

Tracts in SUMA

- Tracts are generated by AFNI's FATCAT toolbox



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

Tracts in SUMA

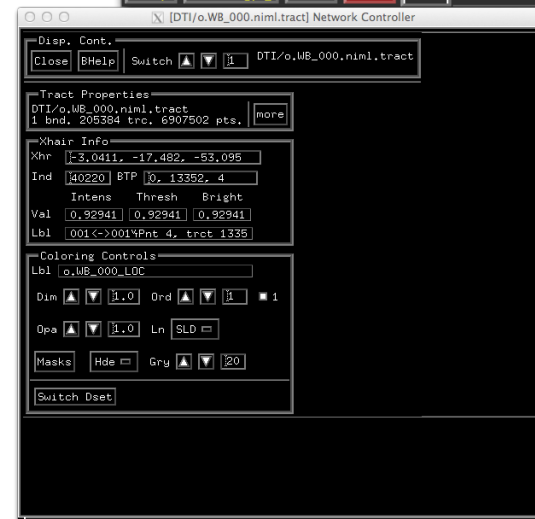
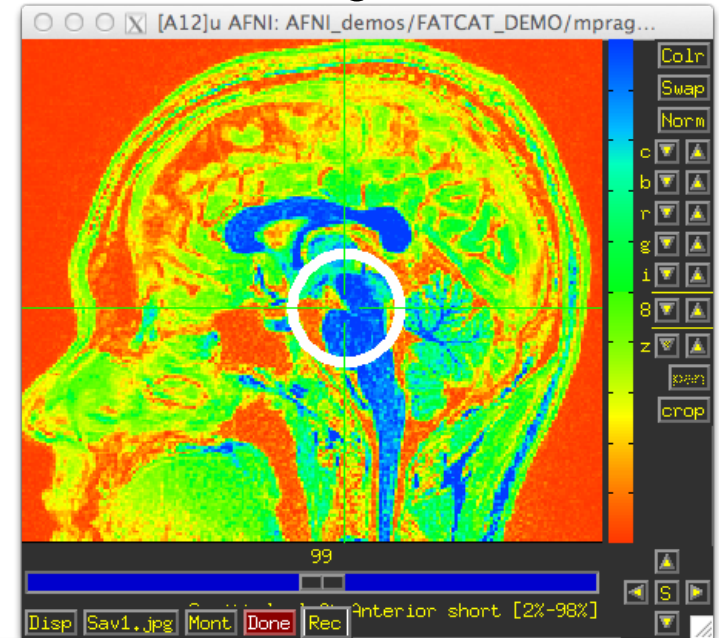
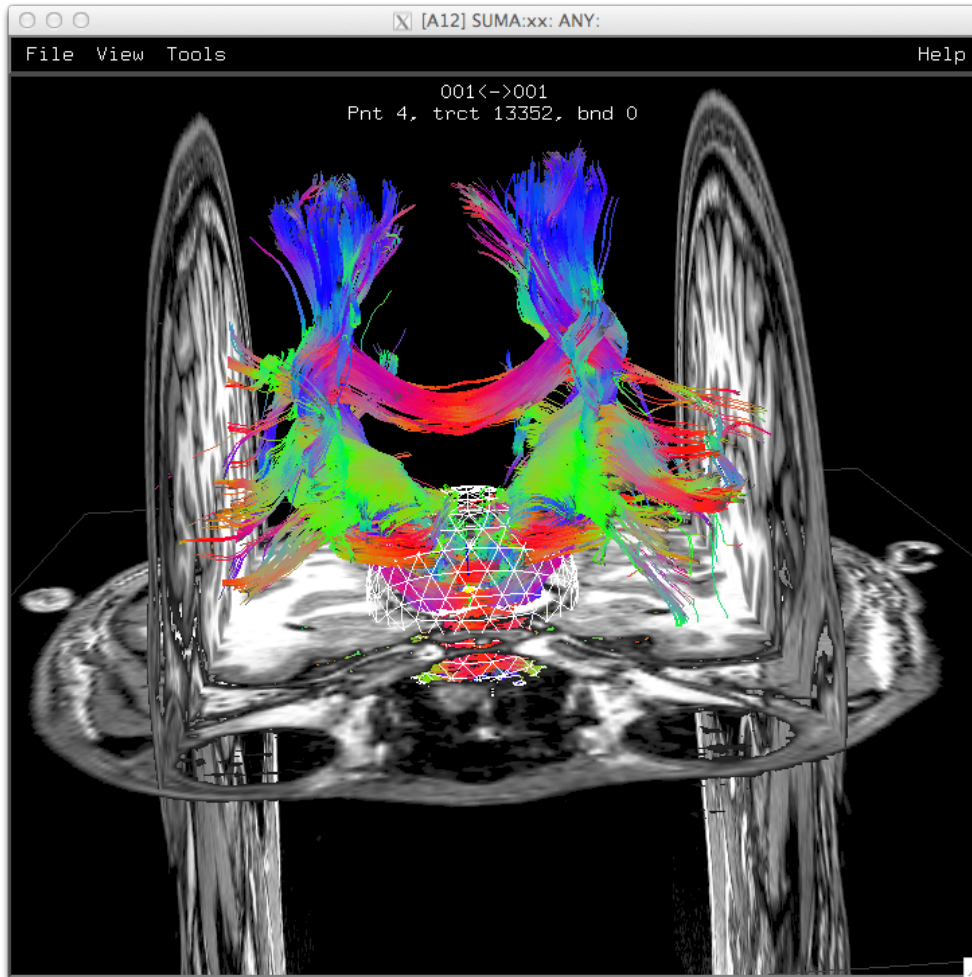


- Tracts are generated by AFNI's FATCAT toolbox
 - If using AFNI bootcamp data:
 - `cd ~/AFNI_demos/FATCAT_DEMO`
 - Else
 - Run `@Install_FATCAT_DEMO` for demo data and scripts
- If you have not done so already
 - Process everything with `tcsh Do_00_PRESTO_ALL_RUNS.tcsh`
- To look at whole brain tracts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

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

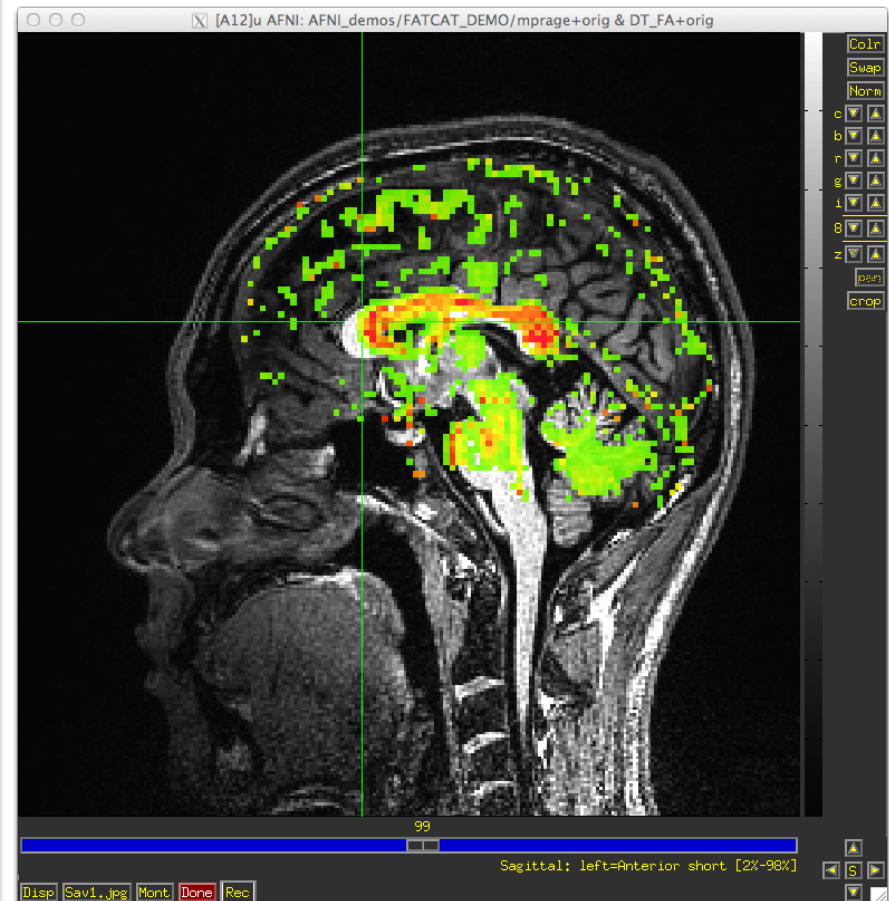
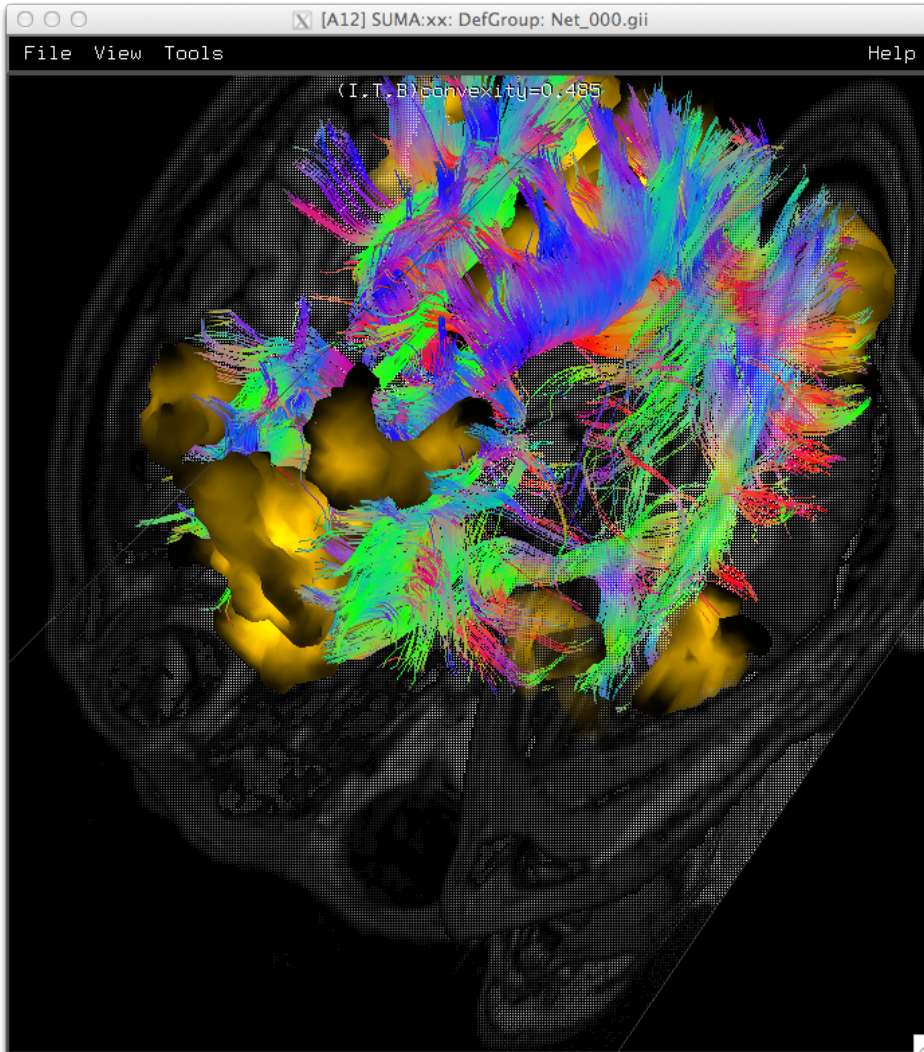
tssh Do_06_VISdti_SUMA_visual_ex1.tssh

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



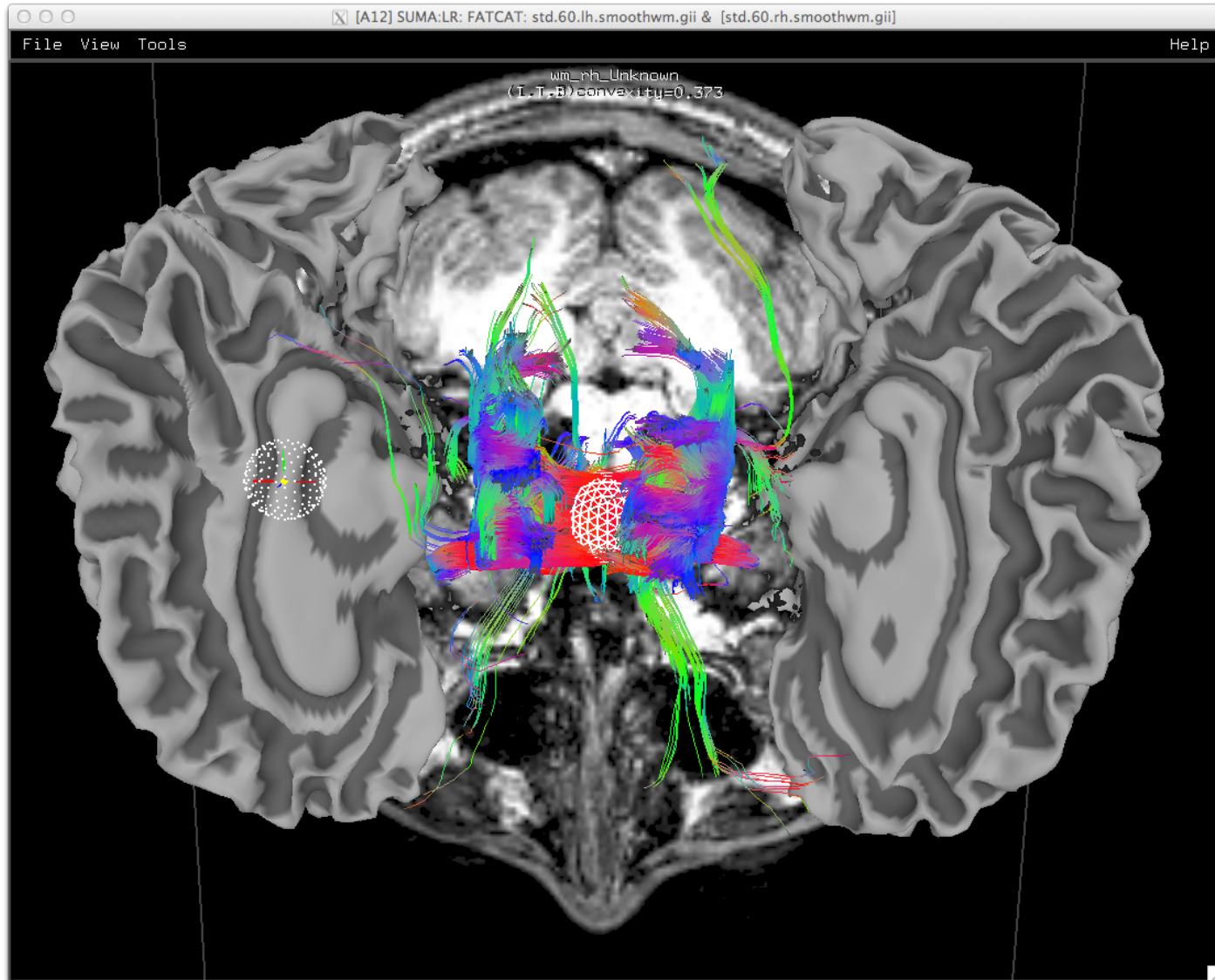
tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

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



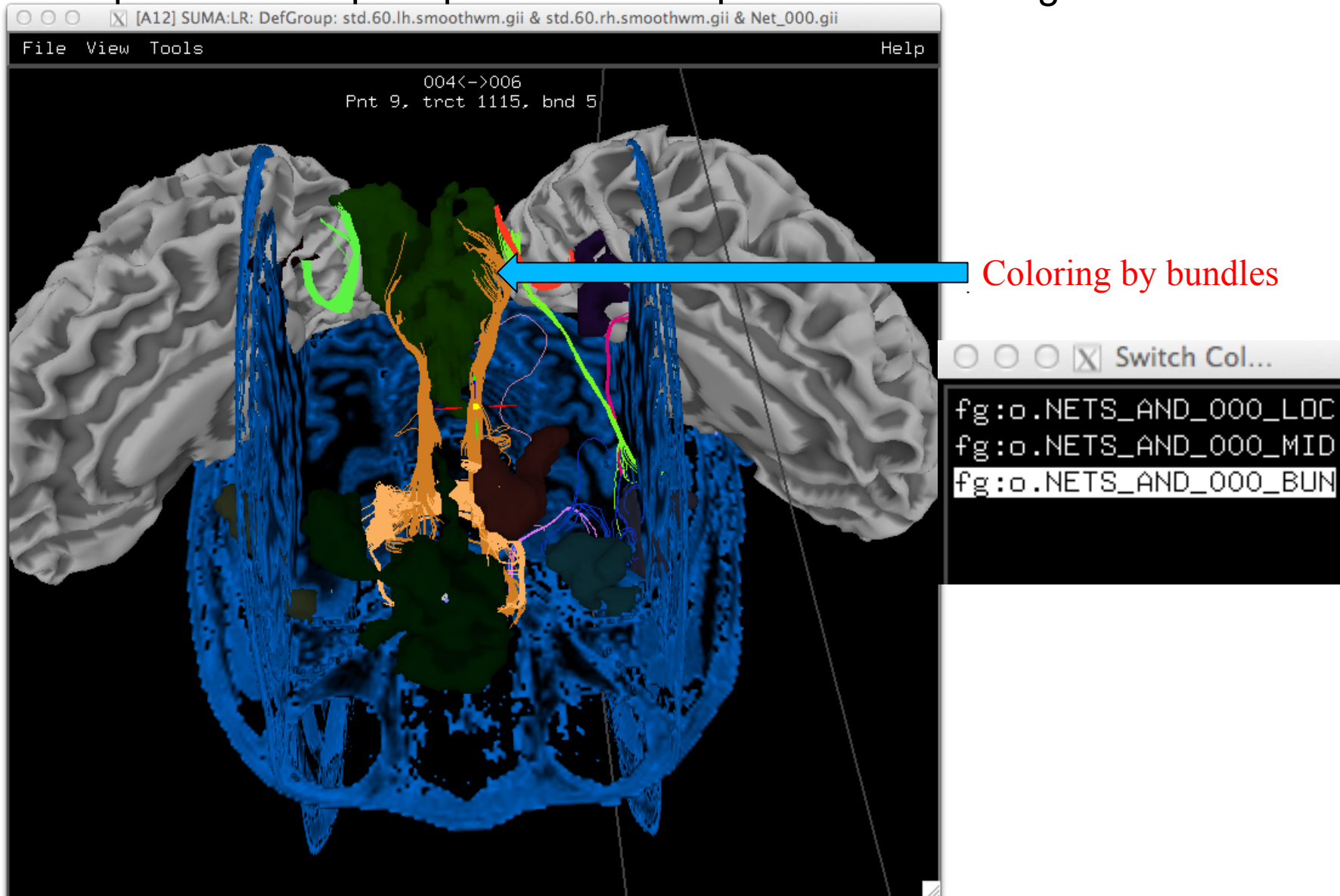
tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

- 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:

