Hands On the FATCAT

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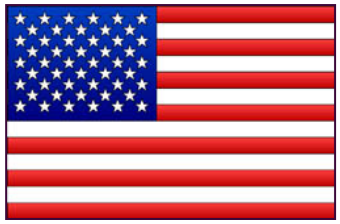

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@Install_FATCAT_DEMO

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

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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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Page 1 of 466 **Pages:** 1 2 3 4 5

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

Help on Message Board & Email

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>

tcsh Do_01_RUNdti_convert_grads.tcsh

Convert gradient vectors, or b matrices for 3dDWItoDT 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.tcsh for other variants, this time to satisfy DTI_Studio (Yeh et al. 2010)

tcsh Do_02_RUNdti_DW_to_DTI.tcsh

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

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tcsh Do_02_RUNdti_DW_to_DTI.tcsh

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

tcsh Do_PostTORTOISE_2014.tcsh

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
```

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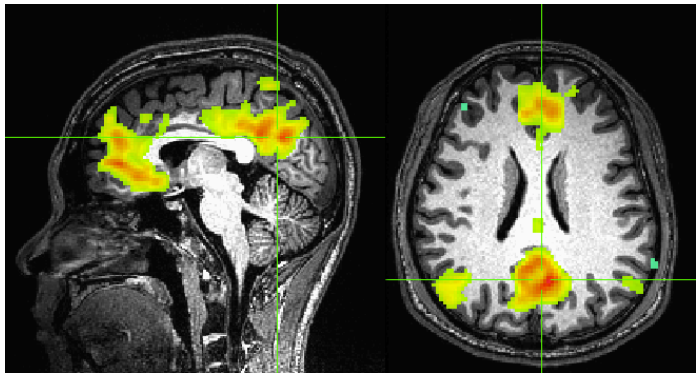
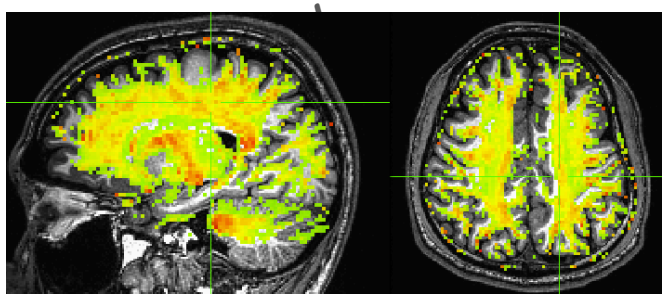
tcsh Do_03_RUNdti_make_network_ROIs.tcsh

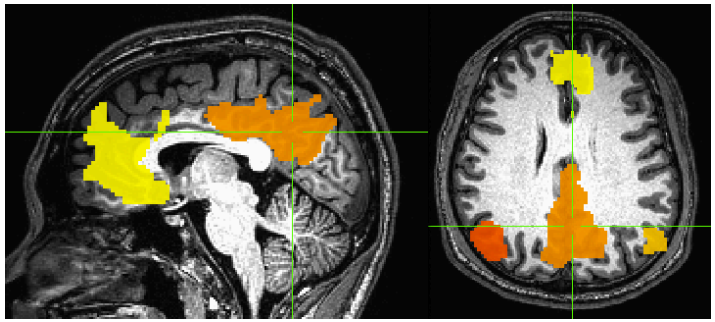
Create fattened gray matter ROIs to serve as tractography targets

```
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 ./:
```

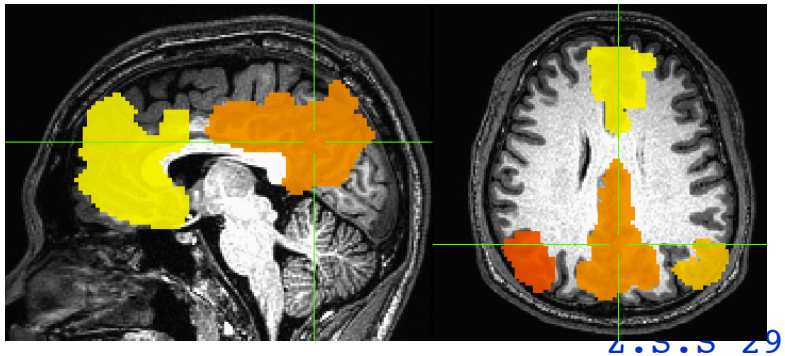




ROI_ICMAP_GM+orig.HEAD



ROI_ICMAP_GMI+orig.HEAD

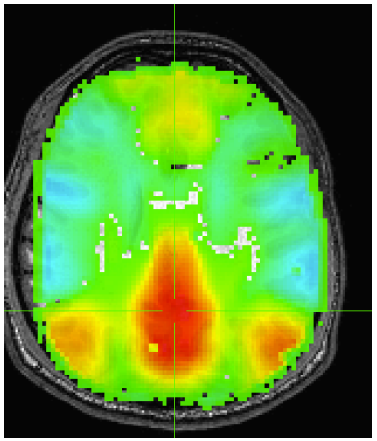


tcsh Do_04_RUNdti_match_network_ROIs.tcsh

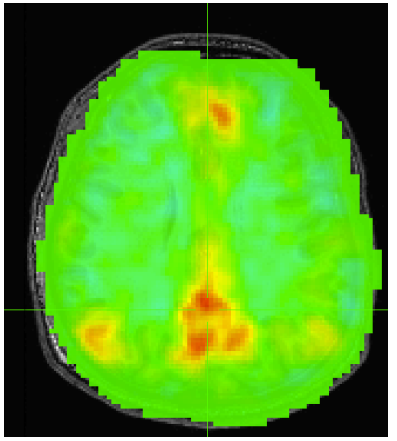
Identify networks by comparing spatial pattern to standard set (Optional)

```
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
```

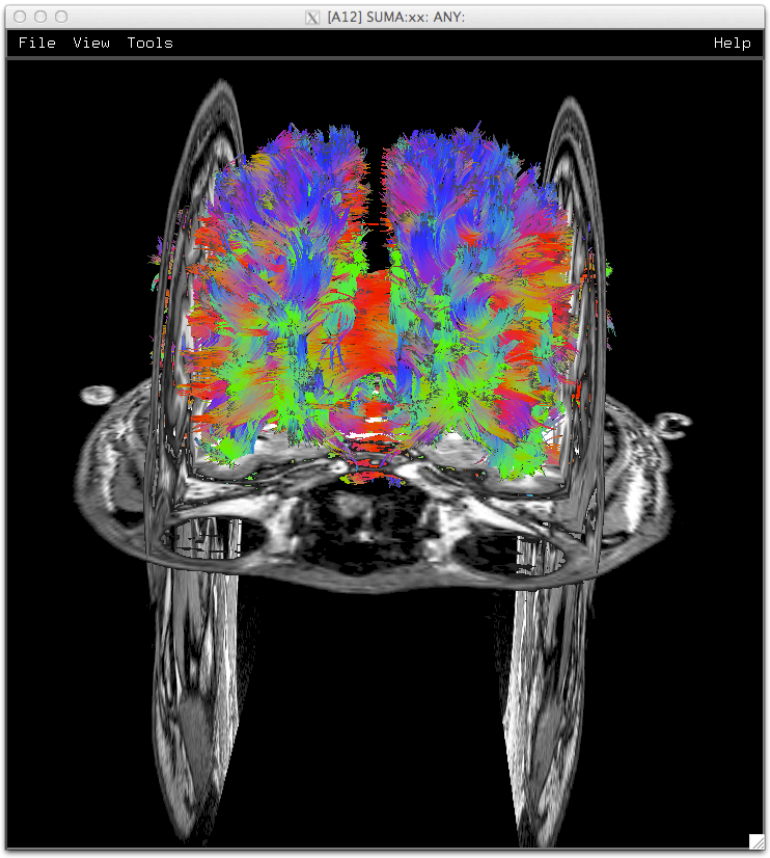
Output in DTI/:

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

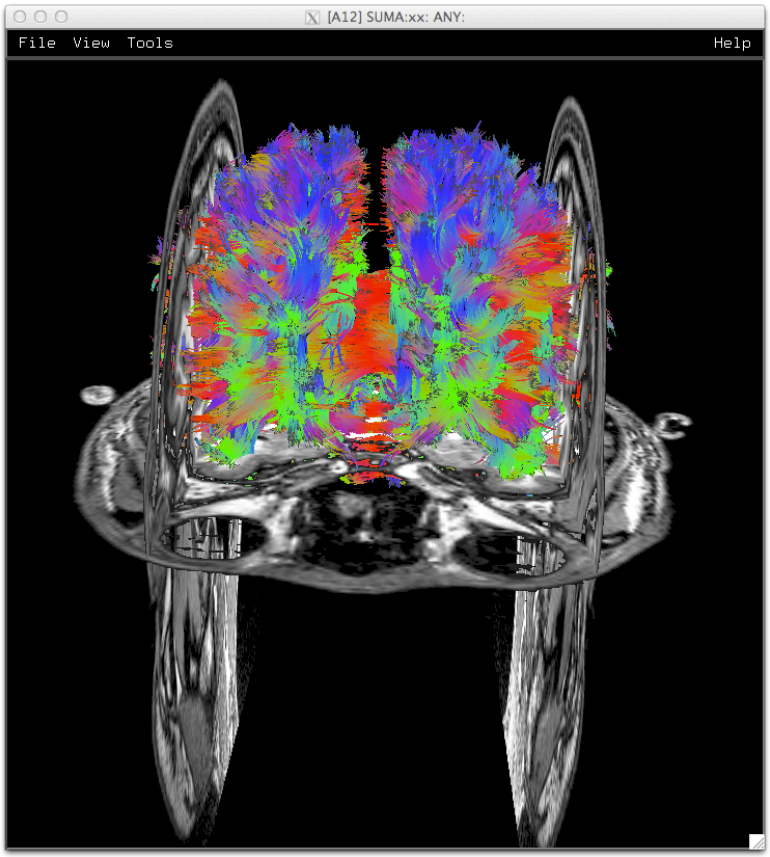
```
suma  -npb 12 -niml                \
      -vol mprage+orig.            \
      -tract DTI/o.WB_000.niml.tract &
```



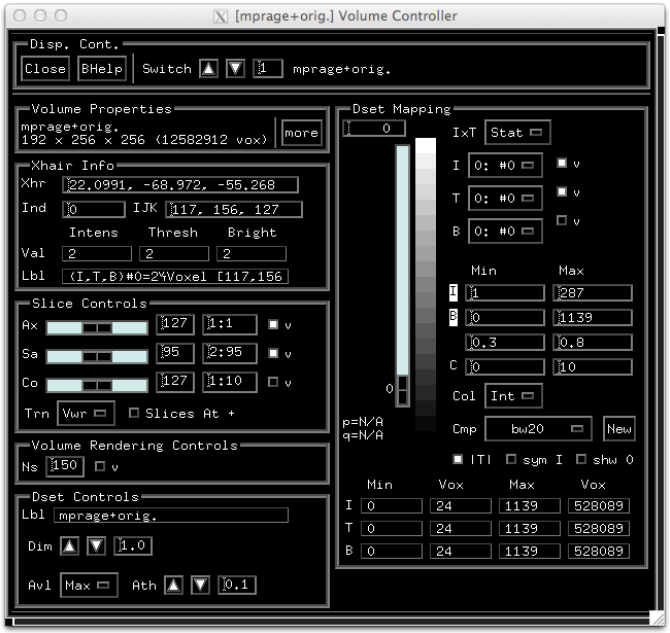
tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

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 volume
View→ Object Controller (ctrl+s)



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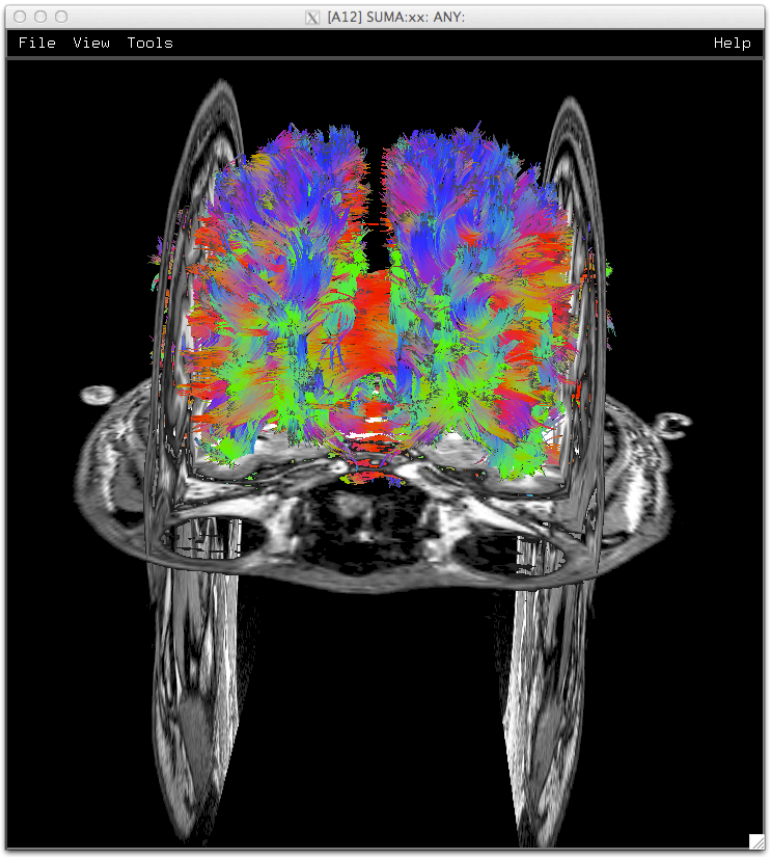
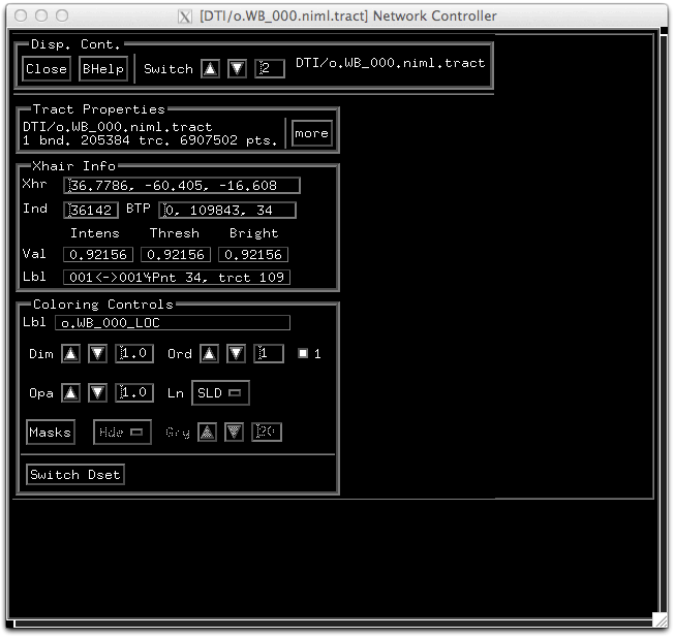
tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

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)



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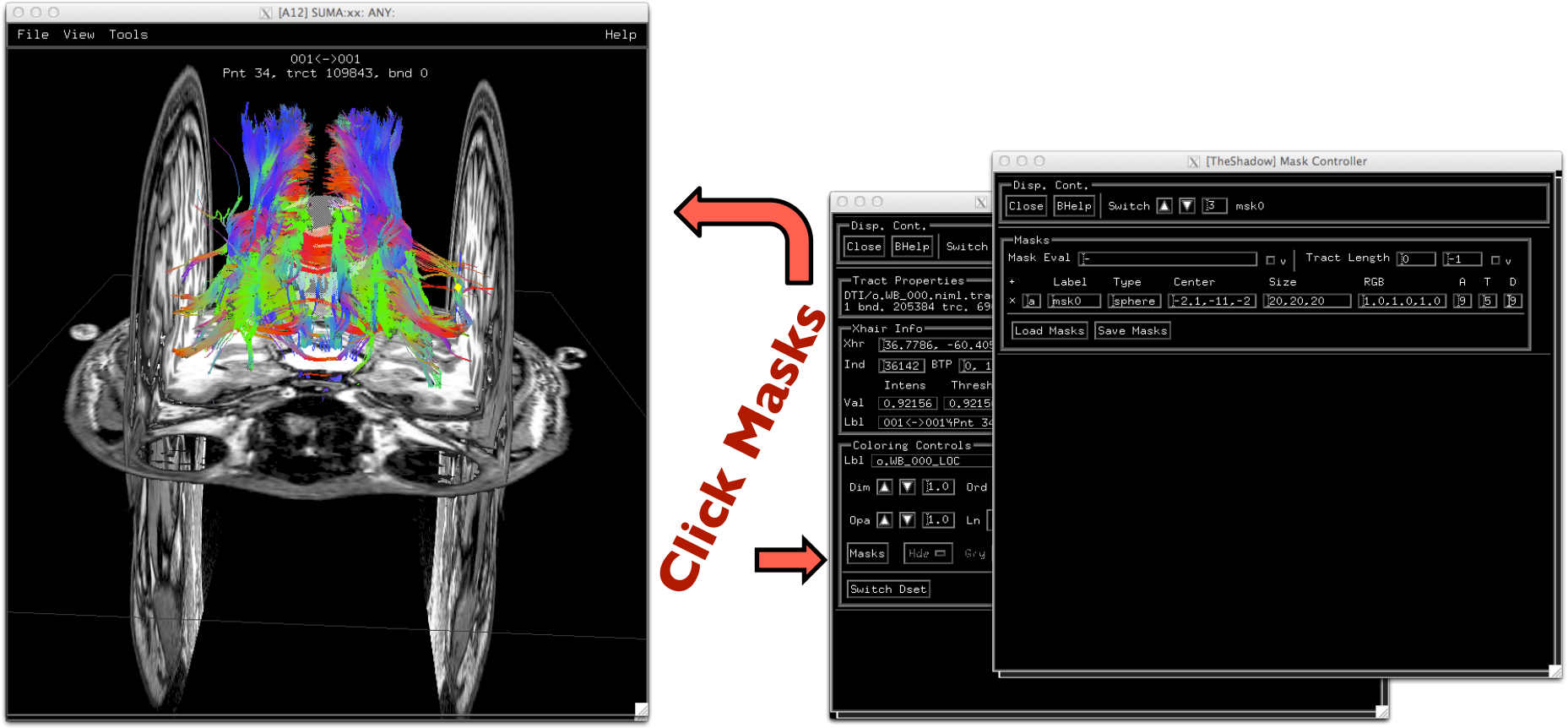
tcsh Do_06_VISdti_SUMA_visual_ex1.tcsh

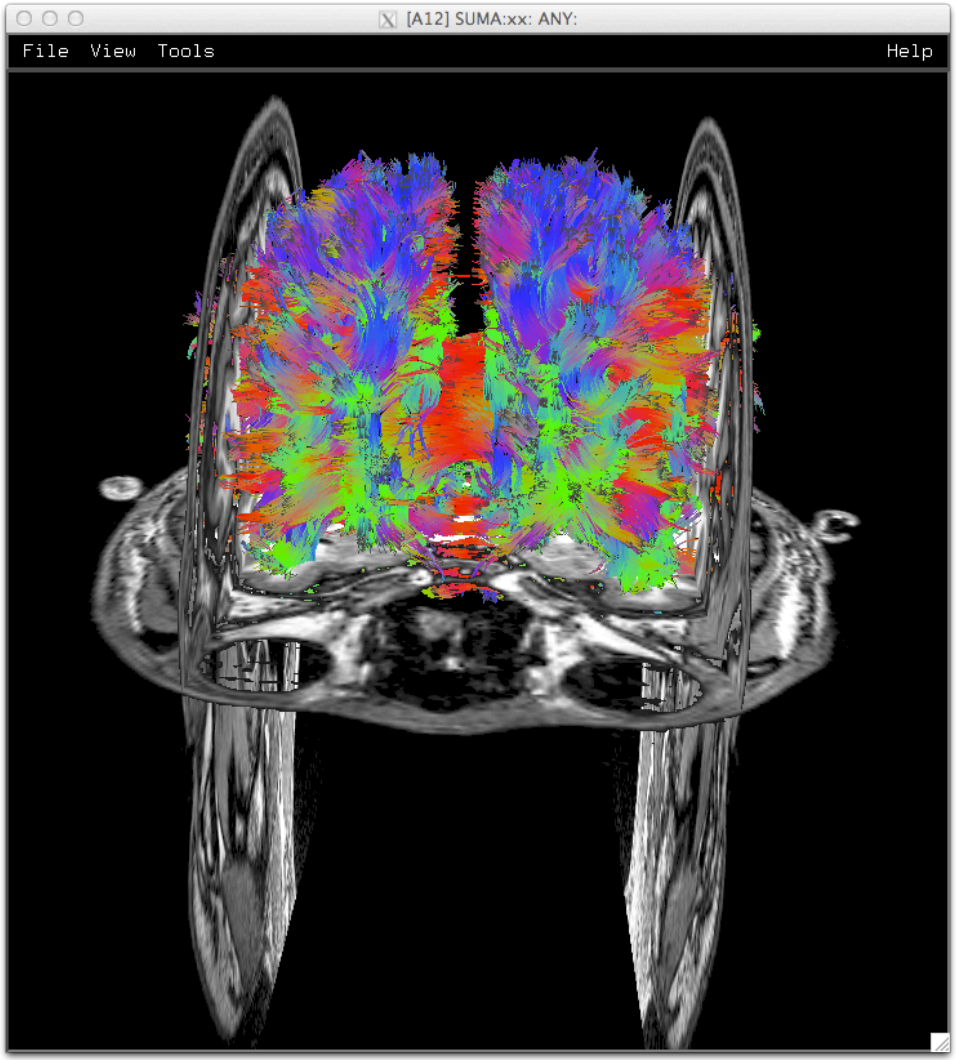
A. Visualize whole brain tracts, check for weirdness

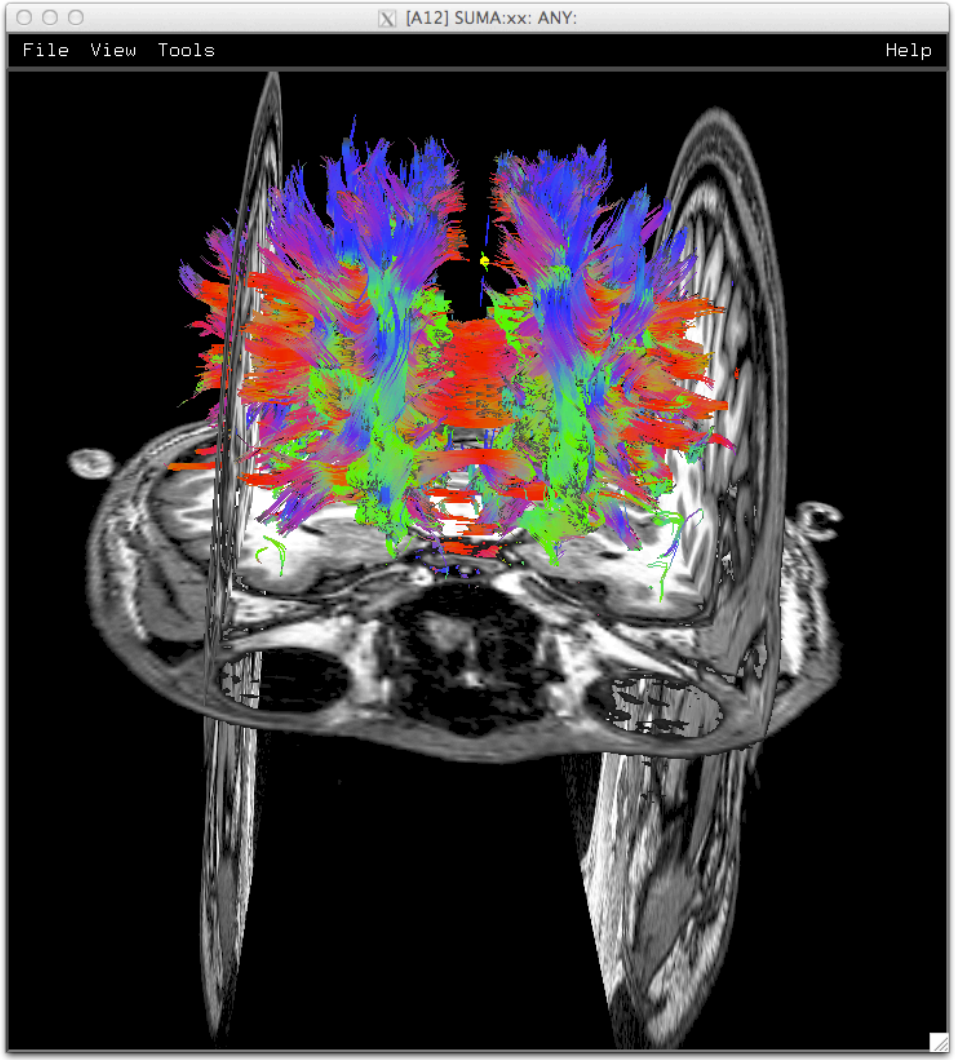
```
suma   -npb 12 -niml                \
       -vol mprage+orig.            \
       -tract DTI/o.WB_000.niml.tract &
```



Good vs. Bad Gradient Directions

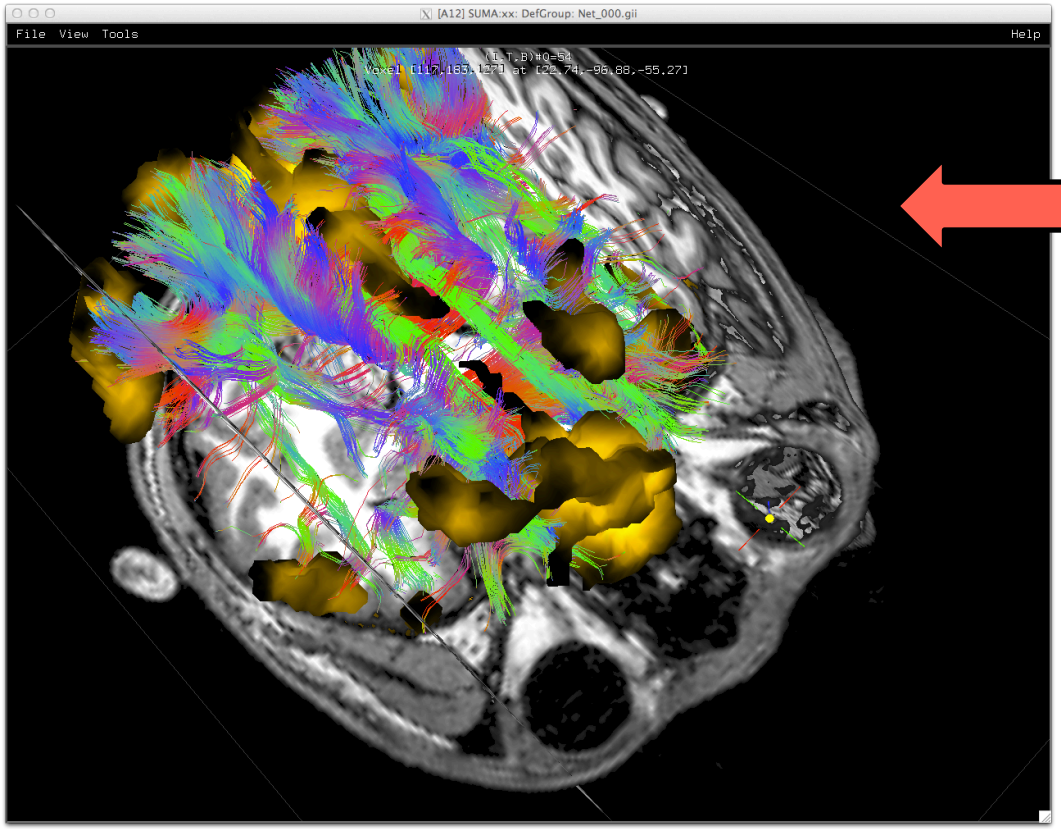
```
suma   -npb 12 -niml                \
       -vol mprage+orig.            \
       -tract DTI/o.WB.bad_000.niml.tract &
```

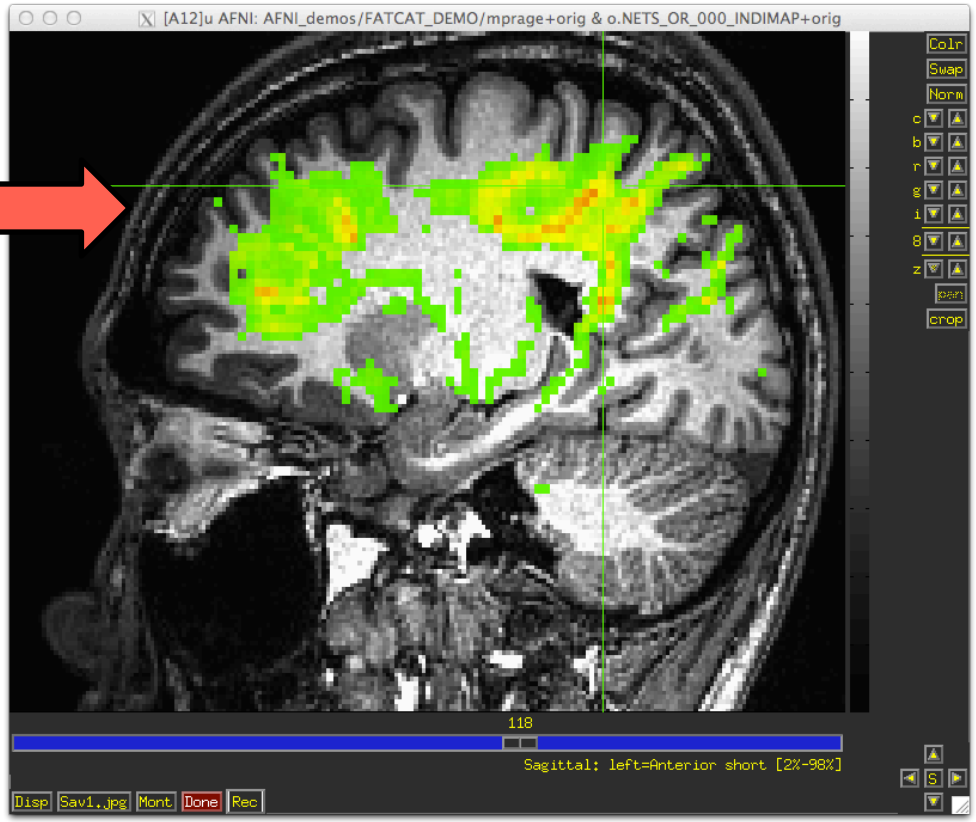




Second half of Do_06 demo

