

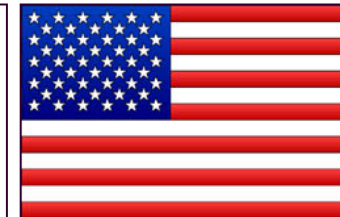
Hands On the FATCAT

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@Install_FATCAT_DEMO

Script in AFNI that downloads data and sample scripts

Illustrates usage of programs in the FATCAT toolbox

Continuously updated to reflect latest additions

Will follow the sequence of Do_* scripts

Script [Do_00_PRESTO_ALL_RUNS.tcsh](#) can be used to run all scripts in one swoop

cd AFNI_demos/FATCAT_DEMO

Comments and Commands

Calculate the correlation matrices of networks of (presumably GM)

ROIs

One can do this simultaneously with multiple networks defined as

sub-bricks. Such is done in this example, using the GM network

...

3dNetCorr |

-inset REST_in_DWI.nii.gz |

-in_rois ROI_ICMAP_GM+orig |

-fish_z |

-prefix FMRI/REST_corr_rz

Help on the Command Line

3dTrackID -help | less ← For all help in GUI text editor

...

Estimate locations of WM associated with target ROIs, particularly between pairs of GM in a network; can process several networks in a given run.

...

B) Mini-probabilistic tracking through a multi-brik network file using a DTI model and AND-logic. Instead of using the thresholded FA map to guide tracking, an extra data set ...:

```
$ 3dTrackID -mode MINIP \
  -dti_in DTI/DT \
  -dti_extra T1_WM_in_DWI.nii.gz \
  -netrois ROI_ICMAP_GMI+orig \
  -logic AND \
```

Purpose, Options, Examples

...

(681 lines and counting)

3dTrackID -h_view ← For all help in GUI text editor

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Subject	Author	Posted
AFNI Bootcamp at NIH – Sep 29–Oct 3 2014 (2 Posts)	Emperor Zhark	06/18/2014 09:09AM
New: FATCAT (3dTrackID, 3dNetCorr) output with 3dMVM statistical modeling (2 Posts)	ptaylor	08/12/2014 04:23AM
t-test – 3dttest++	Marco P	09/29/2014 09:19AM
Changing Cluster Number in Mask	Danny	09/25/2014 05:29PM
● Re: Changing Cluster Number in Mask	ptaylor	09/25/2014 07:34PM
● Re: Changing Cluster Number in Mask	rick reynolds	09/25/2014 08:41PM
● Re: Changing Cluster Number in Mask	Danny	09/26/2014 01:30PM
● Re: Changing Cluster Number in Mask	rick reynolds	09/26/2014 04:27PM

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P Taylor <neon.taylor@gmail.com>



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P Taylor <neon.taylor@gmail.com>



Currently in the
southern hemisphere



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P Taylor <neon.taylor@gmail.com>



Ziad Saad <saadz@mail.nih.gov>



tcsch Do_01_RUNdti_convert_grads.tcsch

Convert gradient vectors, or b matrices for 3dDWltoDT and 3dDWUncert

```
1dDW_Grad_o_Mat \
-in_grad_rows 'bvec[0..32]' \
-flip_y \
-out_grad_cols GRADS_30.dat
```

To illustrate what wrong directions do:

```
1dDW_Grad_o_Mat \
-in_grad_rows 'bvec[0..32]' \
-out_grad_cols GRADS_30.bad.dat
```

***See Do_01_RUNhardi_convert_grads.tcsch for other variants,
this time to satisfy DTI_Studio (Yeh et al. 2010)***

tcsch Do_02_RUNdti_DW_to_DTI.tcsch

Compute tensor from pre-processed (e.g. by TORTOISE) diffusion images

```
3dDWItoDT -echo_edu \  
-prefix DTI/DT \  
-mask mask_DWI+orig \  
-eigs -sep_dsets -nonlinear \  
GRADS_30.dat \  
AVEB0_DWI.nii.gz
```

Output in DTI/:

```
DT_DT+orig.HEAD DT_FA+orig.HEAD  
DT_L1+orig.HEAD DT_V1+orig.HEAD  
DT_L2+orig.HEAD DT_V2+orig.HEAD  
DT_L3+orig.HEAD DT_V3+orig.HEAD  
DT_MD+orig.HEAD
```

Also ran with GRADS_30.bad.dat

tcsch Do_02_RUNdti_DW_to_DTI.tcsch

Compute tensor from pre-processed (e.g. by TORTOISE) diffusion images

```
3dDWItoDT -echo_edu \  
-prefix DTI/DT \  
-mask mask_DWI+orig \  
-eigs -sep_dsets -nonlinear \  
GRADS_30.dat \  
AVEB0_DWI.nii.gz
```

Can also use TORTOISE generated Tensors

Output in DTI/:

```
DT_DT+orig.HEAD DT_FA+orig.HEAD  
DT_L1+orig.HEAD DT_V1+orig.HEAD  
DT_L2+orig.HEAD DT_V2+orig.HEAD  
DT_L3+orig.HEAD DT_V3+orig.HEAD  
DT_MD+orig.HEAD
```

Also ran command with GRADS_30.bad.dat

tcsch Do_PostTORTOISE_2014.tcsch

Processing data from TORTOISE this morning

Need to use diffusion images if doing prob. tractography

... I invoked a -flip_z...

```
1dDW_Grad_o_Mat \  
  -in_bmatT_cols BMTXT.txt \  
  -out_grad_cols GRADS.txt \  
  -flip_z
```

tensor reconstruction-- sep_dsets is useful here;
nonlinear is default anyways.

```
3dDWItoDT -nonlinear -eigs -sep_dsets \  
  -mask mask2.nii.gz \  
  -prefix DT \  
  GRADS.txt \  
  DWI.nii \  
  -overwrite
```

tcsh Do_03_RUNdti_make_network_ROIs.tcsh

Create fattened gray matter ROIs to serve as tractography targets

```
3dROIMaker -echo_edu
```

```
-inset SOME_ICA_NETS_in_DWI+orig →
```

```
-thresh 3.0
```

```
-volthr 130
```

```
-inflate 2
```

```
-wm_skel DTI/DT_FA+orig.
```

```
-skel_thr 0.2
```

```
-skel_stop
```

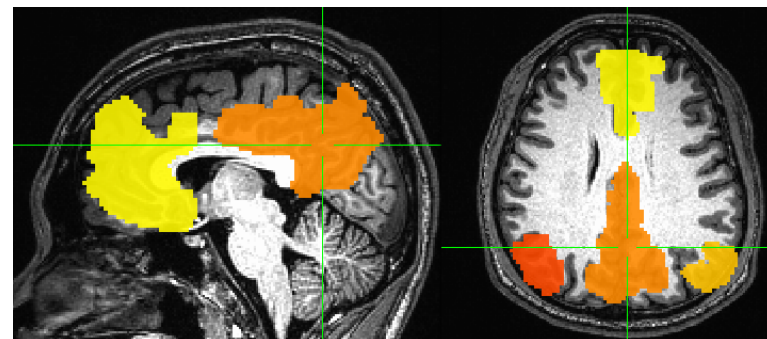
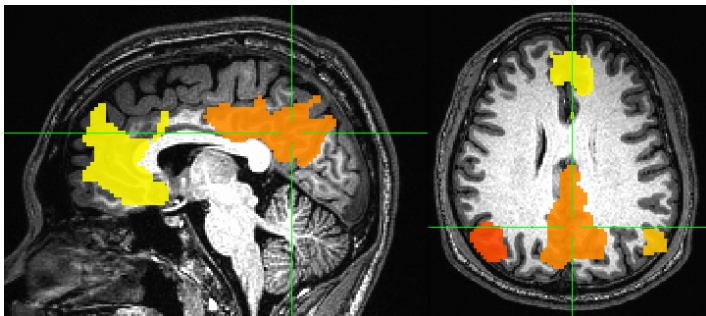
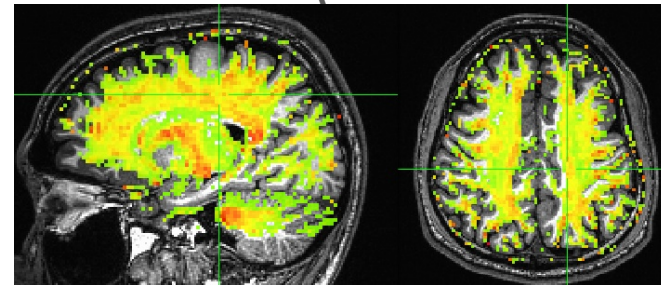
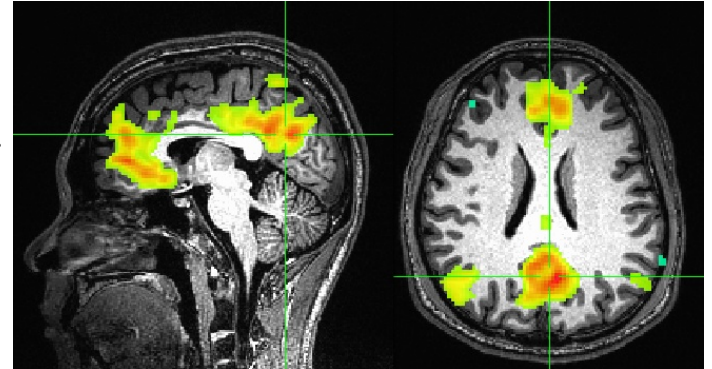
```
-mask mask_DWI+orig
```

```
-prefix ./ROI_ICMAP
```

Output in ./:

ROI_ICMAP_GM+orig.HEAD

ROI_ICMAP_GMI+orig.HEAD



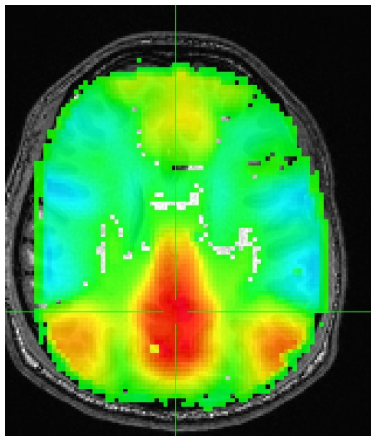
tcsh Do_04_RUNdti_match_network_ROIs.tcsh

Identify networks by comparing spatial pattern to standard set (Optional)

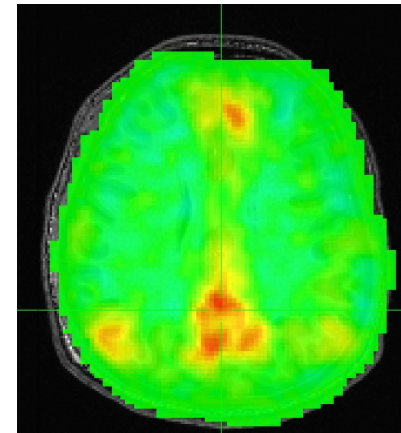
```
3dMatch \
  -inset SOME_ICA_NETS_in_DWI+orig \
  -refset MULTISITE_in_DWI+orig \
  -in_min 1.0 \
  -ref_min 3 \
  -only_dice_thr \
  -prefix MATCHED \
  -overwrite
```

Output in ./:

MATCHED_IN+orig[0]
MATCHED_REF+orig[5]



this input
matched to
this reference



tcsh Do_05_RUNdti_DET_tracking.tcsh

A. Whole brain deterministic tractography

```
3dTrackID -mode DET \  
  -dti_in DTI/DT \  
  -netrois mask_DWI+orig \  
  -logic OR \  
  -alg_Thresh_Len 30 \  
  -prefix DTI/o.WB \  
  -overwrite -echo_edu
```

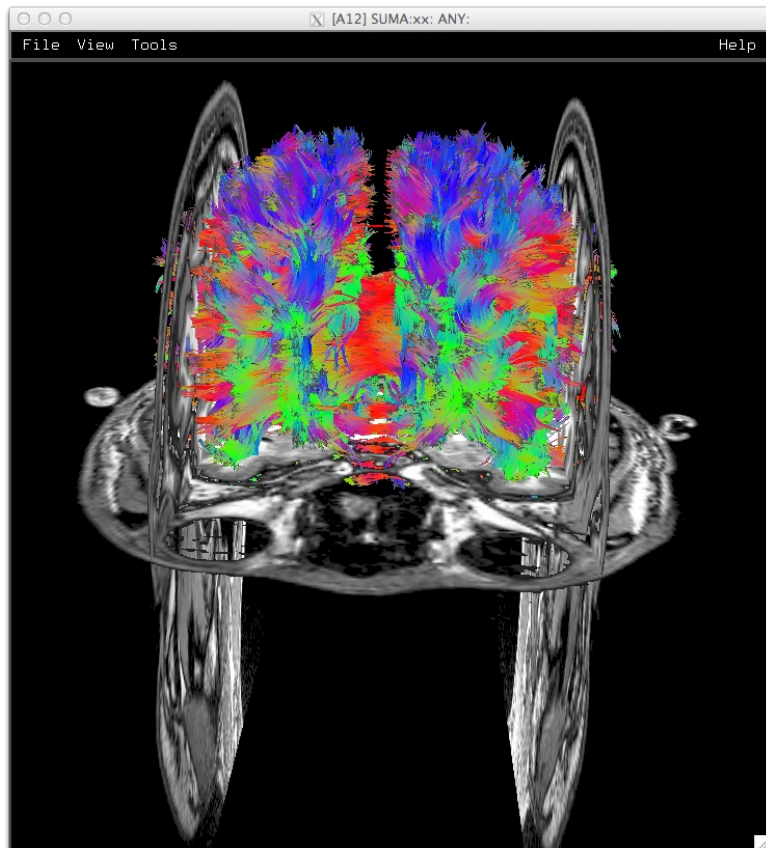
Output in DTI/:

```
o.WB_000.grid ← Stats on WM region  
o.WB_000.niml.dset ← same, in fancy format  
o.WB_000.niml.tract ← Whole brain tracts  
o.WB_000.trk ← same, trackvis format  
o.WB_000_INDIMAP+orig.HEAD ← #of tracts at each  
VOX.  
o.WB_000_PAIRMAP+orig.HEAD ← same, because 1 ROI
```

tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

A. *Visualize whole brain tracts, check for weirdness*

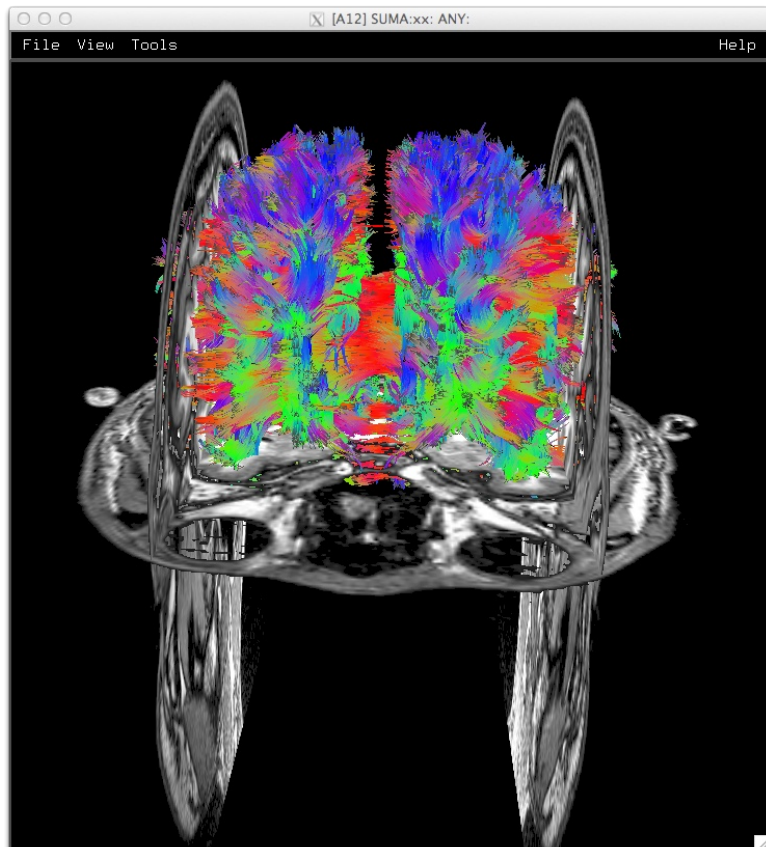
```
suma -npb 12 -niml \
      -vol mprage+orig. \
      -tract DTI/o.WB_000.niml.tract &
```



tcsch Do_06_VISdti_SUMA_visual_ex1.tcsch

A. Visualize whole brain tracts, check for weirdness

```
suma -npb 12 -niml \
      -vol mprage+orig. \
      -tract DTI/o.WB_000.niml.tract &
```



**Right click on volume
View → Object Controller (ctrl+s)**



tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

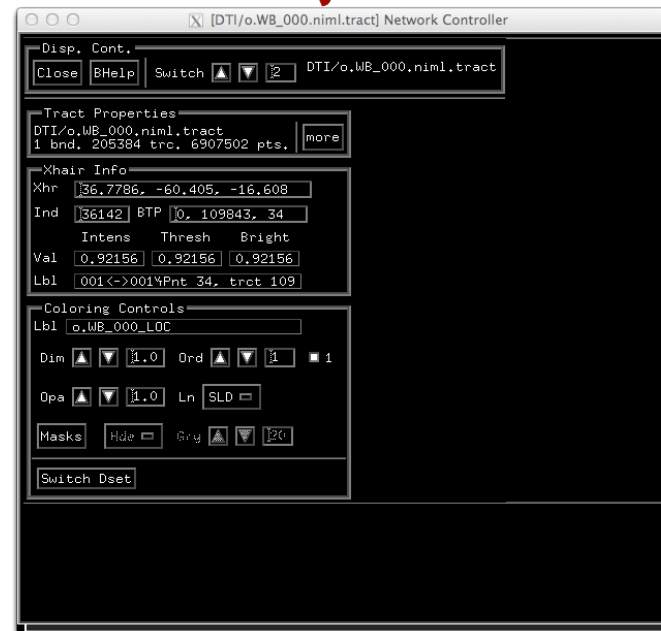
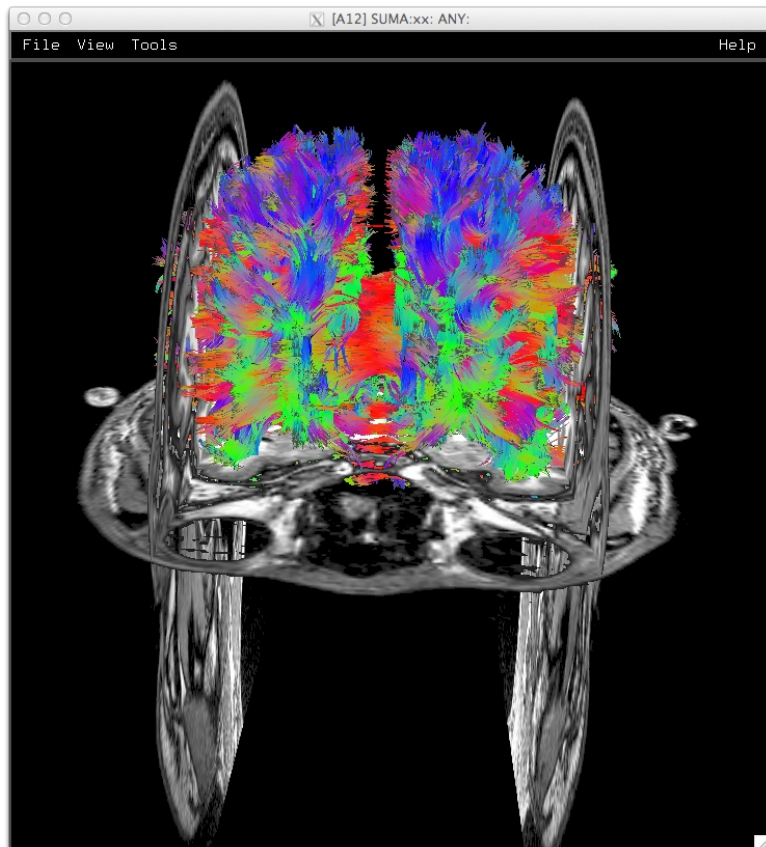
A. Visualize whole brain tracts, check for weirdness

```
suma -npb 12 -niml \
      -vol mprage+orig. \
      -tract DTI/o.WB_000.niml.tract &
```

**Right click on tracts opens tract controller
(another page in controller notebook)**

or

View → Object Controller (ctrl+s)



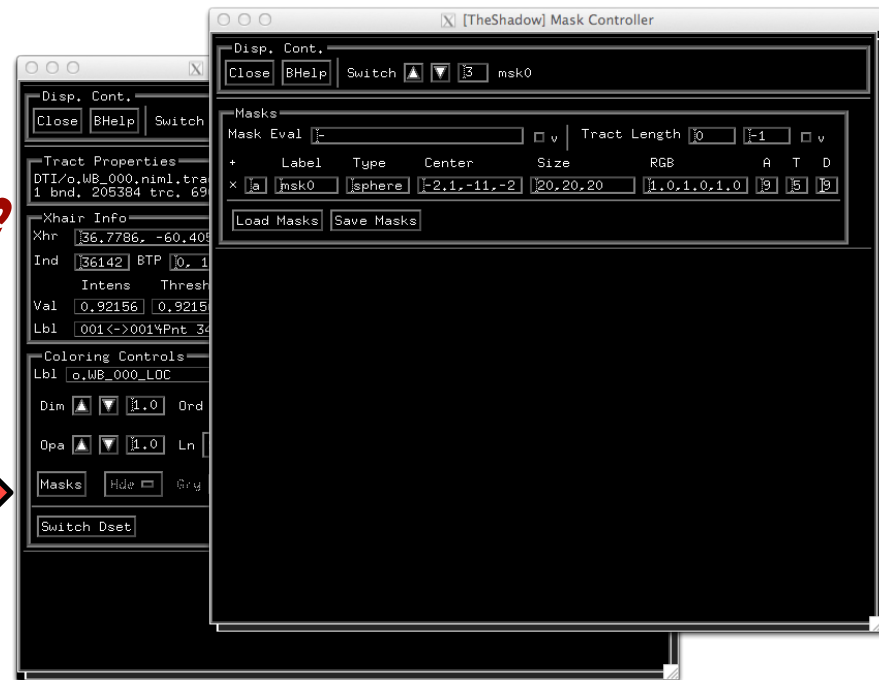
tcsch Do_06_VISdti_SUMA_visual_ex1.tcsch

A. Visualize whole brain tracts, check for weirdness

```
suma -npb 12 -niml \
      -vol mprage+orig. \
      -tract DTI/o.WB_000.niml.tract &
```