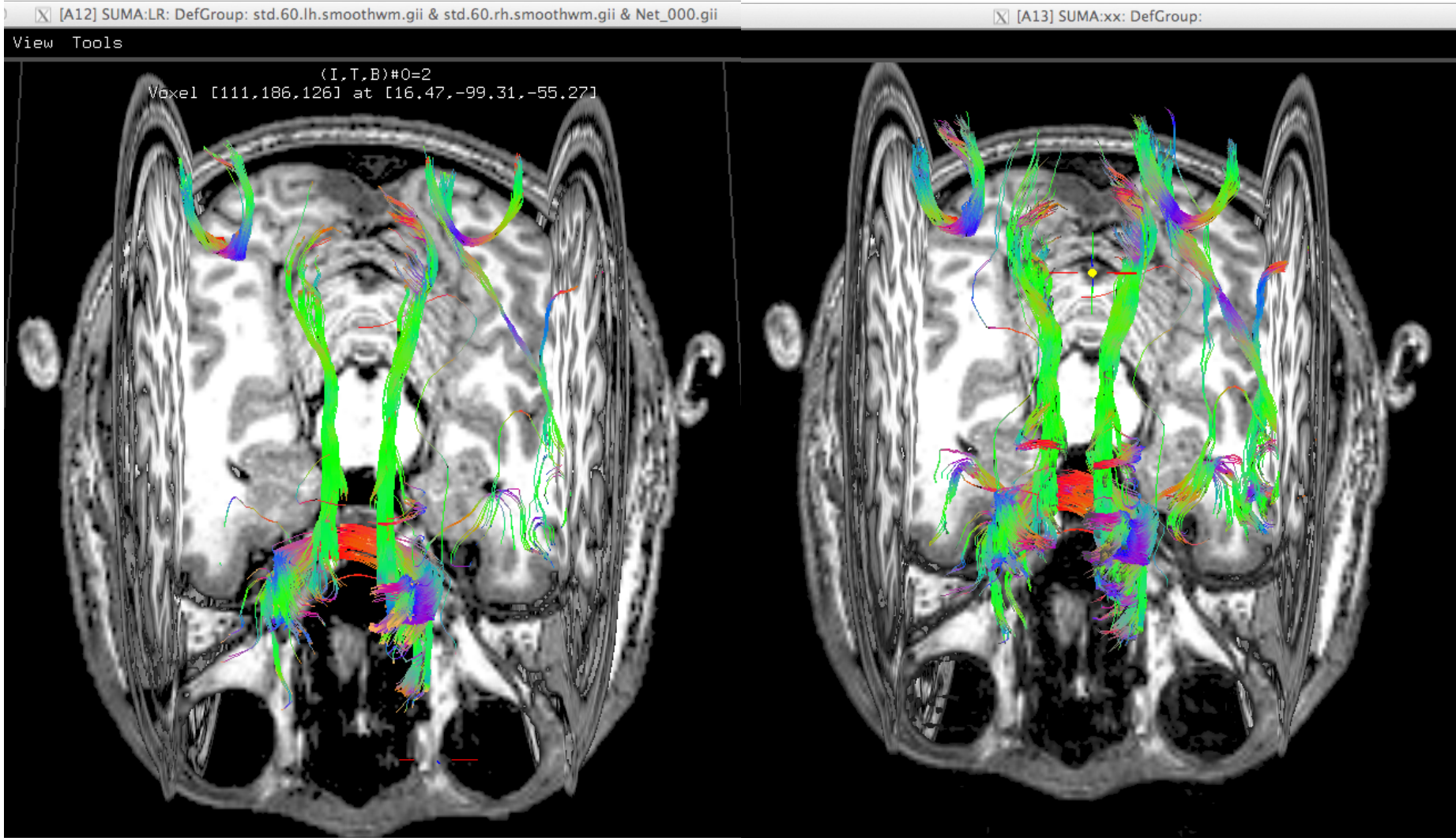


tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

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

Deterministic

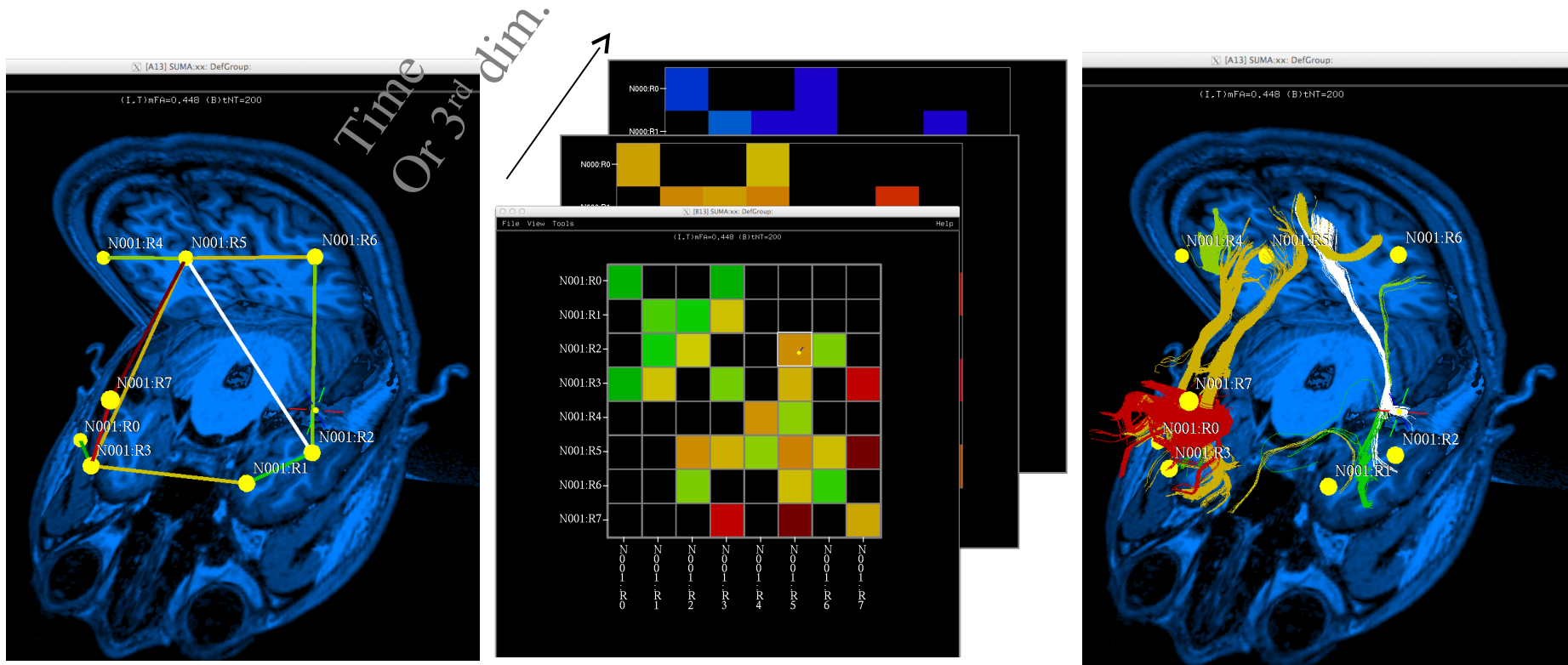
MINIPROB 9 iterations



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)



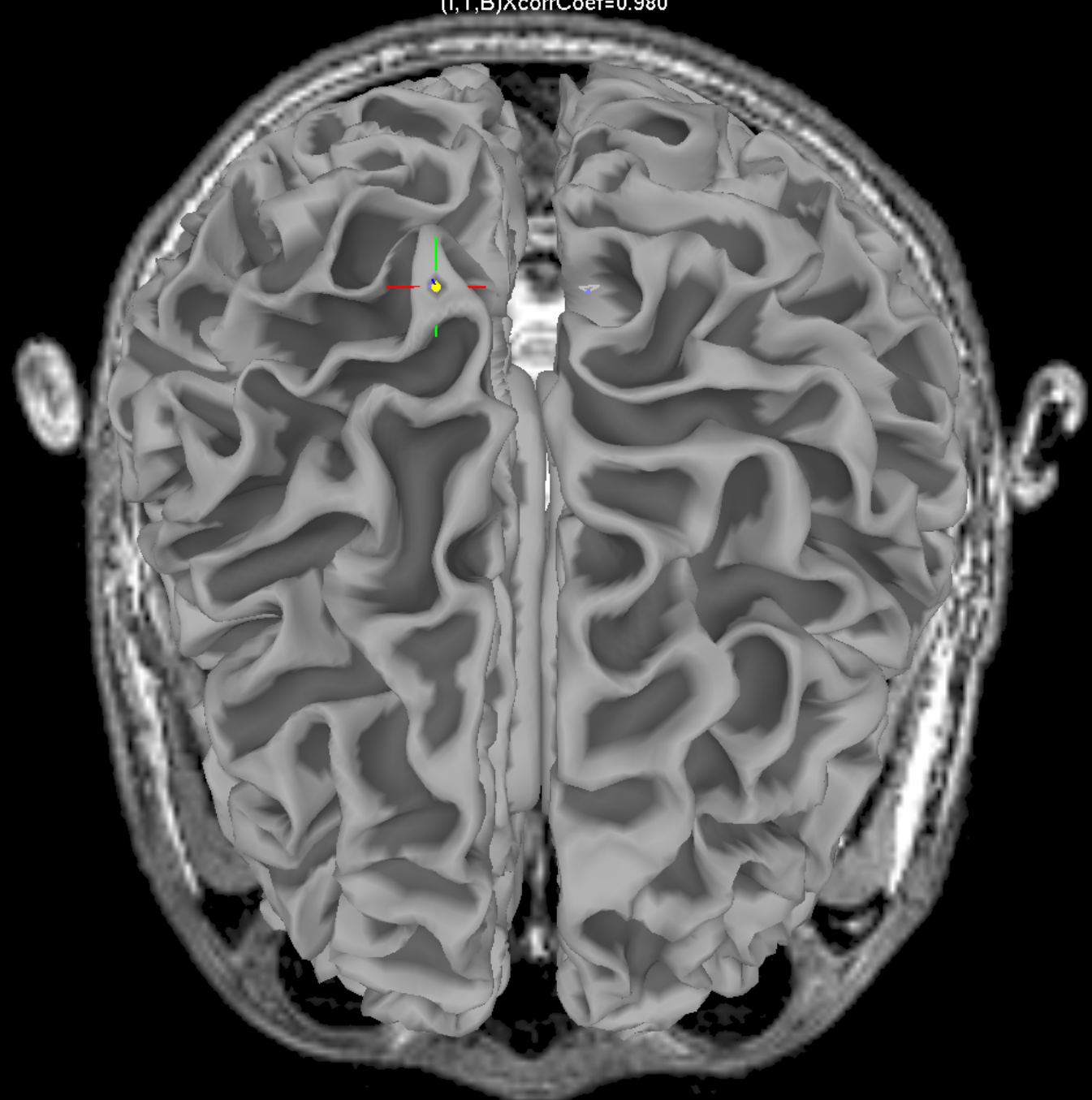
[tcsh Do 09 VISdti SUMA visual ex2.tcsh](#)

Simultaneous InstaCorr & InstaTract

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

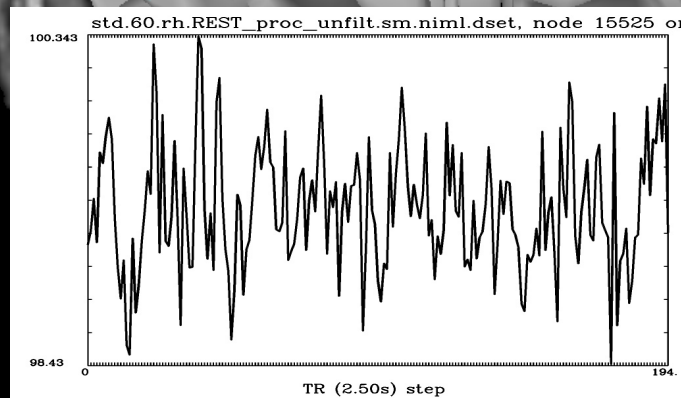
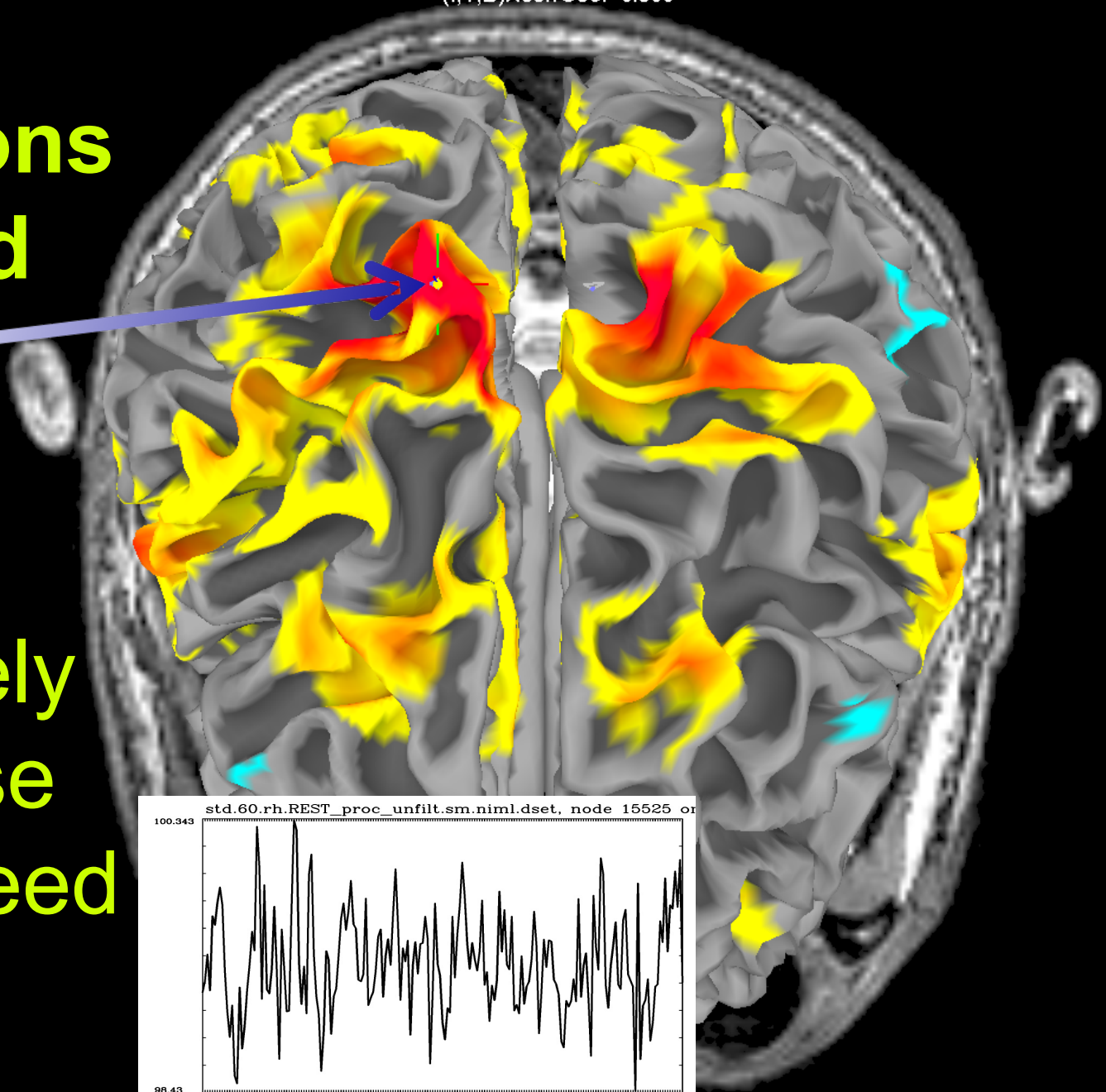
wm_rh_G and S_paracentral
(I,T,B)XcorrCoef=0.980