```
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 &
```





tcsh Do_05_RUNdti_DET_tracking.tcsh

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.

o.NETS_AND_002.grid ← WM stats per region pair

o.NETS_AND_002.niml.dset ← same, in fancy format

o.NETS_AND_002.niml.tract ← Tracts between pairs ONLY

o.NETS_AND_002.trk ← same, trackvis format

o.NETS_AND_002_INDIMAP+orig.HEAD ← #of tracts per ROI

o.NETS_AND_002_PAIRMAP+orig.HEAD ← Masks of voxels between pairs

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

tcsh Do_10_RUNdti_fullprob_track.tcsh

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                  \
    -algopt 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
```

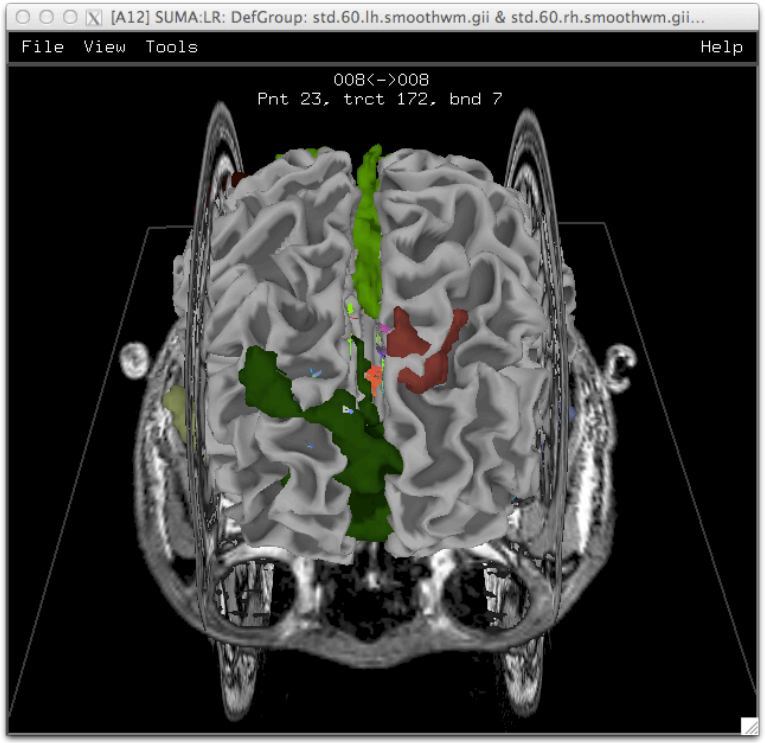
9 perturbations and whole brain tractography only

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 &
```

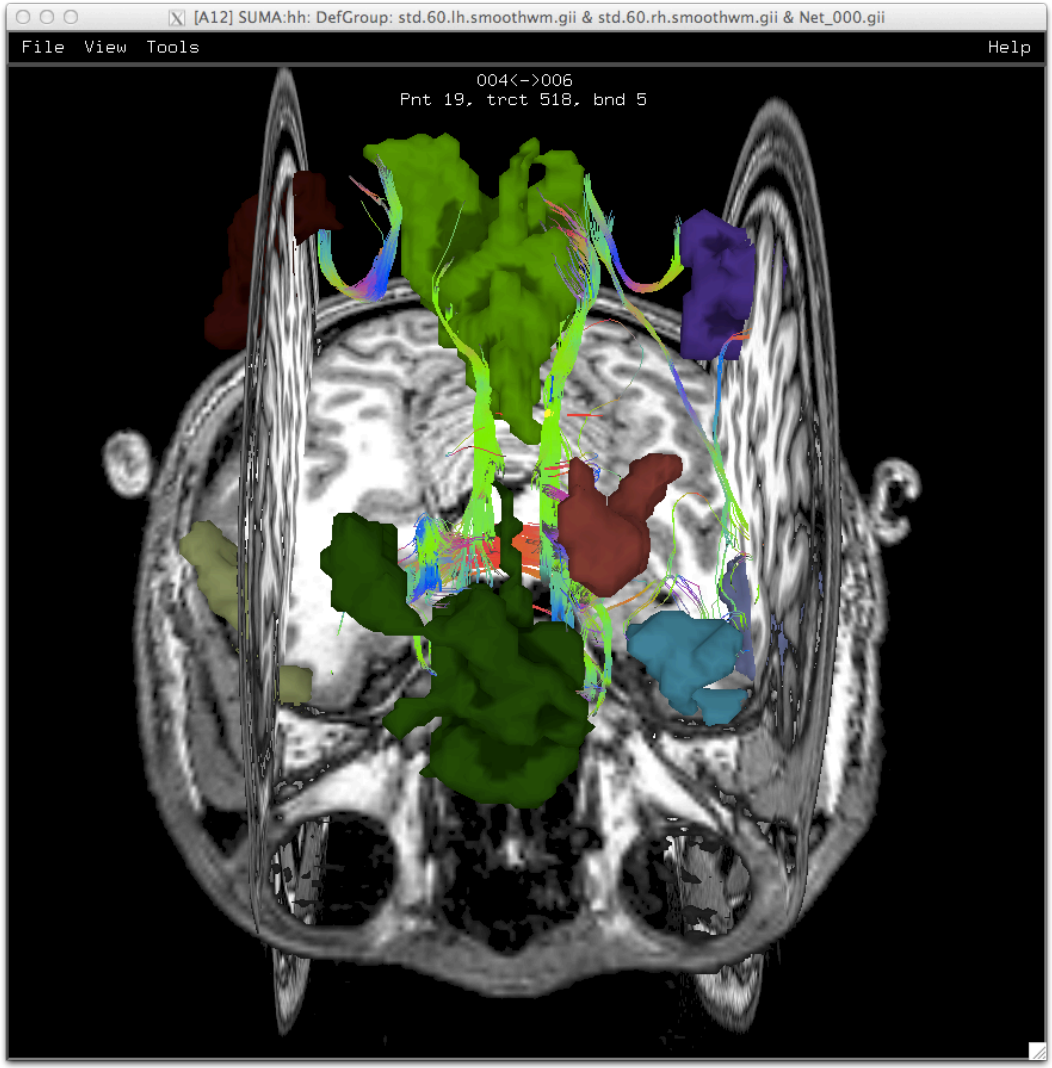


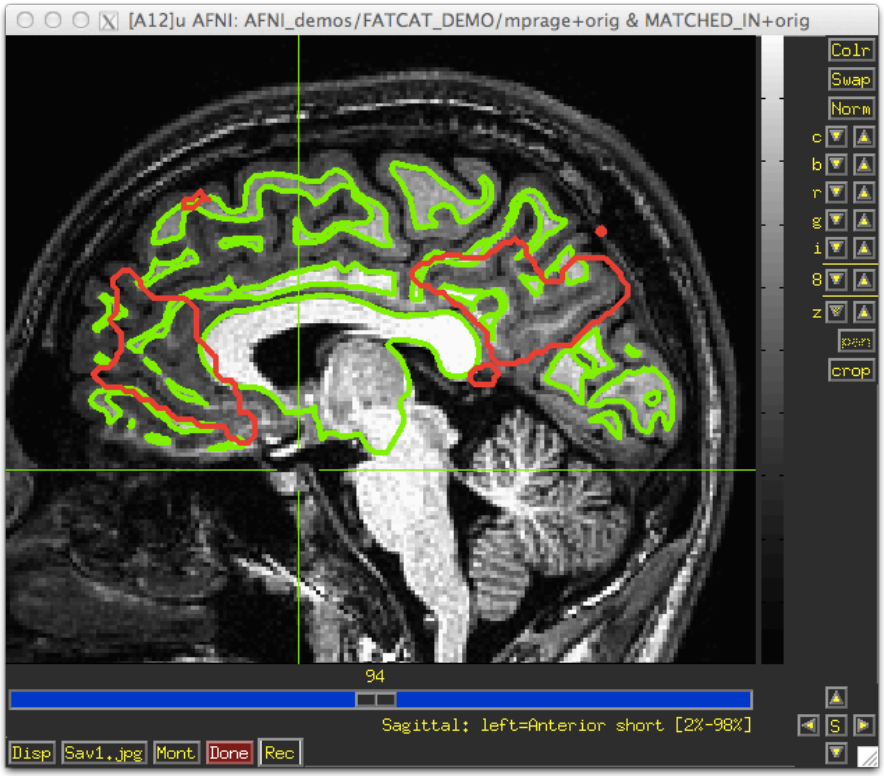
View → Object Controller
Hide surfaces '[' ']'
Select (right-click) objects

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





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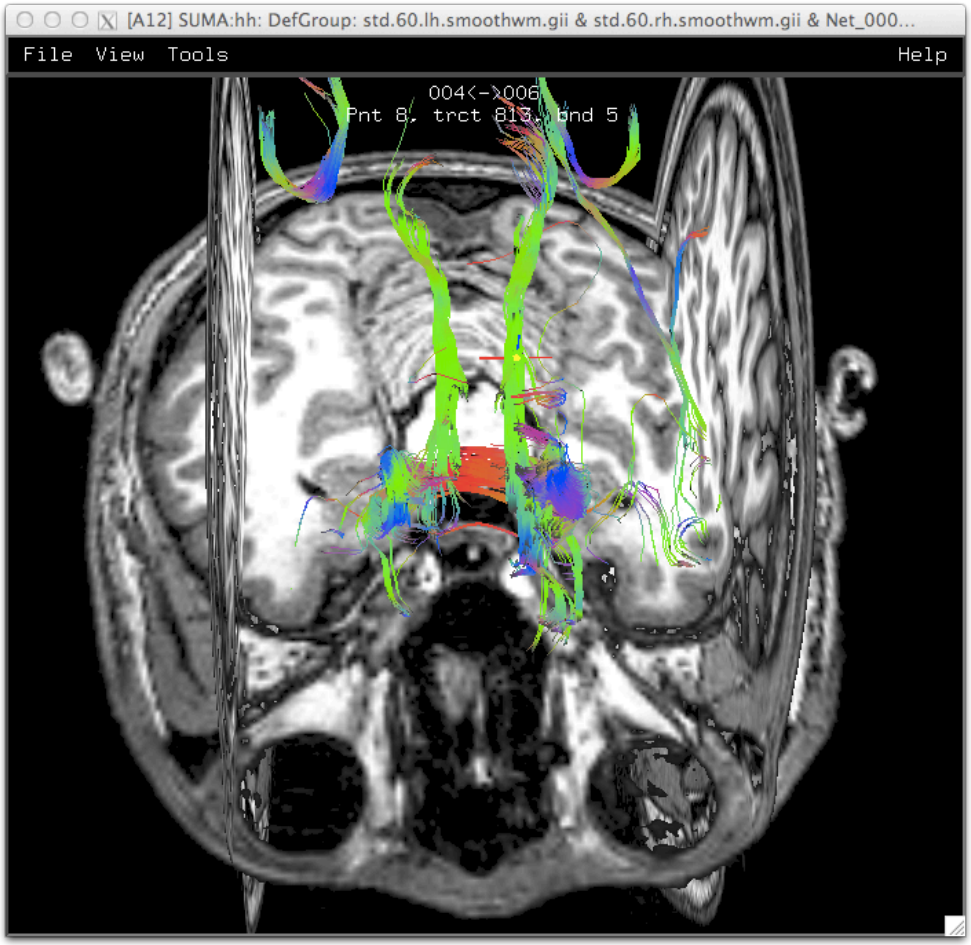
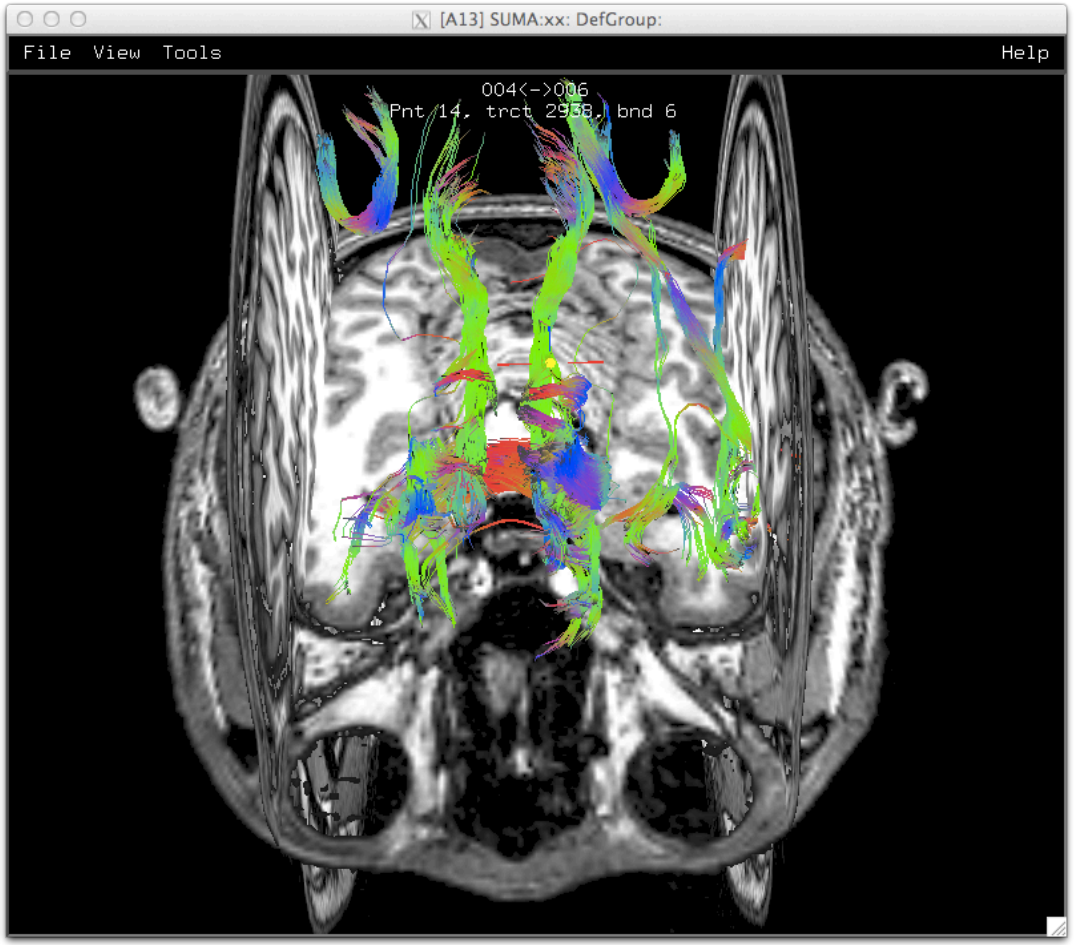
tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Example 2: Det. Tracts vs. Mini Prob.

Det. Tracts



Mini (9) Prob. Tracts

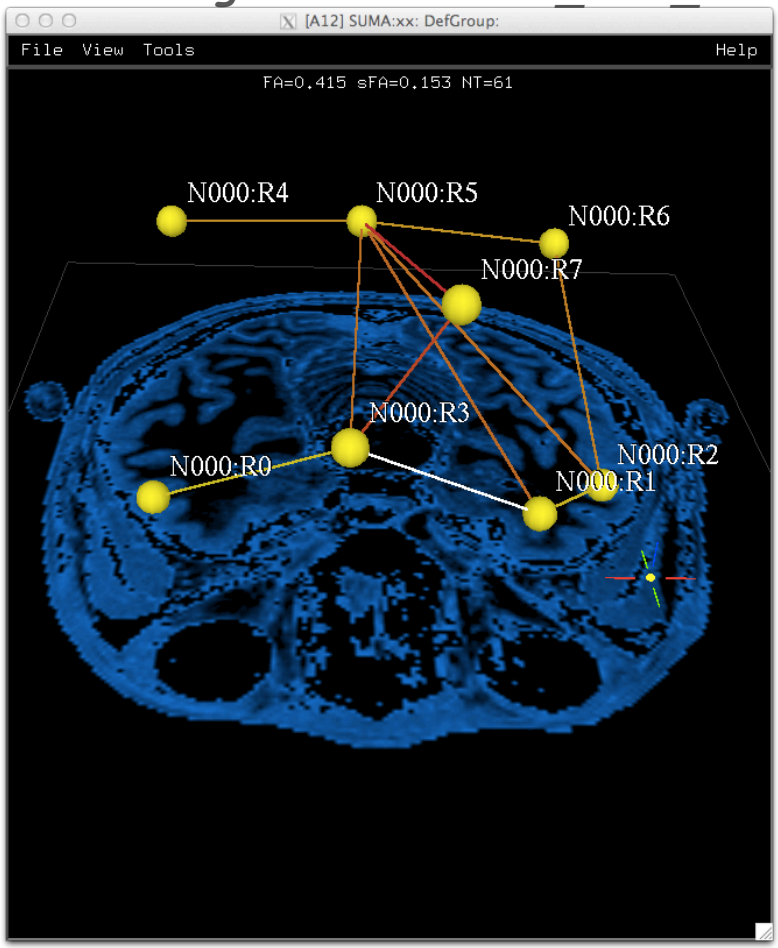


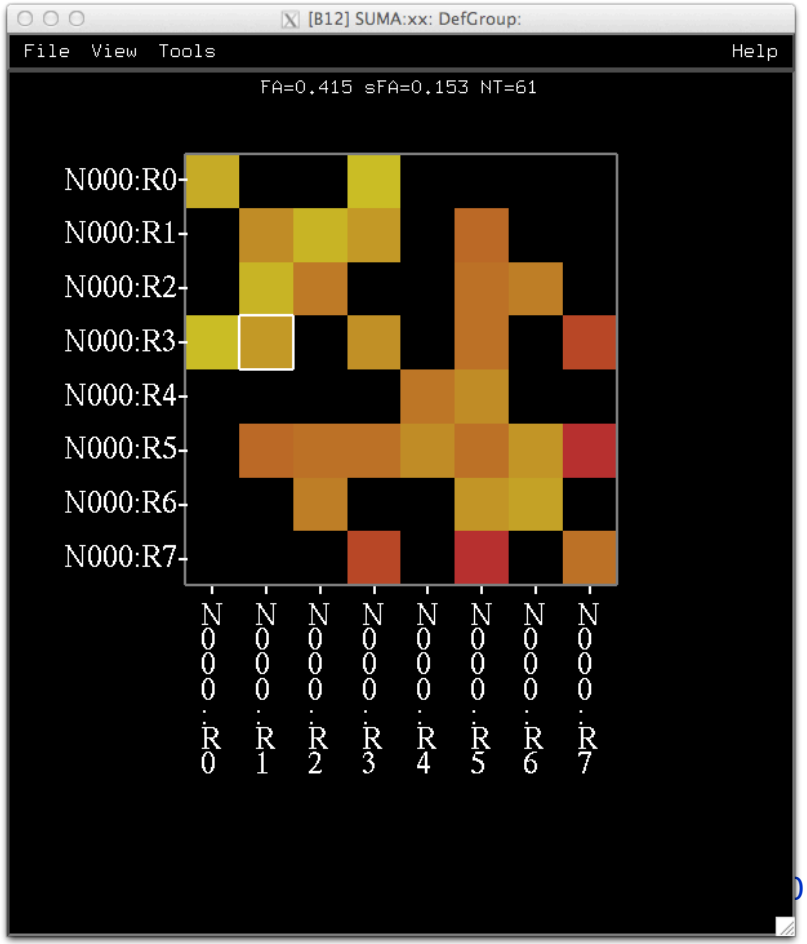
Z.S.S 29/09/14

tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Example 3: The connectivity matrices