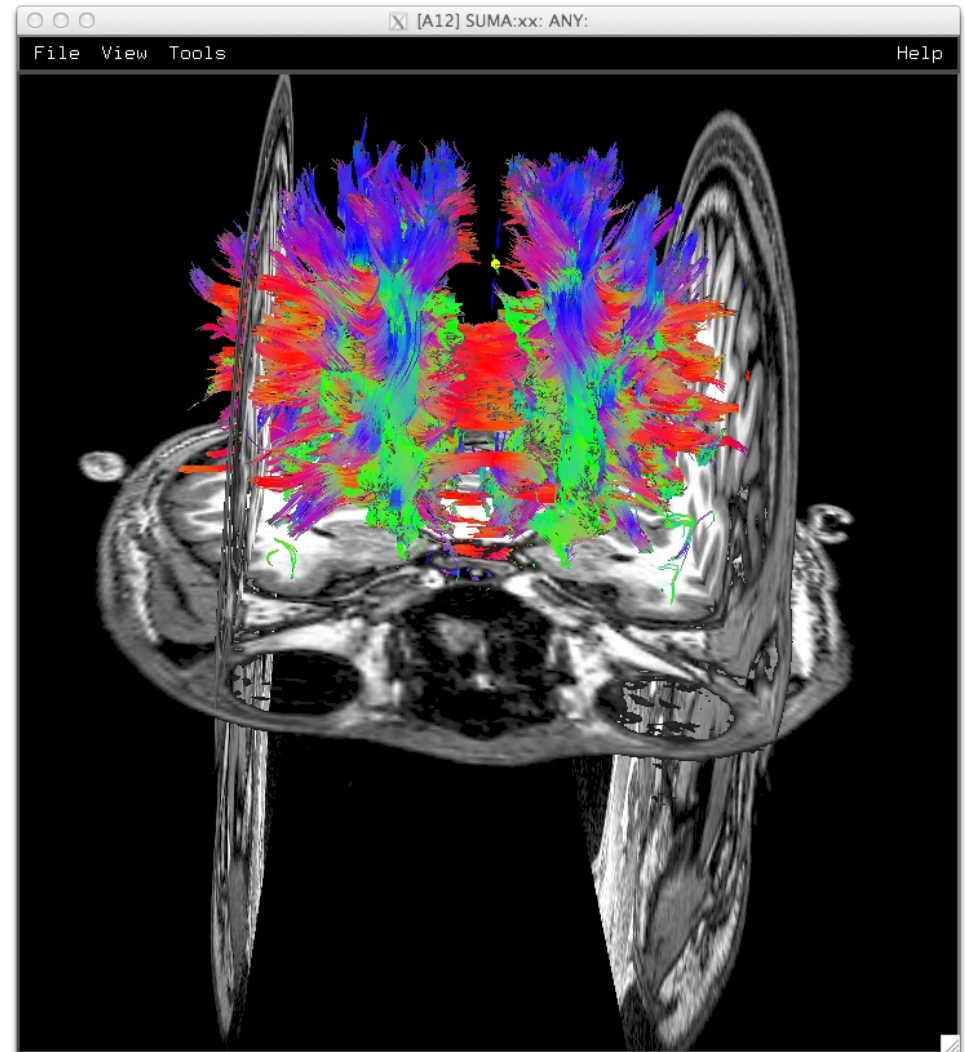
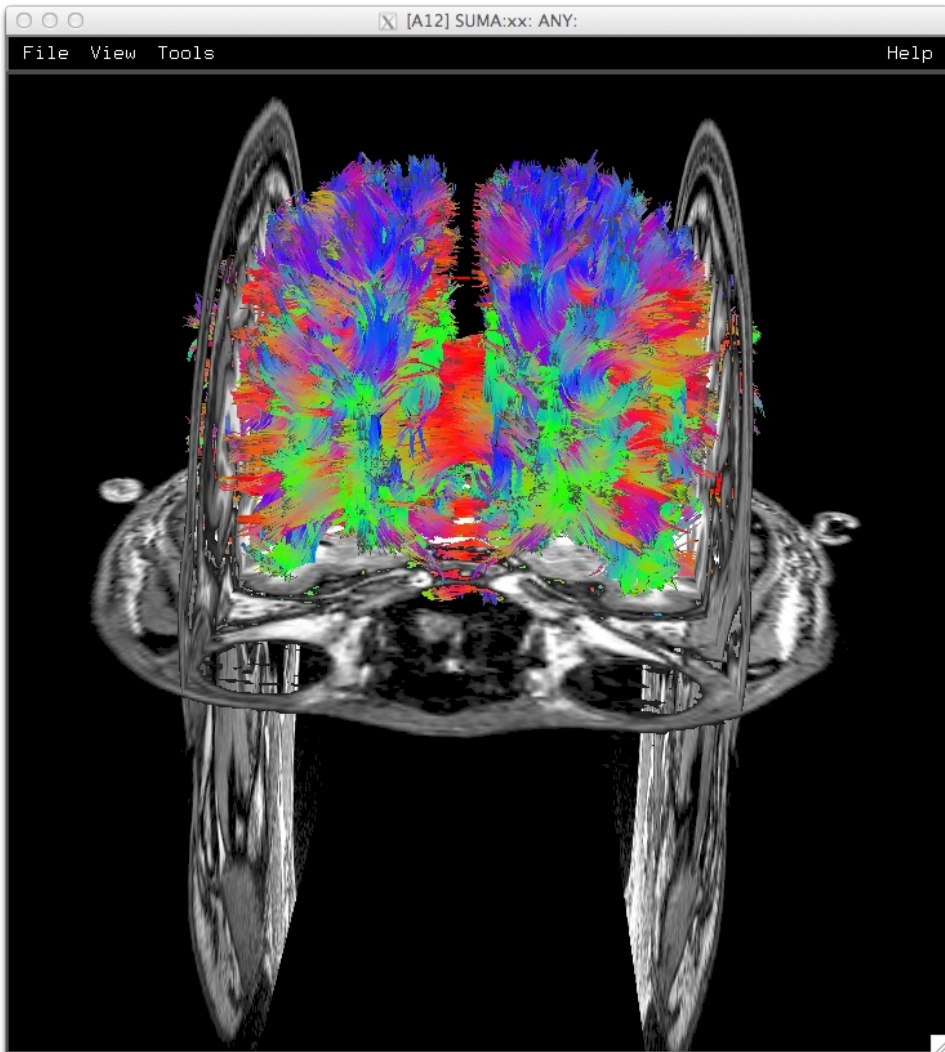


Click Masks



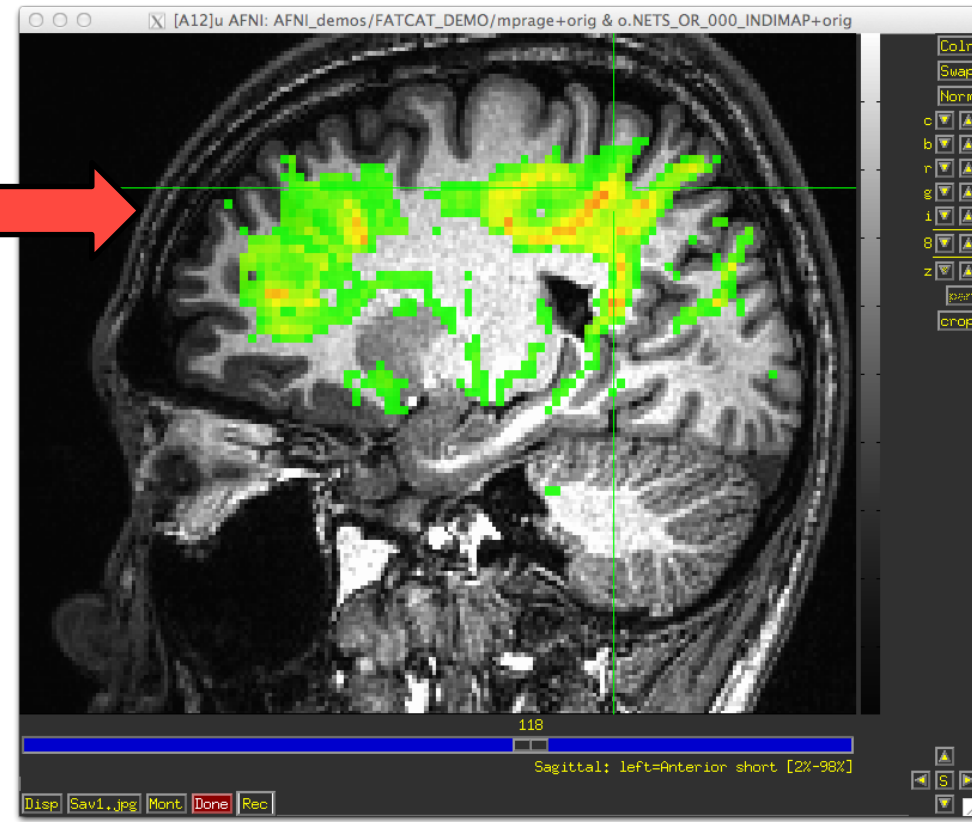
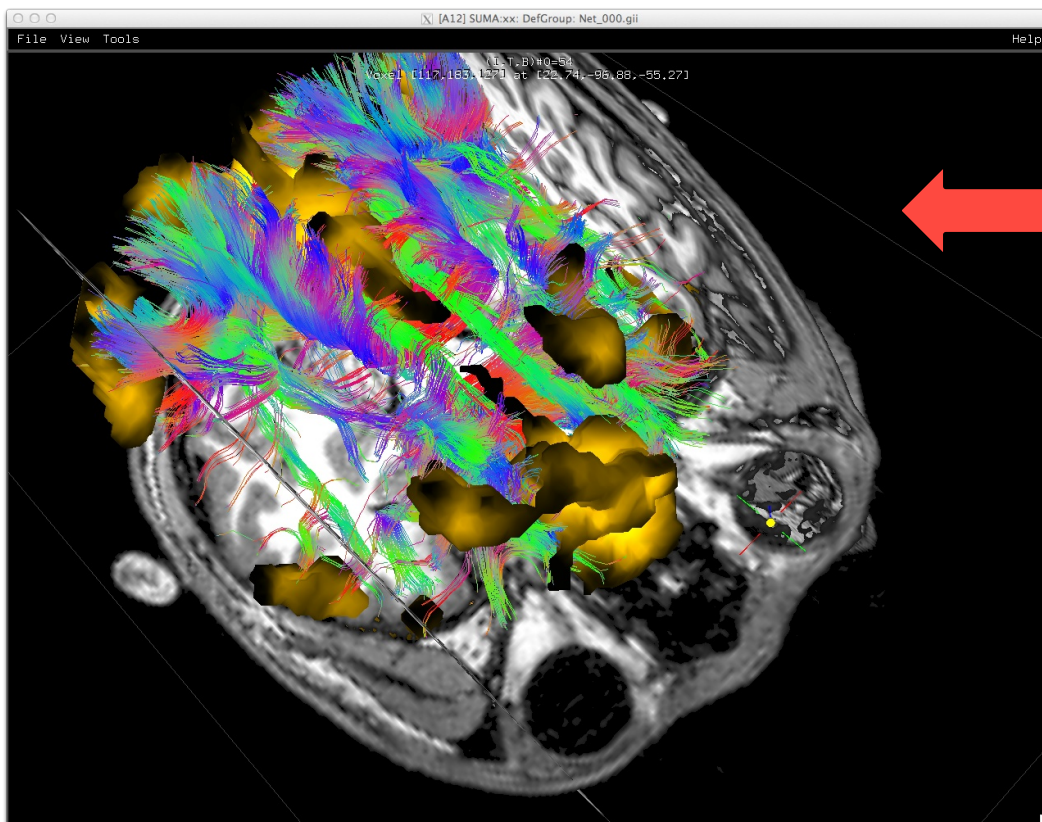
Good vs. *Bad* Gradient Directions

```
suma -npb 12 -niml \
      -vol mprage+orig. \
      -tract DTI/o.WB.bad_000.niml.tract &
```



Second half of Do_06 demo

```
suma -npb 12 -niml \
      -vol mprage+orig. \
      -i Net_000.gii \
      -tract DTI/o.NETS_OR_000.niml.tract &
afni -npb 12 -niml -yesplugouts \
      mprage+orig.HEAD DTI/*.HEAD ROI_ICMAP_GMI+orig.HEAD &
```



tcsch Do_05_RUNdti_DET_tracking.tcsch

B. Whole brain deterministic tractography: AND logic, 4 Networks

```
3dTrackID -mode DET \
  -dti_in DTI/DT \
  -netrois "ROI_ICMAP_GMI+orig" \
  -logic AND \
  -prefix DTI/o.NETS_AND \
  -write_opts \
  -overwrite -echo_edu
```

Output in ***DTI/***:

Only one set for network 002 is listed below.

<i>o.NETS_AND_002.grid</i>	<i>← WM stats per region pair</i>
<i>o.NETS_AND_002.niml.dset</i>	<i>← same, in fancy format</i>
<i>o.NETS_AND_002.niml.tract</i>	<i>← Tracts between pairs ONLY</i>
<i>o.NETS_AND_002.trk</i>	<i>← same, trackvis format</i>
<i>o.NETS_AND_002_INDIMAP+orig.HEAD</i>	<i>← #of tracts per ROI</i>
<i>o.NETS_AND_002_PAIRMAP+orig.HEAD</i>	<i>← Masks of voxels between pairs</i>

Launch afni: ***afni DTI/*** to look at output.

Use option -dump_rois for most detailed WM masks

tcsh Do_07_RUNdti_uncertainty_est.tcsh

B. Estimate uncertainty in principal eigen vector direction and FA estimates

```
time 3dDWUncert -echo_edu \  
-inset AVEB0_DWI.nii.gz \  
-prefix DTI/o.UNCERT \  
-input DTI/DT \  
-grads GRADS_30.dat \  
-iters 50 small number for demo only, use ~200+!
```

Output in DTI/:

o.UNCERT_UNC+orig ← Bias and std of princ. Vec. and FA

Standard deviation estimates are needed for probabilistic tractography

tcsch Do_10_RUNdti_fullprob_track.tcsch

B. *Many perturbations, only keep track of number of tracts at each voxel*

```
3dTrackID -mode PROB \  
-netrois ROI_ICMAP_GMI+orig \  
-uncert DTI/o.UNCERT_UNC+orig \  
-dti_in DTI/DT \  
-mask mask_DWI+orig \  
-algot ALGOPTS_PROB.dat \  
-dump_rois AFNI \  
-prefix DTI/o.PR \  
-overwrite -echo_edu
```

*Output comparable to DET mode, but not tracts are kept.
Also see output of region pair masks in DTI/o.PR/*

afni DTI DTI/o.PR

tcsh Do_08_RUNdti_miniprob_track.tcsh

B. Middle ground. Few perturbations, and keep all tracts

```
3dTrackID -mode MINIP \  
-dti_in DTI/DT \  
-netrois "ROI_ICMAP_GMI+orig" \  
-logic AND \  
-mini_num 9 \  
-uncert DTI/o.UNCERT_UNC+orig. \  
-prefix DTI/o.NETS_AND_MINIP
```

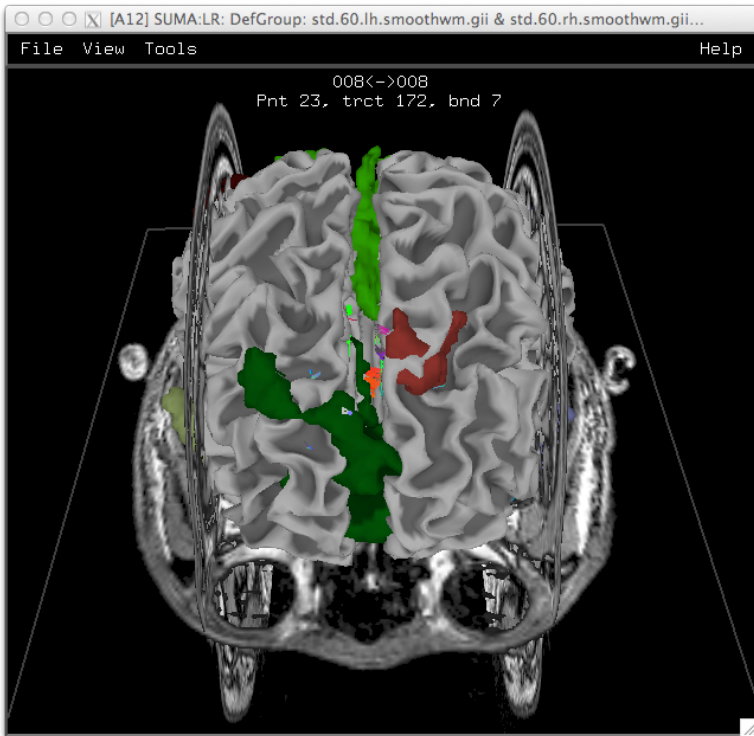
9 perturbations and whole brain tractography only

Will see results next

tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

skip example 0, on to example 1

```
suma -npb $sport -niml \
-onestate \
-i SUMA/std.60.lh.smoothwm.gii \
-i SUMA/std.60.rh.smoothwm.gii \
-i Net_000.gii \
-sv mprage+orig -vol mprage+orig. \
-tract DTI/o.NETS_AND_000.niml.tract &
```

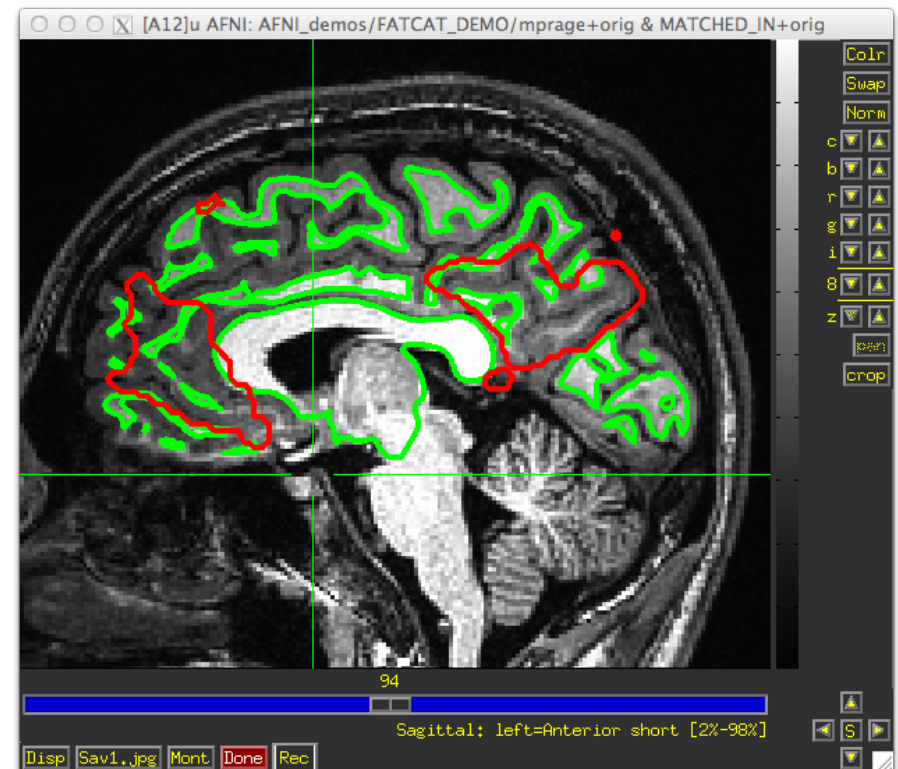


View → Object Controller
Hide surfaces '[' '']'
Select (right-click) objects

tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Example 1: Det. Tracts through ROIs Pairs of Network 0

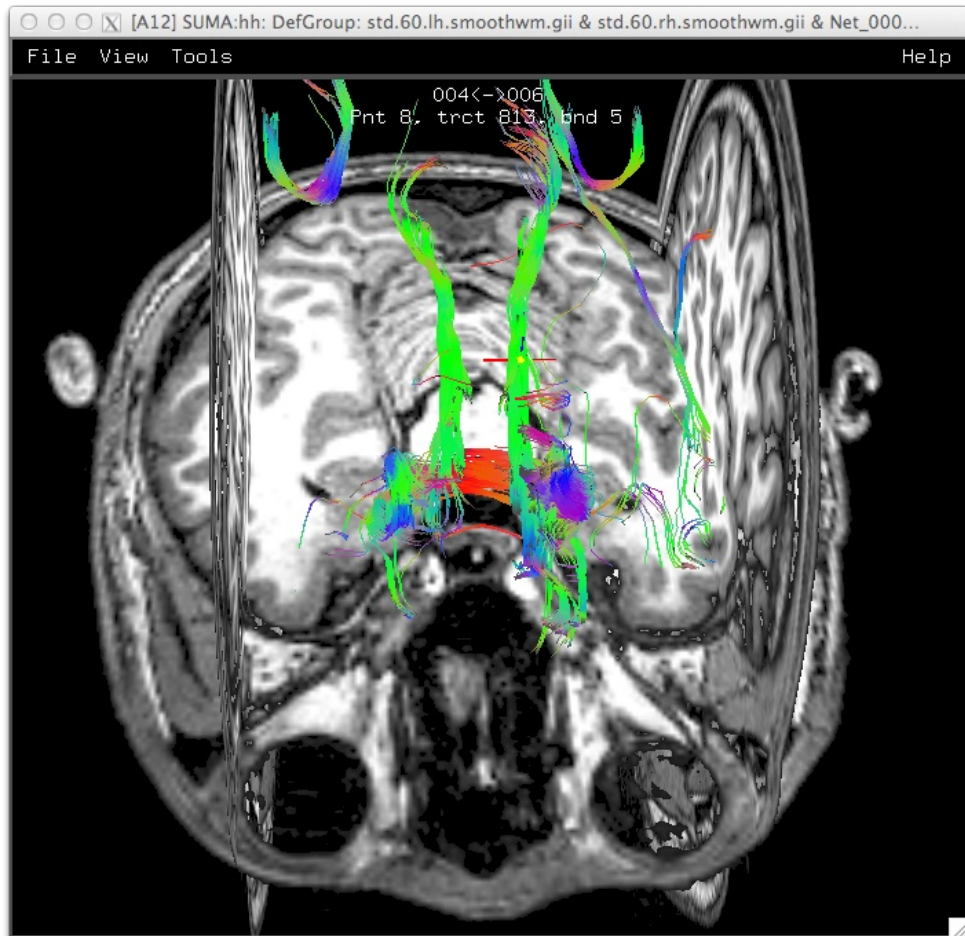
*Selection on any data object
AFNI jumps to same location*



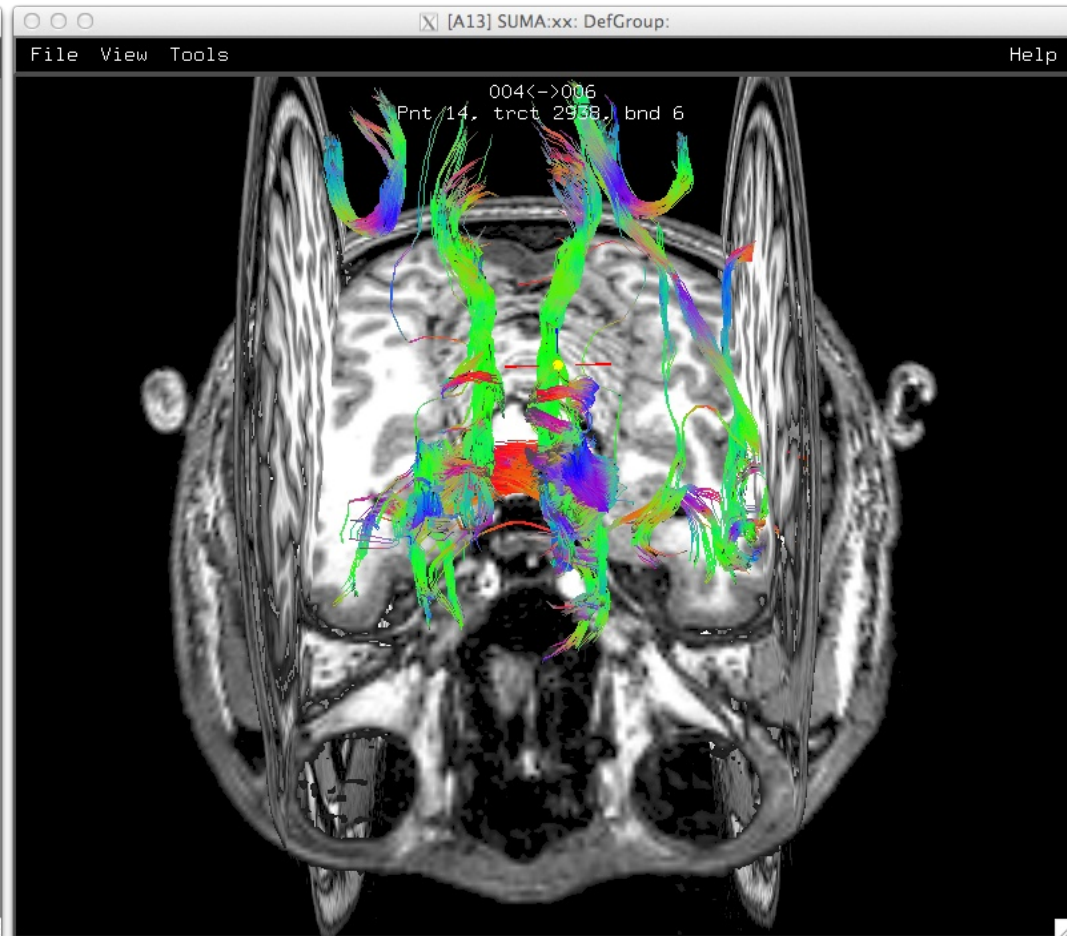
tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Example 2: Det. Tracts vs. Mini Prob.

