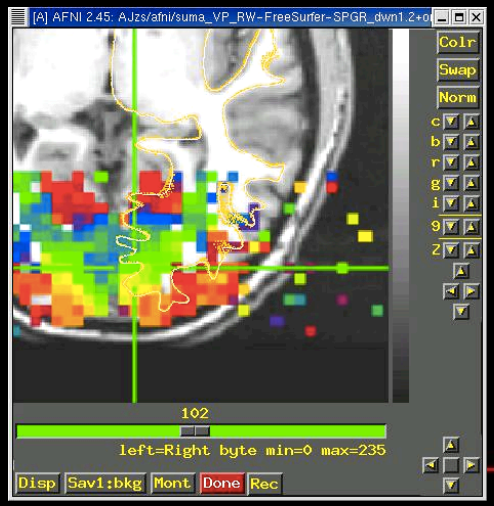
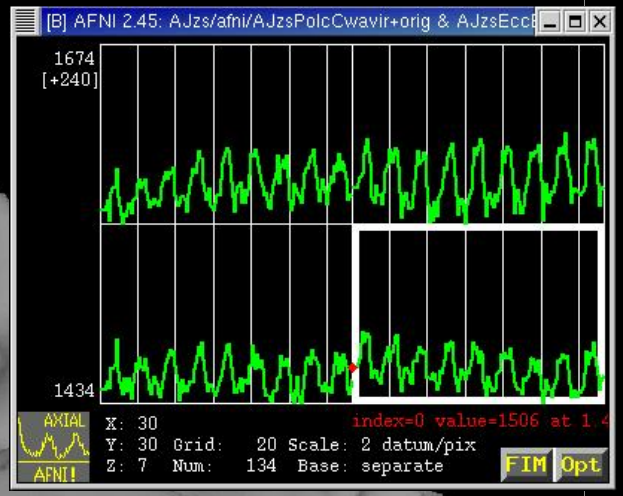
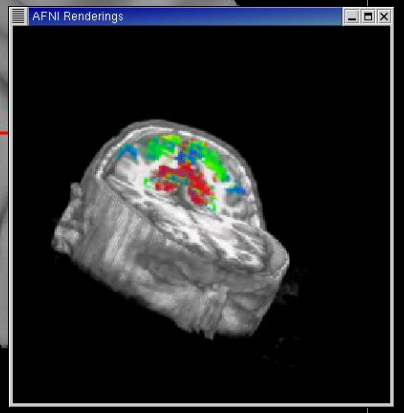
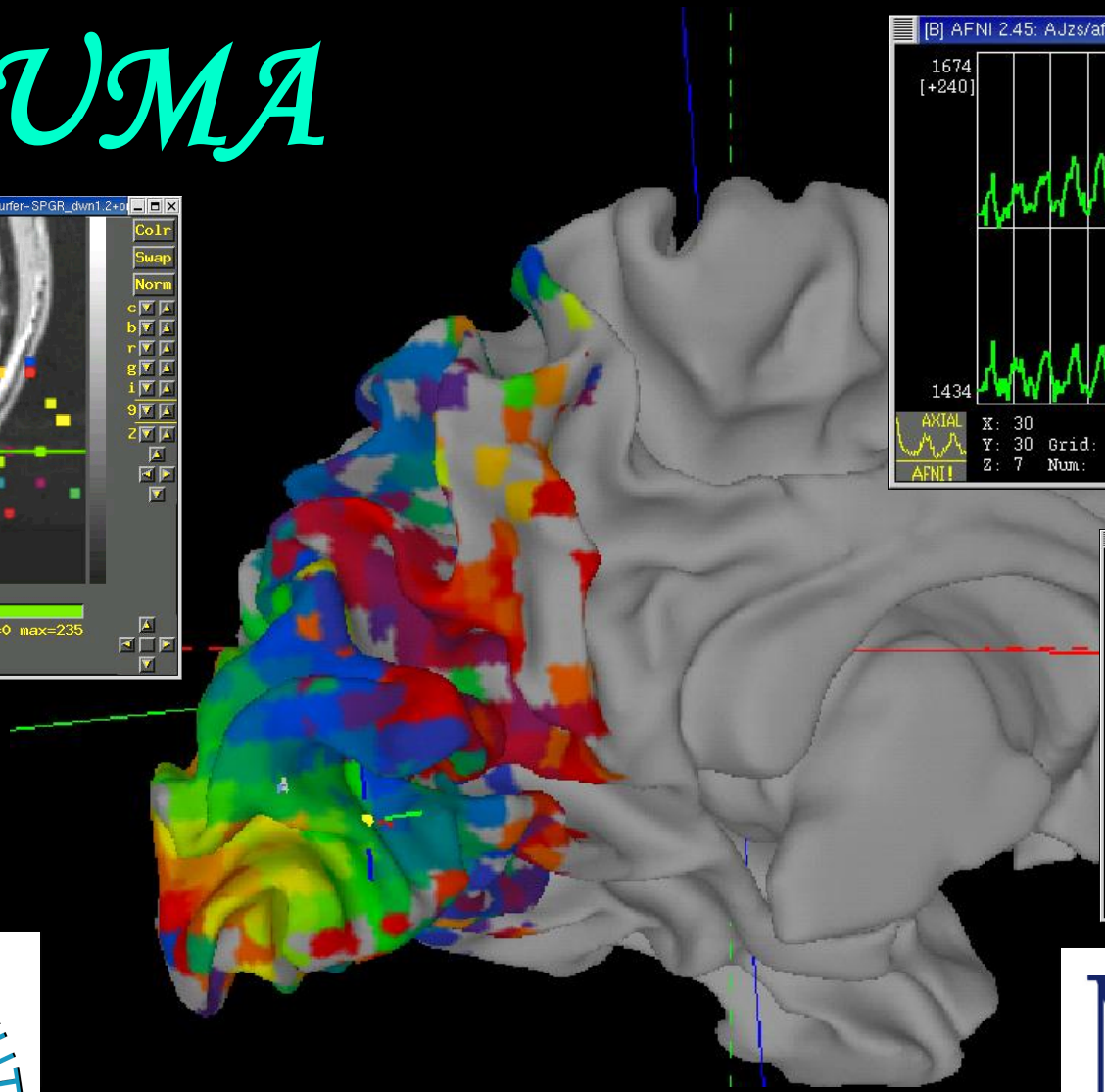
SUMA









Statistical & Scientific Computing Core

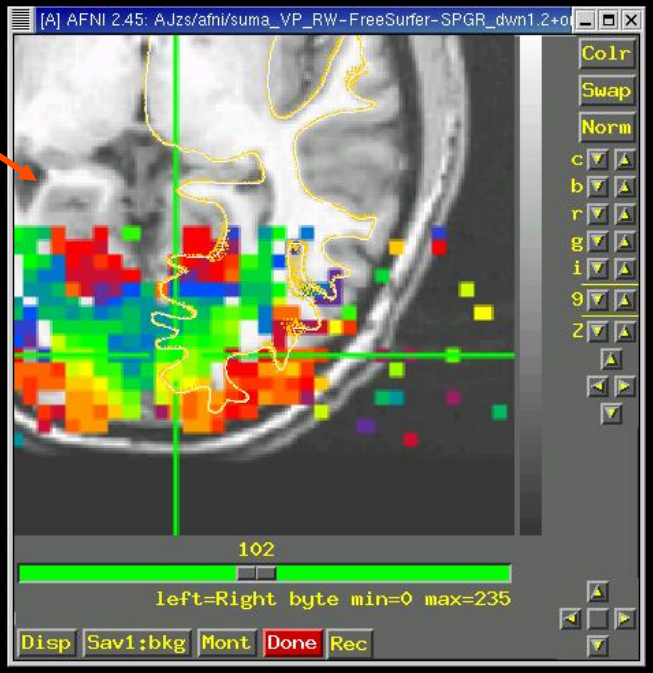
SUMA!

AFNI!

National Institutes of Health

National Institute of Mental Health


AFNI!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Colr
Swap
Norm
c
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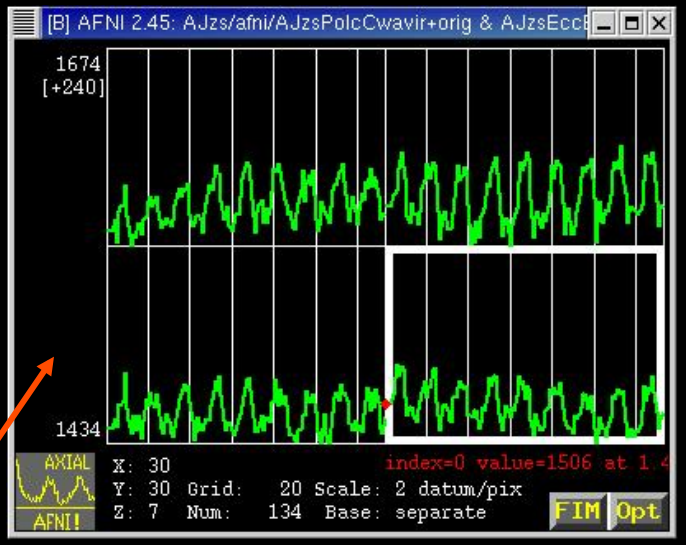
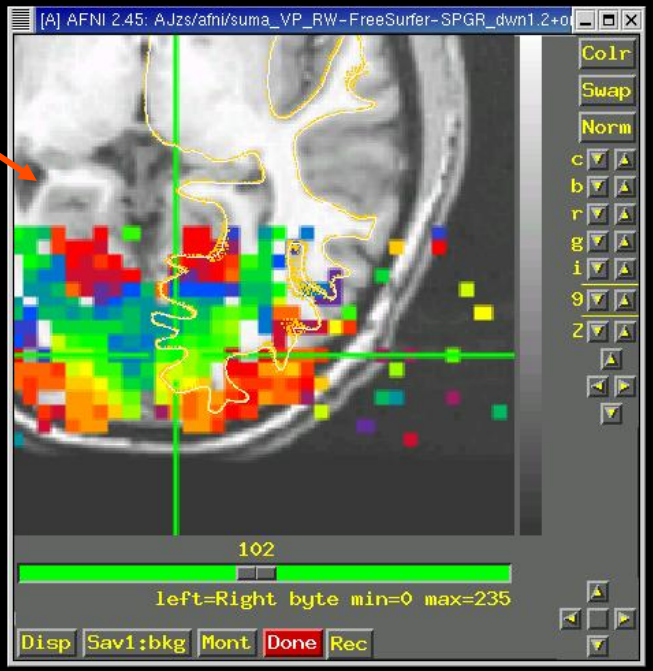
i
9
Z
102
left=Right byte min=0 max=235
Disp
Sav1:bkg
Mont
Done
Rec


[B] AFNI 2.45: AJzs/afni/AJzsPolcCwavir+orig & AJzsEcc
1674
[+240]
1434
AXIAL
AFNI!
X: 30
Y: 30 Grid: 20 Scale: 2 datum/pix
Z: 7 Num: 134 Base: separate
FIM
Opt


AFNI!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left=Right byte min=0 max=235
Disp
Sav1:bkg
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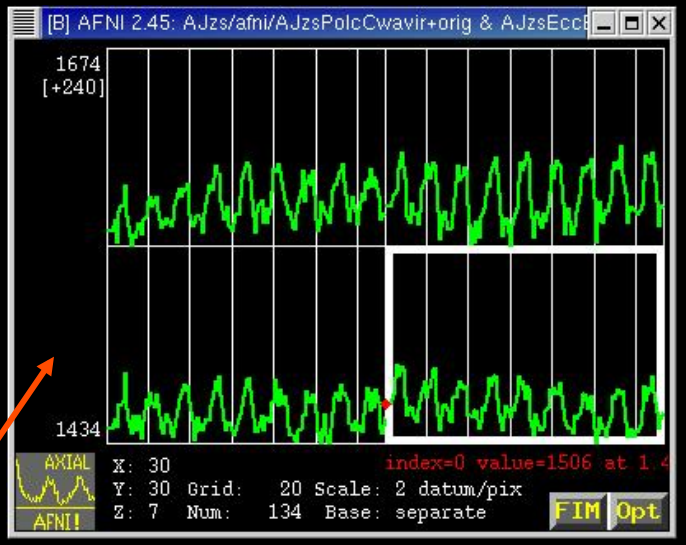
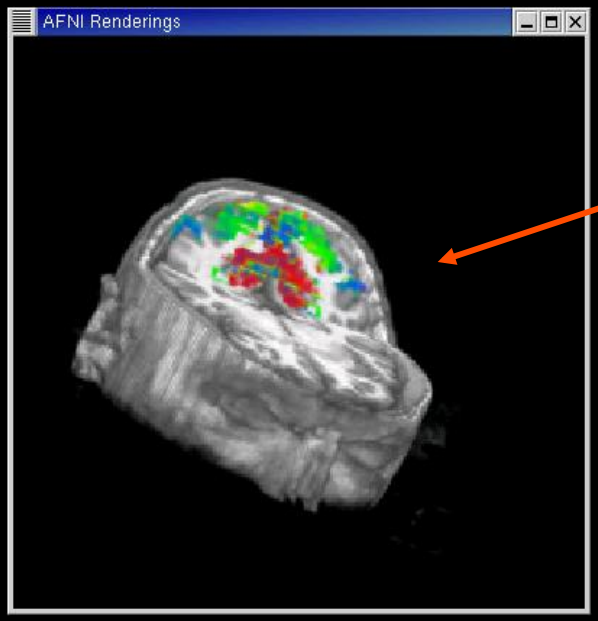
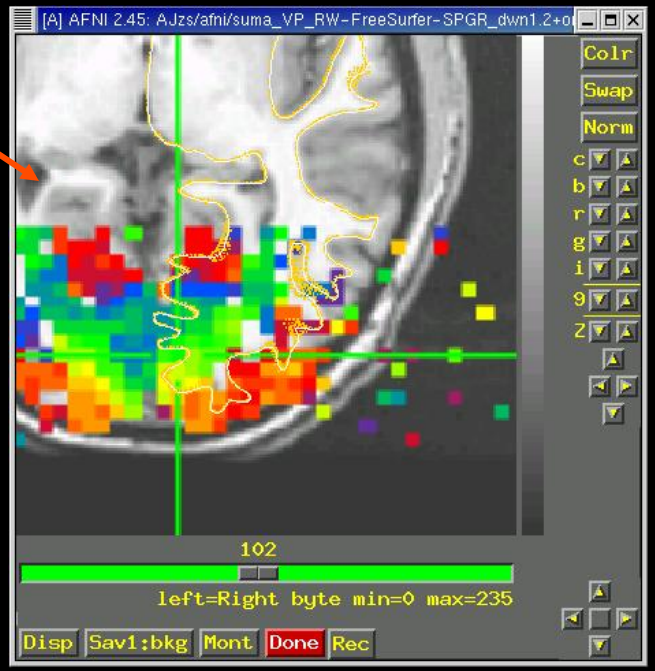
Done
Rec


[B] AFNI 2.45: AJzs/afni/AJzsPolcCwavir+orig & AJzsEcc
1674
[+240]
1434
AXIAL
AFNI!
X: 30
Y: 30 Grid: 20 Scale: 2 datum/pix
Z: 7 Num: 134 Base: separate
FIM
Opt


AFNI Renderings


AFNI!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Colr
Swap
Norm
c
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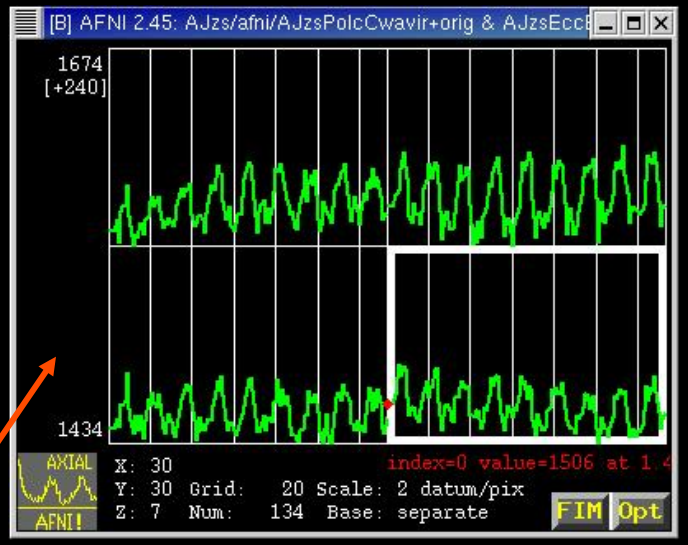
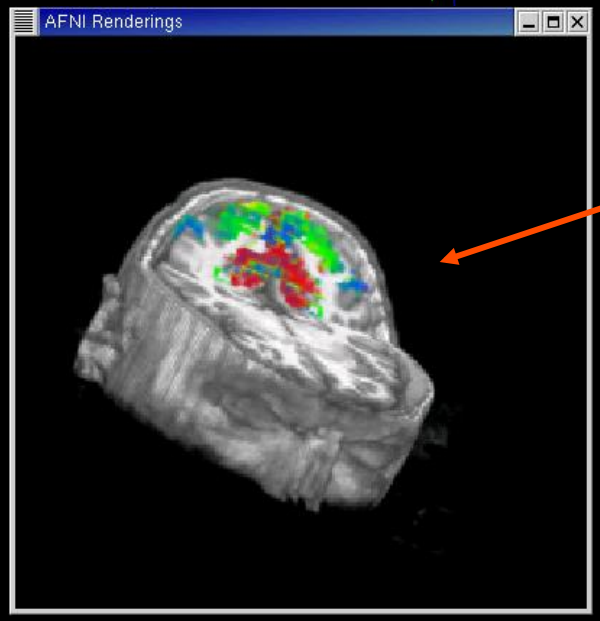
i
9
Z
102
left=Right byte min=0 max=235
Disp
Sav1:bkg
Mont
Done
Rec

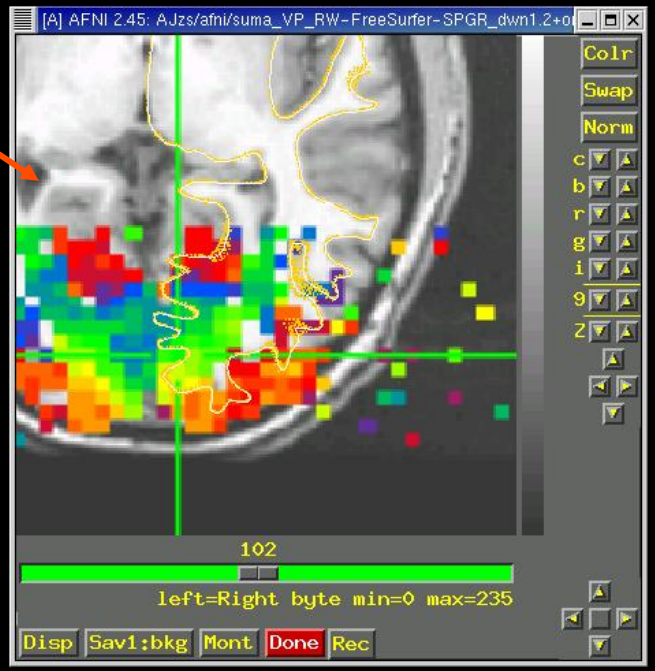

SUMA!

SUMA


[B] AFNI 2.45: AJzs/afni/AJzsPolcCwavir+orig & AJzsEcc
1674
[+240]
1434
AXIAL
AFNI!
X: 30
Y: 30 Grid: 20 Scale: 2 datum/pix
Z: 7 Num: 134 Base: separate
FIM
Opt


AFNI Renderings


AFNI!


[A] AFNI 2.45: AJzs/afni/suma_VP_RW-FreeSurfer-SPGR_dwn1.2+0
Colr
Swap
Norm
c
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r
g
i
9
Z
102
left=Right byte min=0 max=235
Disp
Sav1:bkg
Mont
Done
Rec

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.

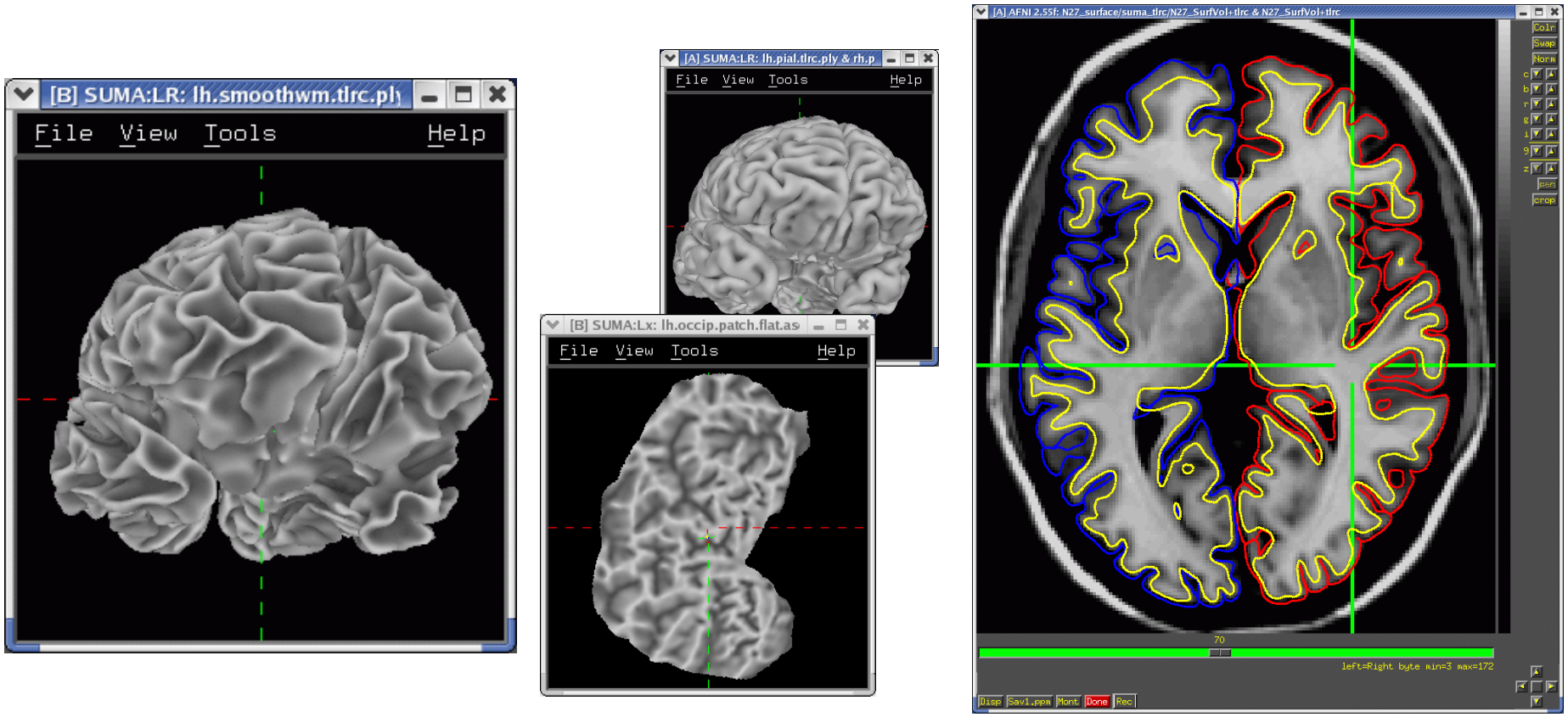
The Process of Using SUMA

- **PreSUMA** (setup phase):
  - Collect, align, and average high-quality, high-resolution anatomical data
    - On NIMH's GE 3 Tesla scanners, 2-4 MPRAGE datasets do well
  - Correct image non-uniformity
    - Using AFNI's 3dUniformize 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

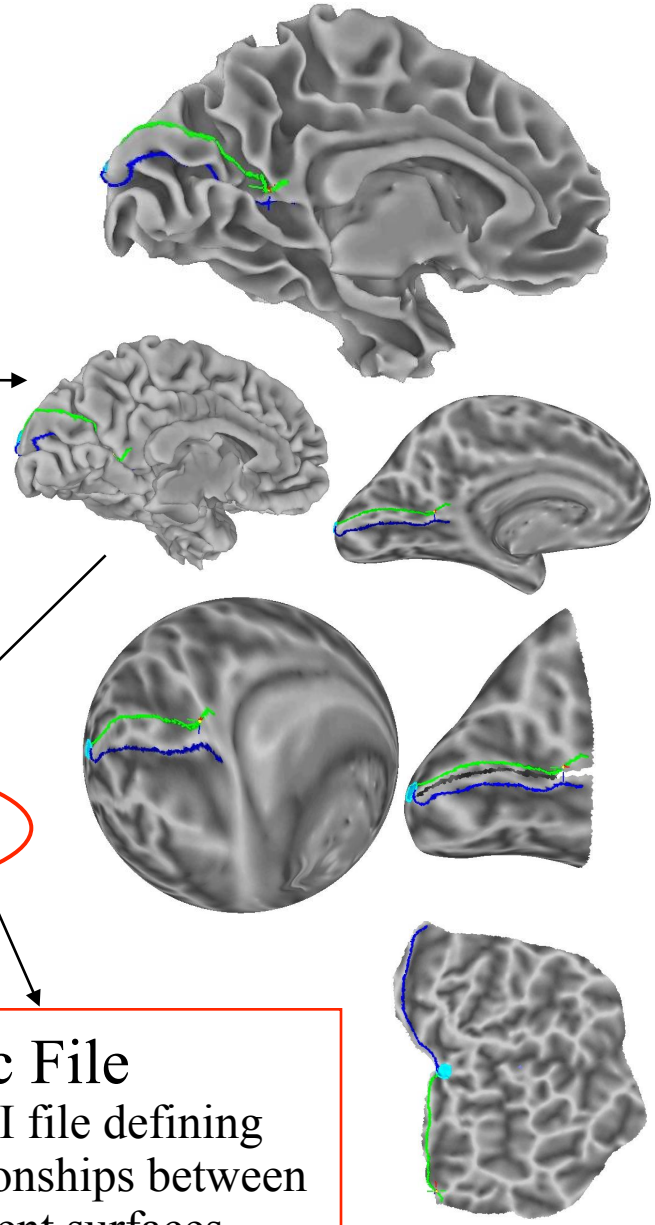
- For display (mostly) of Talairach or MNI data:
  - Use the Talairach (http://afni.nimh.nih.gov/pub/dist/tgz/suma_TT_N27.tgz) or MNI (http://afni.nimh.nih.gov/pub/dist/tgz/suma_MNI_N27.tgz) surfaces created from the N27 brain dataset using FreeSurfer.
  - Ready to use, no surface creation or alignment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



A: Preparing surface models for SUMA

High-Res. Anatomical MRI data

Create Surface Models (FreeSurfer, Caret, etc.)



@SUMA_Make_Spec_*

SurfVol
AFNI-format Surface Volume that is aligned with surface models

Spec File
ASCII file defining relationships between different surfaces

@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.

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 suma_demo/SurfData/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
  - ★ *suma –spec DemoSubj_lh.spec –sv DemoSubj_SurfVol+orig &*
    - ➥or execute the script: *tcsh run_suma*

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.

Hands-On

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

Hands-On

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 at time. In most other circumstances it leads to confusion.
    - ★ Shift+button 1 doubleclick: Undo Z rotation

Hands-On

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

Hands-On

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.

Hands-On

Recording your beautiful SUMA images

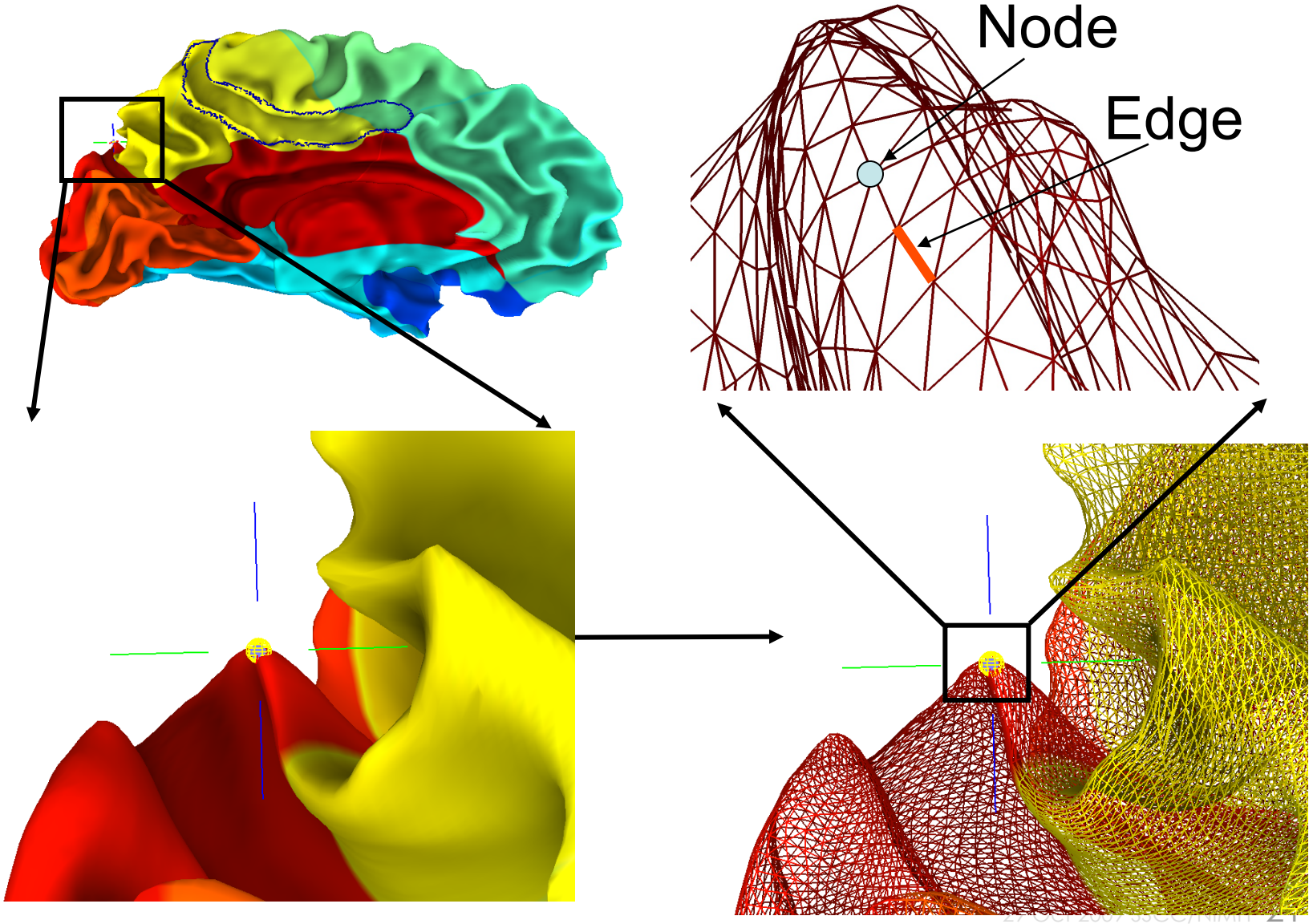
- Using '**r**' in SUMA to record the current scene (a single image).
- Using '**r**' on the colorbar creates an image of the colorbar.
- Using '**R**' to record continuously the rendered scene, as you change it.
- Images are captured by an AFNI-esque image viewer.
  - ★ Identical consecutive images 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

Hands-On

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?

