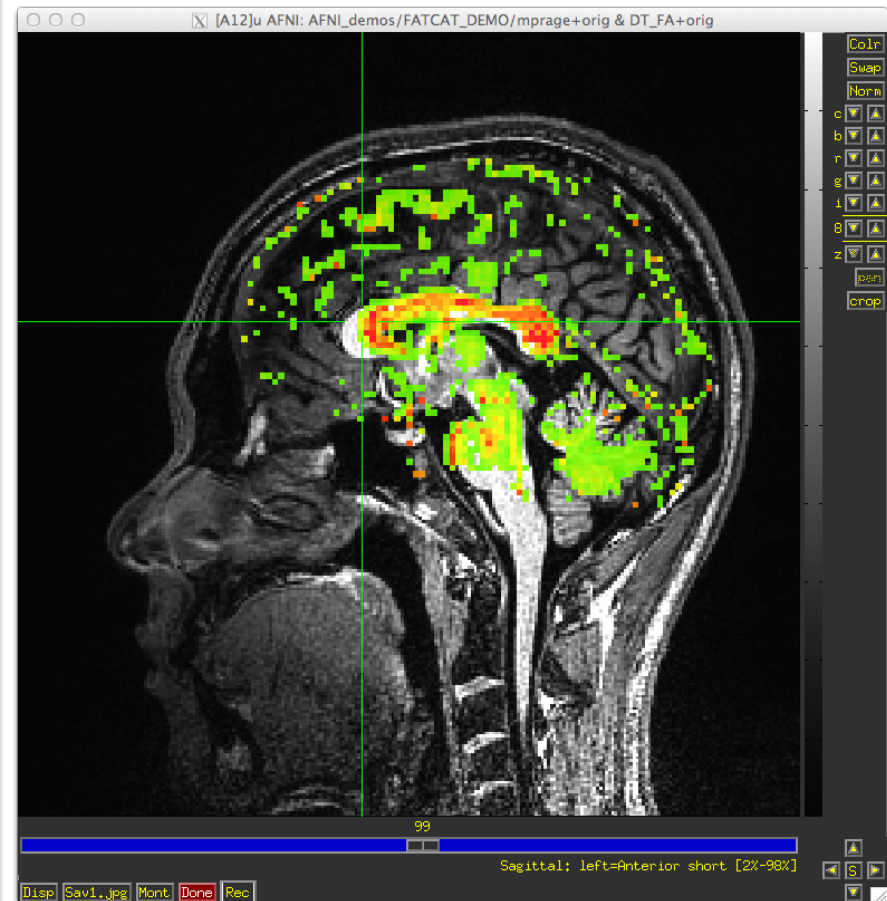
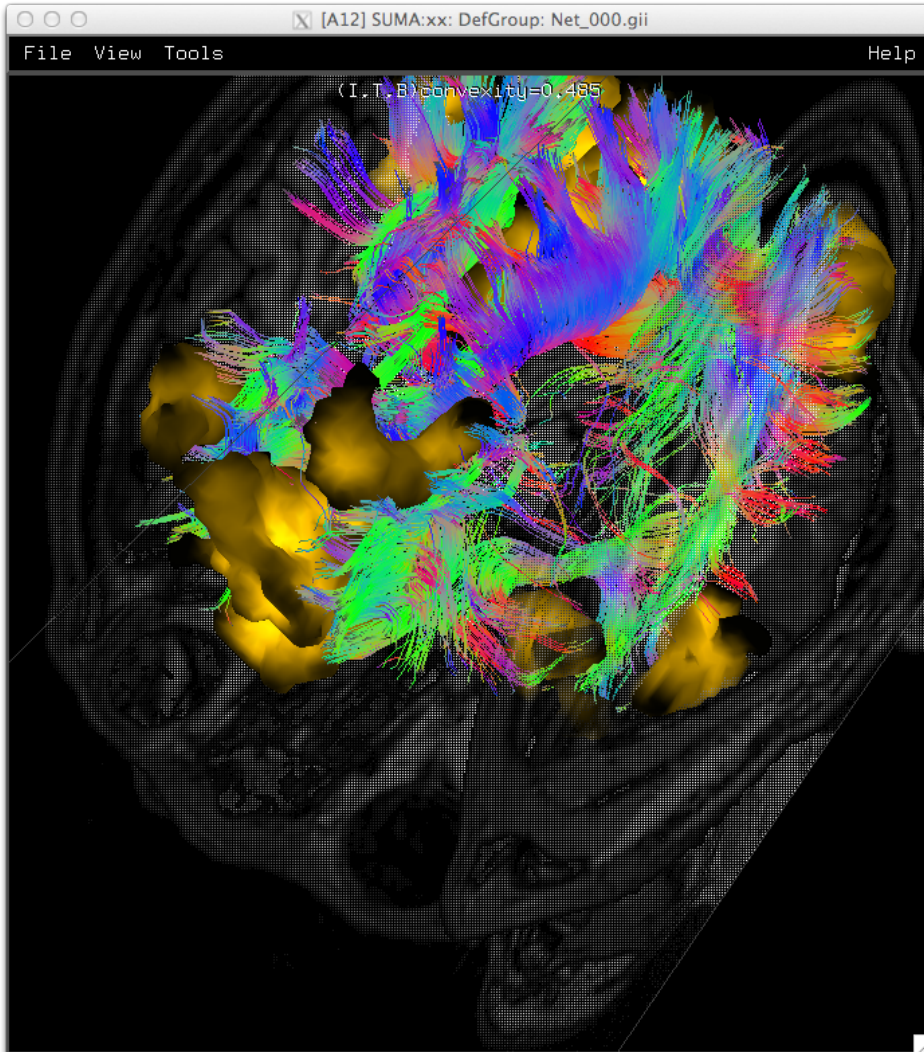
# tcsh Do\_06\_VISdti\_SUMA\_visual\_ex1.tcsh

- Example 0: Follow prompt directions to produce something like this:



# tcsh Do\_06\_VISdti\_SUMA\_visual\_ex1.tcsh

- Example 1: Follow prompt directions to produce something like this:



# tcsh Do\_09\_VISdti\_SUMA\_visual\_ex2.tcsh

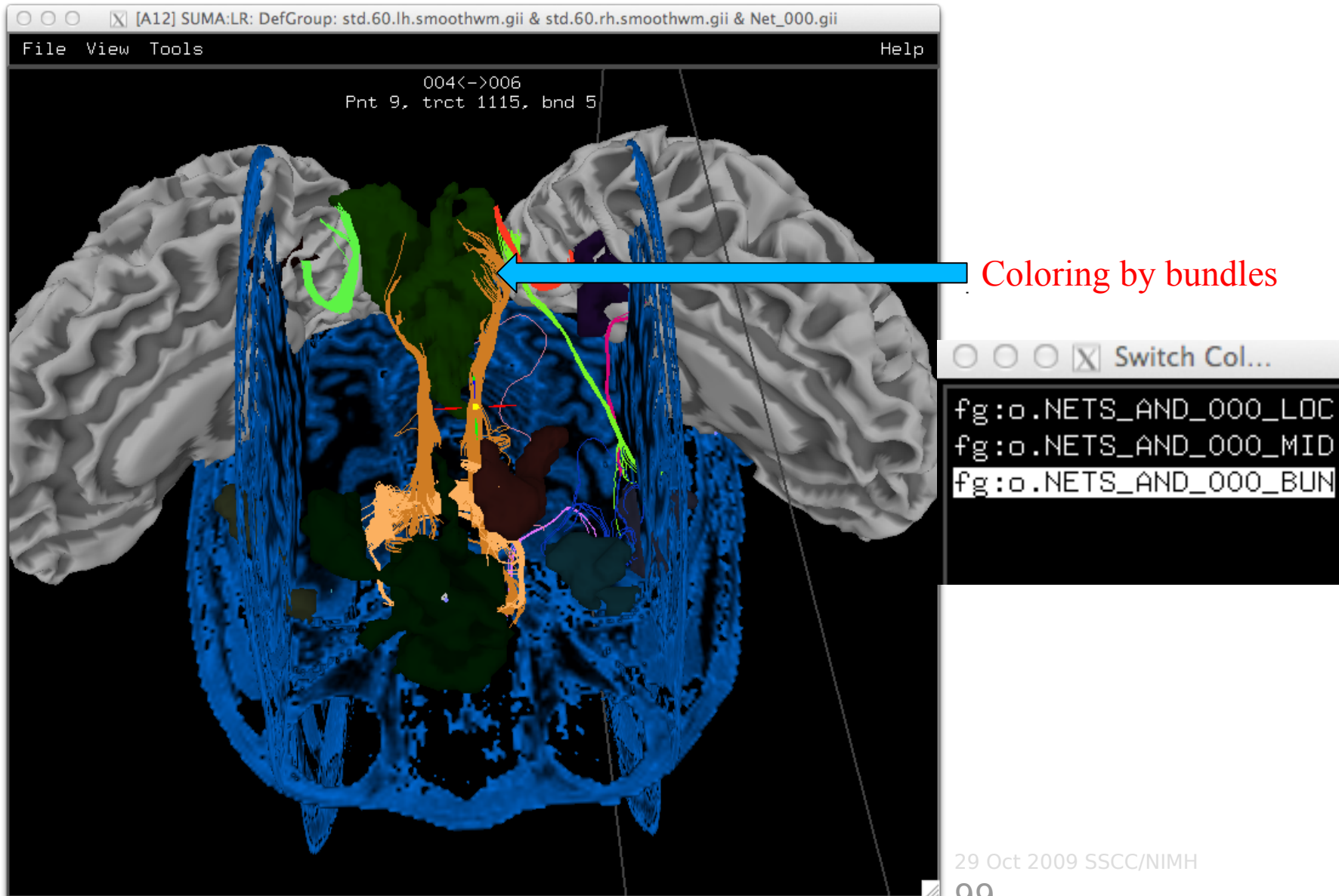
- Example 0: Follow prompt directions to produce something like this:





# tcsh Do\_09\_VISdti\_SUMA\_visual\_ex2.tcsh

- Example 1: Follow prompt directions to produce something like this:

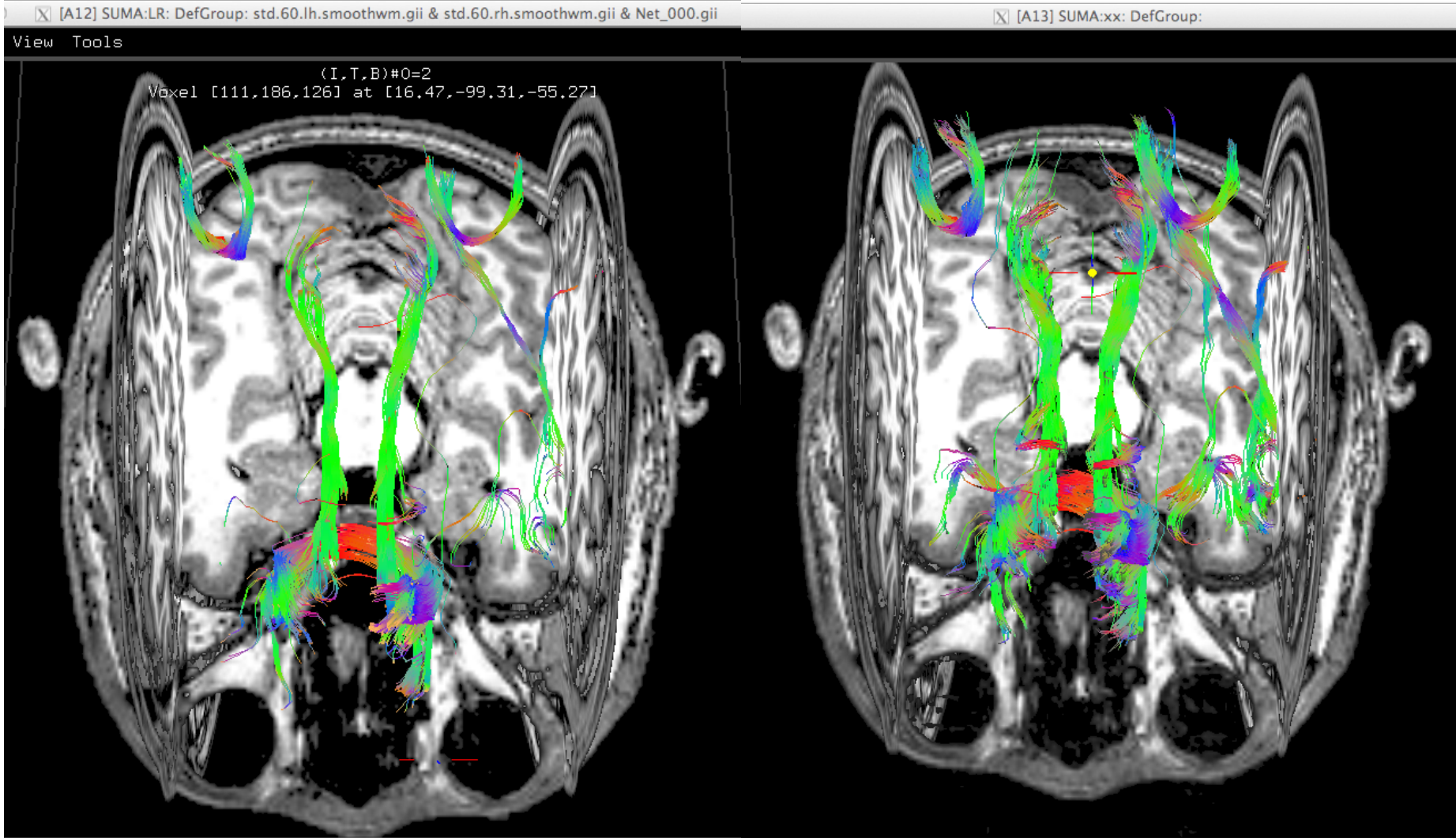


# tcsh Do\_09\_VISdti\_SUMA\_visual\_ex2.tcsh

- Example 2: Compare miniprob results to deterministic (previous):

**Deterministic**

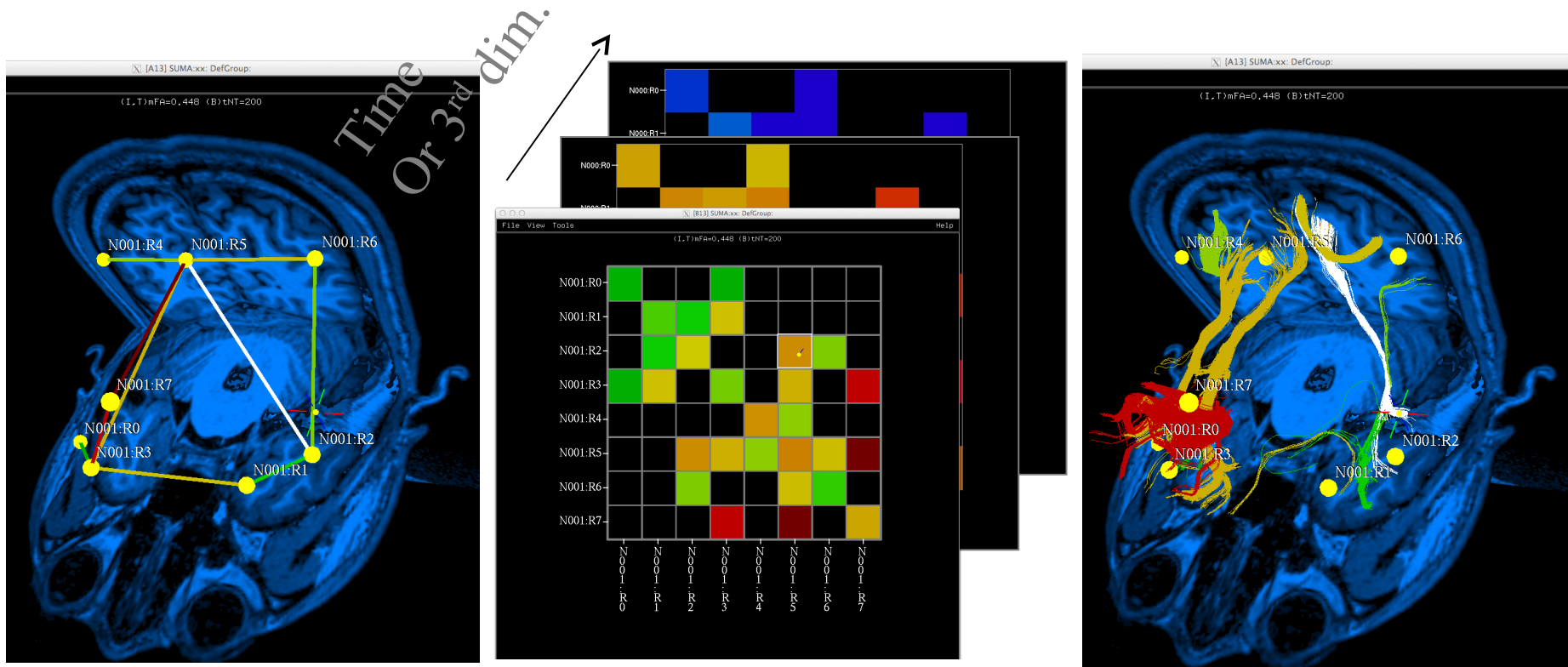
**MINIPROB 9 iterations**



# tcsh Do\_09\_VISdti\_SUMA\_visual\_ex2.tcsh

- Example 3: Should be able to do something like:

**Simultaneous linked rendering in graph and matrix modes  
3D matrices supported (e.g. time varying correlation matrix)**