Det. Tracts



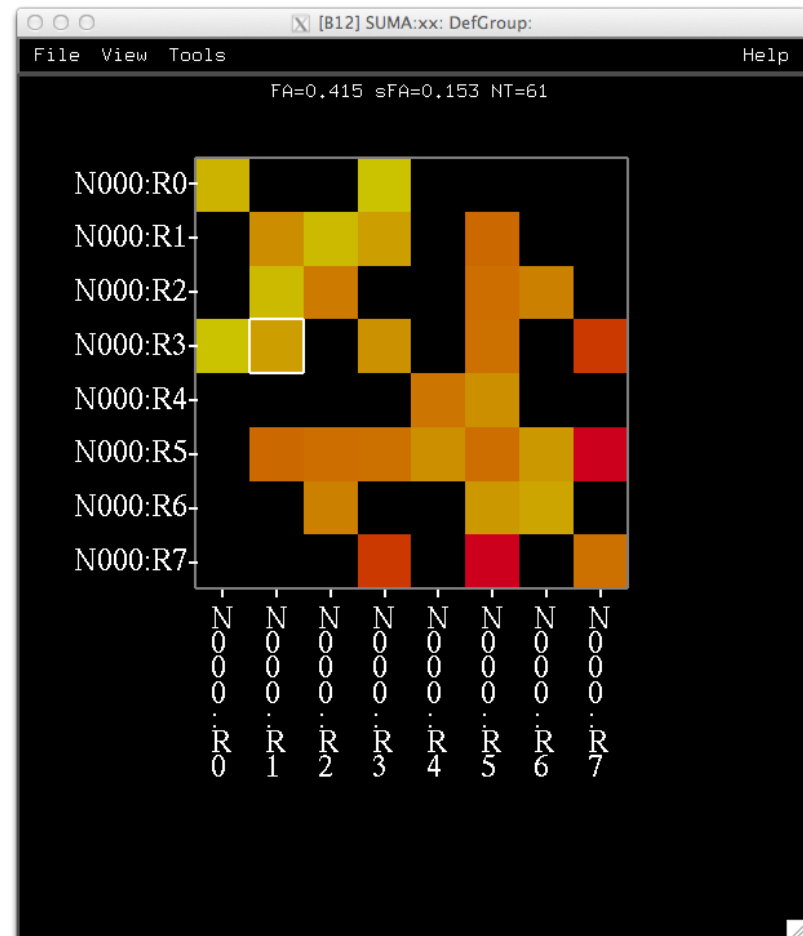
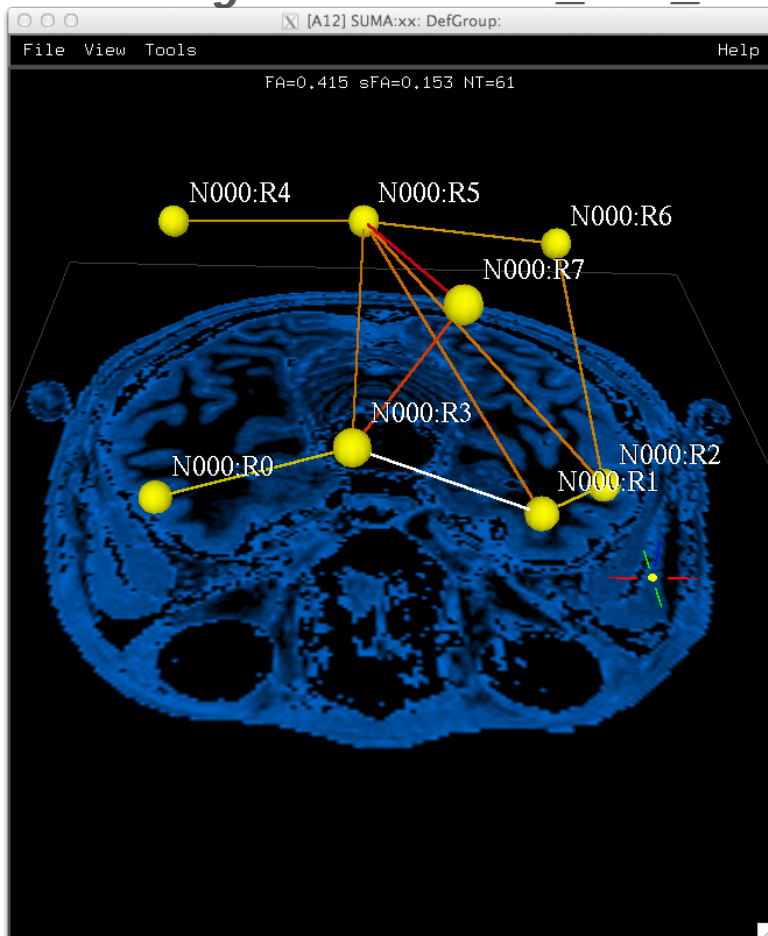
Mini (9) Prob. Tracts



tcsch Do_09_VISdti_SUMA_visual_ex2.tcsch

cd DTI/ Example 3: The connectivity matrices

```
suma -npb $sport -niml -onestate -i ../Net_000.gii \  
-i ../SUMA/std.60.lh.smoothwm.gii \  
-i ../SUMA/std.60.rh.smoothwm.gii \  
-sv ../mprage+orig -vol ../mprage+orig. \  
-gdset o.NETS_AND_MINIP_000.niml.dset &
```



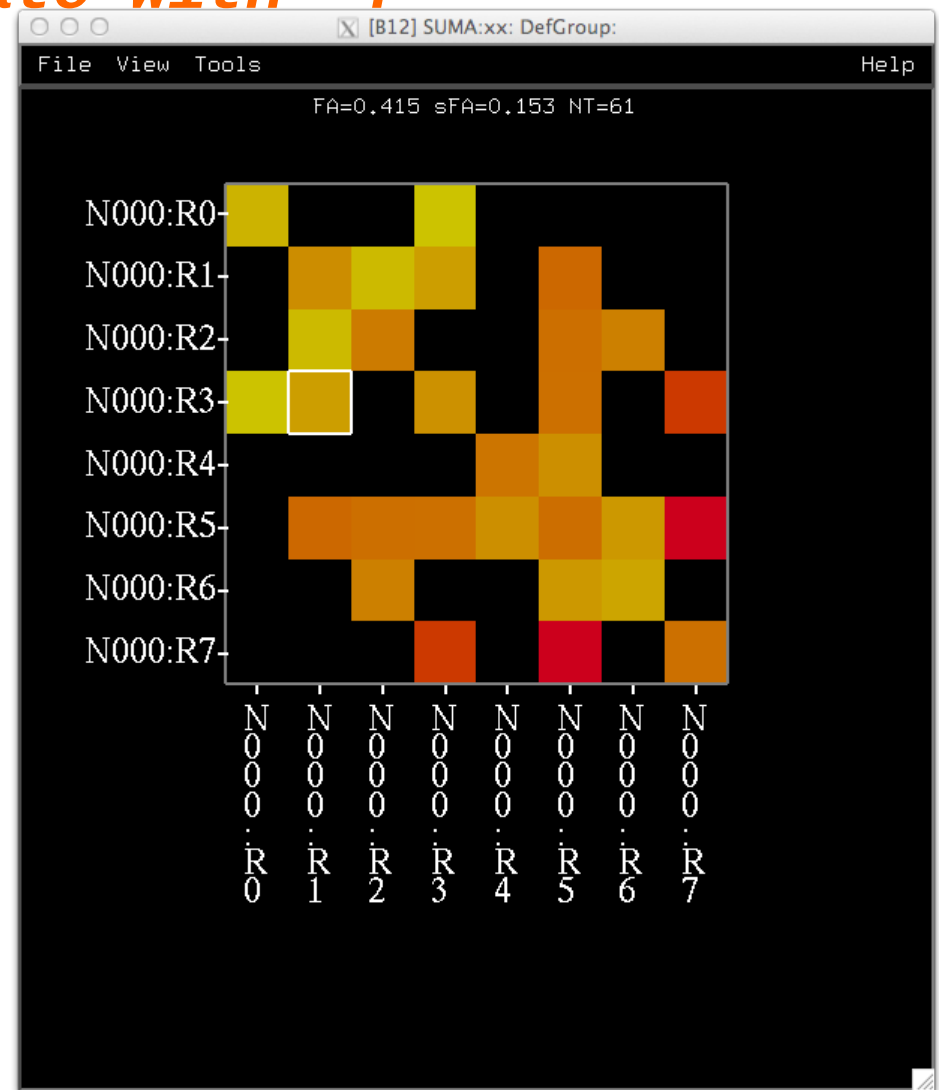
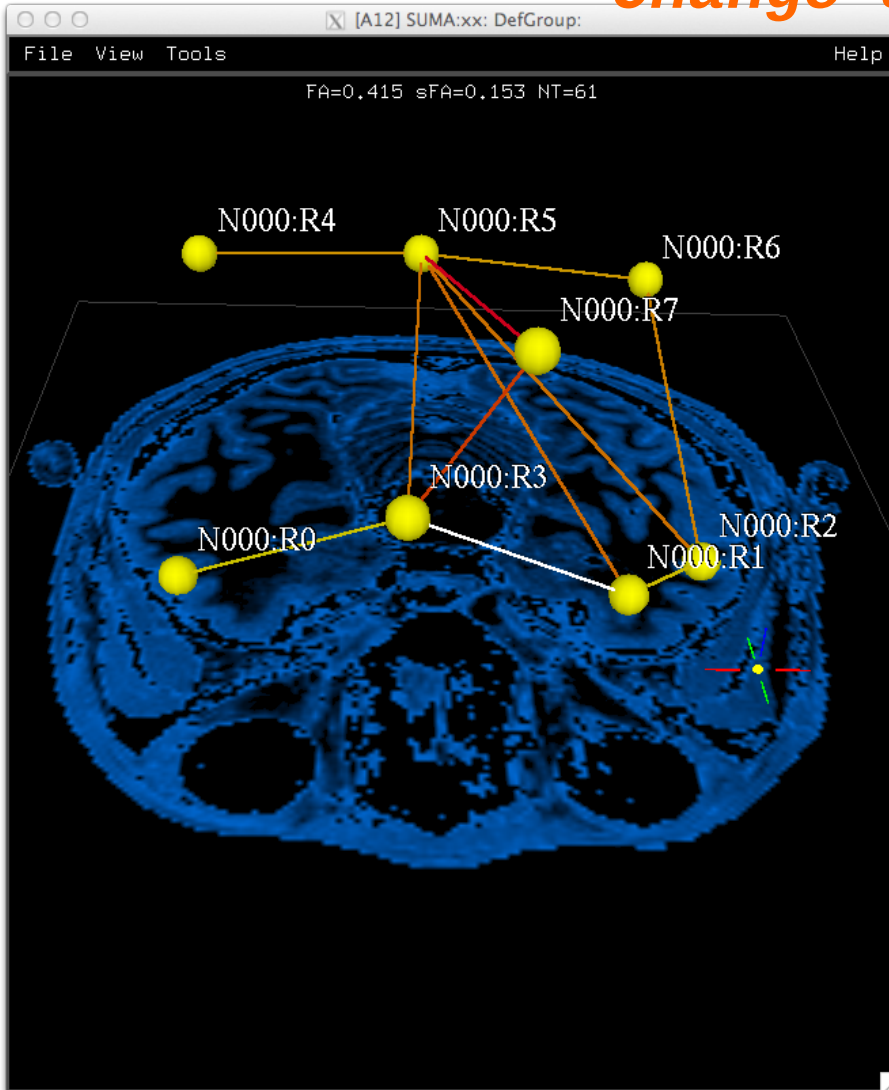
tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Example 3: Matrices in dual form

View → Object Controller

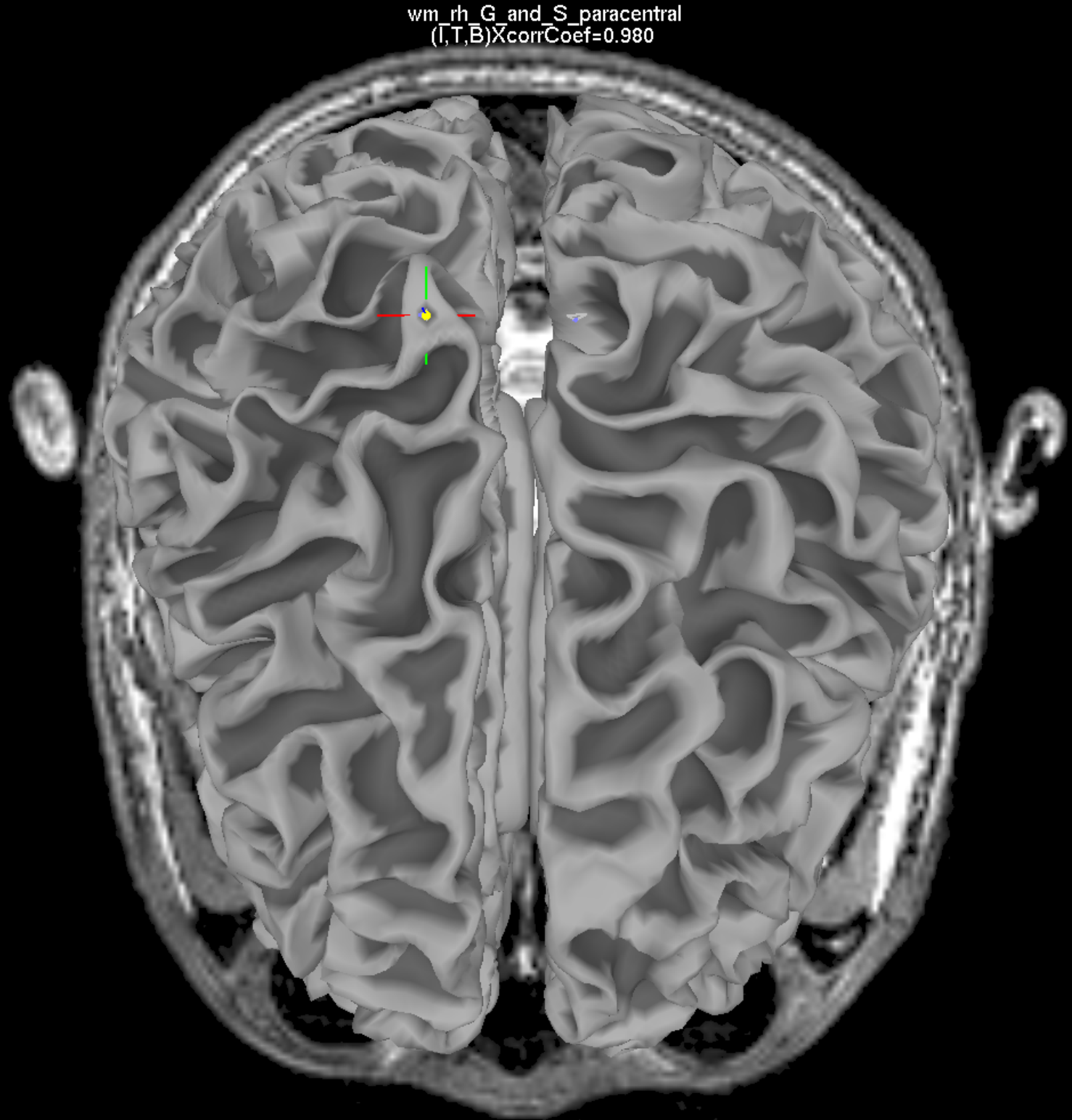
Open new window (ctrl+n)

Change state with '.'



tcsch Do_09_VISdti_SUMA_visual_ex3.tcsch
Simultaneous InstaCorr & InstaTract

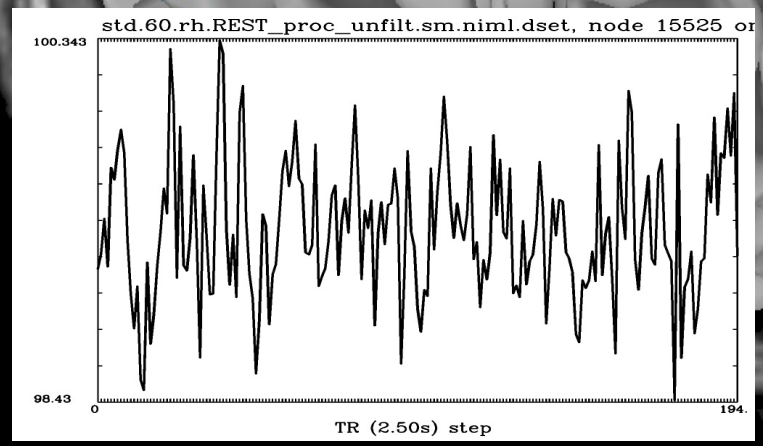
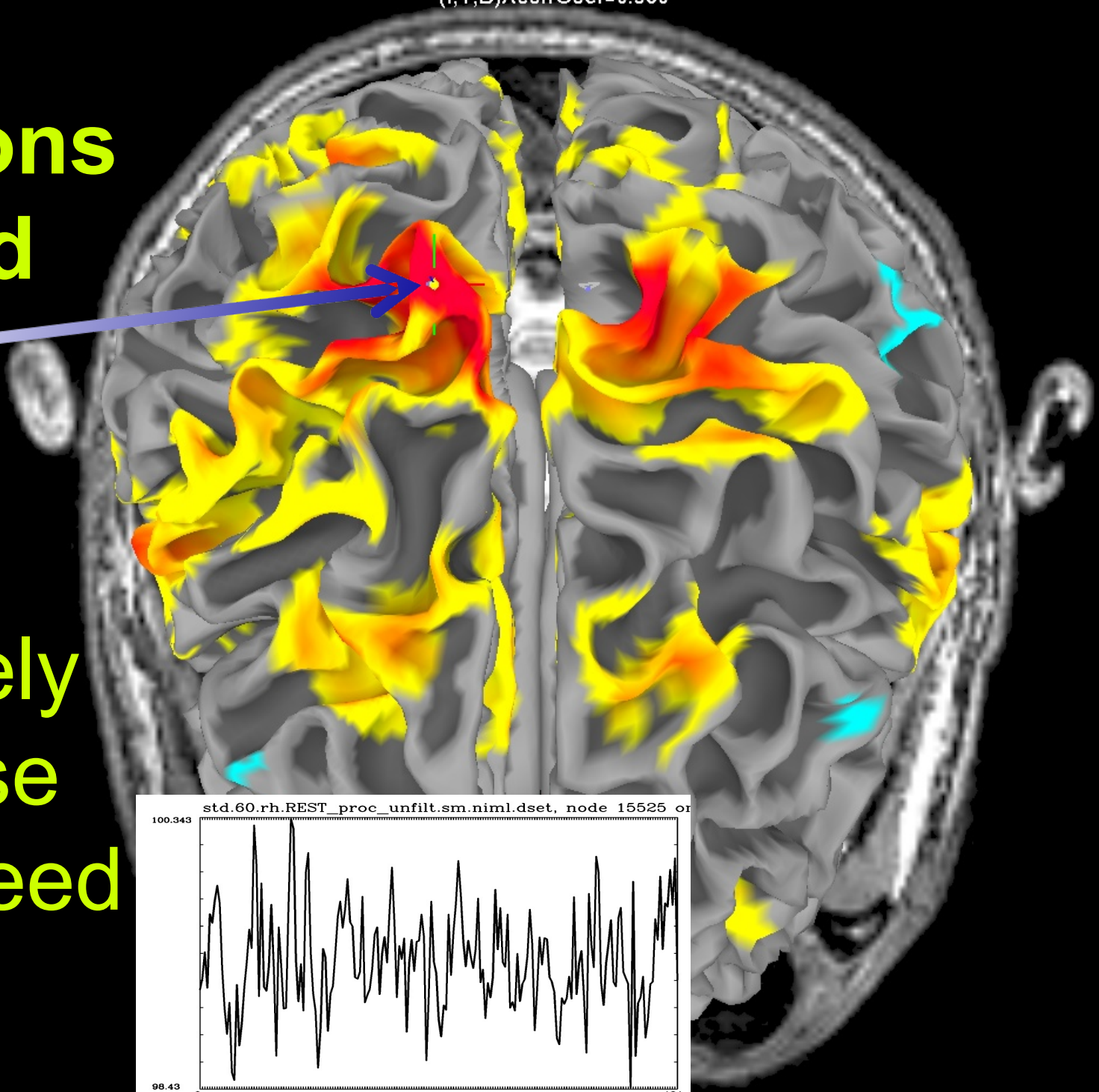
Naked brain surface



wm rh G and S paracentral
(I,T,B)XcorrCoef=0.980

**RS-FMRI
correlations
from seed
voxel**

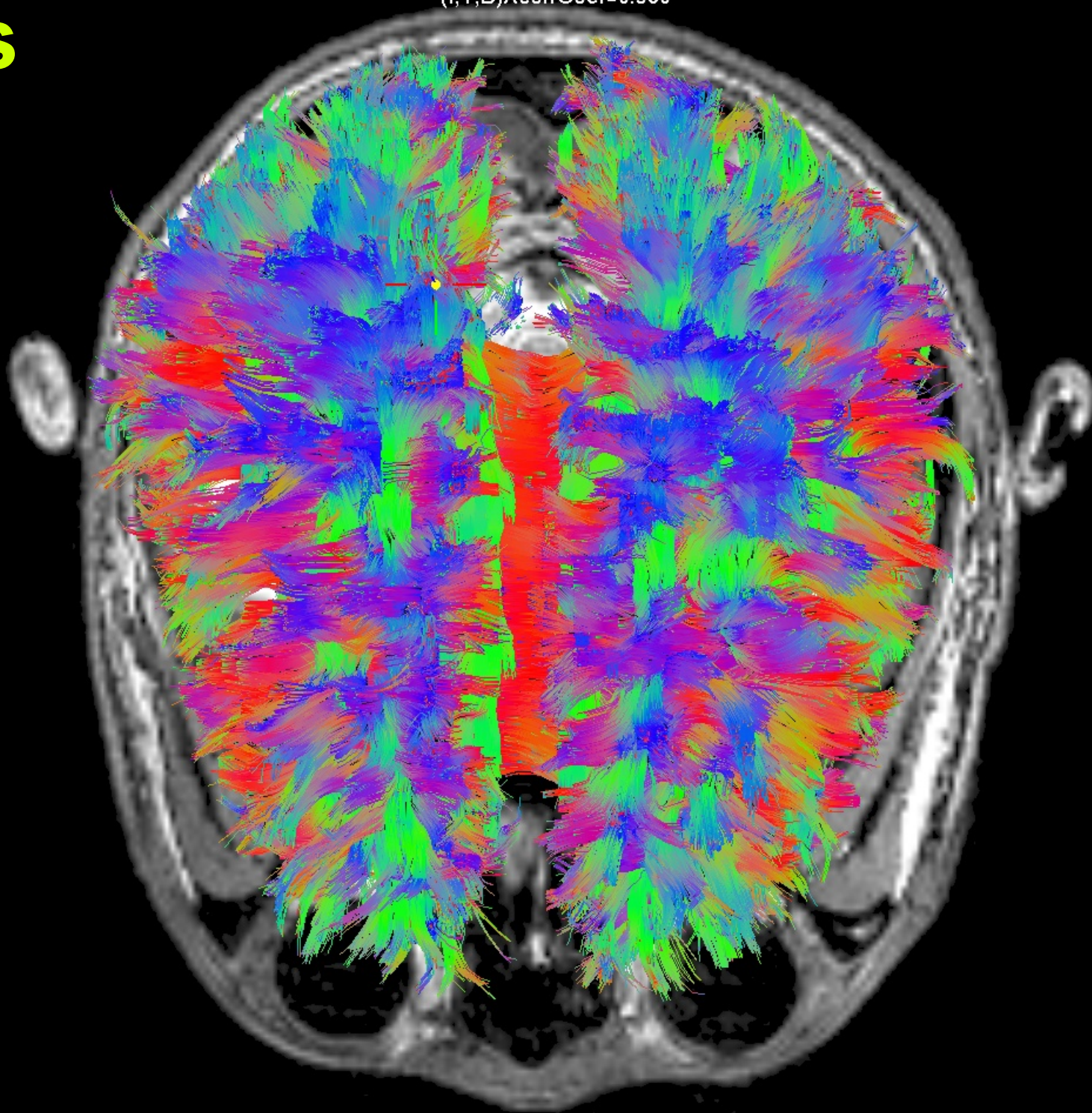
**computed
interactively
with mouse
click on seed**