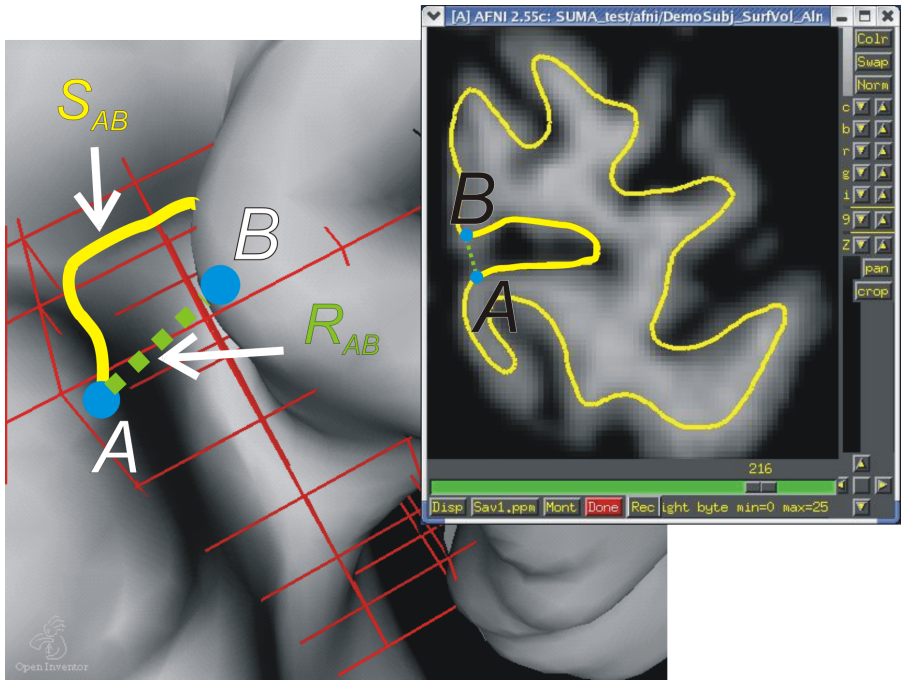


Relationships between surface models

- 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

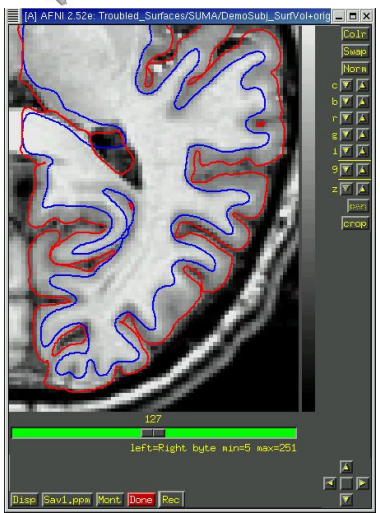
Inflated

Pial

Inflated, Occipital cut

Spherical

Overlay of anatomically correct Pial and SmoothWm surfaces over anatomical volume



Flattened, Occipital cut

Sample Spec File

```
# delimits comments
# define the group
        Group = DemoSubj

# define various States
        StateDef = smoothwm
        StateDef = pial
        StateDef = inflated

NewSurface
        SurfaceFormat = ASCII
        SurfaceType = FreeSurfer
        FreeSurferSurface =
lh.smoothwm.asc
        LocalDomainParent = SAME
        SurfaceState = smoothwm
        EmbedDimension = 3

NewSurface
        SurfaceFormat = ASCII
        SurfaceType = FreeSurfer
        FreeSurferSurface = lh.pial.asc
        LocalDomainParent =
lh.smoothwm.asc
        SurfaceState = pial
        EmbedDimension = 3
```

```
NewSurface
        SurfaceFormat = ASCII
        SurfaceType = FreeSurfer
        FreeSurferSurface = lh.inflated.asc
        LocalDomainParent = lh.smoothwm.asc
        SurfaceState = inflated
        EmbedDimension = 3

NewSurface
        SurfaceFormat = ASCII
        SurfaceType = FreeSurfer
        FreeSurferSurface = lh.sphere.asc
        LocalDomainParent = lh.smoothwm.asc
        SurfaceState = sphere
        EmbedDimension = 3
```

Details of the Spec file:

- The Spec file contains information about the surfaces that will be viewed.
  - ★ Information is specified in the format: *field = value*.
  - ★ The = sign must be preceded and followed by a space character.
  - ★ **#** delimit comment lines, empty lines and tabs are ignored.
  - ★ In addition to fields, there is also the **NewSurface** tag which is used to announce a new surface.
  - ★ Unrecognized text will cause the program parsing a Spec file to complain and exit.

Details of the Spec file:

- The fields are:
  - ★ Group: Usually the Subject's ID. In the current SUMA version, you can only have one group per spec file. All surfaces read by SUMA must belong to a group.
  - ★ FreeSurferSurface: Name of the FreeSurfer surface.
  - ★ SurfaceFormat: ASCII or BINARY
  - ★ SurfaceType: FreeSurfer, Caret, BrainVoyager, Ply, etc.
  - ★ SurfaceState: Surfaces can be in different states such as inflated, flattened, etc. The label of a state is arbitrary and can be defined by the user. The set of available states must be defined with StateDef at the beginning of the Spec file.

Details of the Spec file:

- The fields are:
  - ★ StateDef: Used to define the various states. This must be placed before any of the surfaces are specified.
  - ★ Anatomical: Used to indicate whether surface is anatomically correct (Y) or not (N). Anatomically correct surfaces are sent to AFNI.
  - ★ LocalDomainParent: Name of a surface whose mesh is shared by other surfaces in the spec file.

    The default for FreeSurfer surfaces is the smoothed gray matter/ white matter boundary. For SureFit it is the fiducial surface. Use SAME when the LocalDomainParent for a surface is the surface itself.

    ➥A node-to-node correspondence is maintained across surfaces sharing the same domain parent.
  - ★ EmbedDimension: Embedding Dimension of the surface, 2 for surfaces in the flattened state, 3 for other.

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)

Hands-On

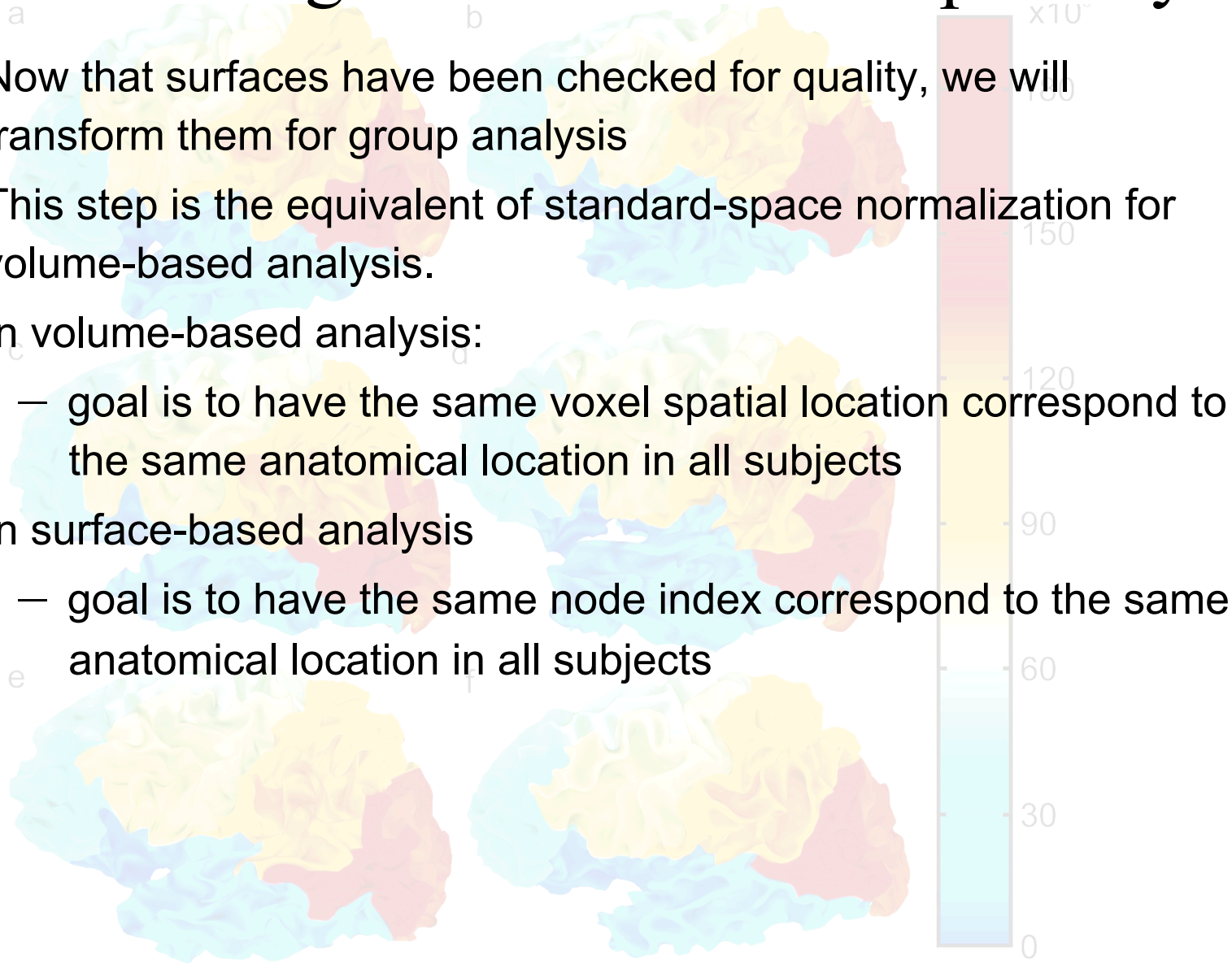
Viewing the group of surfaces

- 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

Hands-On

Standardizing Surfaces For Group Analysis

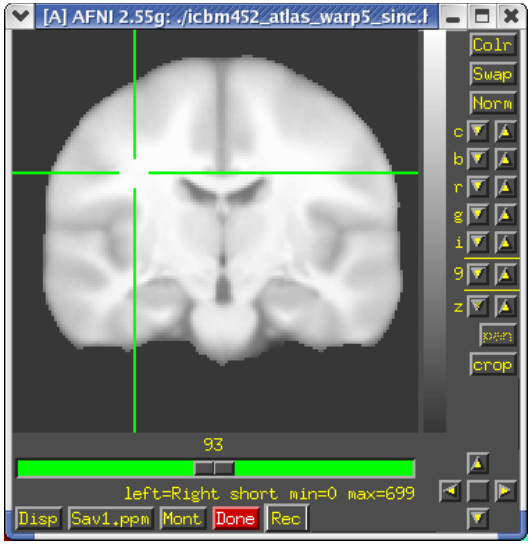
- Now that surfaces have been checked for quality, we will transform them for group analysis
- This step is the equivalent of standard-space normalization for volume-based analysis.
- In volume-based analysis:
  - goal is to have the same voxel spatial location correspond to the same anatomical location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

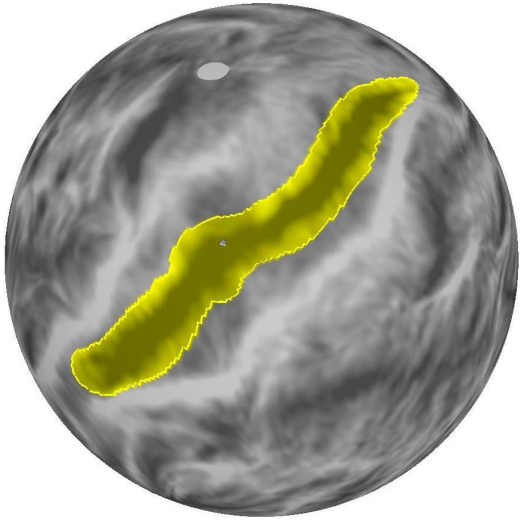


Group analysis

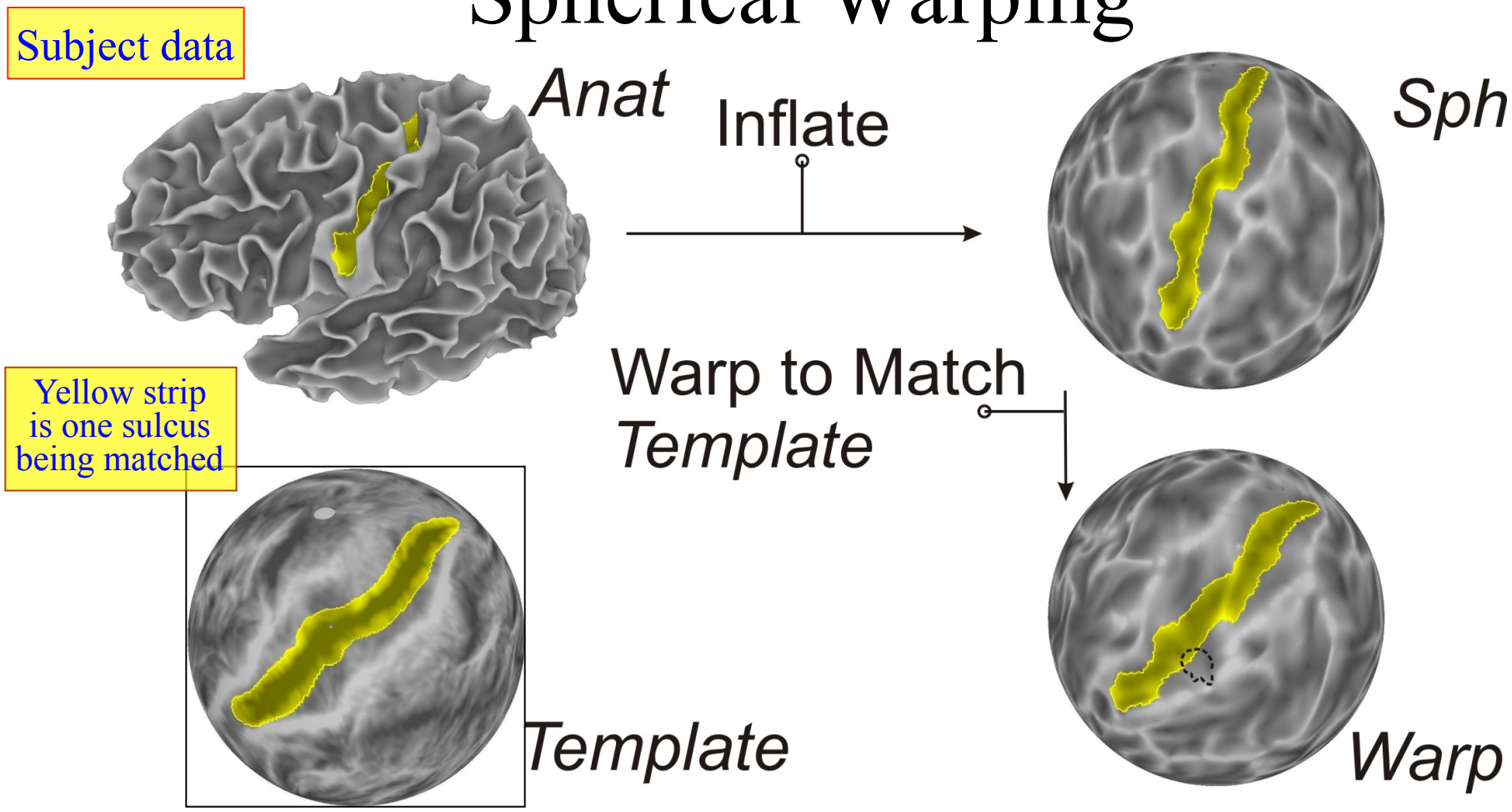
- Group analysis requires data defined over a spatial domain common to all subjects
  - ★ Talairach space for volume-based analysis
    - ★ With low order registration
      - \+ Small amount of geometric distortion
      - \- No respect for topology of activation
    - ★ With high order registration
      - \+ 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 <u>Good</u> in general and crucial for
  - ★ Retinotopy
  - ★ Plasticity
  - ★ High-resolution Mapping





Spherical Warping



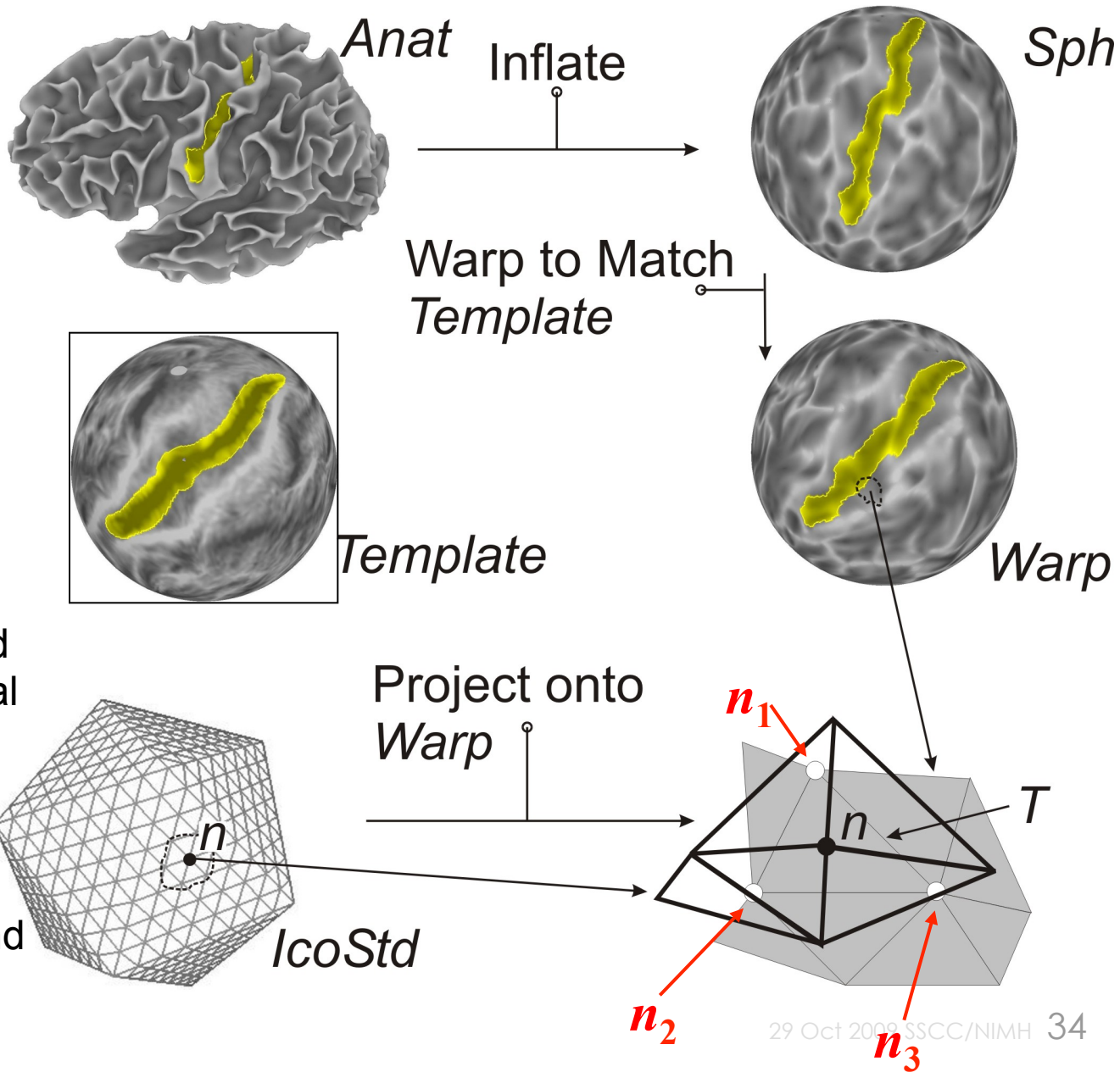
Surface-based warping (based on matching geometrical features like sulci and gyri) is more accurate than the more common low order Talairach volume-based analysis because it preserves the topology of the cortical sheet *and* uses more landmarks for the warping

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

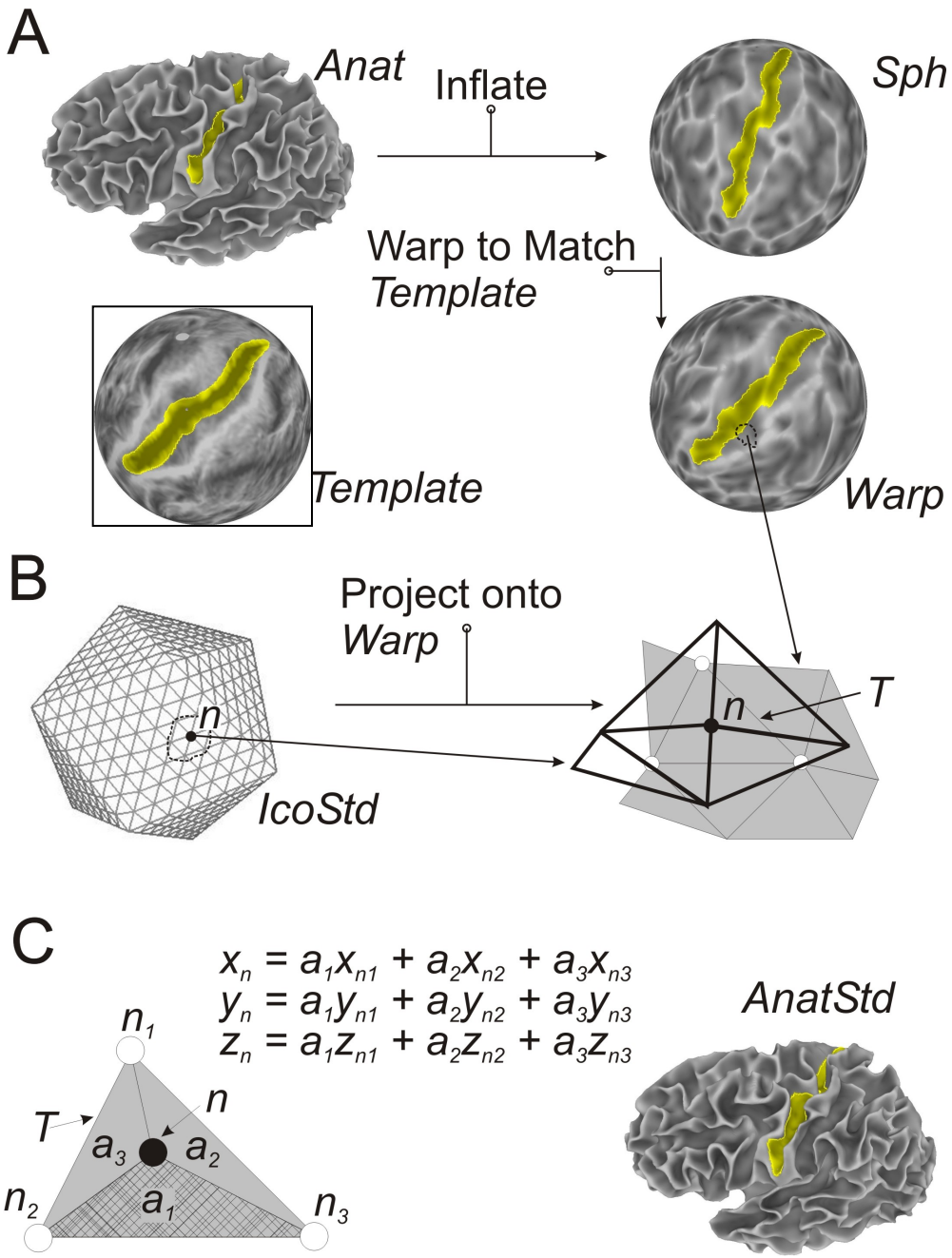


Our Way

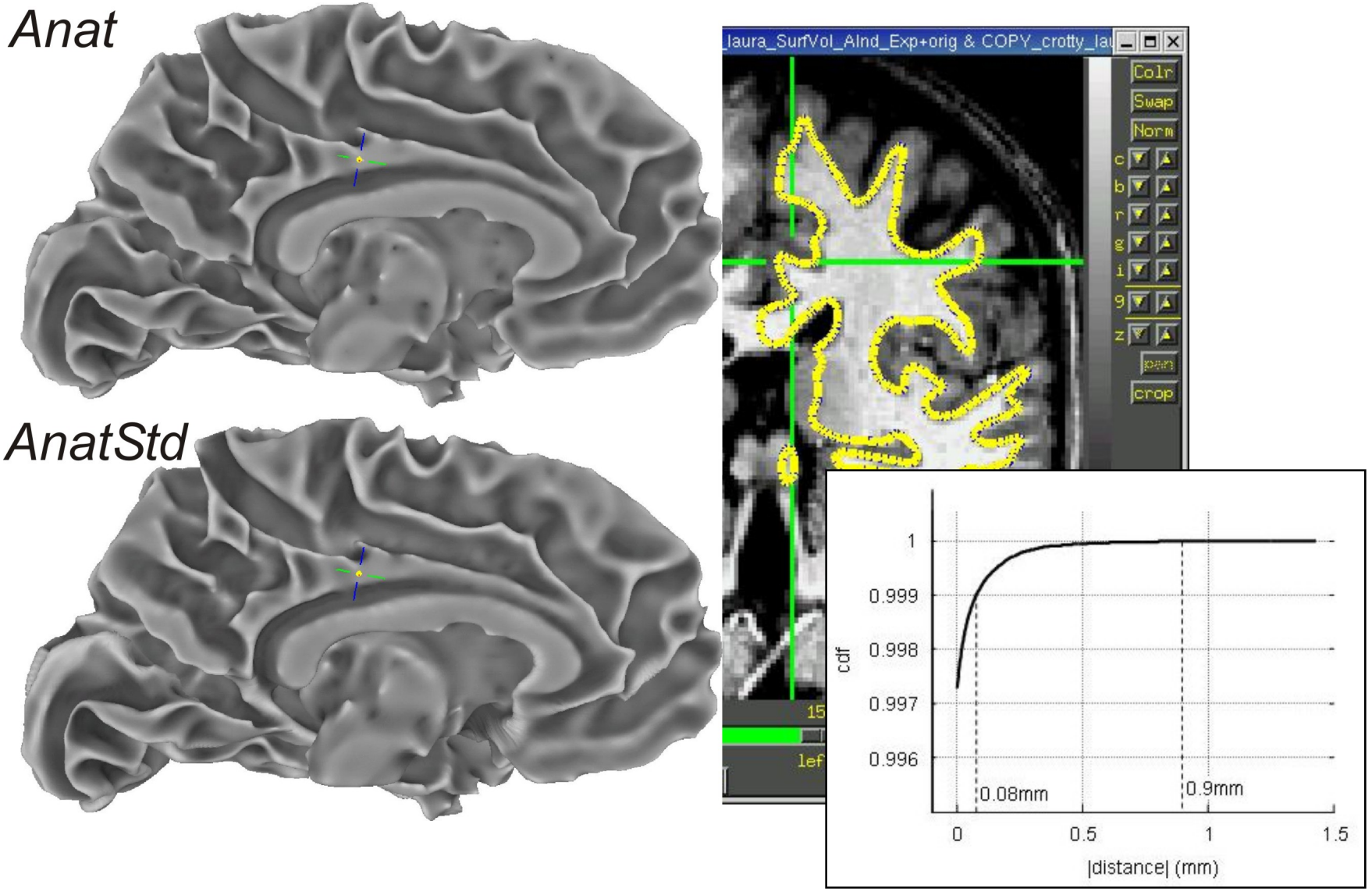
Instead of interpolating data values to the icosahedral nodes, interpolate using the coordinates of the original surface's node.

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

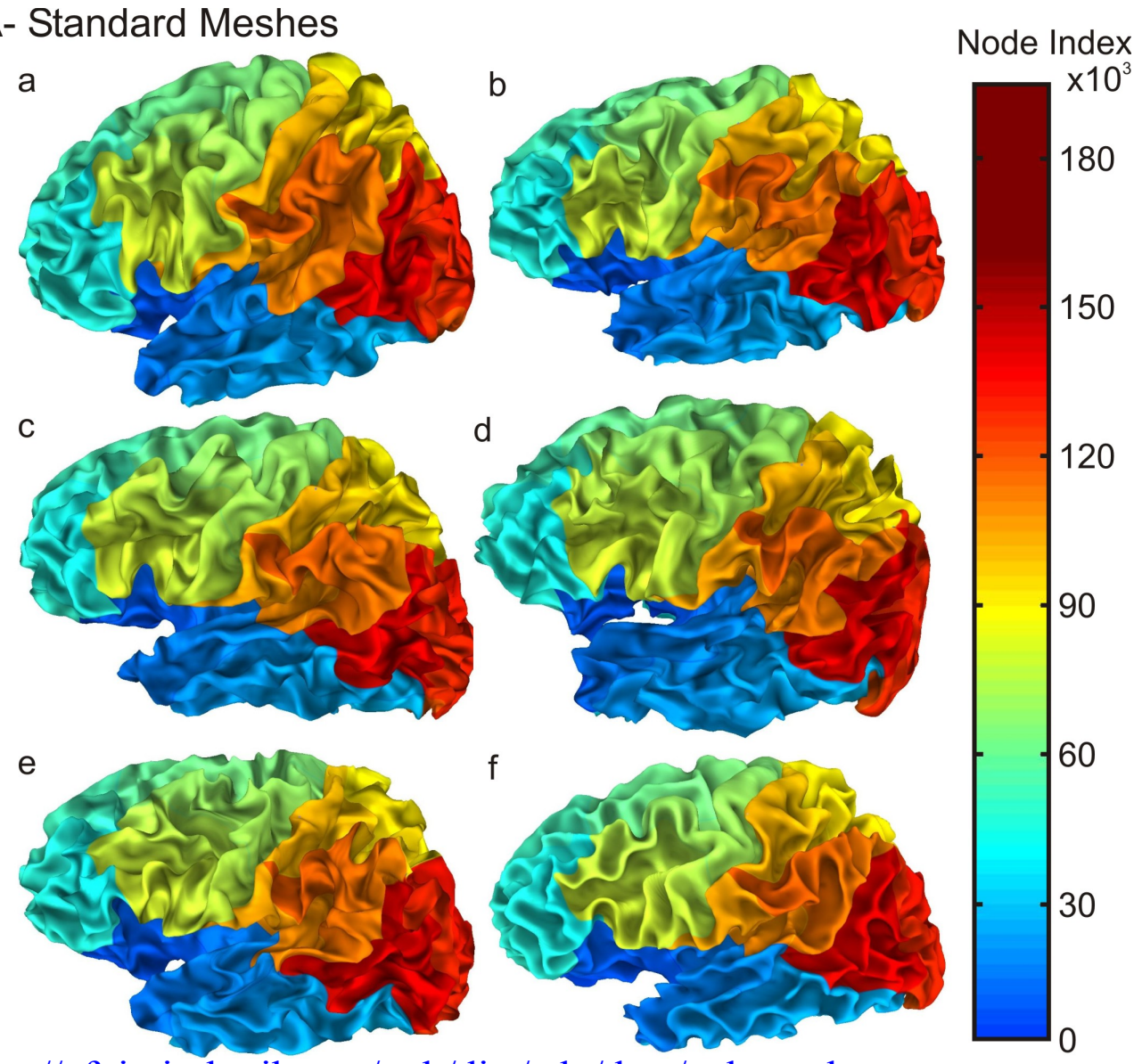


Compare surfaces: Original and Standard



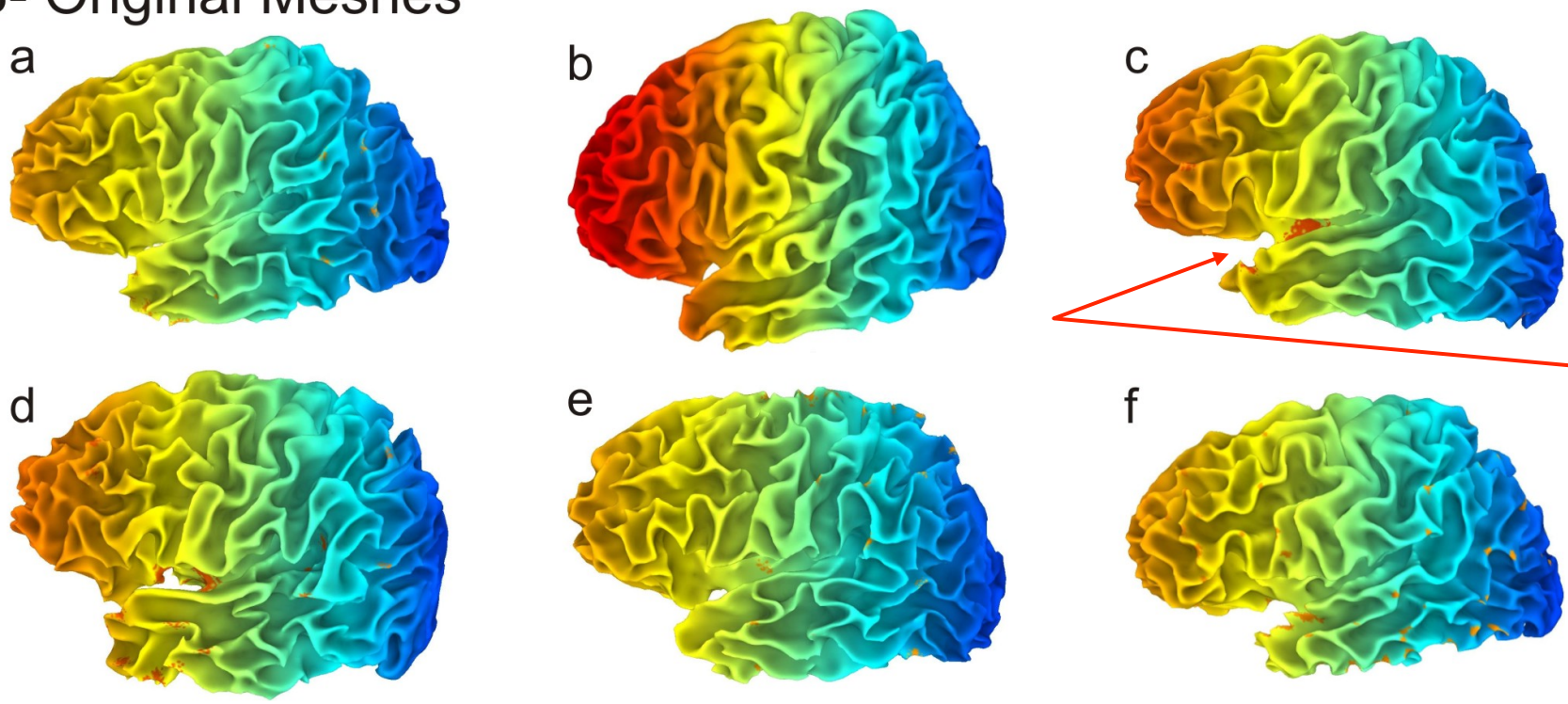
Standard meshes for 6 subjects

- 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: tcsh run_stdmesh_demo

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.