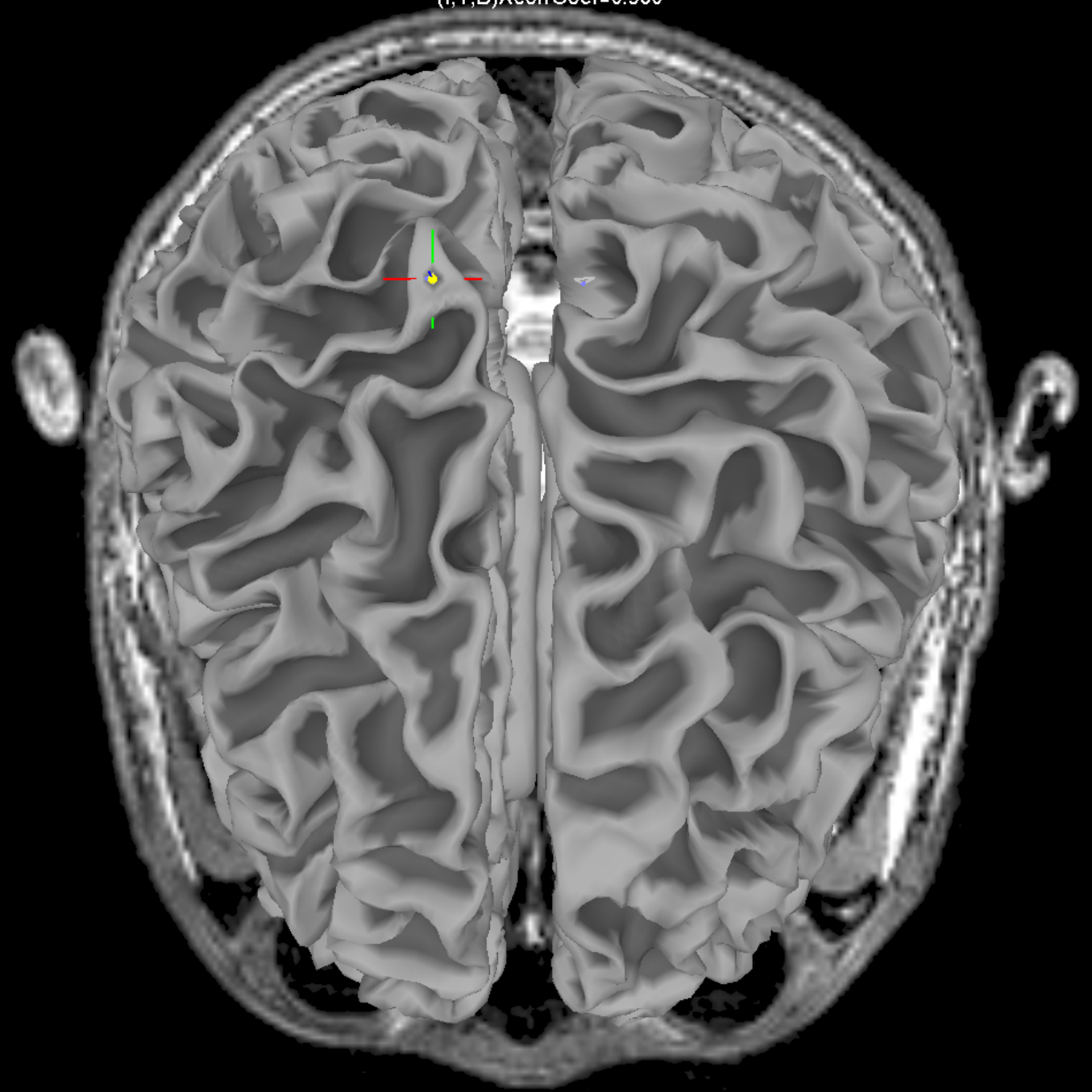
[tcsh Do 09 VISdti SUMA visual ex2.tcsh](#)

## ***Simultaneous InstaCorr & InstaTract***

- Follow directions to do something like in the next bunch o slides

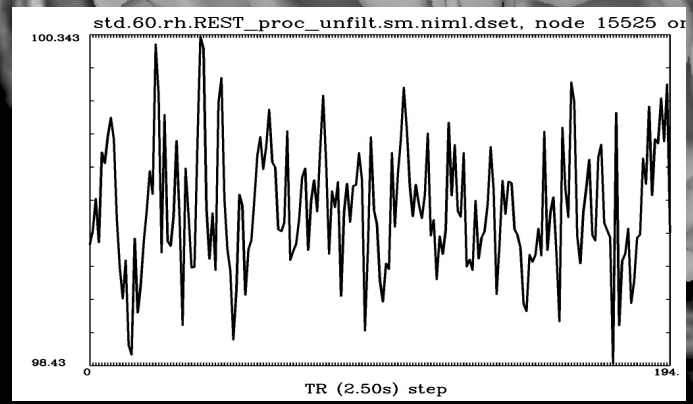
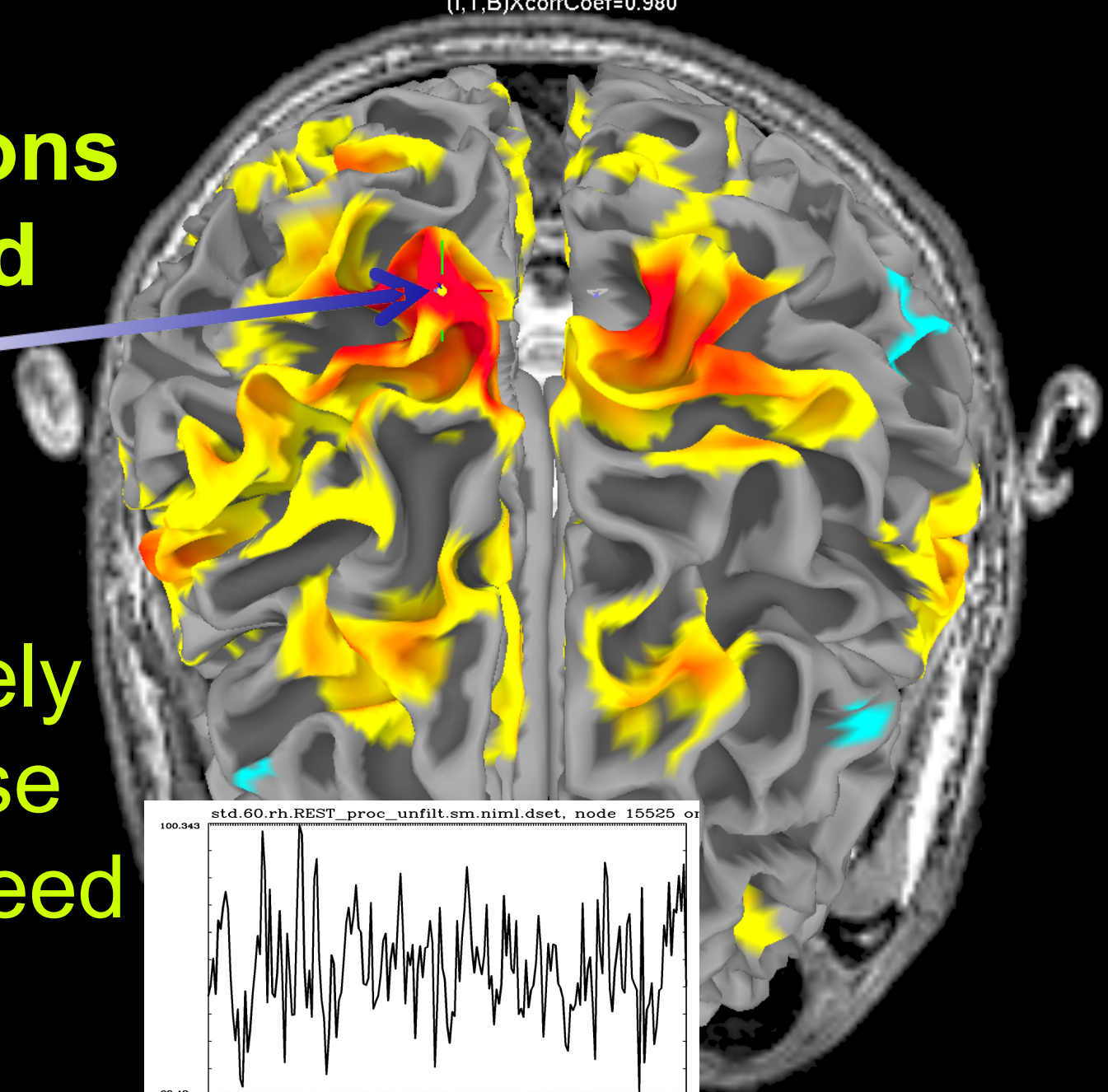
wm rh\_G and S\_paracentral  
(I,T,B)XcorrCoef=0.980

# Naked brain surface



**RS-FMRI  
correlations  
from seed  
voxel**

**computed  
interactively  
with mouse  
click on seed**

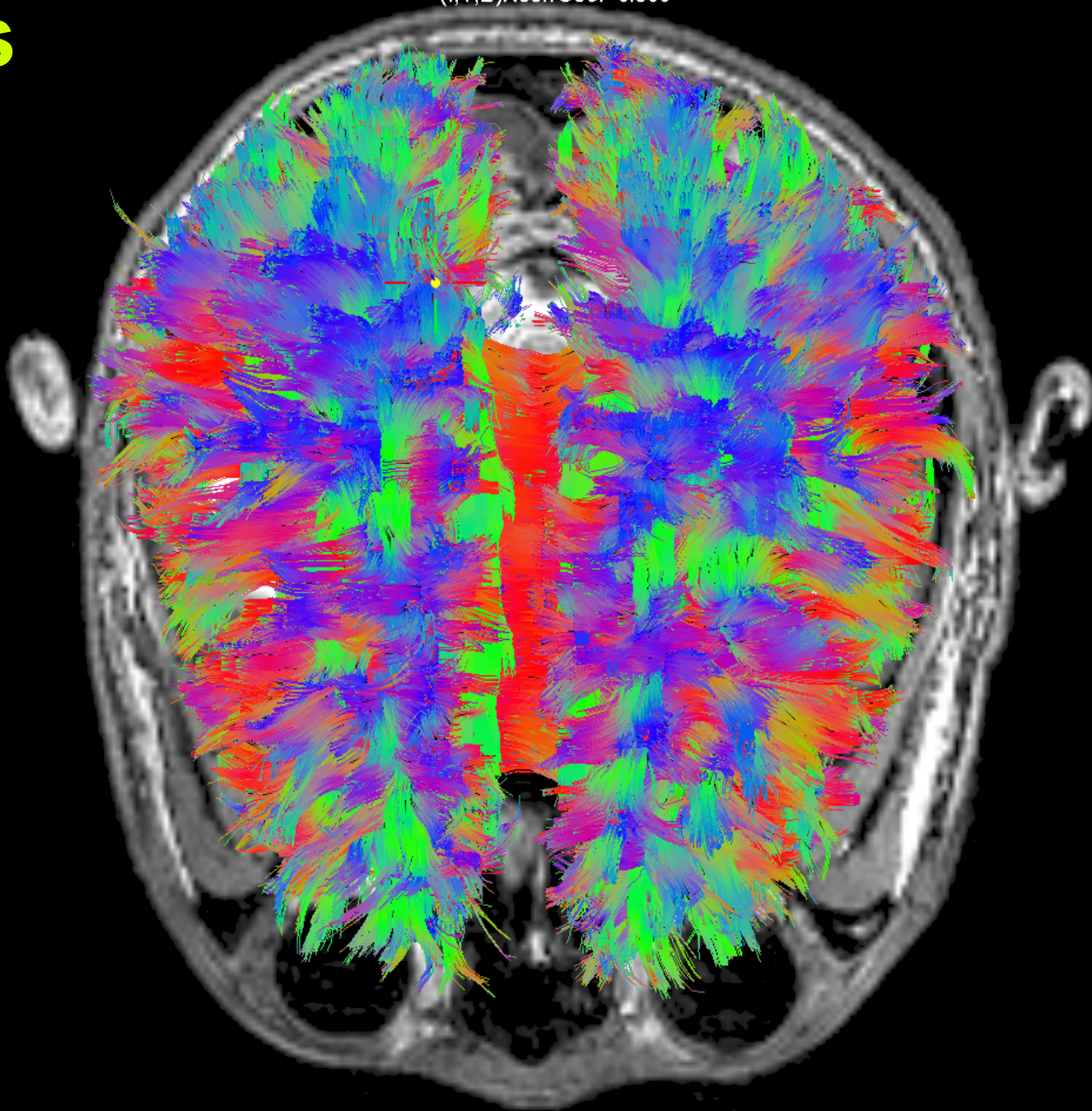


wm rh\_G and S\_paracentral  
(I,T,B)XcorrCoef=0.980

# DTI tracts

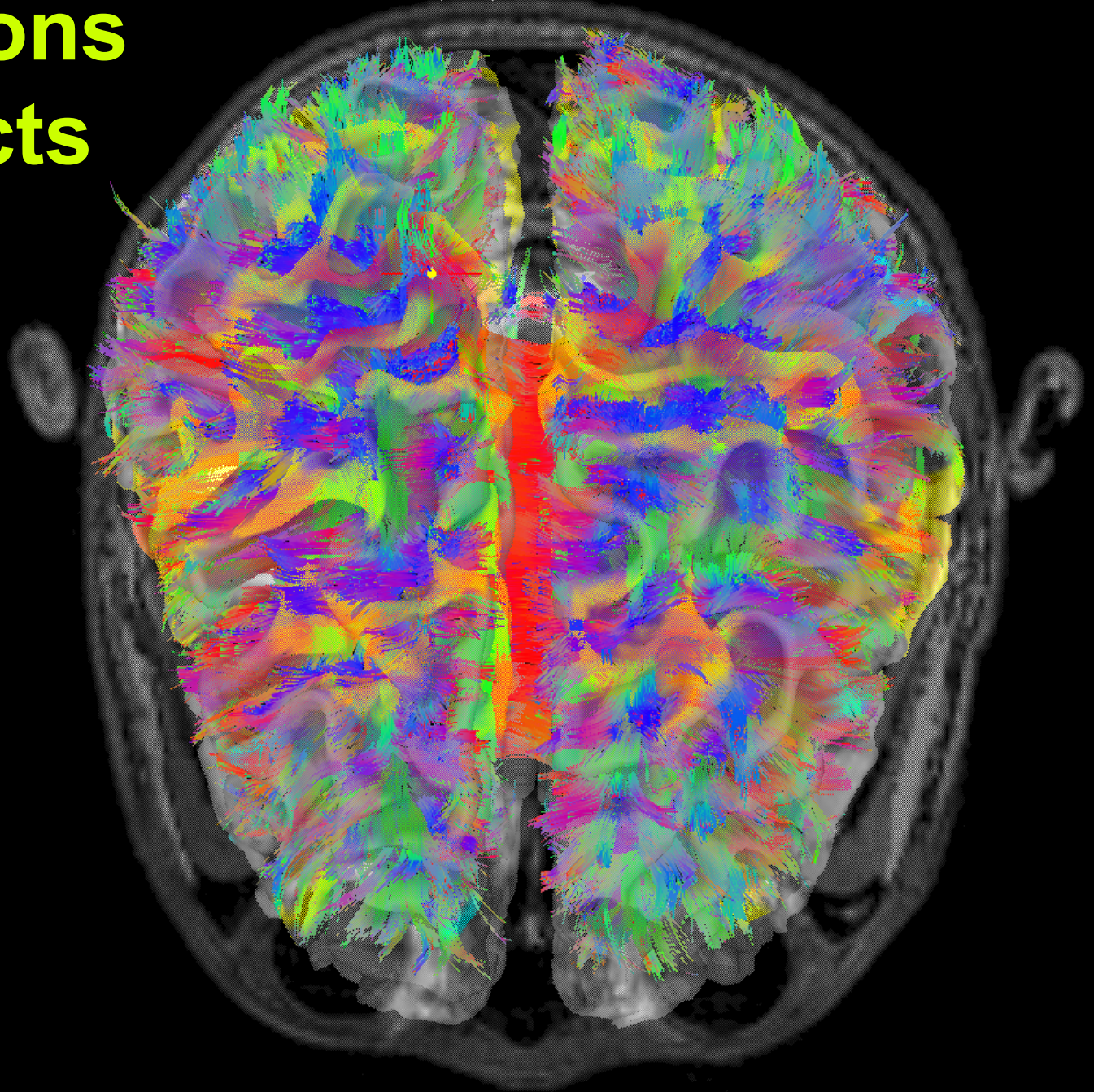
[brain is  
hidden]

Just too  
much to  
take in!