DTI tracts

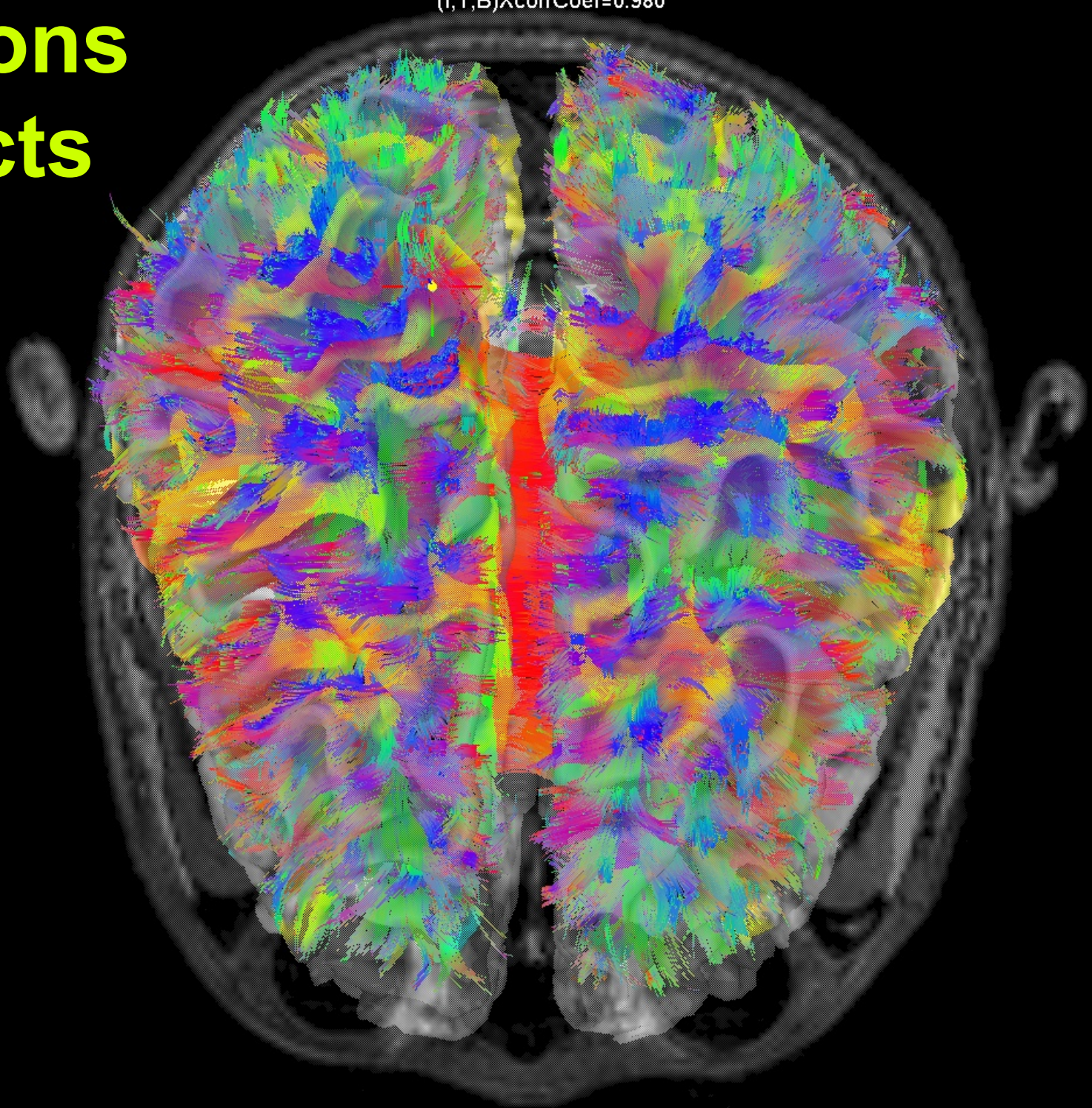
[brain is hidden]

Just too much to take in!



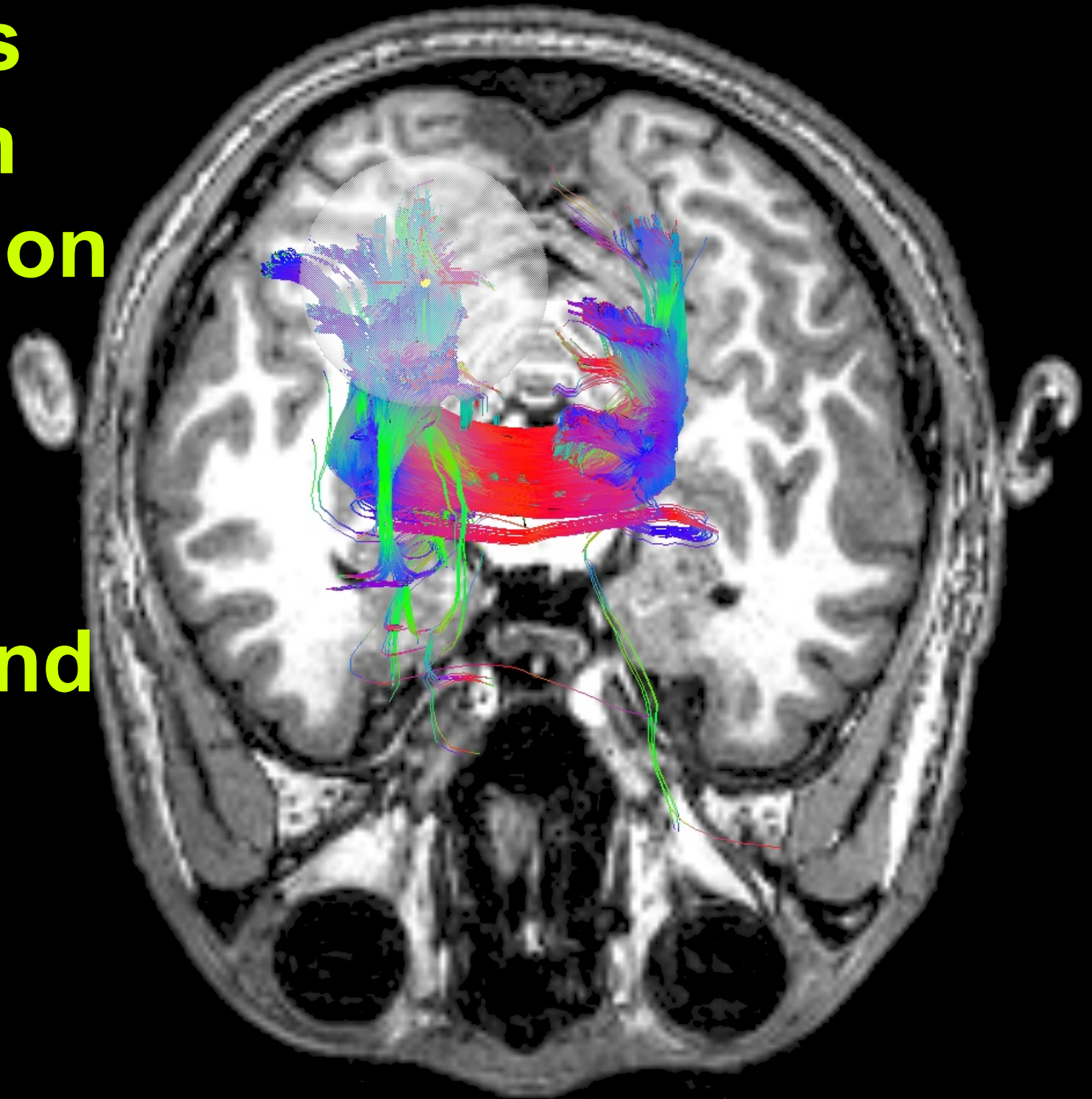
Correlations + DTI tracts + Brain

*Way too
much to
take in!*



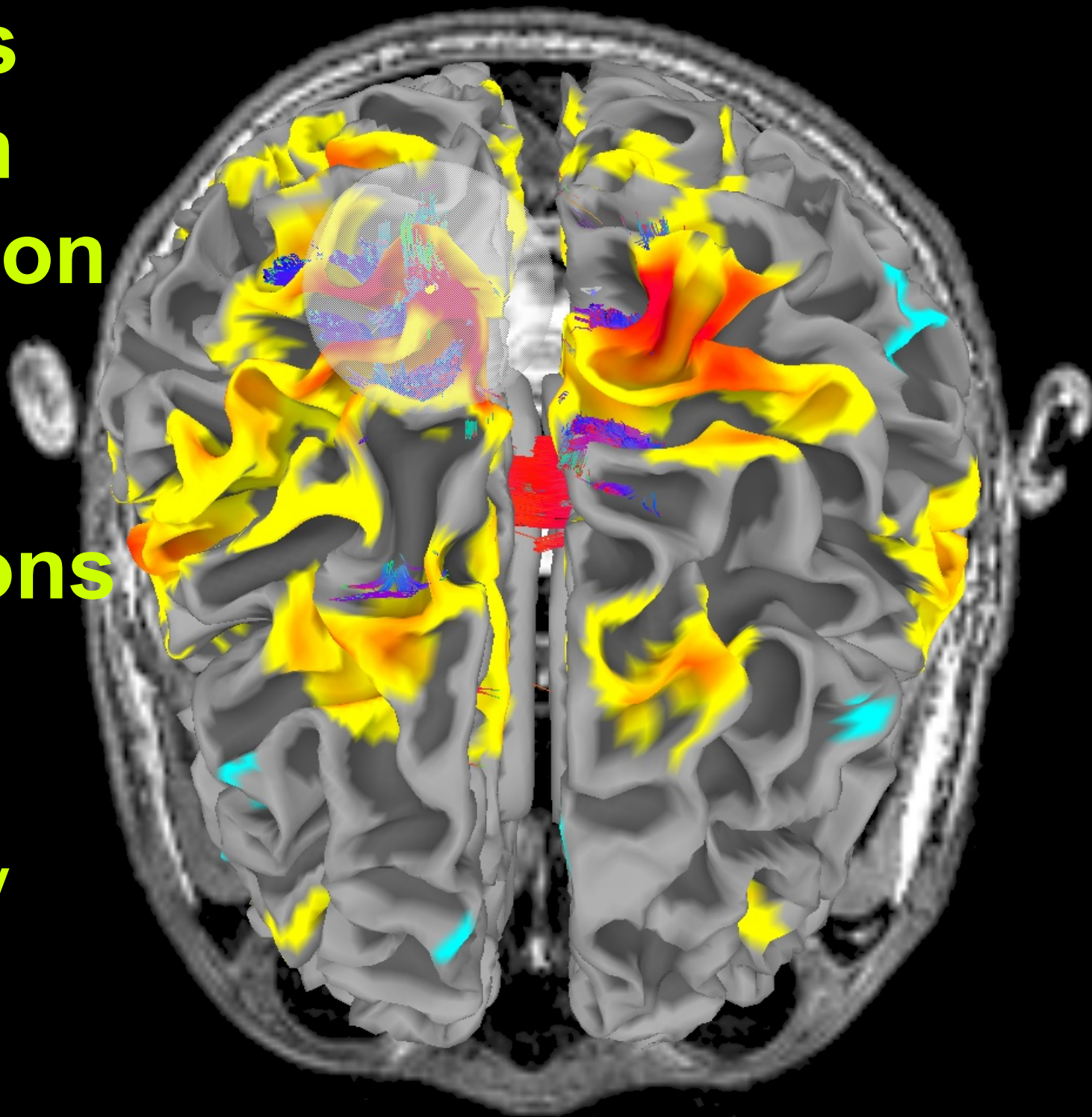
**DTI tracts
only from
seed region**

***Much
easier to
understand***



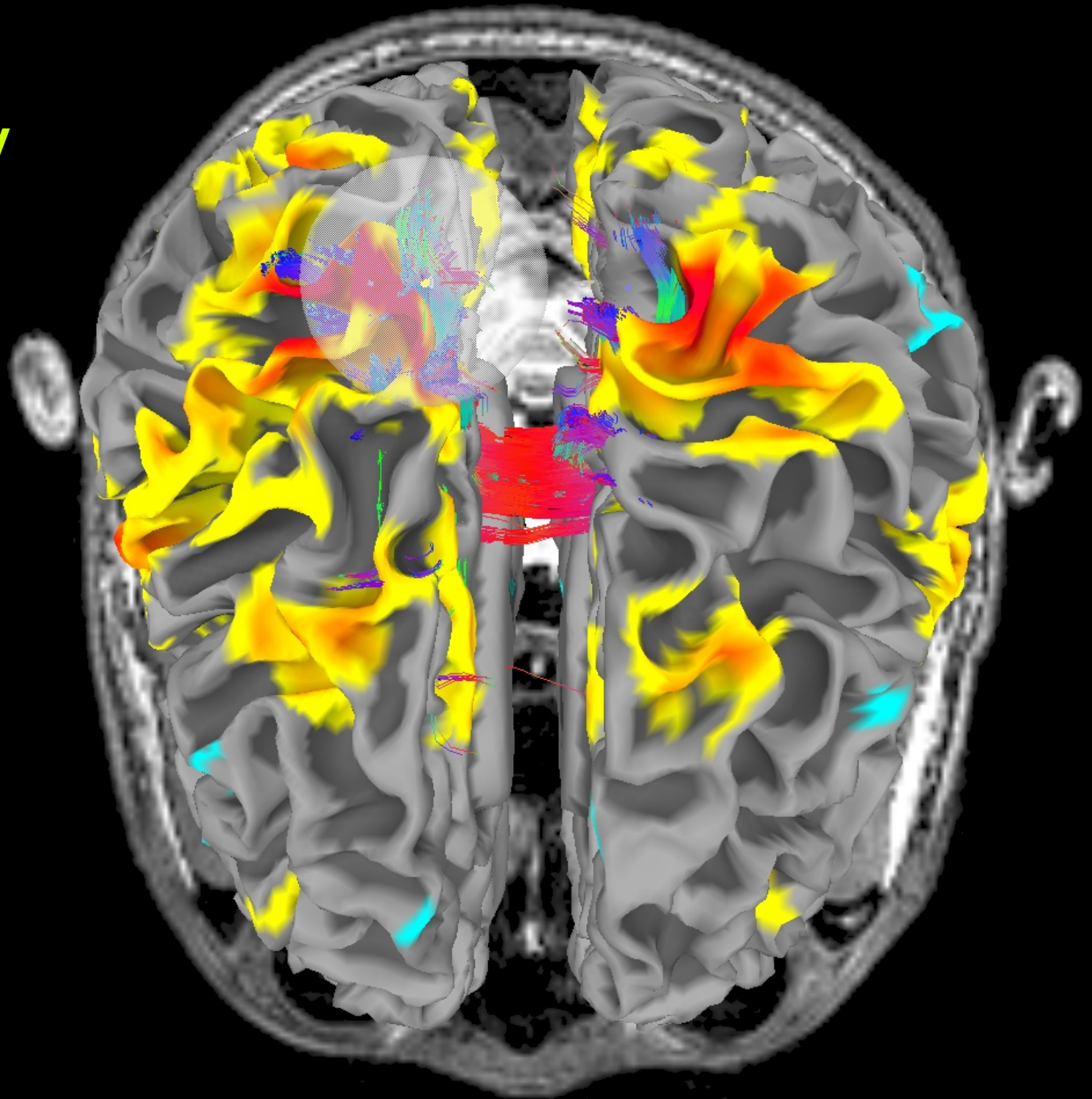
**DTI tracts
only from
seed region
+ time
series
correlations**