```
cd DTI/
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 &
```





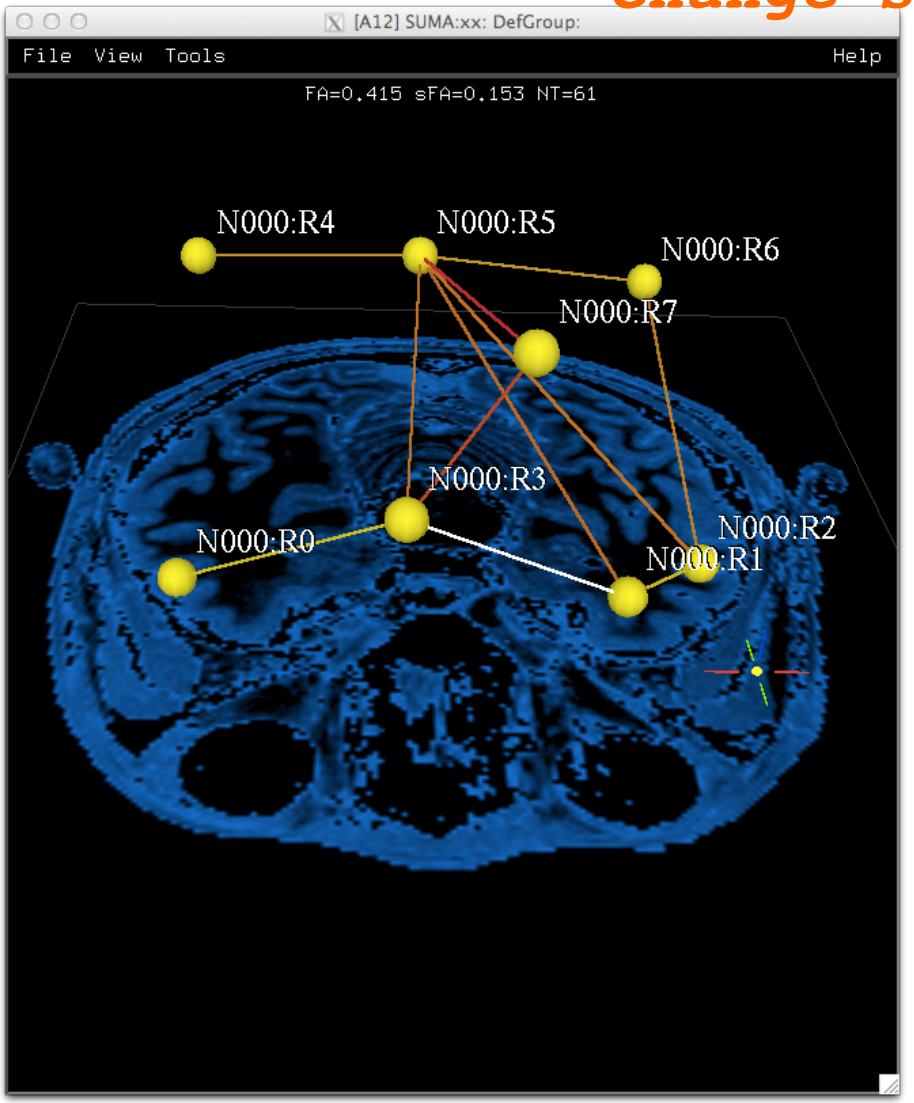
tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

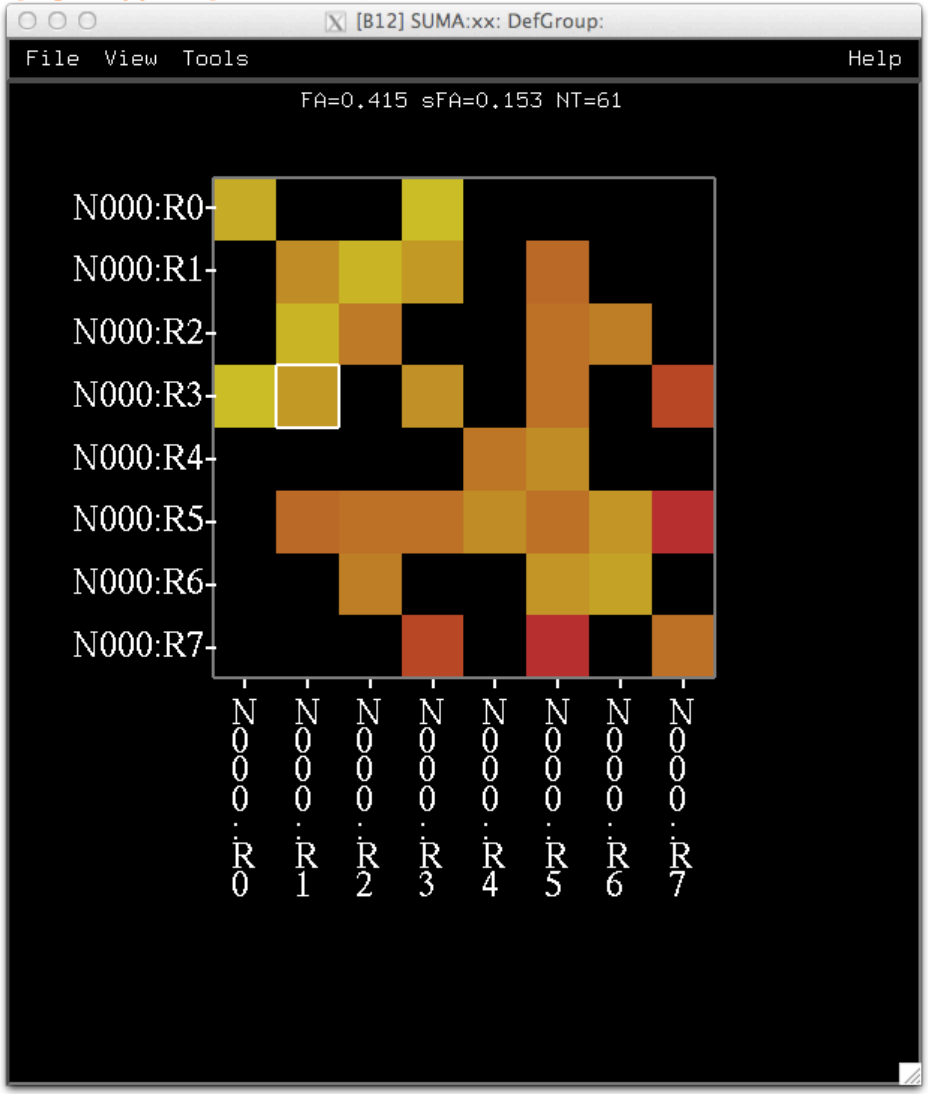
Example 3: Matrices in dual form

View → Object Controller

Open new window (ctrl+n)

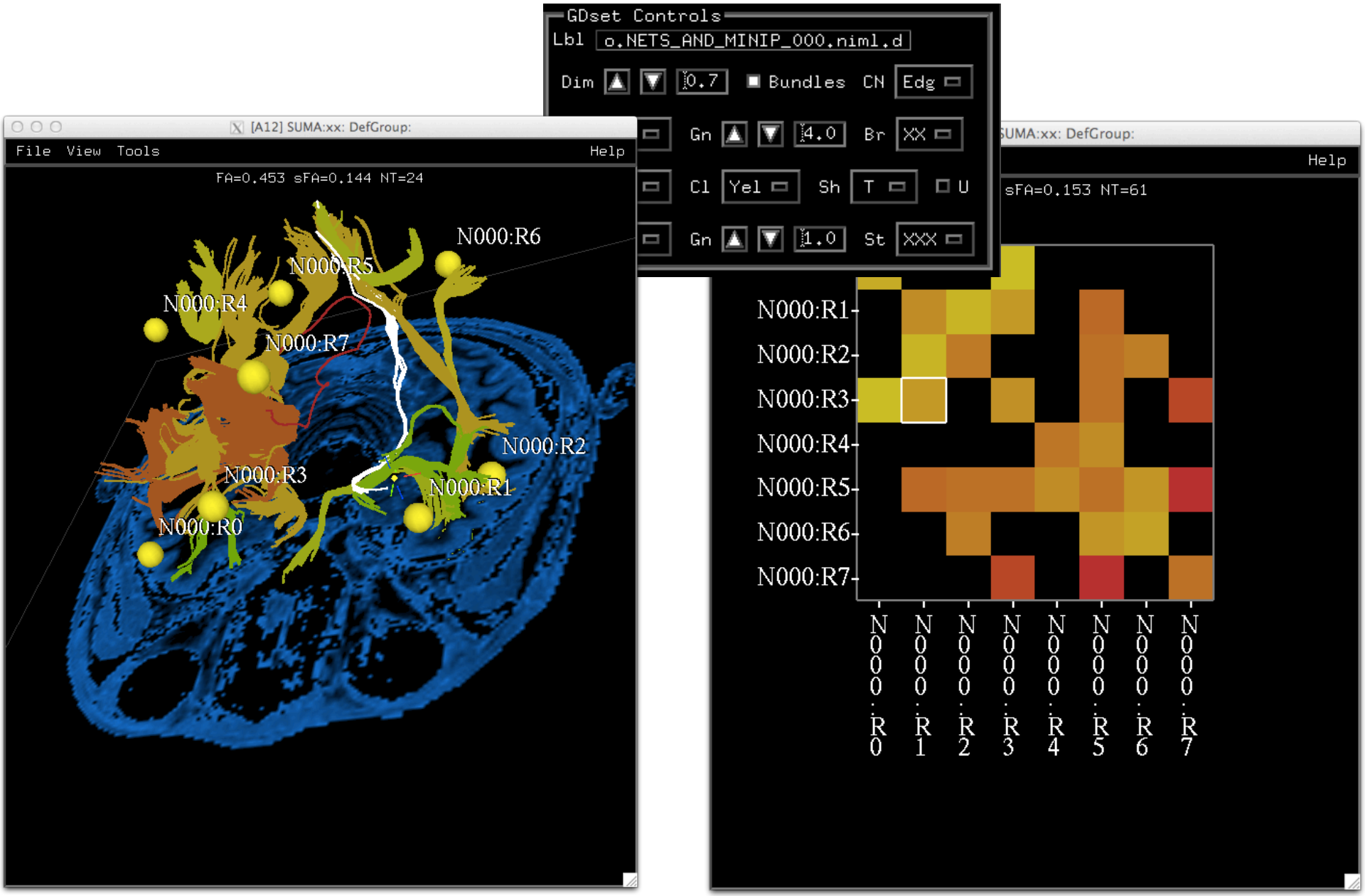
Change state with '.'





tcsh Do_09_VISdti_SUMA_visual_ex2.tcsh

Example 3: Graph edges rendered by bundles



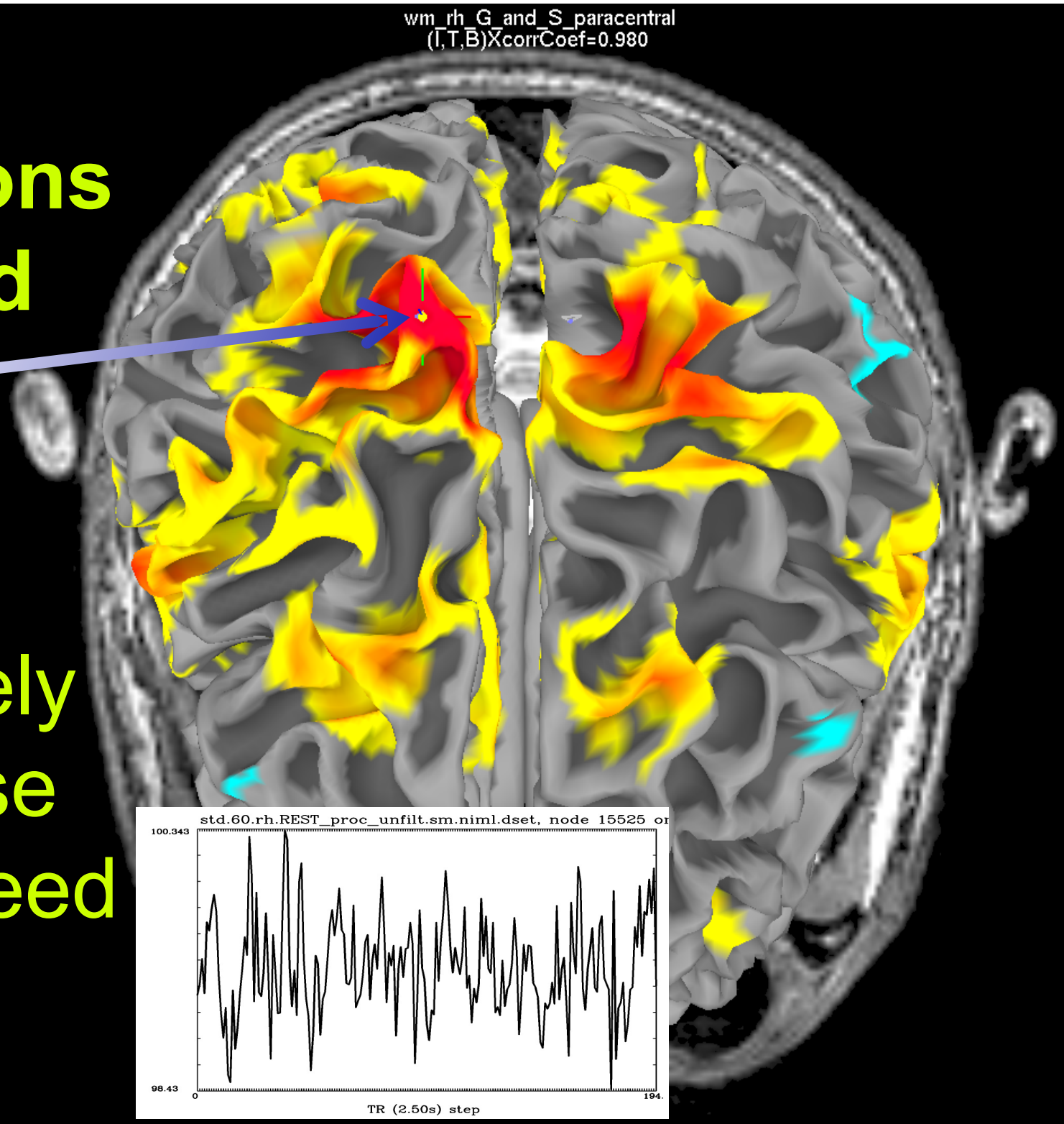
tcsh Do_09_VISdti_SUMA_visual_ex3.tcsh

Simultaneous InstaCorr & InstaTract

Naked brain surface

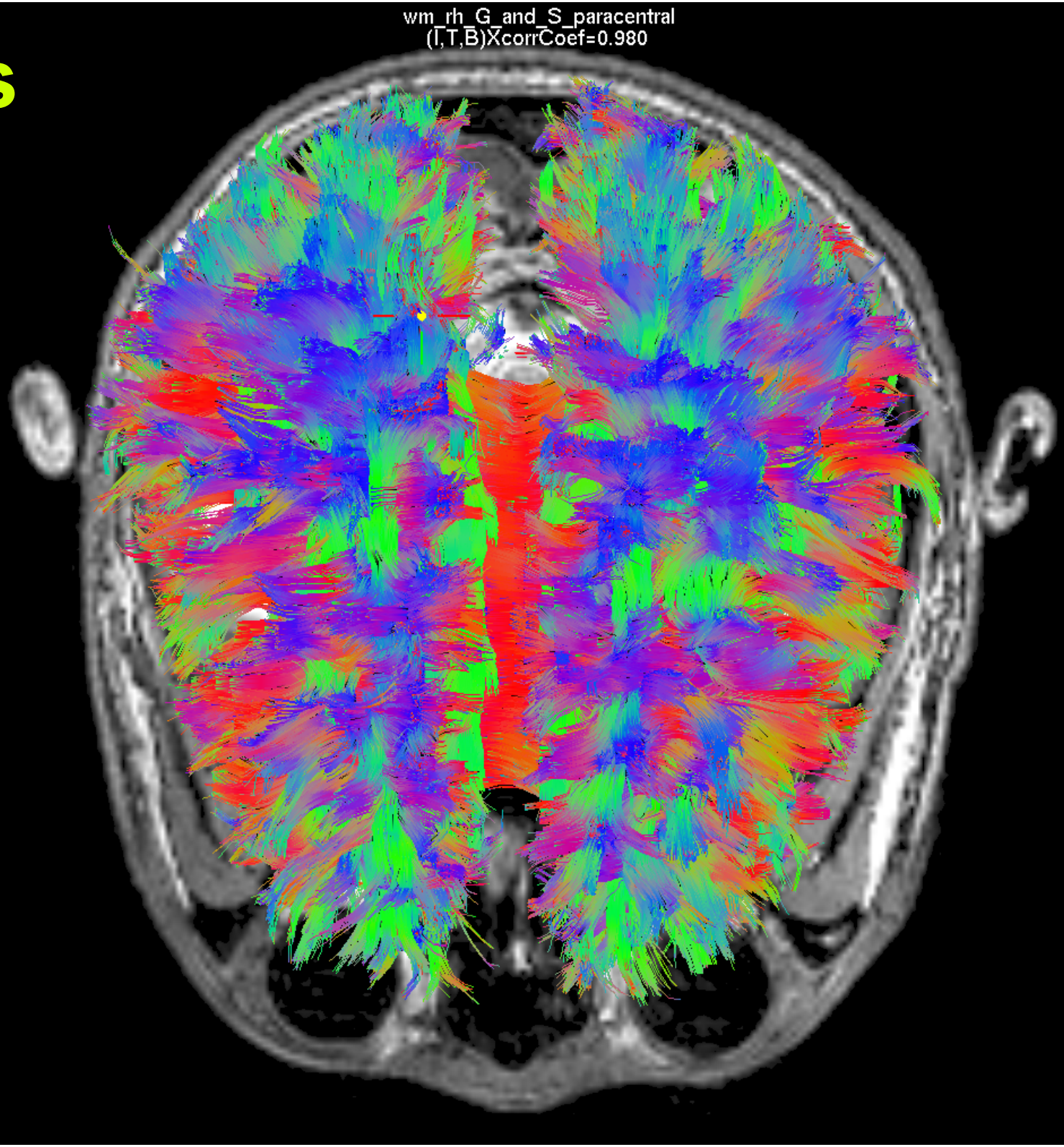
RS-FMRI correlations from seed voxel

computed interactively with mouse click on seed



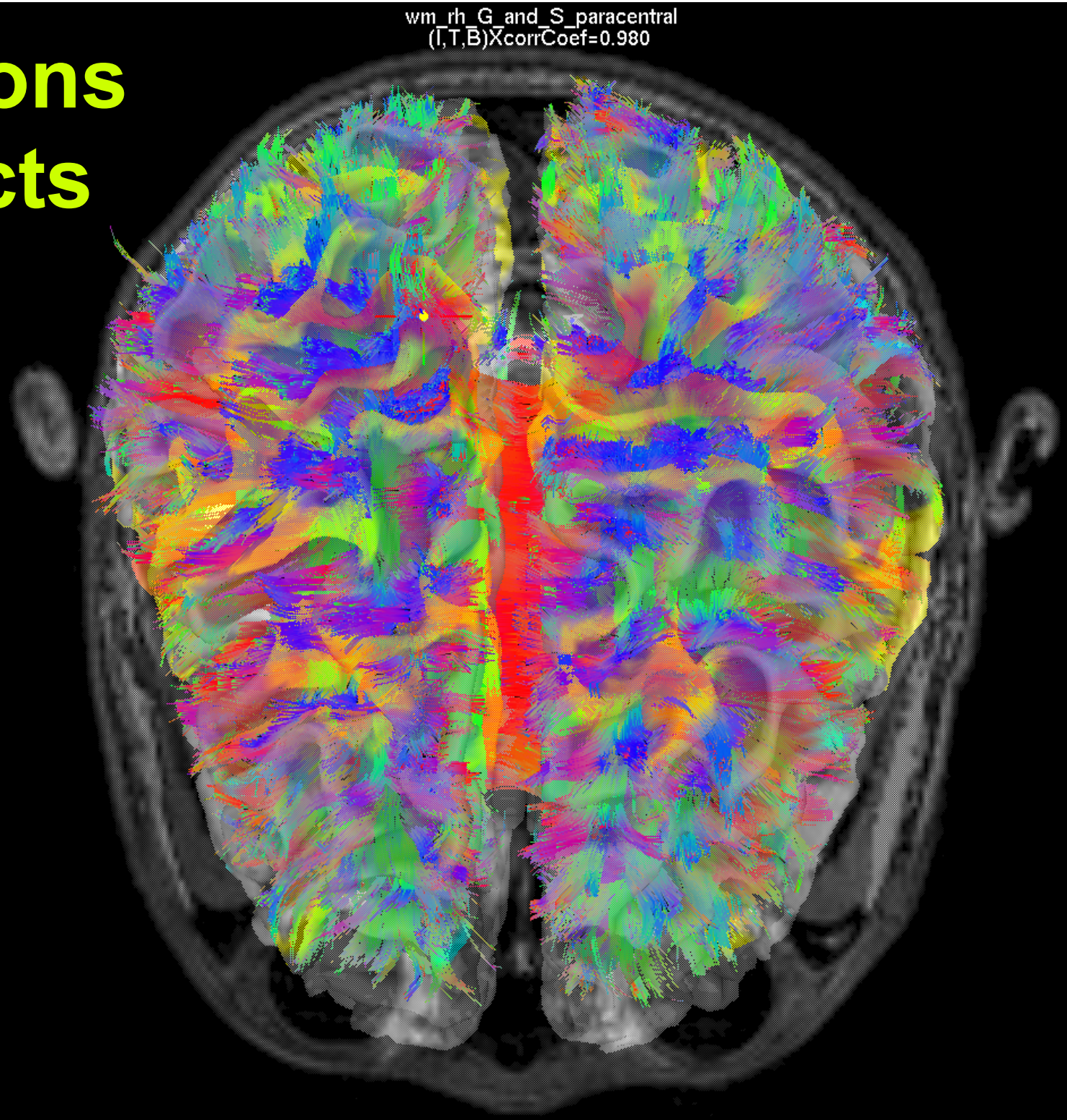