**Correlations  
+ DTI tracts  
+ Brain**

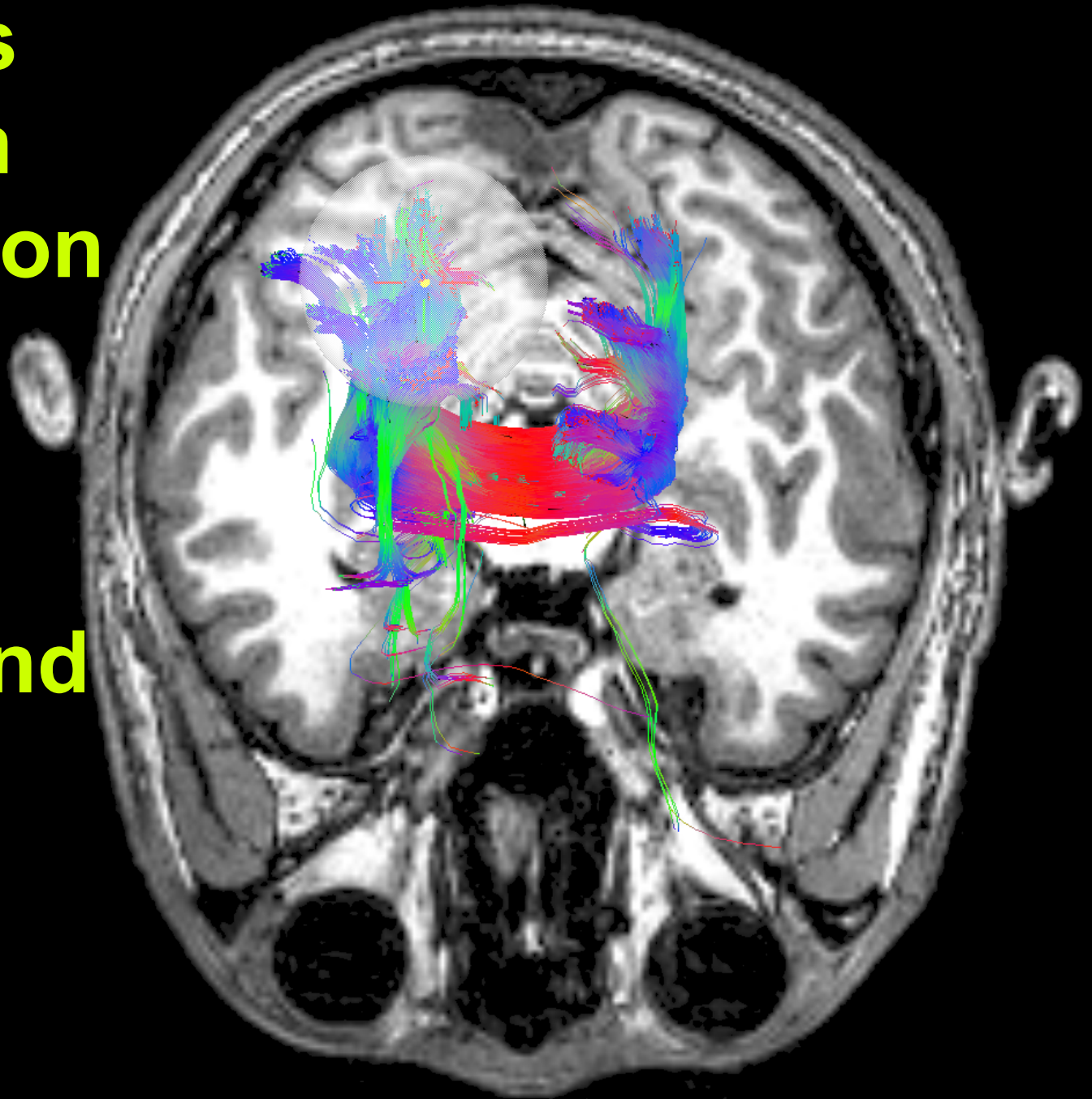
**Way too  
much to  
take in!**





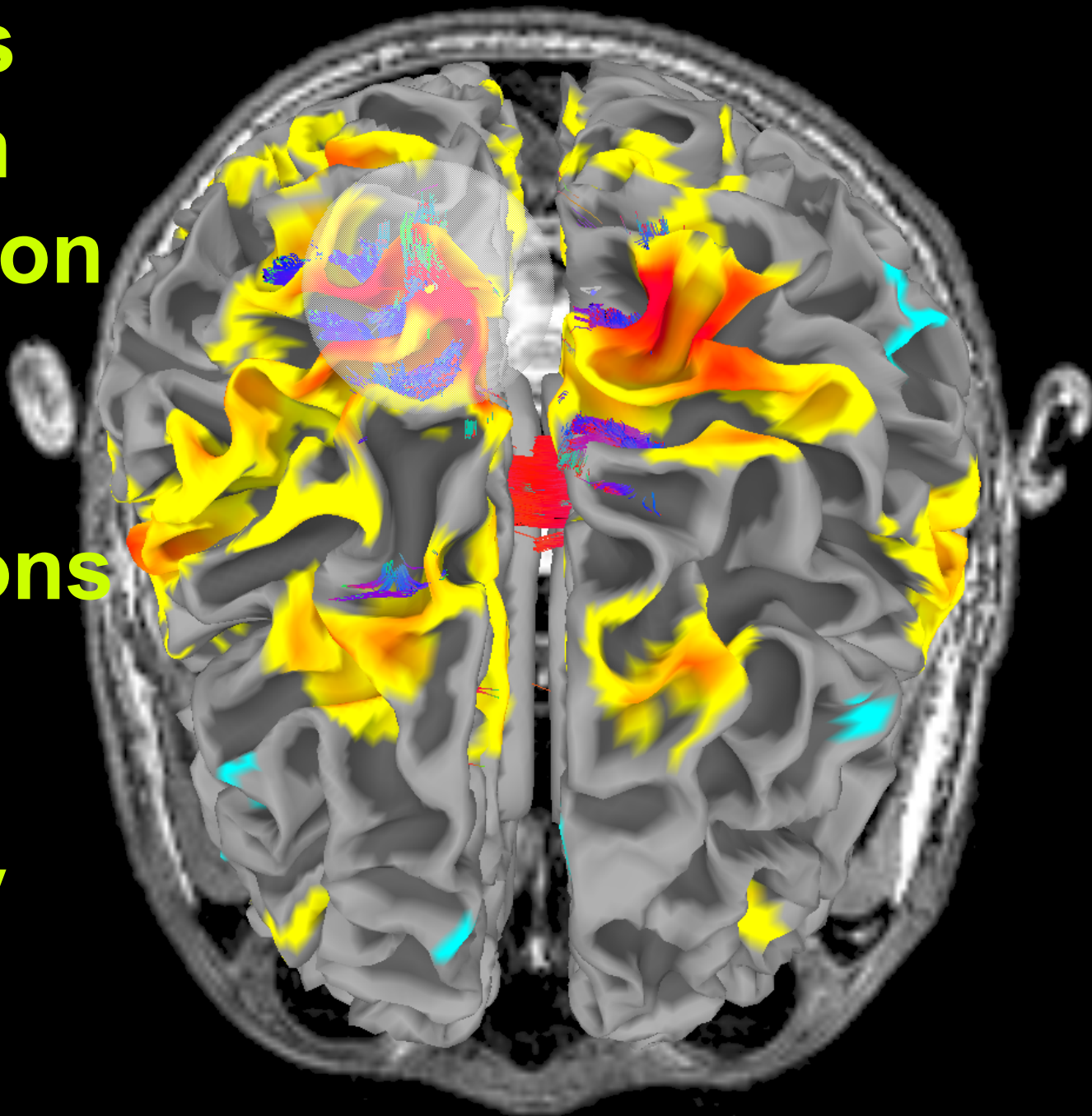
**DTI tracts  
only from  
seed region**

***Much  
easier to  
understand***



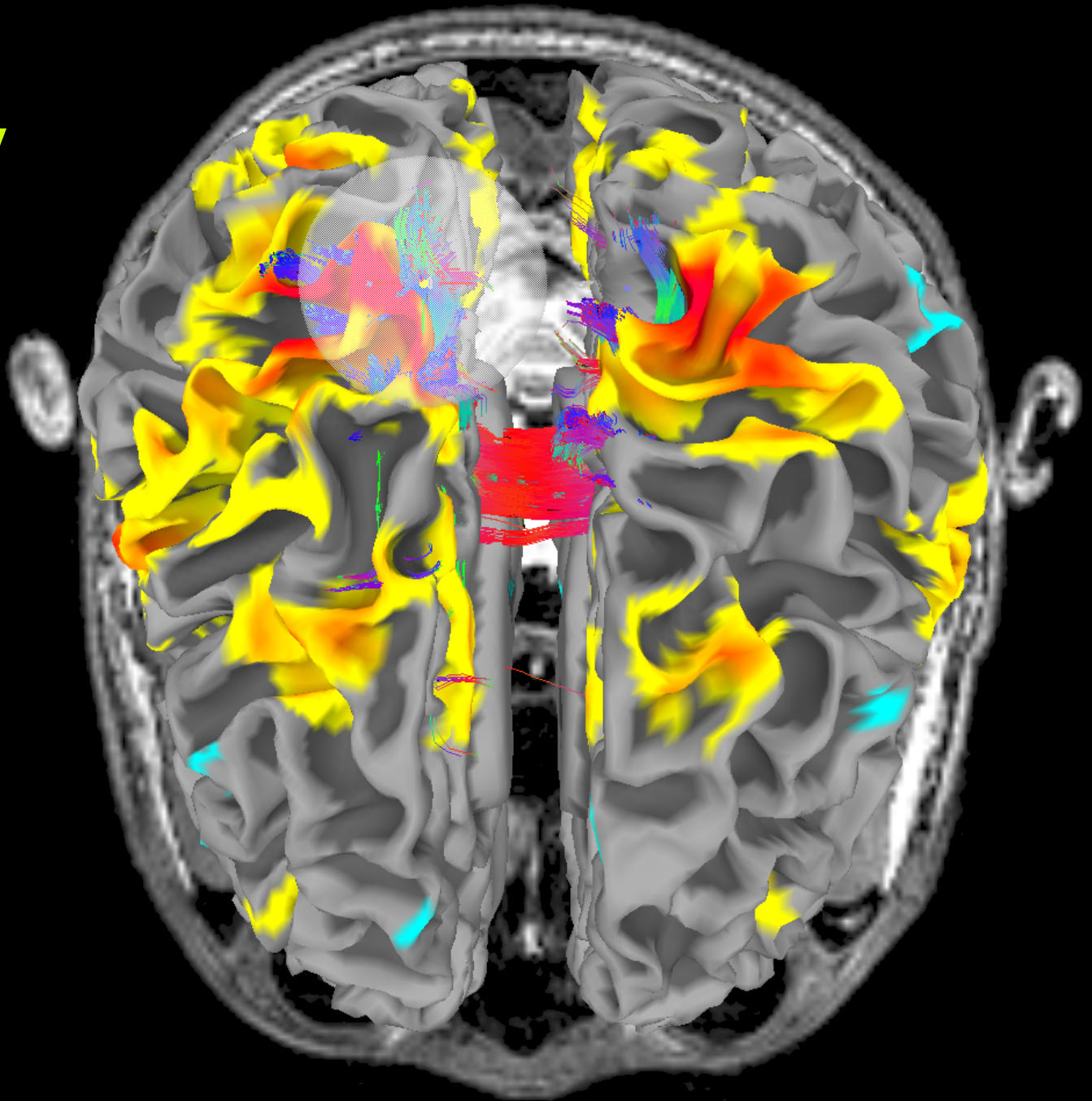
**DTI tracts  
only from  
seed region  
+ time  
series  
correlations**