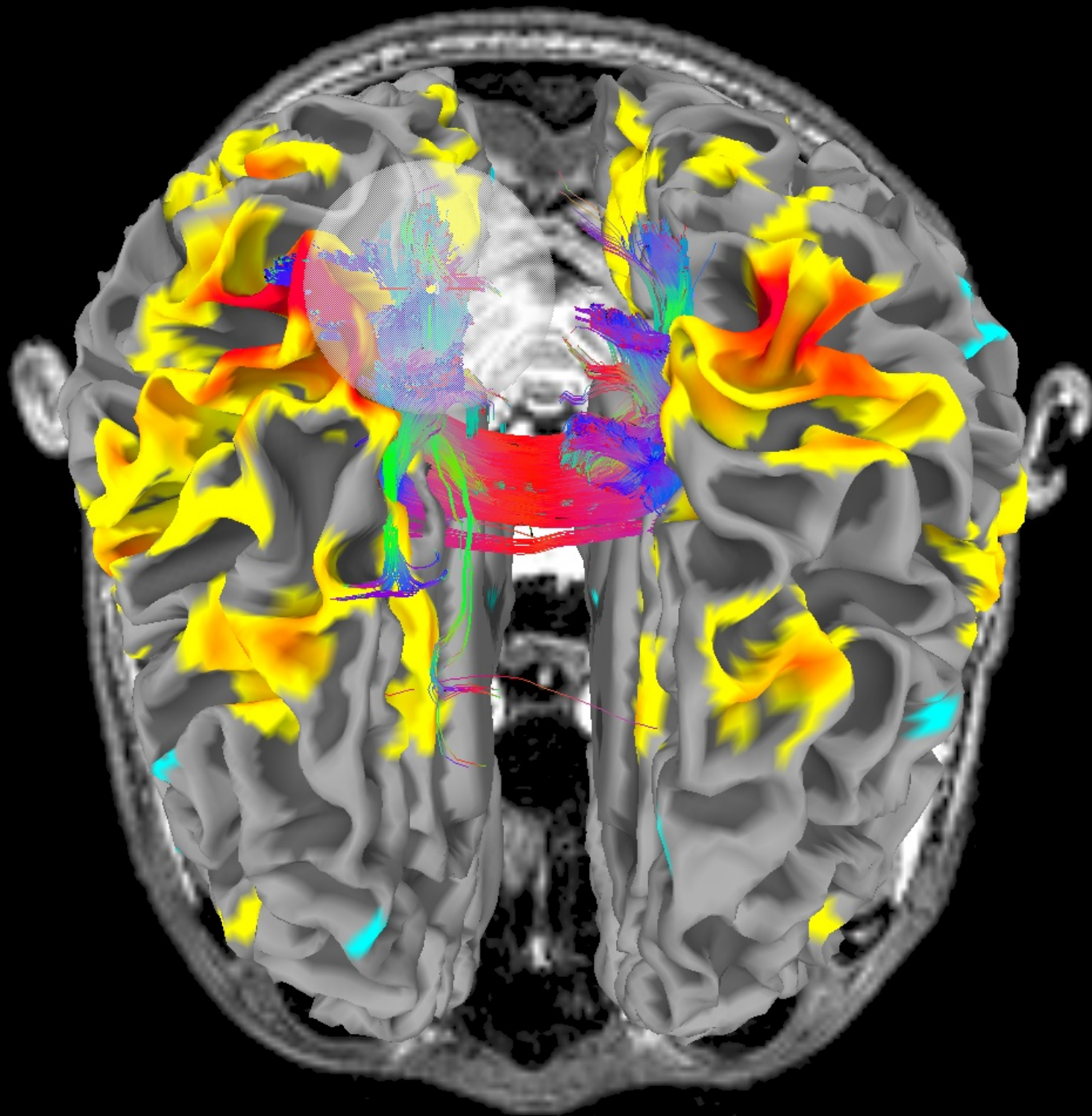
**Brain is
in the way**

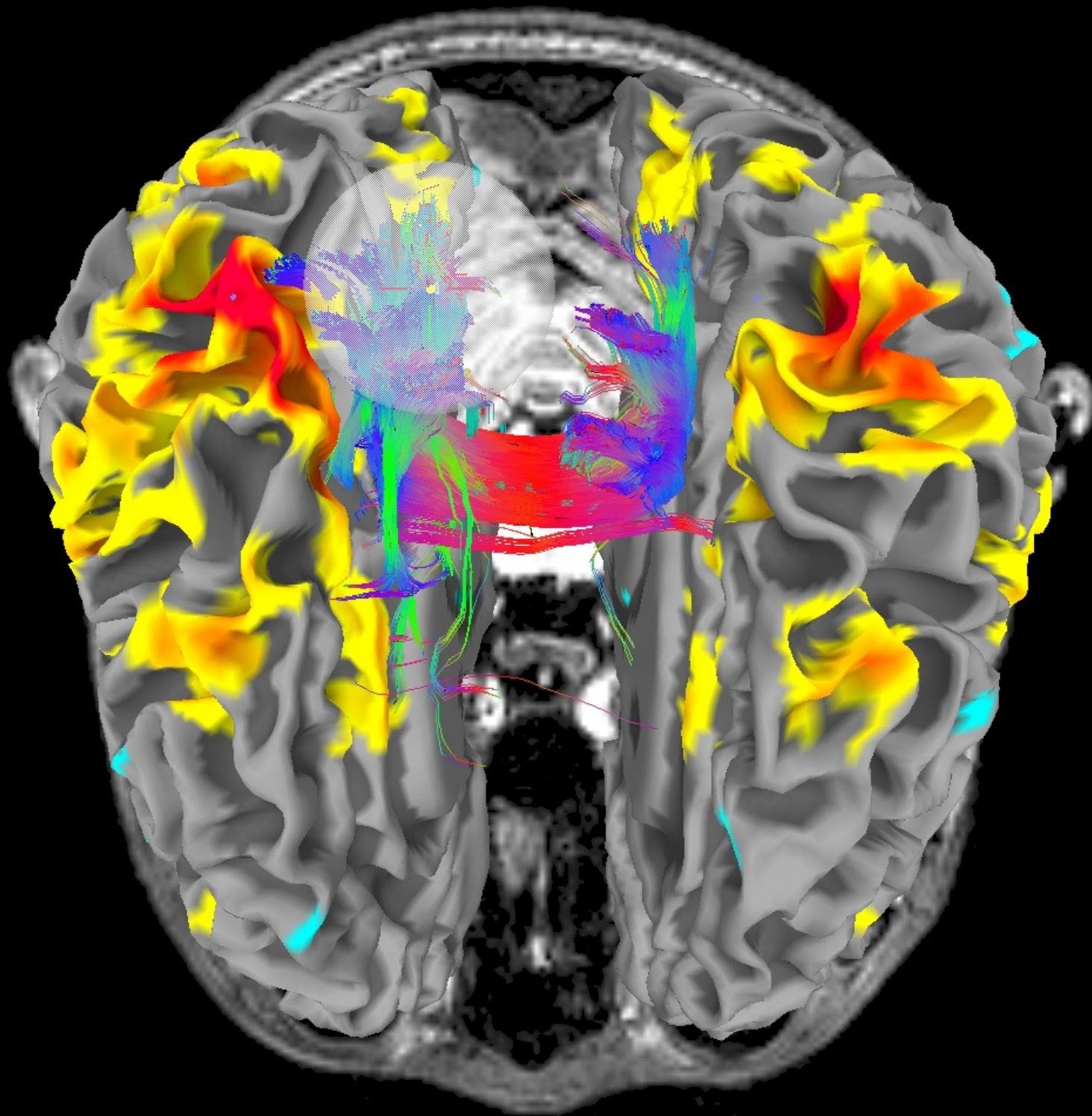


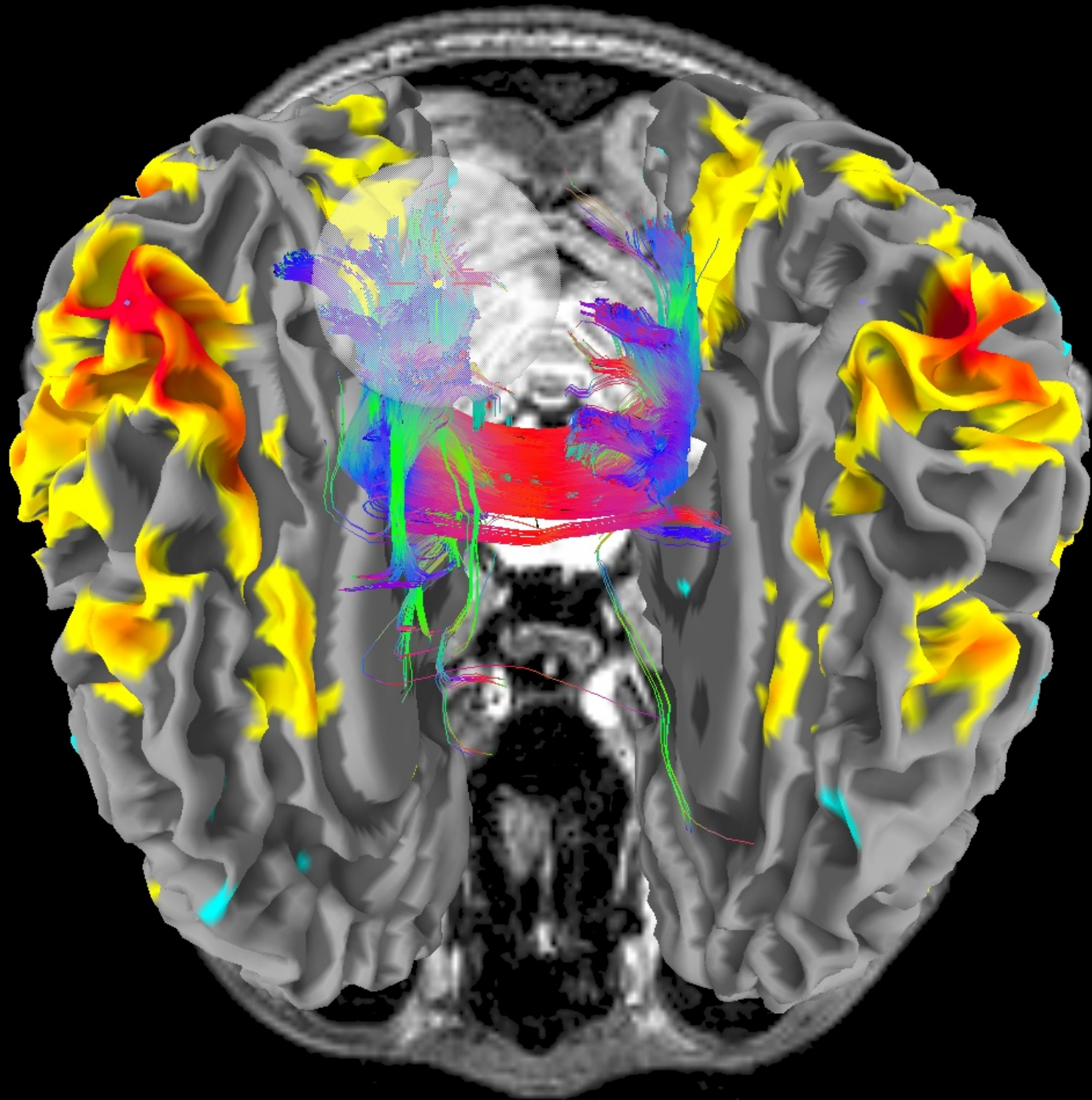
Brain is
in the way

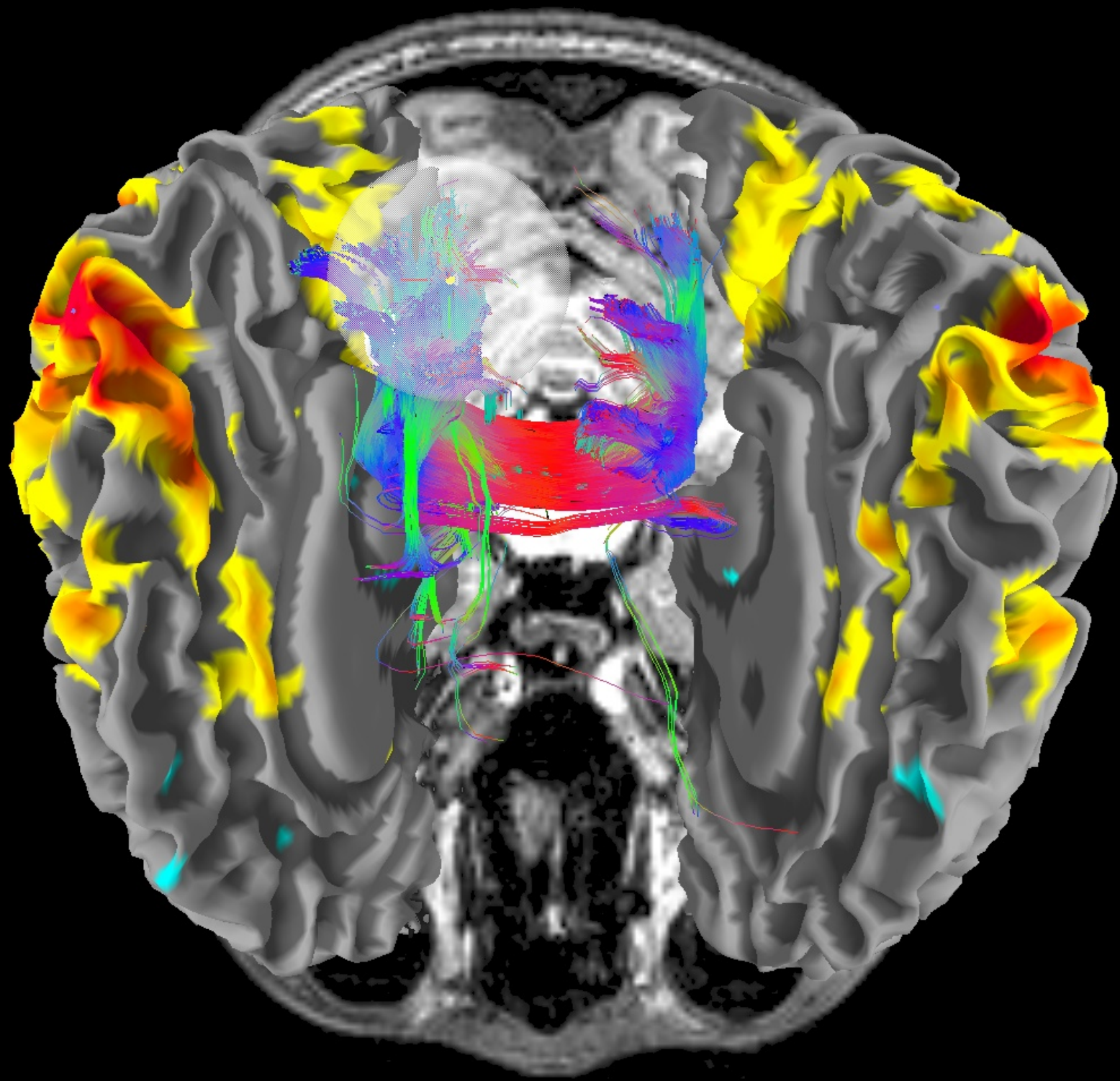
So move
it aside!

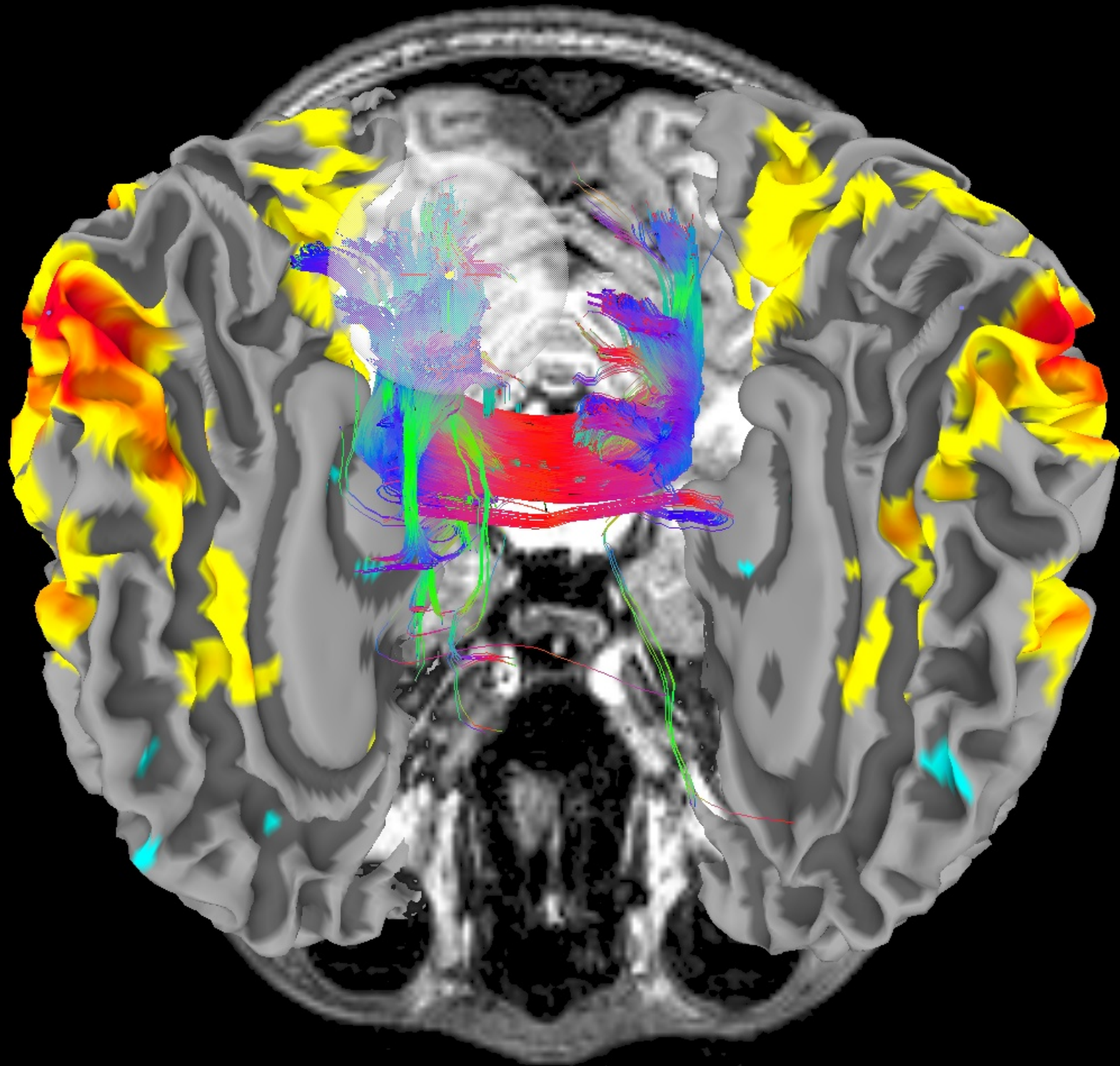




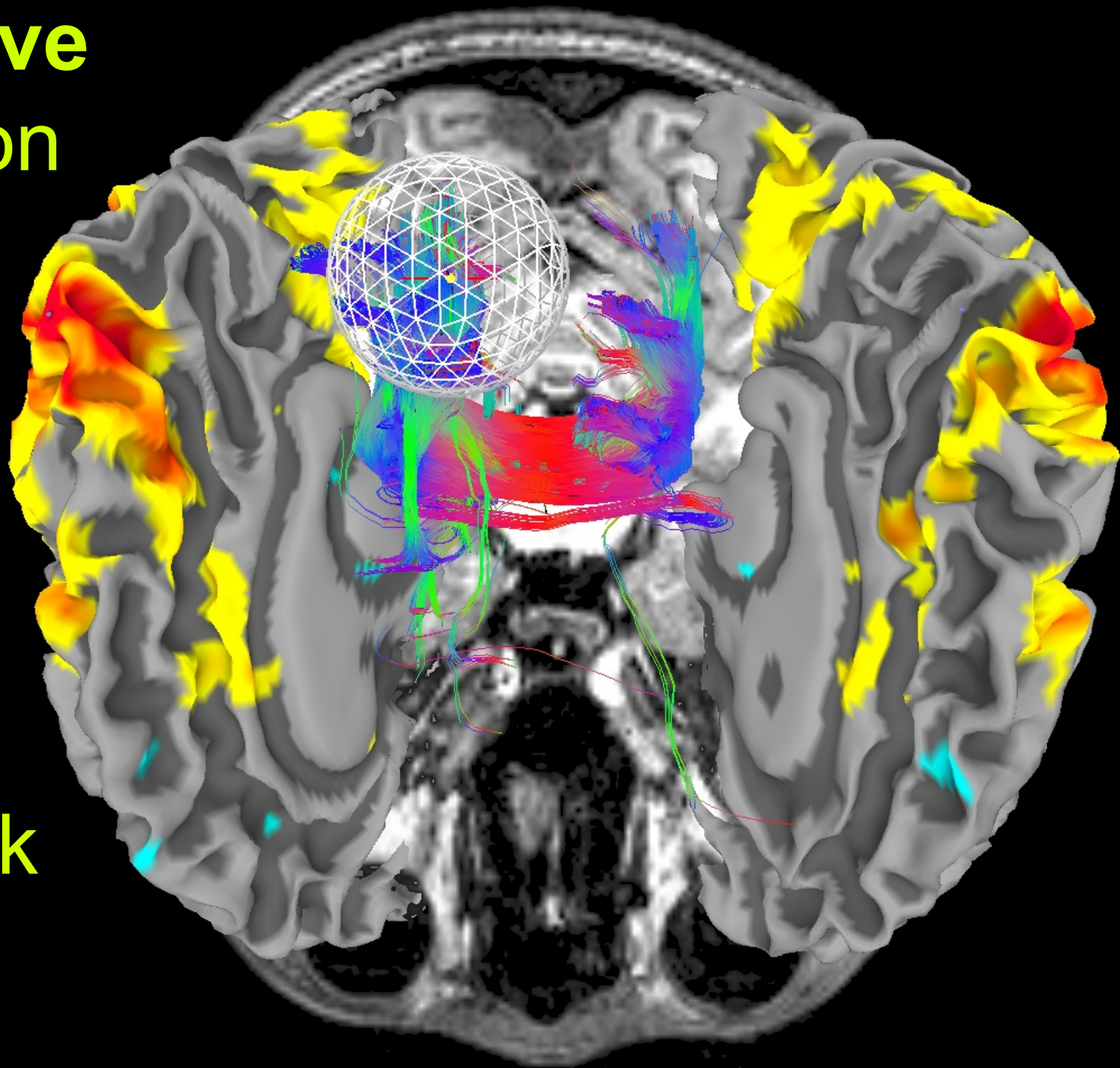




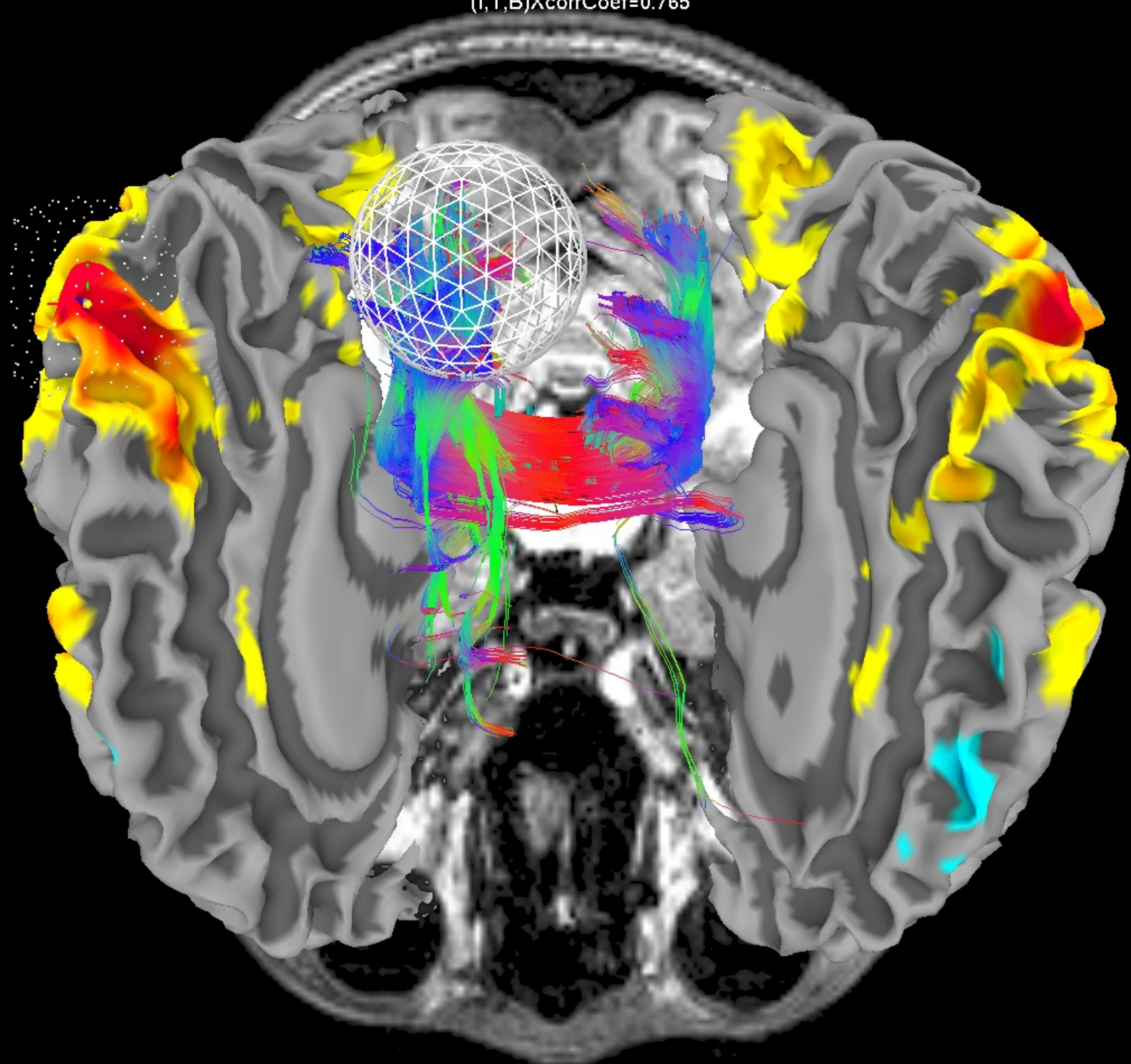




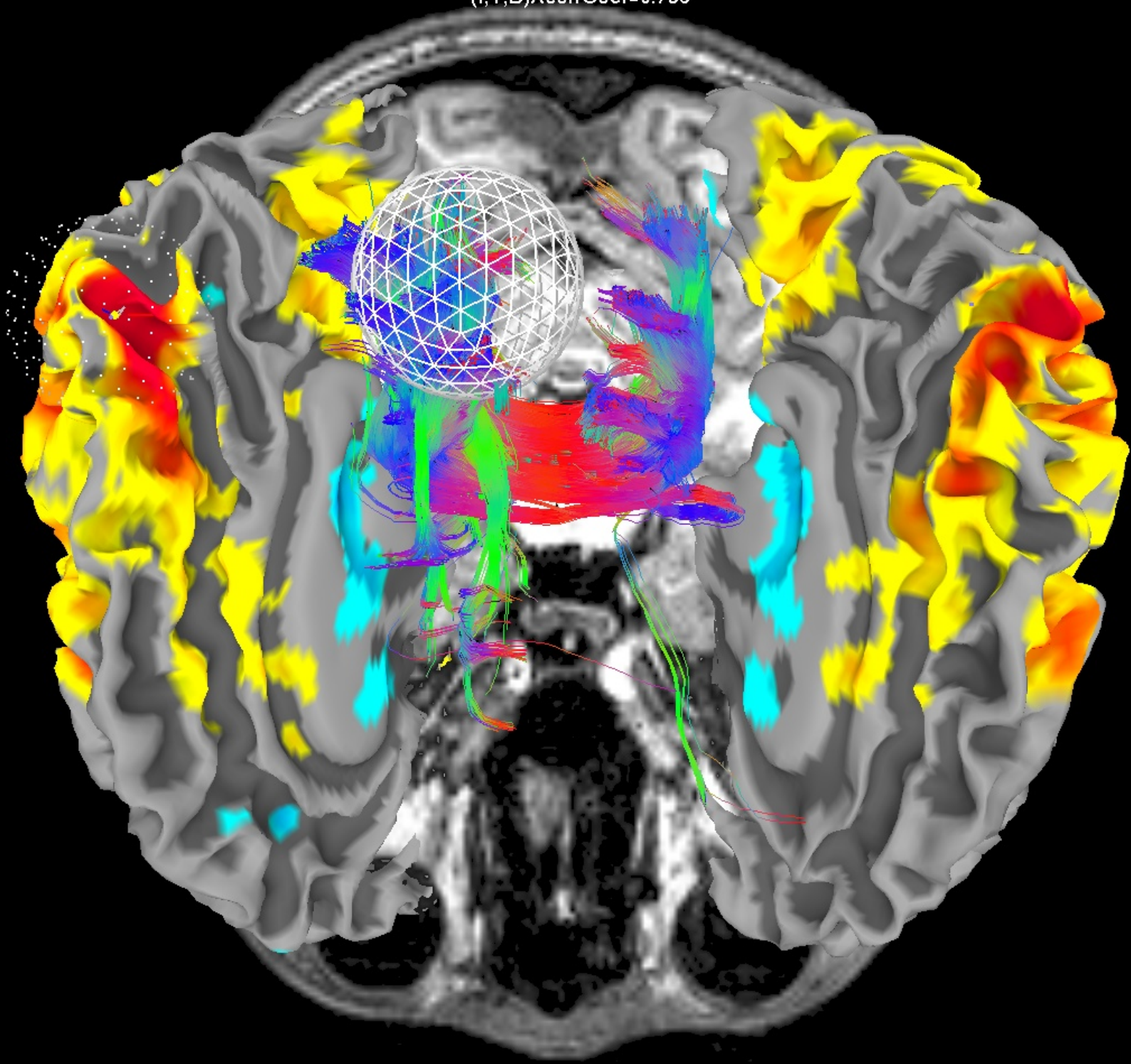
**Now move
correlation
and
tract
seed
along
the
sulcus
from back
to front**