$Nv = 2 + 10n^2$ (198812 vertices)

$Nt = 20n^2$ (397620 triangles)

$Ne = 30n^2$ (596430 edges)

-prefix: prefix assigned to standard mesh surfaces

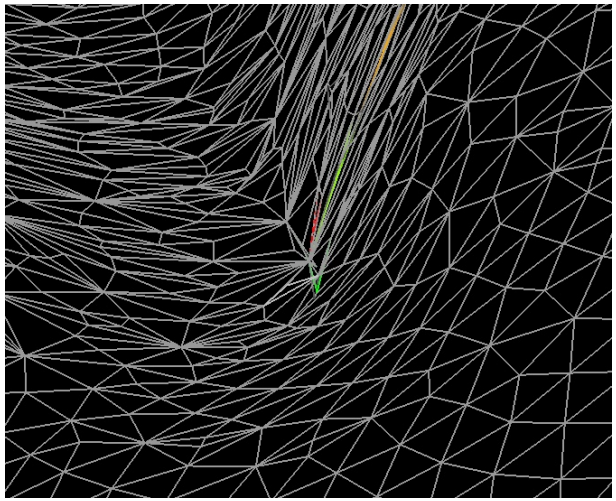
- @SUMA_Make_Spec_FS now generates standard-mesh surfaces by default. See @SUMA_Make_Spec_FS –help for details.
- Script *run_stdmeshes* was used to generate standard-mesh surfaces for the hands-on material

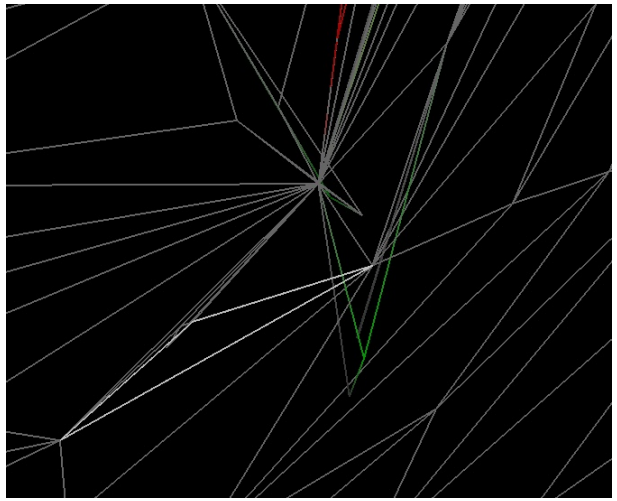
Using Standard-Mesh Surfaces

- 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

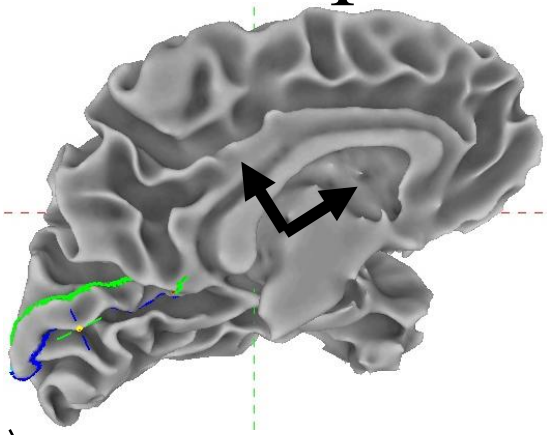
- In the past, there have been localized distortions between the standard-mesh surface and the original surface.
- These had **all** been caused by topological errors in the original spherical surfaces.
- SurfQual was written to highlight these errors
  - ★ if causing distortions, errors must be fixed 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



SurfVol
Surface Volume

Anatomically correct surface

@SUMA_AlignToExperiment

SurfVol_Alnd_Exp
(SurfVol Aligned to ExpVol
W/ Alignment Xform)

ExpVol
Experiment Volume

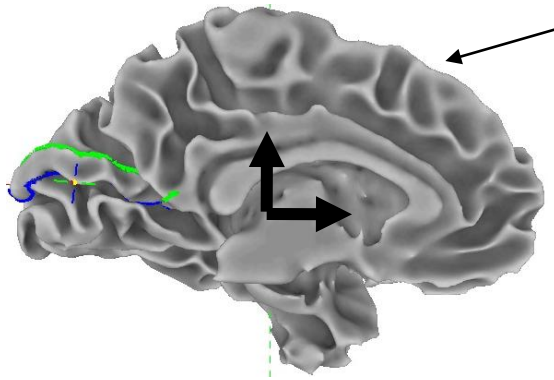
Apply Alignment Xform

Func. 1

Func. 2

Func. *N*

AFNI



Cortical Surface Aligned to 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_Alnd_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_Alnd_Exp+orig &

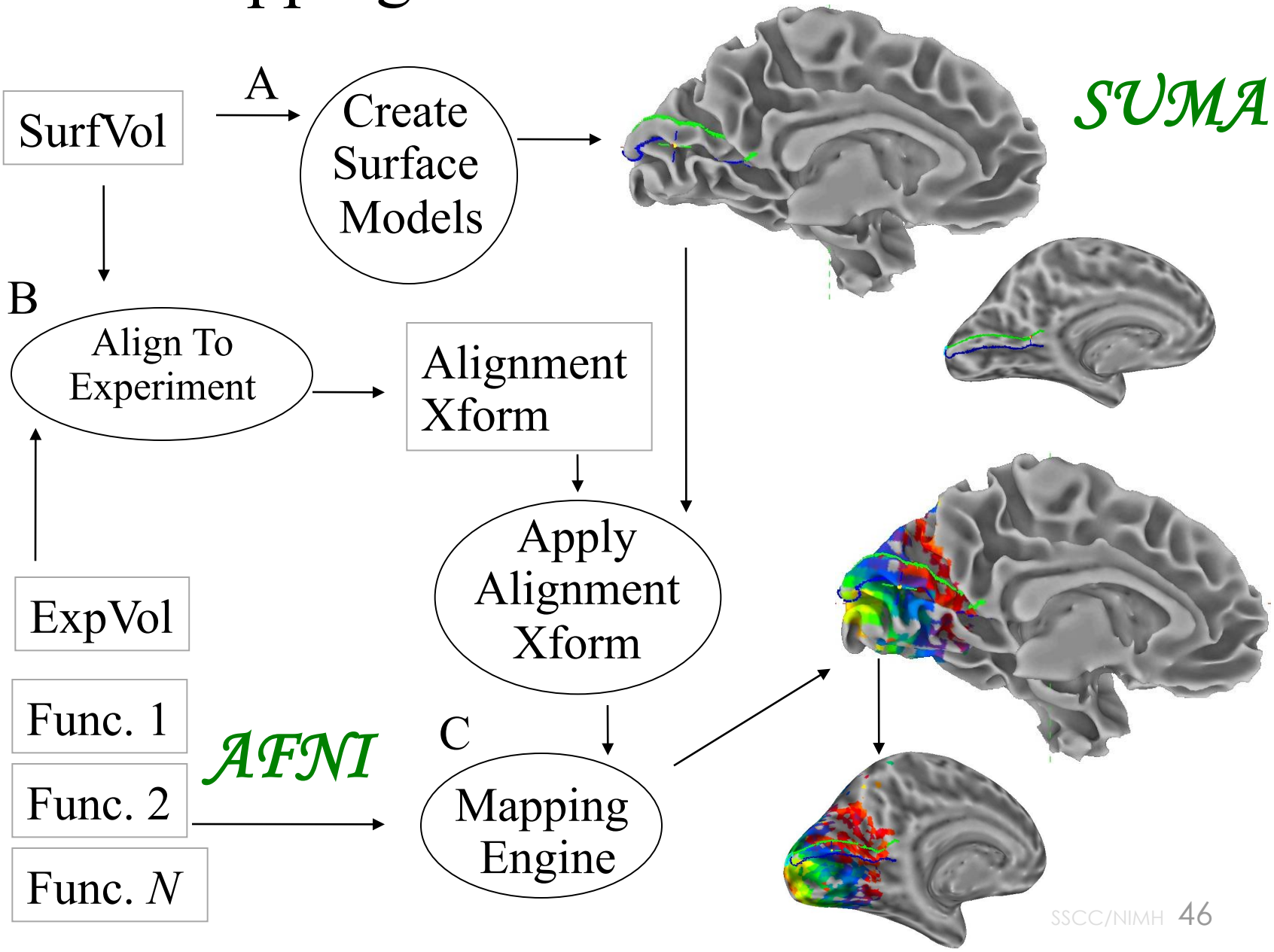
➥ or execute the script: *tcsh run_suma*

Press '**t**' to talk to AFNI

➥ You should see a surface overlaid onto DemoSubj_SurfVol_Alnd_Exp+orig

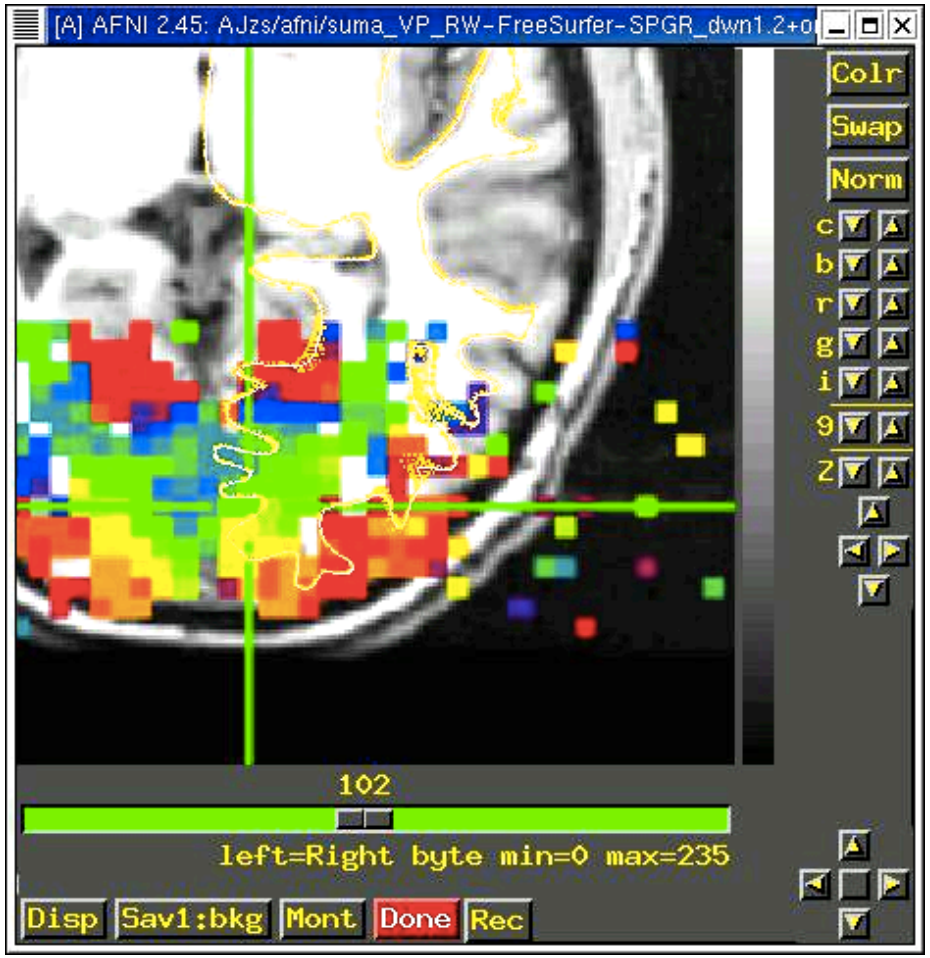
➥ Alignment should be proper, otherwise you have a problem.

C: Mapping FMRI Data Onto Surface

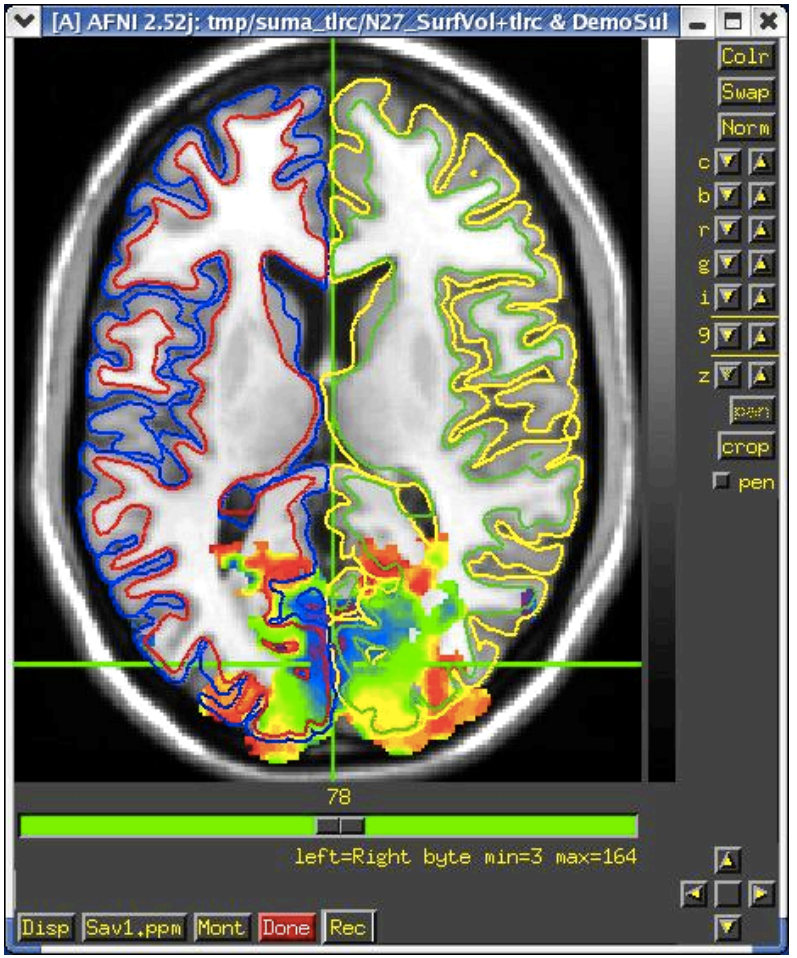


Mapping Options

- Surface/volume Intersection



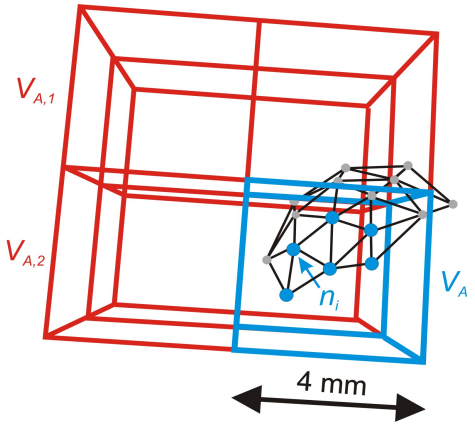
- Shell/volume Intersection



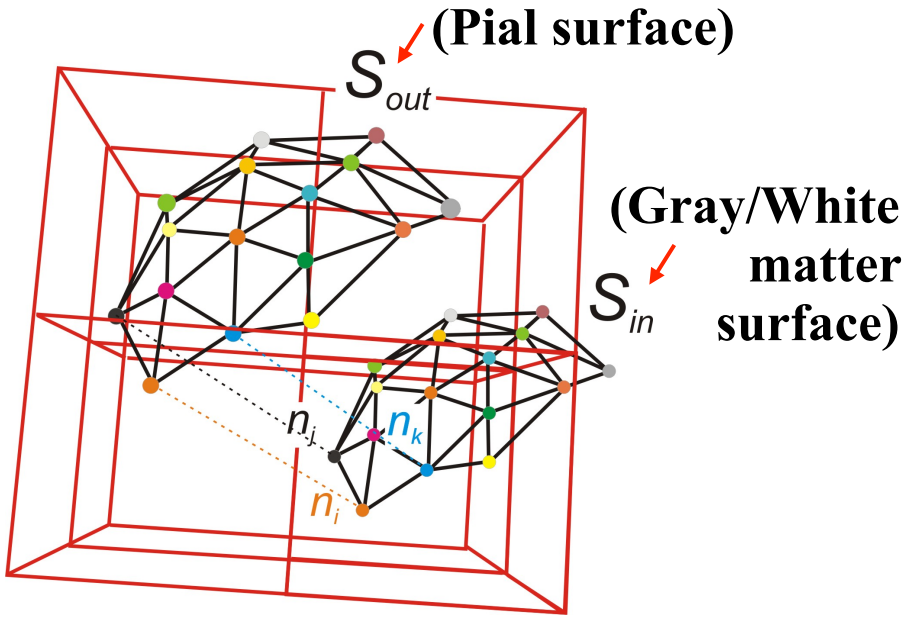
Mapping options

- Surface/volume Intersection
  - ★ One voxel per node

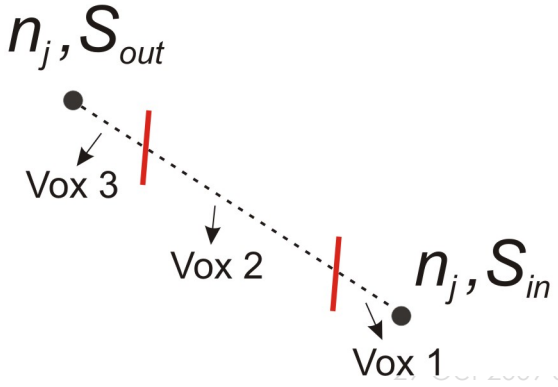
  (whatever voxel that node lies inside of)



- 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 3d*XXX* 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

Hands-On

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_Alnd_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

Hands-On

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 progams)
  - 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)

A trivial cross-subject analysis

- Calculate the mean value at each node from 3 subjects:

```
1deval  -a 'DataSurf_s1.1D.dset[6]'        \
        -b 'DataSurf_s2.1D.dset[6]'        \
        -c 'DataSurf_s3.1D.dset[6]'        \
        -expr '(a + b + c) / 3'            \
        -index 'DataSurf_s1.1D.dset[0]'  > DataSurf_mean.1D.dset
```

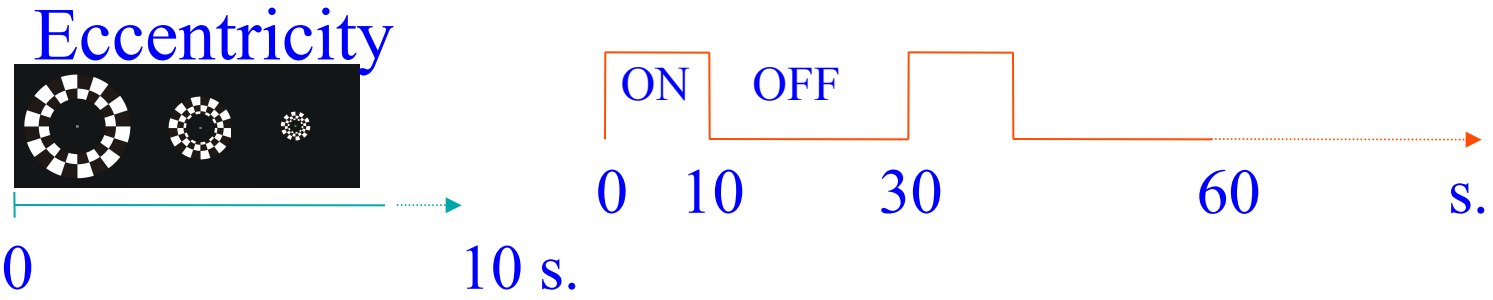
- 1deval works much like 3dcalc but with 1D files
  - -index option allows the addition of an index column (node indices) to the output.
  - DataSurf_mean.1D.dset will contain 2 columns: node index and mean value
- Appreciate why we forced an output for all node indices
- Things to be careful about:
  - ★ 1D files do not explicitly encode domain information
    - ➥ Up to you to make sure that the i^{th} entry in all 1D files corresponds to the same node.
    - ➥ You must have the same number of values in all files

Full versus Sparse Datasets

- Sparse dsets contain entries for a subset of surface nodes
  - Efficient but can cause trouble in 3d* programs
    - Same row in two datasets may not correspond to the same node
- Full dsets contain entries for each surface node
  - Big files but safe for 3d* programs where row *i* has data for node *i* in all datasets.
  - ConvertDset's *-pad_to_node* converts a sparse dset to a full one.
  - See practical examples in run_ROIdump
  - Option *-pad_to_node* also available in ROI2dataset

Sample FMRI data: Eccentricity Mapping

- Scan Parameters:
  - ★ EPI: NIH-EPI, TR=2sec, 17 Coronal Slices, 134 samples, 3.75 x 3.75 x 4 mm
  - ★ Anat: SPGR, 0.94 x 0.94 x 1.1, 120 axial slices
- Stimulus Timing:

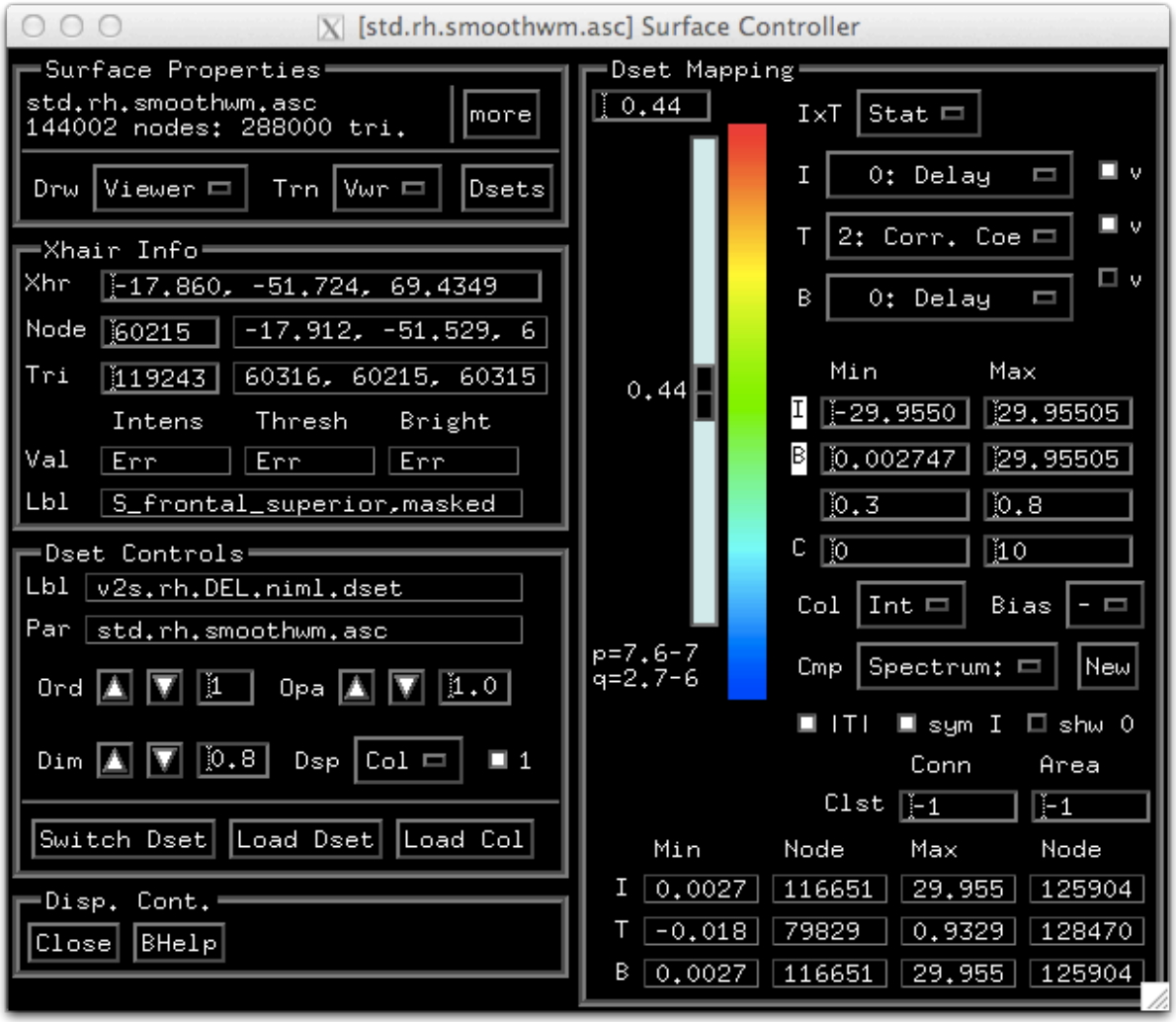


- Activation delay estimated with 3ddelay
- Demo:
  - ★ Rotate color map in AFNI and watch changes in SUMA
    - ➥note how colors progress along the calcarine sulcus
    - ➥try the dance on inflated and spherical surfaces

Surface-based Datasets (Dsets)

- These datasets form matrices with one column representing the node index (*ni*, a.k.a node id) followed by *k* values (*i_val. 0 … i_val. k-1*) associated with each node.
- Those *k* values can potentially be any assortment of parameters, though some dataset formats will be limited.
- In some instances, the node index column may be missing and the node's index is assumed to be equal to the row index.
- Unlike its volumetric counterpart, the domain over which the data are defined is not implicitly defined in the dataset.
  - ★ Such a dataset alone cannot be visualized without specifying its surface domain (location and connectivity of the nodes).
- Dsets can be colorized interactively (the fun way) using SUMA's Object (used to be Surface) Controller interface
  - ★ or offline using ScaleToMap
- A colorized dataset is called a "color plane" in SUMA

Colorizing Results Interactively

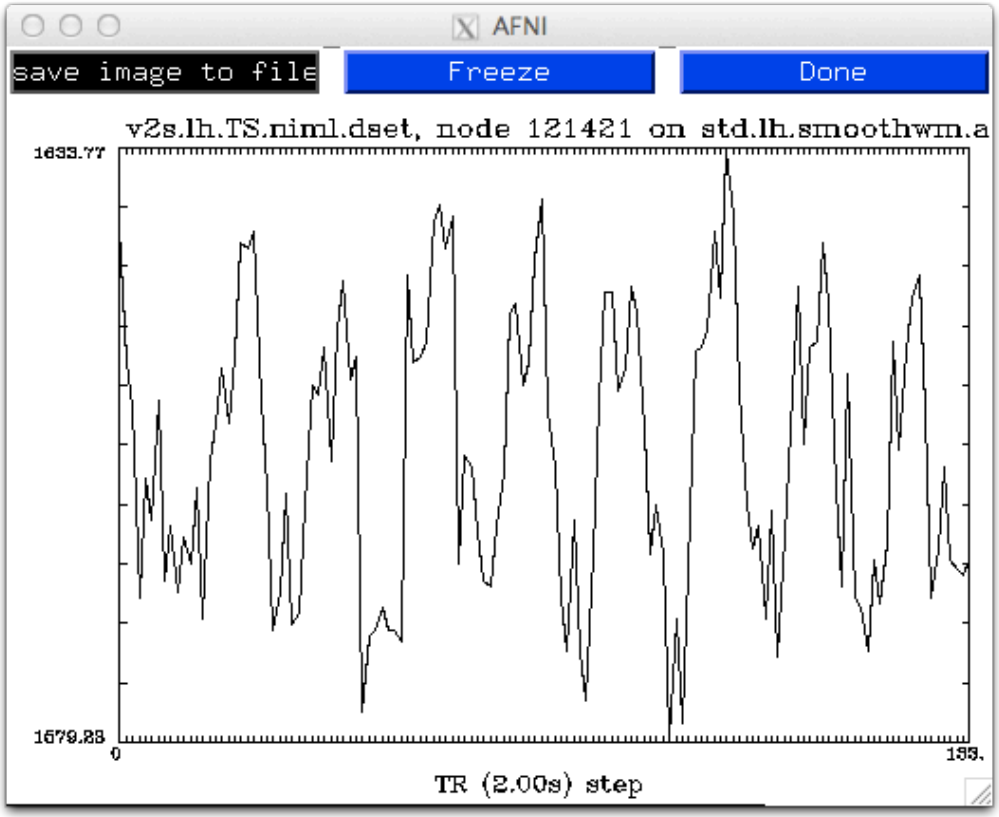


- Demo *(continued):*
  - ★ In SUMA, press ‘ctrl+s’ to open Object Controller.
    - ➥Use View→Object Controller if you were born after 1981.

Hands-On

Graphing Time Series

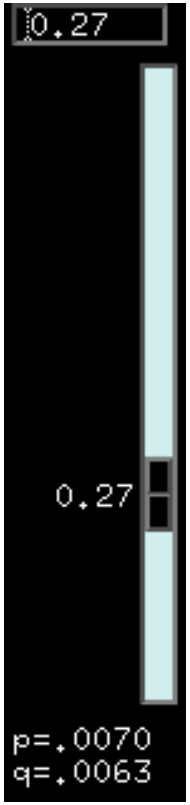
- Demo *(continued):*
  - ★ Press "Load Dset" and read in "v2s.lh.TS.niml.dset"
    - ★ Contralateral dataset, if sanely named, gets automatically loaded too
    - ➥ In SUMA, press '**g**' to graph data points at the selected node
    - ➥ Select other nodes (or right-click+drag) to see data at other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



Hands-On

Colorizing results interactively

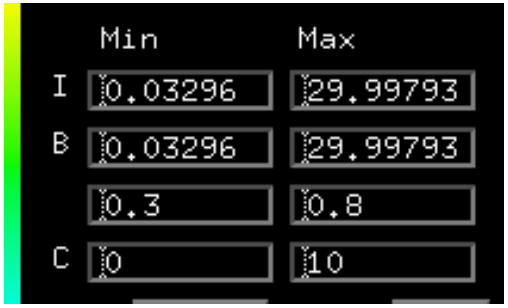
- Demo *(continued):*
  - ★ Press "Load Dset" and read in "v2s.lh.DEL.niml.dset"
    - ➥ SUMA will colorize the loaded Dset (create a color plane for Dset) and display it on the top of pre-existing color planes.
    - ➥ We begin by describing the right side block "Dset Mapping" which is used to colorize 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.

Hands-On

Dset Mapping block



- 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 < min then v = min**
  - ★ Column **Max**:
    - ➥Maximum clip value. Clips values (v) in the Dset larger than Maximum (max): **if v > max then v = 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

Hands-On

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

Hands-On

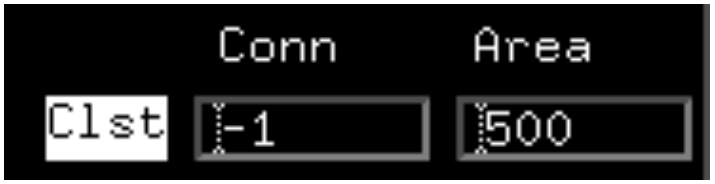
Dset Mapping block

- Demo *(continued):*
- **|T| :**
  - ★ Toggle Absolute thresholding.
    - ➥OFF: Hide node color for nodes ‘n’ that have:
      T(n) < Tscale
    - ➥ON: Hide node color for nodes that have:
      |T(n)| < Tscale

  where: Tscale 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

Hands-On

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.