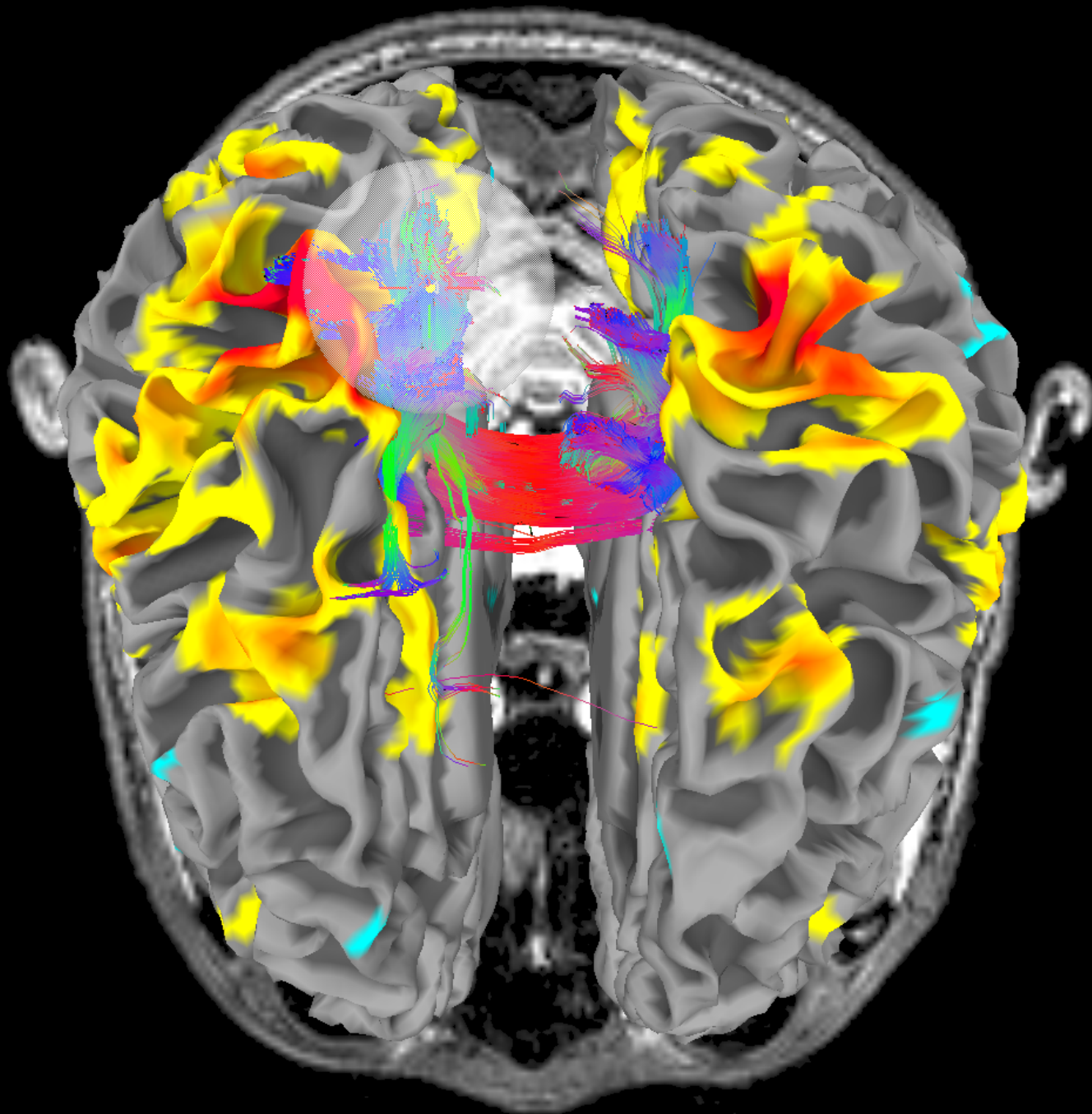
**Brain is  
in the way**

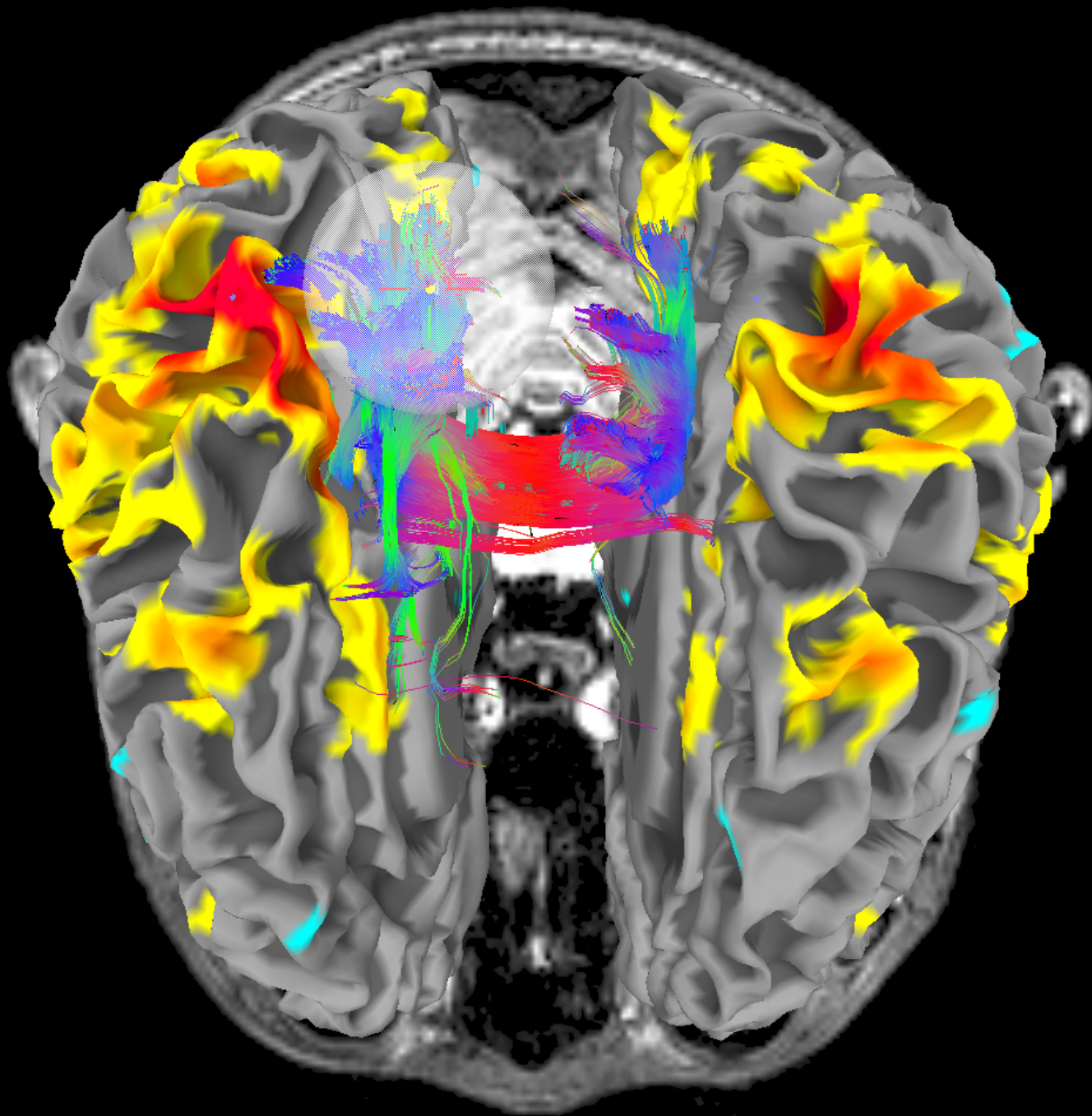


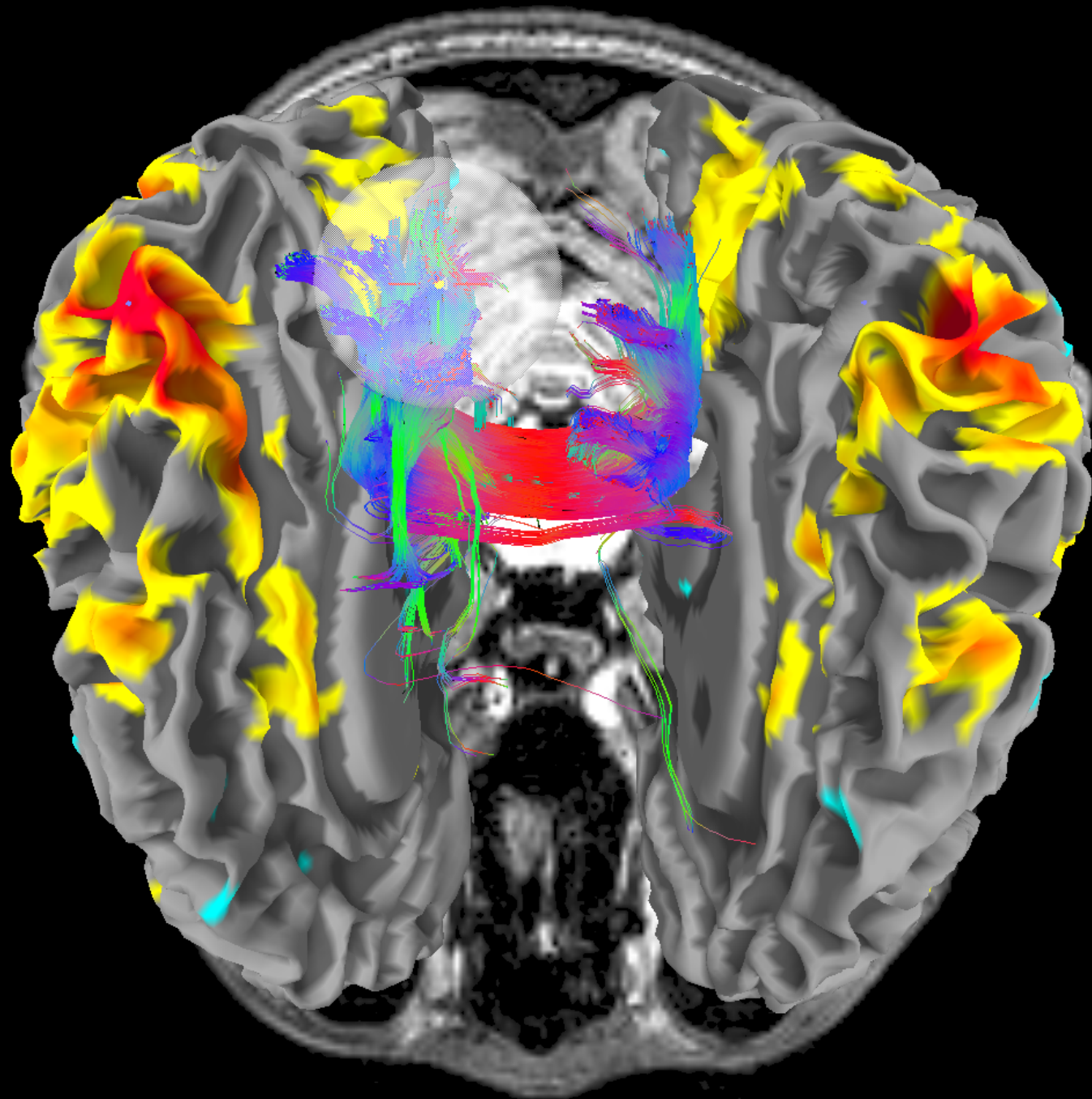
Brain is  
in the way

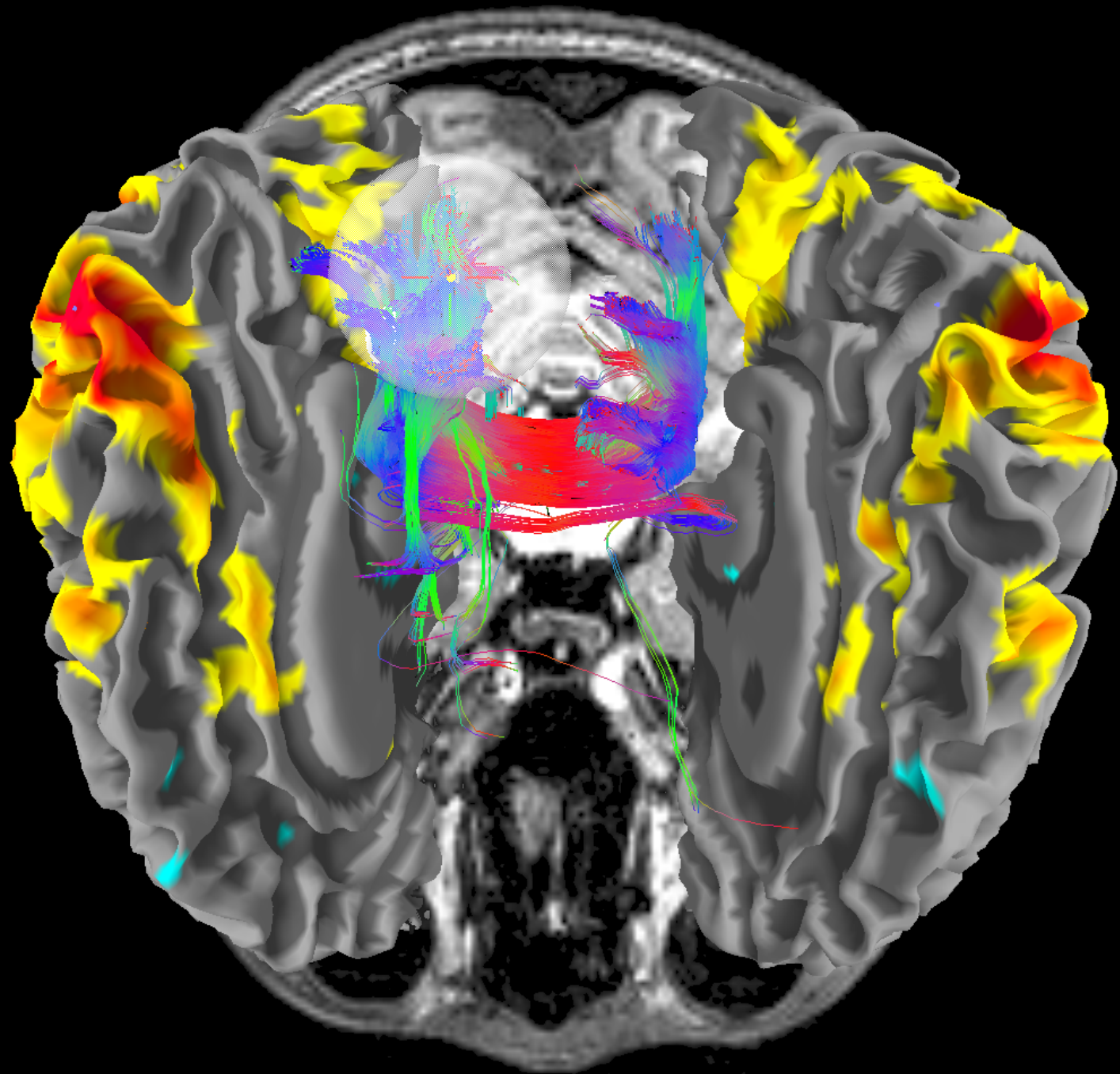
So move  
it aside!

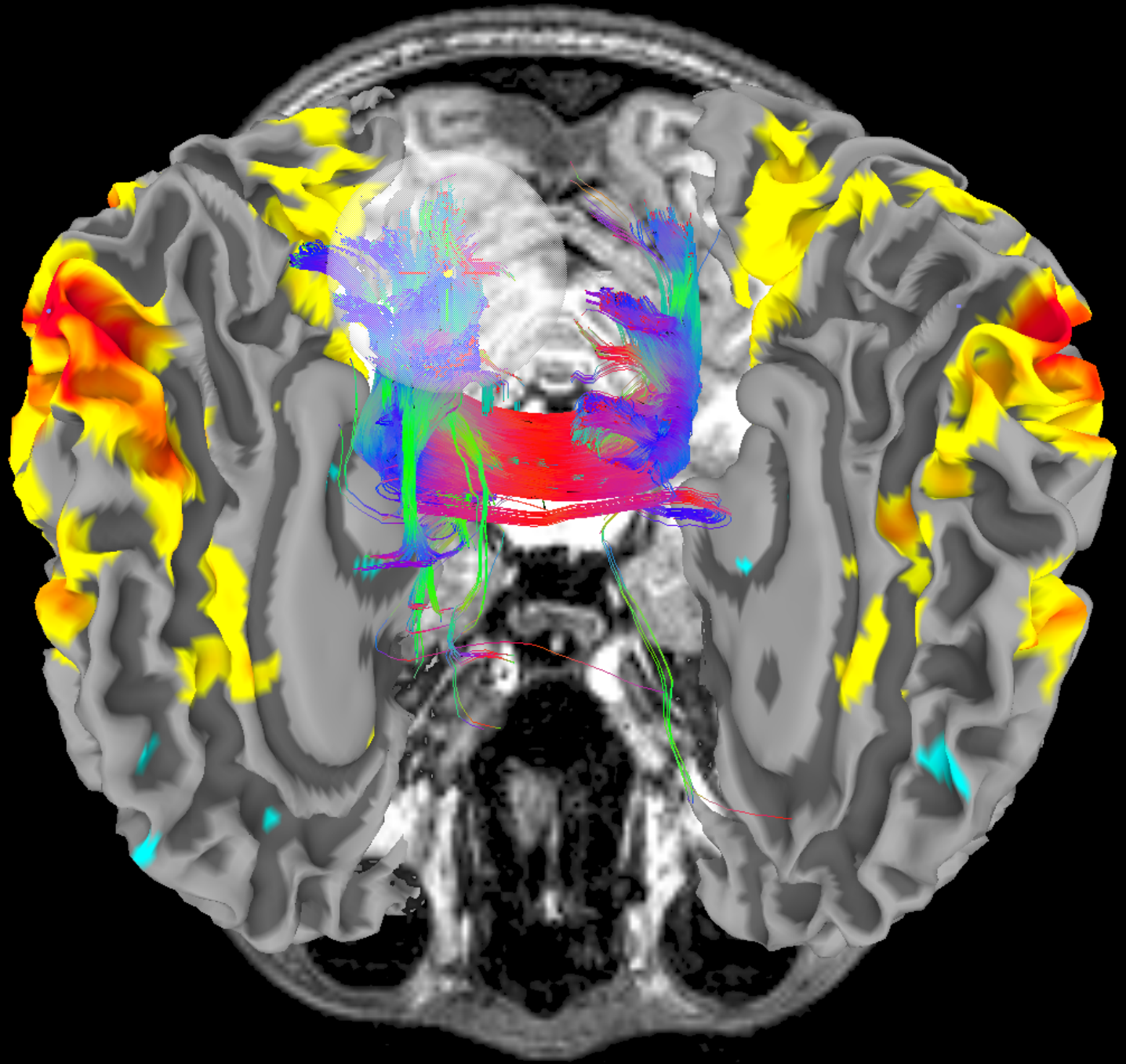






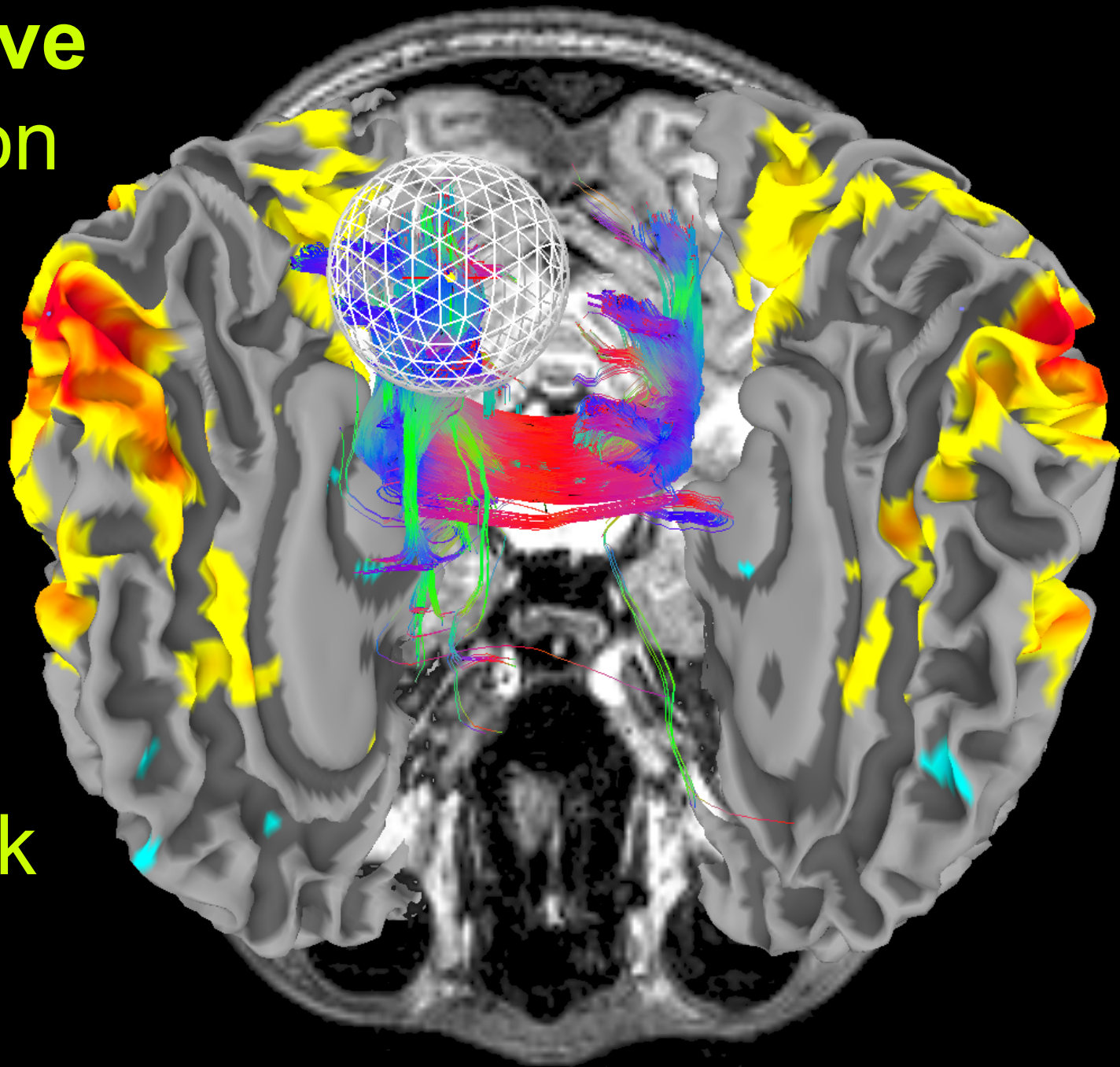




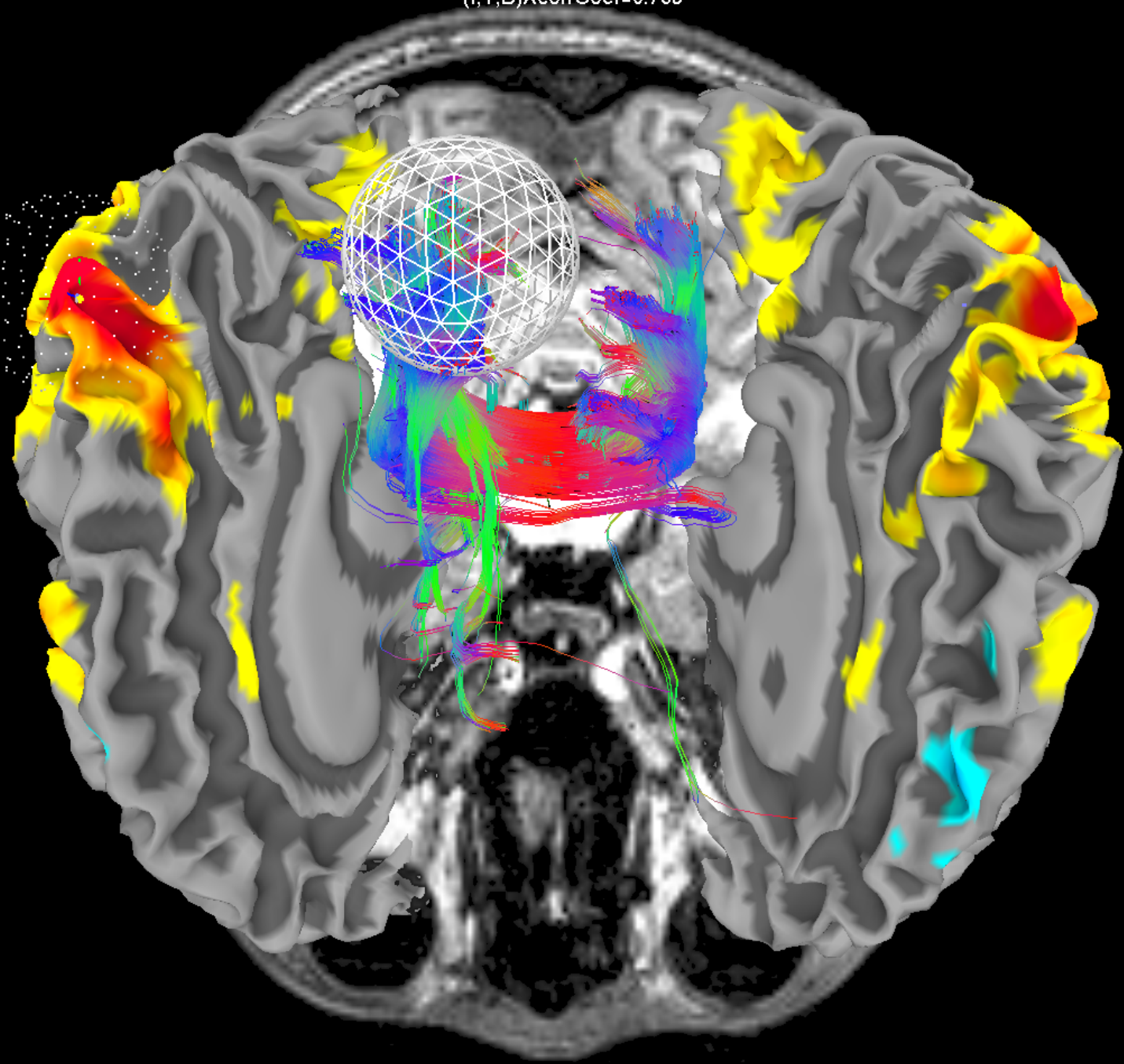




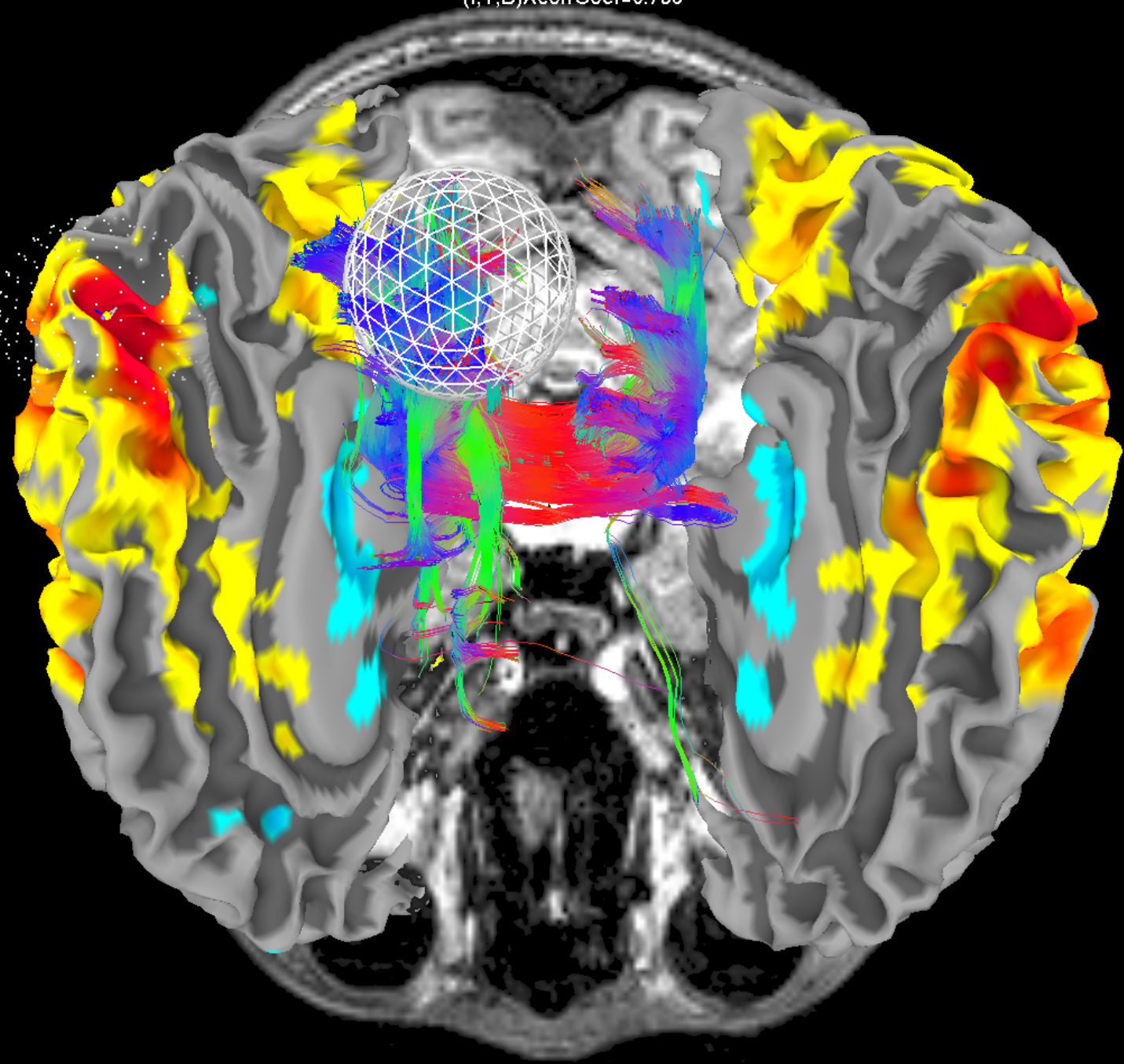
**Now move  
correlation  
and  
tract  
seed  
along  
the  
sulcus  
from back  
to front**