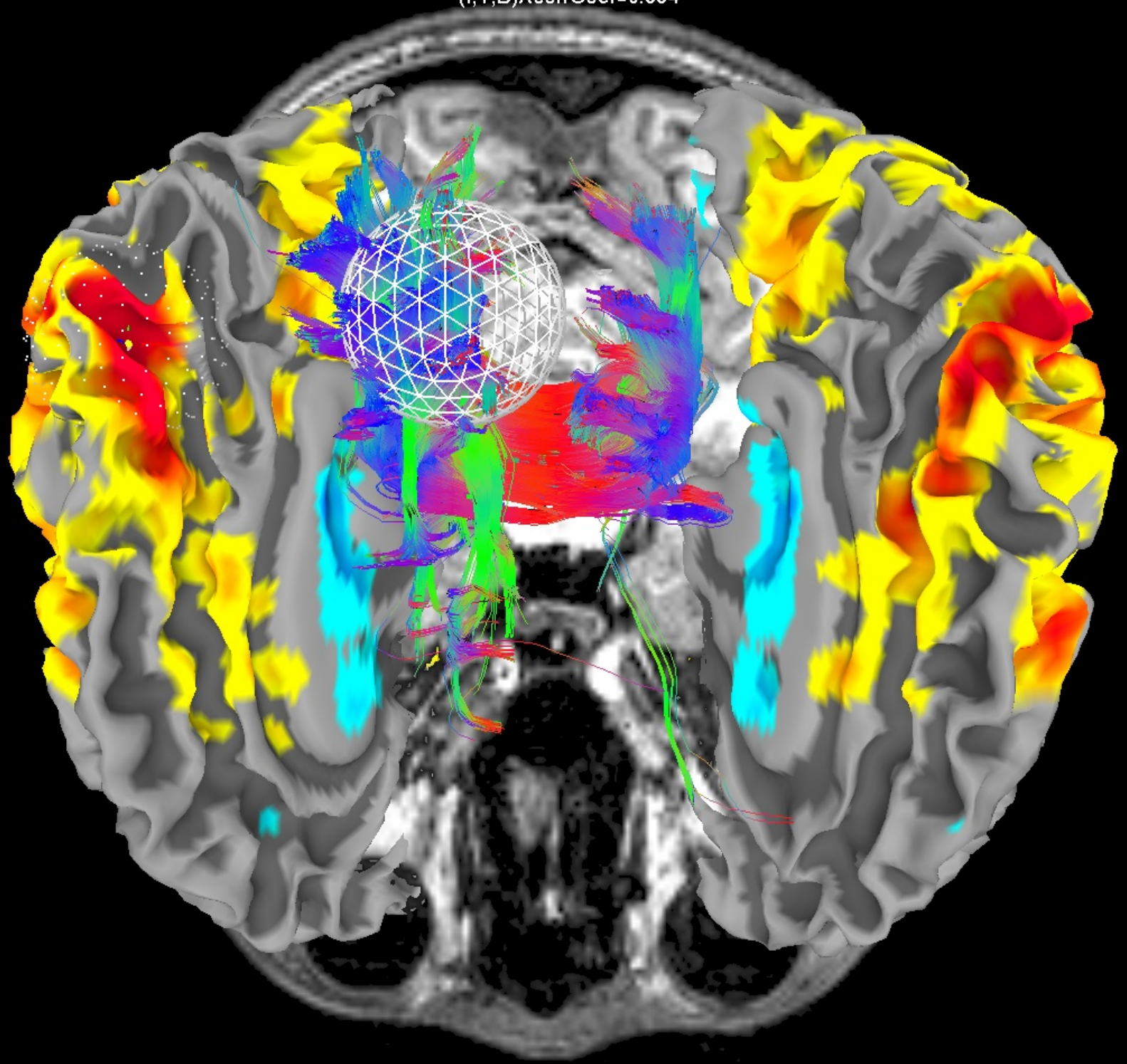
wm rh G and S paracentral
(I,T,B)XcorrCoef=0.765



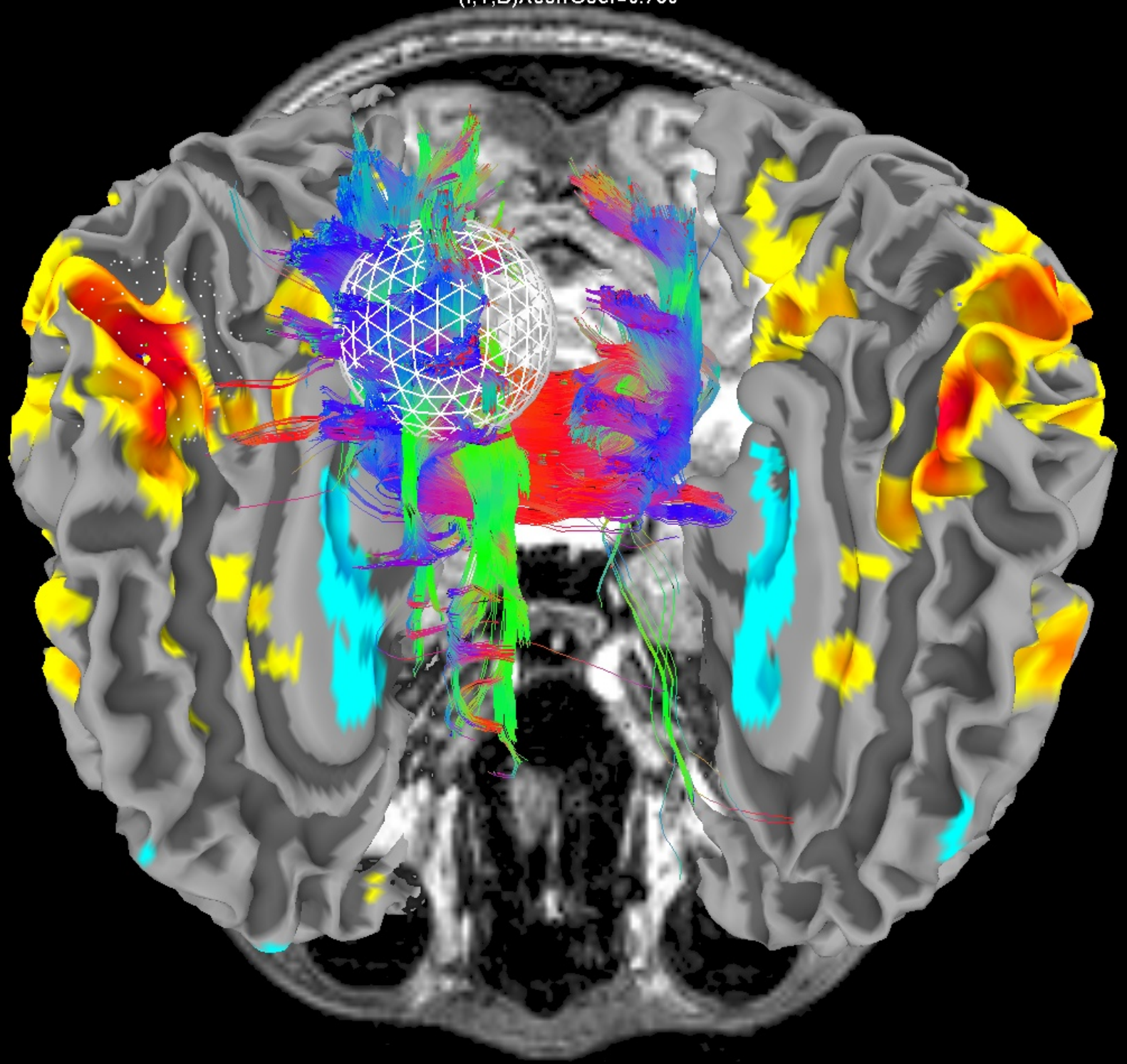
wm rh G and S paracentral
(I,T,B)XcorrCoef=0.753



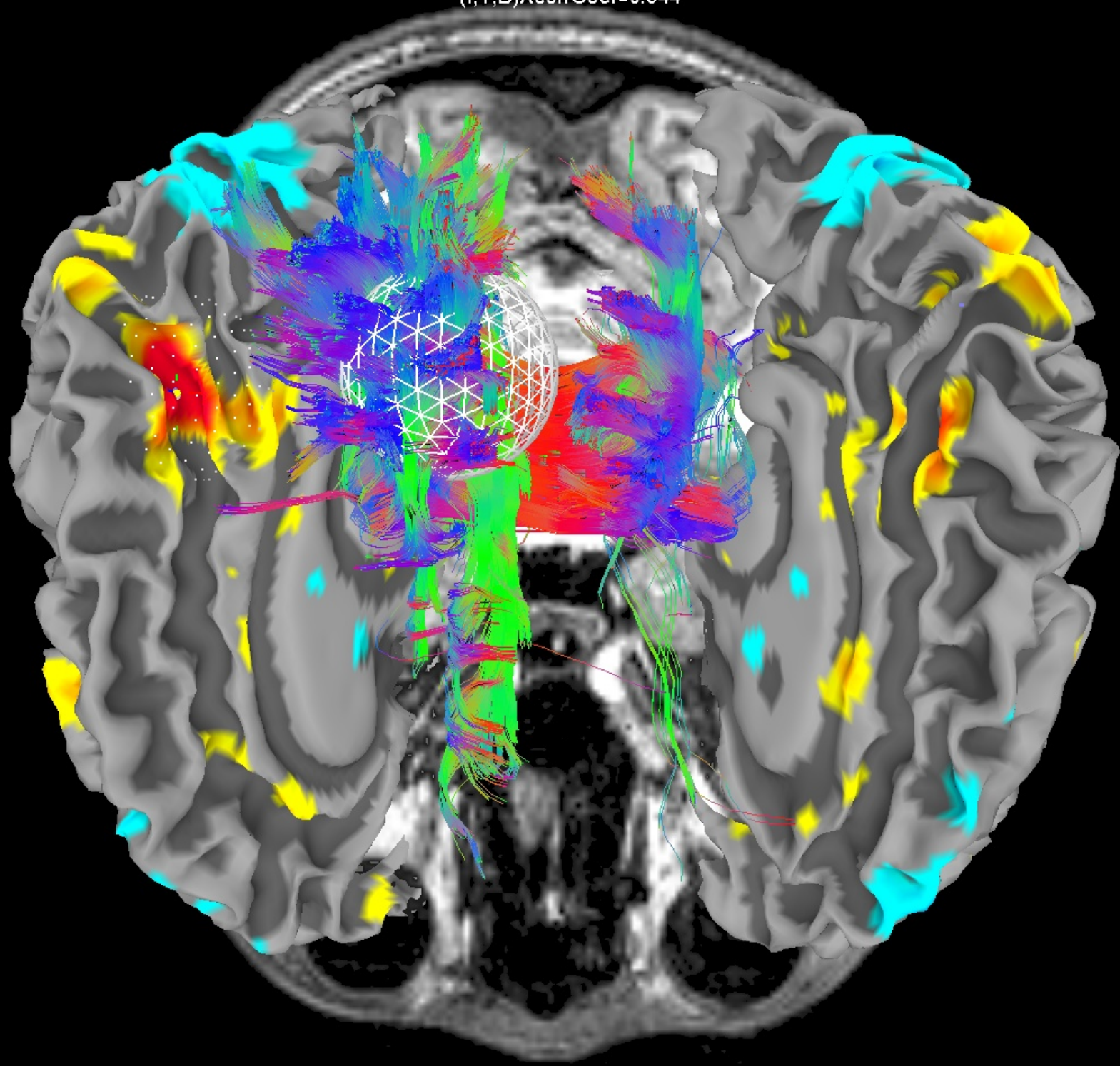
wm rh S cingul-Marginalis
(I,T,B)XcorrCoef=0.884



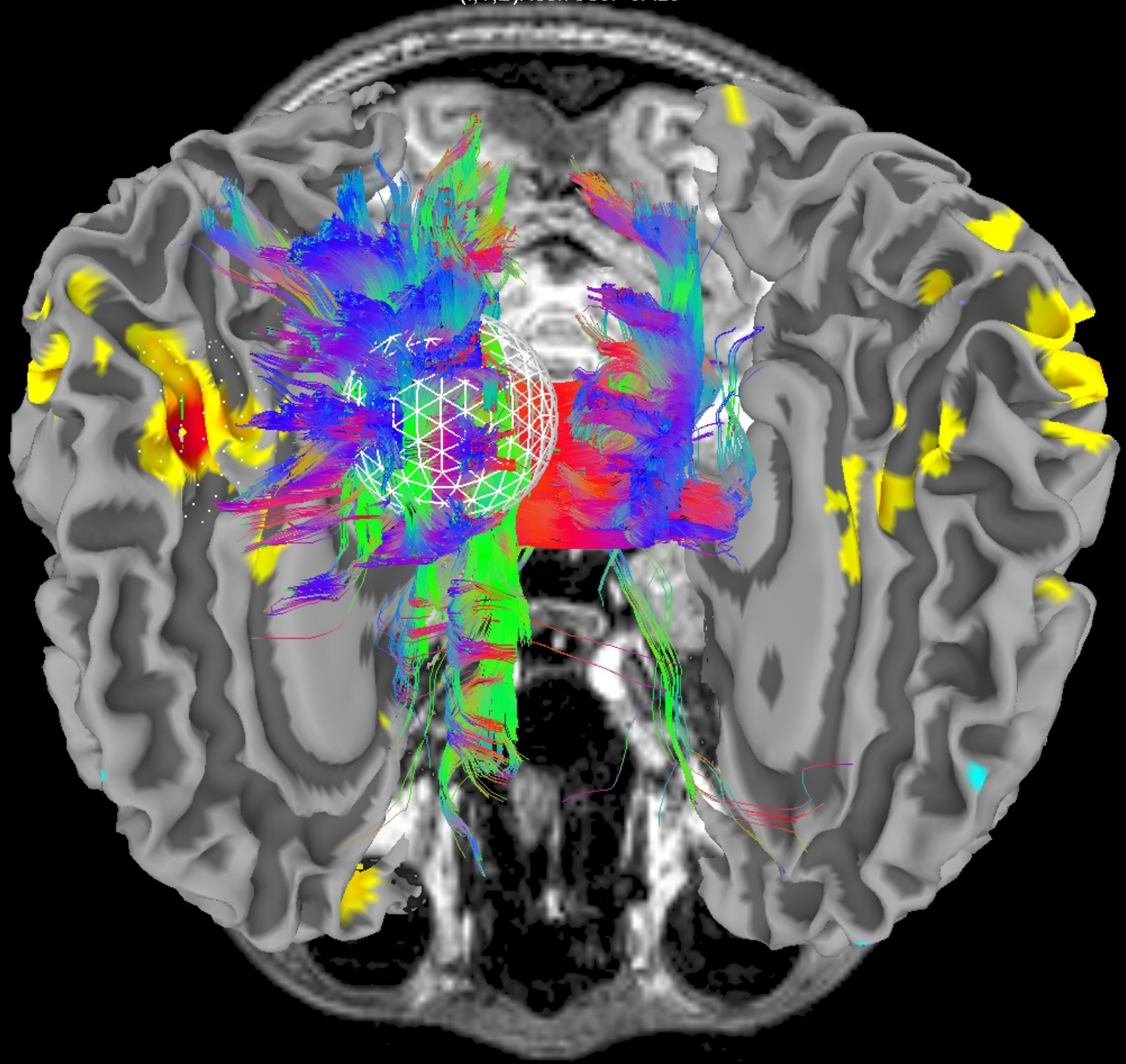
wm rh S cingul-Marginalis
(I,T,B)XcorrCoef=0.780



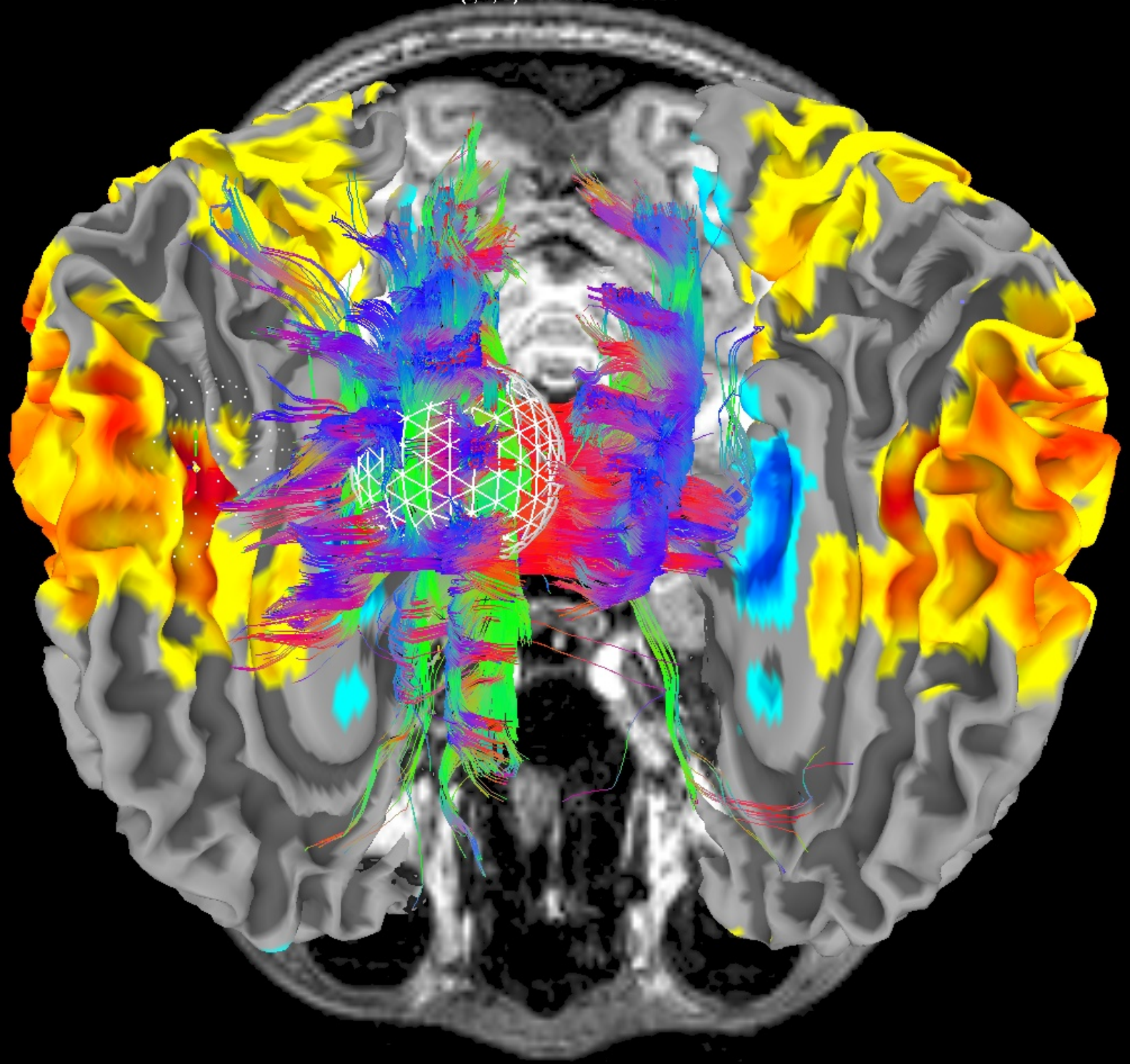
wm rh S cingul-Marginalis
(I,T,B)XcorrCoef=0.644



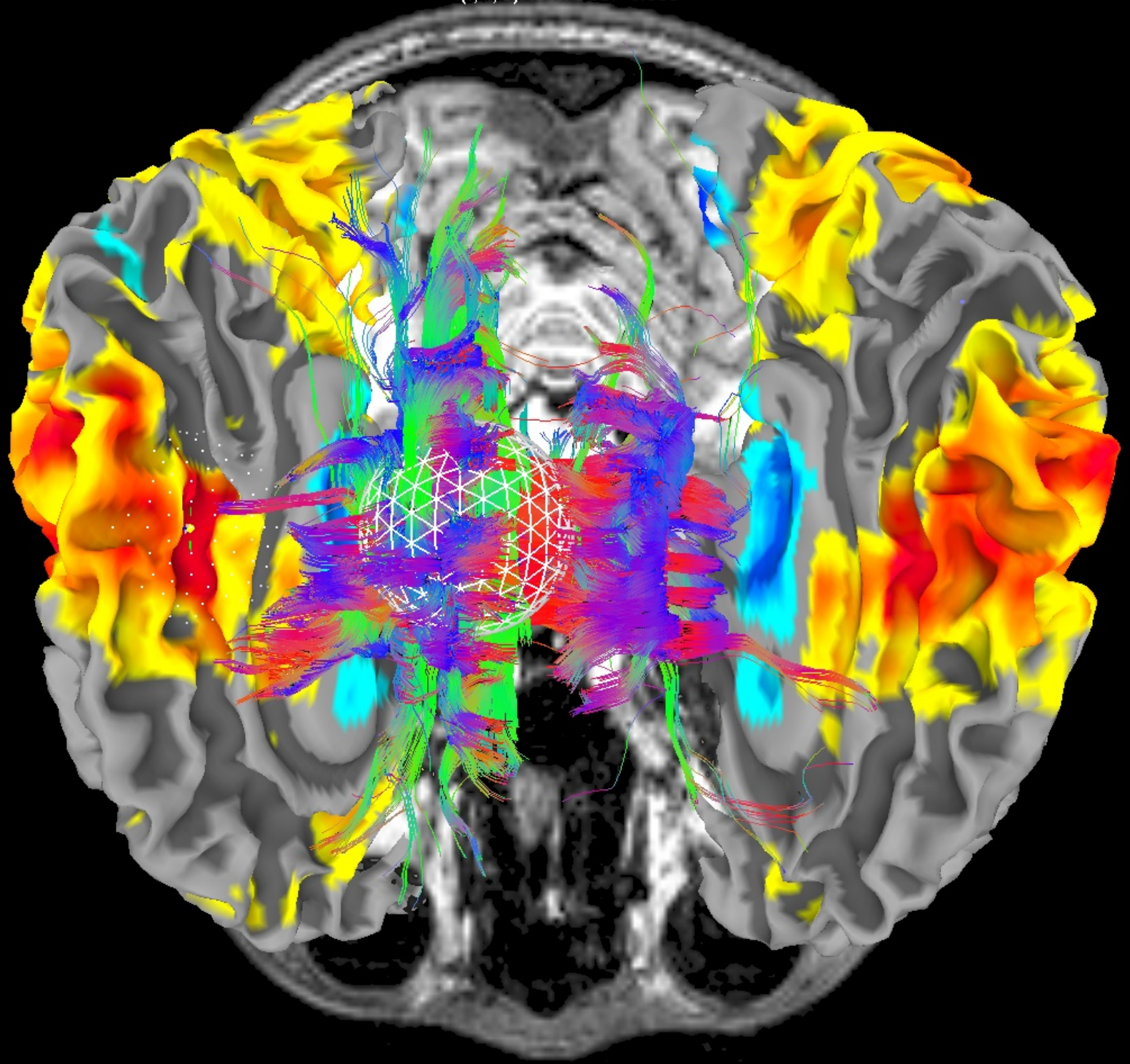
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.423