DTI tracts [brain is hidden]

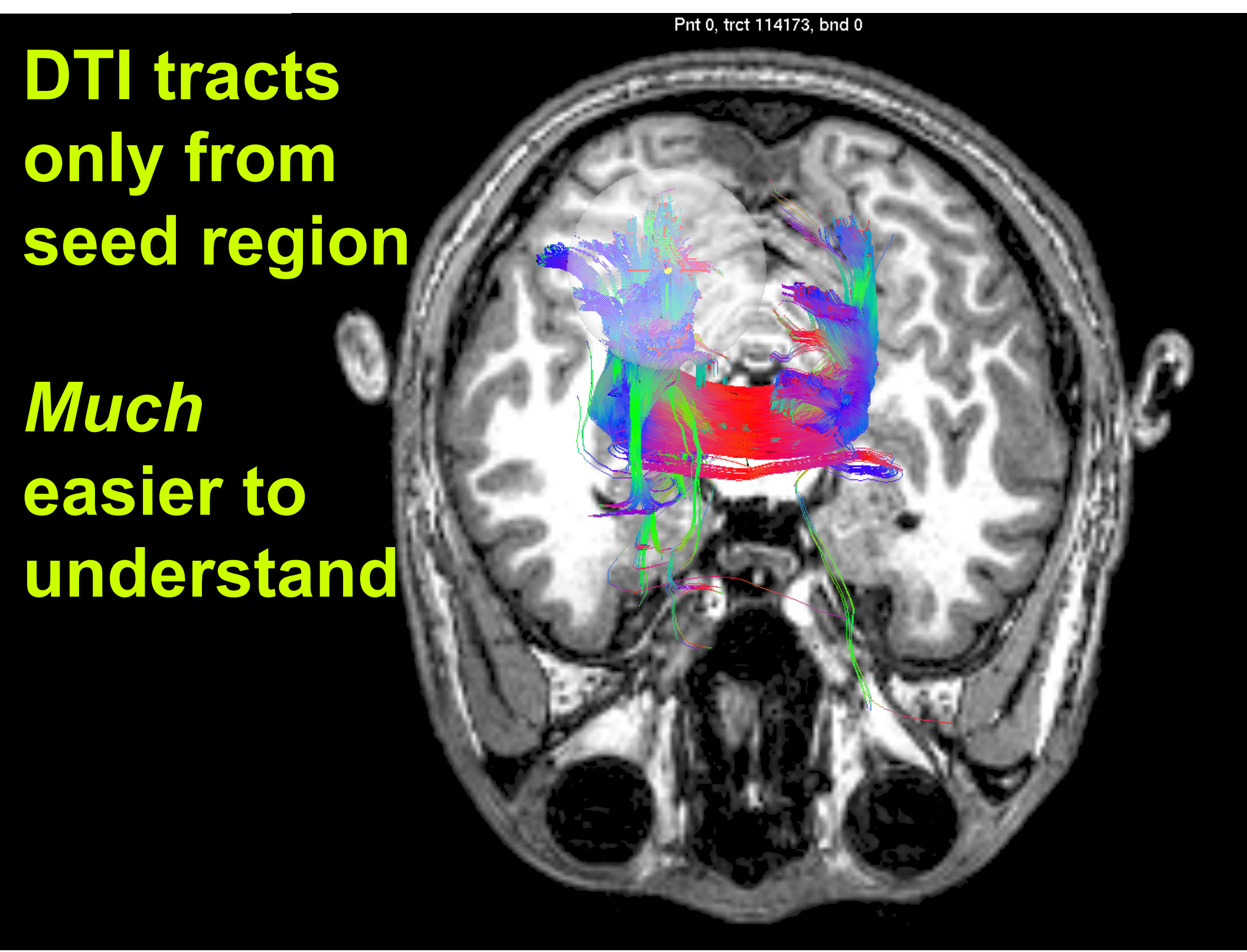
Just too much to take in!

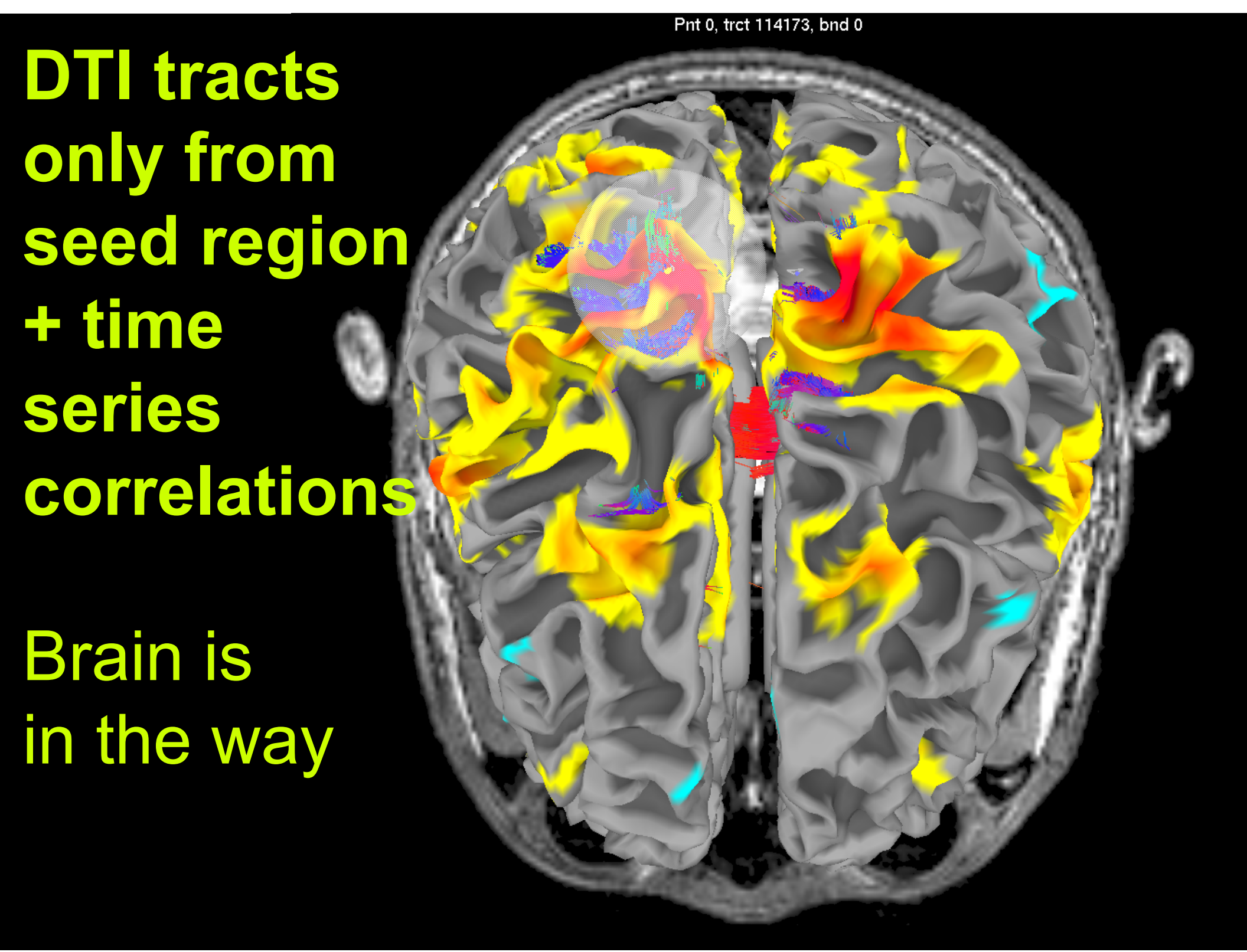


Correlations + DTI tracts + Brain

Way* too much to take in*!

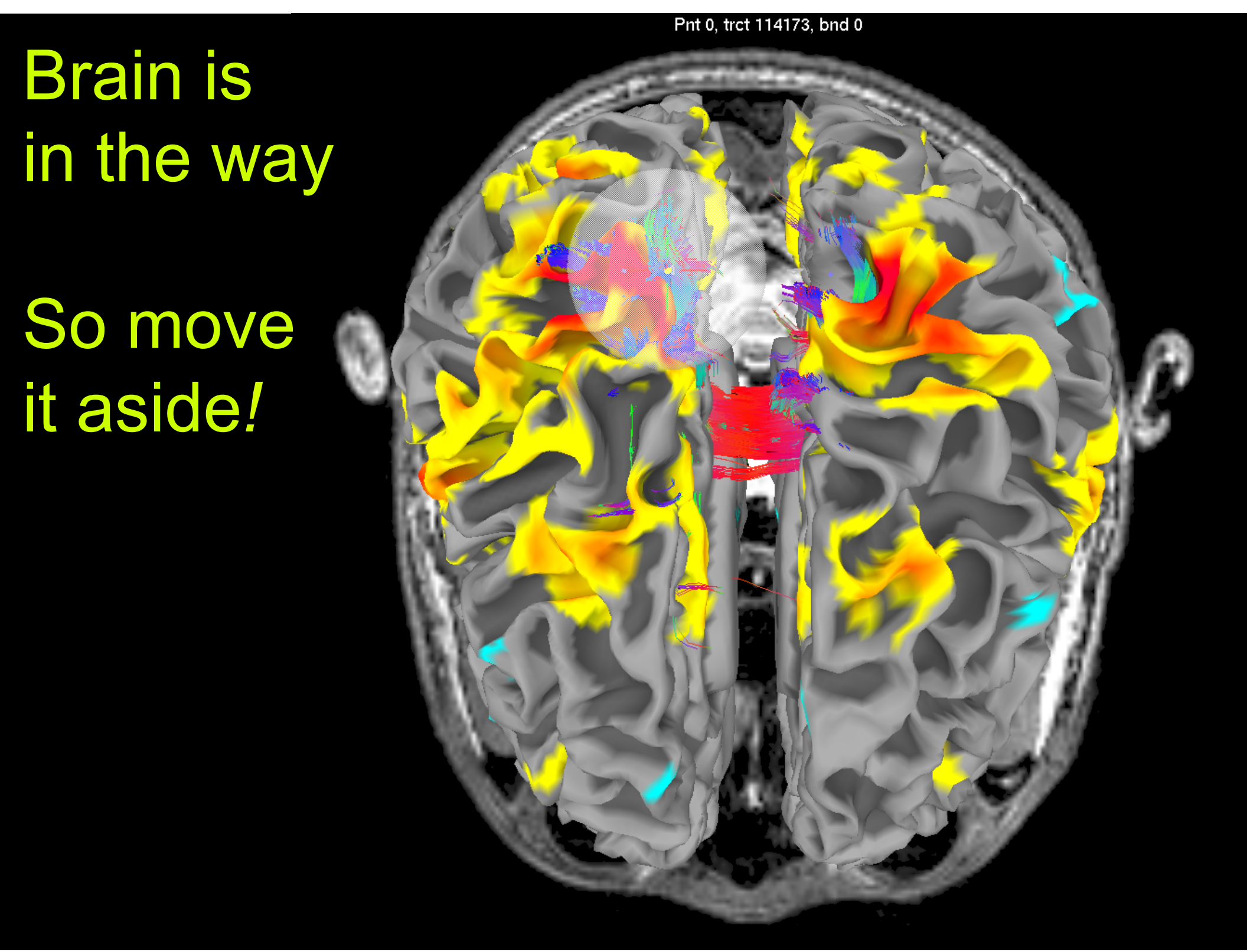


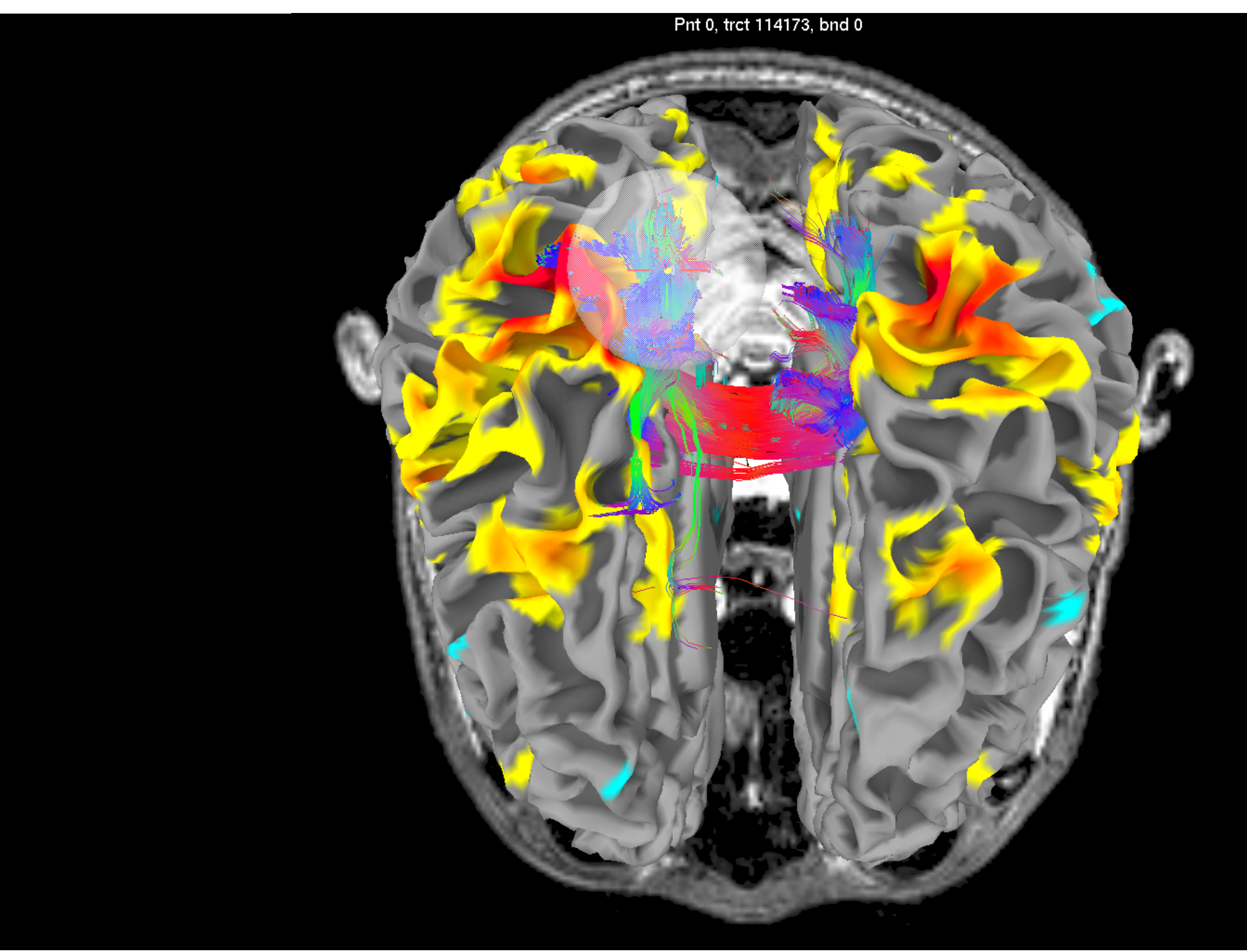

Pnt 0, trct 114173, bnd 0
DTI tracts only from seed region
Much easier to understand

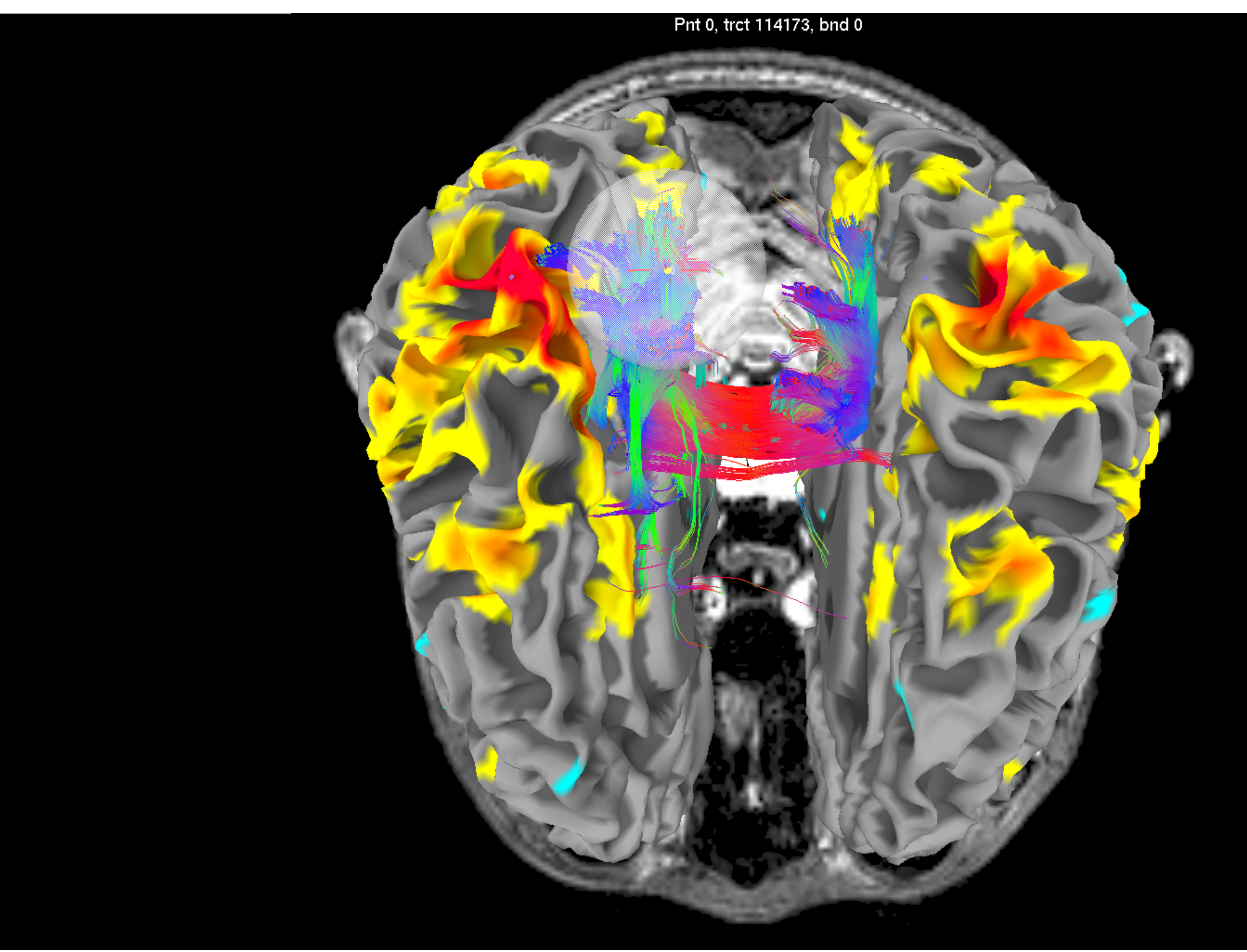

Pnt 0, trct 114173, bnd 0
DTI tracts only from seed region + time series correlations
Brain is in the way

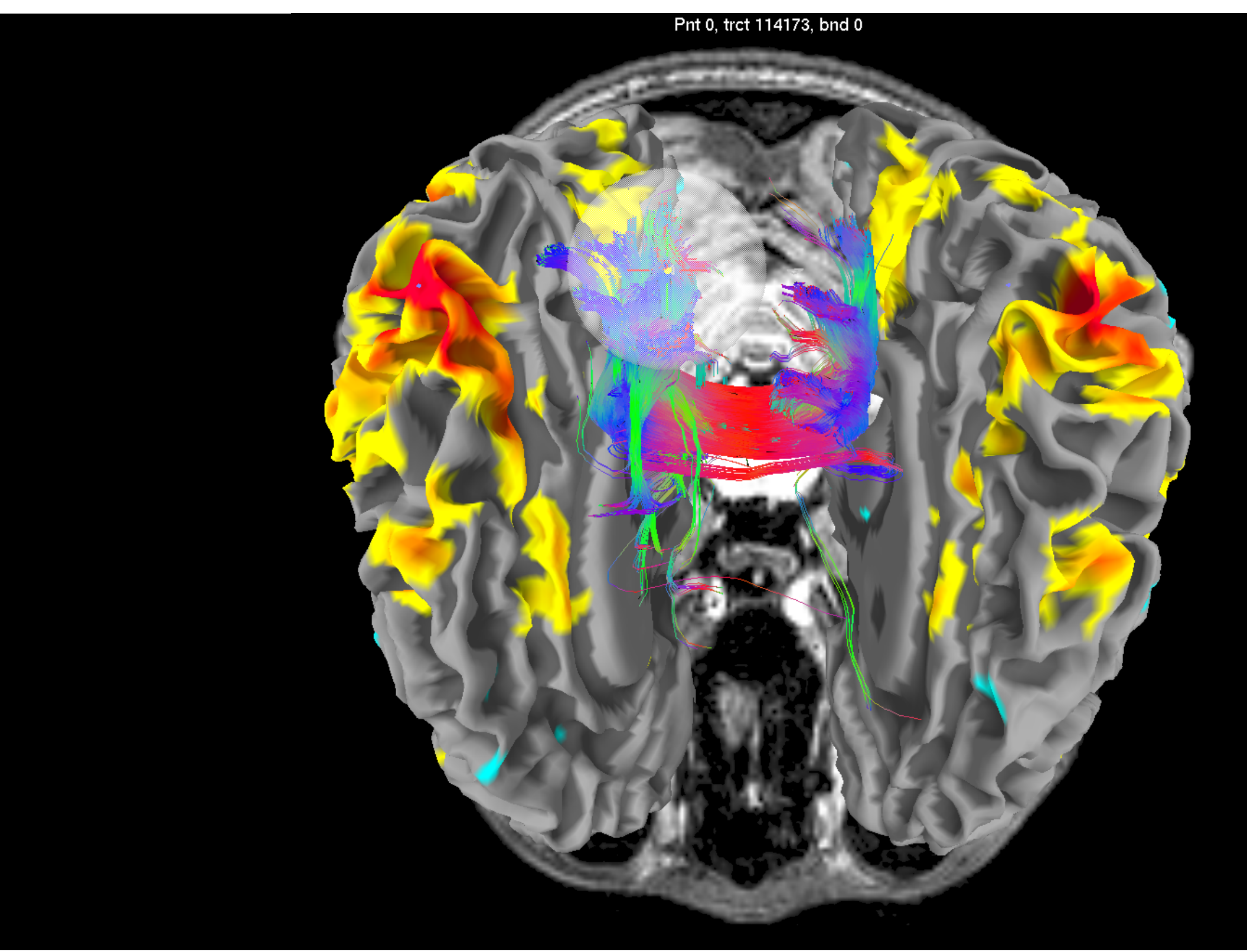
Brain is
in the way

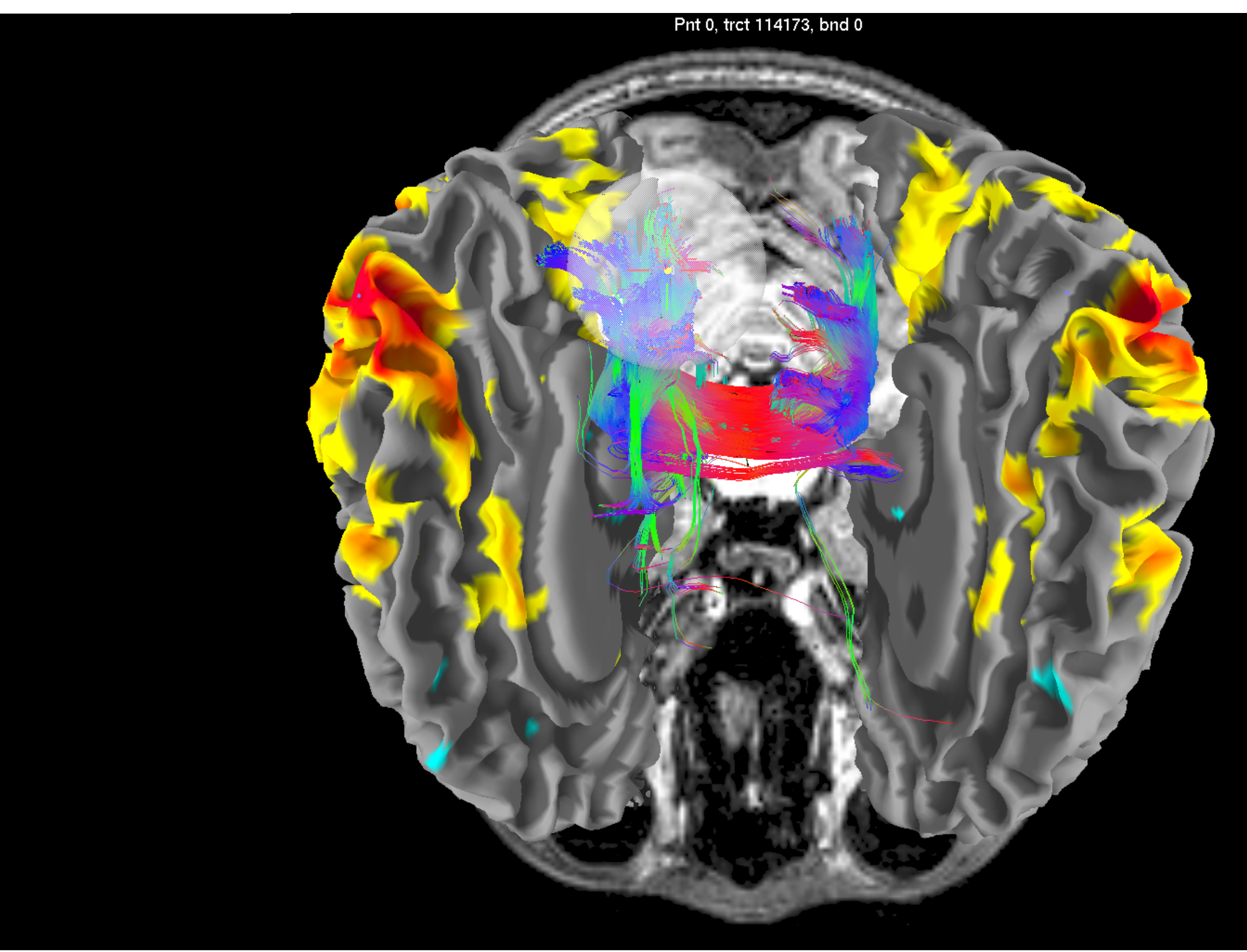
So move
it aside*!*

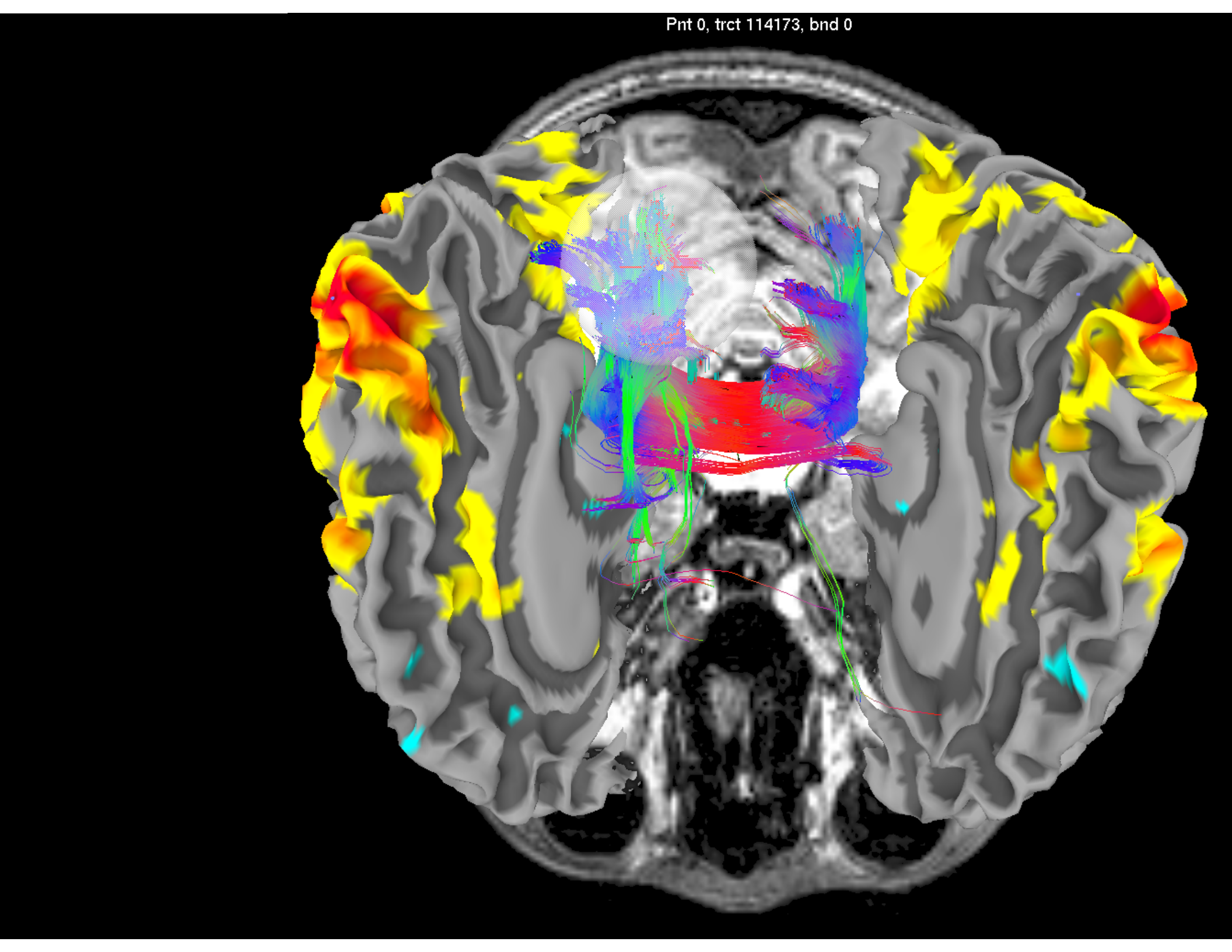


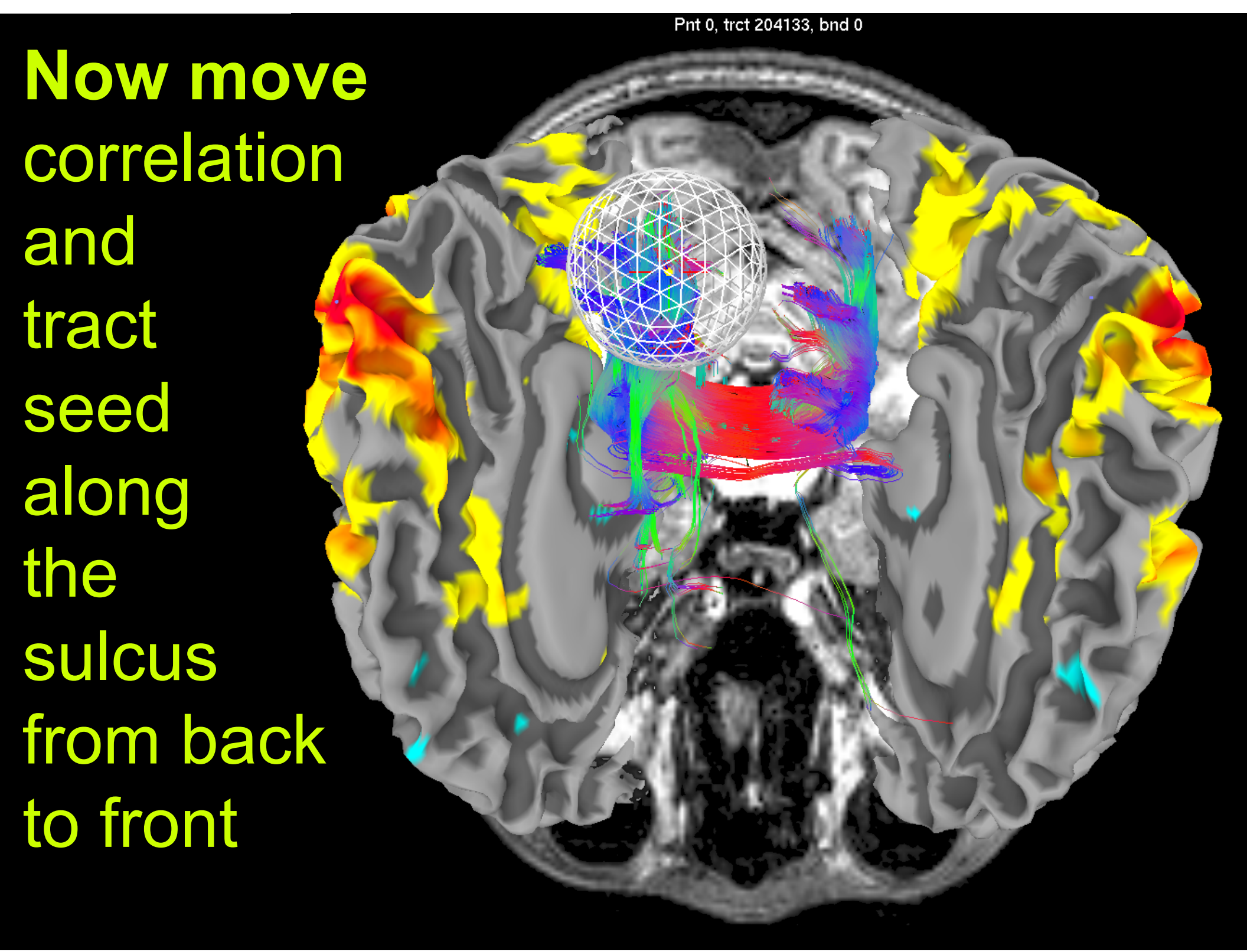

Pnt 0, trct 114173, bnd 0