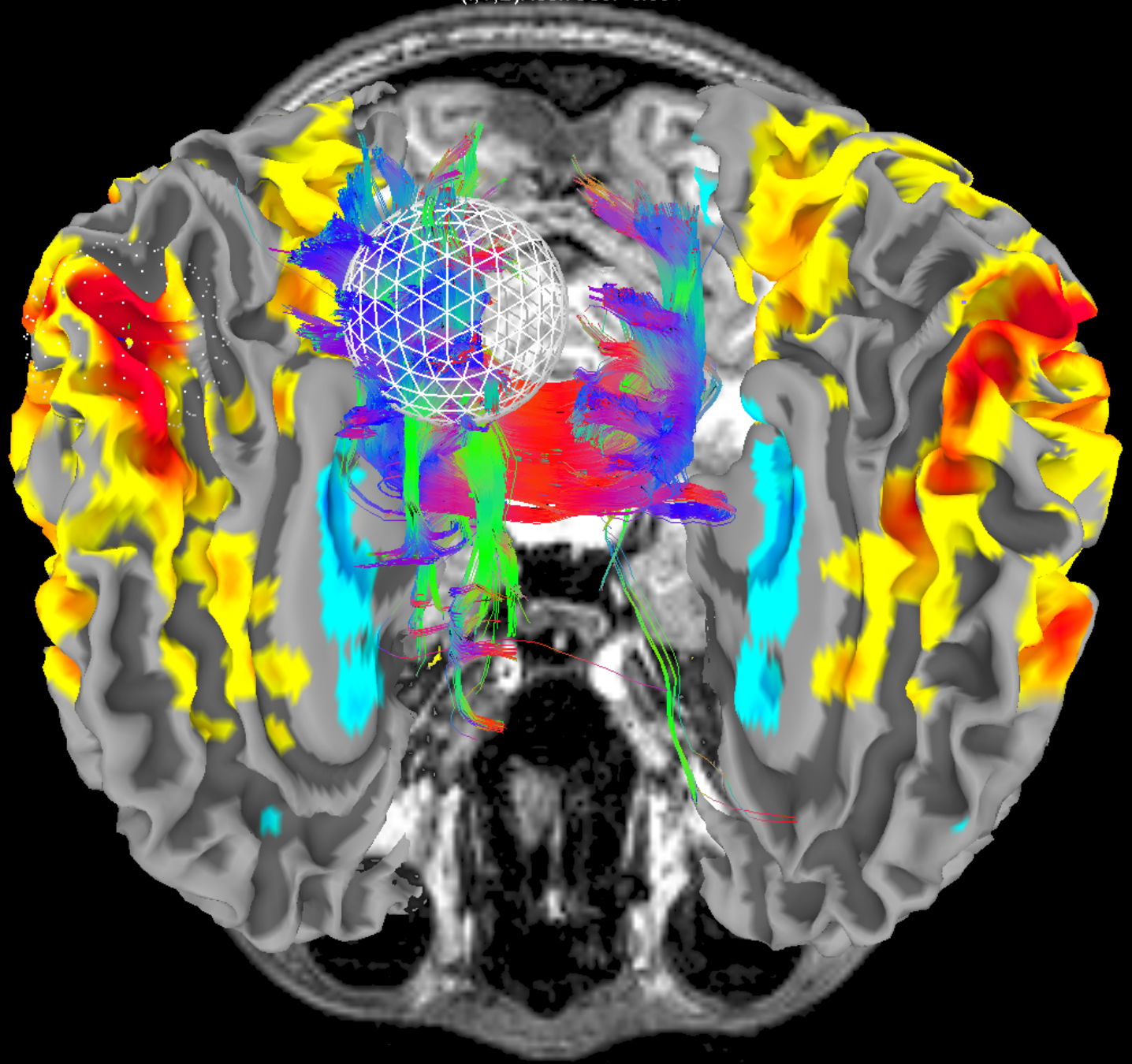
wm rh G and S\_paracentral  
(I,T,B)XcorrCoef=0.765



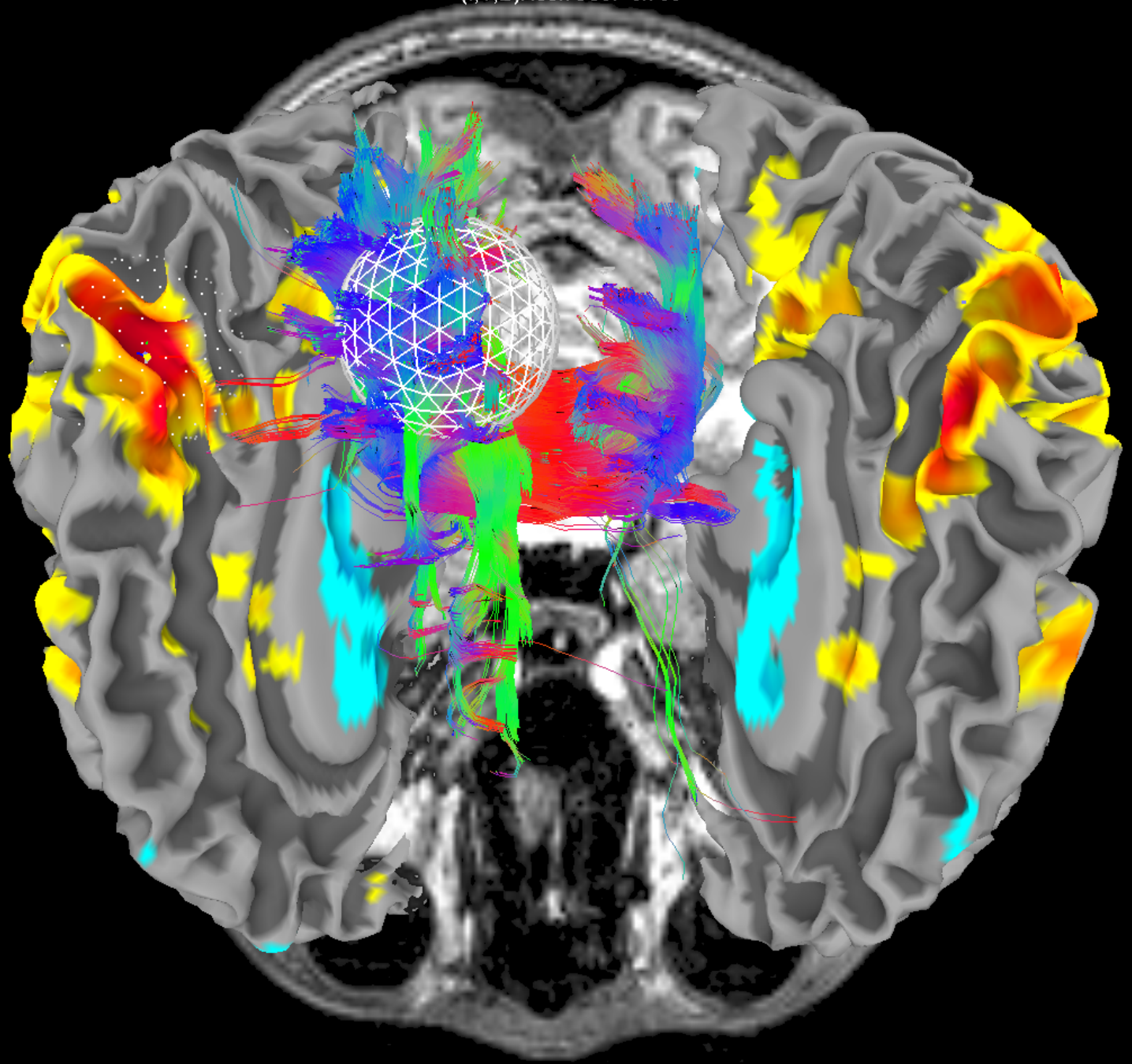
wm rh G and S\_paracentral  
(I,T,B)XcorrCoef=0.753



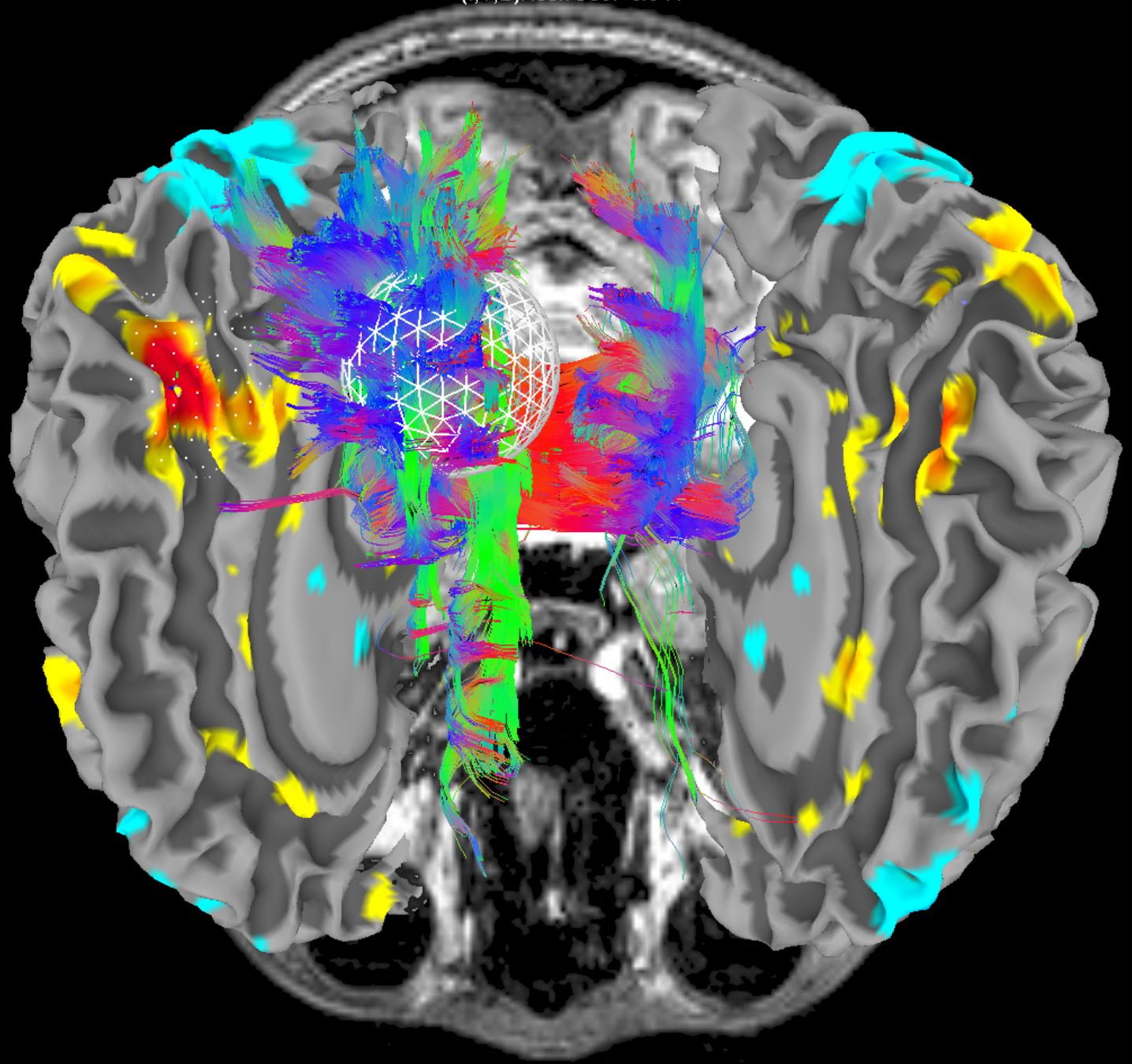
wm\_rh\_S\_cingul-Marginalis  
(I,T,B)XcorrCoef=0.884



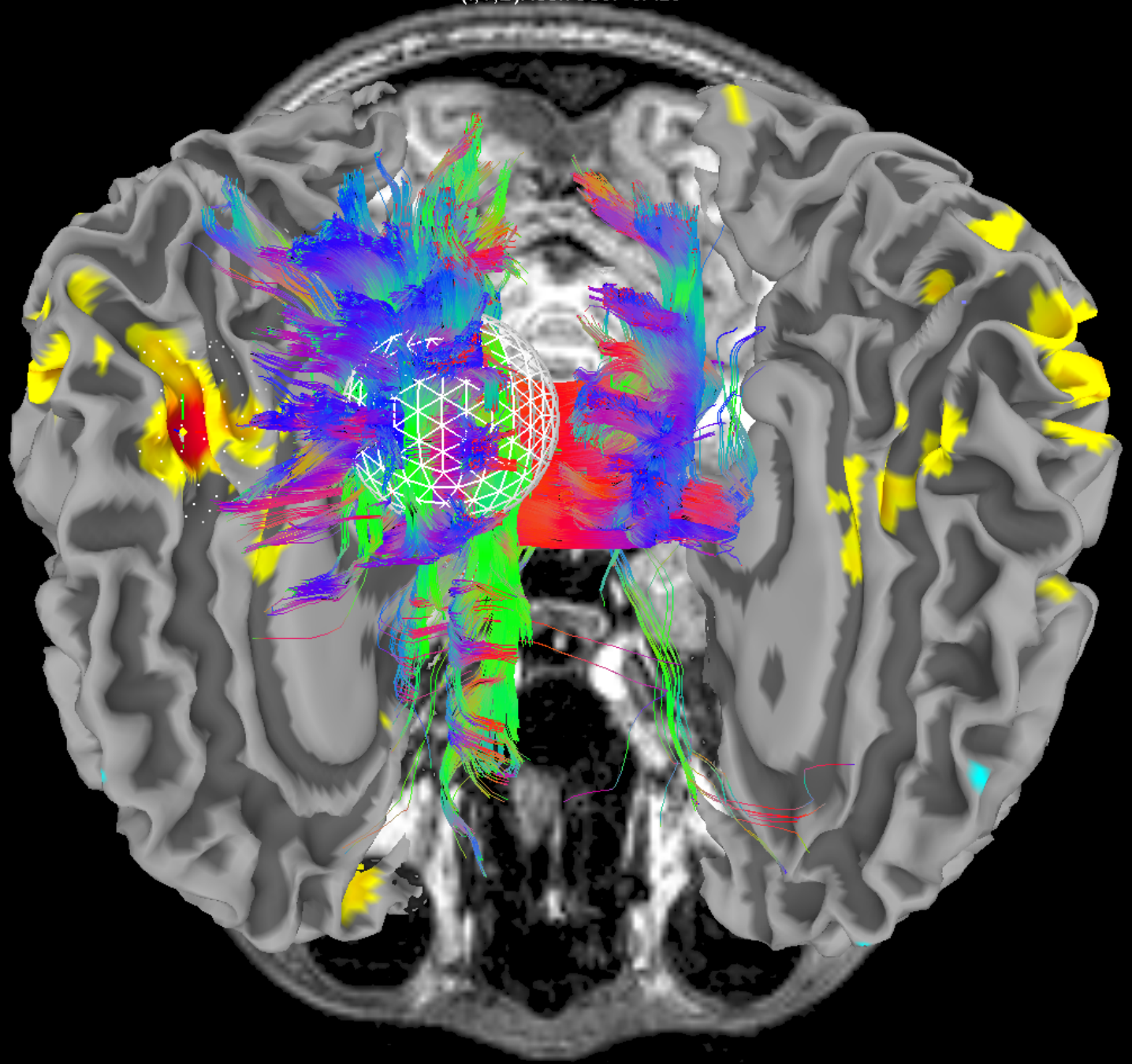
wm\_rh\_S\_cingul-Marginalis  
(I,T,B)XcorrCoef=0.780