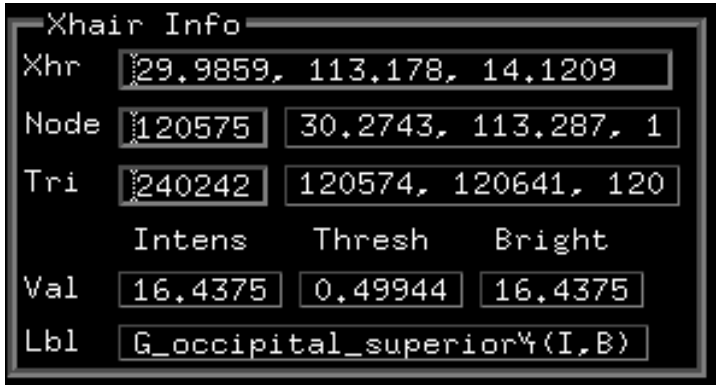
	Min	Node	Max	Node
I	0.0329	80378	29.997	109447
T	-0.024	115153	0.9420	111286
B	0.0329	80378	29.997	109447

- **Data Range Table:**
  - ★ Full range of values in Dset.
    - ➥ Right click in "Node" columns to have crosshairs jump to that node's location.
      - ➥ You might have to move the surface around to see where the crosshairs have jumped

Hands-On

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.

Hands-On

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 exits 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.

Hands-On

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.

Hands-On

Colorizing results with ScaleToMap:

- This step is **no longer necessary** with SUMA's new interface for colorizing
- Formerly: ScaleToMap was only way for getting node-based results into SUMA
- Execute: *tcsh run_ScaleToMap*
- *ScaleToMap -input v2s.lh.DEL.1D.dset 0 6 *
  *-cmap afni_p20 *
  *-apr 30 *
  *-msk -3.0 -0.1 *
  -nomsk_col > out_Del.1D.col
  - ★ -input : Specify the 1D format input file and the columns containing the node index and the node data
  - ★ -cmap : Specify the colormap to use.
    - ➥ Here we are using AFNI's standard colormaps (positive, 20 colors).
    - ➥ Could use your own colormaps, see MakeColorMap
  - ★ -apr: AFNI positive range value.
    - ➥ Scaling a là AFNI, other scaling methods that do not require 0 → range or –range → range are also available
    - ➥ When data are integer valued (such as ROI datasets), you can use a direct mapping where a node with value i gets mapped to the ith color in the map.
  - ★ -msk: Mask data values in the specified range (inclusive)
  - ★ -nomsk_col: Do not color masked nodes (default is a dark gray).
    - ➥ You can specify your own mask color
  - ★ The output of ScaleToMap goes to stdout, which can be redirected with ' > ' symbol to a text file

Viewing a color file in SUMA

- A color file, such as ScaleToMap's output out_Del.1D.col is of the format:

#Node_Index	R	G	B
23	0.3	0.8	0.6
127	0.8	0.91	0.12
...	...	....	...

- You can load it into SUMA with the '**c**' key or 'Load Col'
  - ★ The color data is loaded into a new dataset (Dset) of the type RGB. No "Dset Mapping" block is available for RGB Dsets.
  - ★ The recently loaded Dset obscures planes below it because it has a default opacity of 1
    - ➥ We will discuss color plane opacity and order next.
      - ➥ Unlike AFNI, SUMA allows you to overlay multiple datasets in color at the same time

Color overlay planes

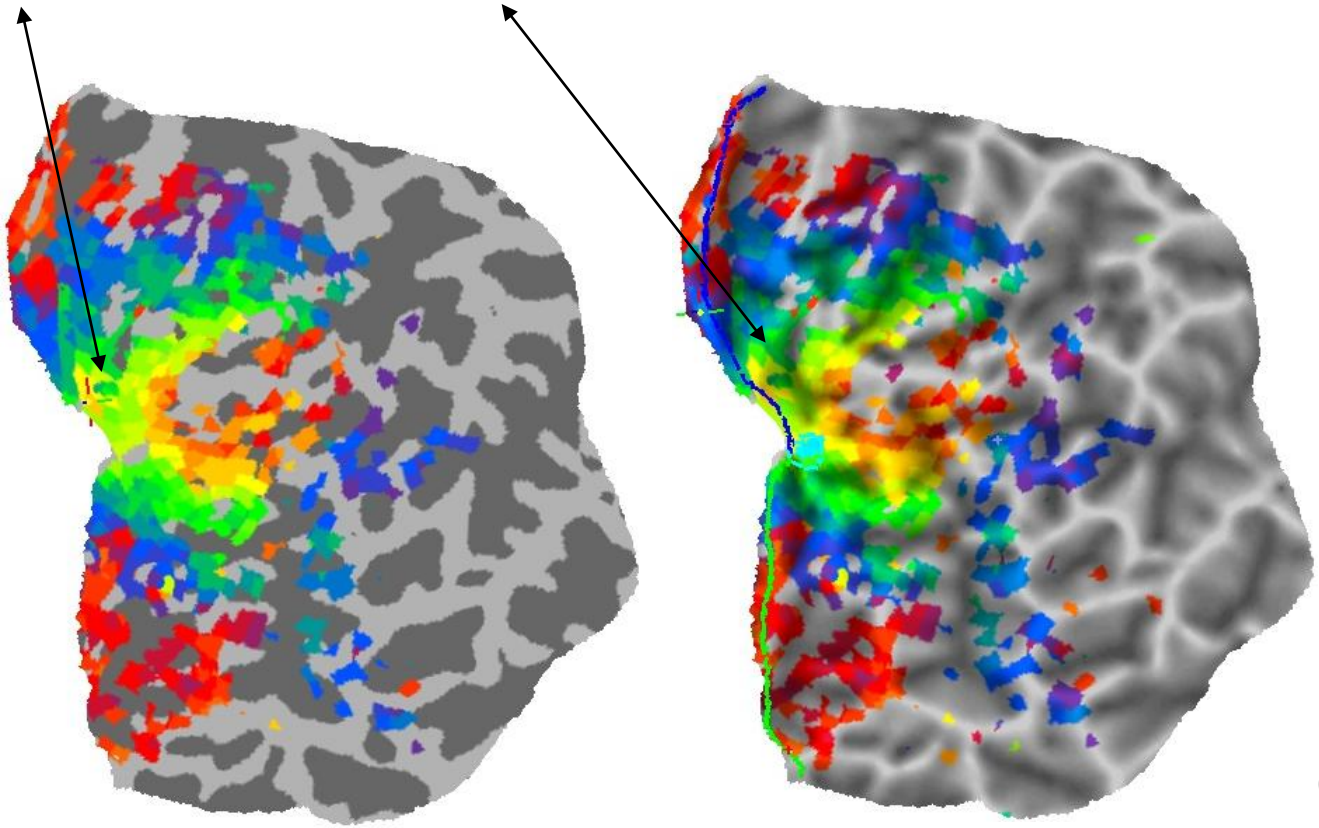
- Colorized Dsets are organized into layered color planes
  - ★ 2 commonly used planes are:
    - ➥ Surface Convexity (usually in gray scale)
    - ➥ AFNI Function (usually in color)
  - ★ Planes are assigned to two groups
    - ➥ Background planes (like Convexity)
    - ➥ Foreground planes (like AFNI 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

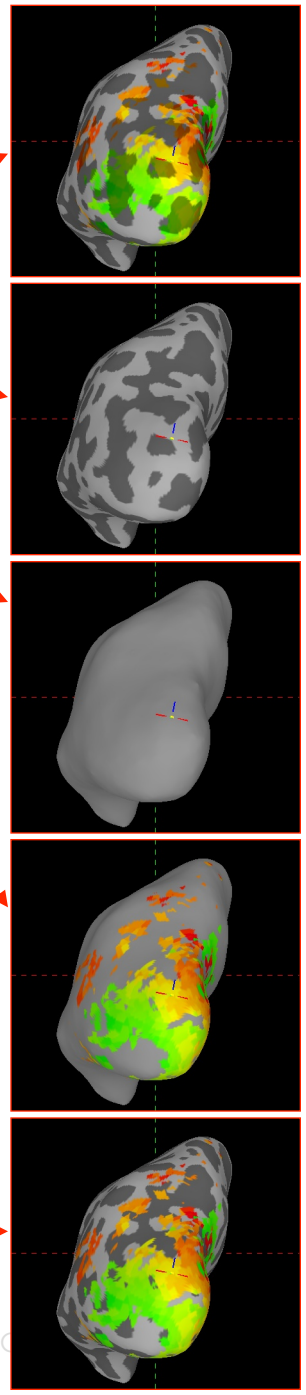
Color overlay planes

- 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

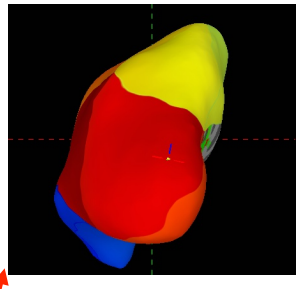
- Demo *(continued):*
  - ★ View an inflated surface with function from AFNI
  - ★ Turn foreground plane(s) off by pressing '**f**' once
    - ➥Now all you see is the background plane(s)
  - ★ Turn background planes off by pressing '**b**' once
    - ➥Now all you see is "No Color" color on all nodes
  - ★ 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.

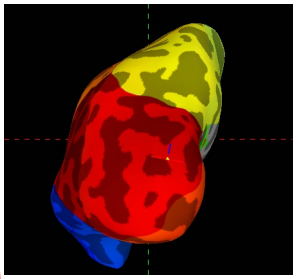


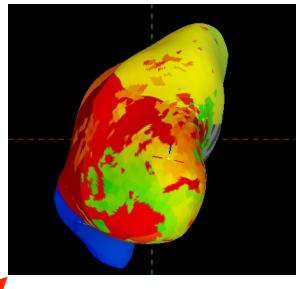
Hands-On

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







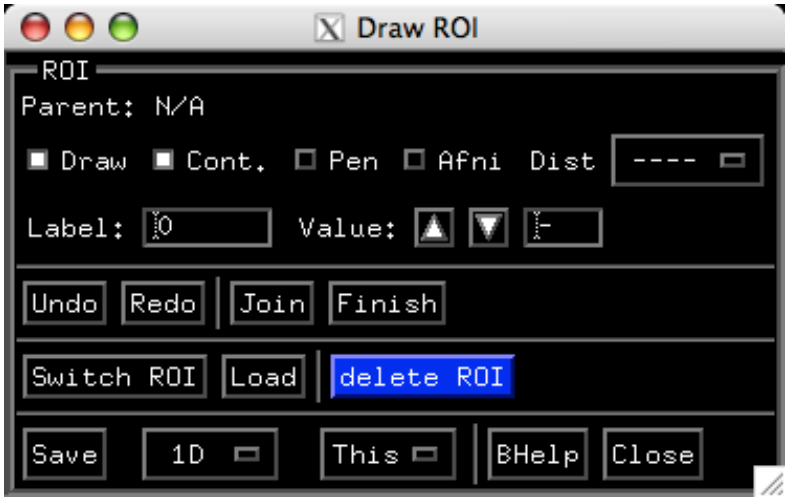
Playing with color plane order

- 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.

Hands-On

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

Hands-On

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.

Hands-On

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_Alnd_Exp+orig  \
            -grid_parent    DemoSubj_SurfVol_Alnd_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

Hands-On

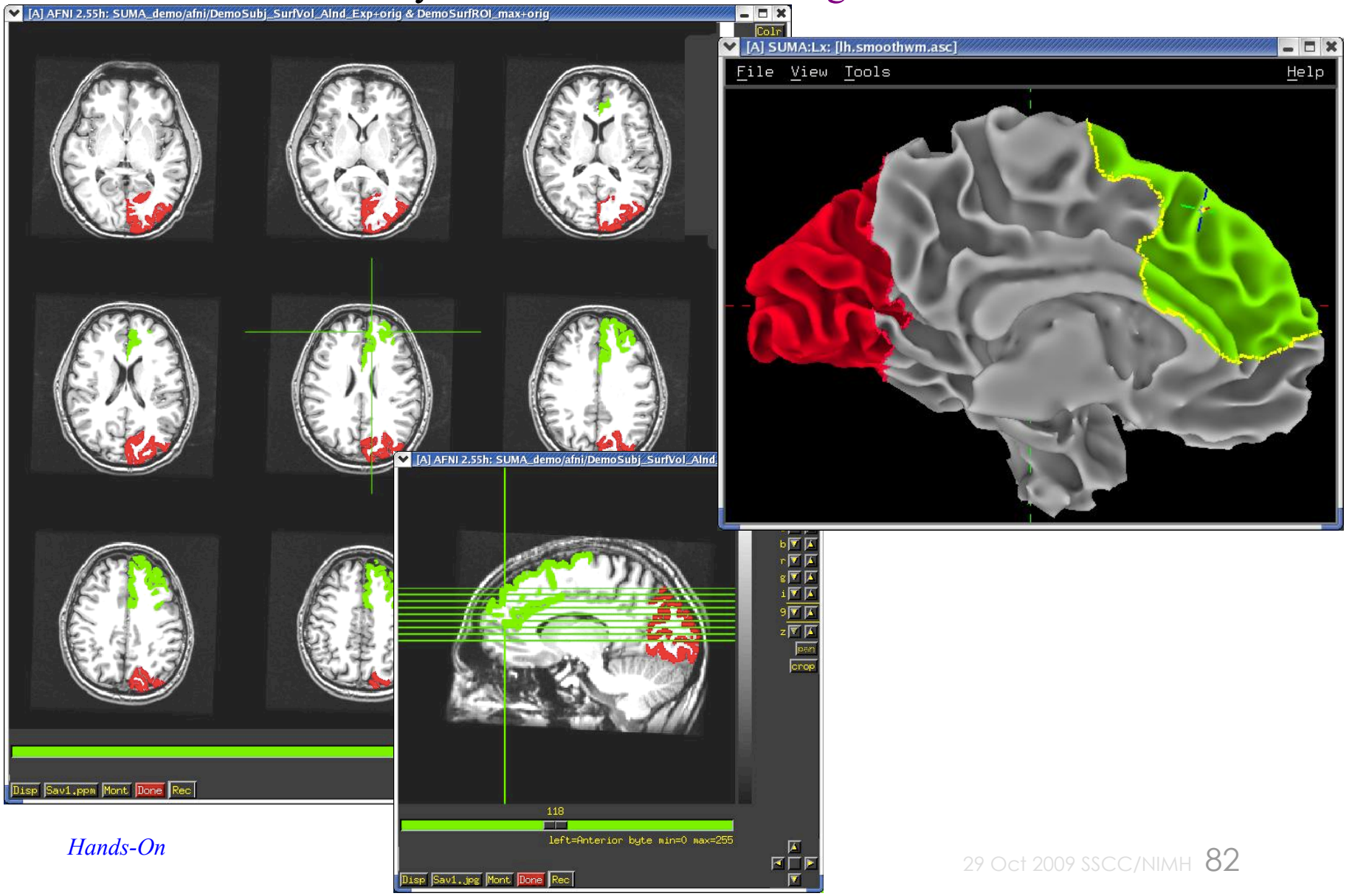
Surface ROI Utilities

- 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

Hands-On

Surface ROI → Volume ROI

check your own lh.OccROIs+orig in AFNI



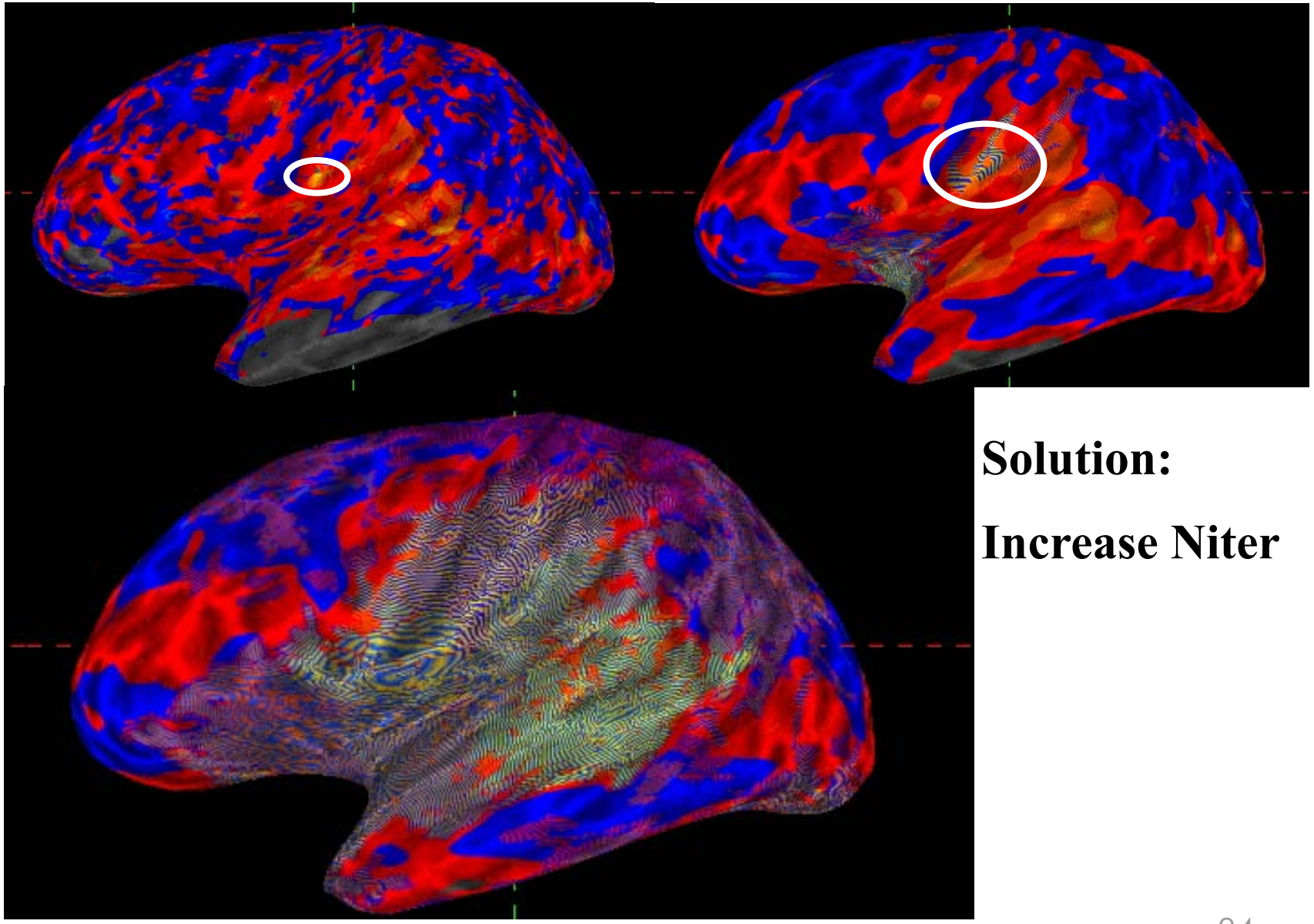
Hands-On

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 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.

Hands-On

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)

Hands-On

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

Hands-On

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 regresion 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

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

- CreateIcosahedron (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
- If you can't get help here, please get help somewhere.

Tracts in SUMA

- Tracts are generated by AFNI's FATCAT toolbox

FATCAT: **F**unctional **A**nd **T**ractographic **C**onnectivity **A**nalysis **T**oolbox (Taylor & Saad, 2013)

Tracts in SUMA

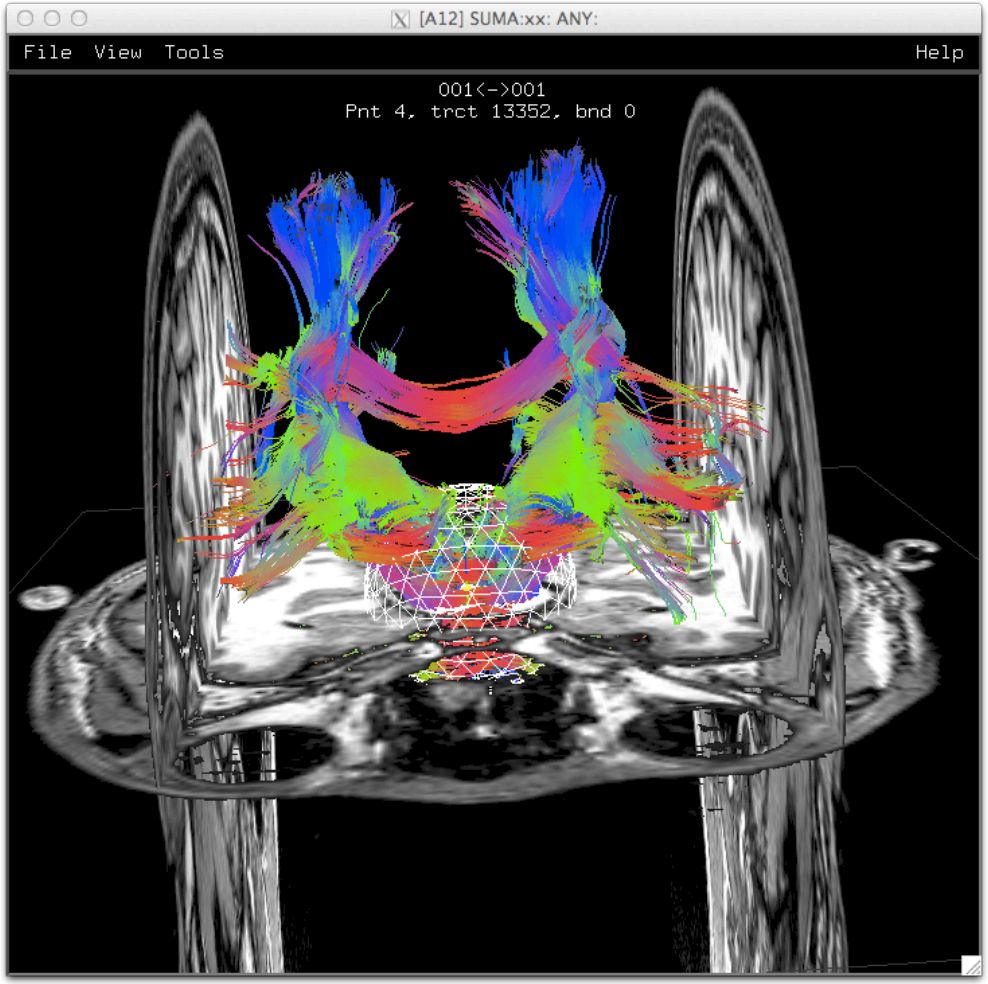
- Tracts are generated by AFNI's FATCAT toolbox
  - If using AFNI bootcamp data:
    - cd ~/AFNI_demos/FATCAT_DEMO

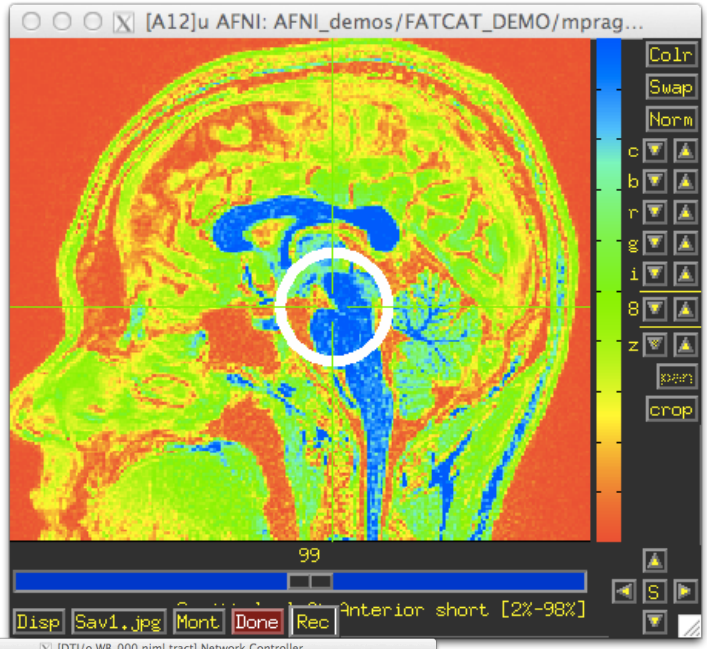
  Else
    - Run @Install_FATCAT_DEMO for demo data and scripts
- If you have not done so already
  - Process everything with tcsh Do_00_PRESTO_ALL_RUNS.tcsh
- To look at whole brain tracts
  - tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

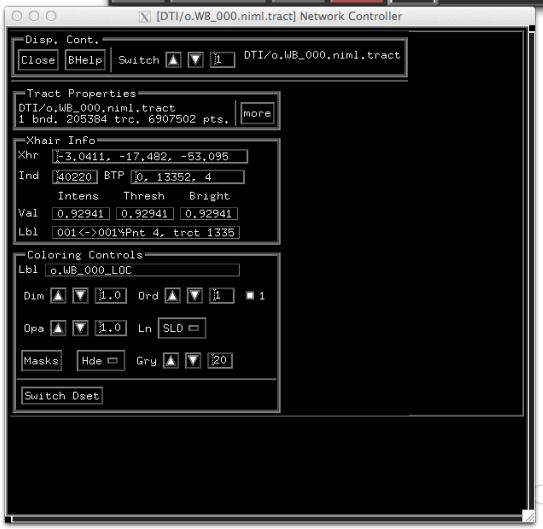
FATCAT: **F**unctional **A**nd **T**ractographic **C**onnectivity **A**nalysis **T**oolbox (Taylor & Saad, 2013)

tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

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

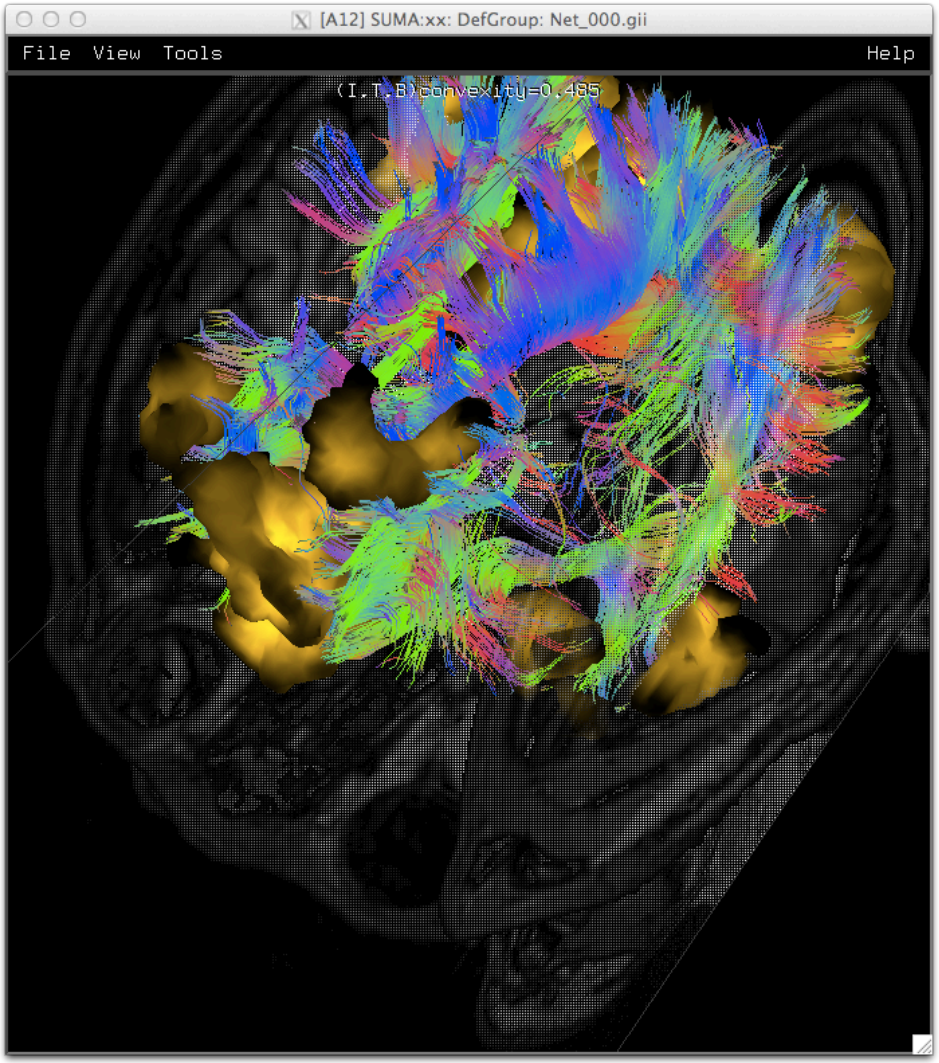


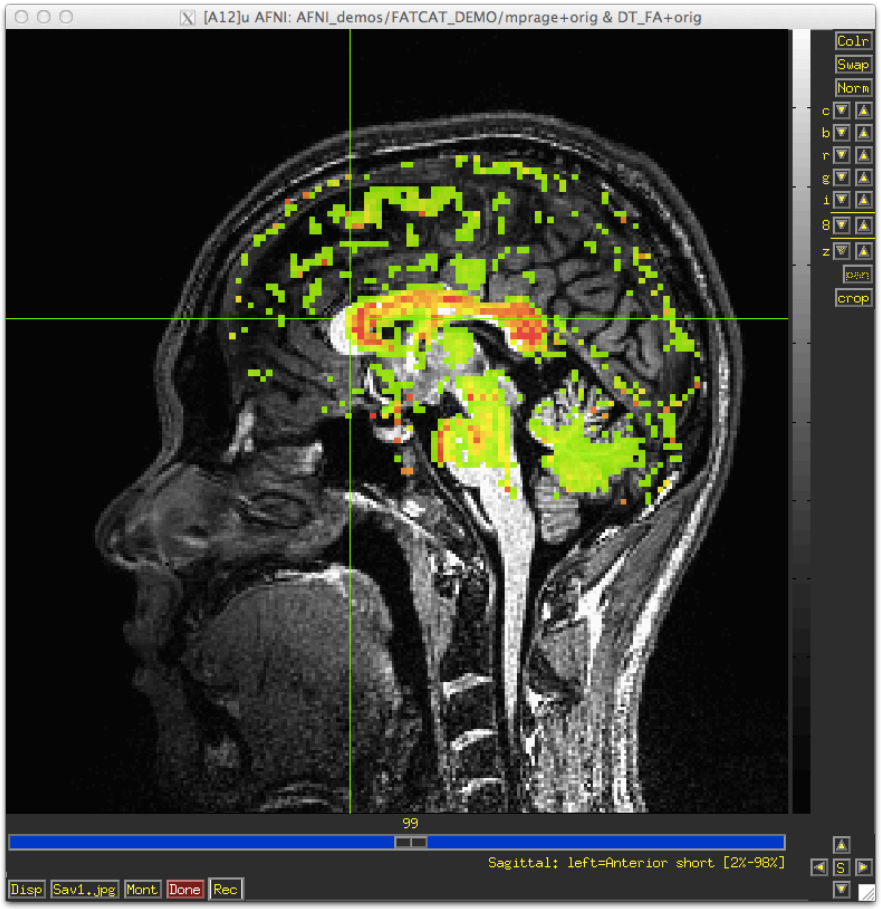




tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

- 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

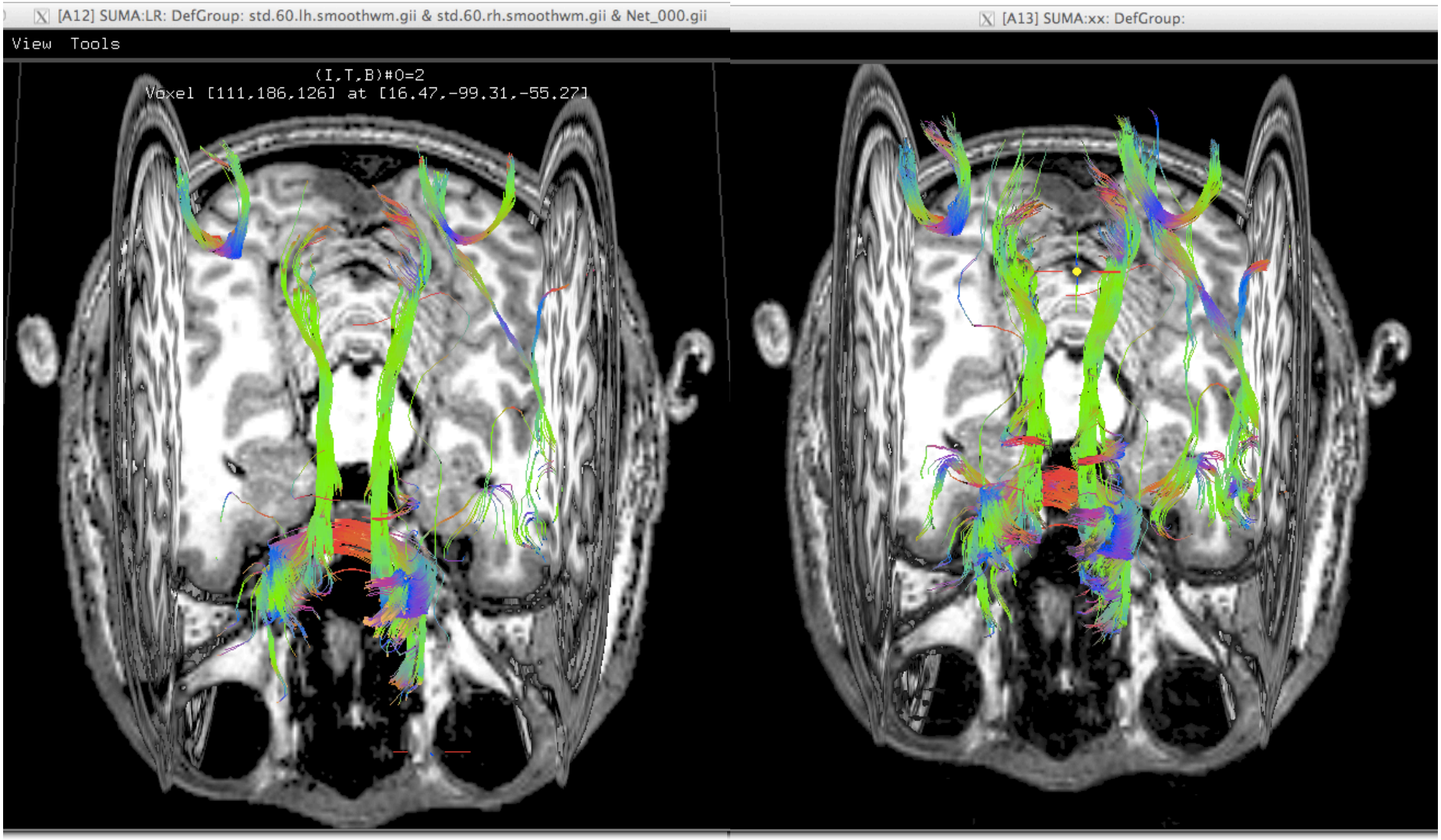
- Example 1: Follow prompt directions to produce something like this:

tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

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

Deterministic

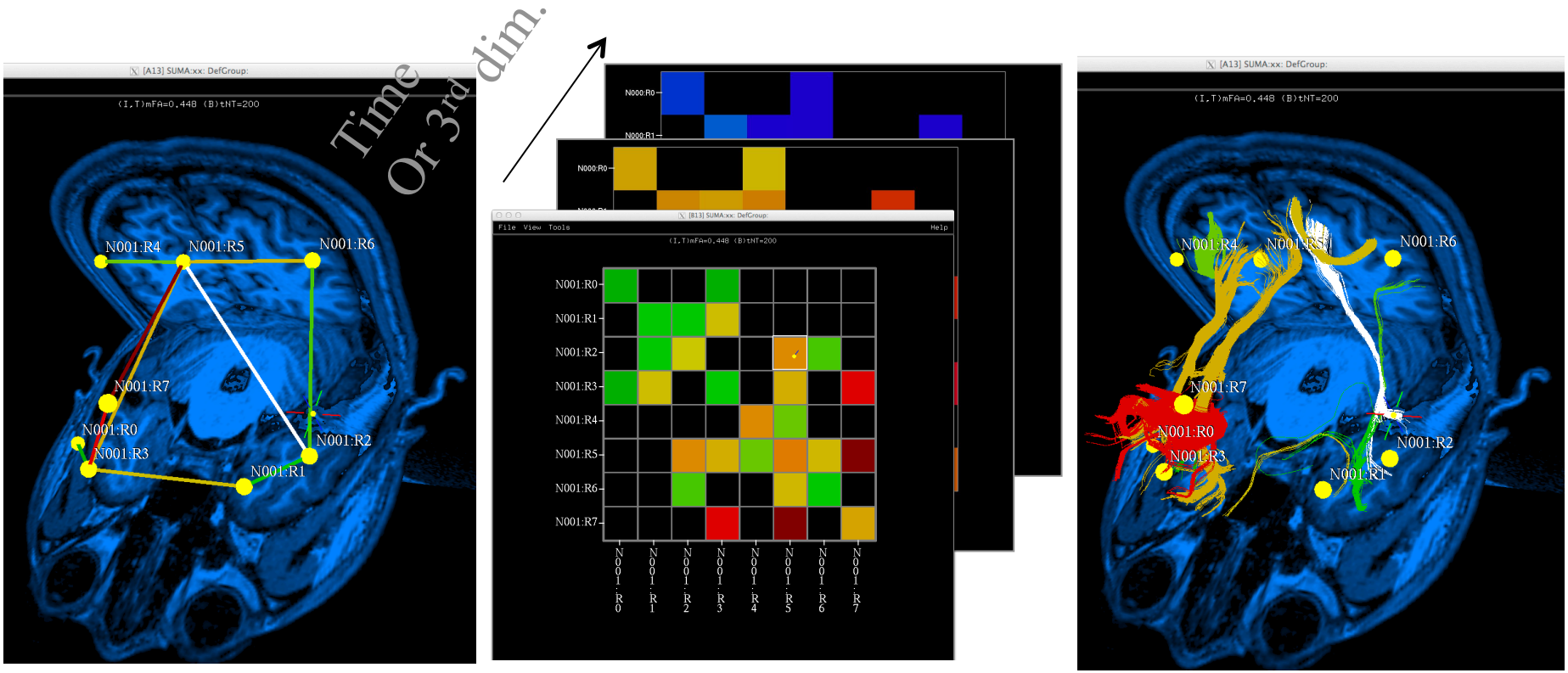
MINIPROB 9 iterations



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)

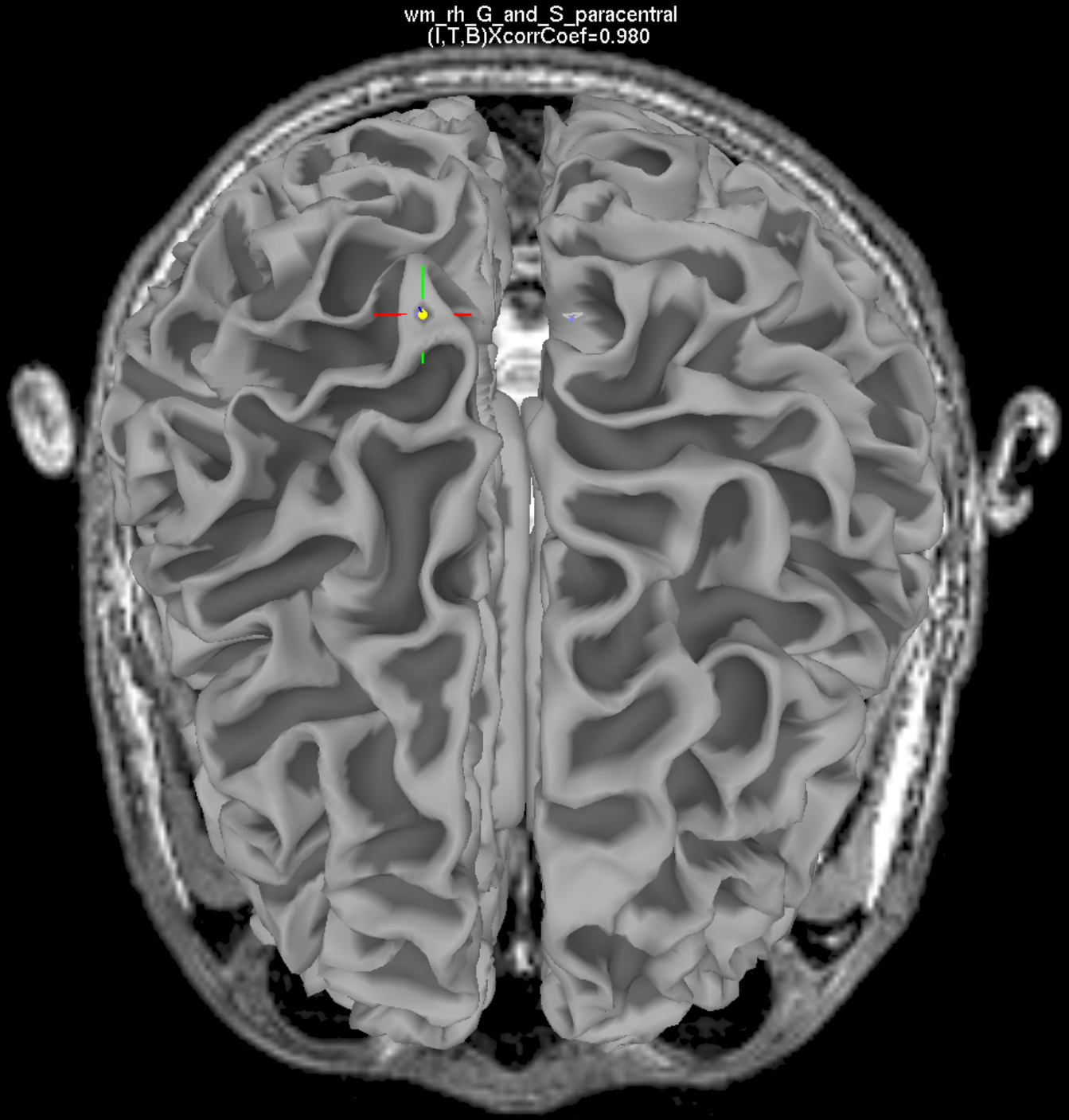


tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Simultaneous InstaCorr & InstaTract

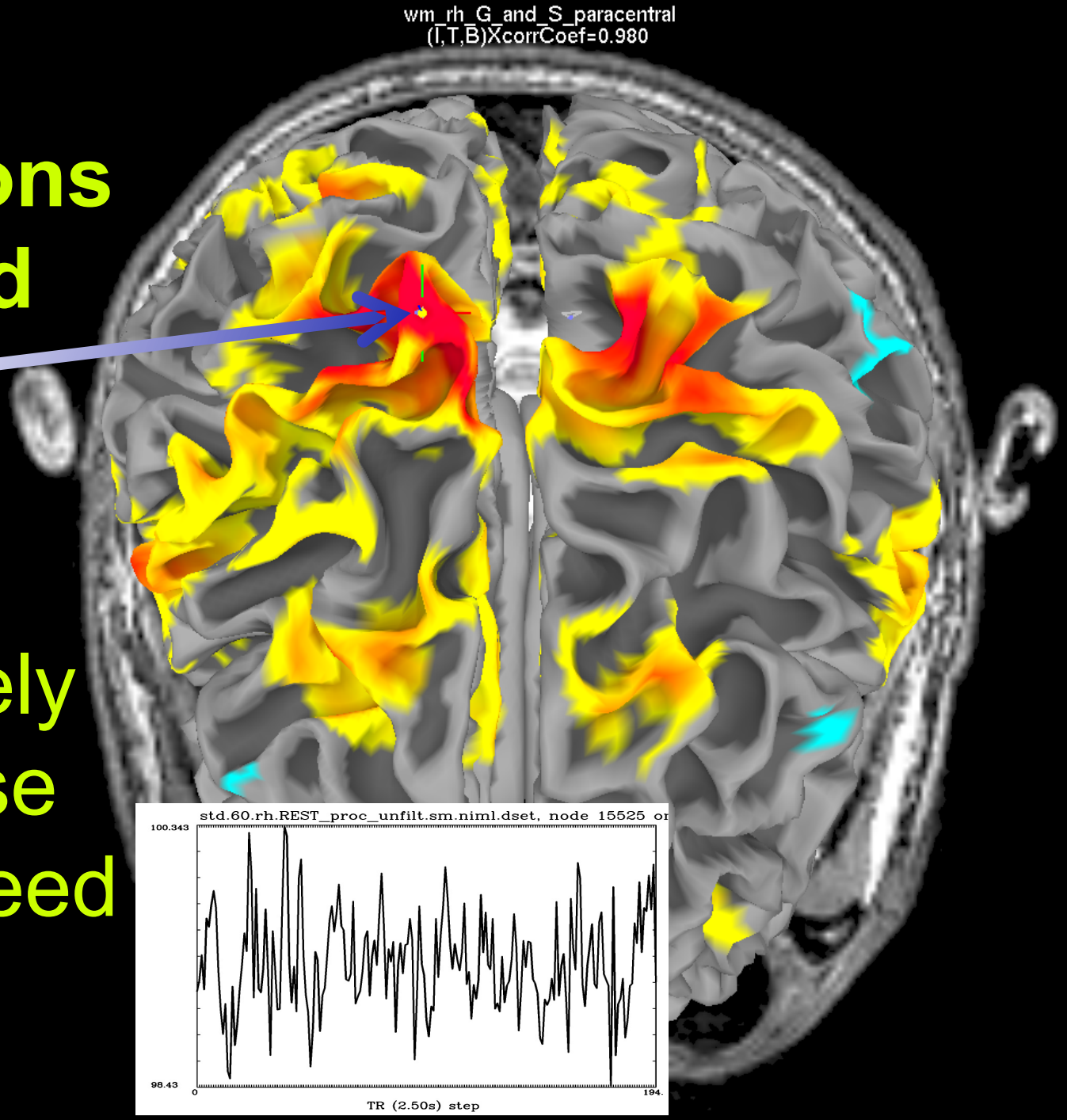
- Follow directions to do something like in the next bunch o slides

Naked brain surface



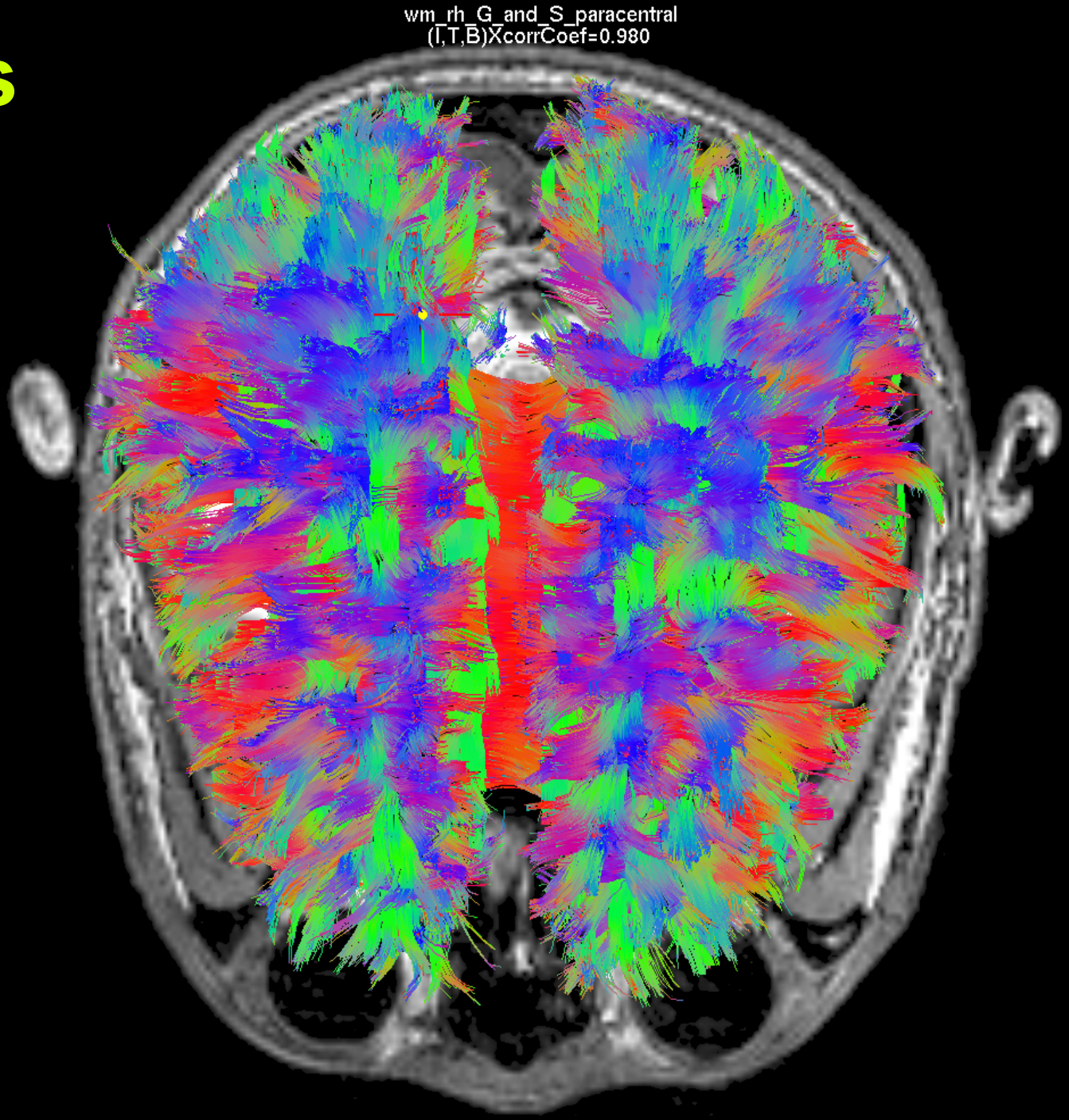
RS-FMRI correlations from seed voxel

computed interactively with mouse click on seed



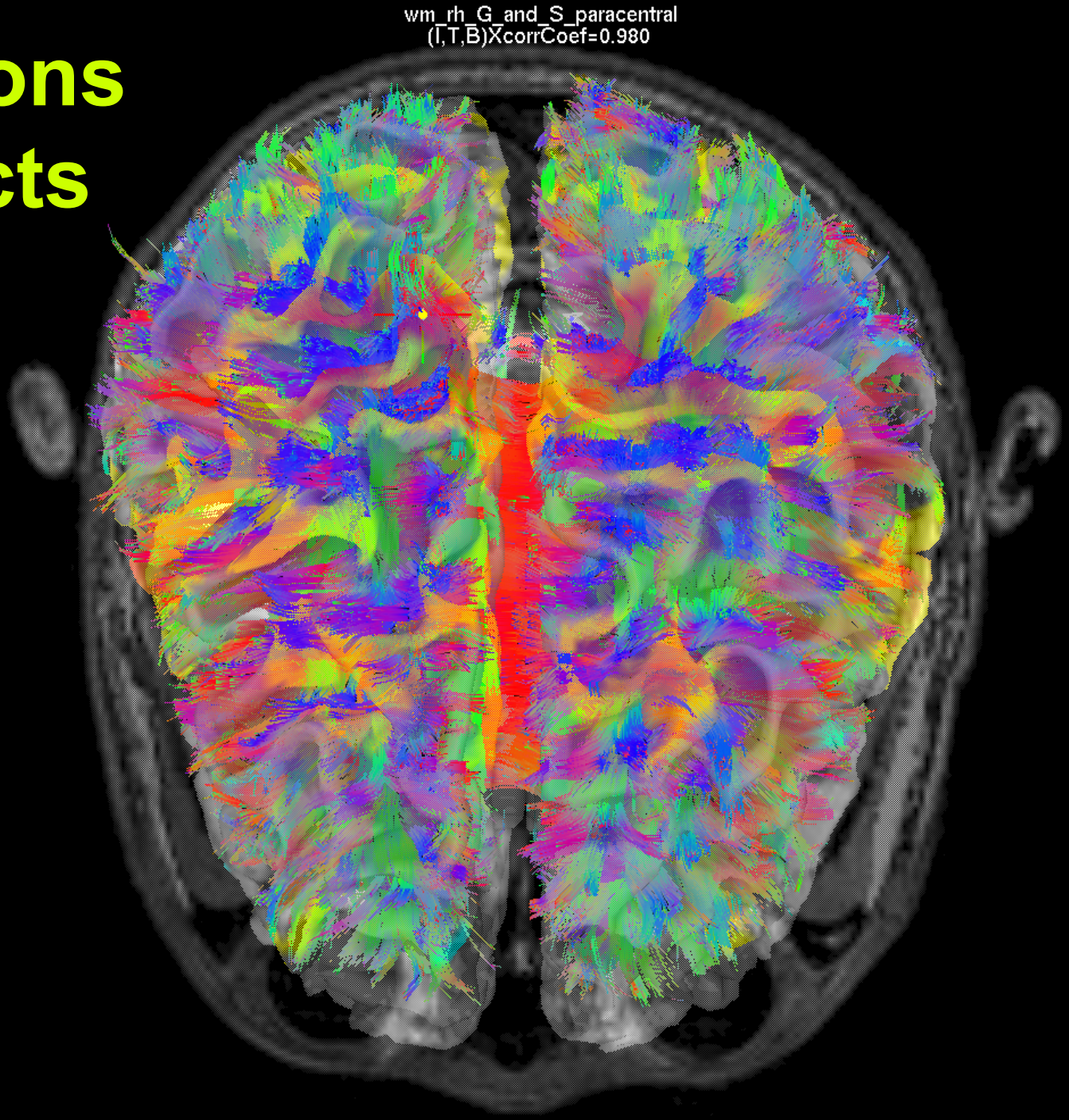
DTI tracts
[brain is hidden]