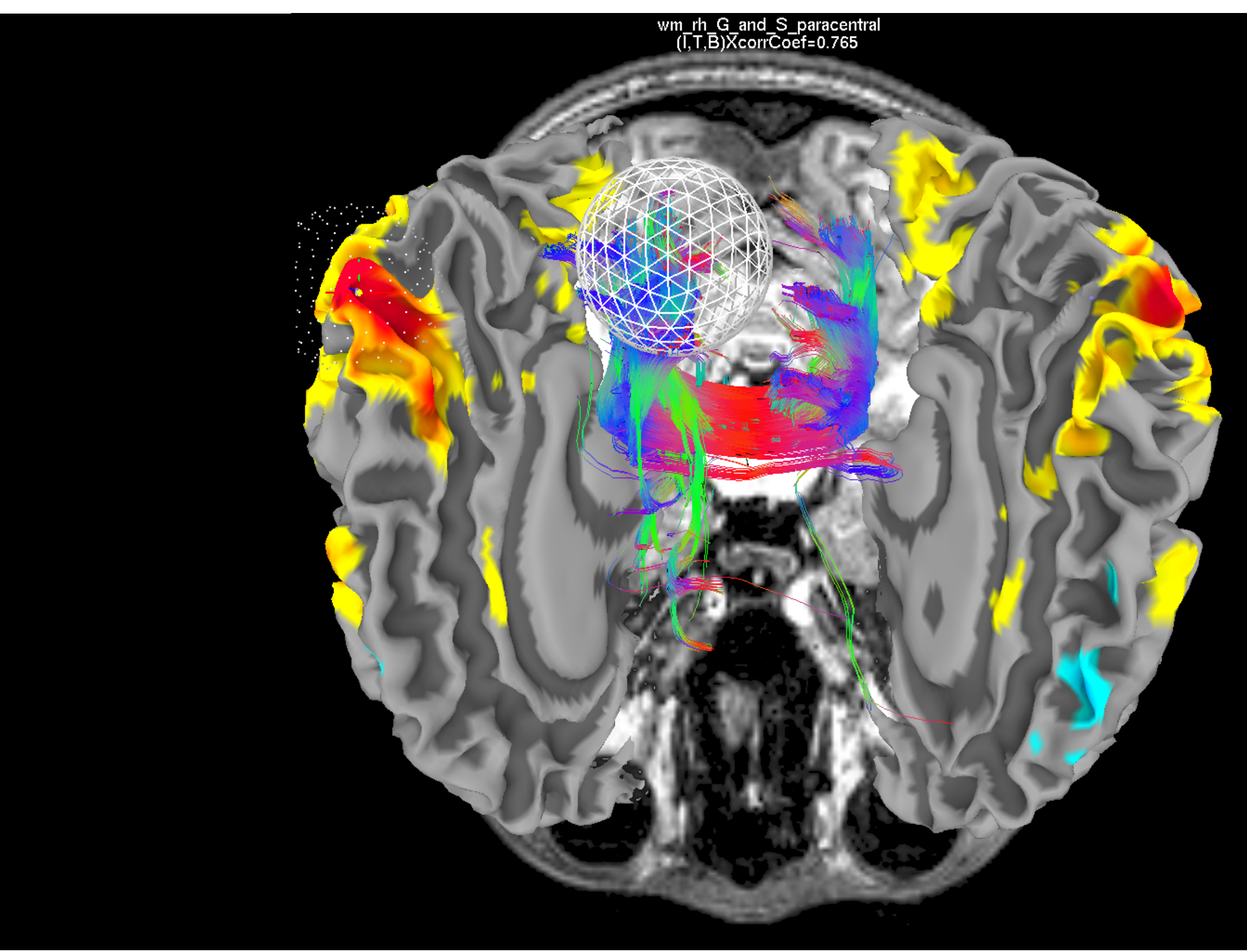

Pnt 0, trct 114173, bnd 0

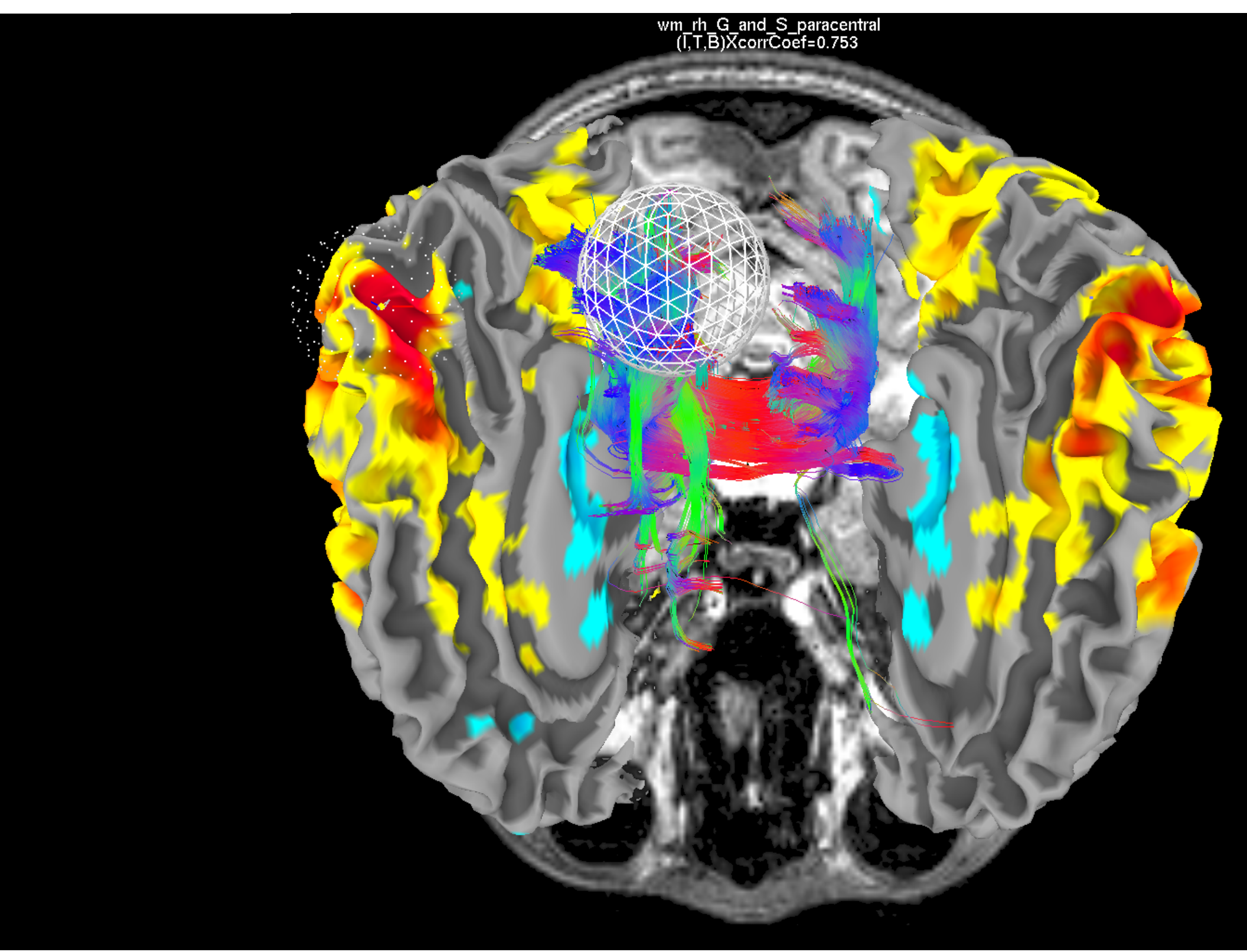

Pnt 0, trct 114173, bnd 0

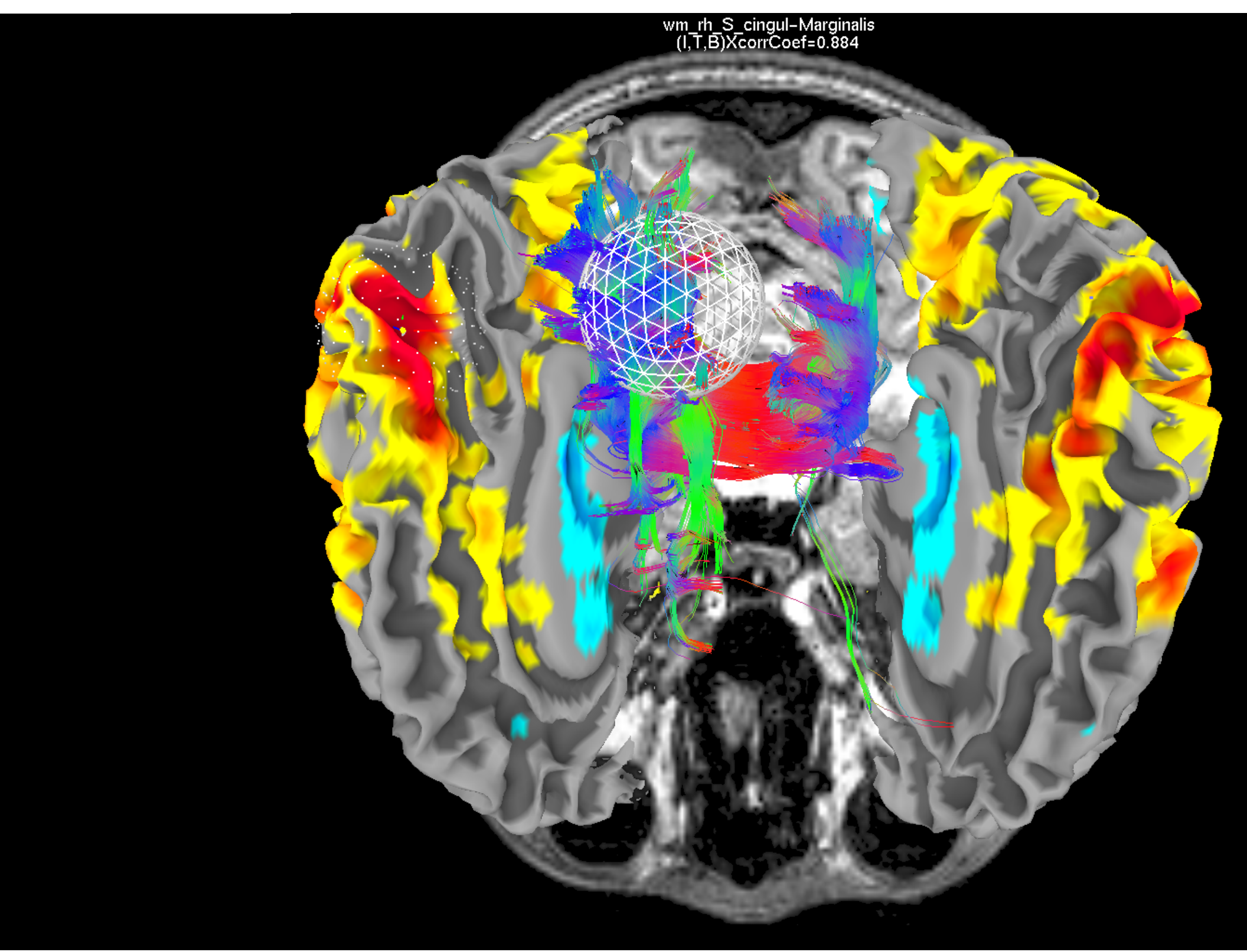

Pnt 0, trct 114173, bnd 0

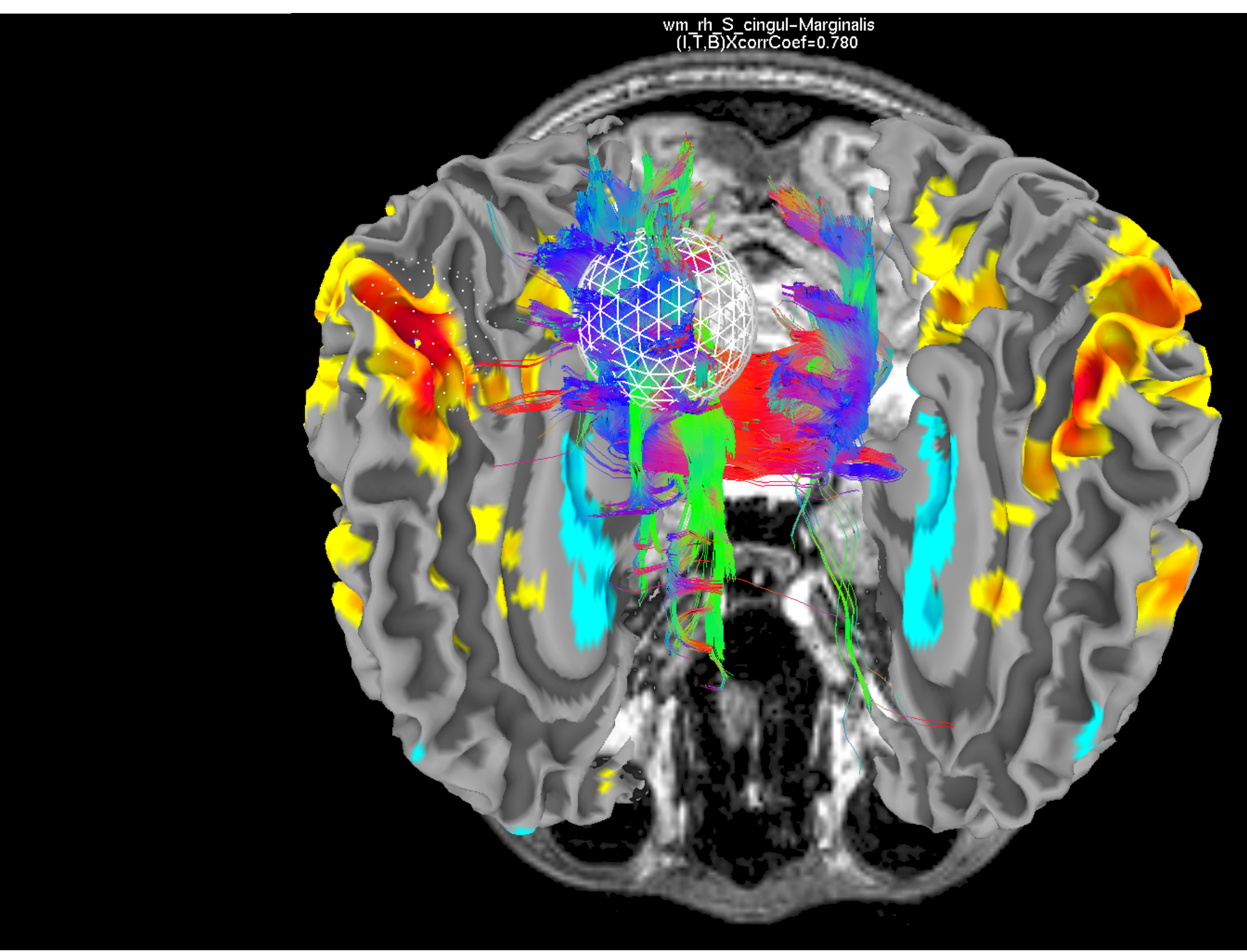

Pnt 0, trct 114173, bnd 0

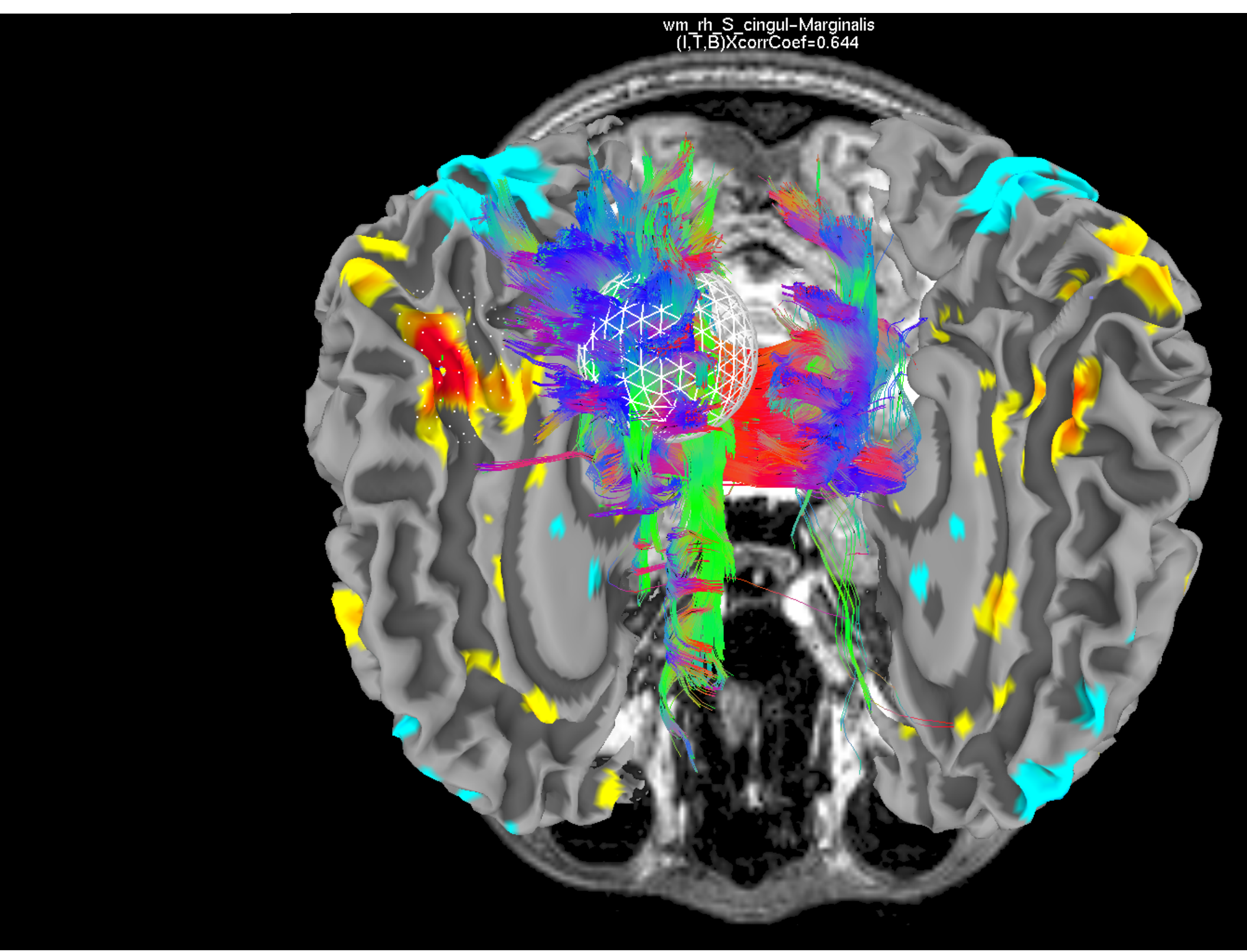

Pnt 0, trct 204133, bnd 0
Now move
correlation
and
tract
seed
along
the
sulcus
from back
to front

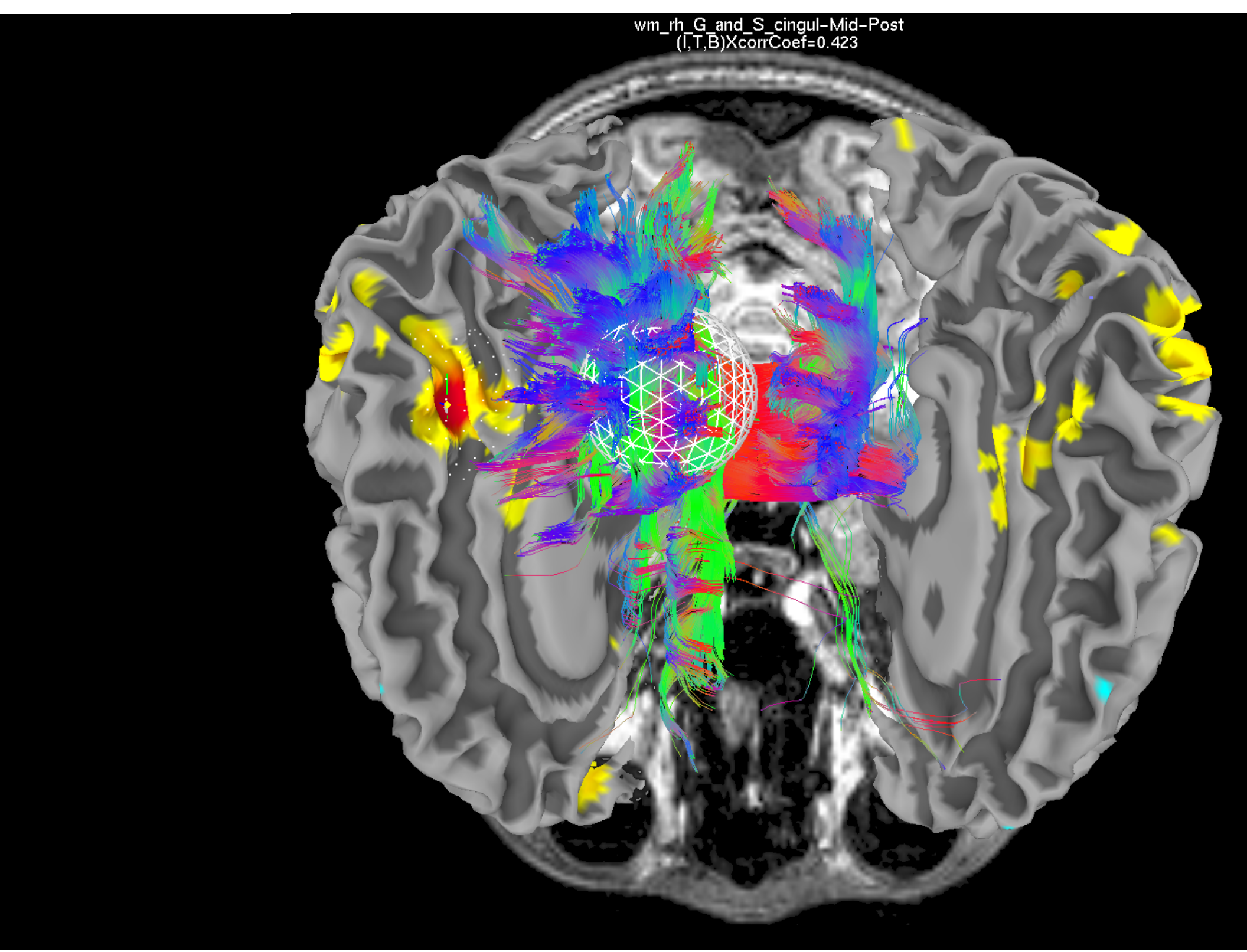

wm_rh_G_and_S_paracentral
(I,T,B)XcorrCoef=0.765

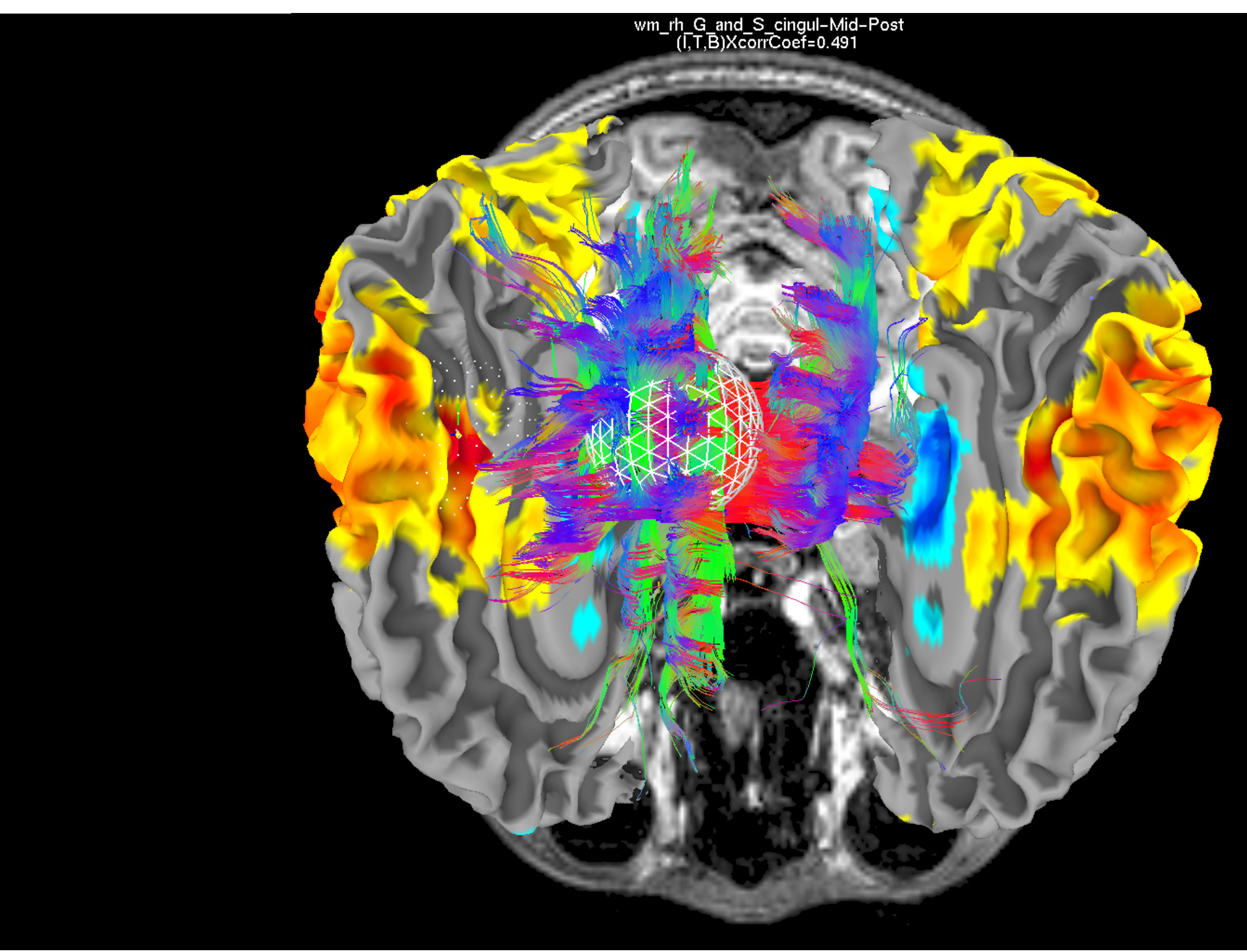

wm_rh_G_and_S_paracentral
(I,T,B)XcorrCoef=0.753

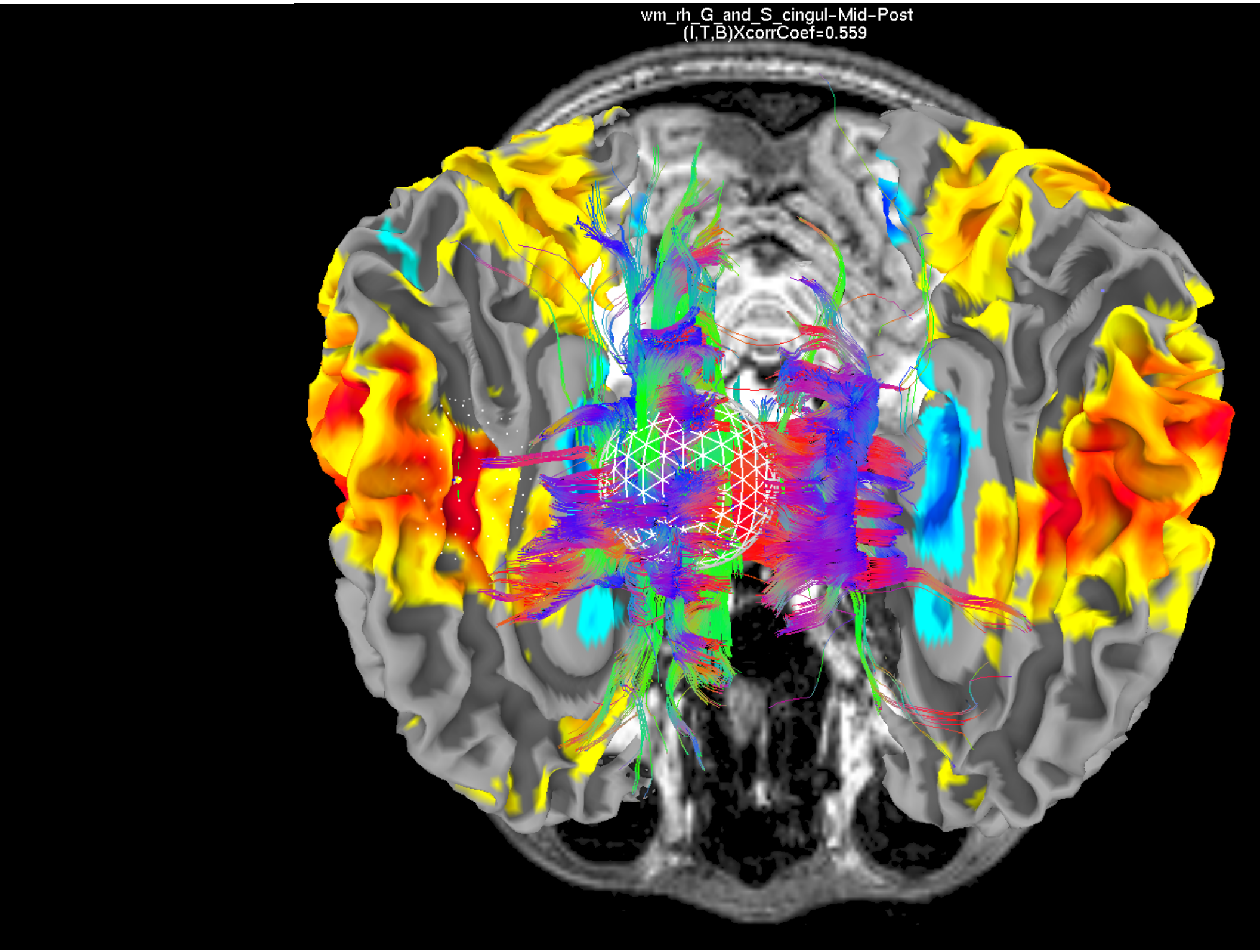

wm_rh_S_cingul-Marginalis
(I,T,B)XcorrCoef=0.884

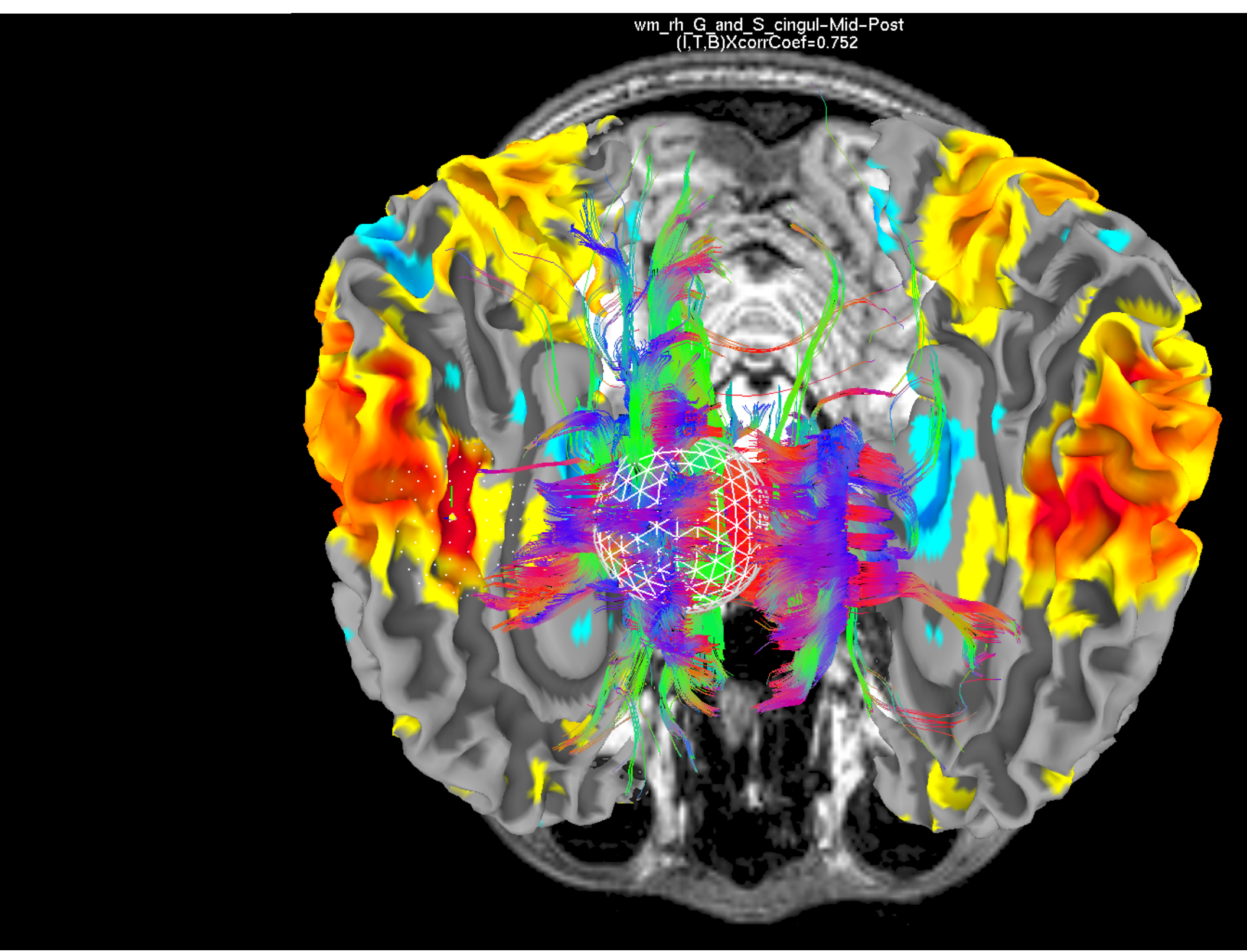

wm_rh_S_cingul-Marginalis
(I,T,B)XcorrCoef=0.780