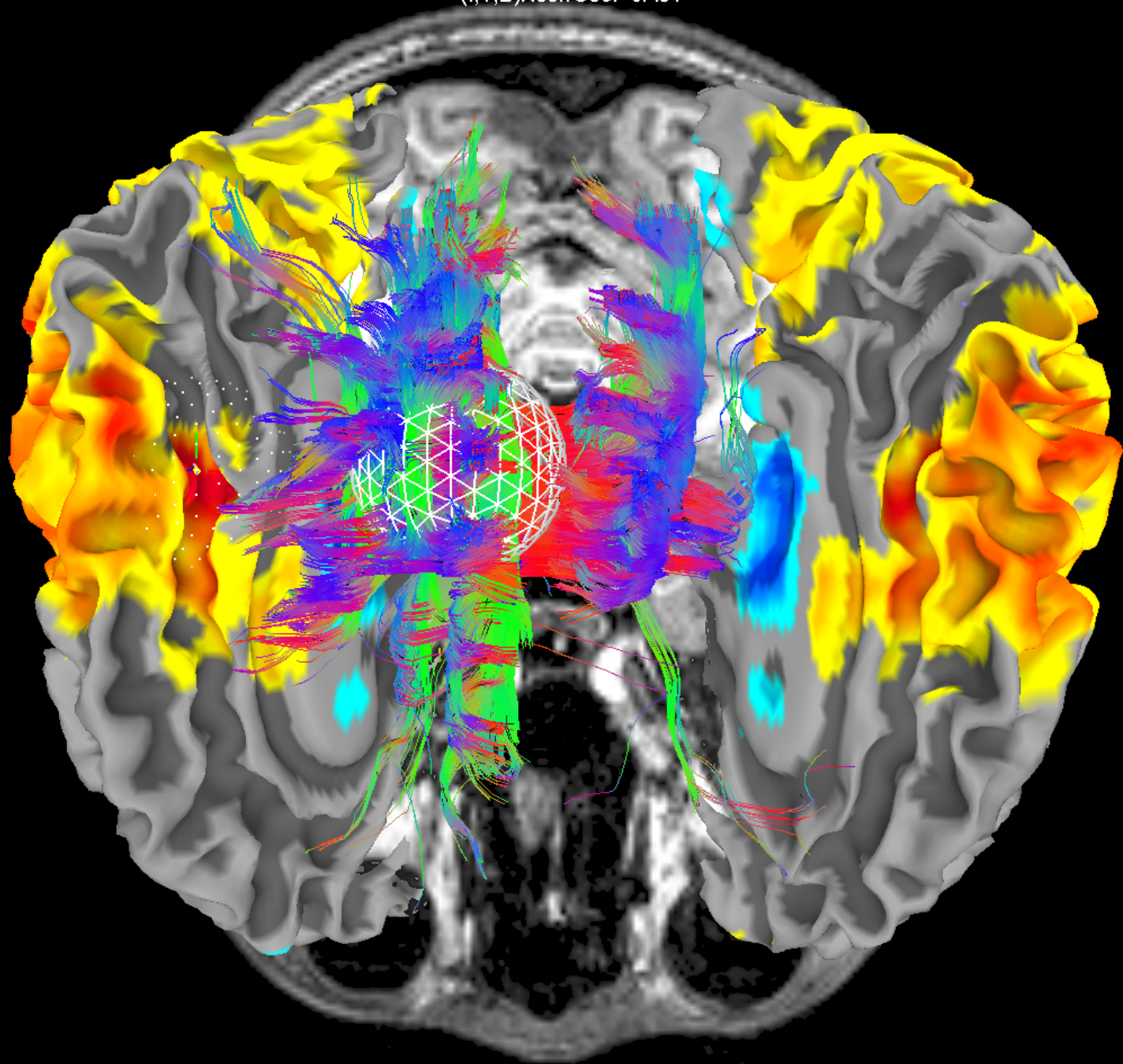
wm\_rh\_S\_cingul-Marginalis  
(I,T,B)XcorrCoef=0.644



wm\_rh\_G and S\_cingul-Mid-Post  
(I,T,B)XcorrCoef=0.423

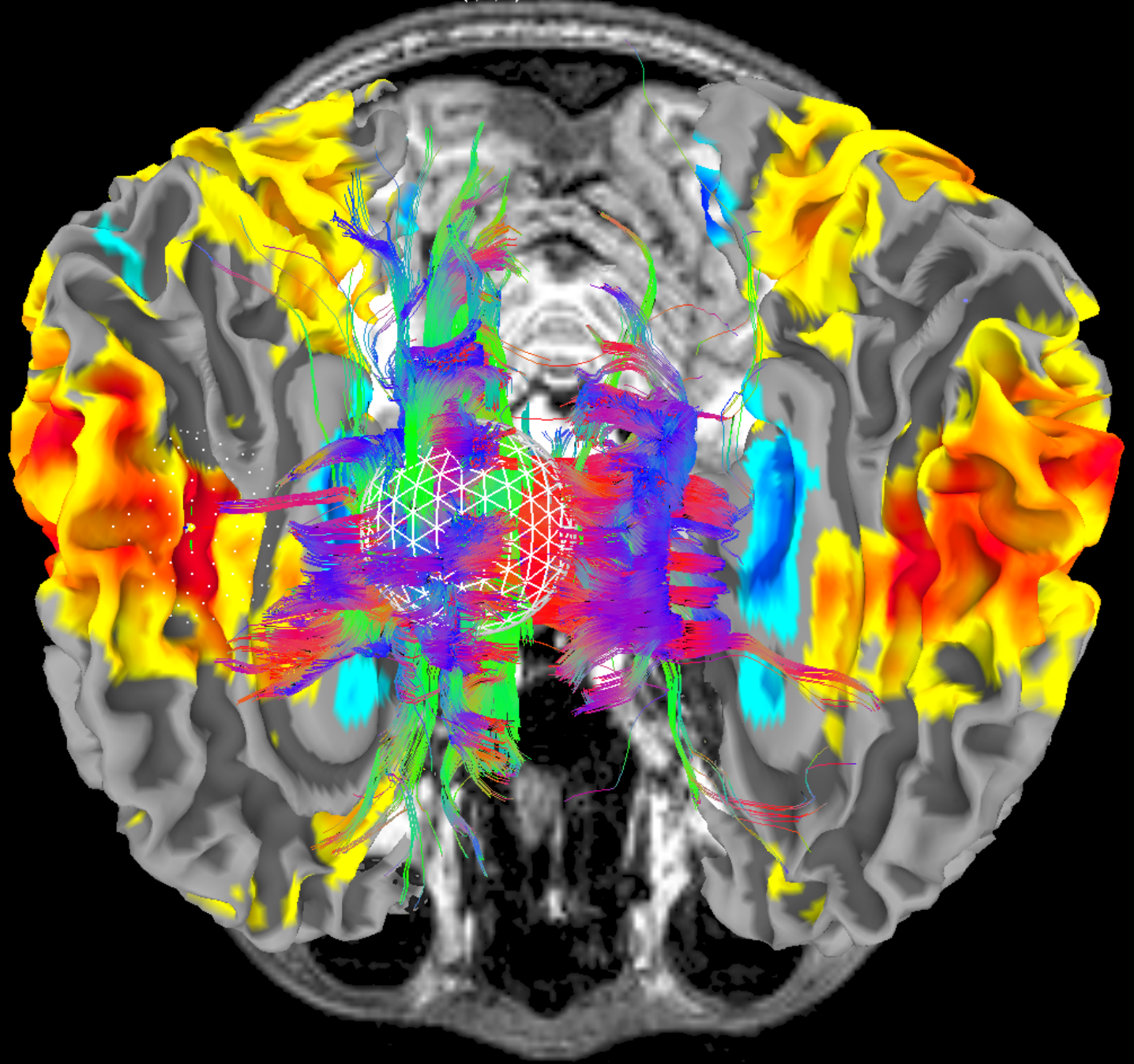


wm\_rh\_G and S\_cingul-Mid-Post  
(I,T,B)XcorrCoef=0.491

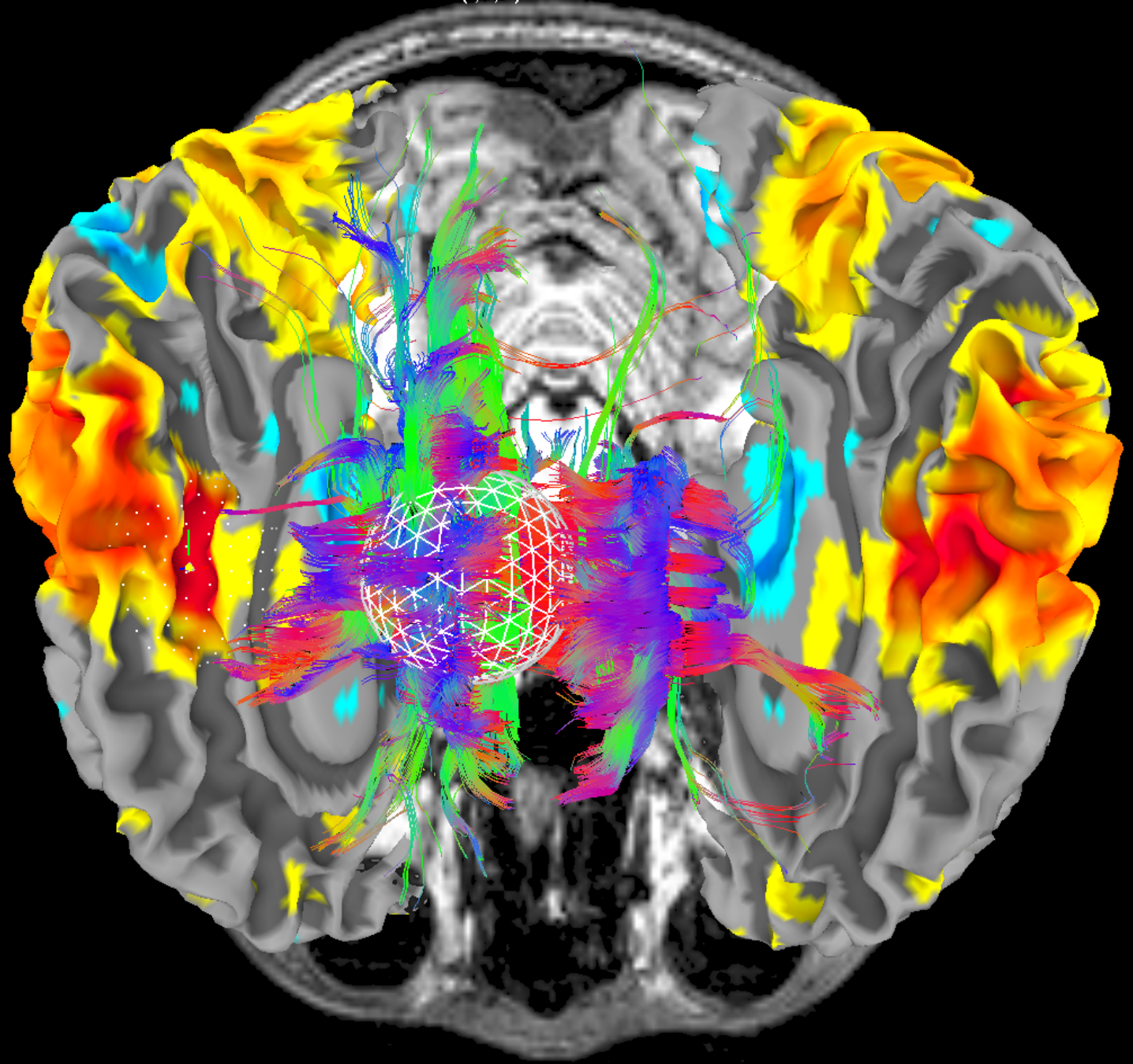




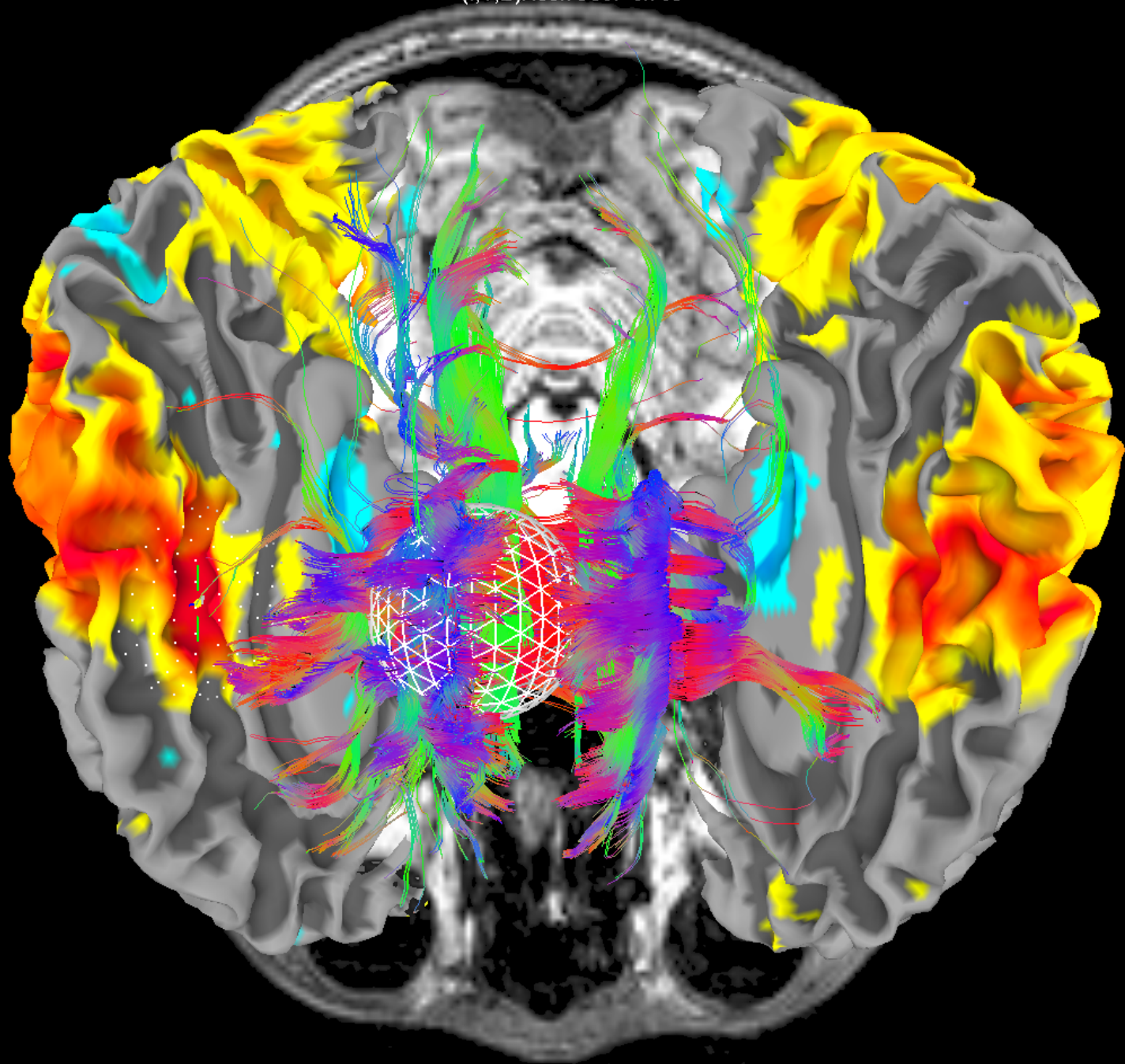
wm\_rh\_G and S\_cingul-Mid-Post  
(I,T,B)XcorrCoef=0.559



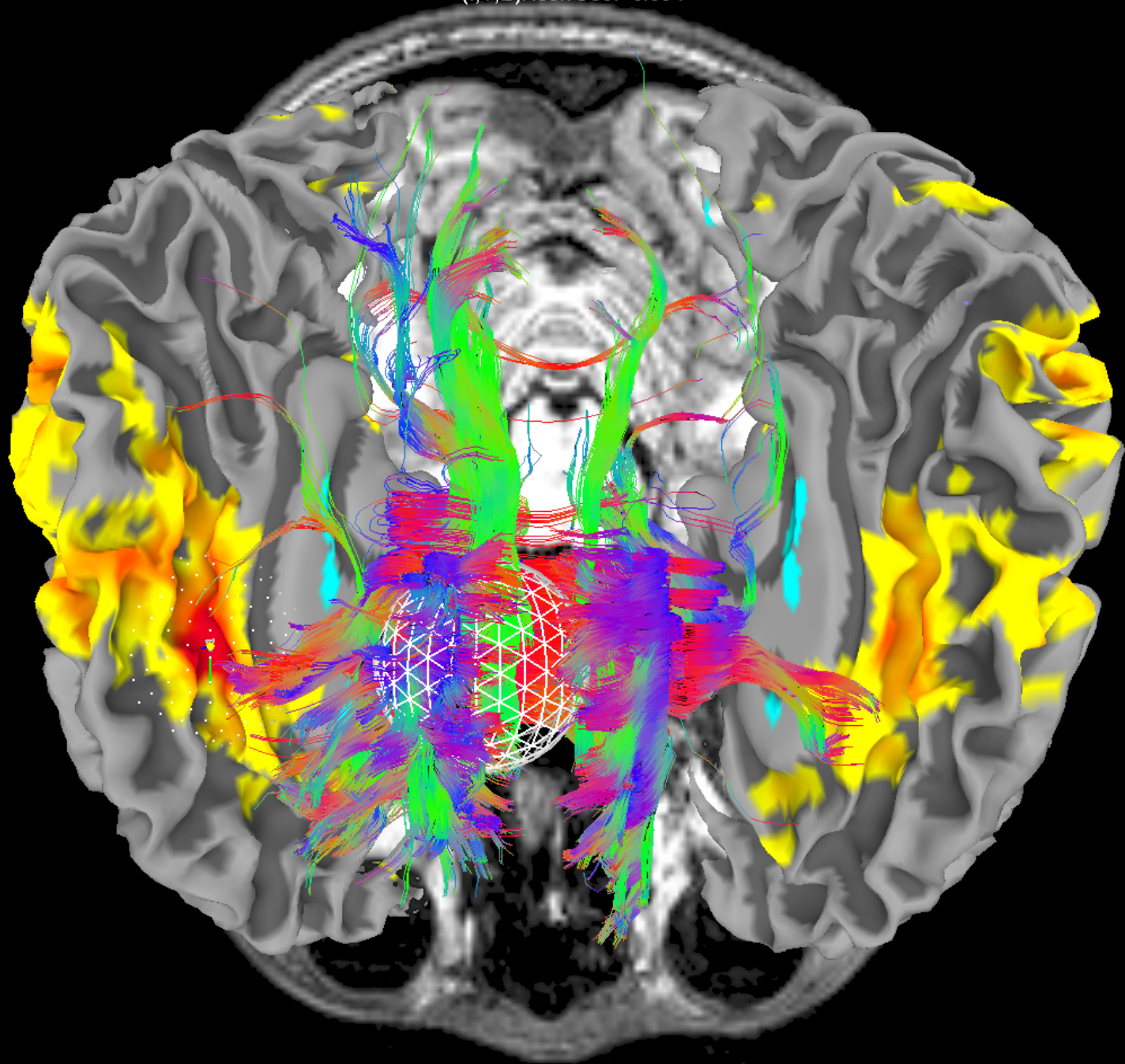
wm\_rh\_G and S\_cingul-Mid-Post  
(I,T,B)XcorrCoef=0.752