**Naked
brain
surface**



**RS-FMRI
correlations
from seed
voxel**

**computed
interactively
with mouse
click on seed**

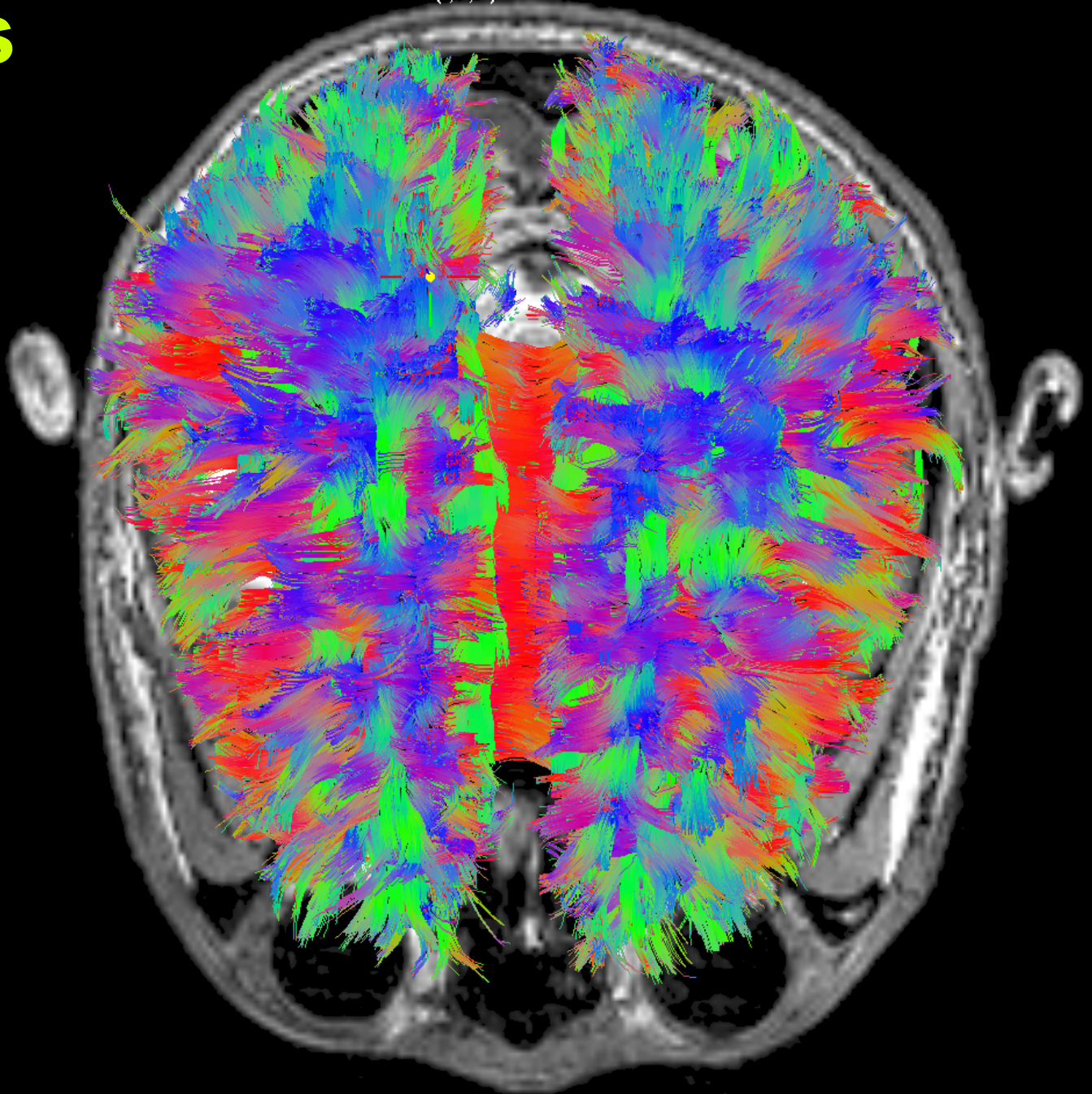


wm_rh_G and S_paracentral
(T,T,B)XcorrCoef=0.980

DTI tracts

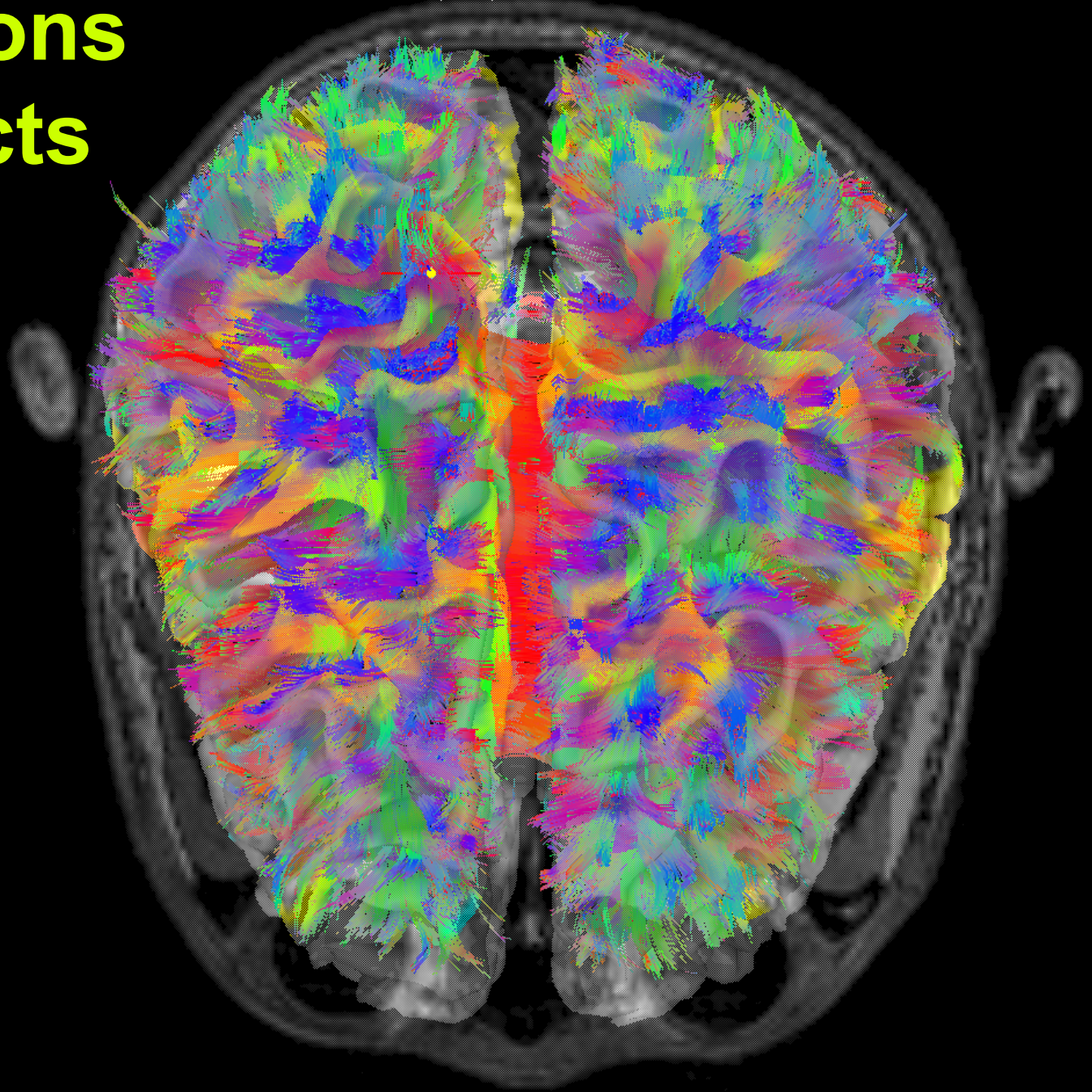
[brain is
hidden]

Just too
much to
take in!



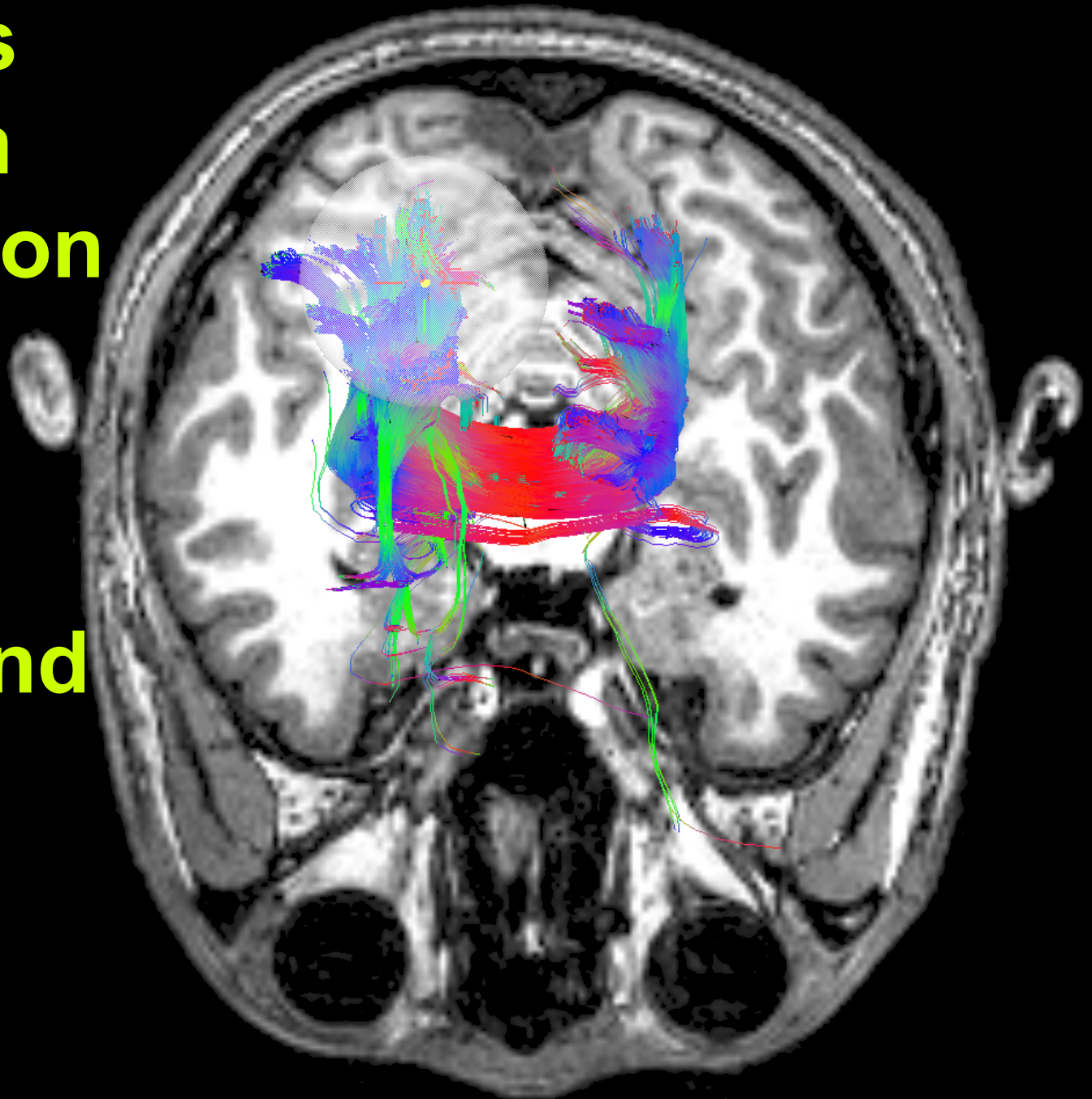
**Correlations
+ DTI tracts
+ Brain**

**Way too
much to
take in!**



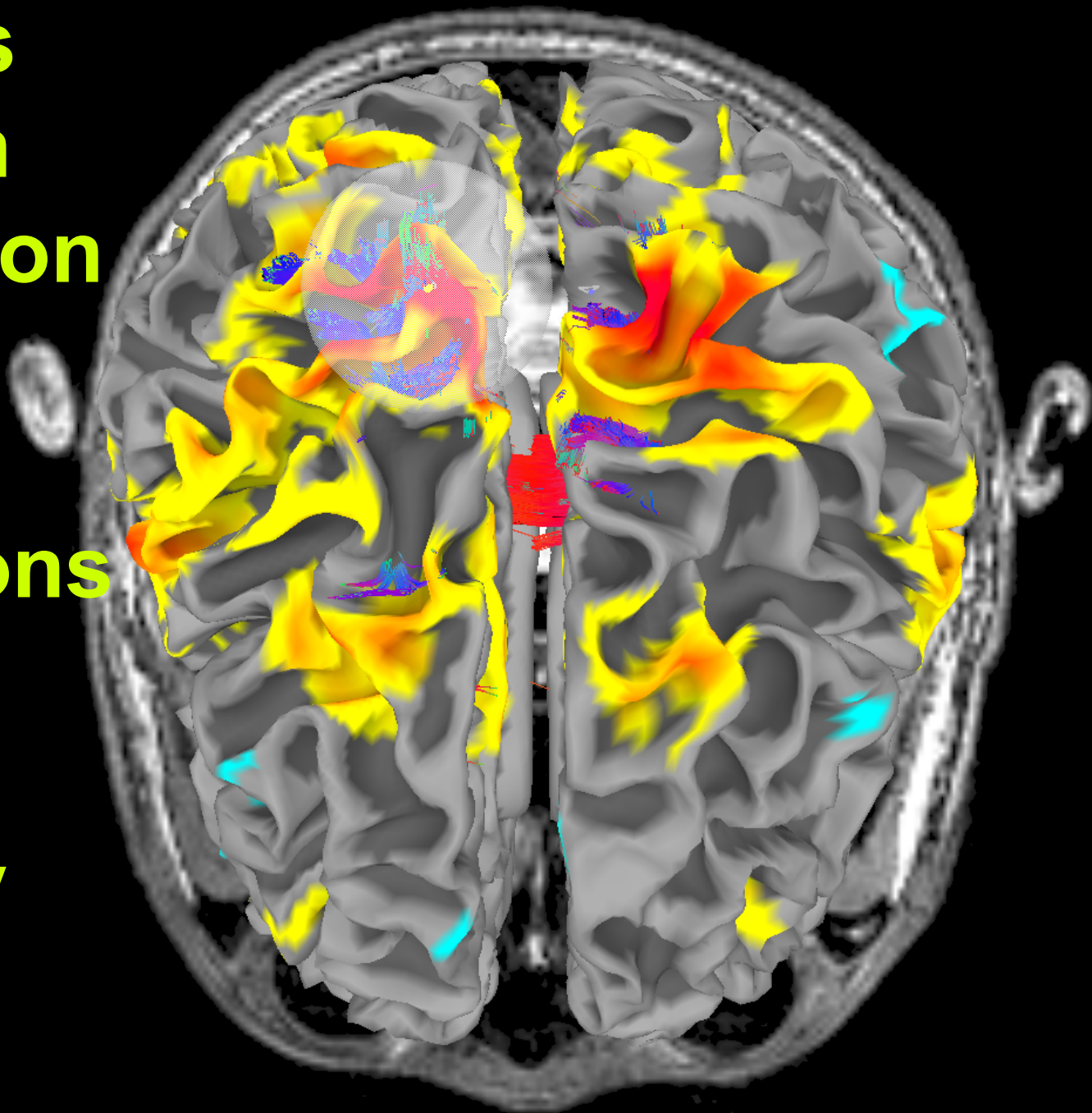
**DTI tracts
only from
seed region**

***Much
easier to
understand***



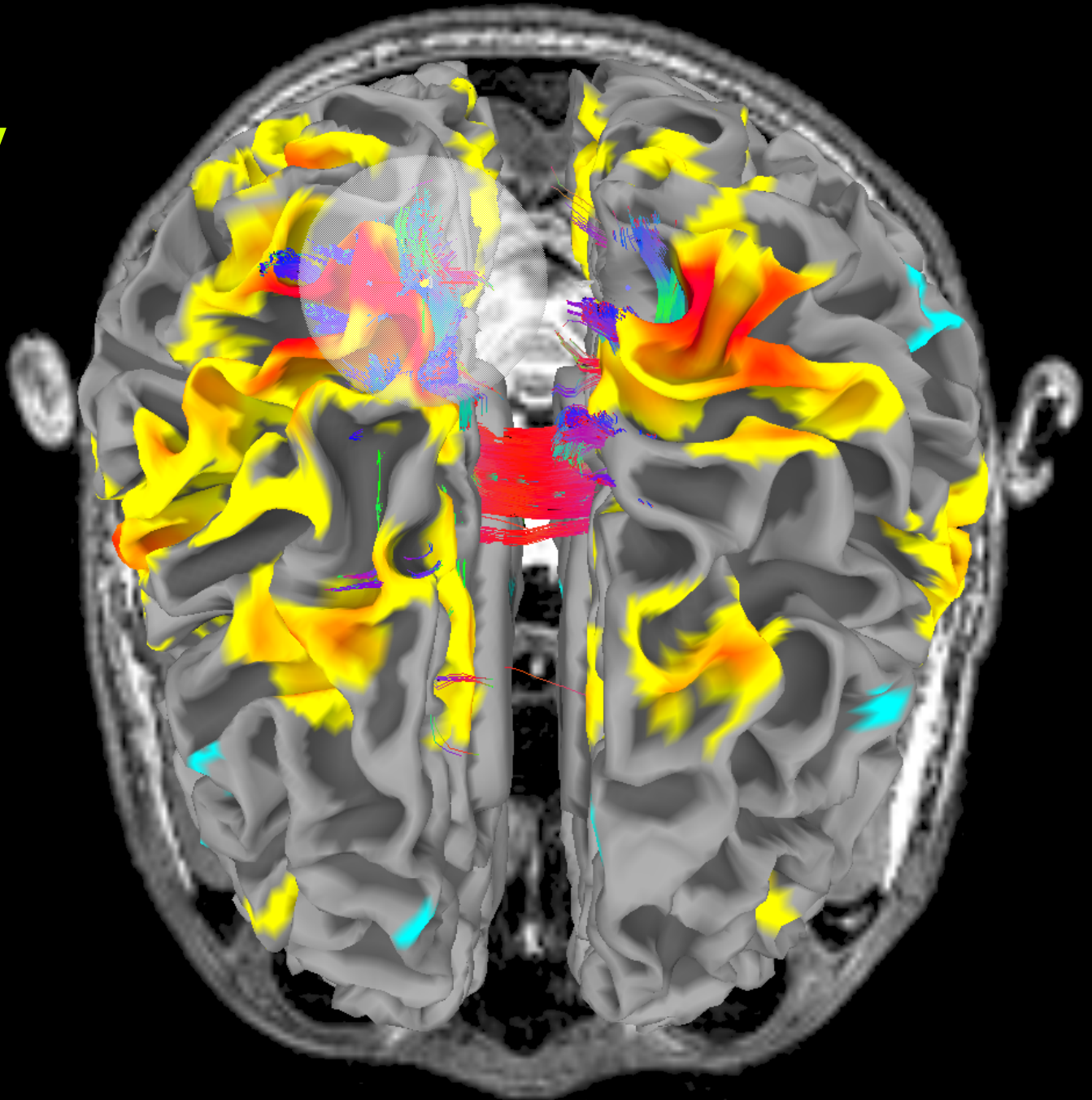
**DTI tracts
only from
seed region
+ time
series
correlations**