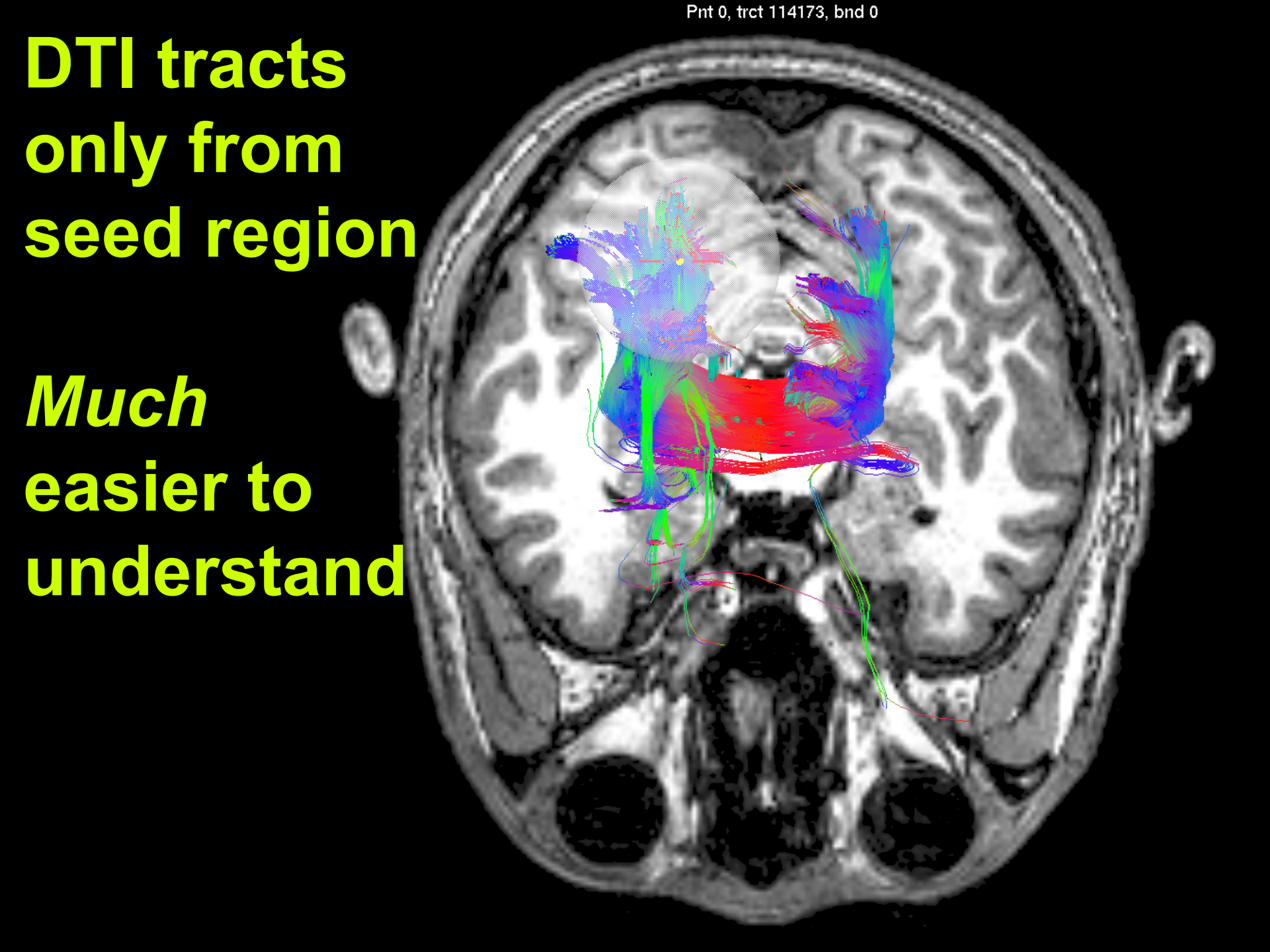
Just too much to take in*!*

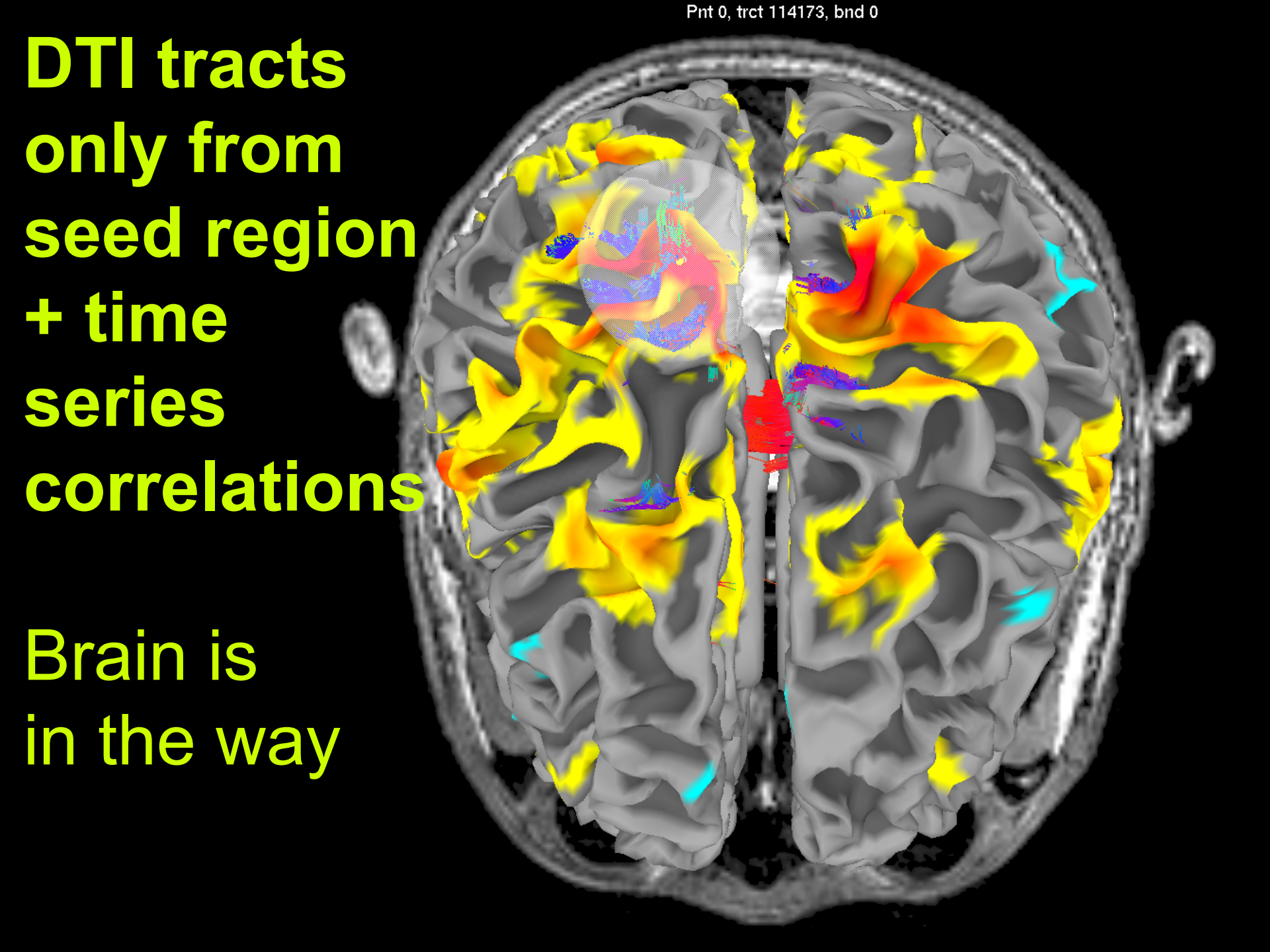


Correlations + DTI tracts + Brain

Way too much to take in*!*

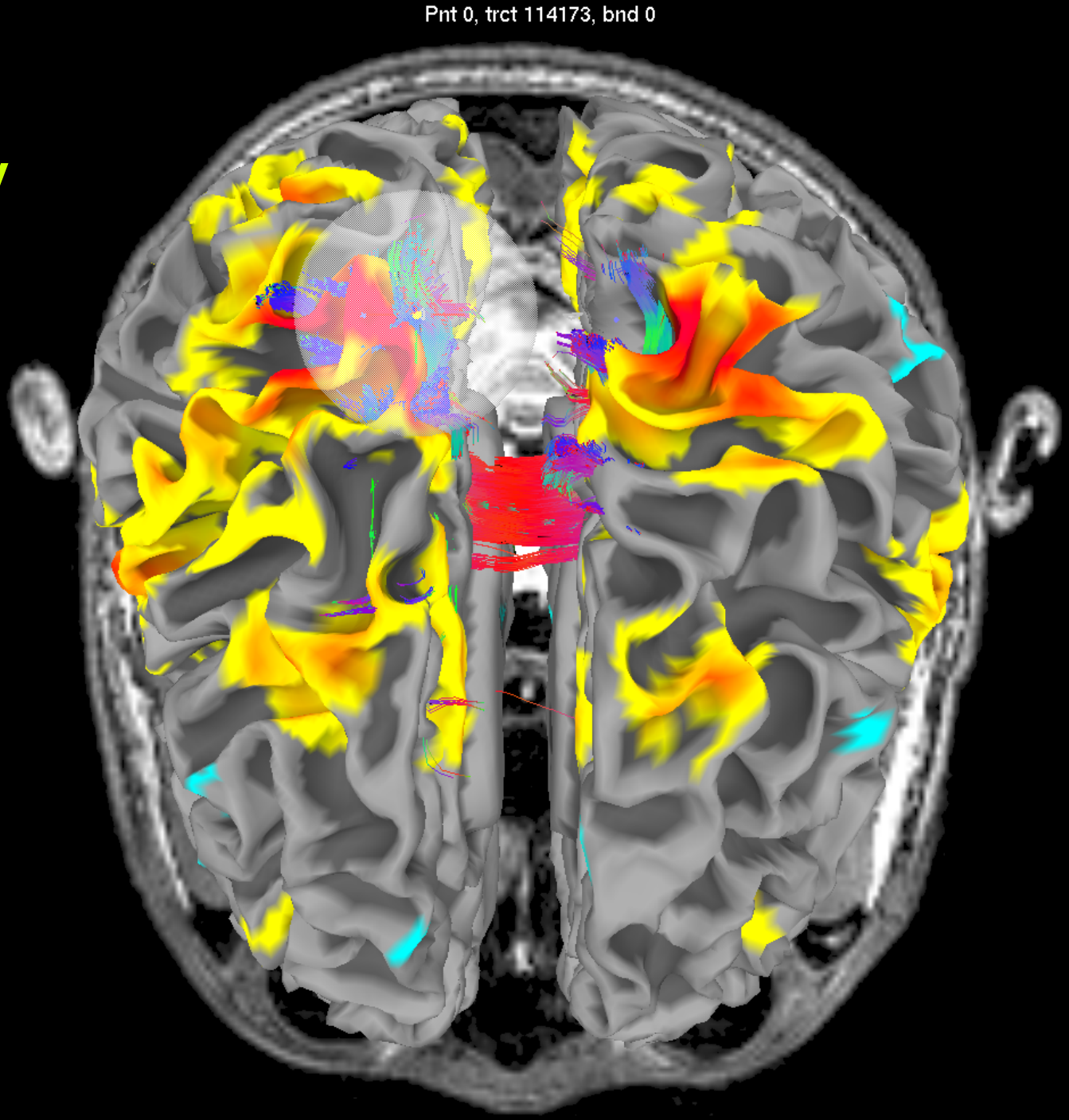


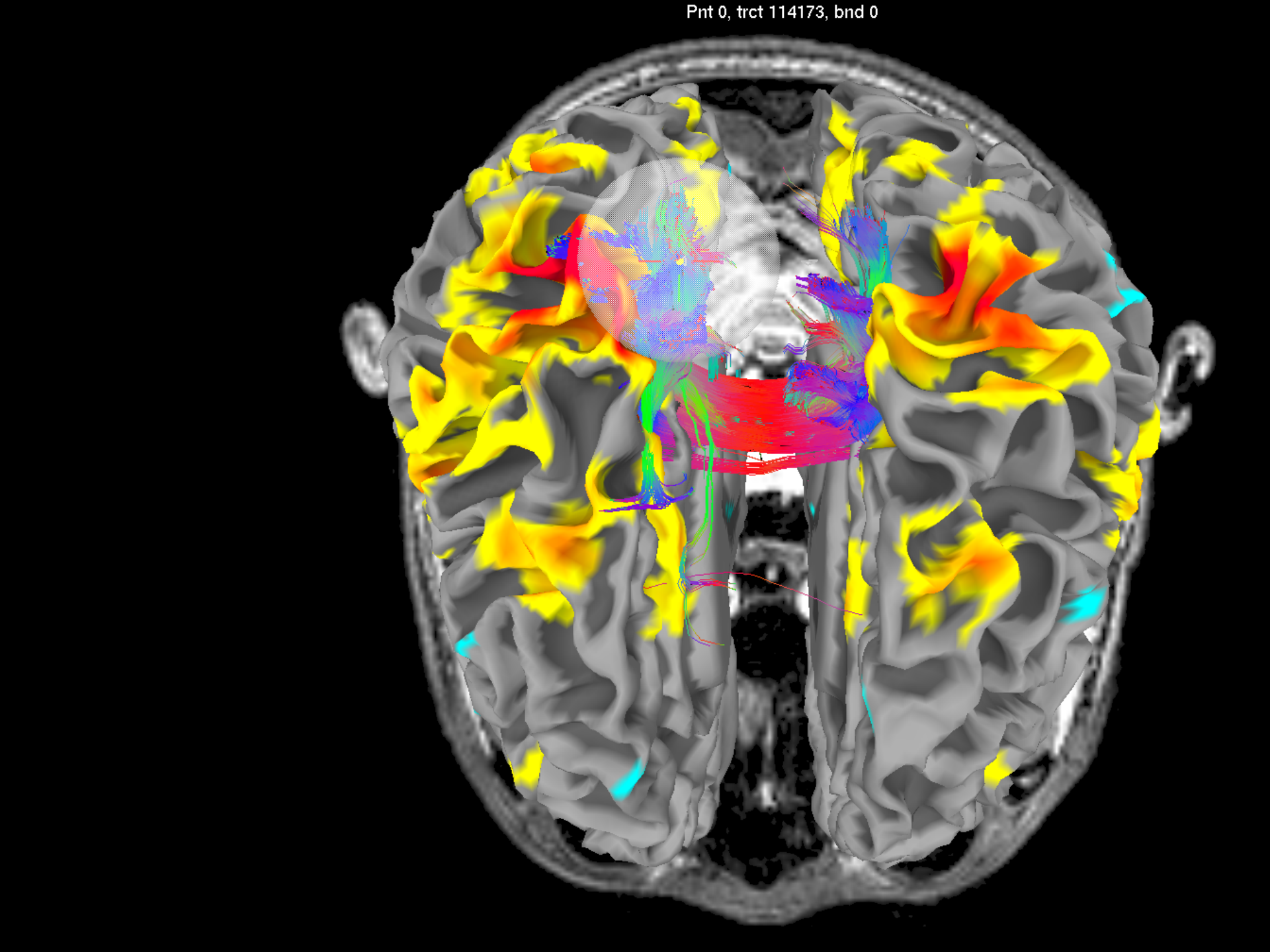

Pnt 0, trct 114173, bnd 0
DTI tracts only from seed region
Much easier to understand


Pnt 0, trct 114173, bnd 0
DTI tracts only from seed region + time series correlations
Brain is in the way

Brain is
in the way

So move
it aside!

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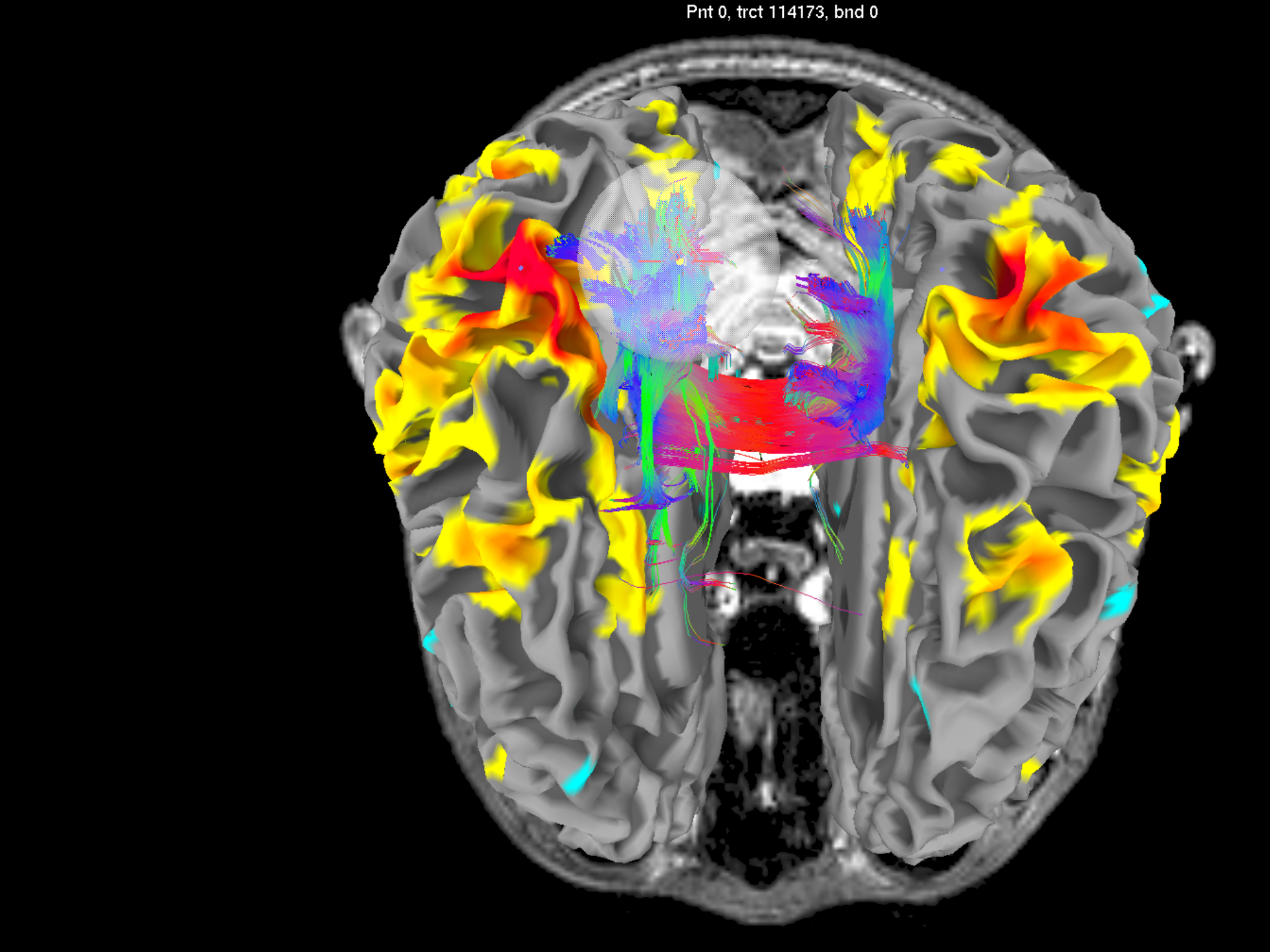
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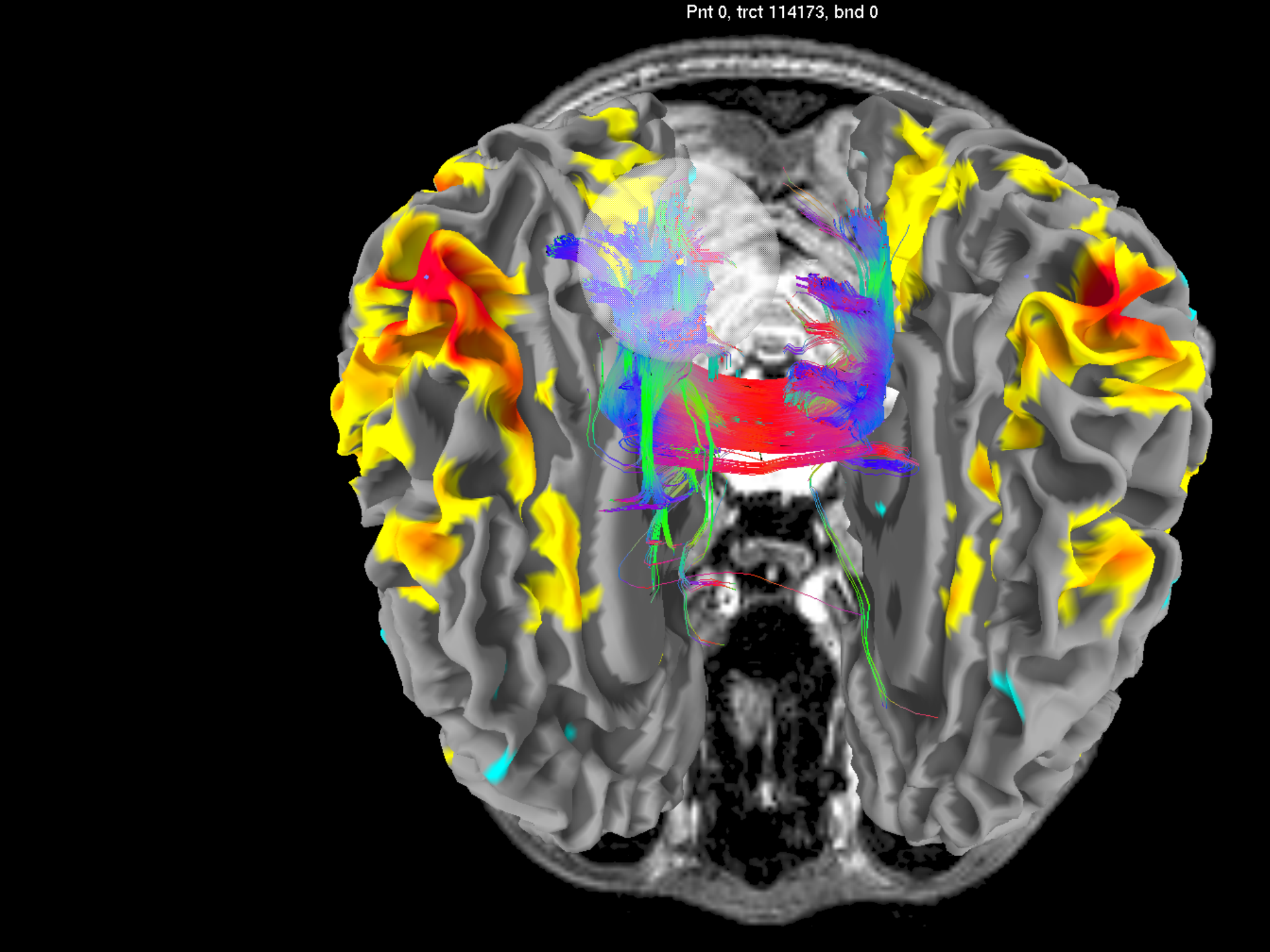
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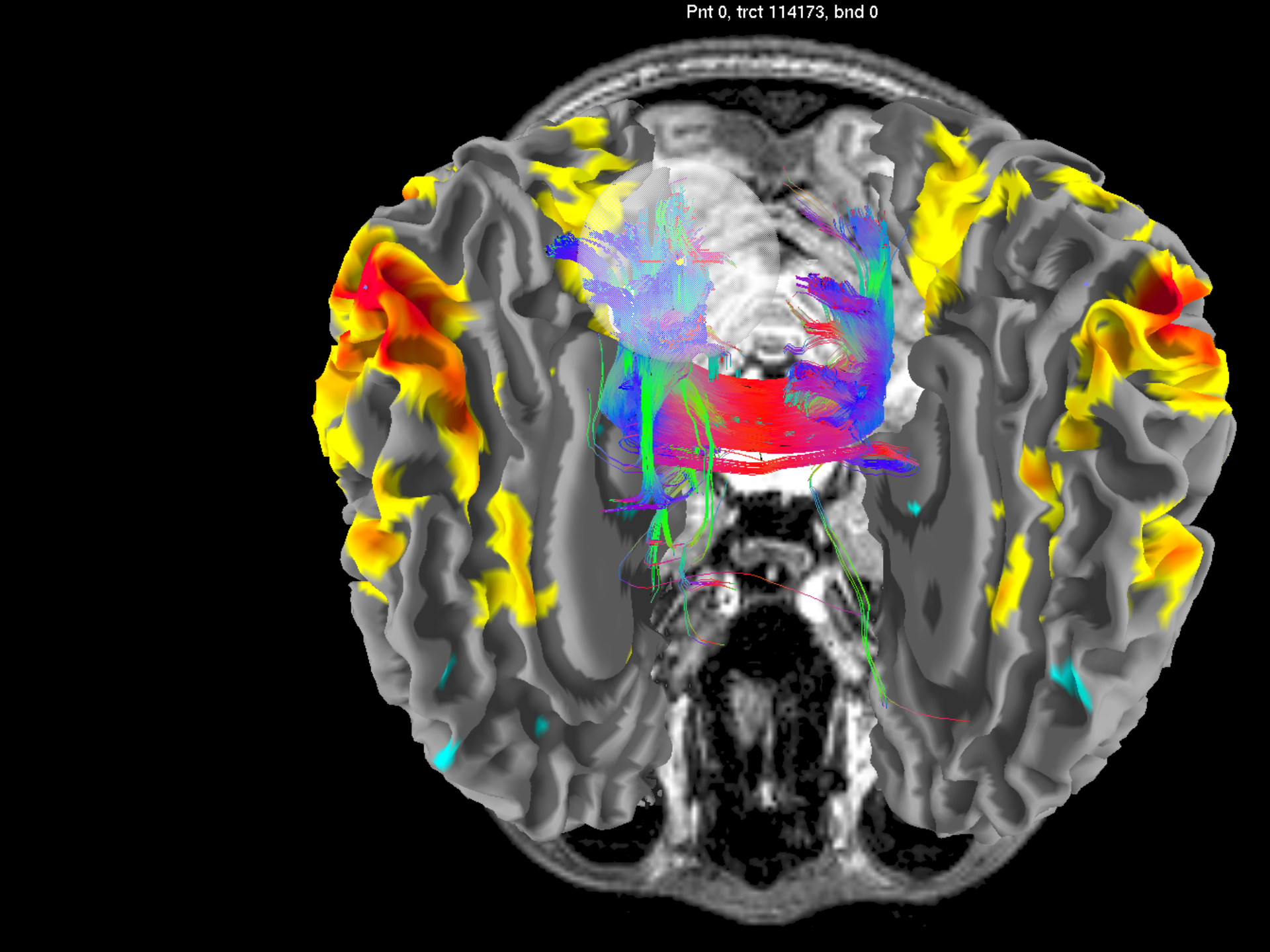
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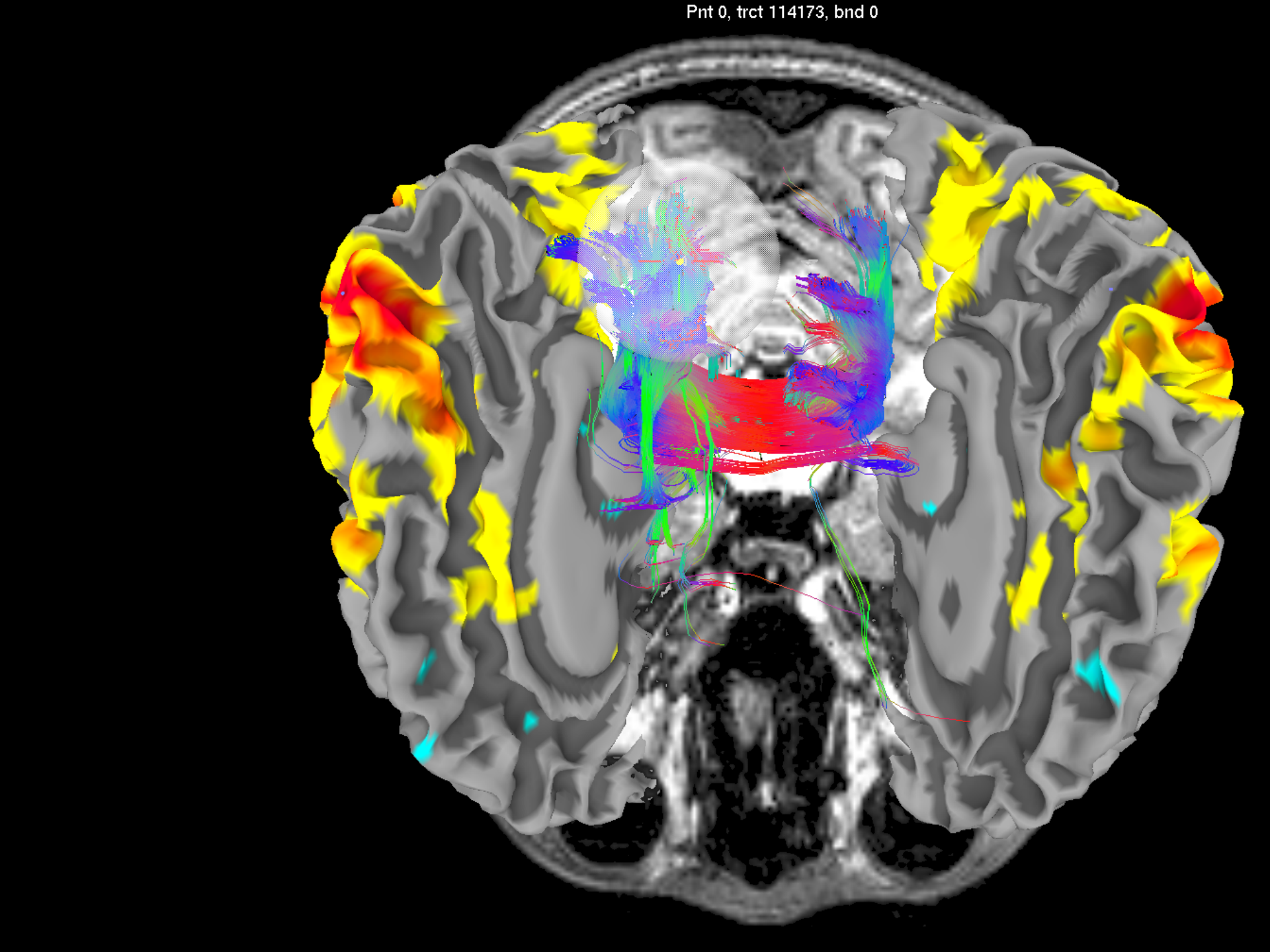
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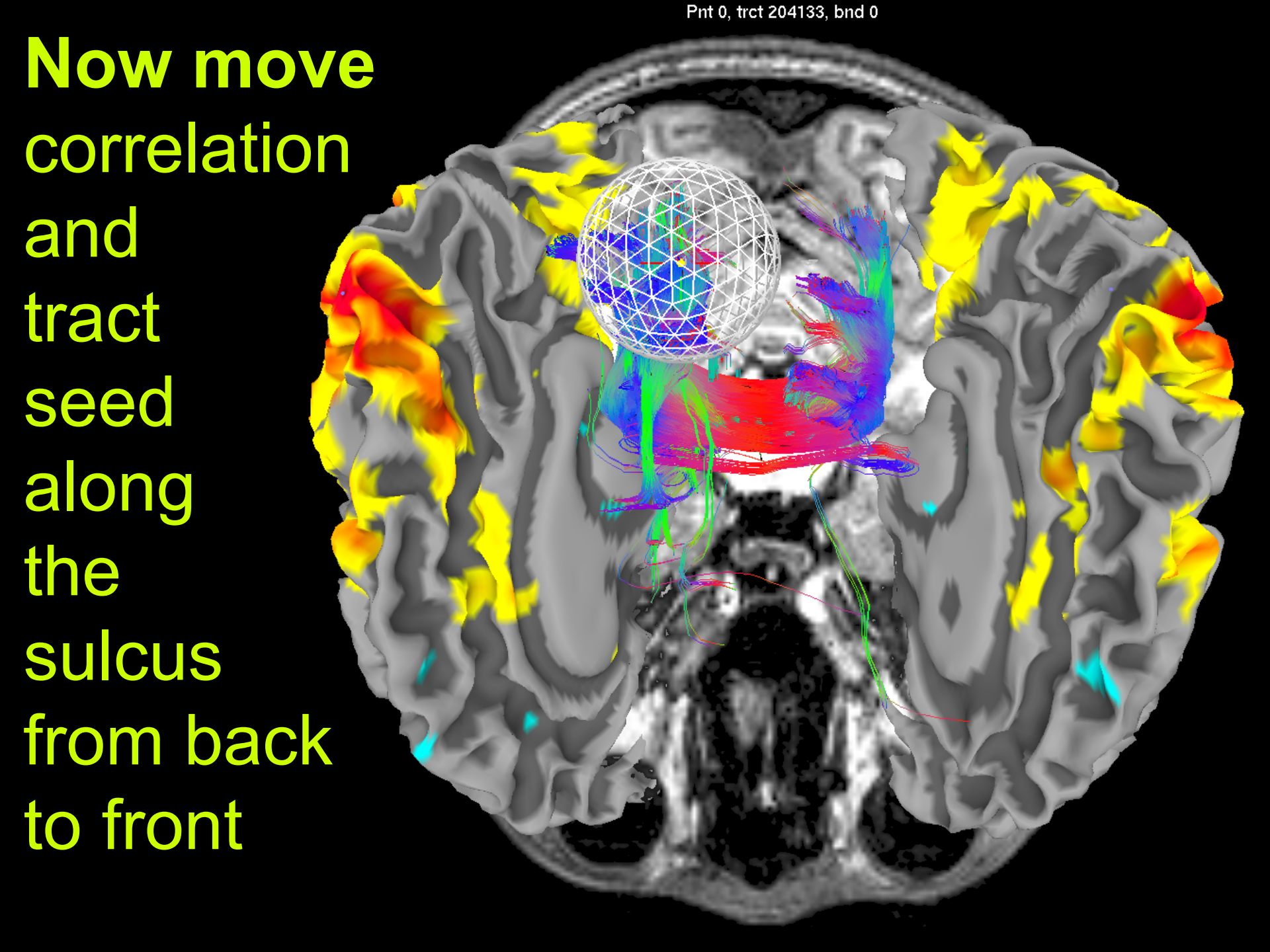
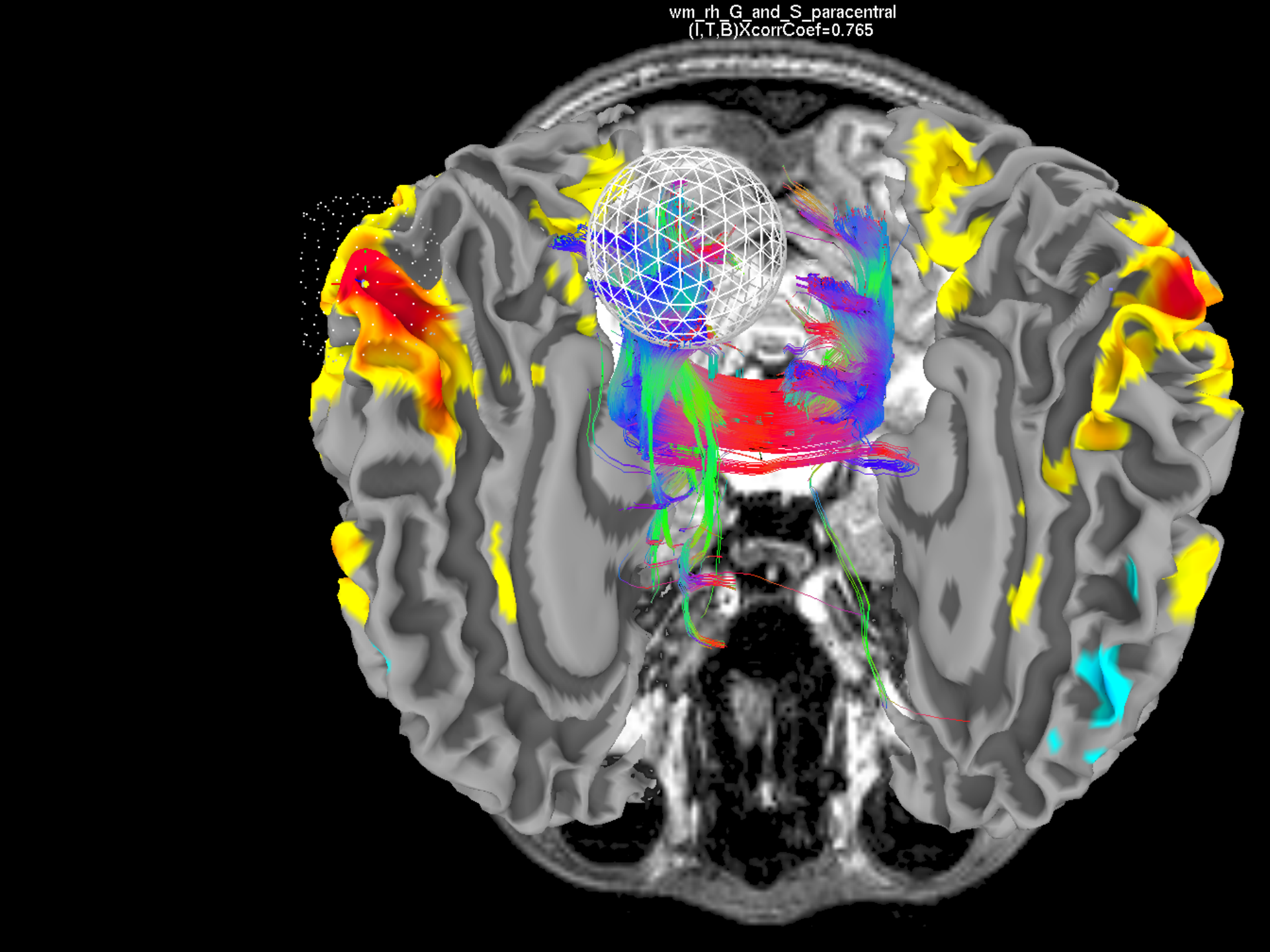