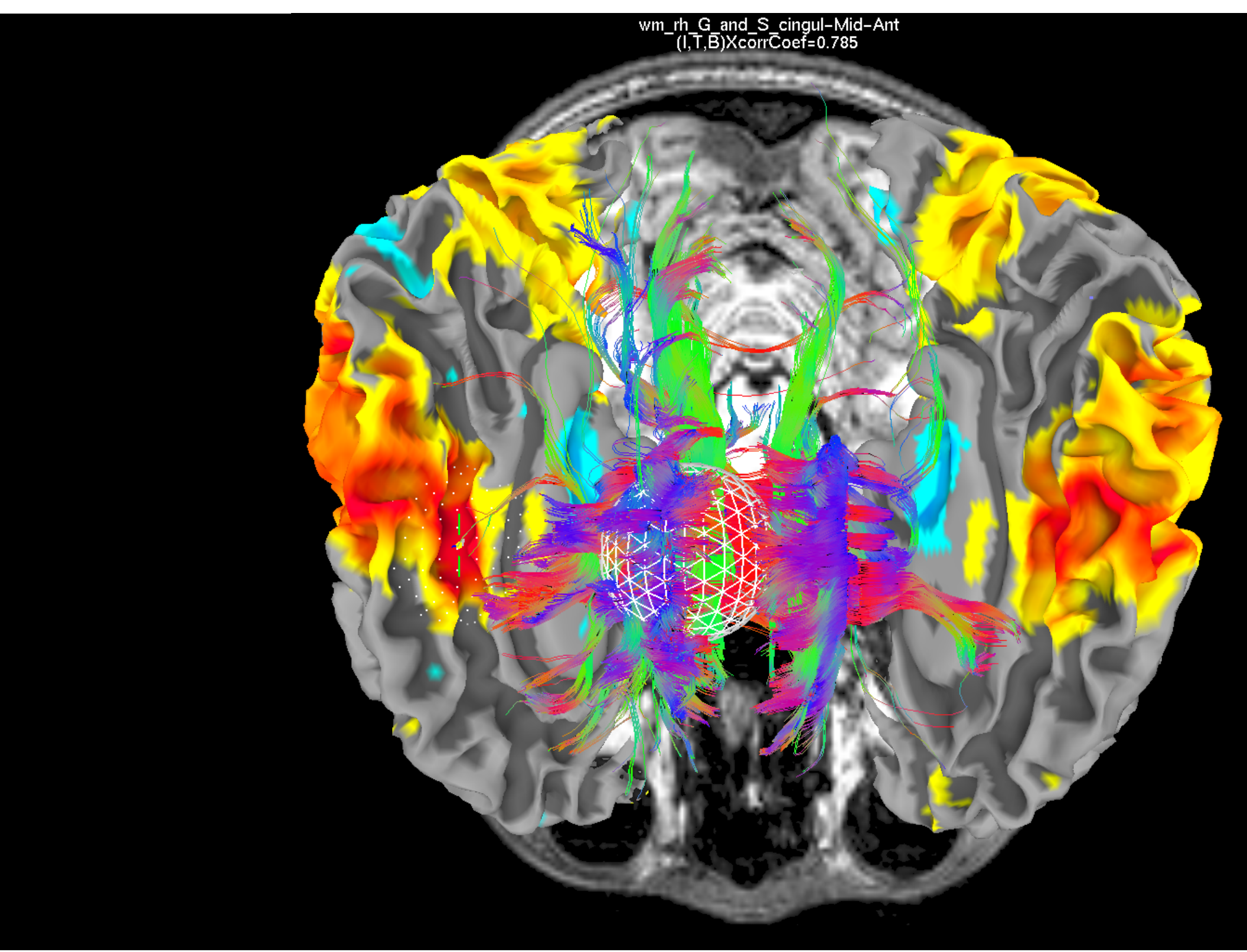

wm_rh_S_cingul-Marginalis
(I,T,B)XcorrCoef=0.644

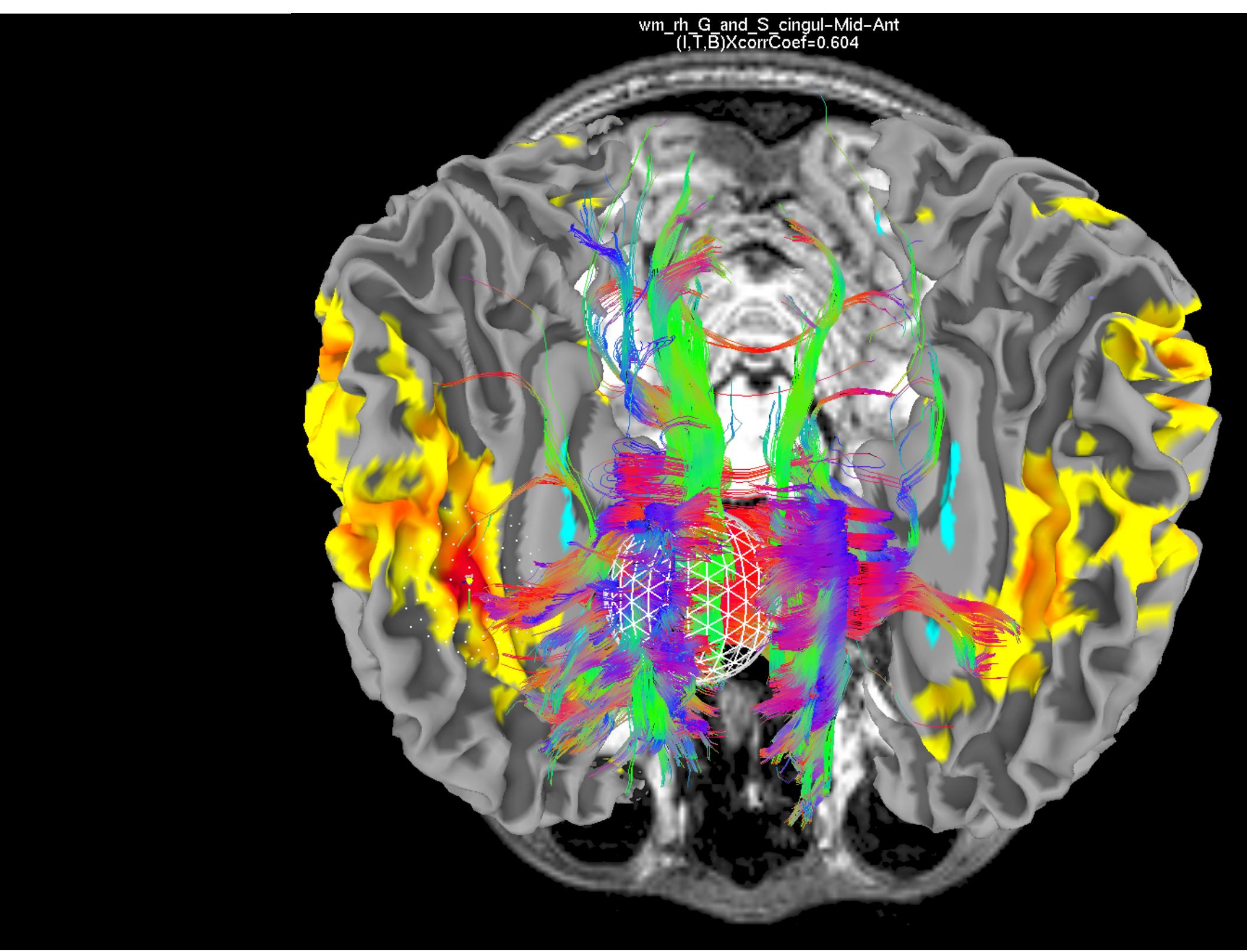

wm_rh_G_and_S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.423

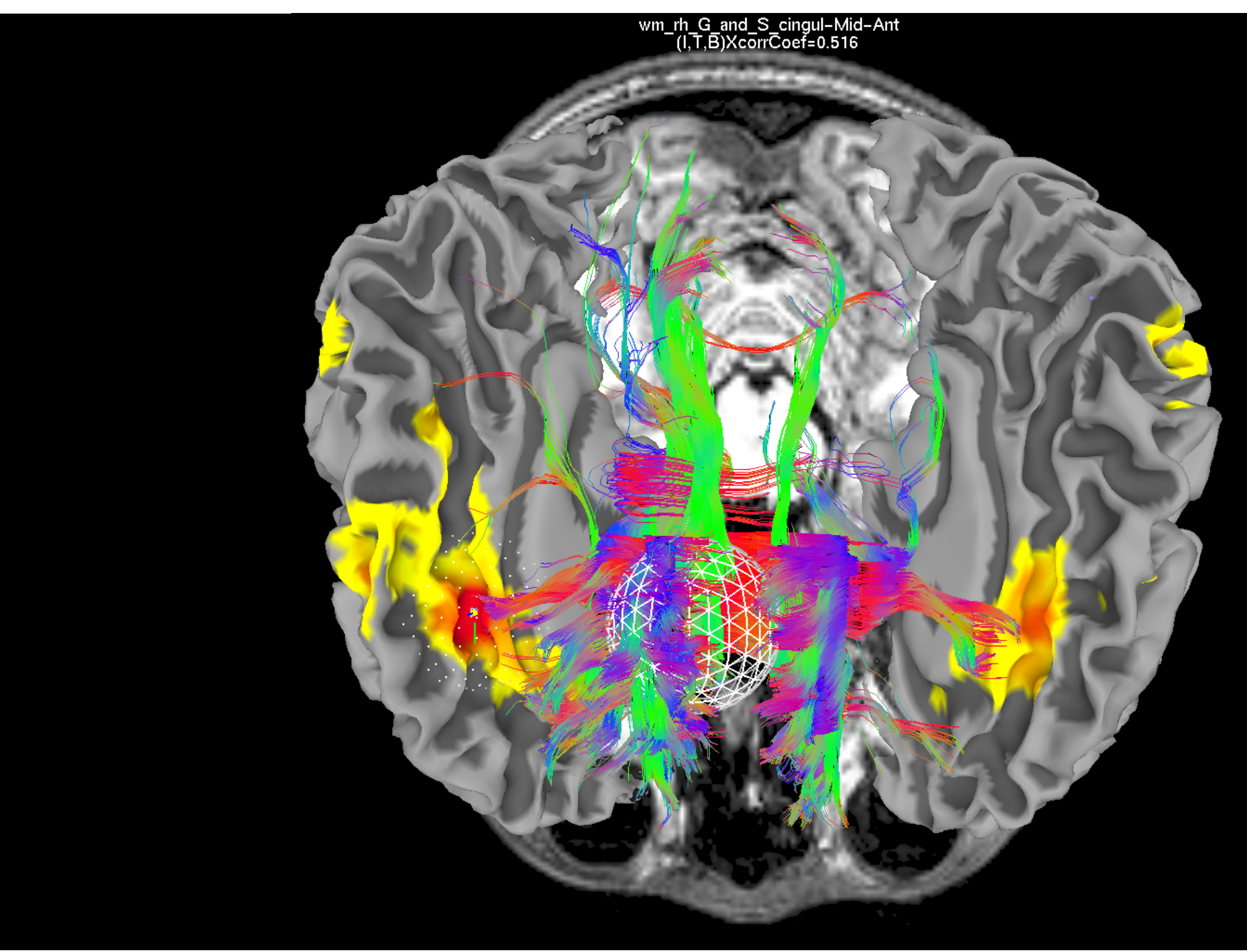

wm_rh_G_and_S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.491


wm_rh_G_and_S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.559

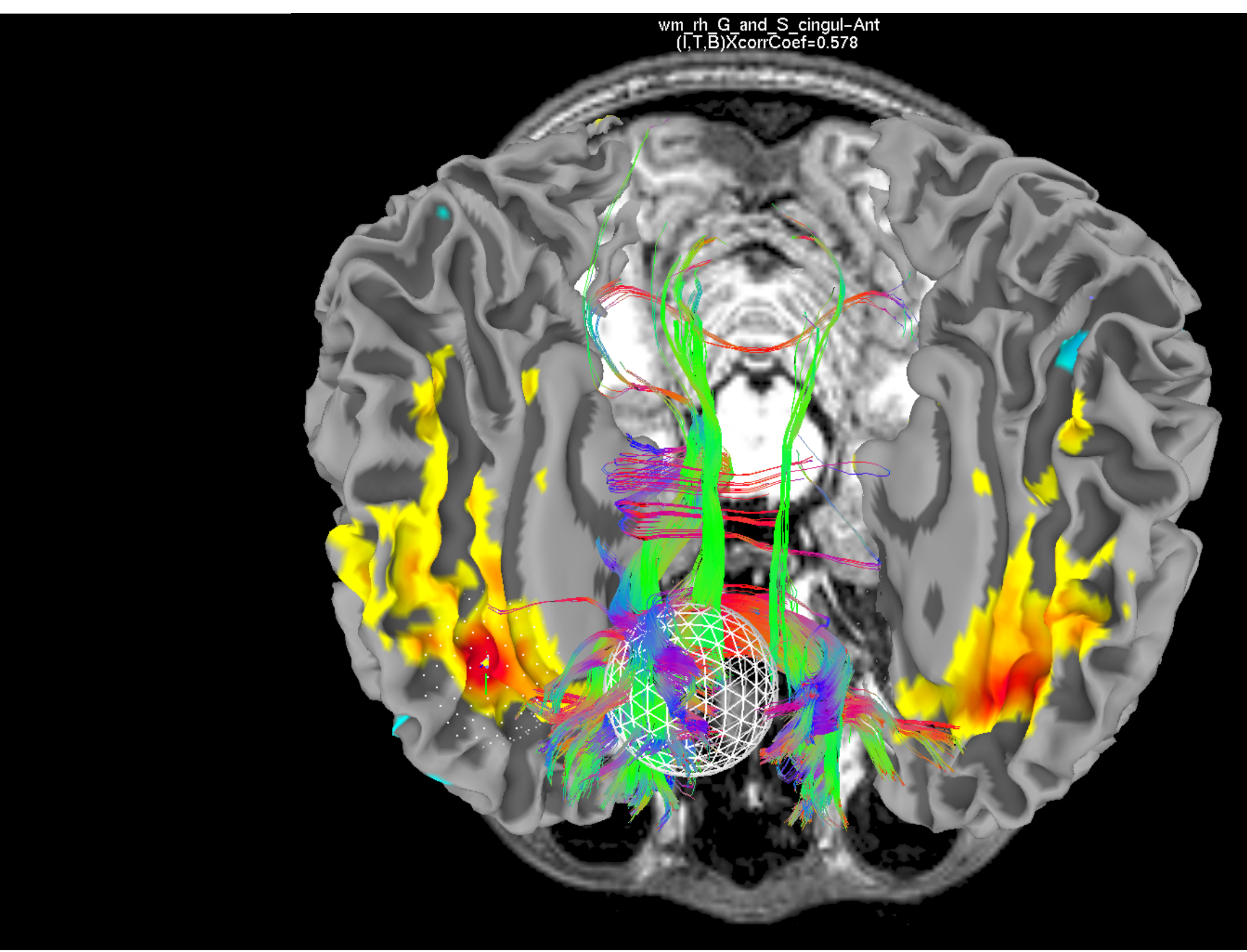

wm_rh_G_and_S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.752

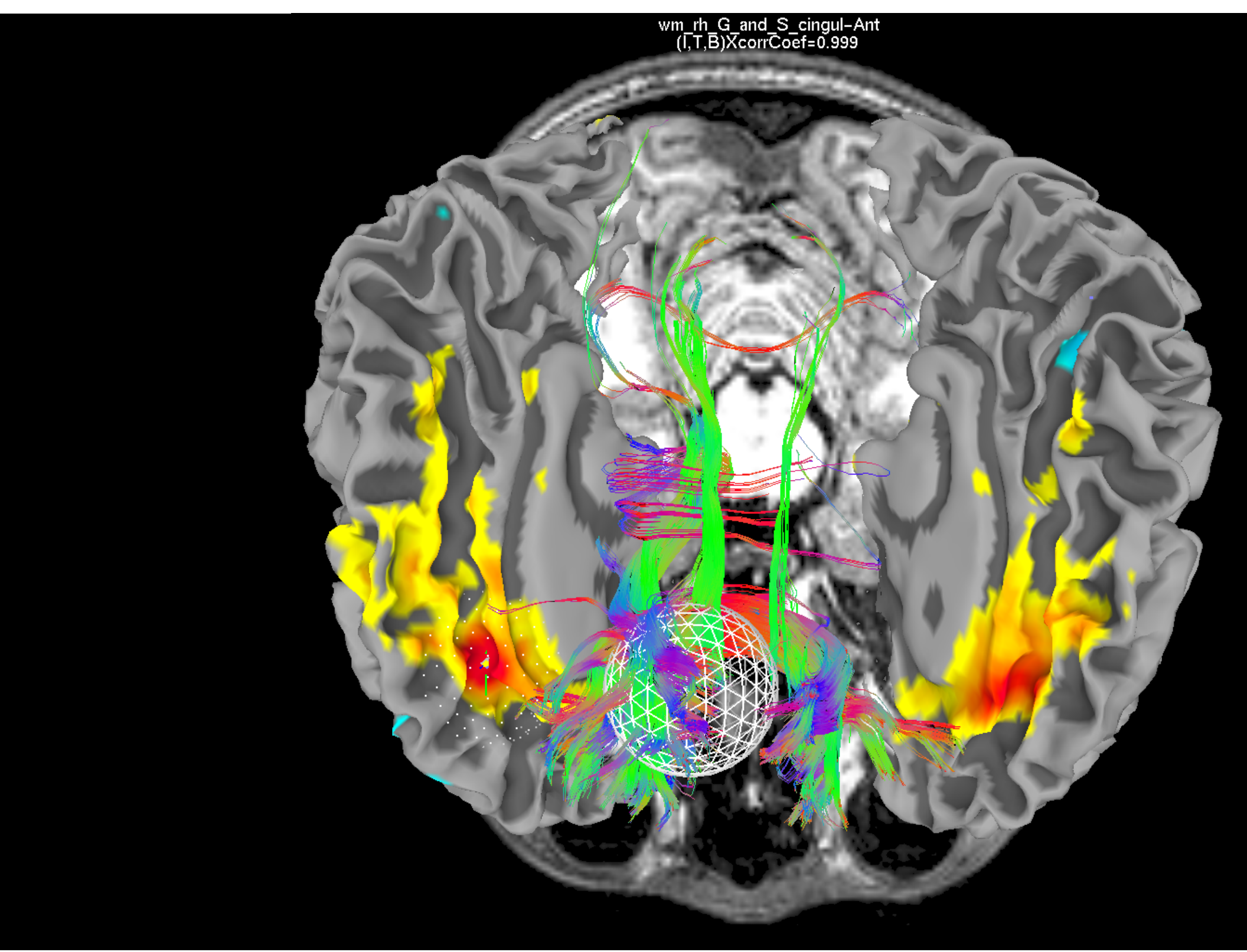

wm_rh_G_and_S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.785

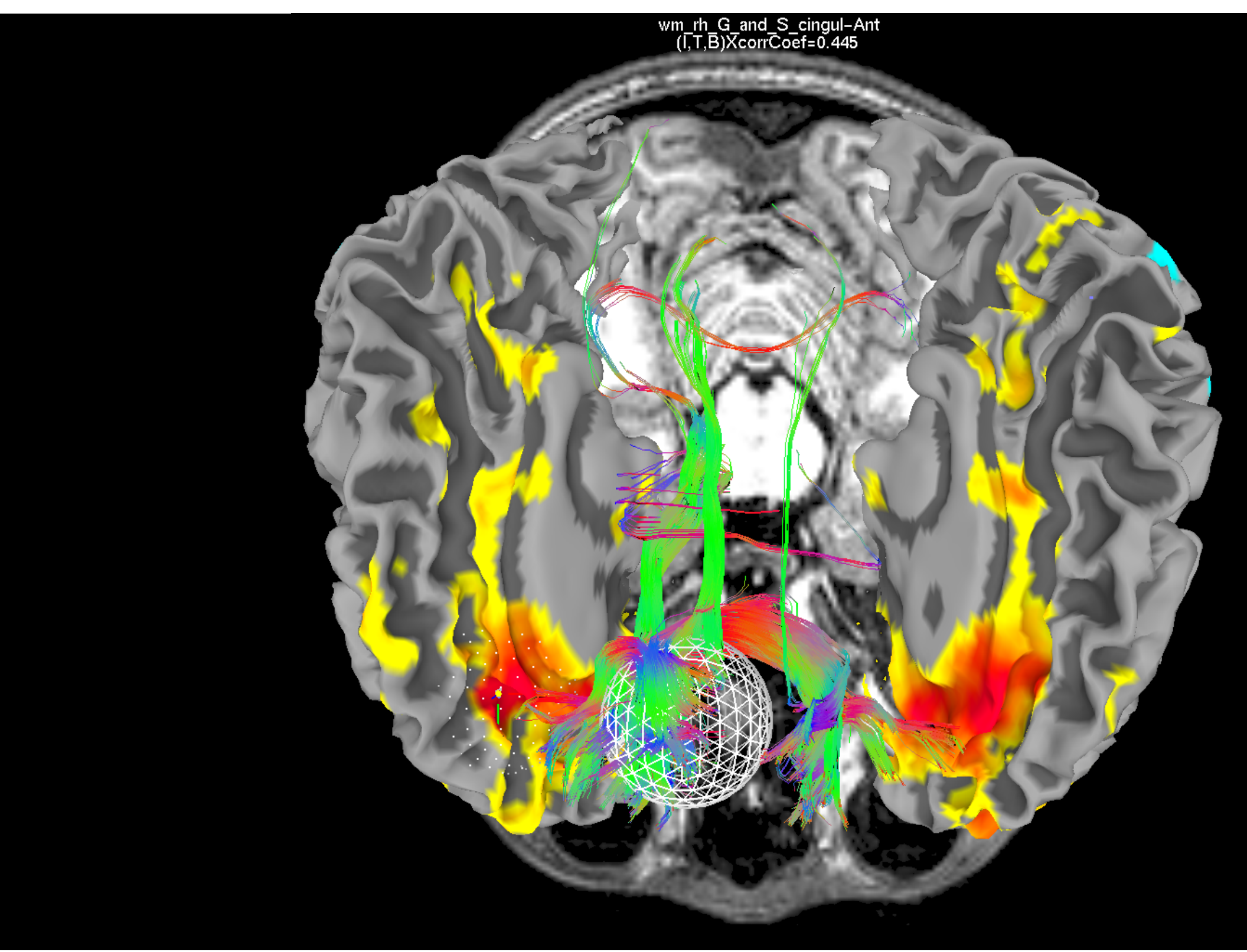

wm_rh_G_and_S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.604

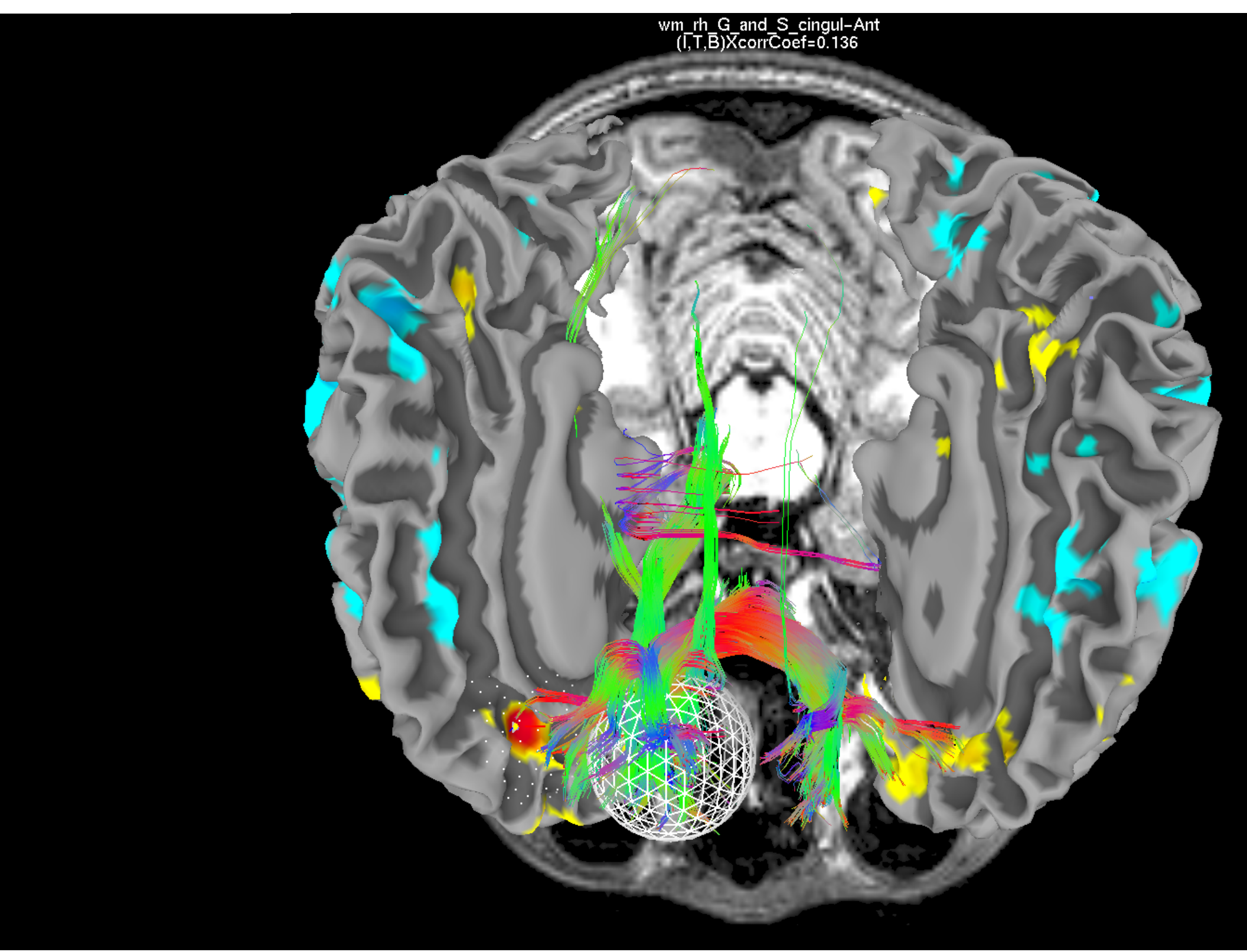