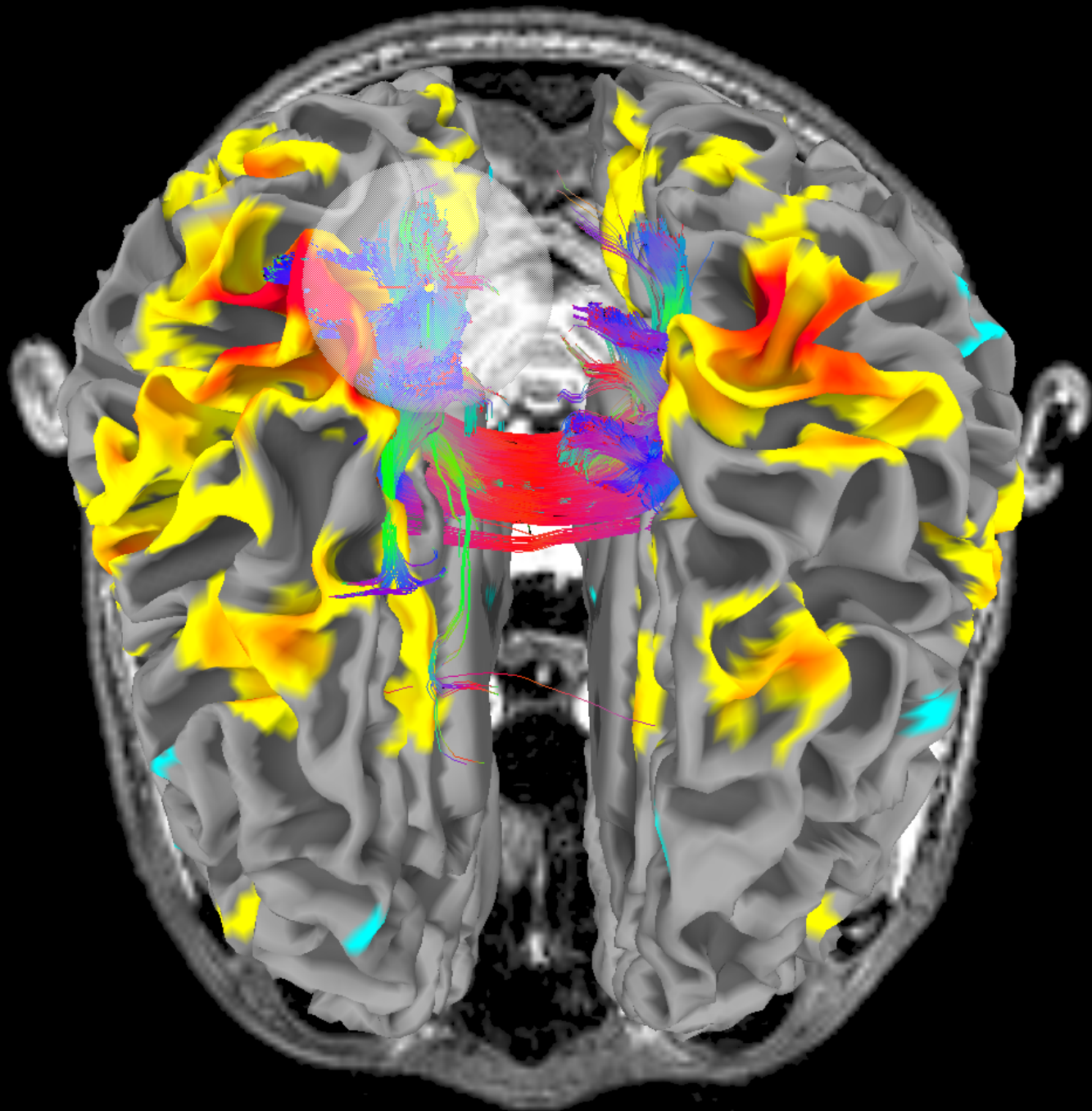
**Brain is
in the way**

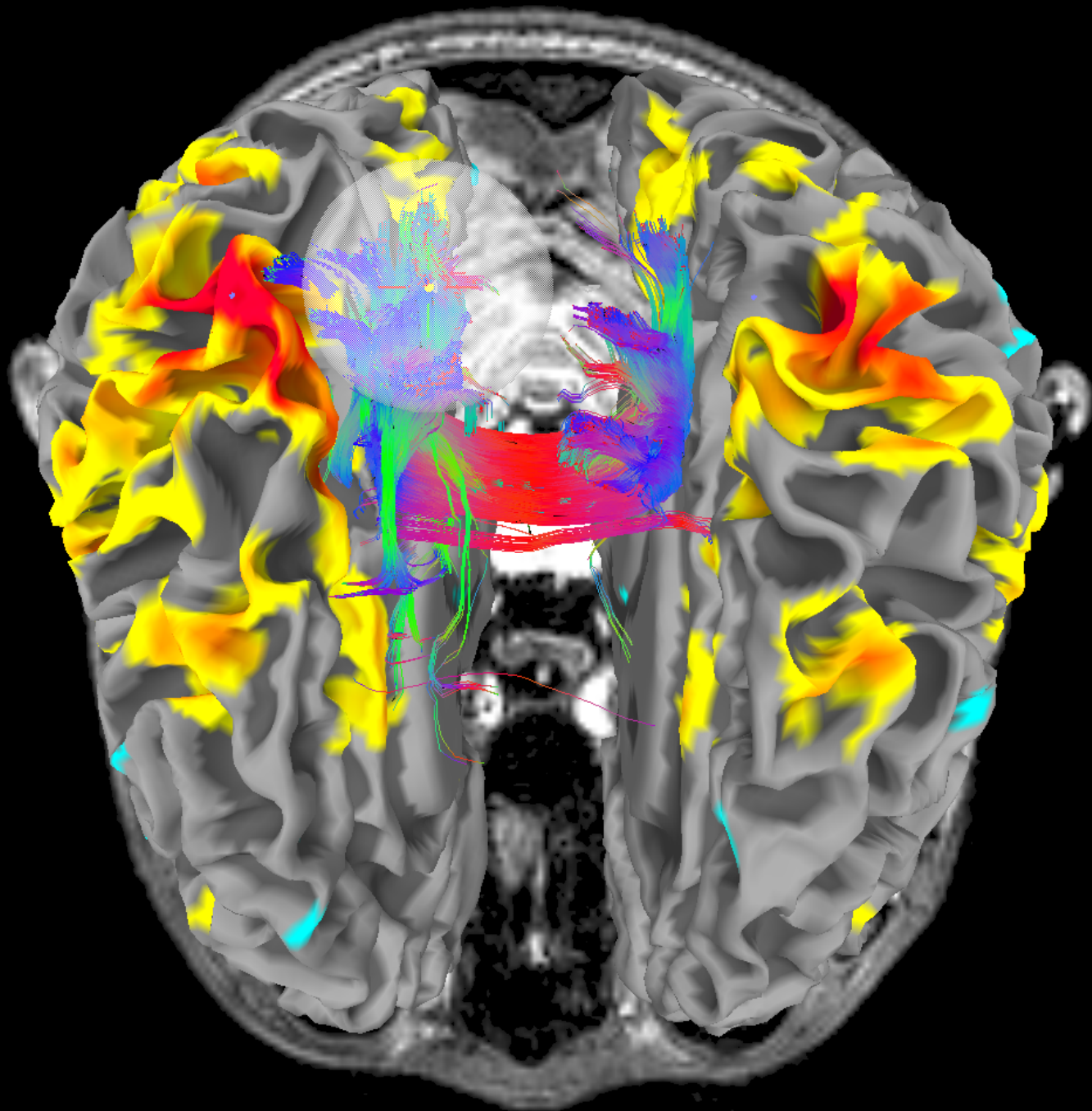


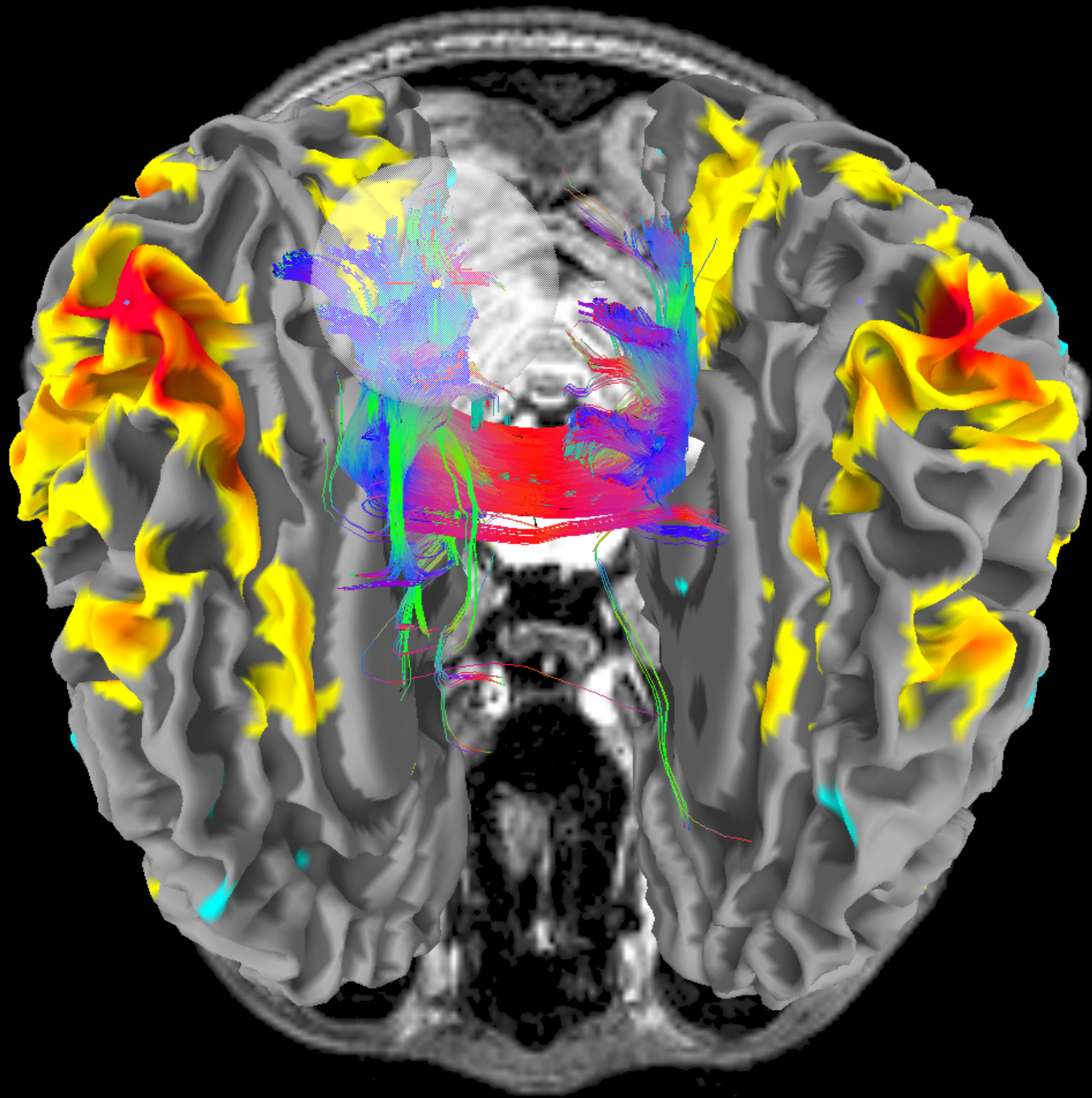
Brain is
in the way

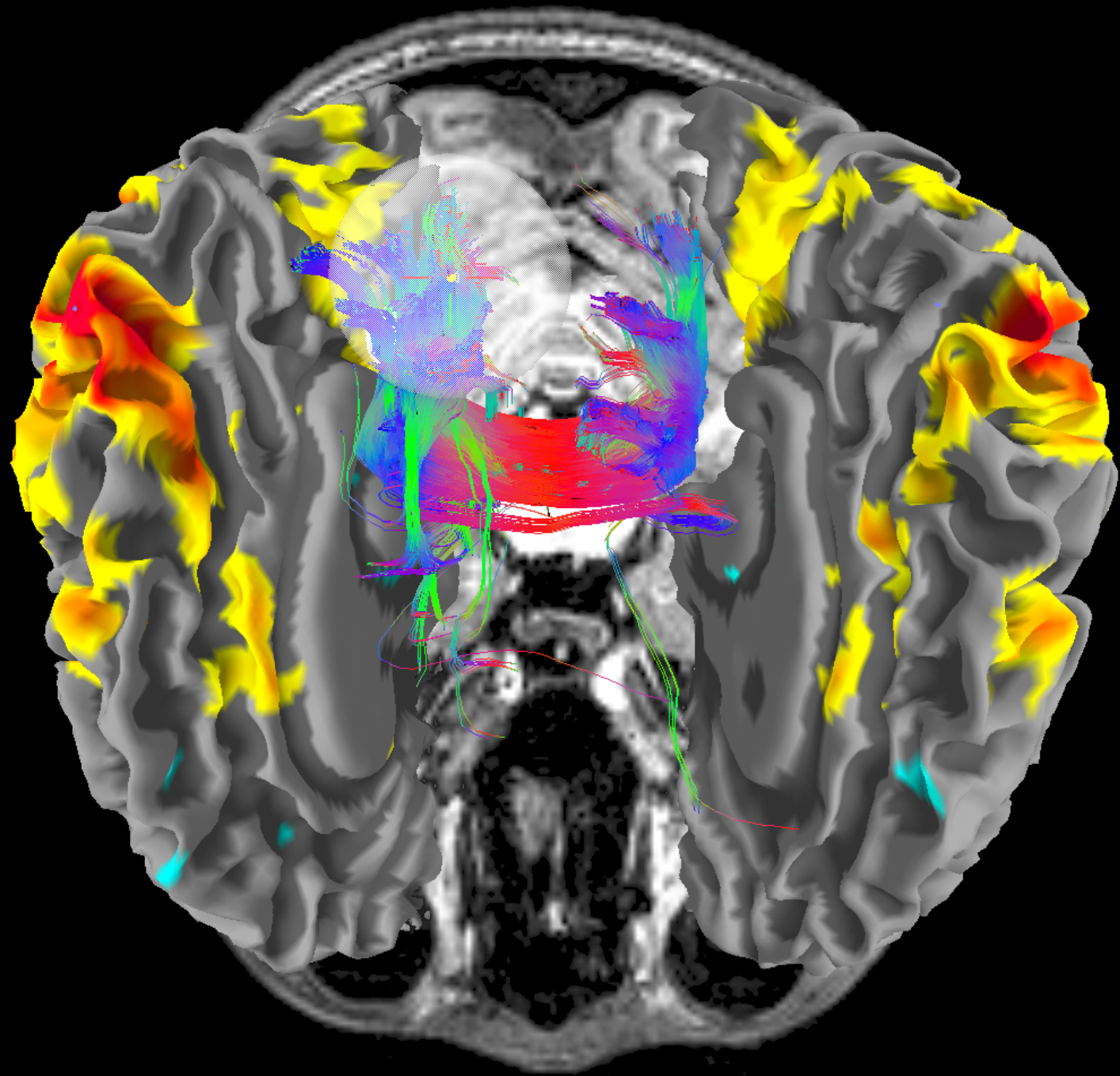
So move
it aside!