Pnt 0, trct 204133, bnd 0
Now move
correlation
and
tract
seed
along
the
sulcus
from back
to front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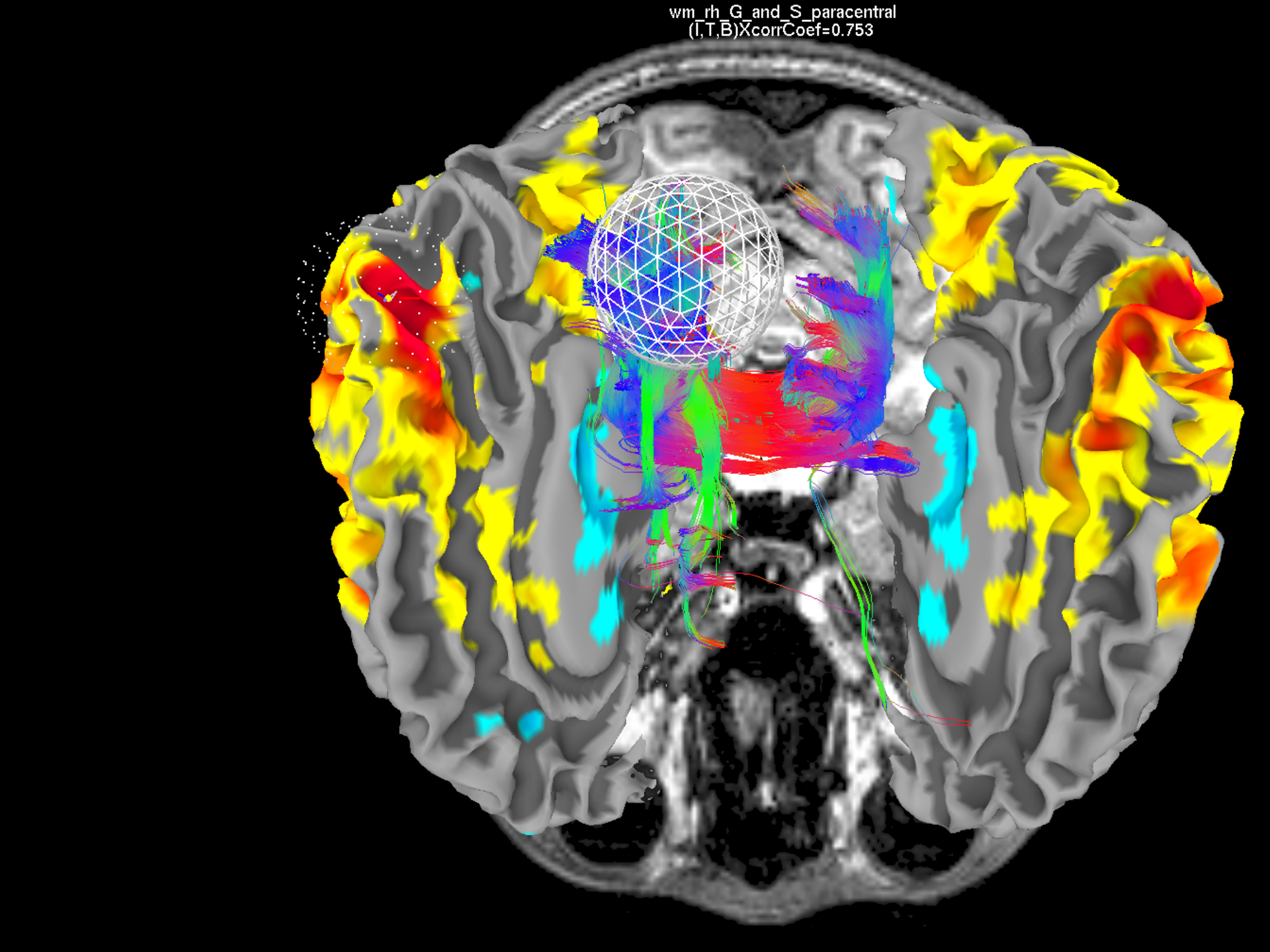
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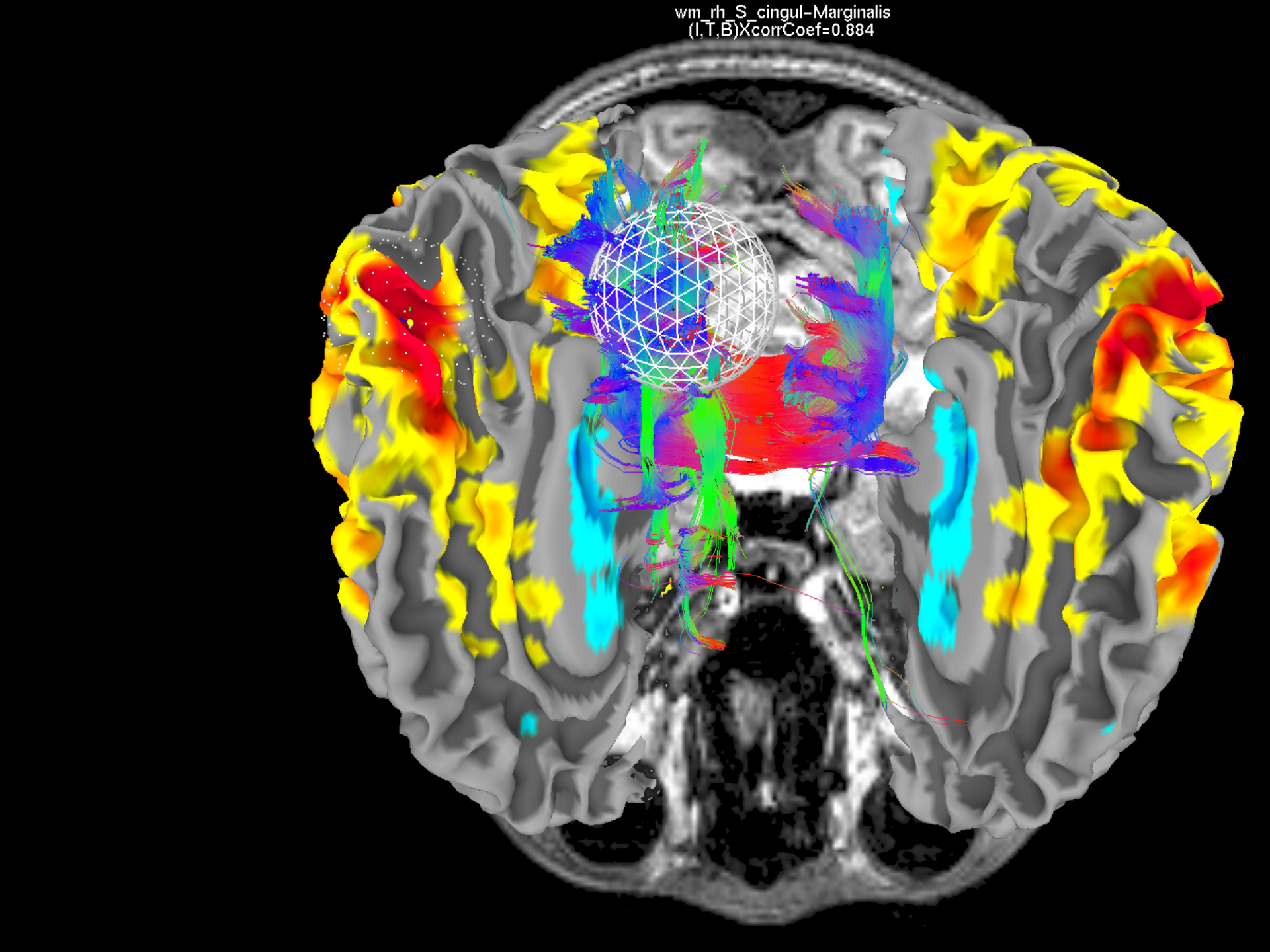
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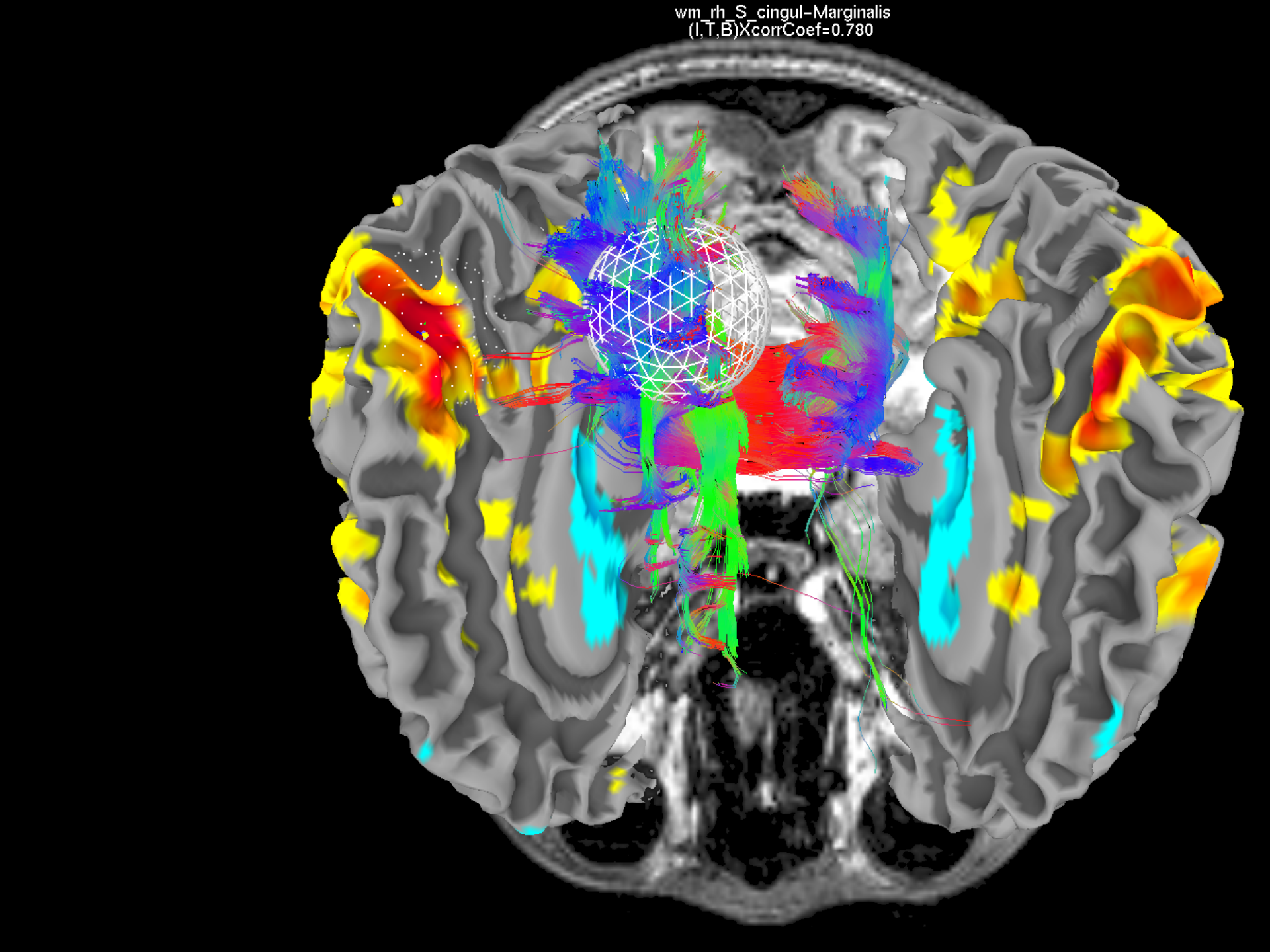
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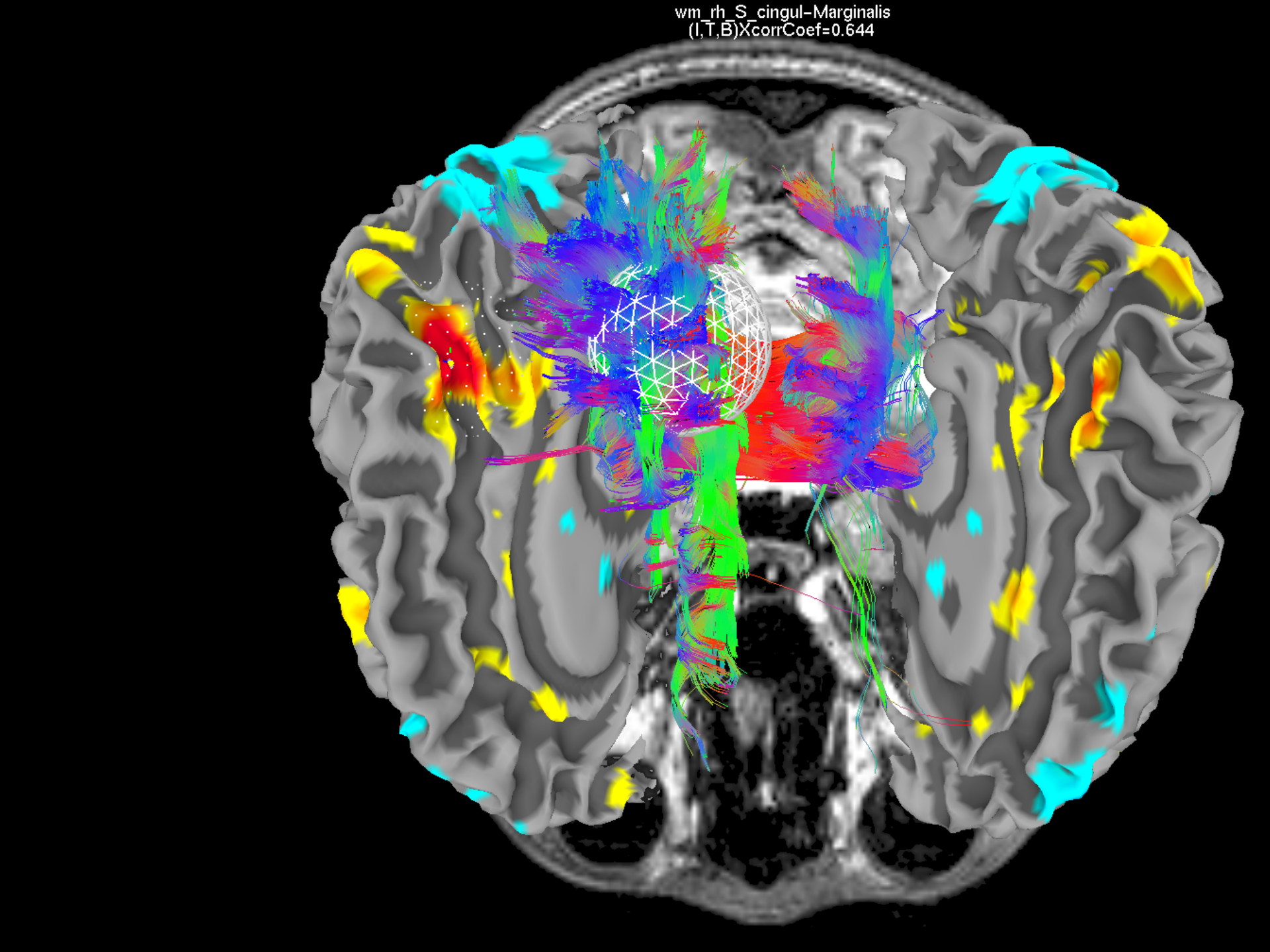
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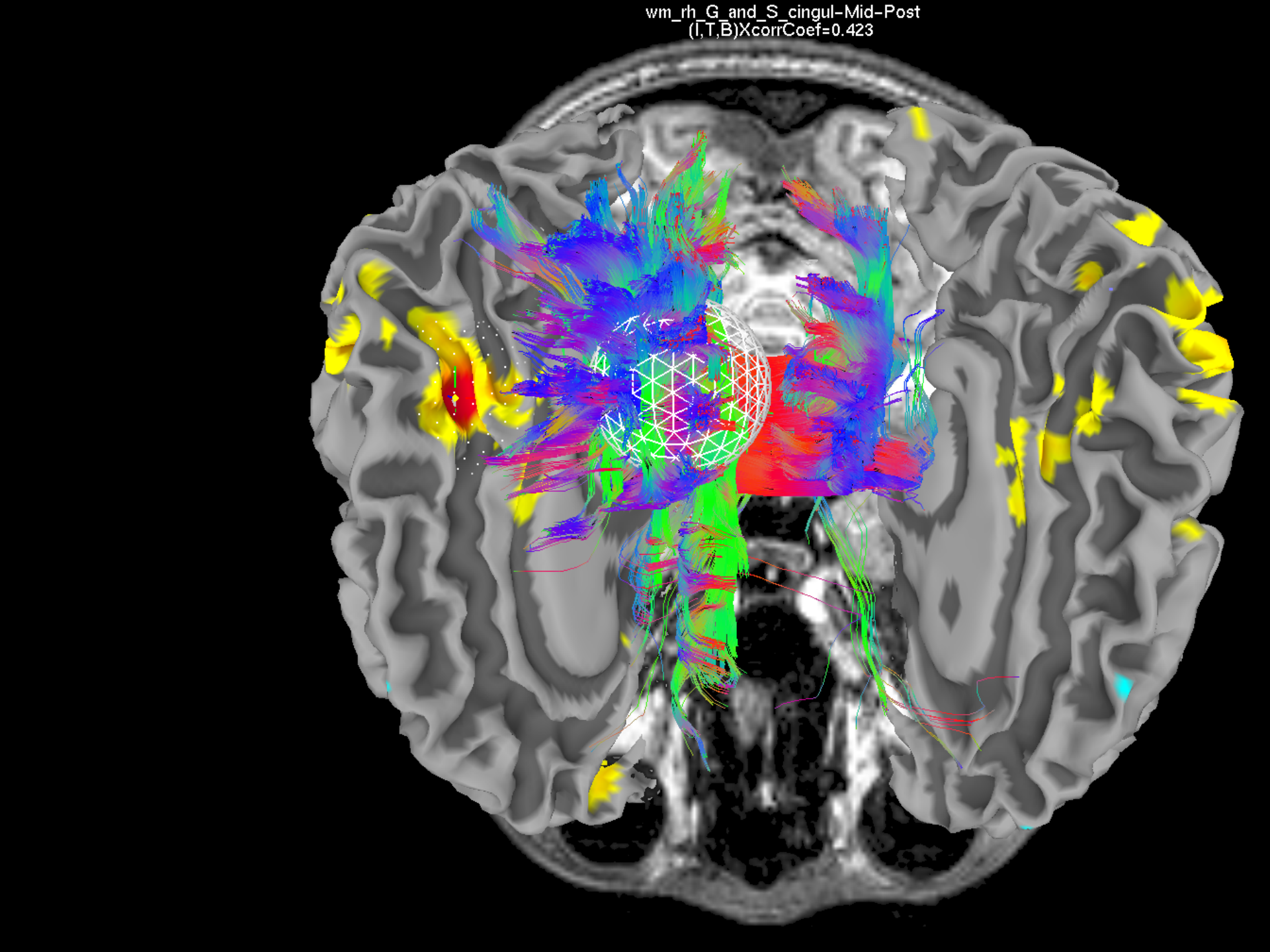
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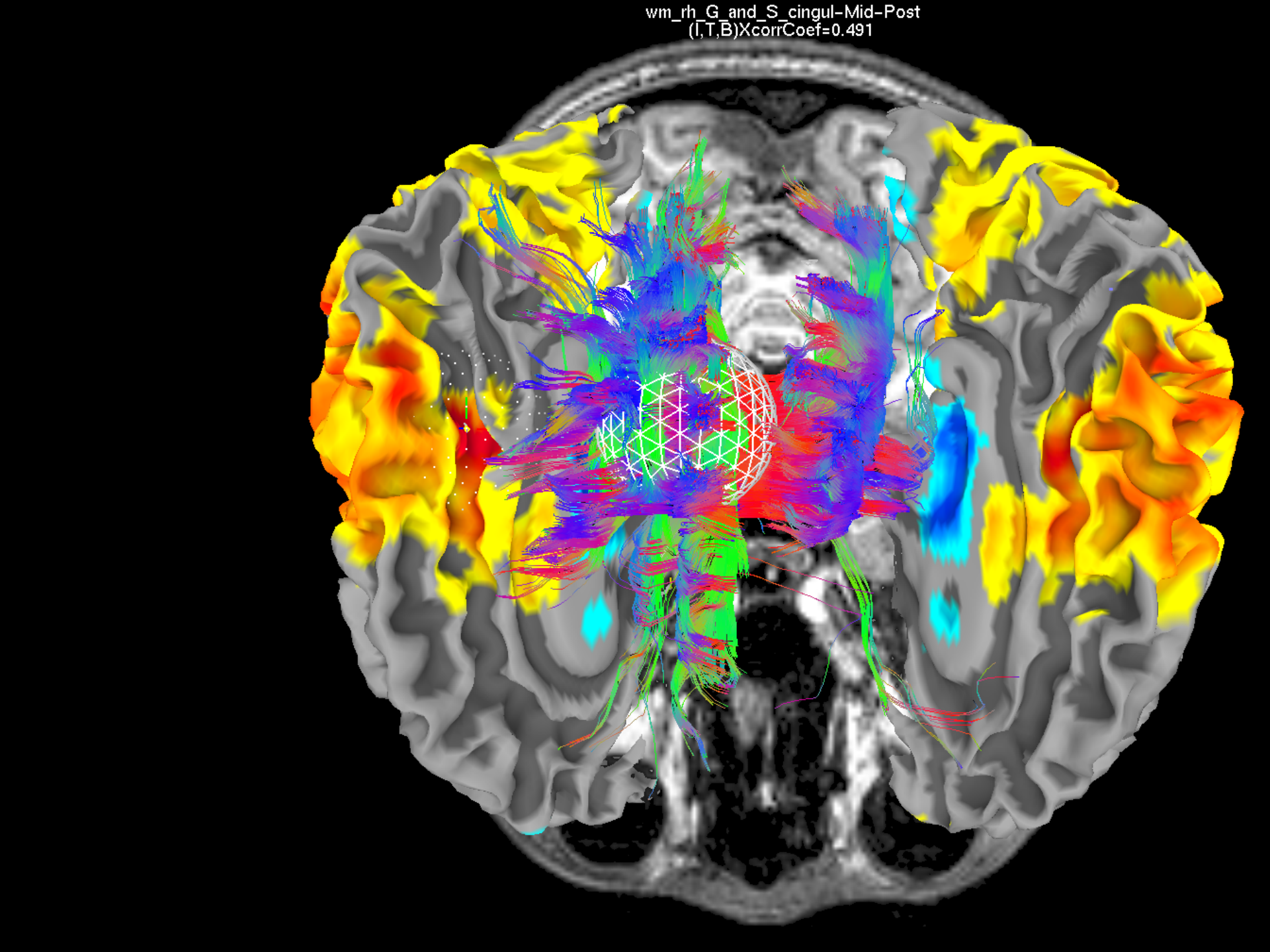
(I,T,B)XcorrCoef=0.423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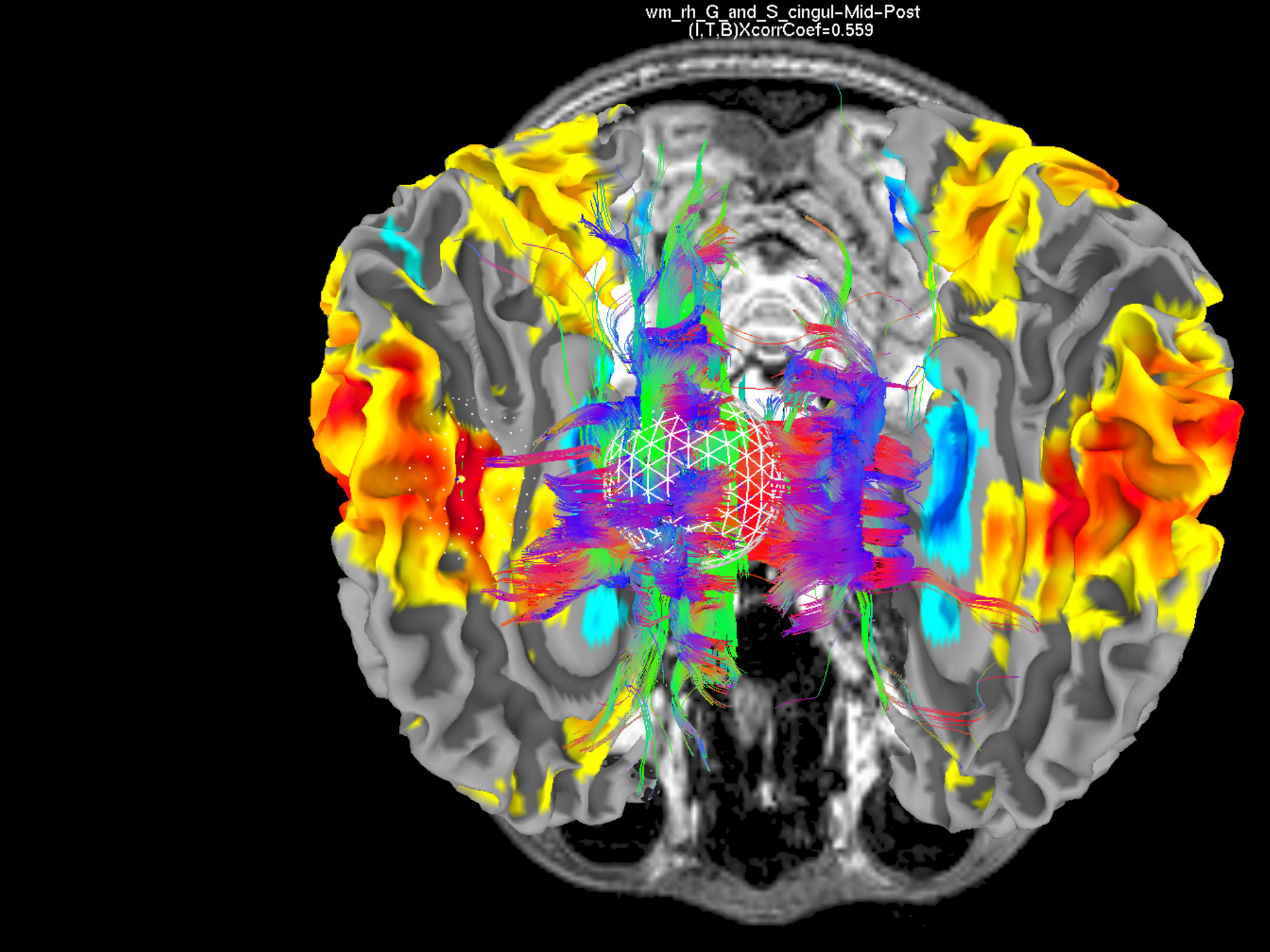
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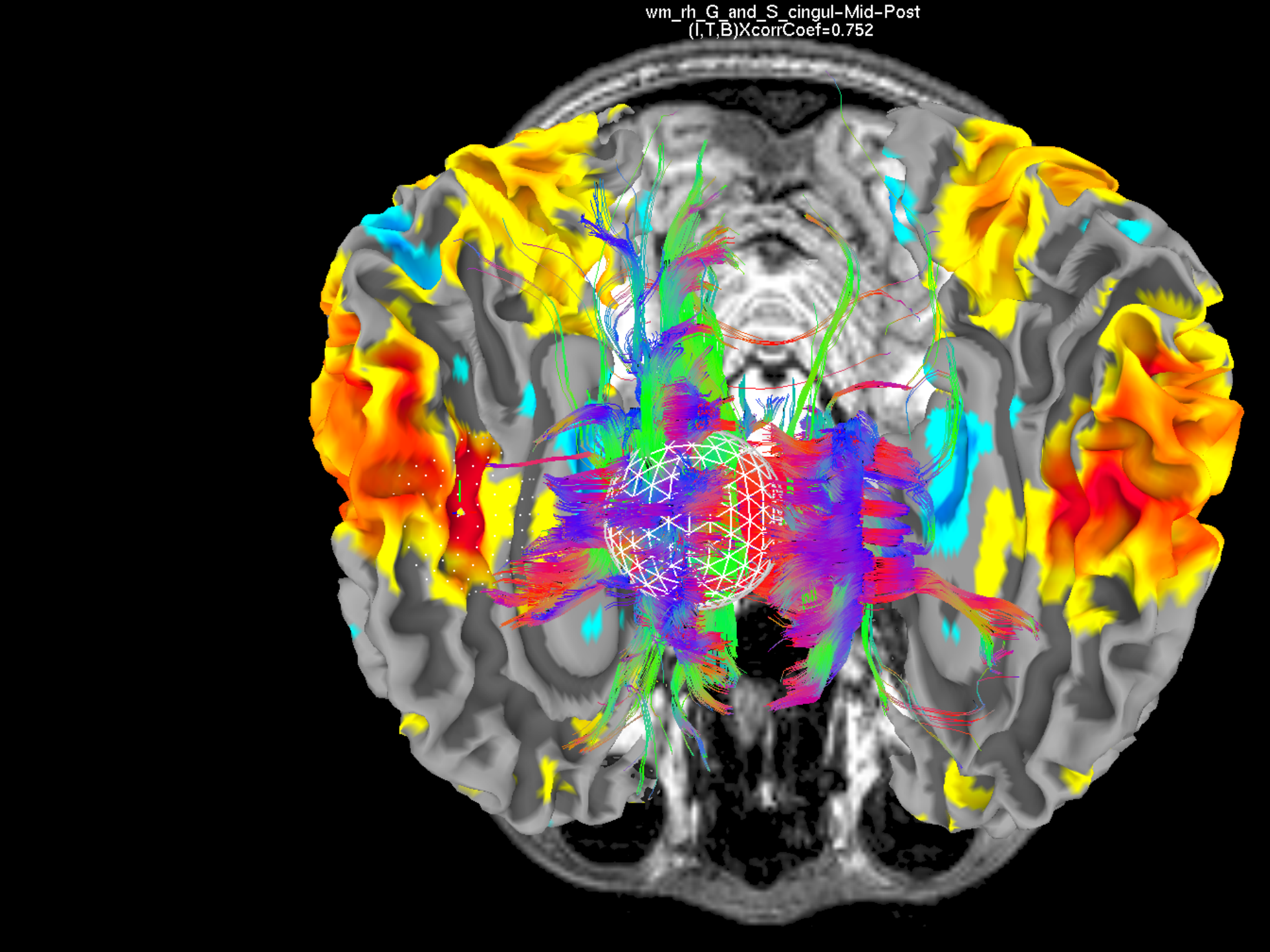
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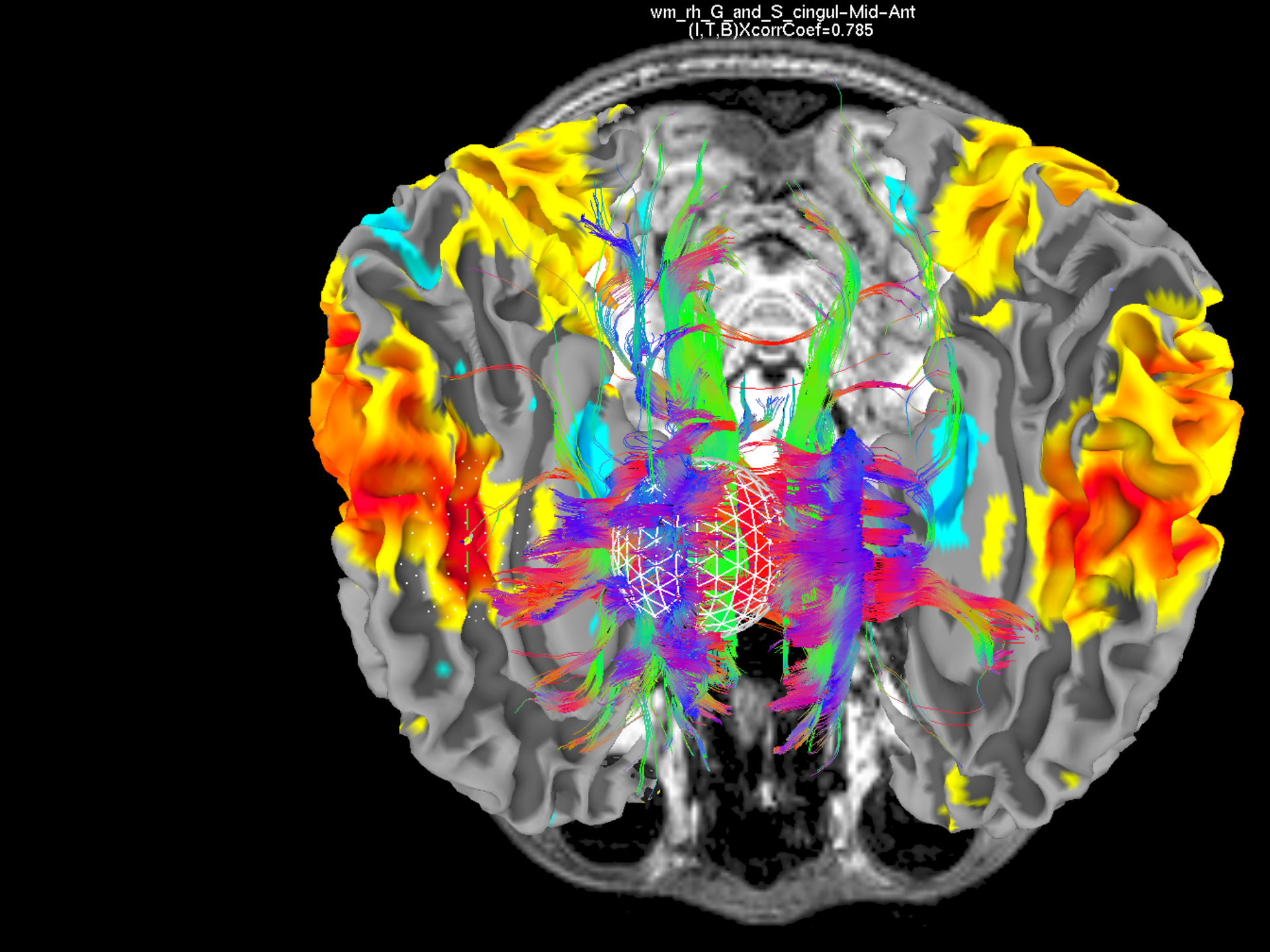
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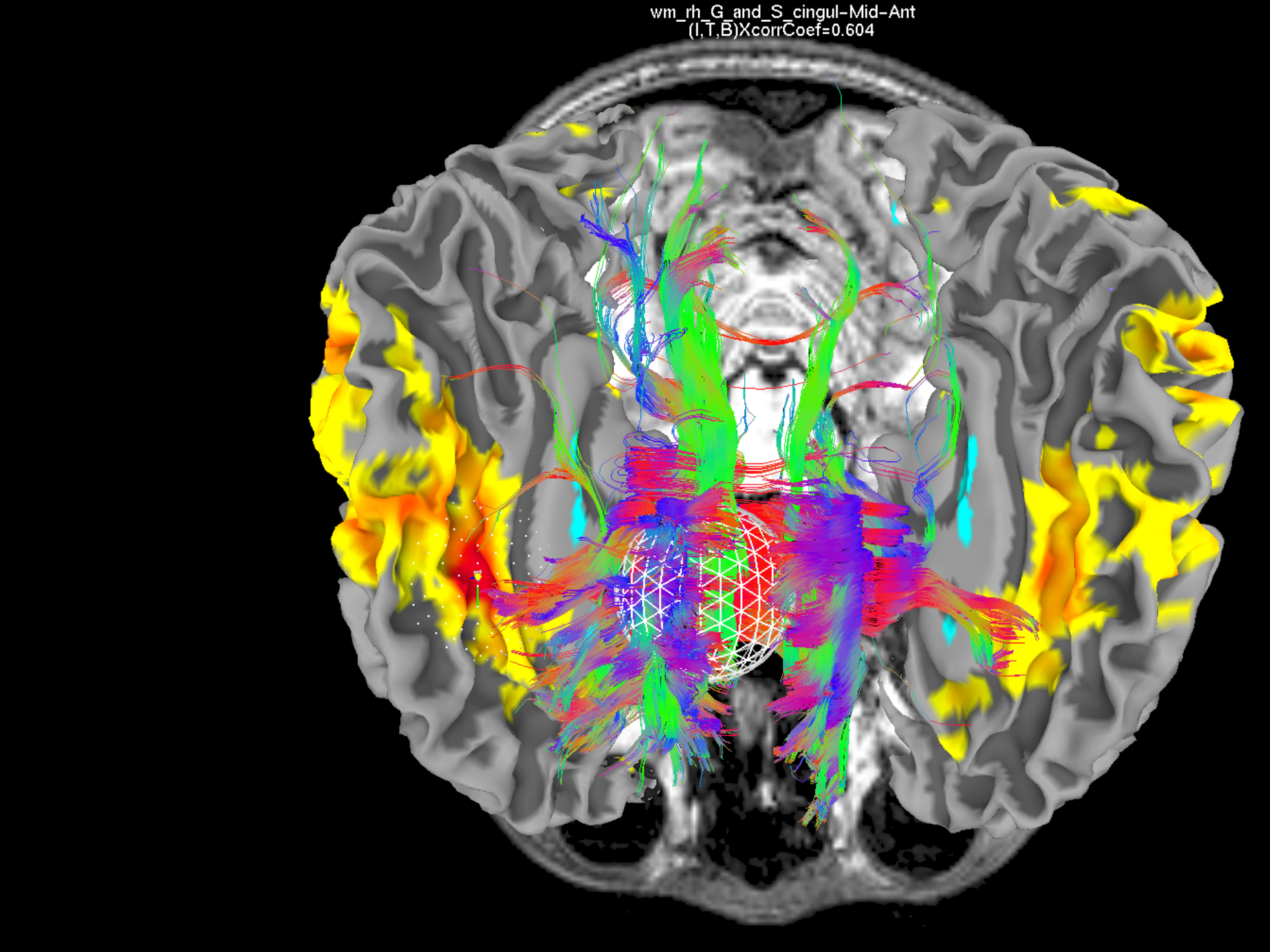
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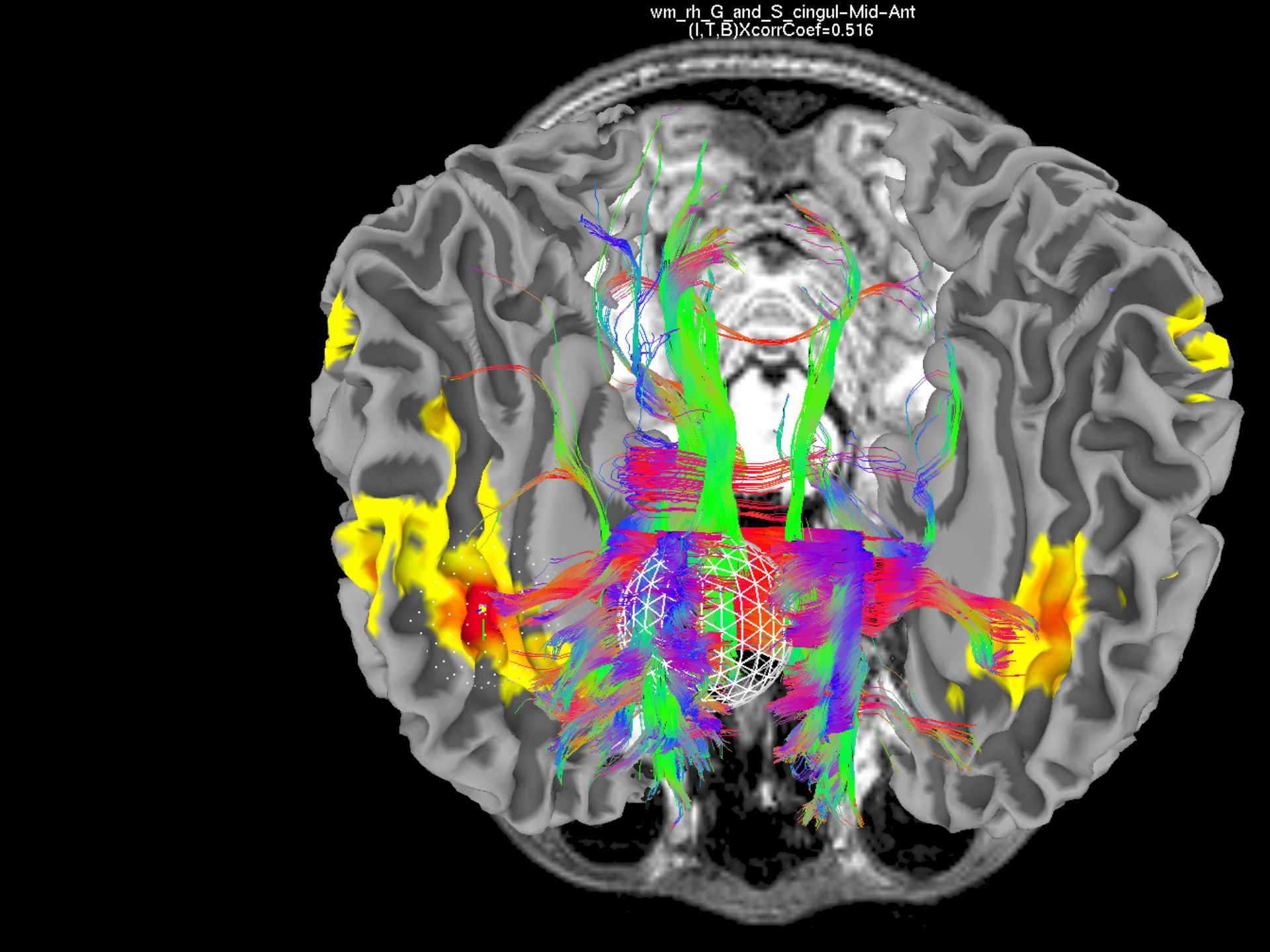
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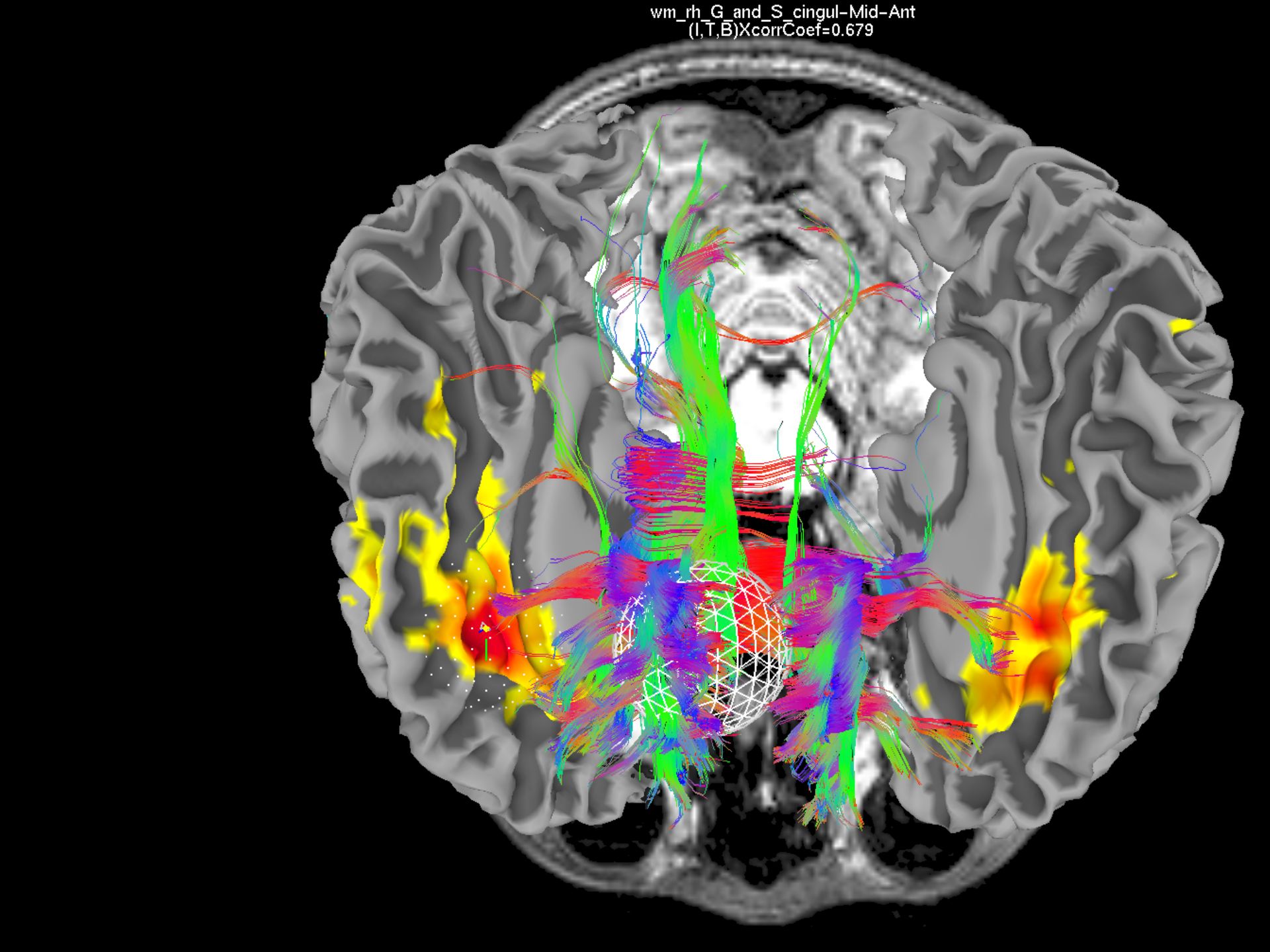
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wm_rh_G_and_S_cingul-Ant
(I,T,B)XcorrCoef=0.578