wm_rh_G_and_S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.516

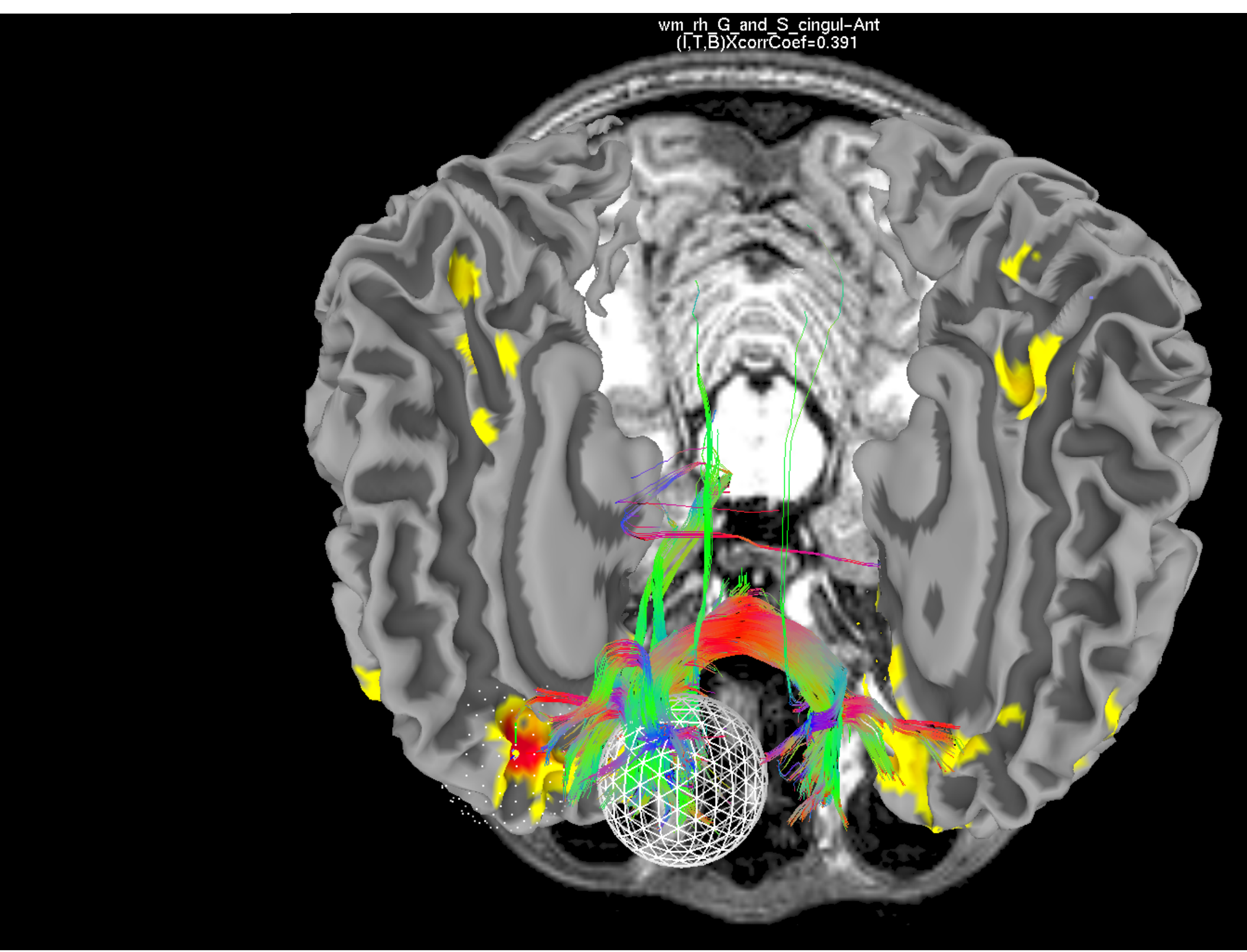

wm_rh_G_and_S_cingul-Mid-Ant
(I,T,B)XcorrCoef=0.679


wm_rh_G_and_S_cingul-Ant
(I,T,B)XcorrCoef=0.578

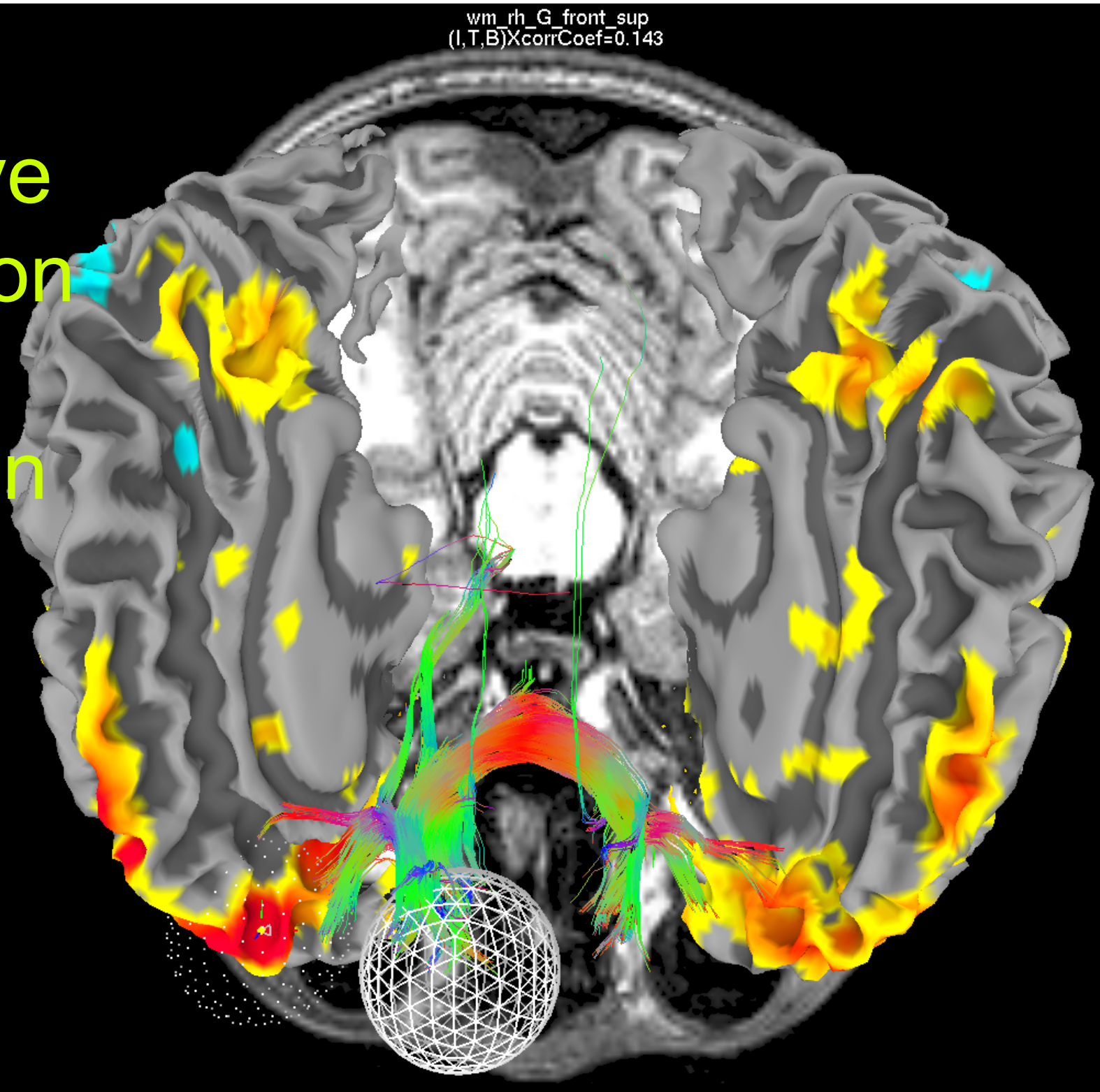

wm_rh_G_and_S_cingul-Ant
(I,T,B)XcorrCoef=0.999


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)

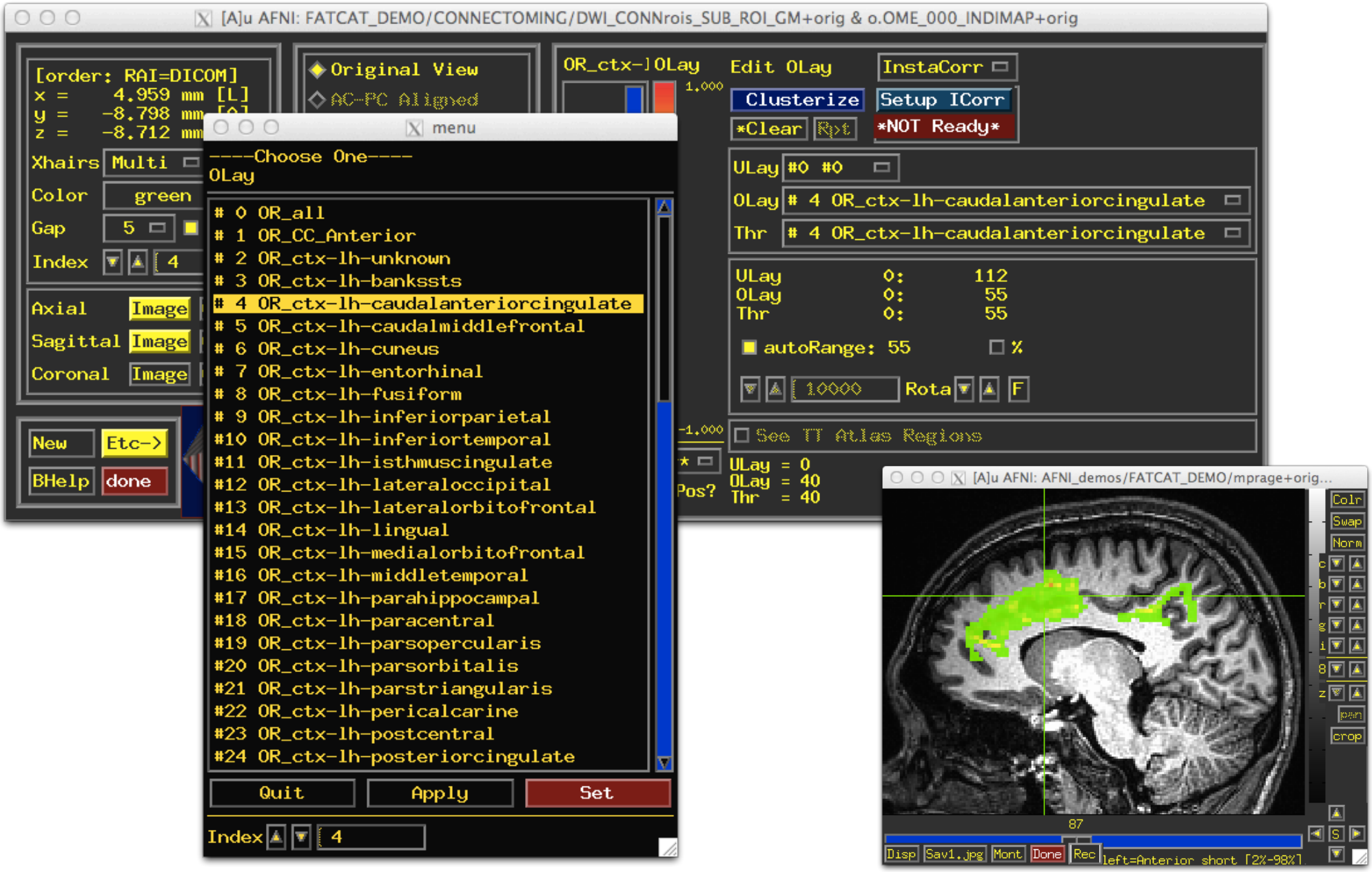
```
set outdir = CONNECTOMING
3dTrackID -mode DET                                          \
    -netrois ${outdir}/DWI_CONNrois_SUB_ROI_GMI+orig         \
    -logic AND                                               \
    -dti_in ${FATPATH}/DTI/DT                                \
    -prefix ${outdir}/o.OME8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