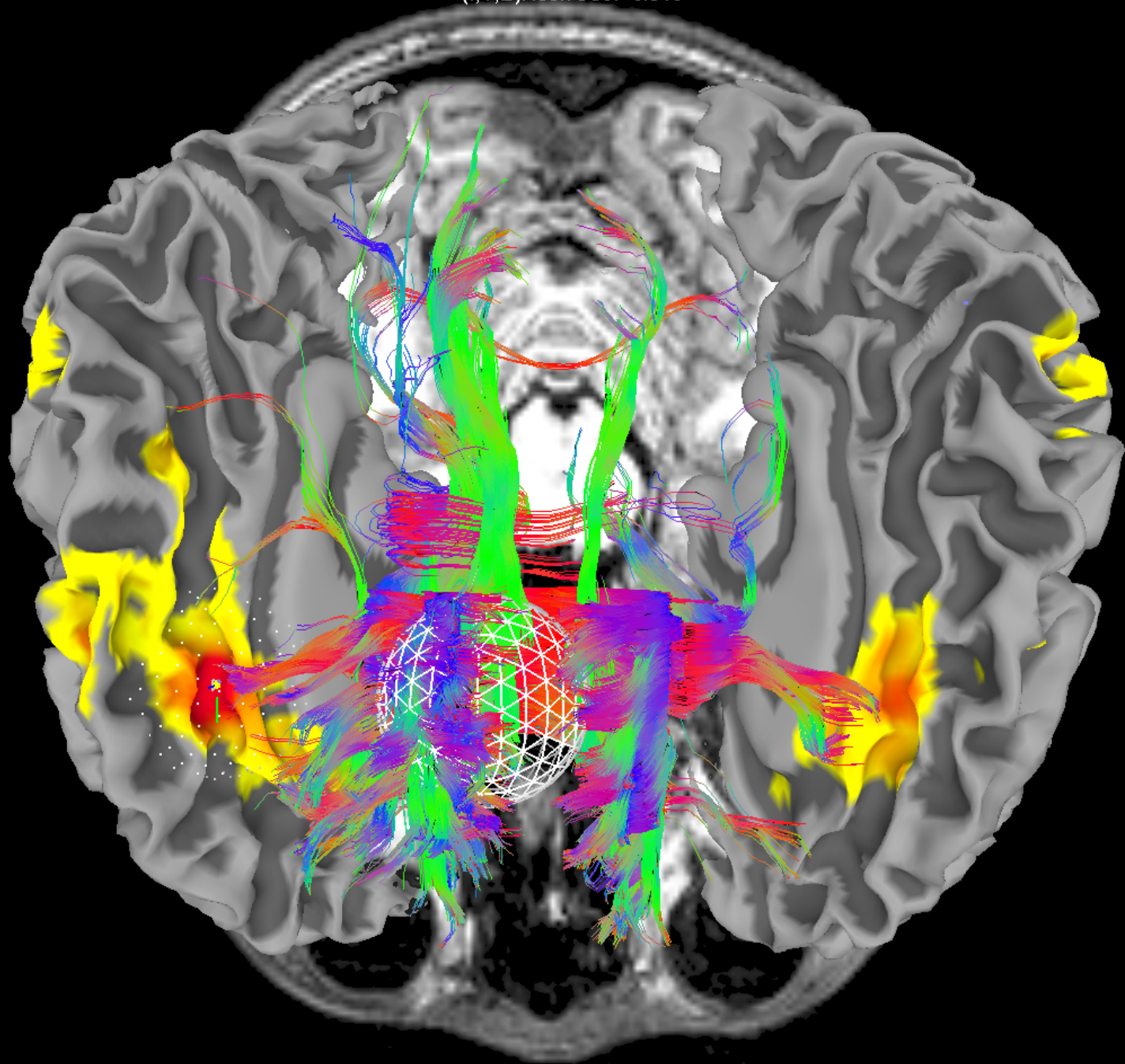
wm\_rh\_G and S\_cingul-Mid-Ant  
(I,T,B)XcorrCoef=0.785



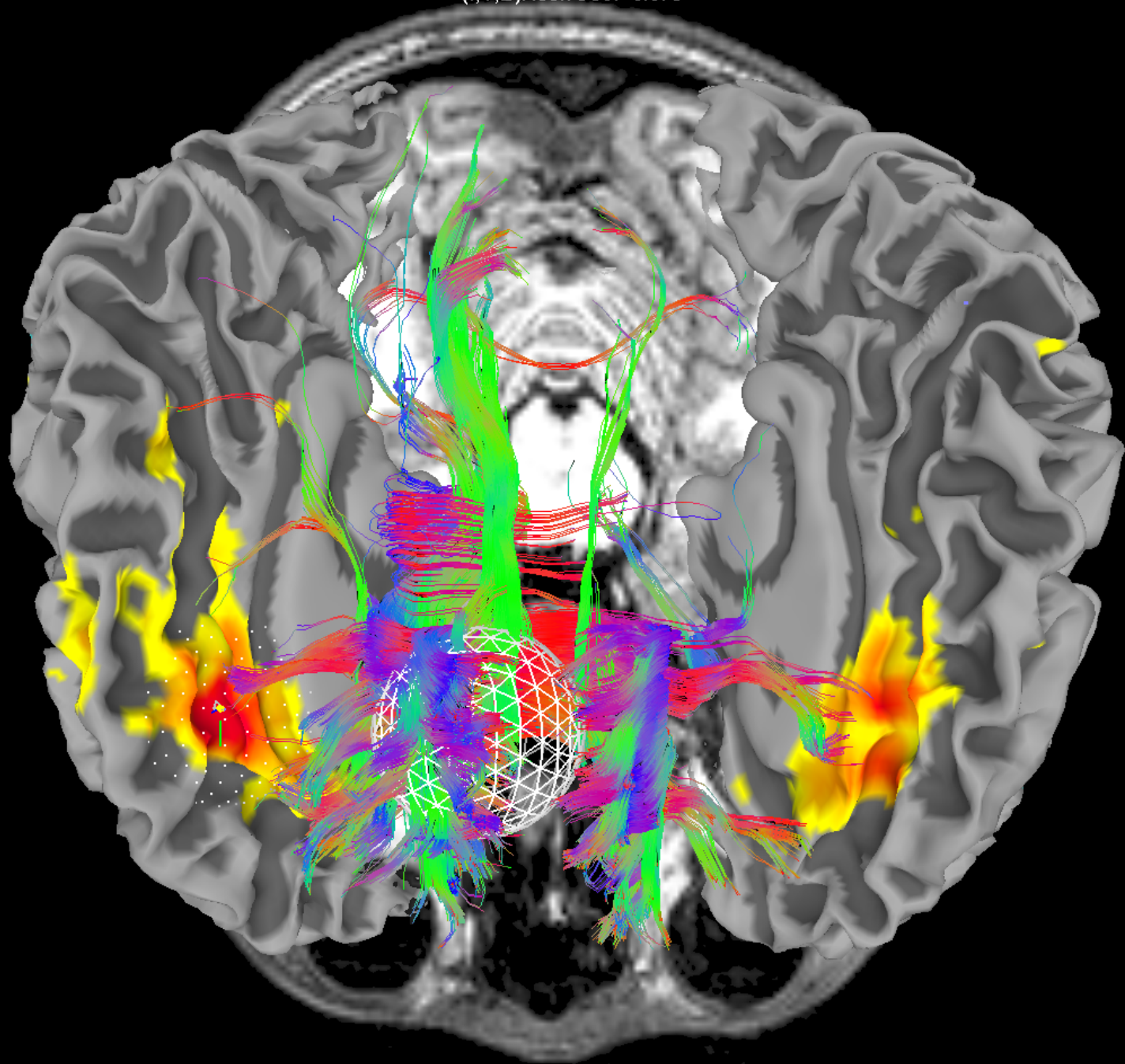
wm\_rh\_G and S\_cingul-Mid-Ant  
(I,T,B)XcorrCoef=0.604



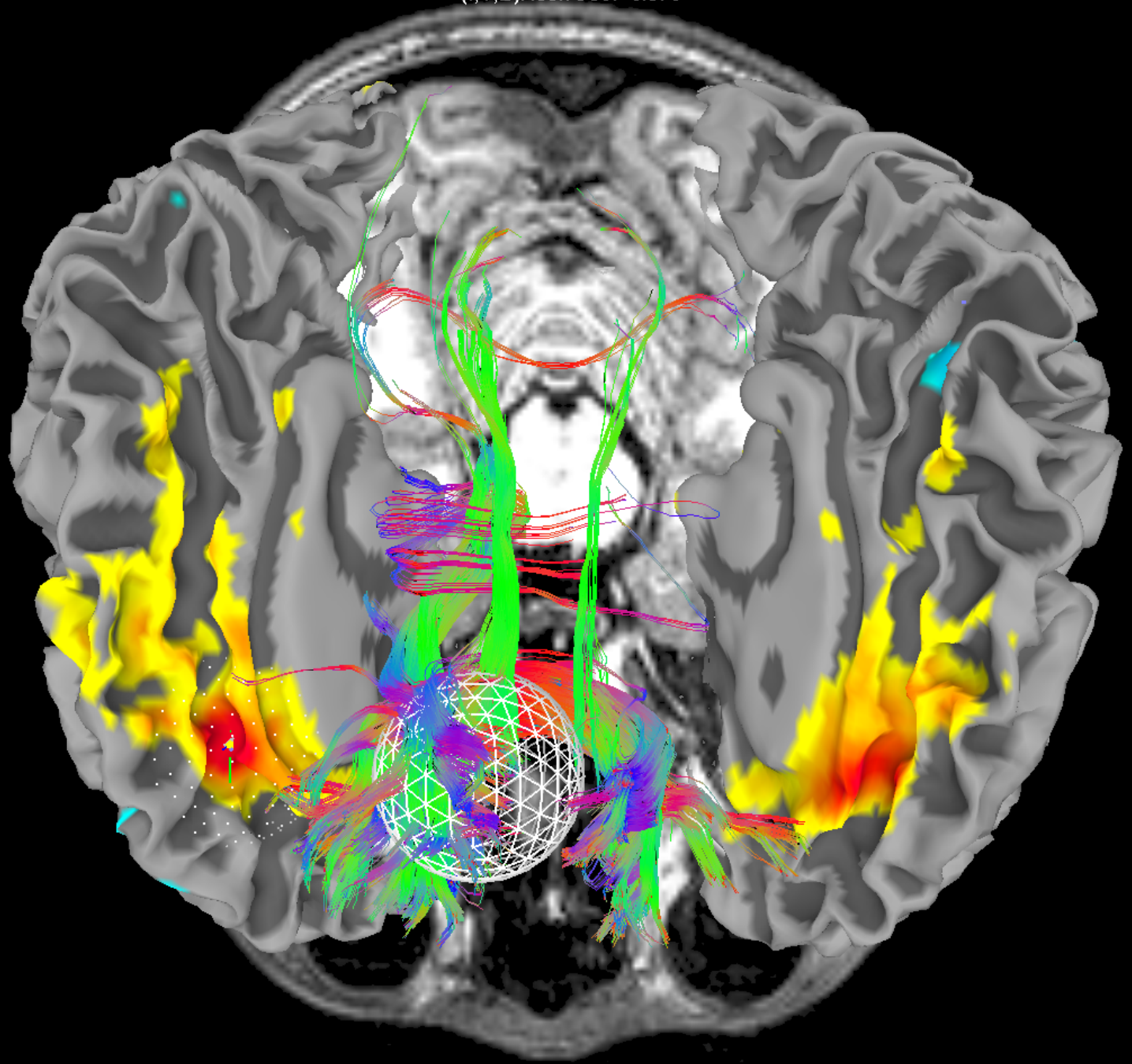
wm\_rh\_G and S\_cingul-Mid-Ant  
(I,T,B)XcorrCoef=0.516



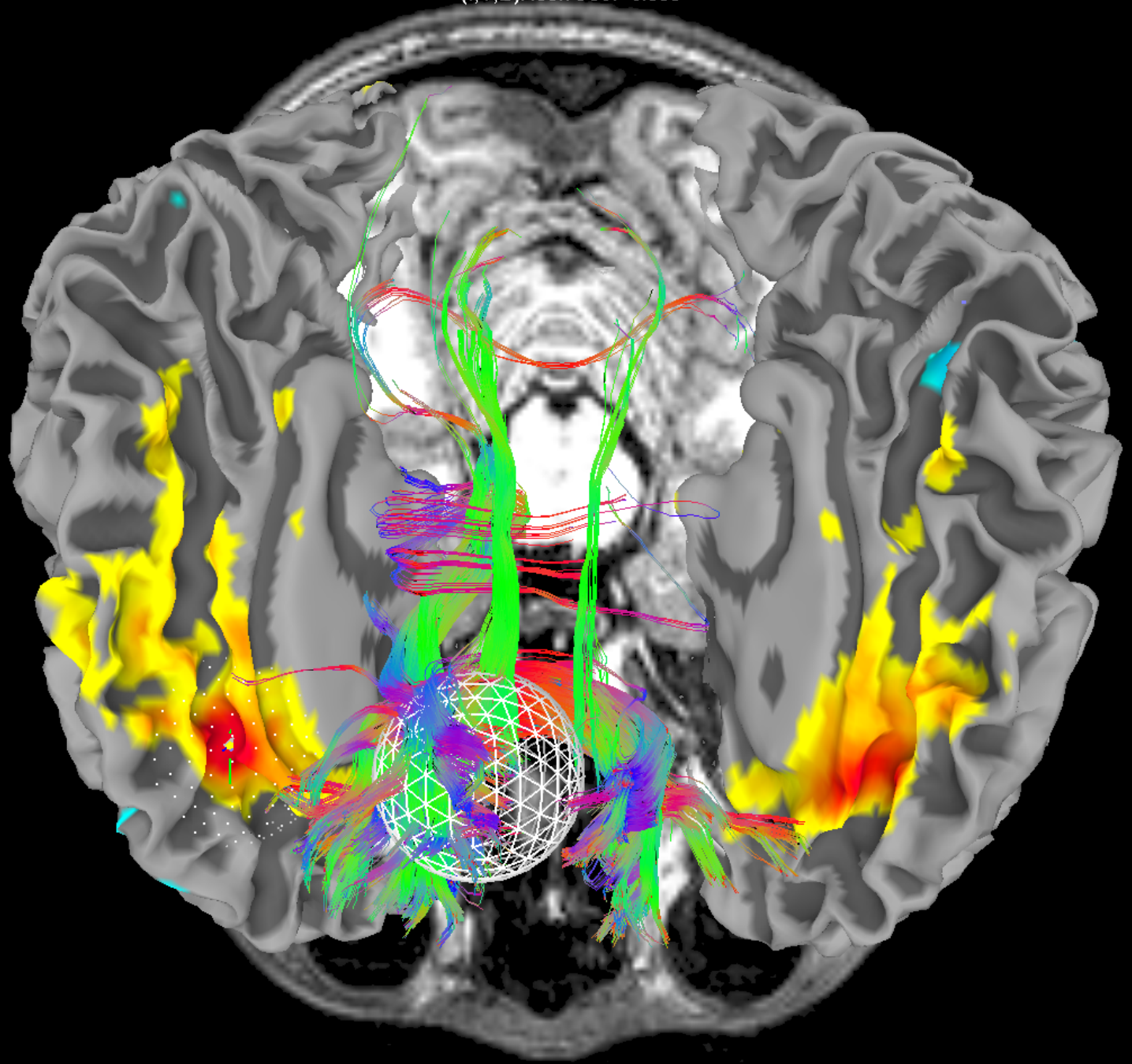
wm\_rh\_G and S\_cingul-Mid-Ant  
(I,T,B)XcorrCoef=0.679