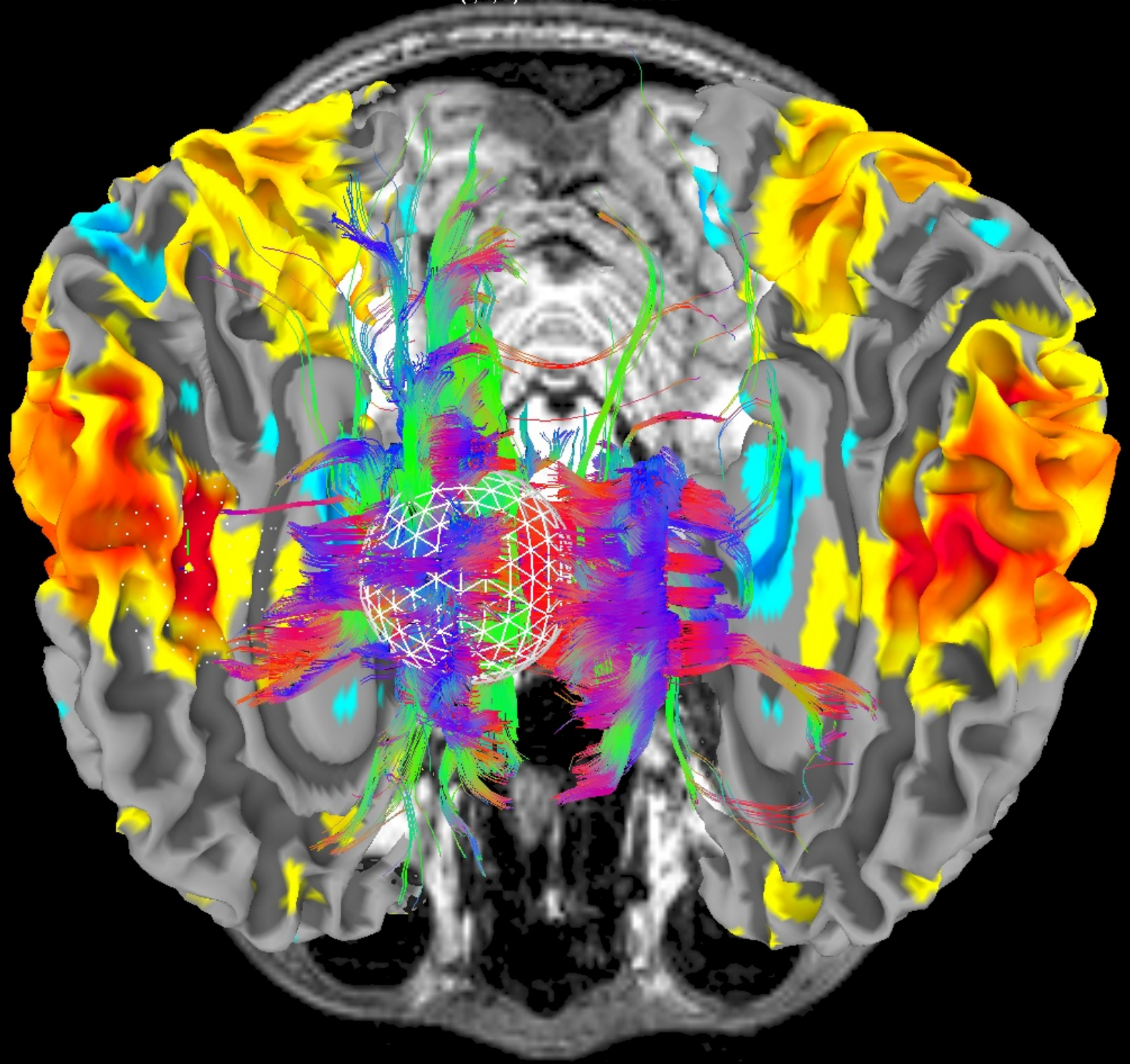
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.491



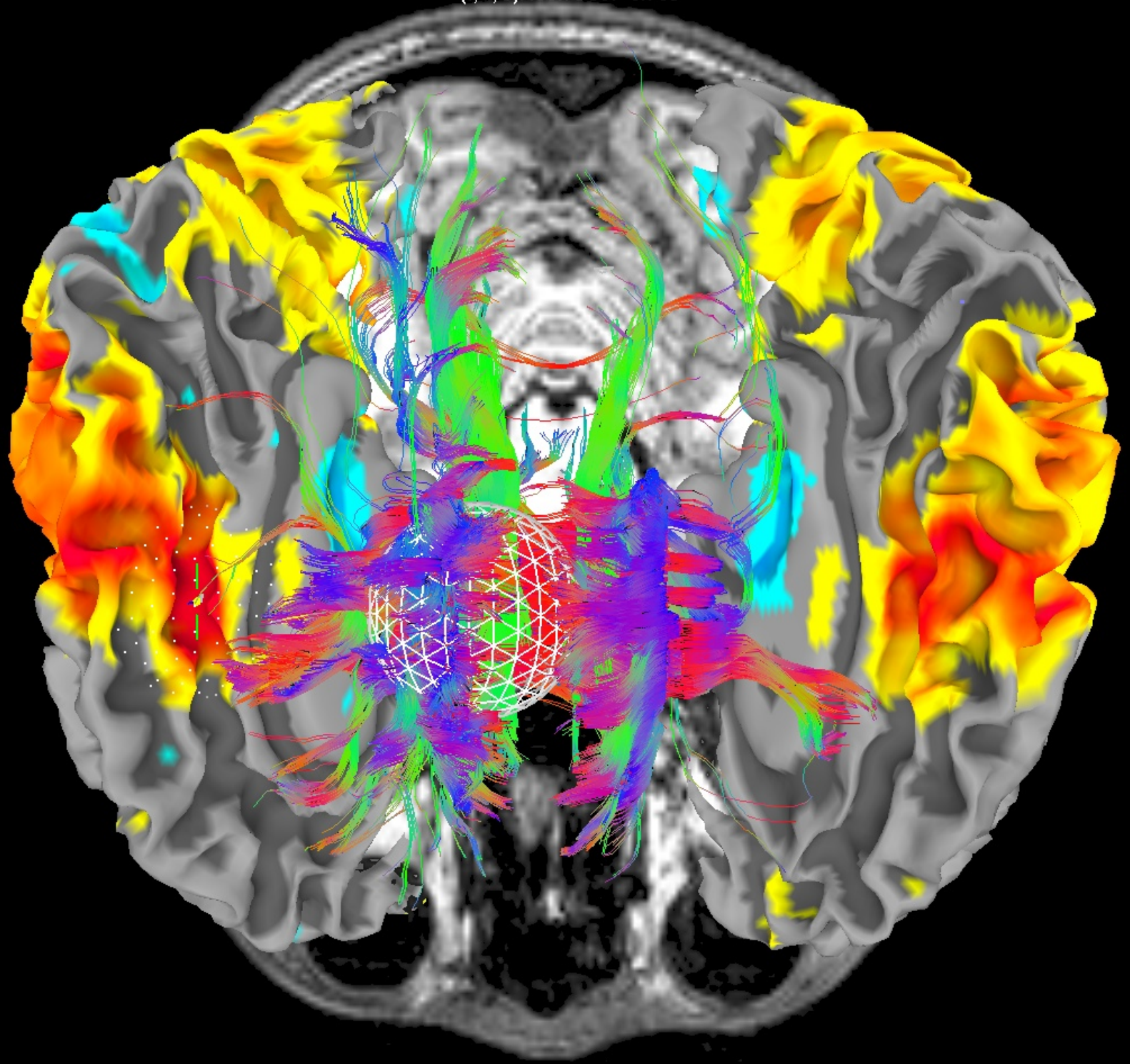
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.559



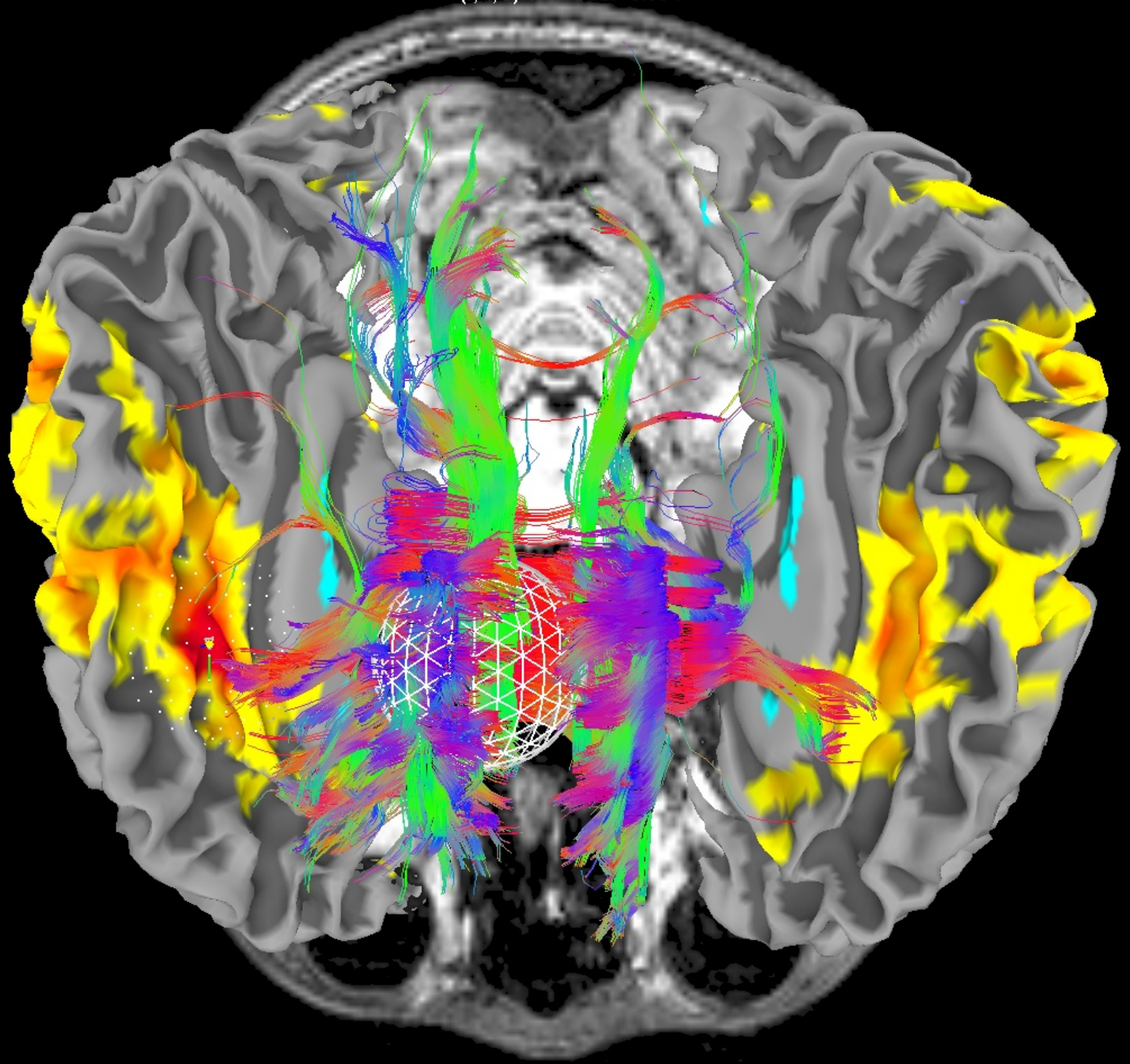
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.752



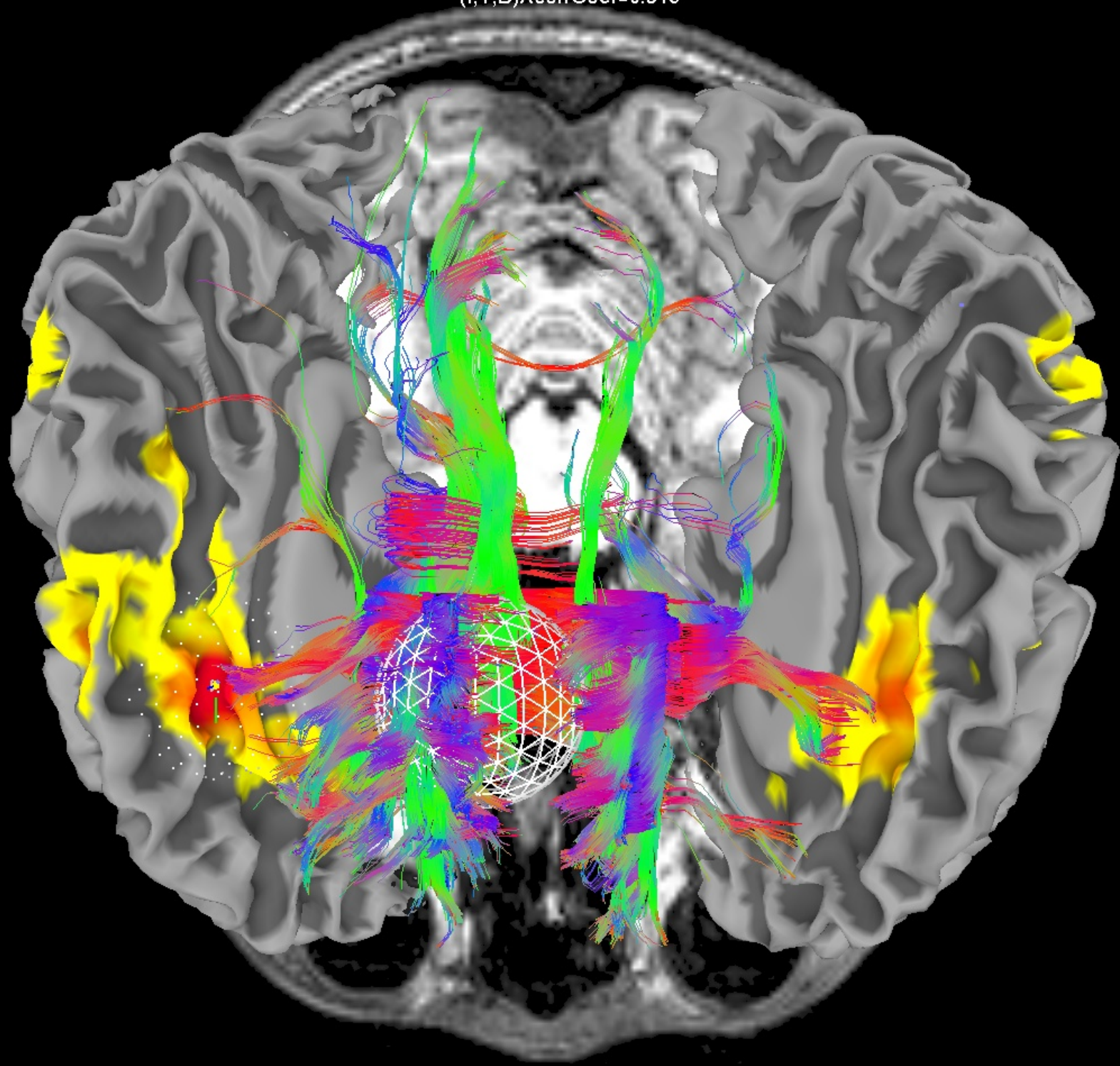
wm_rh_G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.785



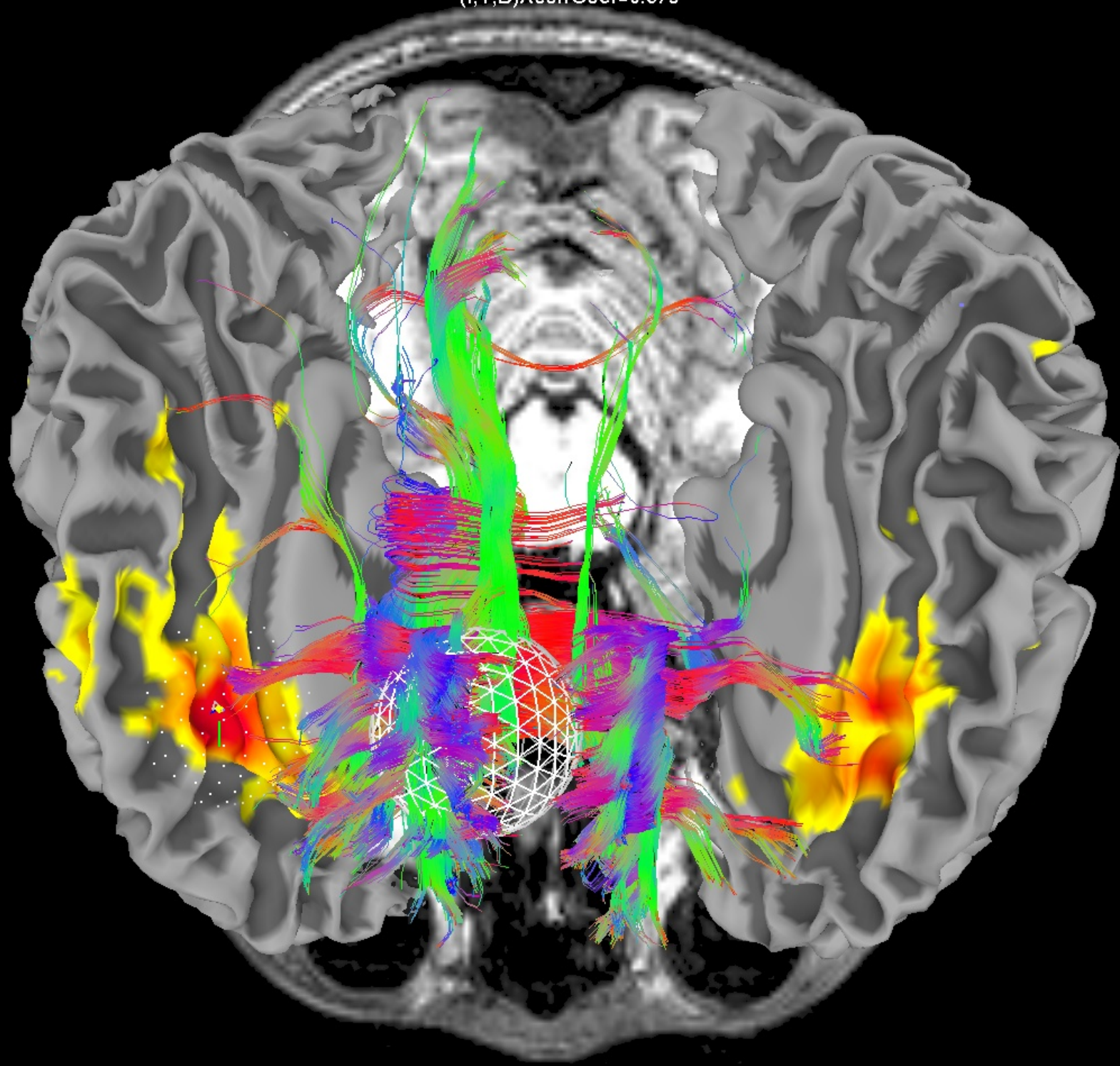
wm_rh_G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.604



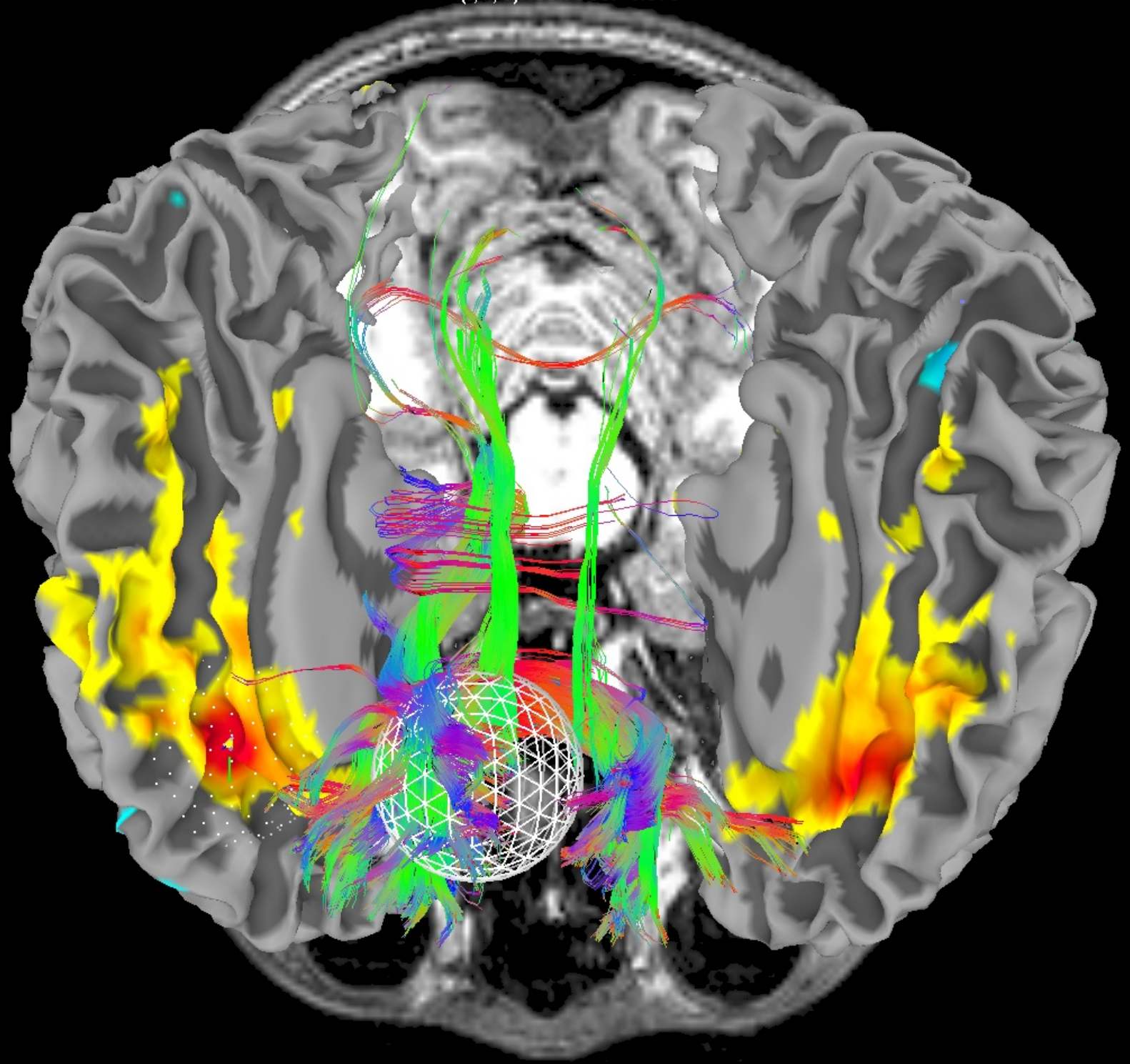
wm_rh G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.516



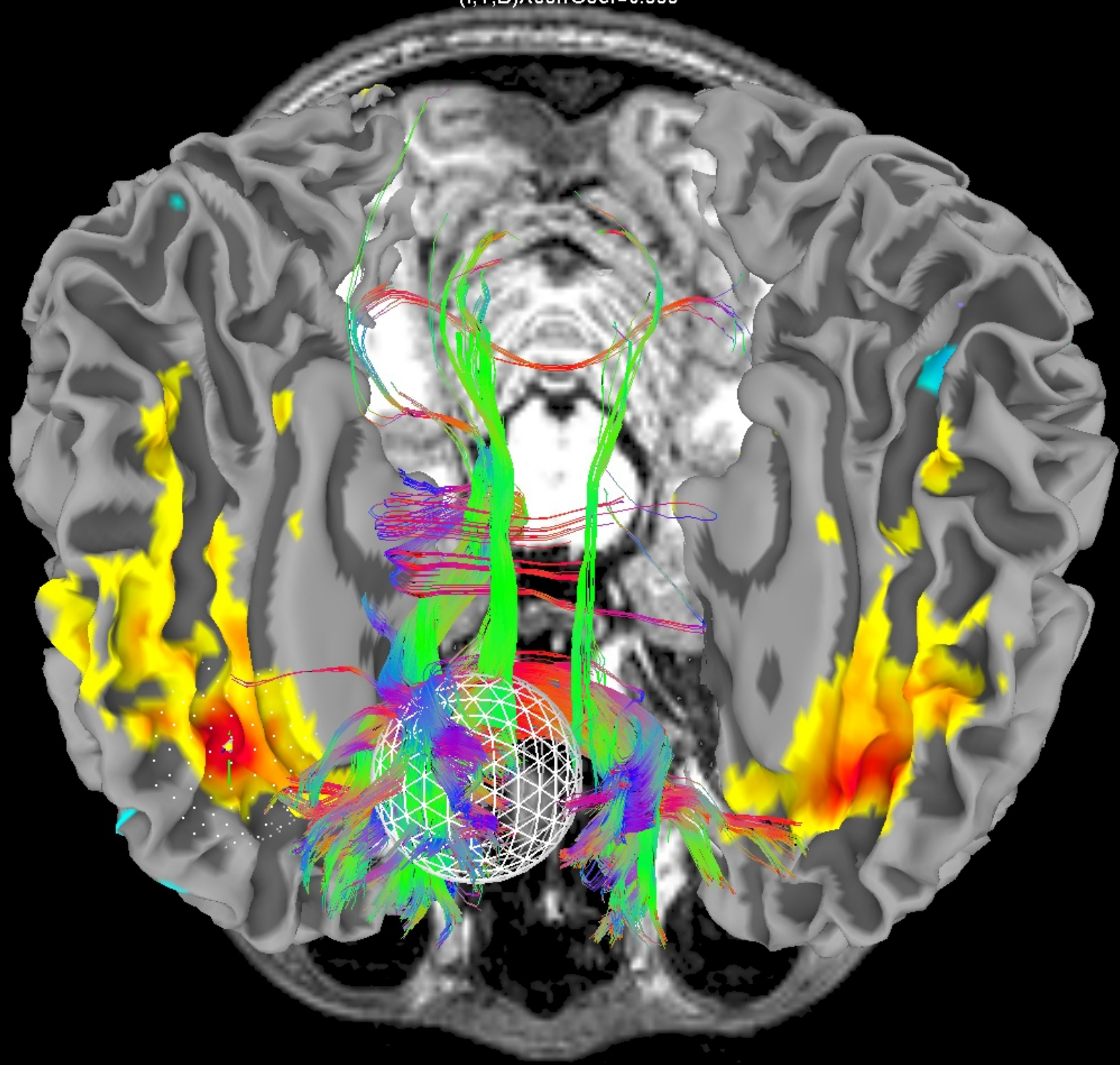
wm_rh G and S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.679