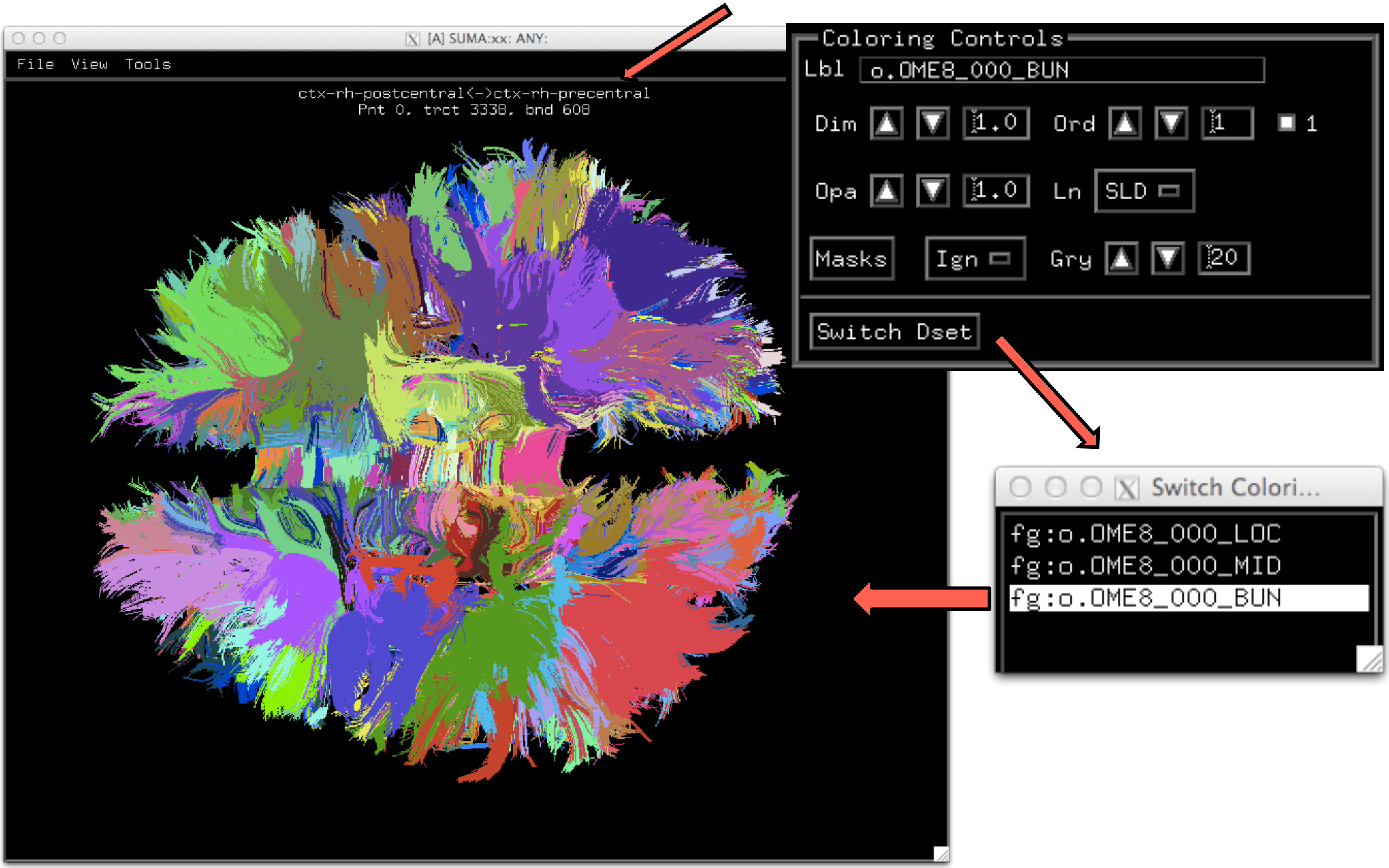
Subbricks are labeled with ROI names



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

Z.S.S 29/09/14

Tracts and Grid files are labeled with ROI names



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

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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**

tcsh Do_13_RUNrsfc_RSFCfilt_param.tcsh

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
```

tcsh @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)