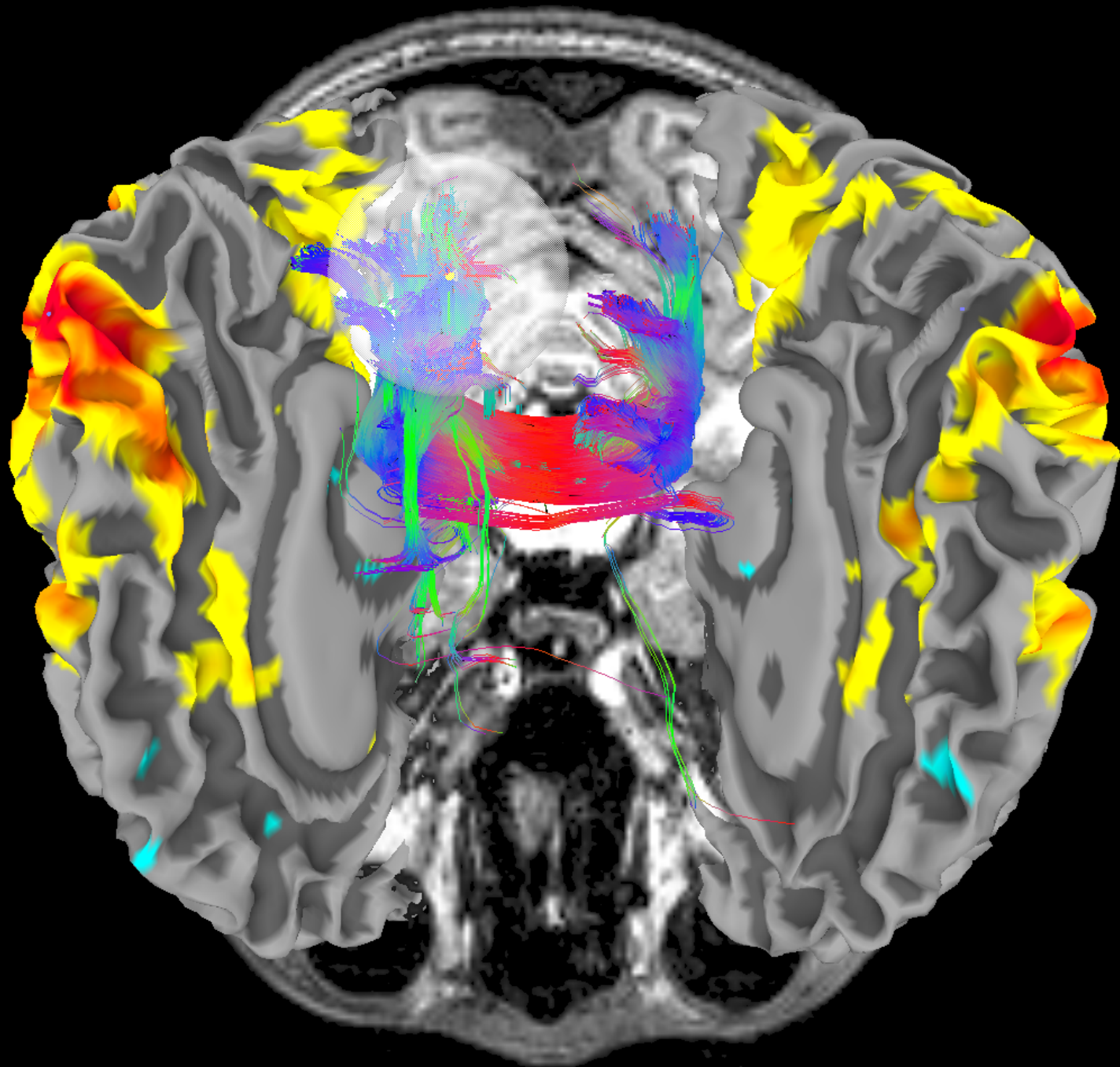




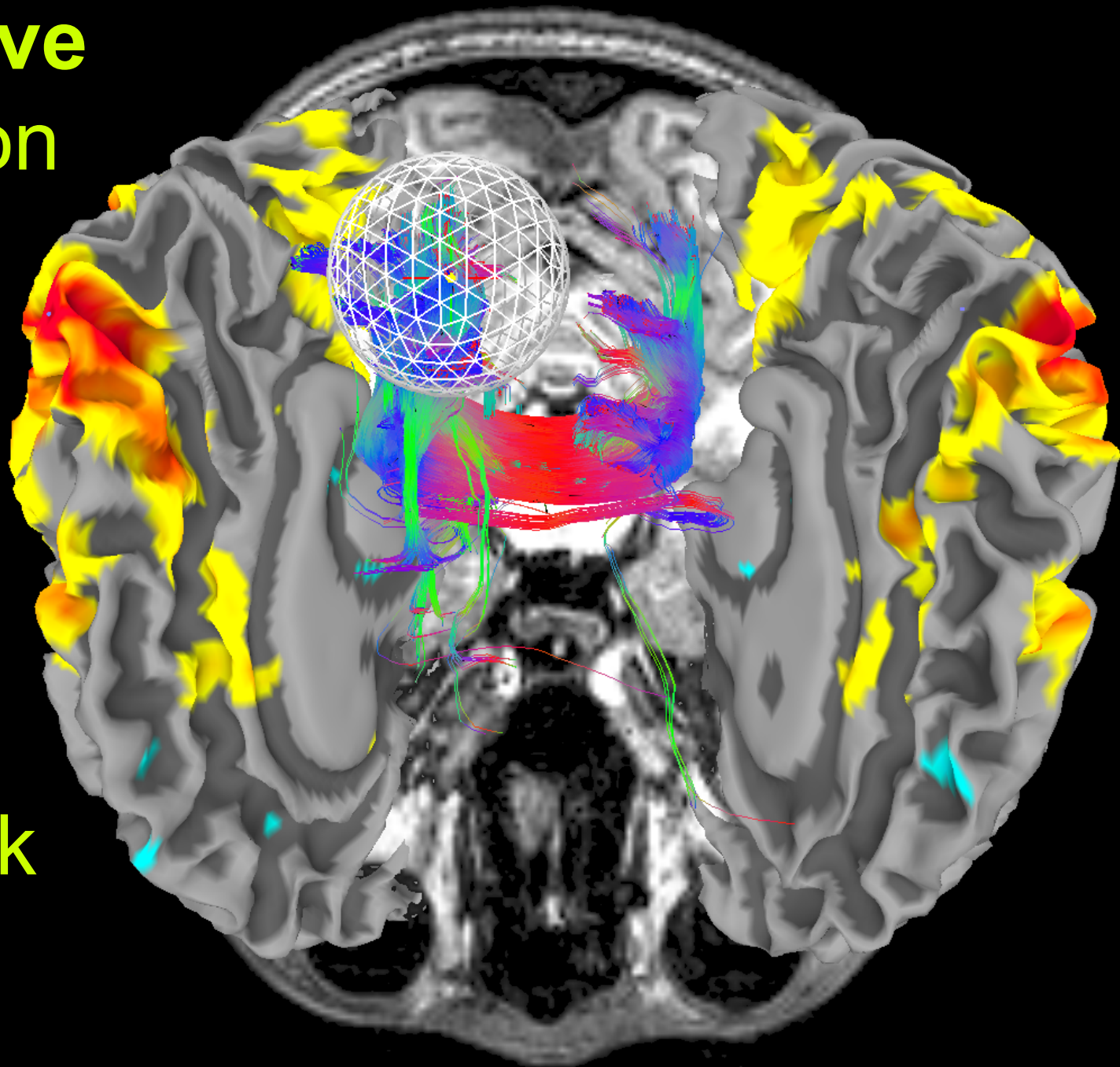




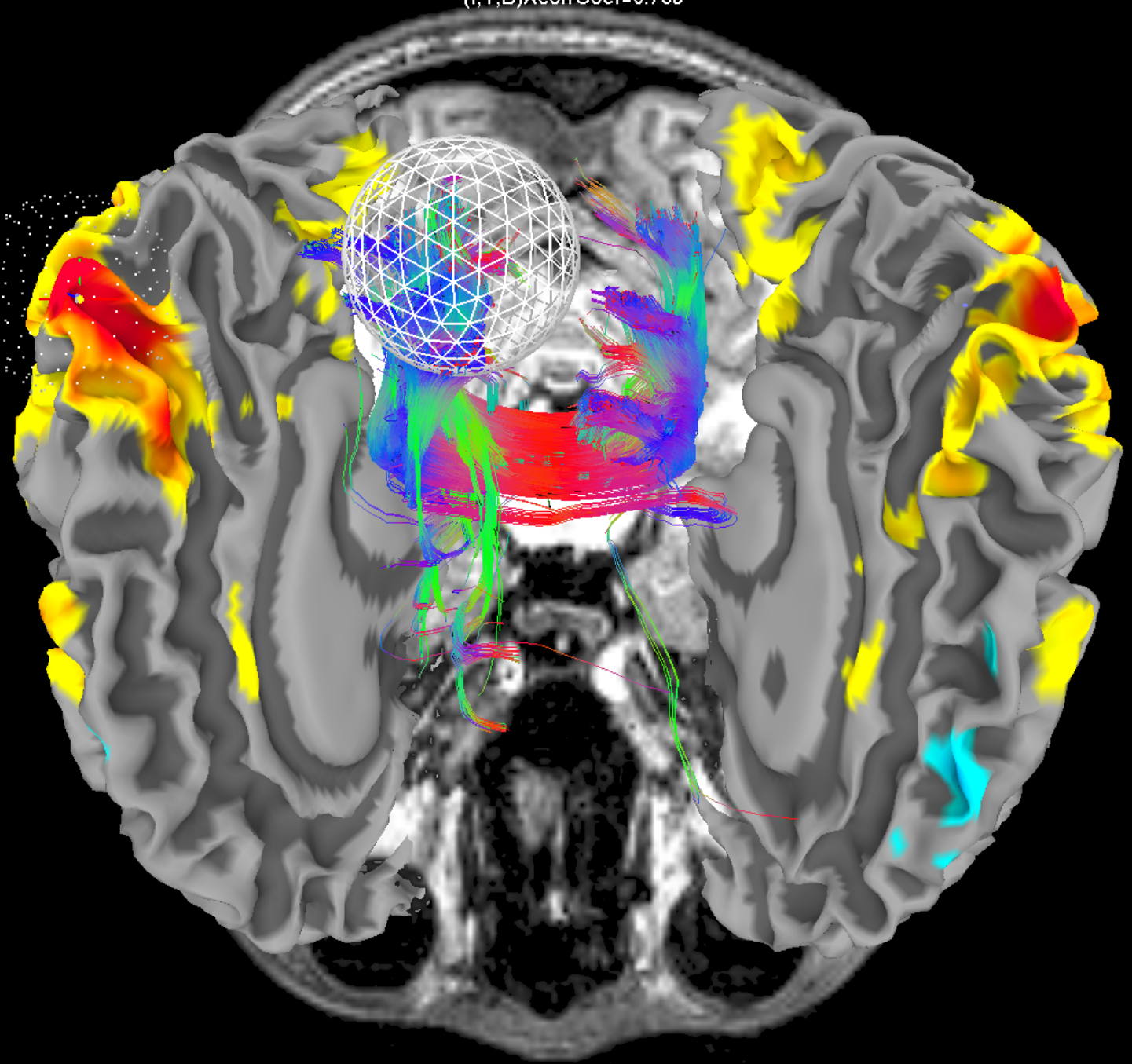




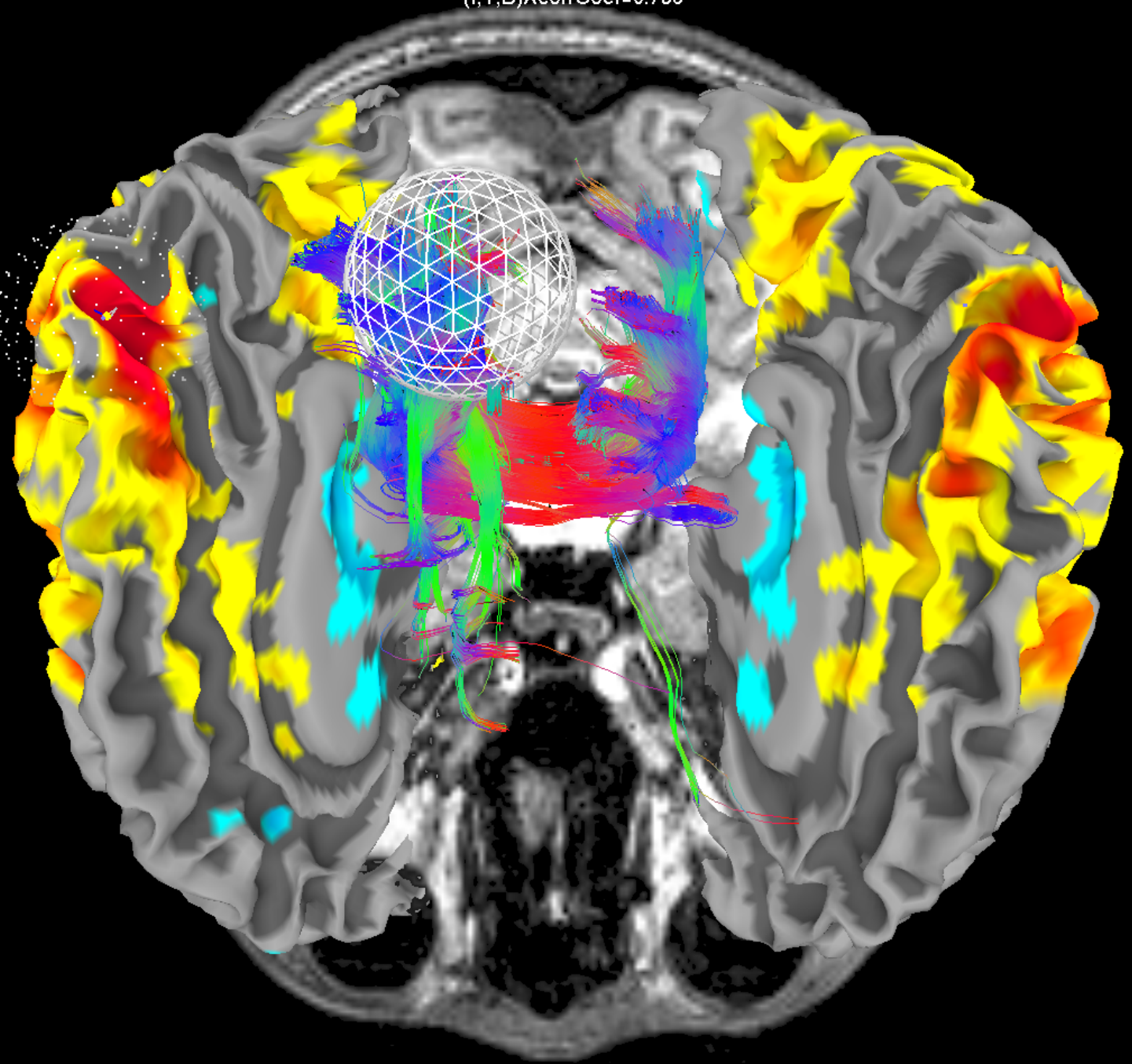
**Now move
correlation
and
tract
seed
along
the
sulcus
from back
to front**



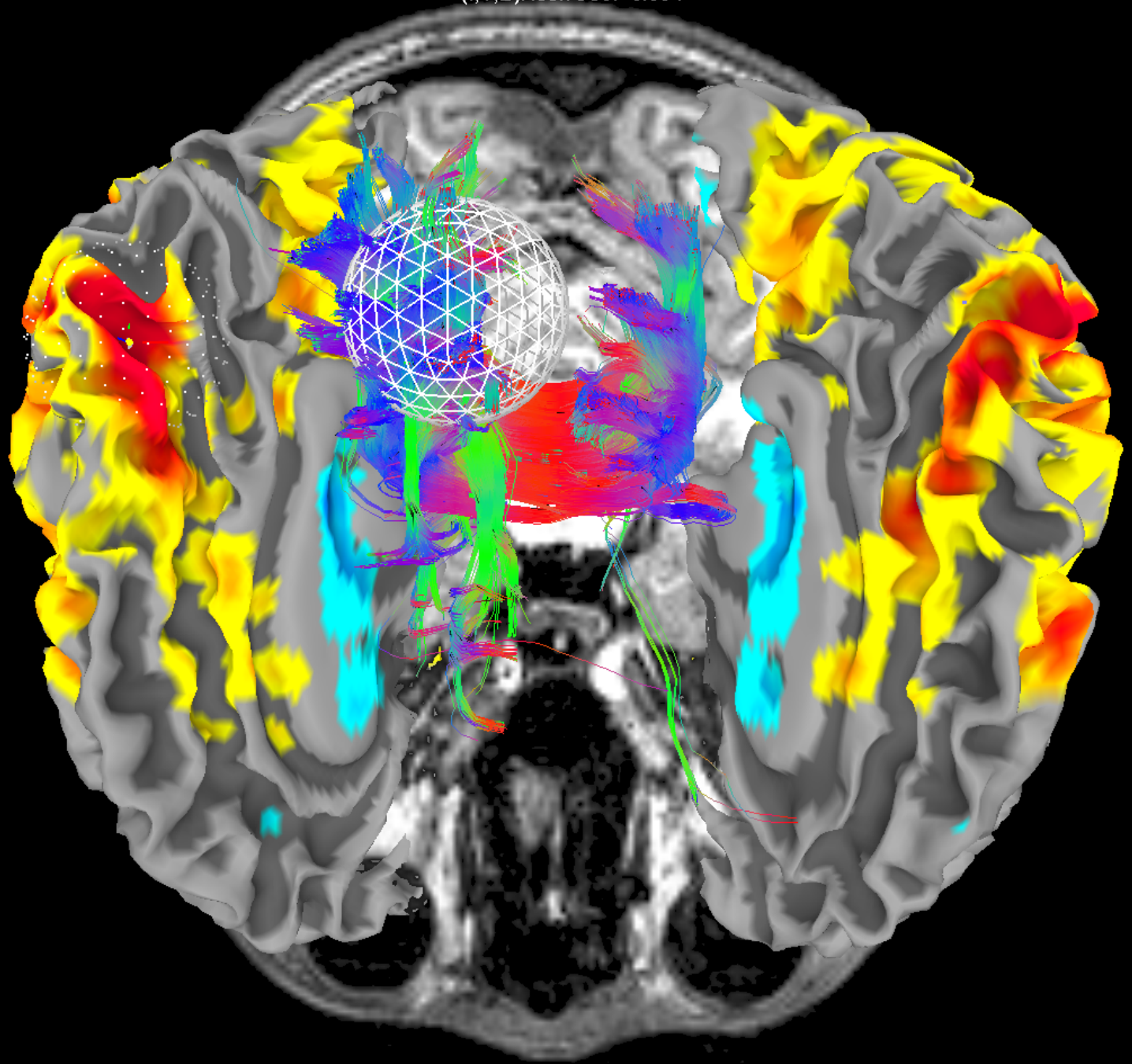
wm rh G and S_paracentral
(I,T,B)XcorrCoef=0.765



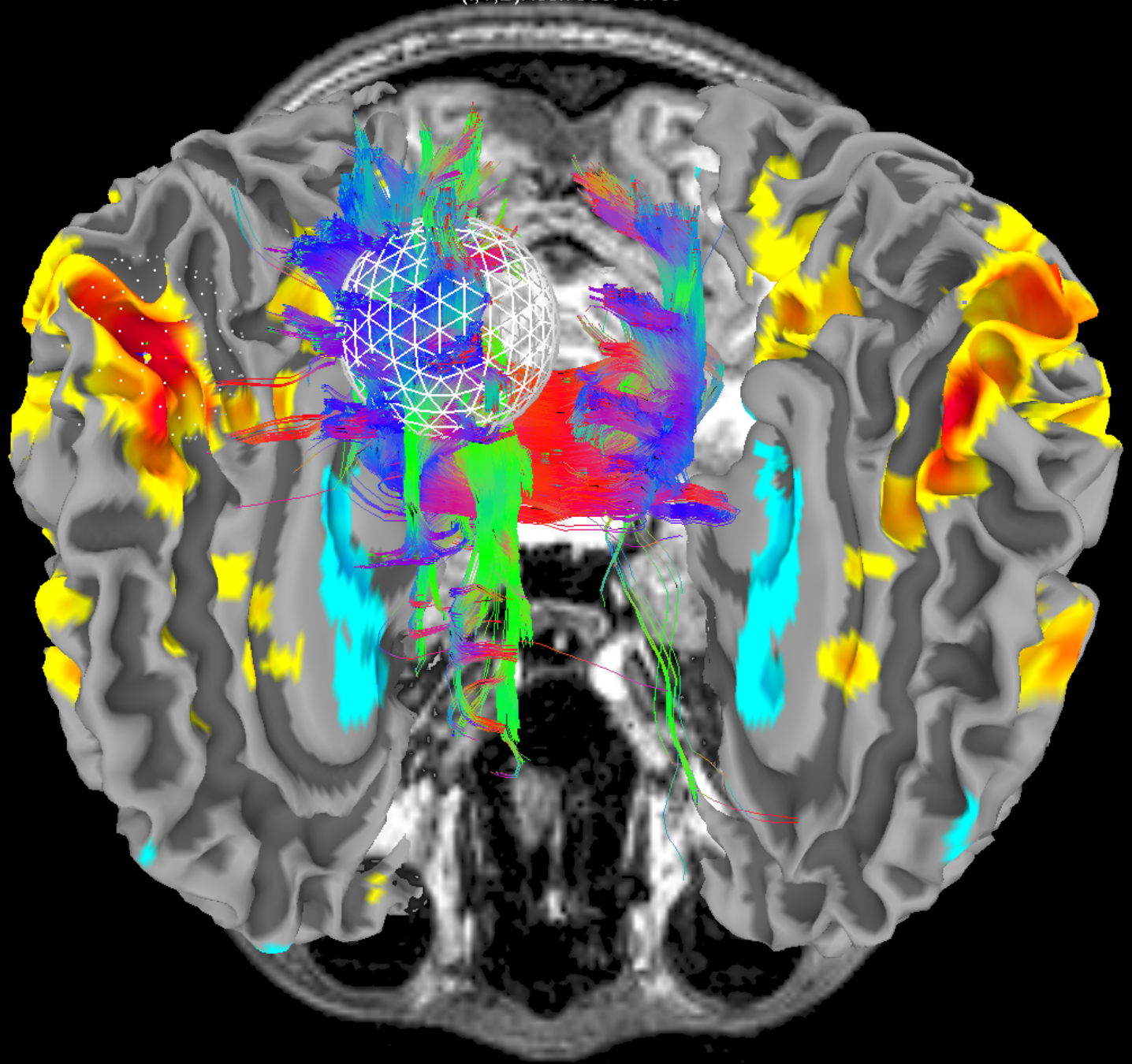
wm rh G and S_paracentral
(I,T,B)XcorrCoef=0.753



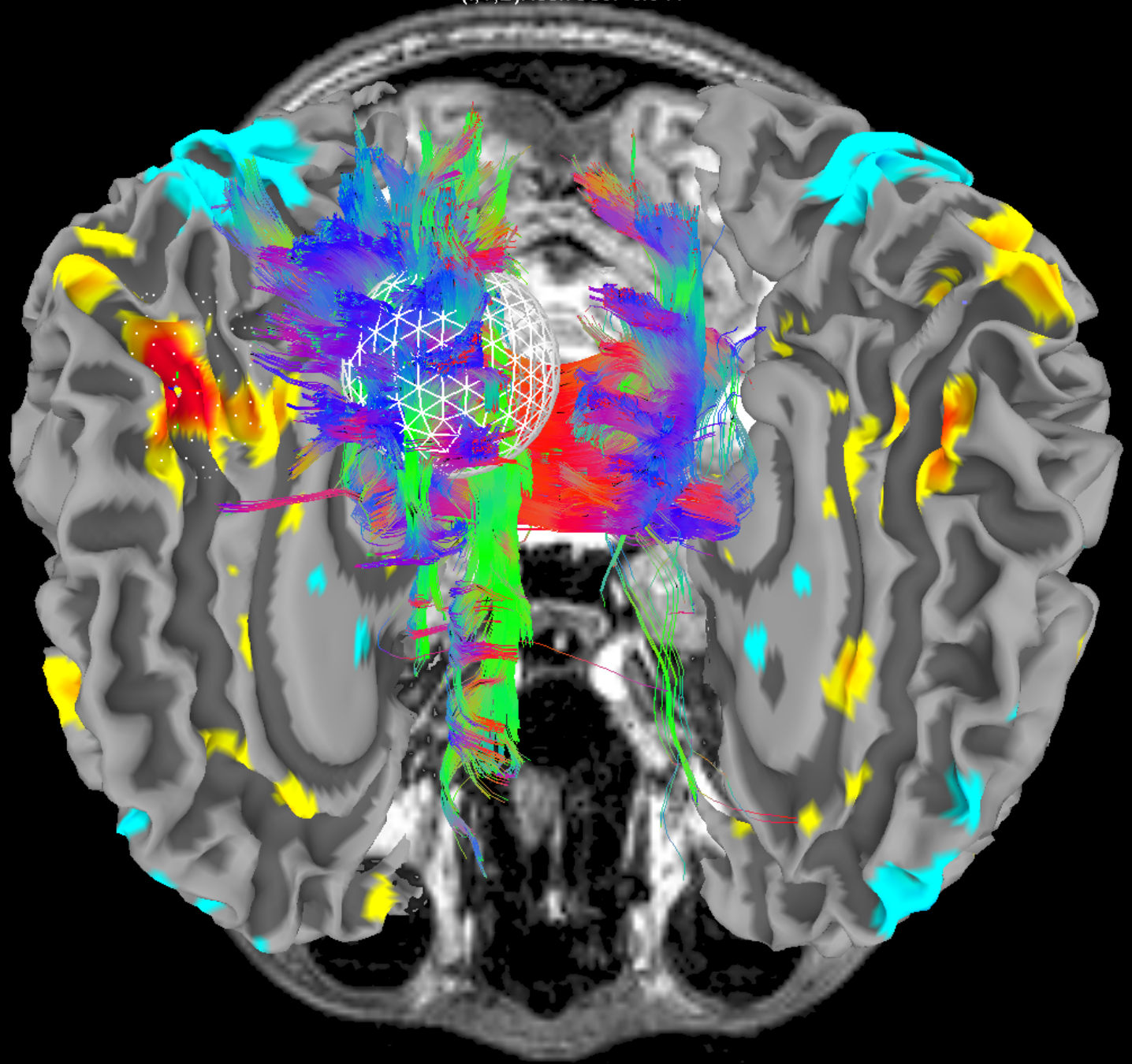
wm_rh_S_cingul-Marginalis
(I,T,B)XcorrCoef=0.884