wm\_rh\_G and S\_cingul-Ant  
(I,T,B)XcorrCoef=0.578

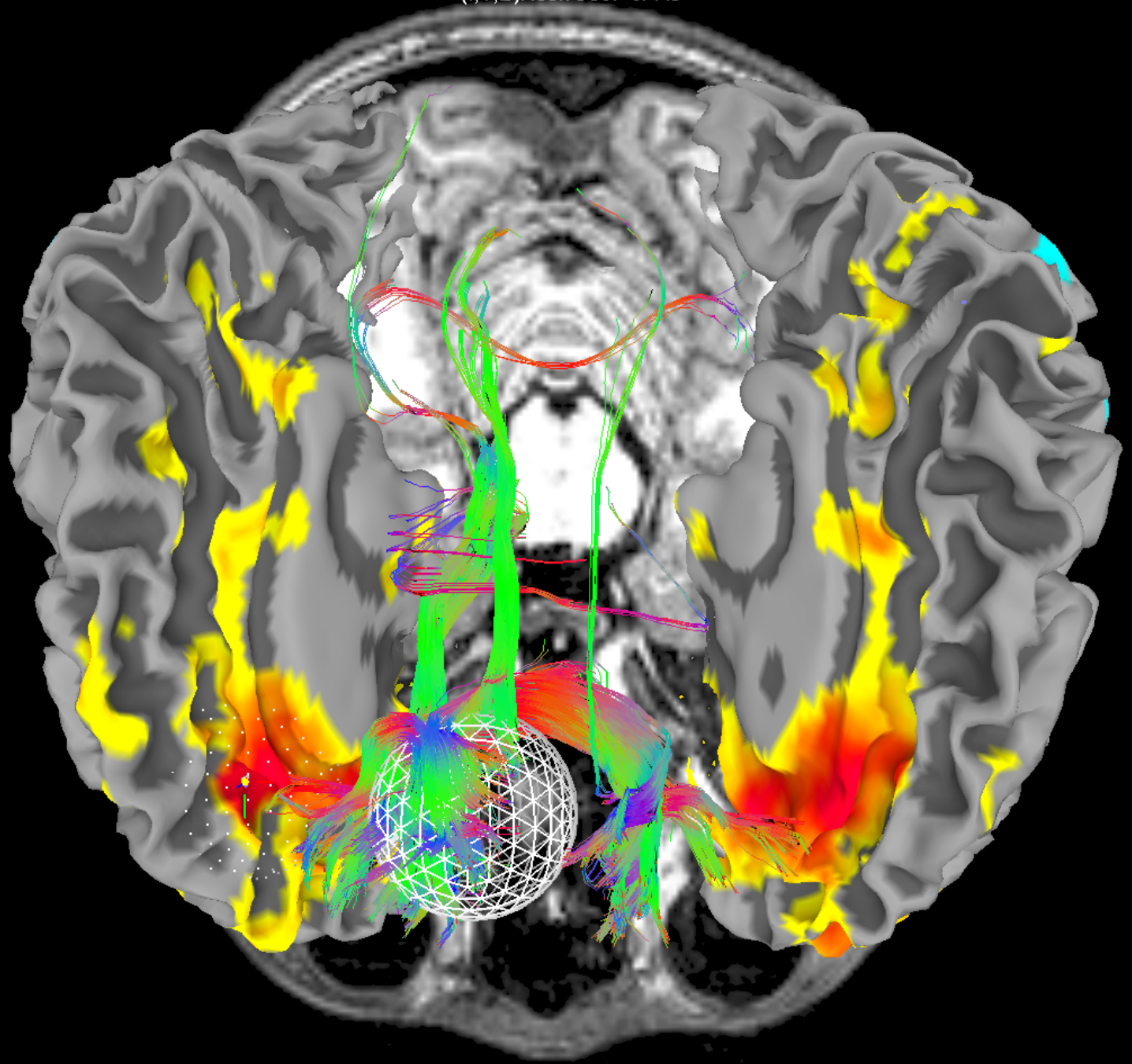


wm\_rh\_G and S\_cingul-Ant  
(I,T,B)XcorrCoef=0.999

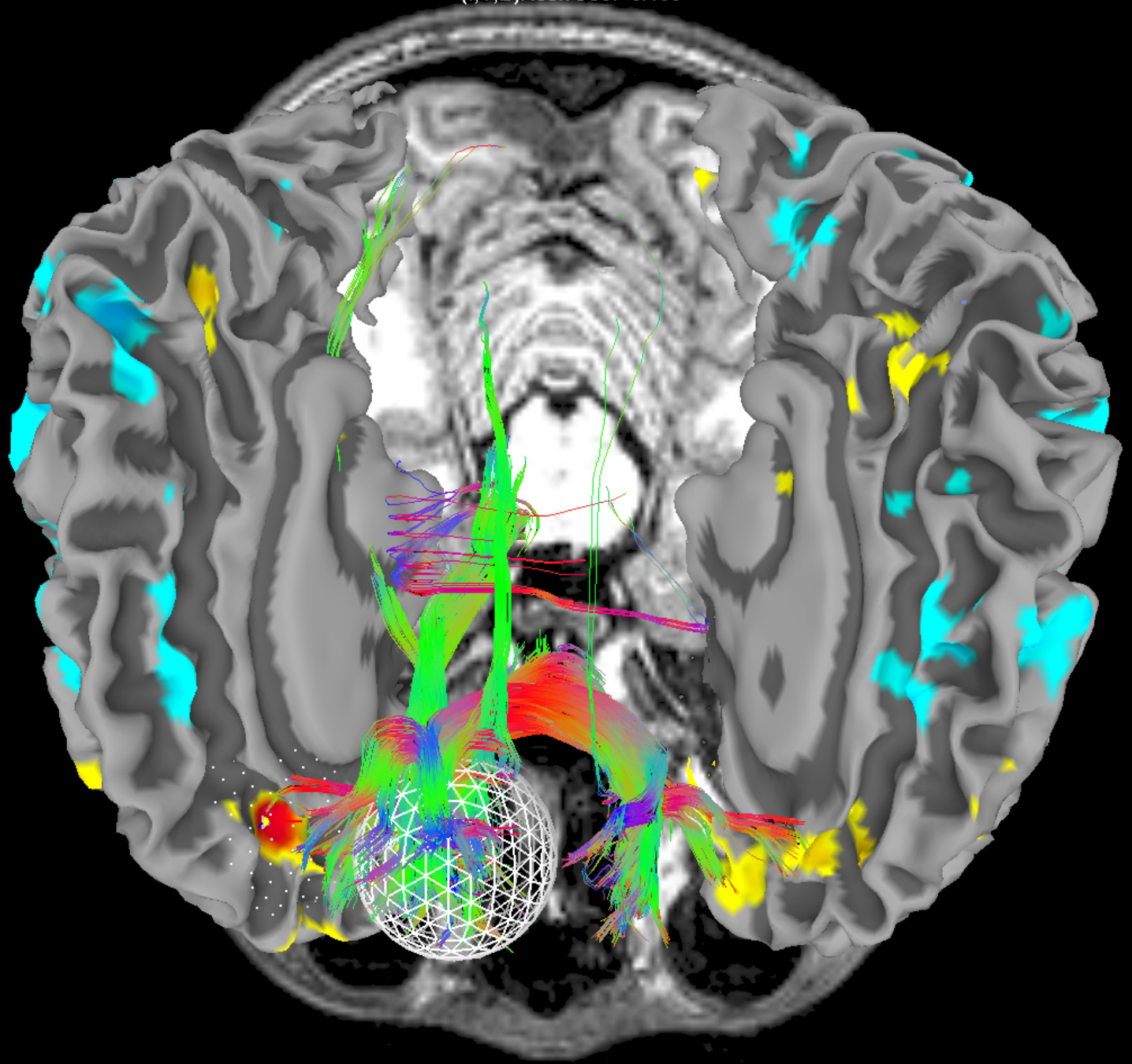




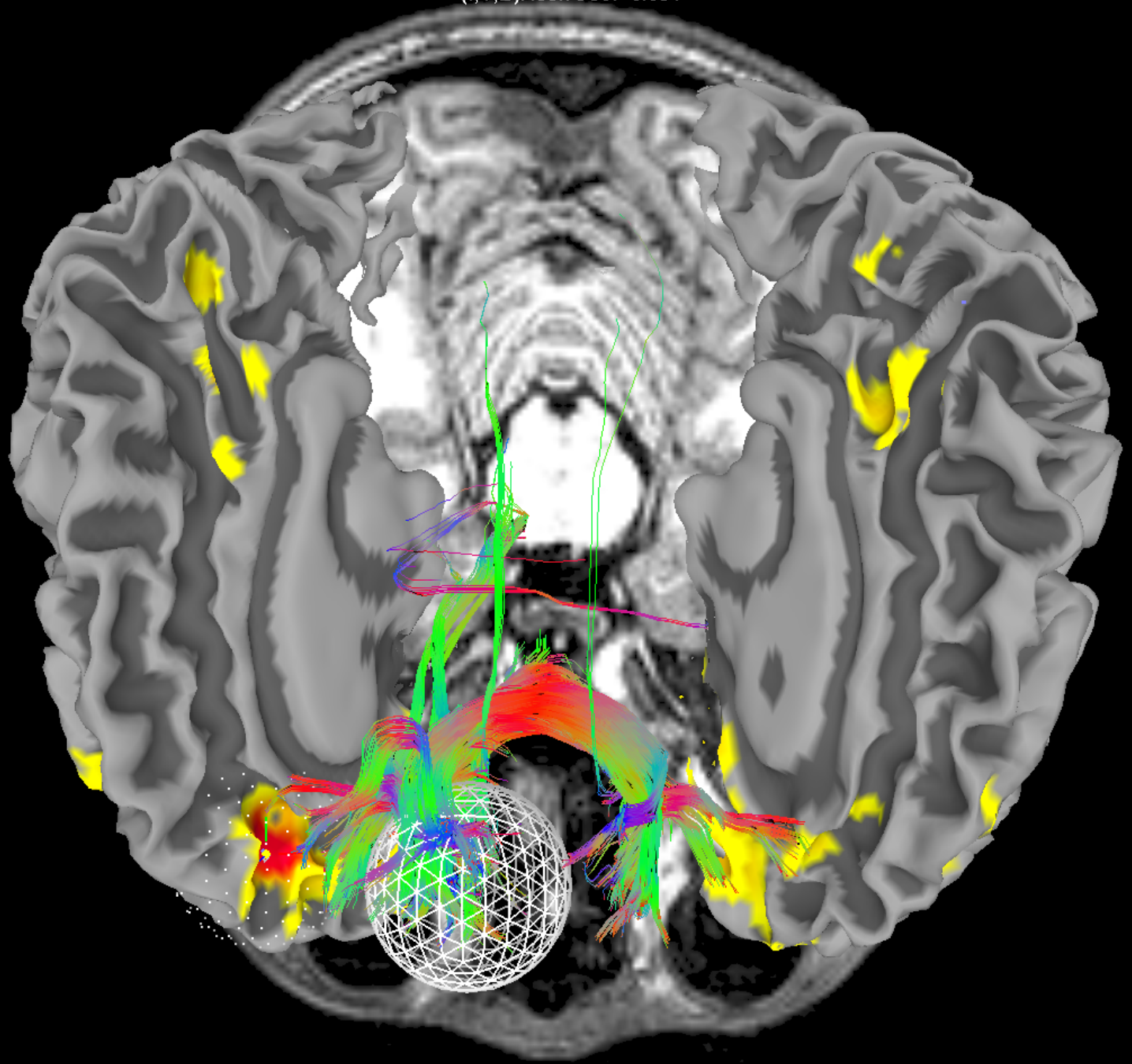
wm\_rh\_G and S\_cingul-Ant  
(I,T,B)XcorrCoef=0.445



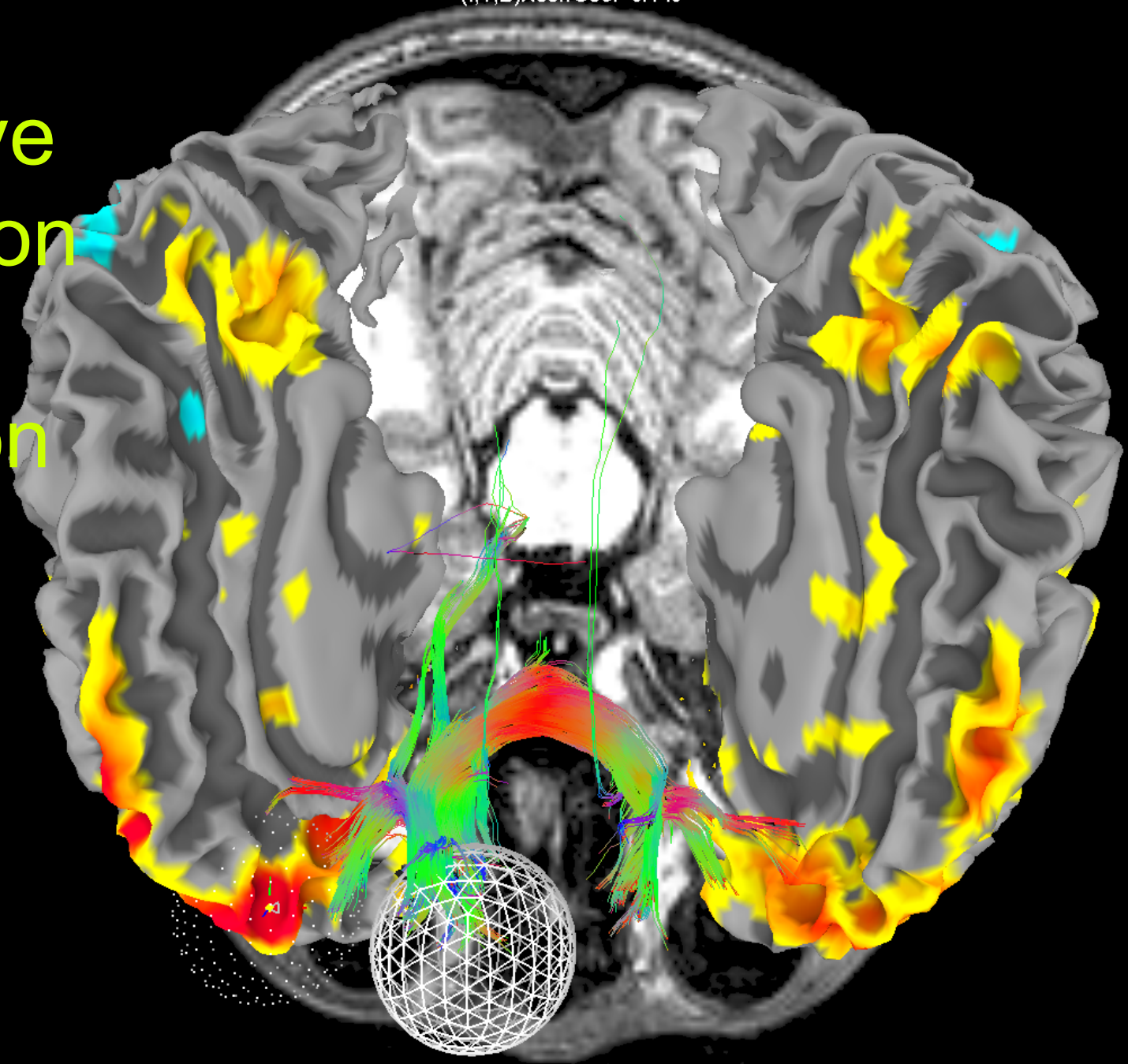
wm\_rh\_G and S\_cingul-Ant  
(I,T,B)XcorrCoef=0.136



wm\_rh\_G and S\_cingul-Ant  
(I,T,B)XcorrCoef=0.391

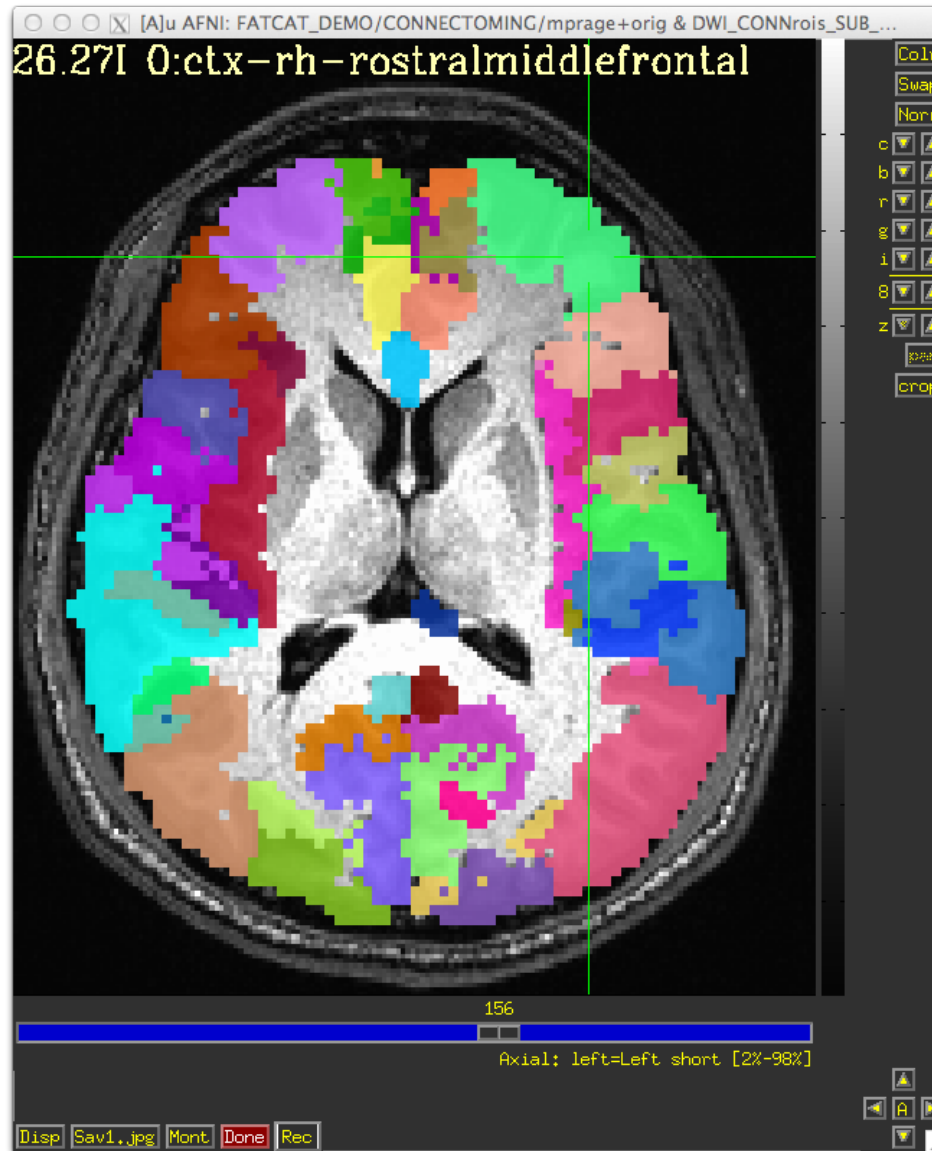


**Goal:**  
Interactive  
exploration  
of high  
dimension  
complex  
datasets



# tcsh Do\_11\_RUNdti\_Connectome\_Examp.tcsh

- Example 1: Tract tracing between large numbers of ROIs



*Hands-On*

29 Oct 2009 SSCC/NIMH

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# Tracts and Grid files are labeled with ROI names

The image shows a screenshot of the SUMA software interface. The main window displays a brain tract visualization with various colored fibers. The title bar reads "[A] SUMA:xx: ANY:". The menu bar includes "File View Tools". The main text area shows "ctx-rh-postcentral<->ctx-rh-precentral" and "Pnt 0, tret 3338, bnd 608". To the right, the "Coloring Controls" panel is visible, with "Lbl" set to "o.OME8\_000\_BUN". Below this, there are sliders for "Dim" (1.0) and "Opa" (1.0), and dropdowns for "Ord" (1) and "Ln" (SLD). There are also checkboxes for "Masks" and "Ign", and a "Gry" slider (20). A "Switch Dset" button is at the bottom of the panel. A red arrow points from the "Switch Dset" button to a smaller window titled "Switch Colori...". This window lists three foreground ROI names: "fg:o.OME8\_000\_LDC", "fg:o.OME8\_000\_MID", and "fg:o.OME8\_000\_BUN". A red arrow points from the "fg:o.OME8\_000\_BUN" line back to the main visualization. Another red arrow points from the main window's title bar area to the "Coloring Controls" panel.

```
suma -tract CONNECTOMING/o.OME8_000.niml.tract
```

# Thanks to:

## Developers:

Brenna Argall  
Shruti Japee  
Rick Reynolds



## Critics:

Mike Beauchamp  
Pat Bellgowan

## Data and Documentation:

Peggy Christidis



## Getting Help Somewhere:

Karen Dutton



## SysAdmin:

Brian Pittman

## MRI Pulse Sequence and Segmentation

Hauke Heekeren  
Sean Marrett



Testing: Samia Saad