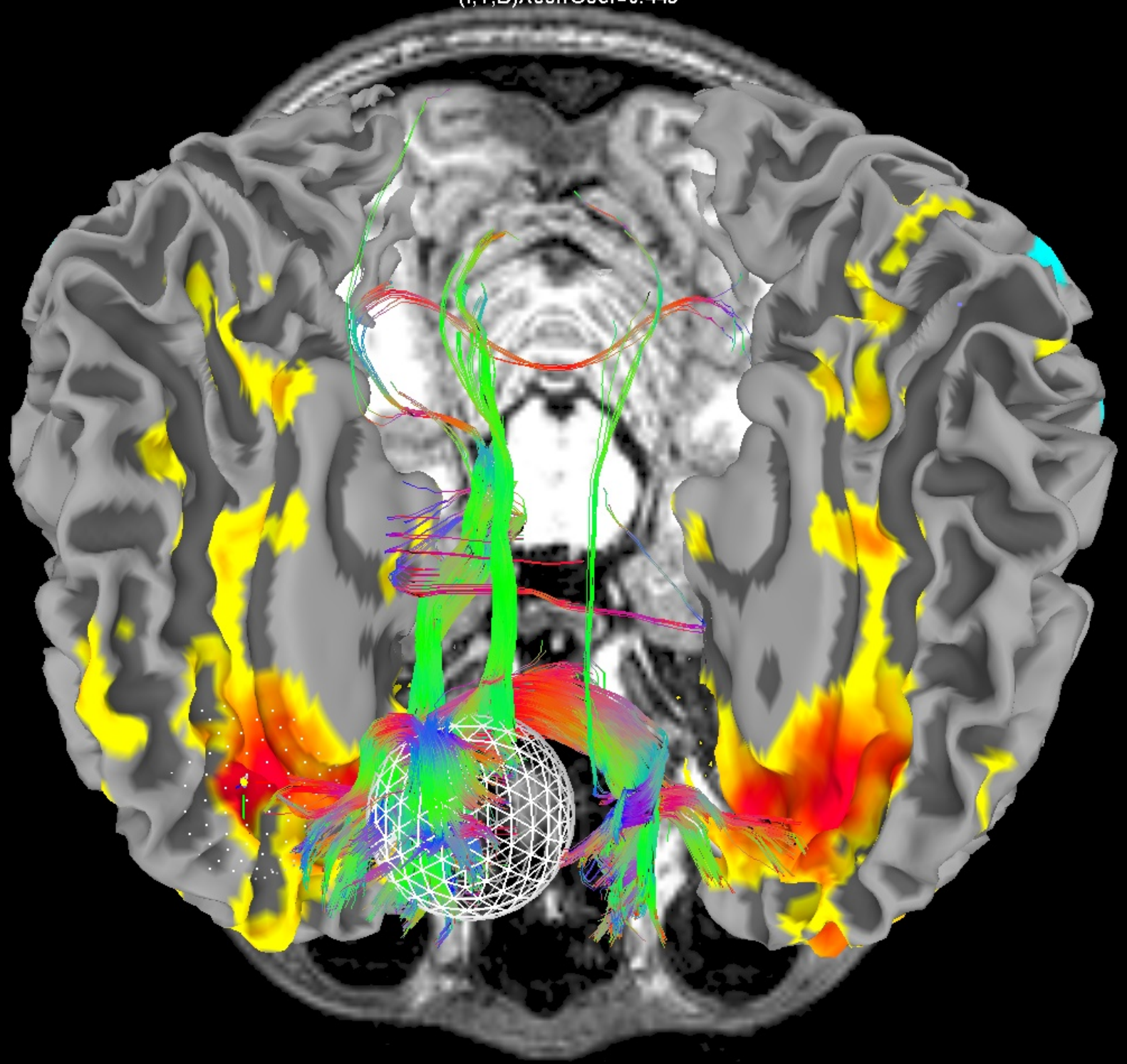
wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.578



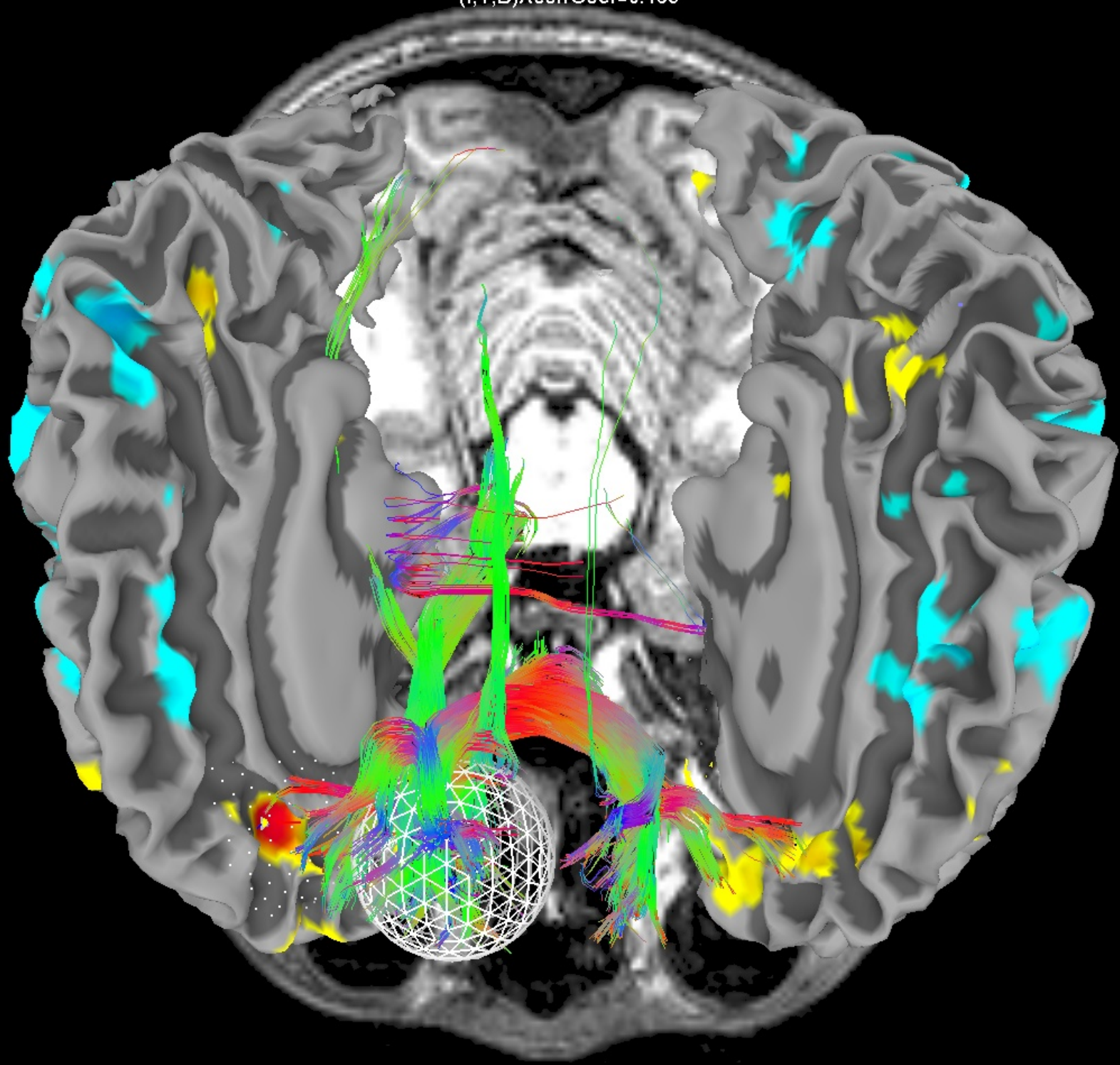
wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.999



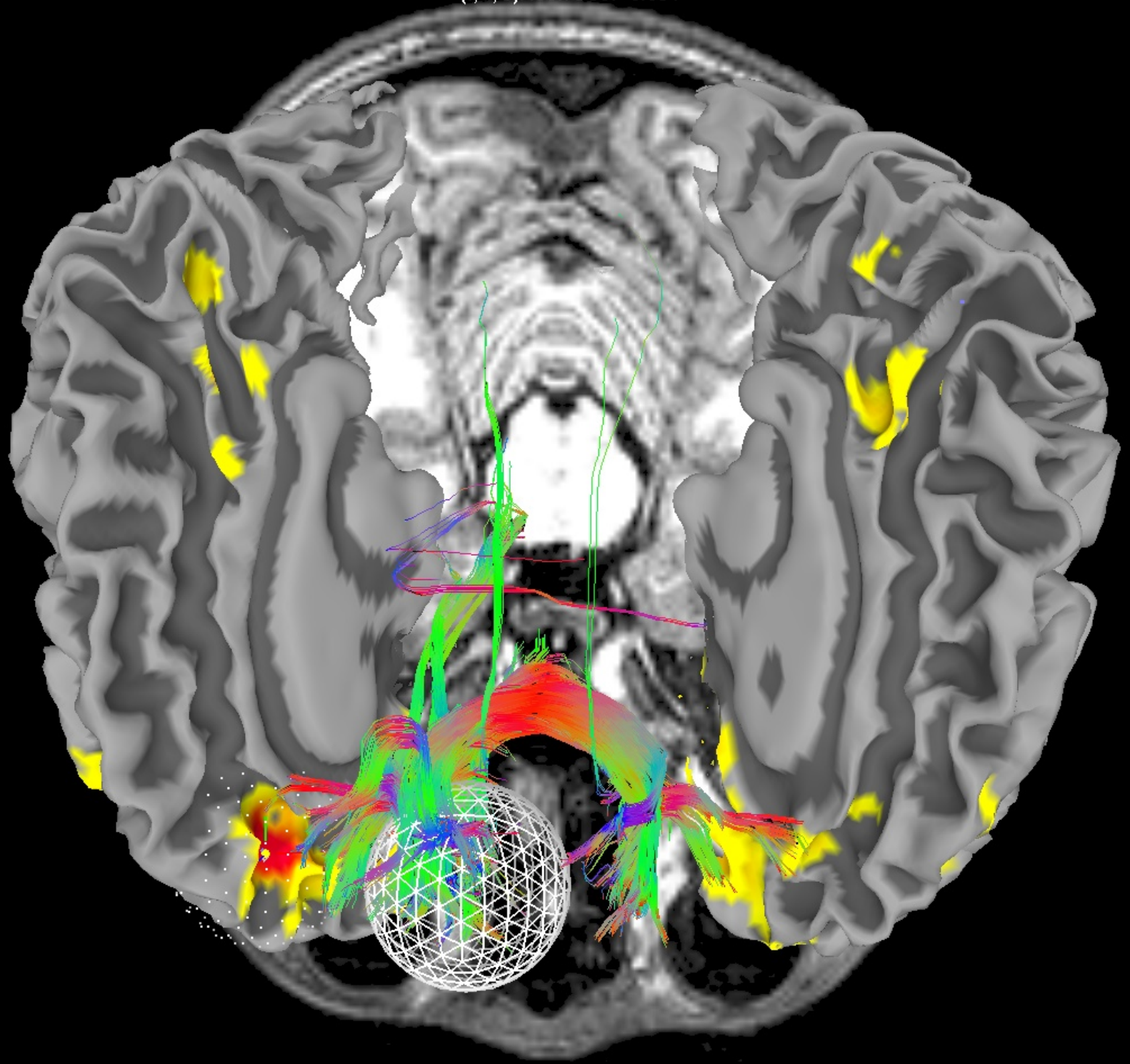
wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.445



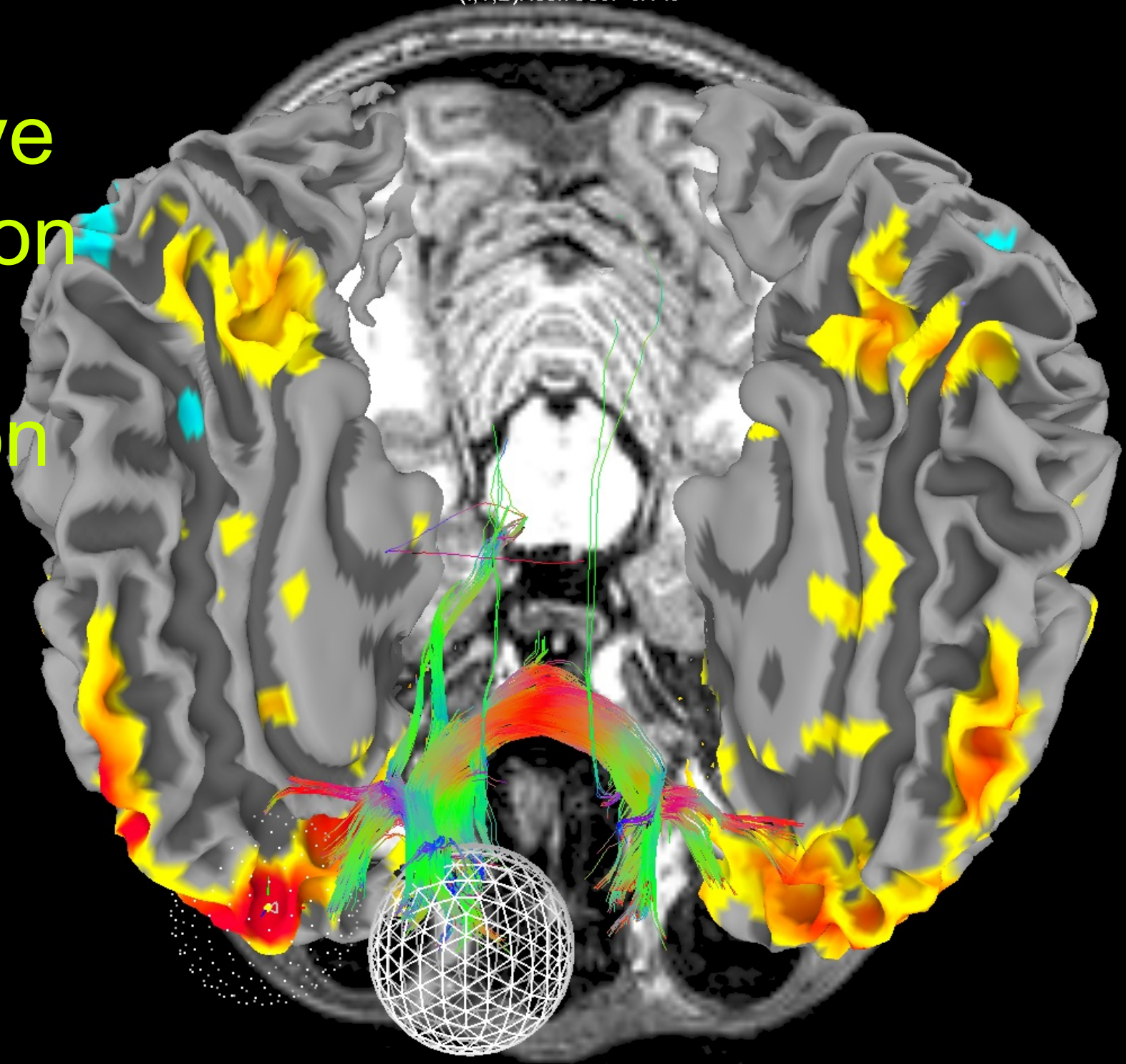
wm rh G and S cingul-Ant
(I,T,B)XcorrCoef=0.136



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

ROIs covering whole brain (here 71 FreeSurfer ROIs)

```
set outdir = CONNECTOMING
```

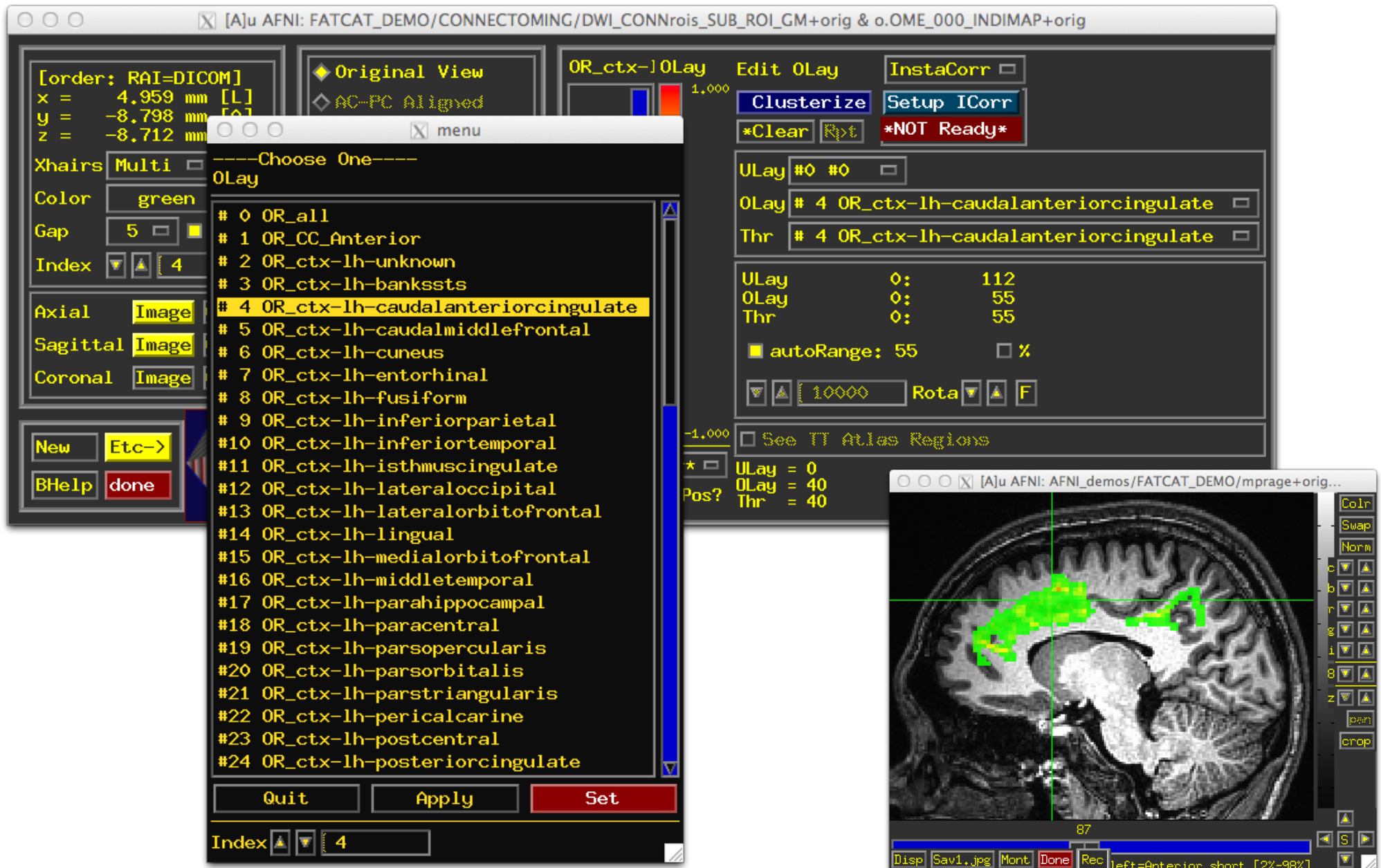
```
3dTrackID -mode DET \  
-netrois ${outdir}/DWI_CONNrois_SUB_ROI_GMI+orig \  
-logic AND \  
-dti_in ${FATPATH}/DTI/DT \  
-prefix ${outdir}/o.OME8 \  
-dump_rois AFNI
```

New utilization of ROI labels in naming:

e.g.: NET_000_ROI_ctx-rh-rostralmiddlefrontal_ctx-rh-rostralmiddlefrontal+orig

For mask of white matter connecting ctx-rh-rostralmiddlefrontal with ctx-rh-rostralmiddlefrontal

Subbricks are labeled with ROI names



afni mprage+orig. CONNECTOMING/o.OME8*HEAD

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 multi-colored, fibrous structure. The title bar reads "[A] SUMA:xx: ANY:". The menu bar includes "File View Tools". The status bar shows "ctx-rh-postcentral<->ctx-rh-precentral Pnt 0, tract 3338, bnd 608".

Overlaid on the right is the "Coloring Controls" panel. It features a text field for "Lbl" containing "o.OME8_000_BUN". Below this are several control elements: "Dim" with up/down arrows and a value of "1.0"; "Ord" with up/down arrows and a value of "1"; "Opa" with up/down arrows and a value of "1.0"; "Ln" with a dropdown menu set to "SLD"; "Masks" and "Ign" buttons; and "Gry" with up/down arrows and a value of "20". A "Switch Dset" button is located at the bottom of the panel.

Below the "Coloring Controls" panel is a "Switch Colori..." dialog box. It contains a list of ROI names: "fg:o.OME8_000_LOC", "fg:o.OME8_000_MID", and "fg:o.OME8_000_BUN". The "fg:o.OME8_000_BUN" entry is highlighted.

Red arrows indicate the flow of information: one arrow points from the "Coloring Controls" panel to the "Switch Colori..." dialog box, and another arrow points from the dialog box to the main brain tract visualization.

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

tcsh Do_12_RUNrsfc_netw_corr.tcsh

correlation matrix of ROI avg. time series

3dNetCorr

-inset REST_in_DWI.nii.gz

-in_rois ROI_ICMAP_GM+orig

-fish_z

-prefix FMRI/REST_corr_rz

-overwrite

-echo_edu

\
\
\
\
\

Output in FMRI/:

REST_corr_rz_000.netcc ← *Corr. matrix of network 0 ROIs*

REST_corr_rz_001.netcc ← *Corr. matrix of network 1 ROIs*

tcsch Do_13_RUNrsfc_RSFCfilt_param.tcsch

filtering and calculating some RSFC components

```
3dRSFC \
-nodetrend \
-prefix FMRI/REST_filt \
0.01 0.1 \
REST_proc_unfilt.nii.gz \
-overwrite
```

tcsh Do_14_RUNrsfc_ReHo_param.tcsh

```
# Case C-- NB: a map of `case A' values is also  
# calculated by default.  
# The ROI network values are output in *.vals and *.chi  
# text files, one network per line (in order of  
# subbrick).
```

```
3dReHo \  
-inset REST_in_DWI.nii.gz \  
-mask mask_DWI+orig \  
-in_rois ROI_ICMAP_GM+orig \  
-prefix FMRI/REST_in_DWI_REHO_ROI \  
-overwrite
```

tcsch @Install_FATMVM_DEMO

Group level inference on connectivity matrices

Example set for taking a group's connectivity output from 3dTrackID (*.grid files), combining it in a simply-formatted table with subject information from a CSV file (e.g., dumped from a spreadsheet), and building a script to run 3dMVM for statistical modeling.

Chen, G., et al. Neuroimage 2014

Taylor, P.A., et al. HBM 2014 (in press)