wm_rh_G_and_S_cingul-Ant
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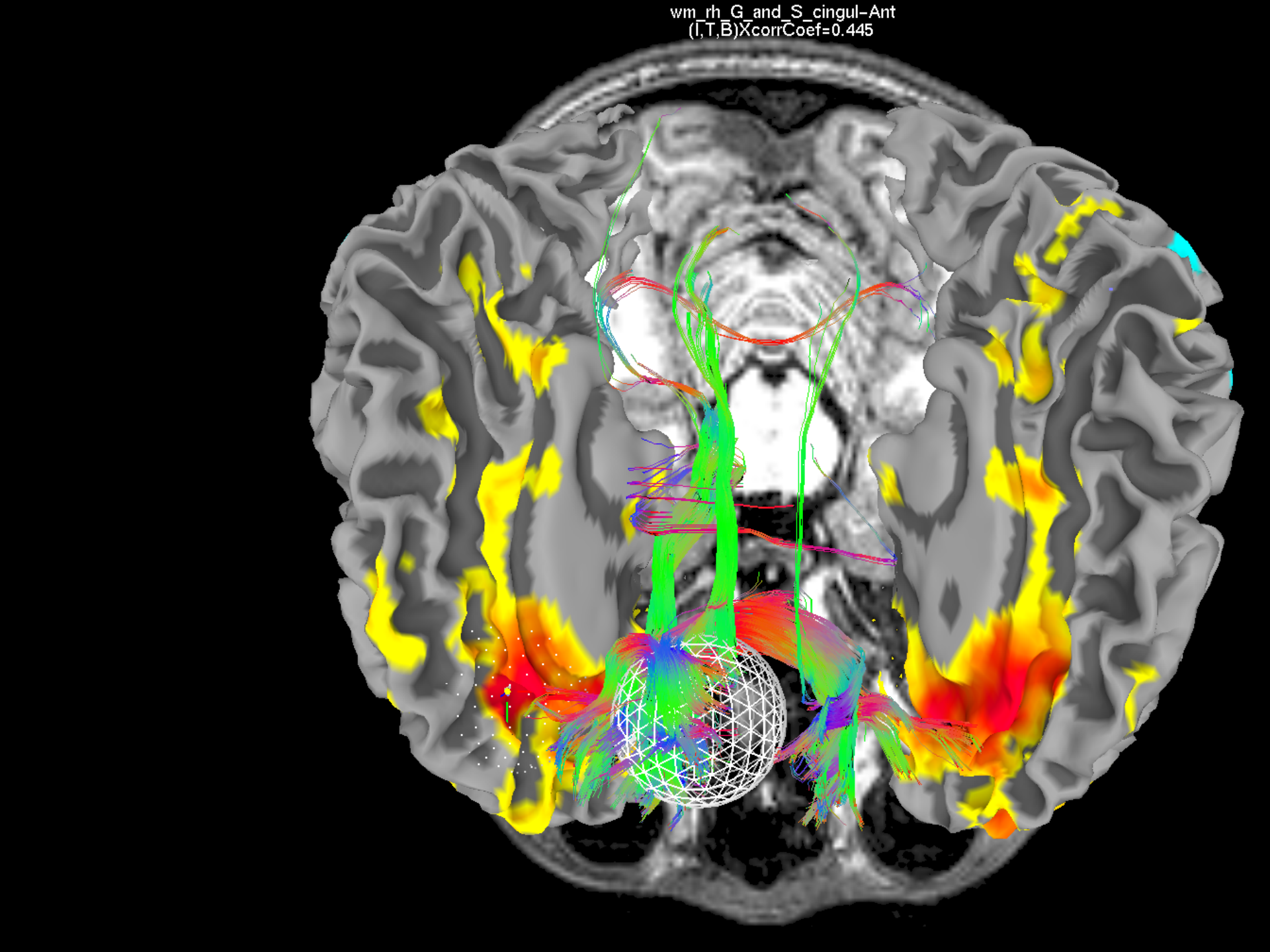
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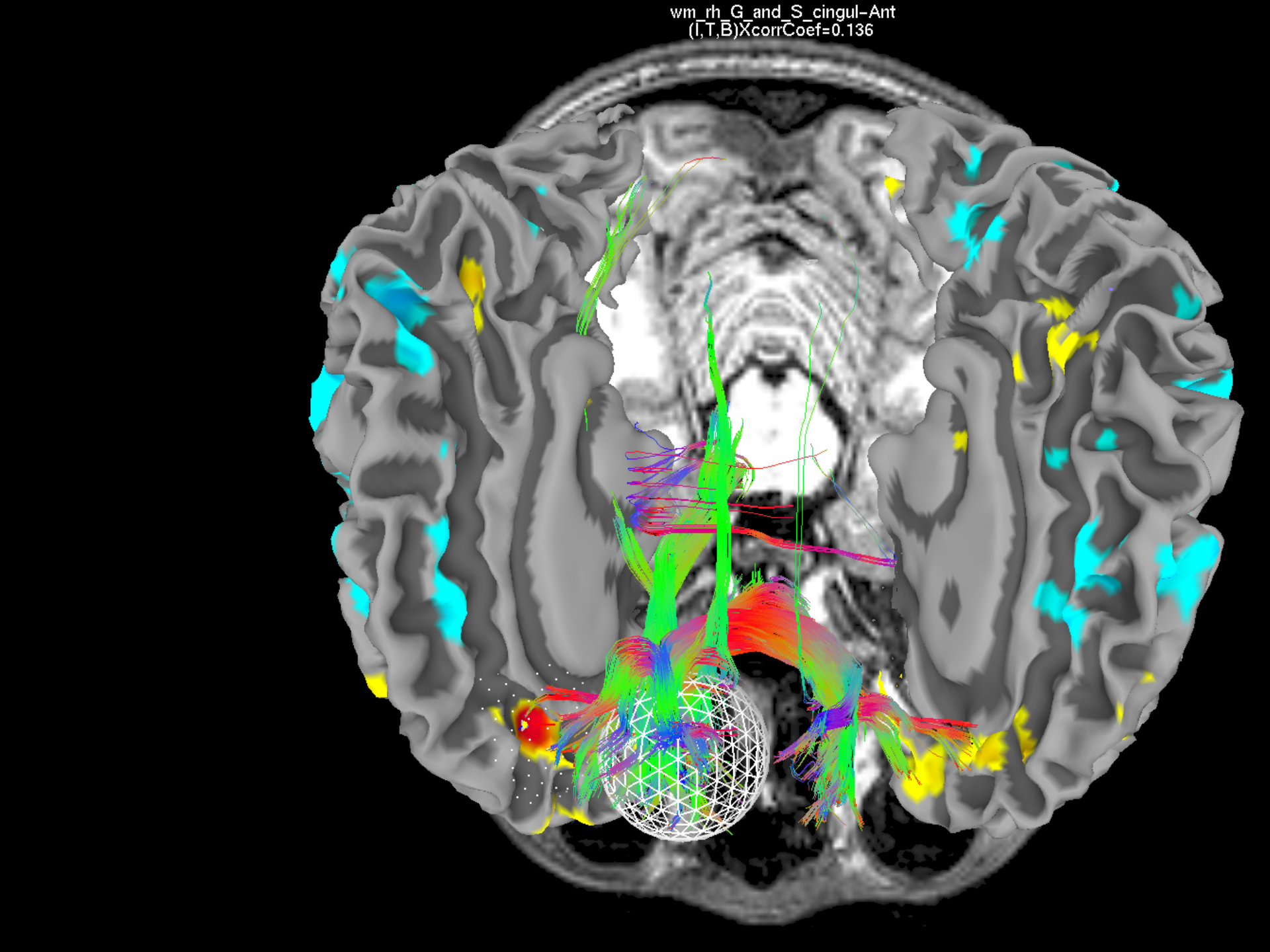
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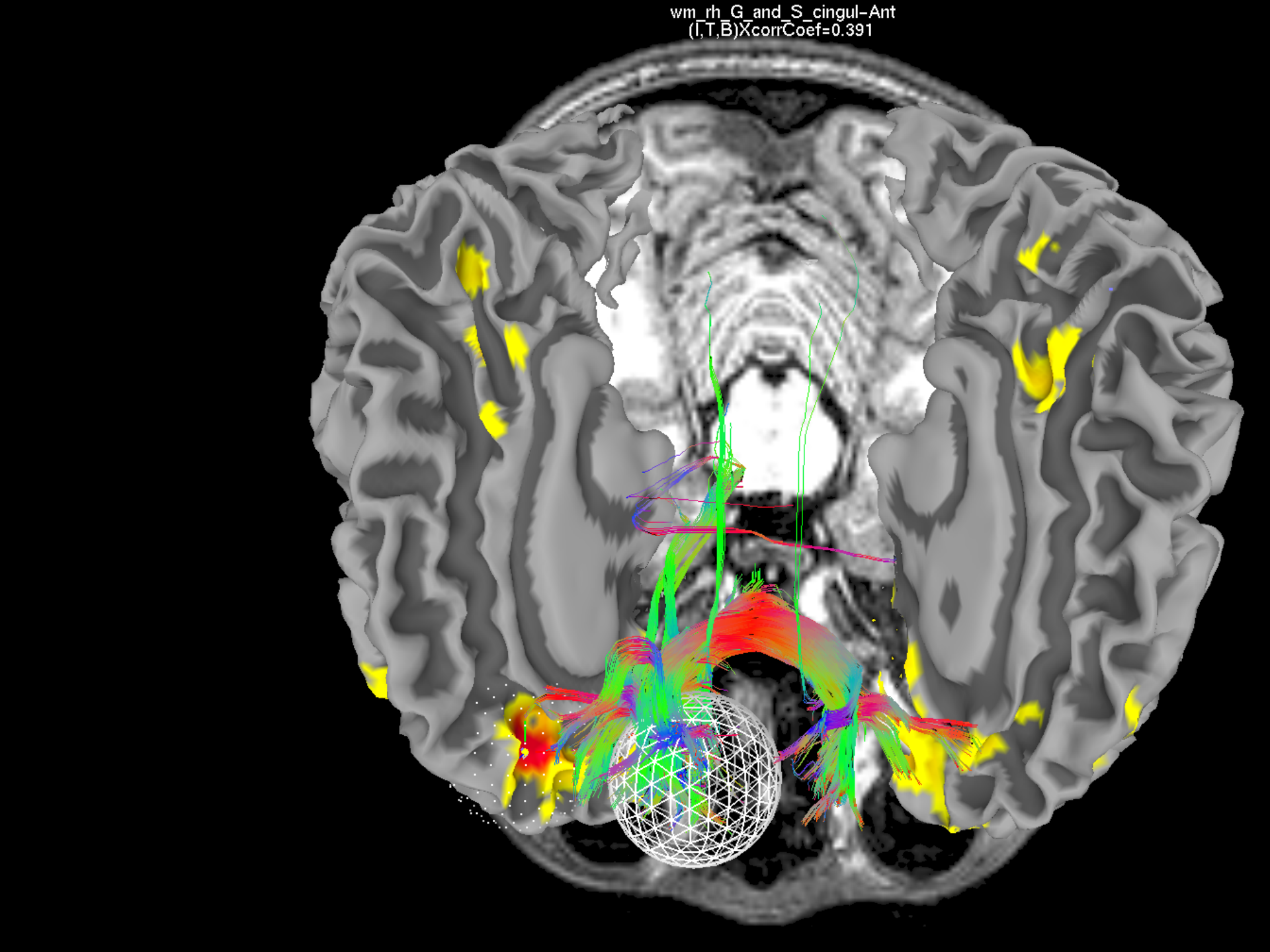
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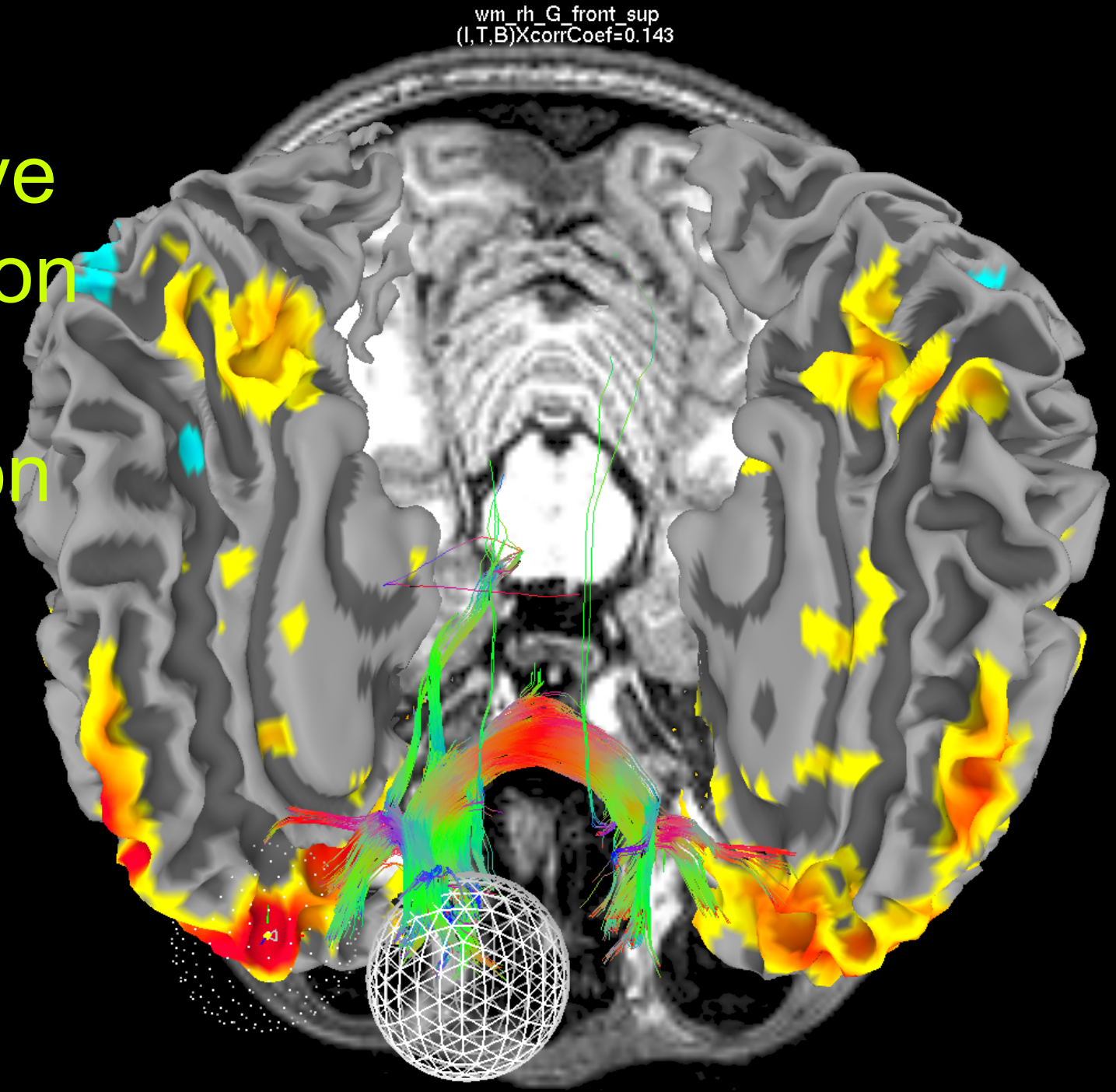
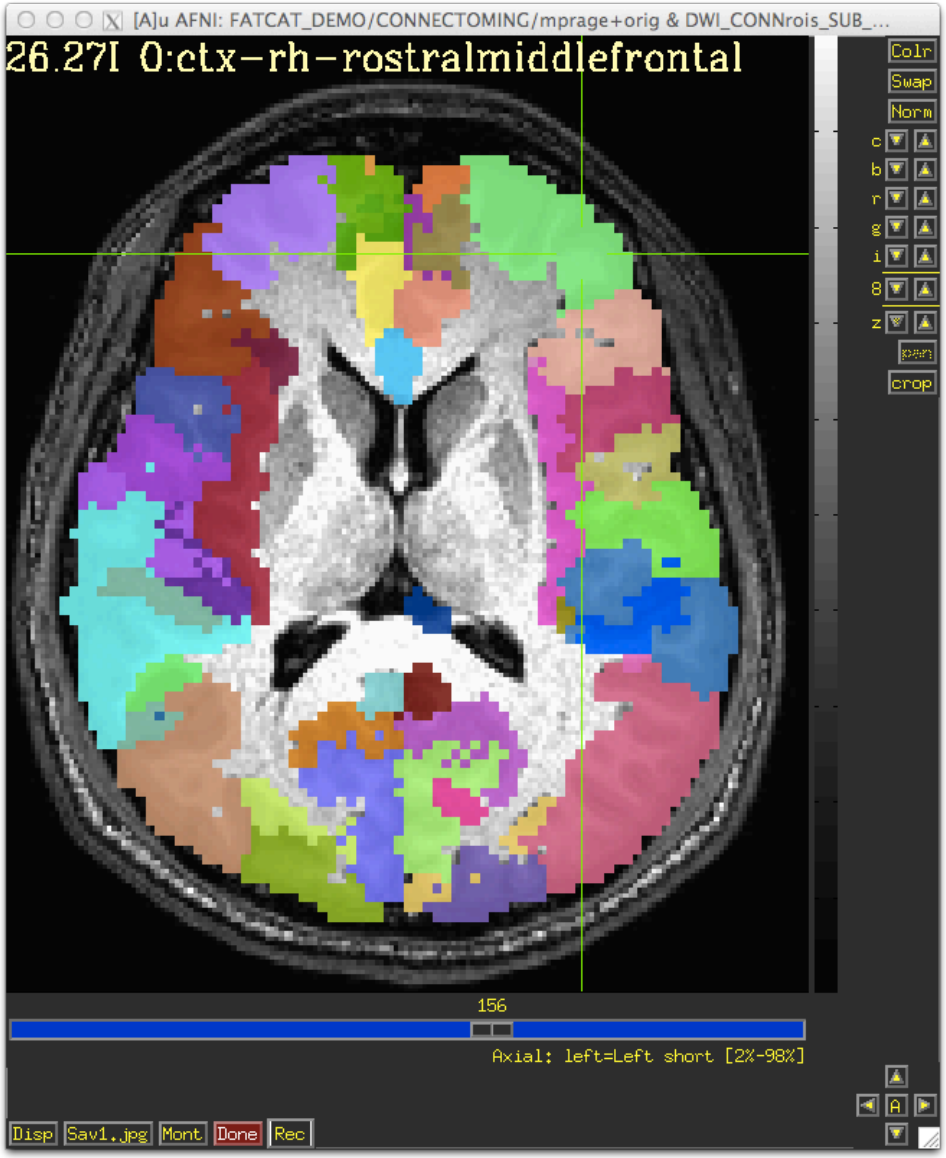
Goal:
Interactive exploration of high dimension complex datasets



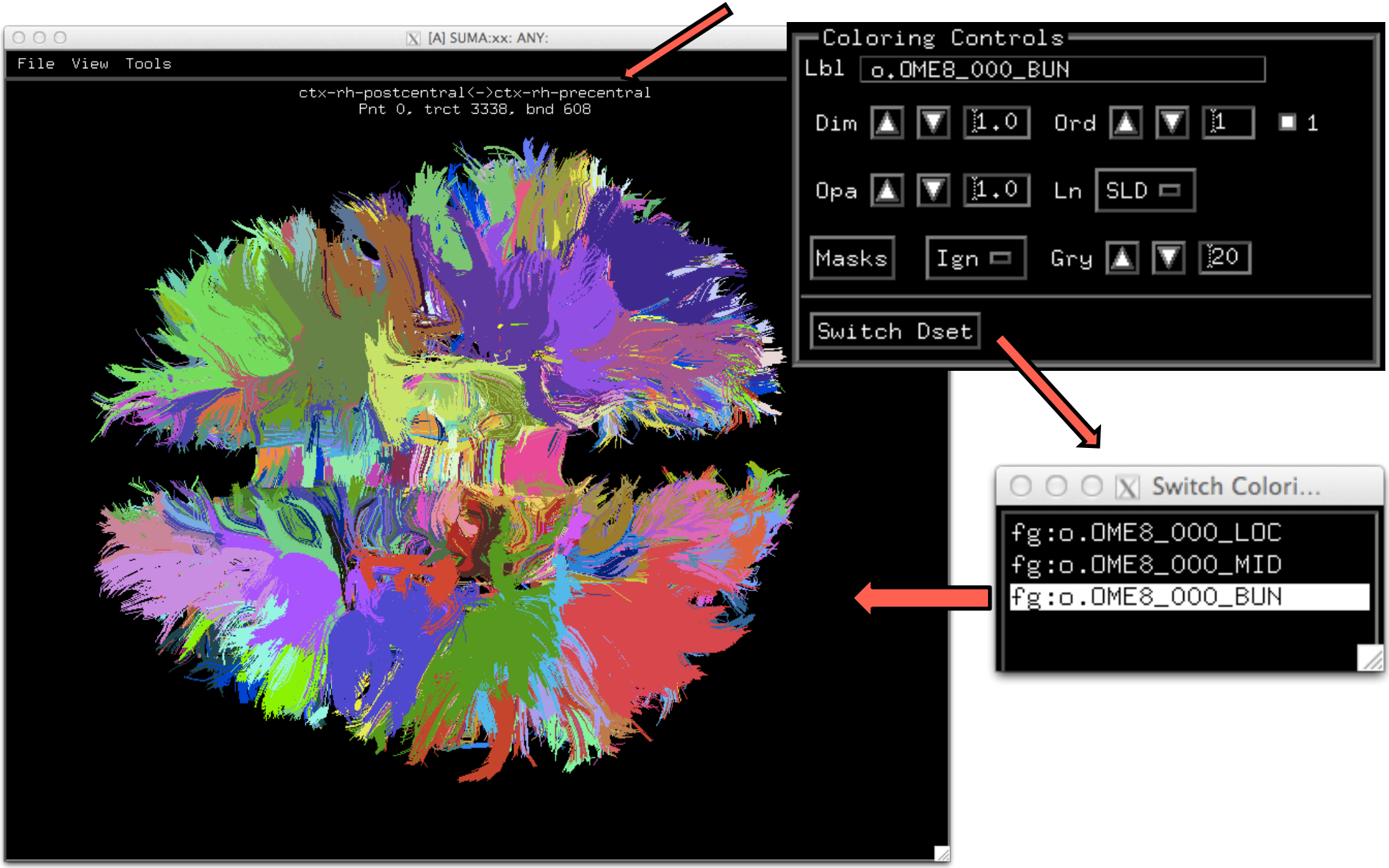
tcsh Do_11_RUNdti_Connectome_Examp.tcsh

- Example 1: Tract tracing between large numbers of ROIs



Hands-On

Tracts and Grid files are labeled with ROI names



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

Z.S.S 29/09/14

Thanks to:

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- Brenna Argall
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- Rick Reynolds

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- Pat Bellgowan

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Testing: Samia Saad

SysAdmin:
- Brian Pittman

MRI Pulse Sequence and Segmentation
- Hauke Heekeren
- Sean Marrett