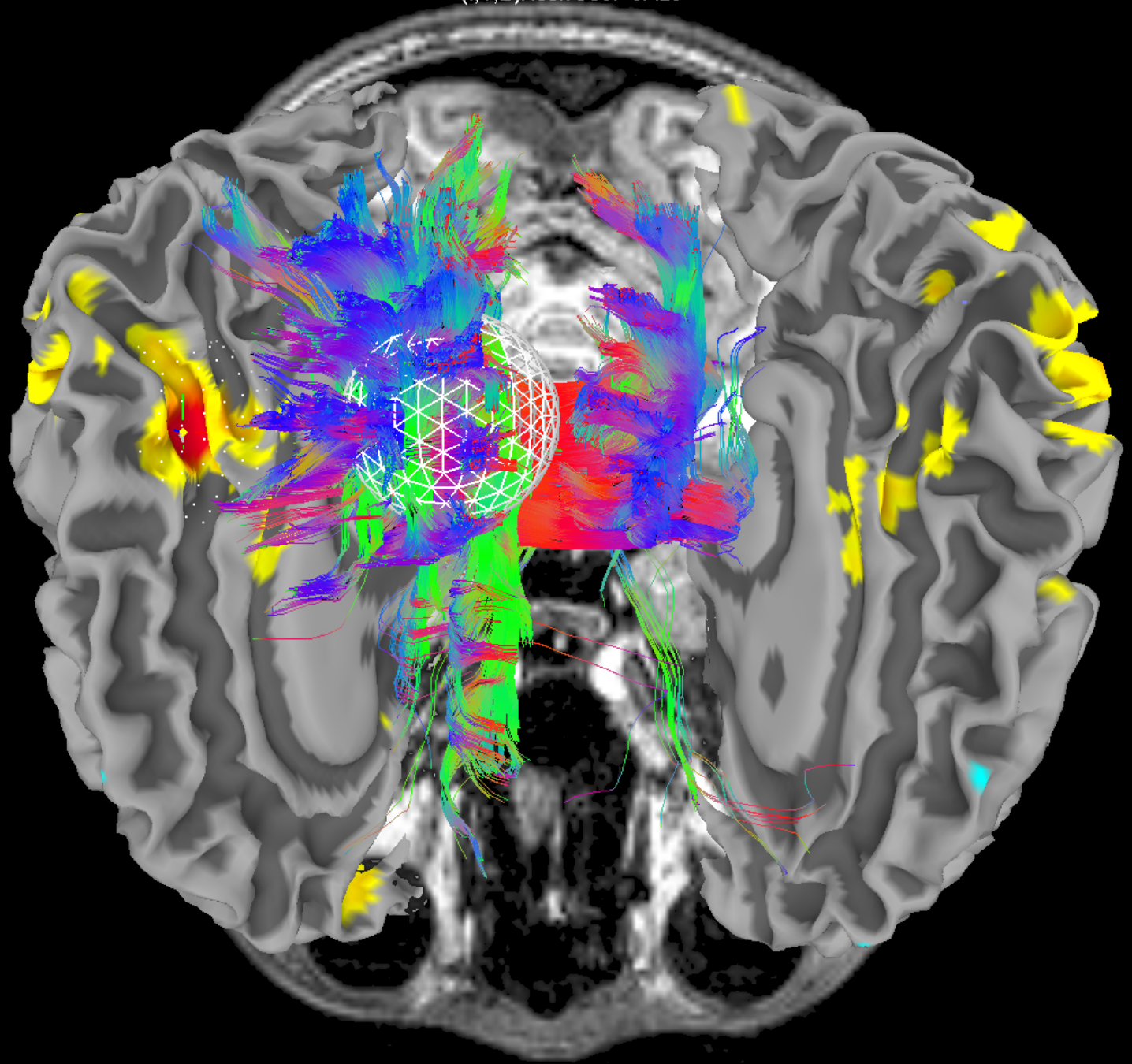
wm_rh_S_cingul-Marginalis
(I,T,B)XcorrCoef=0.780



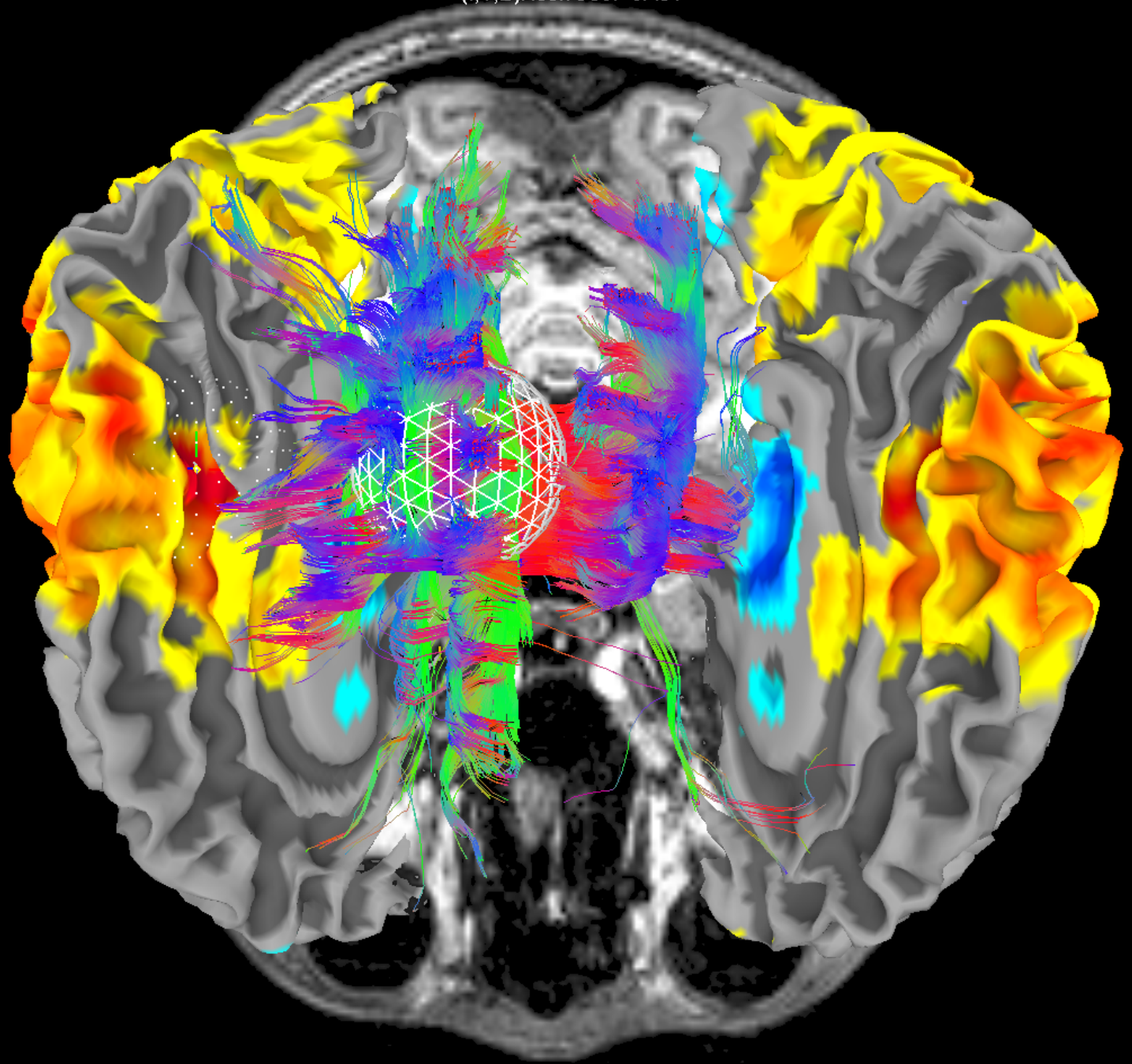
wm_rh_S_cingul-Marginalis
(I,T,B)XcorrCoef=0.644



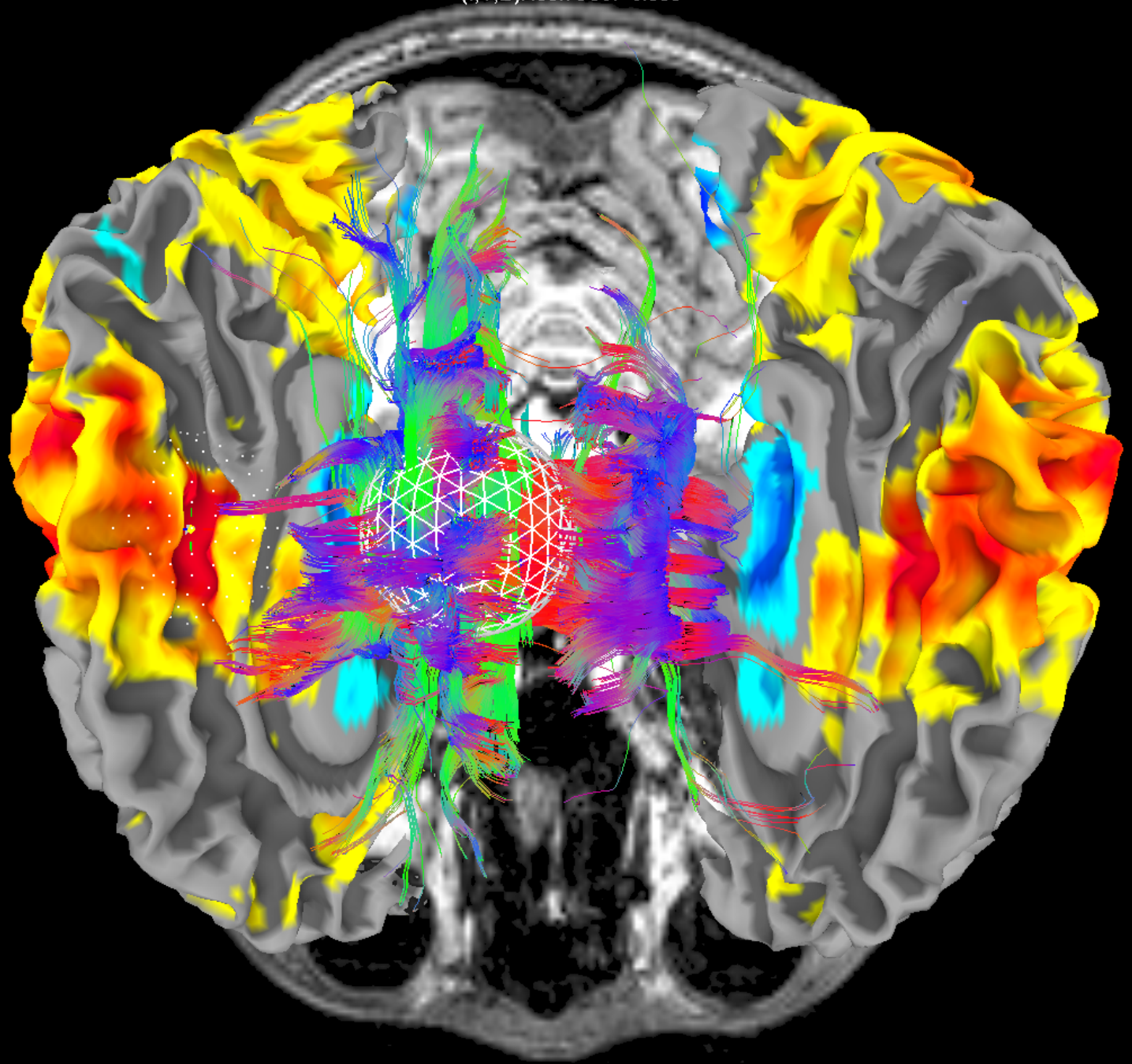
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.423



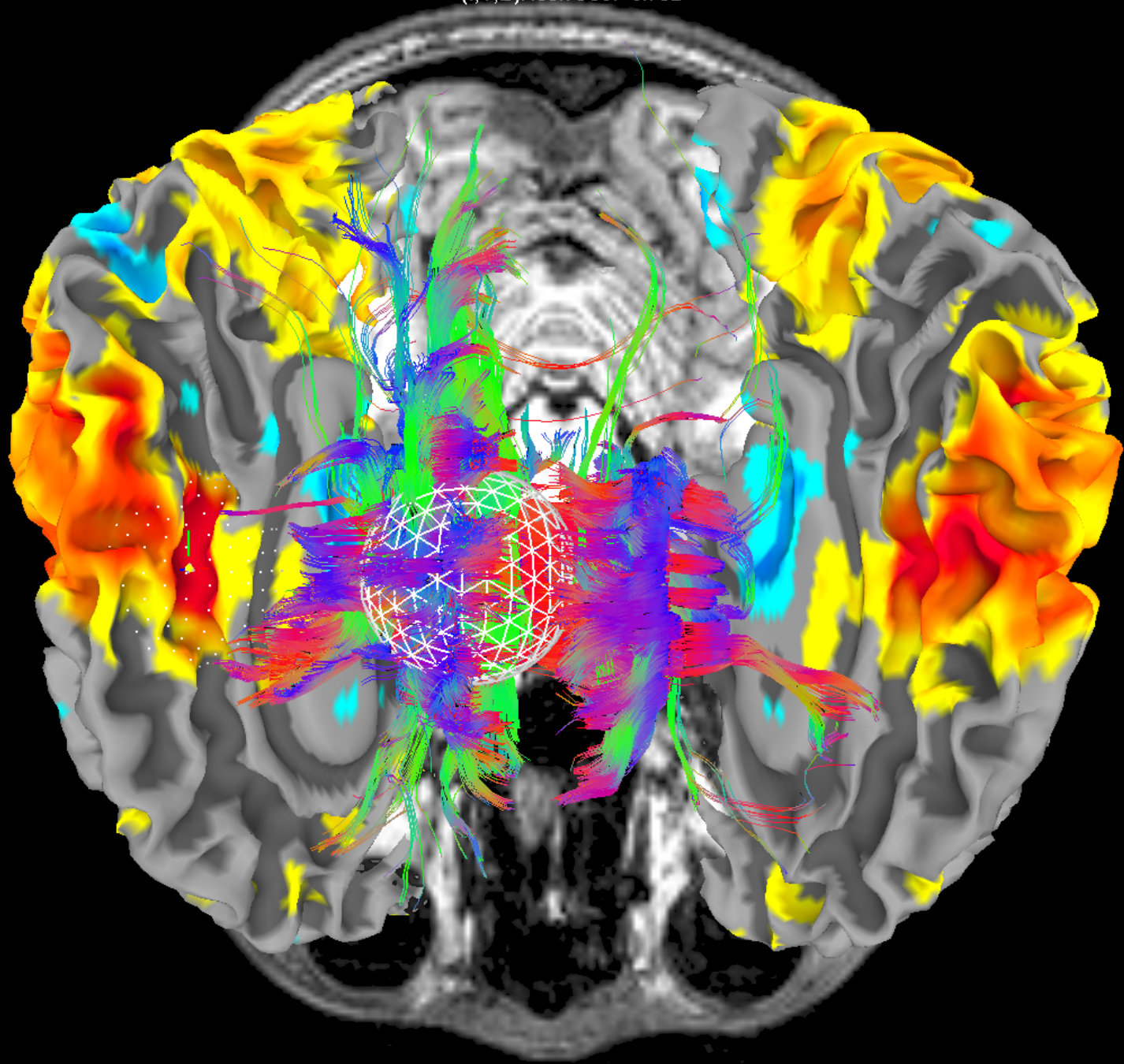
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.491



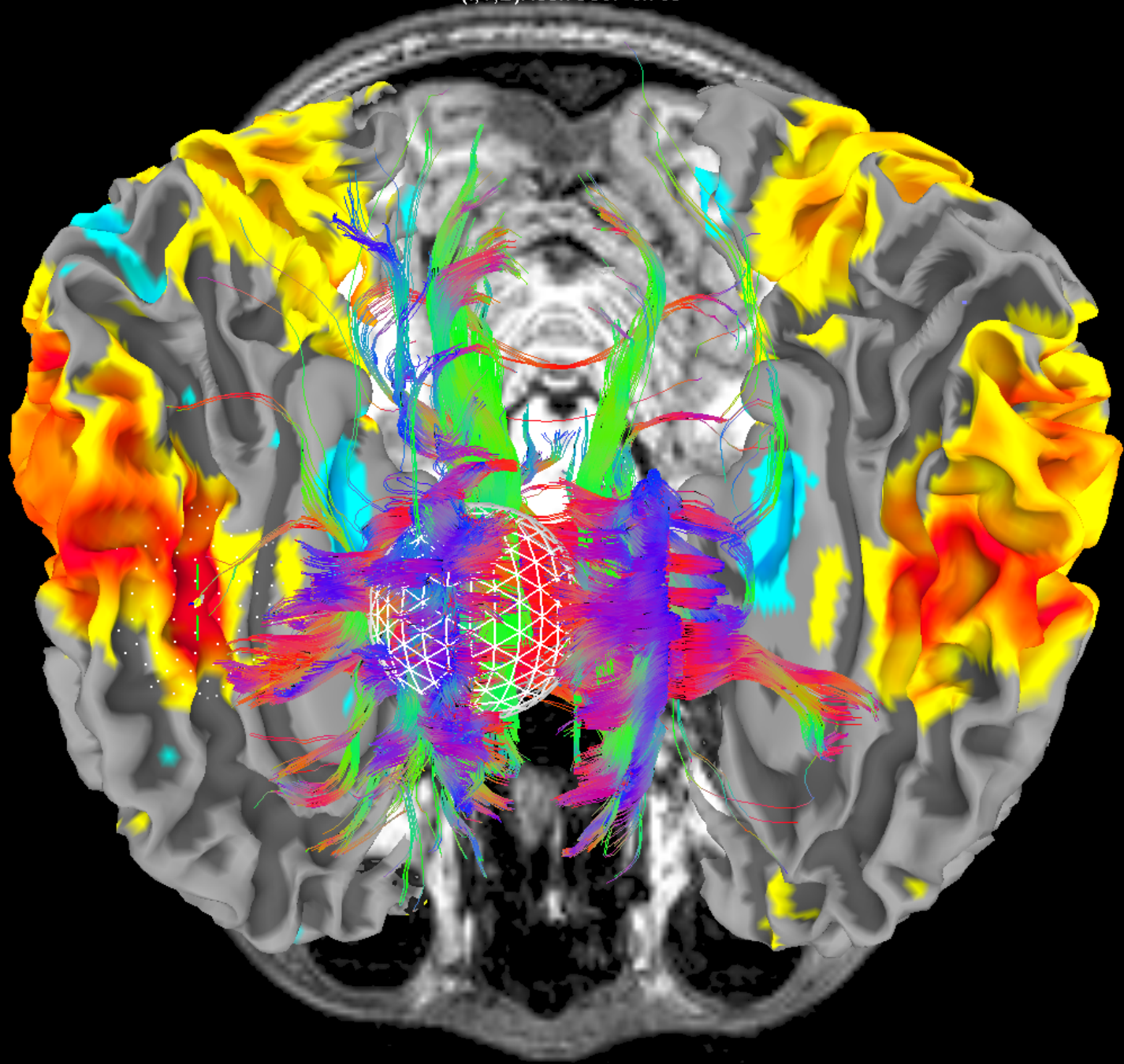
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.559



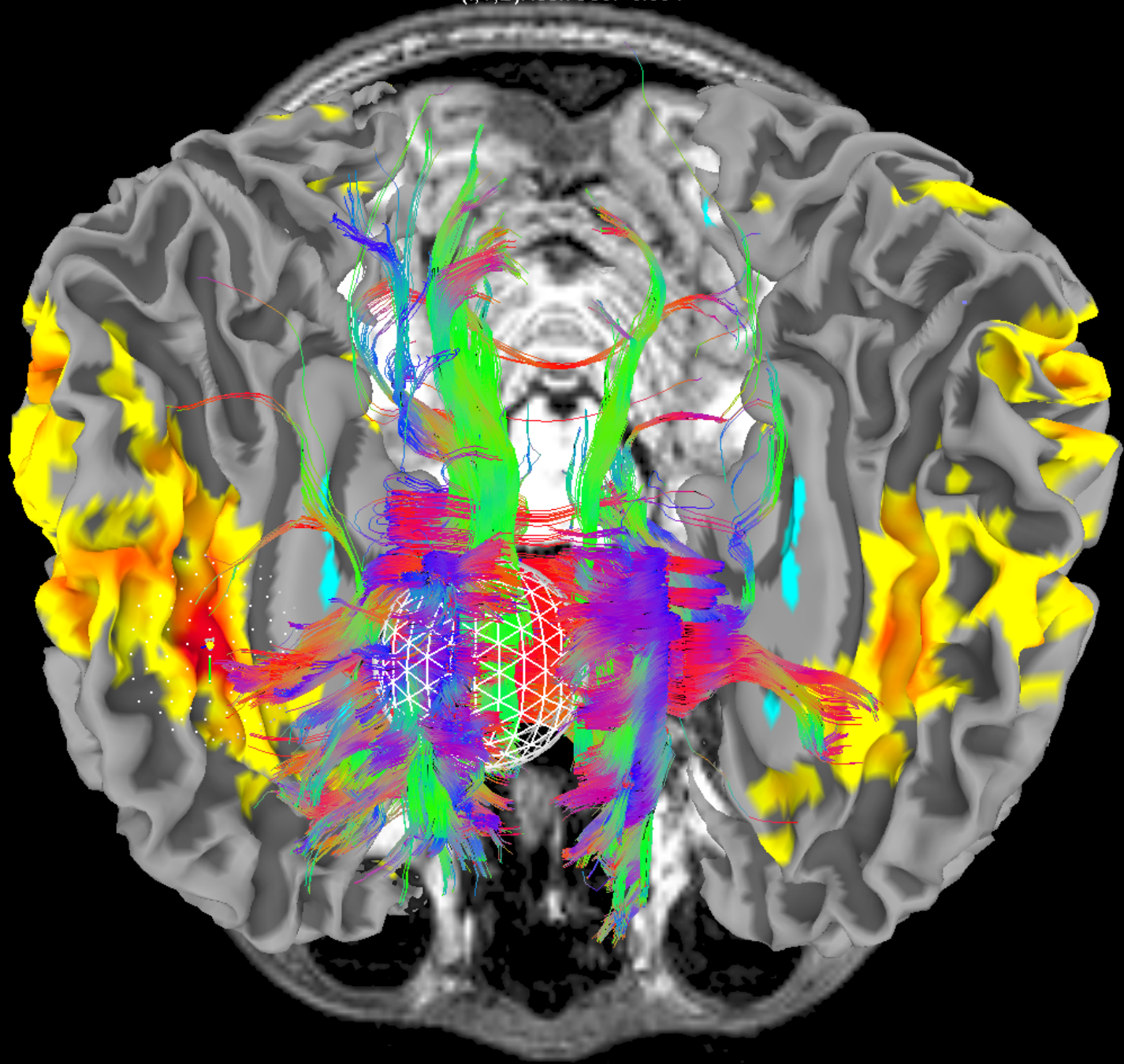
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.752



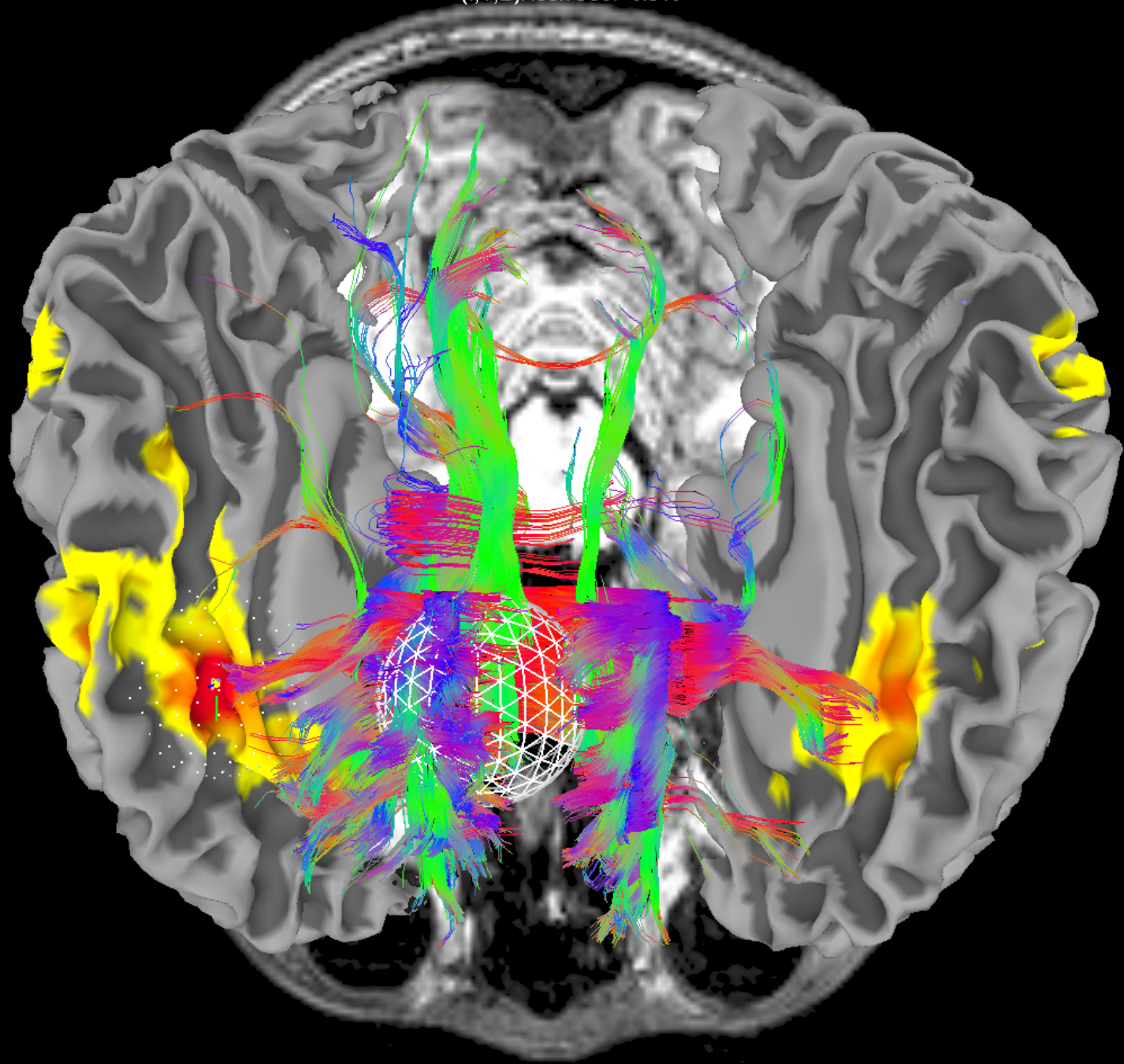
wm_rh_G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.785



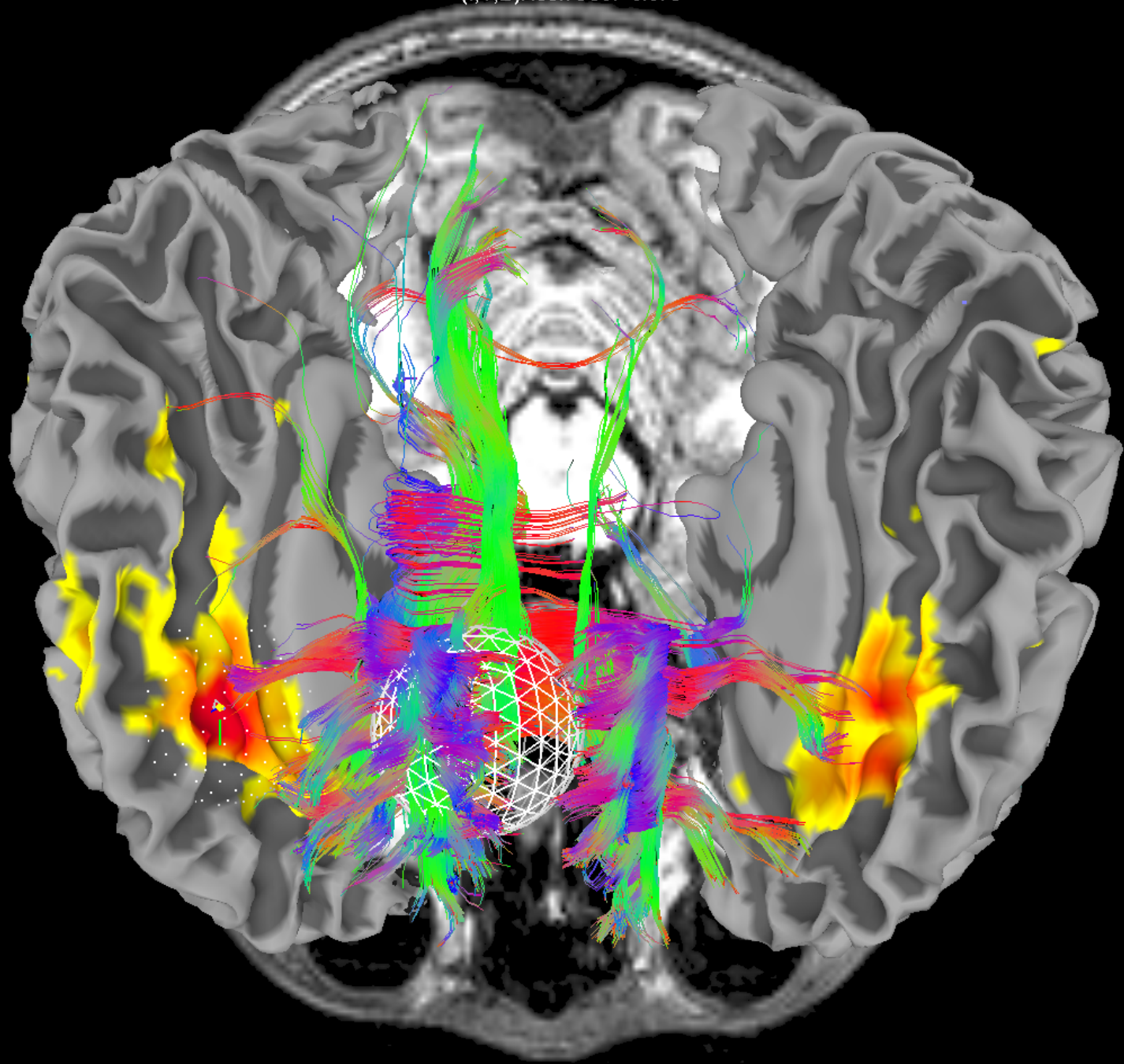
wm_rh_G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.604



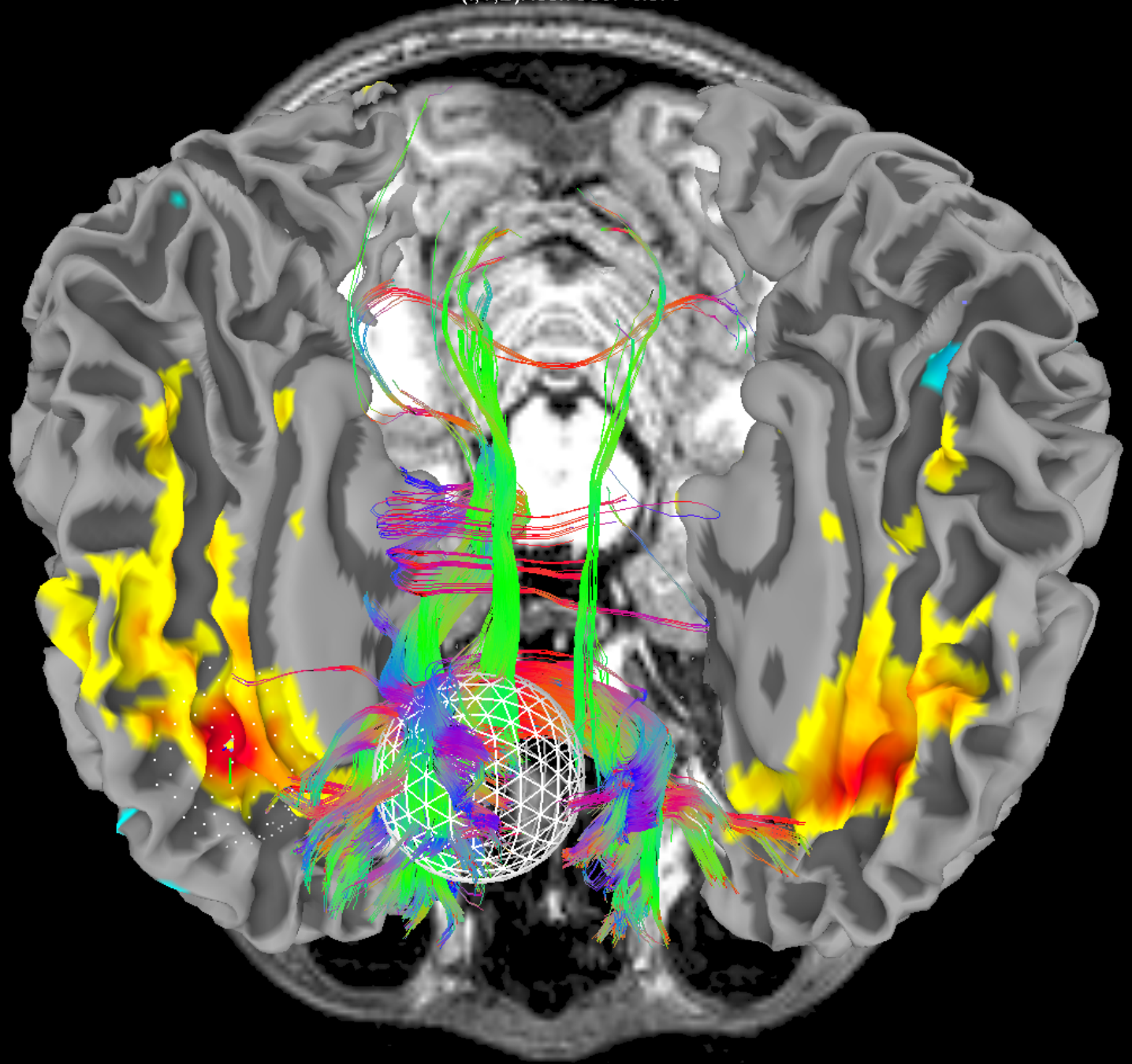
wm_rh_G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.516



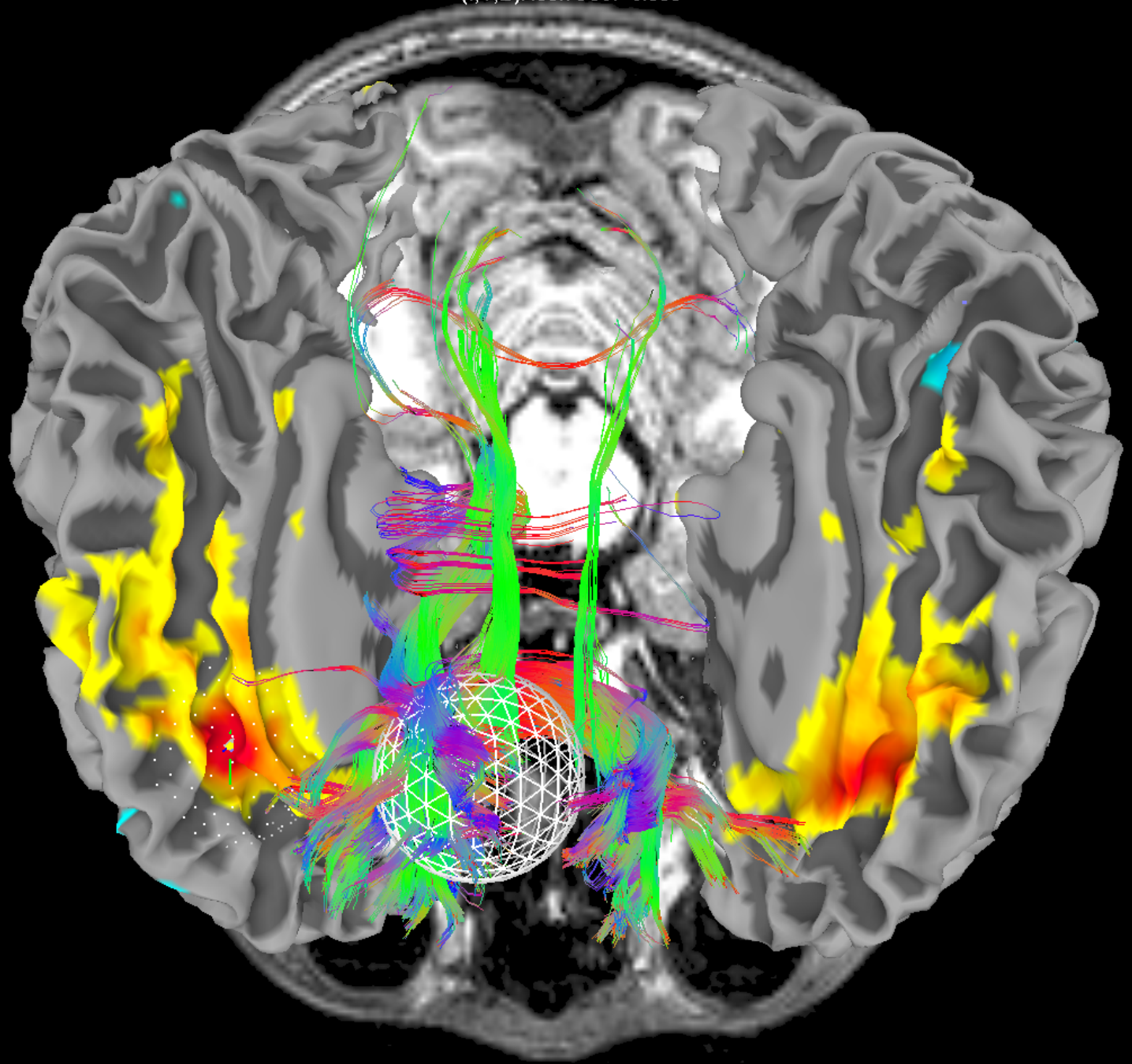
wm_rh_G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.679



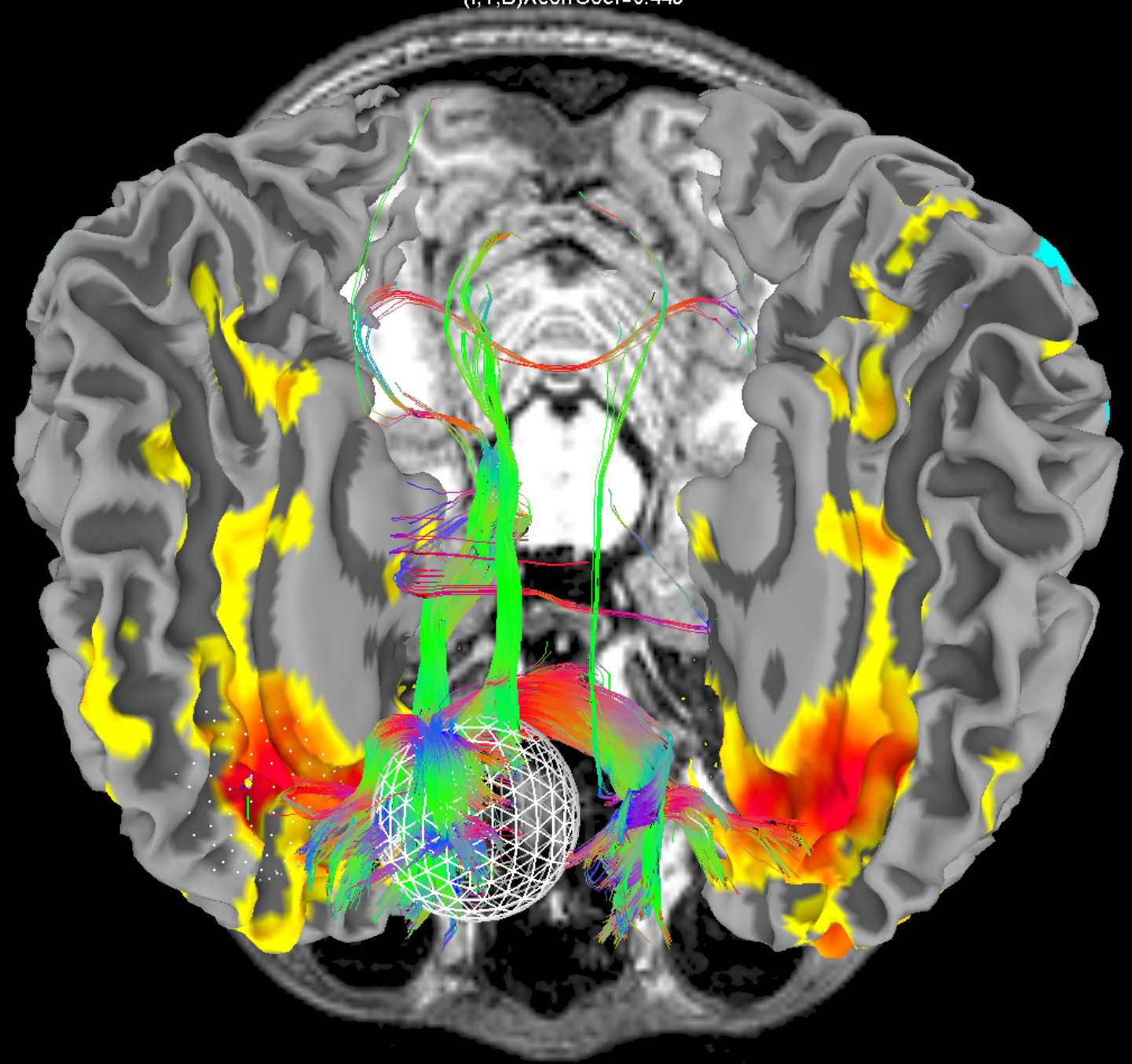
wm_rh_G and S_cingul-Ant
(I,T,B)XcorrCoef=0.578



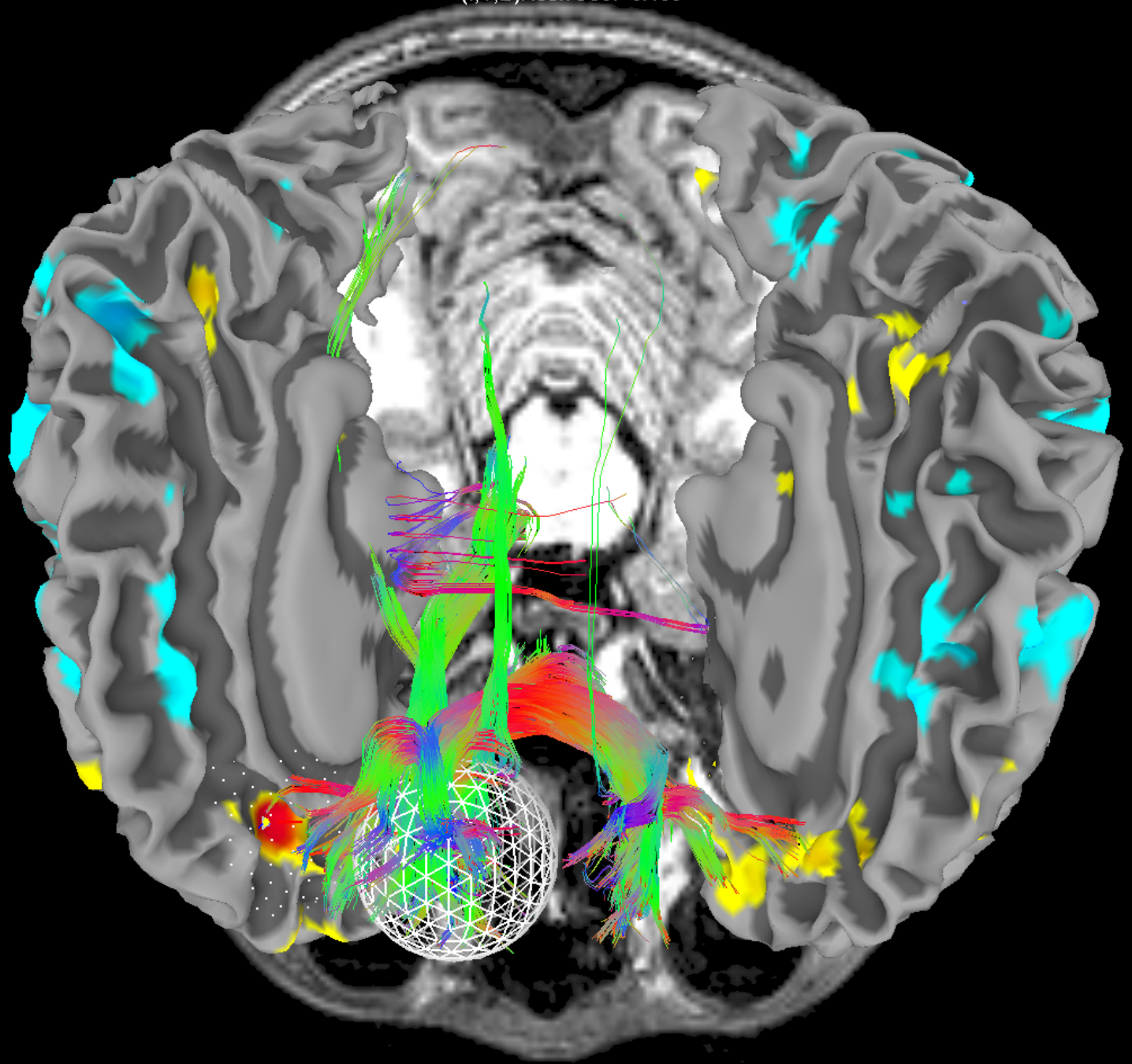
wm_rh_G and S_cingul-Ant
(I,T,B)XcorrCoef=0.999



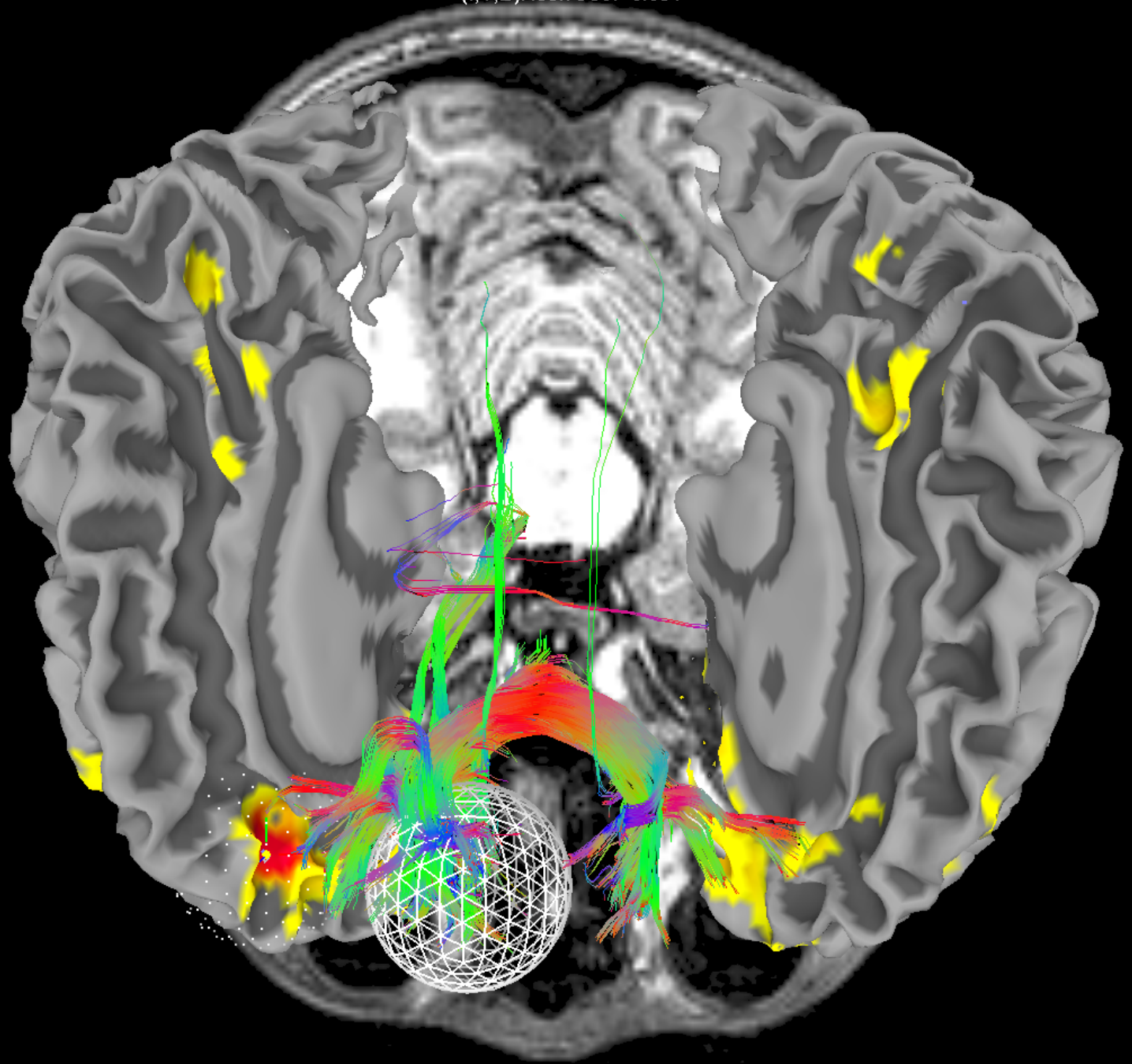
wm_rh_G and S_cingul-Ant
(I,T,B)XcorrCoef=0.445



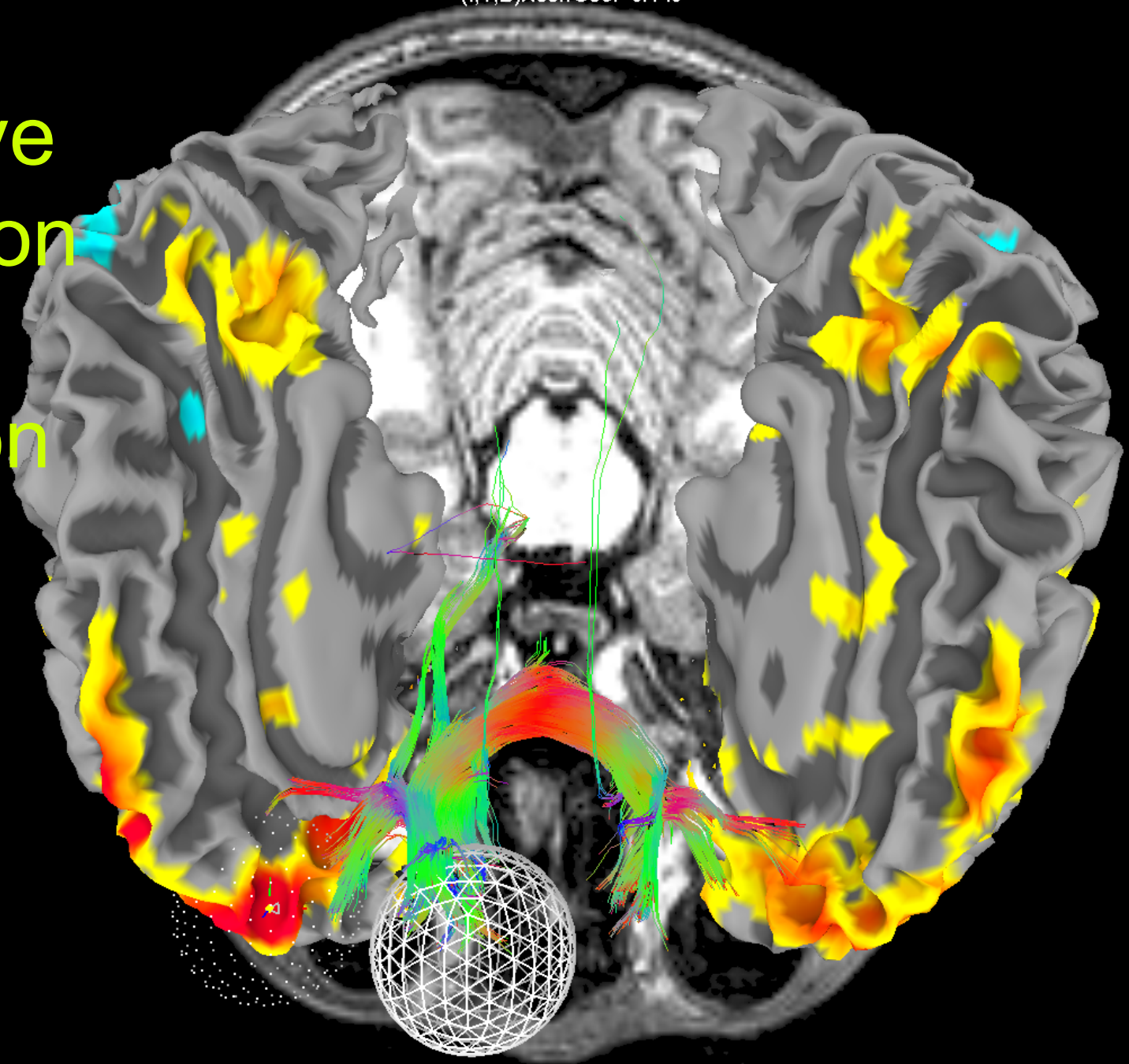
wm_rh_G and S_cingul-Ant
(I,T,B)XcorrCoef=0.136



wm_rh_G and S_cingul-Ant
(I,T,B)XcorrCoef=0.391

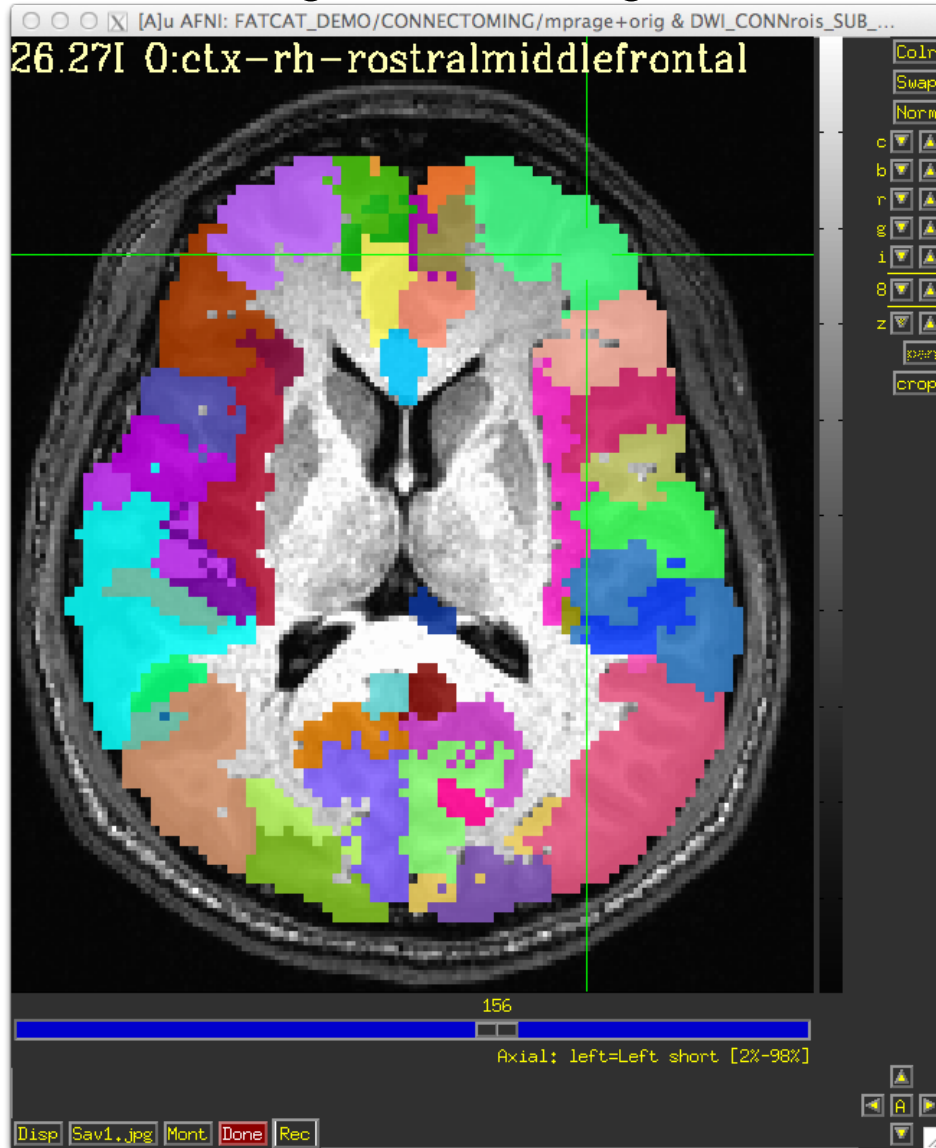


Goal:
Interactive
exploration
of high
dimension
complex
datasets



tcsh Do_11_RUNdti_Connectome_Examp.tcsh

- Example 1: Tract tracing between large numbers of ROIs



Hands-On

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 a colorful, multi-colored fiber-like structure. The title bar of the window reads "[A] SUMA:xx: ANY:". Below the title bar, the menu bar includes "File View Tools". The main content area shows the text "ctx-rh-postcentral<->ctx-rh-precentral" and "Pnt 0, tret 3338, bnd 608". To the right of the main window is a "Coloring Controls" panel. This panel includes a "Lbl" field with the value "o.OME8_000_BUN". Below this are several control fields: "Dim" with a value of "1.0", "Ord" with a value of "1", "Opa" with a value of "1.0", "Ln" with a dropdown menu set to "SLD", "Masks", "Ign" with a checkbox, and "Gry" with a value of "20". At the bottom of the "Coloring Controls" panel is a "Switch Dset" button. A red arrow points from the "Switch Dset" button to a smaller window titled "Switch Colori...". This window displays a list of 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 window.

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