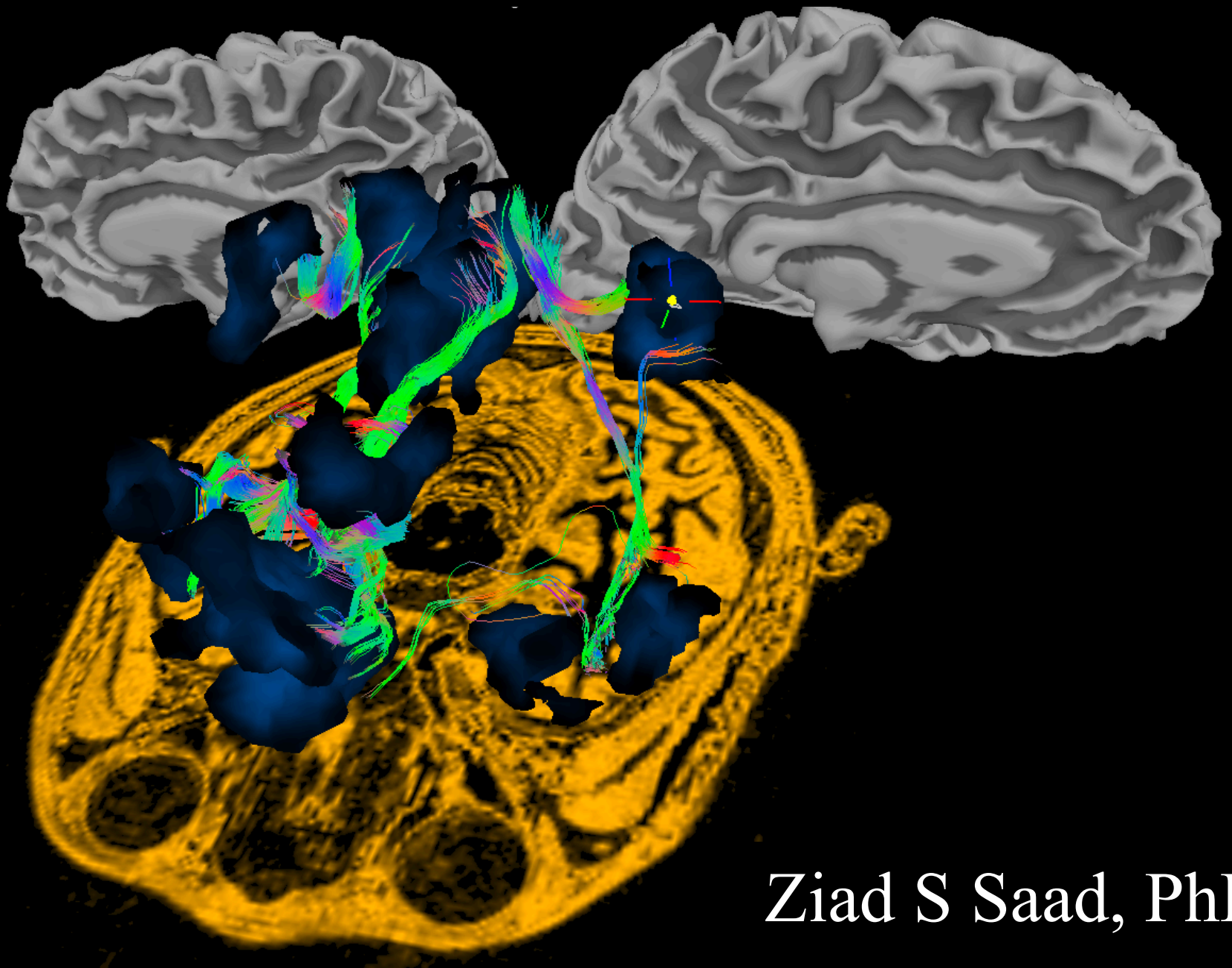


AFNI in 45 minutes

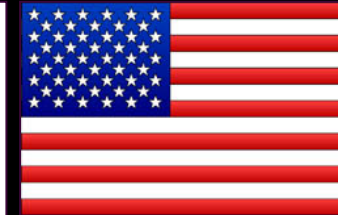


Ziad S Saad, PhD

30
AFNI in 45 minutes!

Ziad S Saad, PhD

SSCC / NIMH & NINDS / NIH / DHHS / USA /
EARTH



30

AFNI in 45 minutes!

No Conflicts of Interest to Declare

Ziad S Saad, PhD

SSCC / NIMH & NINDS / NIH / DHHS / USA /
EARTH



AFNI in 1 minute

A suite of programs for analyzing MRI data



AFNI in 1 minute

Single subject analyses – task based and rest

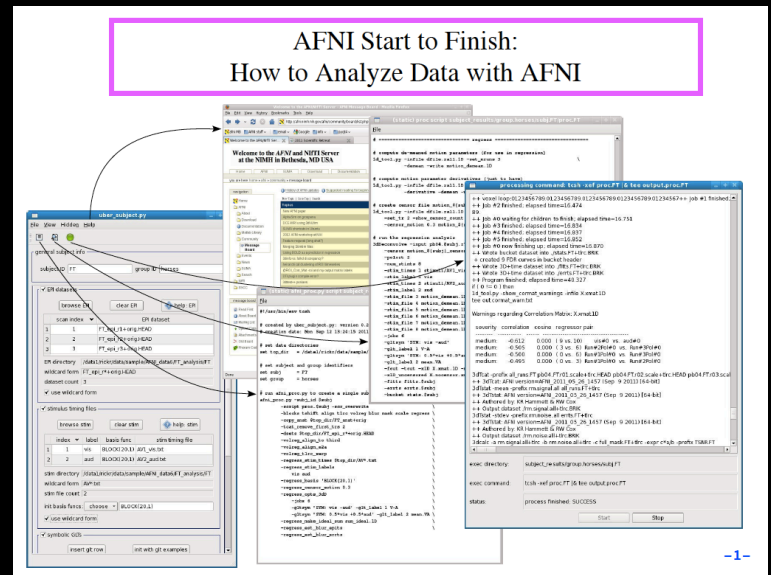
afni_proc.py & uber_subject.py

Rick Reynolds

afni_proc.py: Command-line pipeline creator

uber_subject.py: GUI to create afni_proc.py

command and assemble pipeline



Start with the processing script from these programs and modify if you need to.

See http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/afni_handouts/afni16_start_to_finish.pdf

AFNI in 1 minute

Single subject analyses – task based and rest

afni_proc.py & uber_subject.py

Rick Reynolds

AFNI Start to Finish: How to Analyze Data with AFNI

The image displays the AFNI software interface, showing the process of analyzing data. It includes a terminal window with the command `afni_proc.py` and its output, a window for setting up the analysis (AFNI Start to Finish), and a window for the processing command (processing command: `tcsh -xsf proc.FT / & tee output.proc.FT`).

The terminal window shows the execution of the `afni_proc.py` script, which is used to process the data. The output includes a list of jobs and their status, as well as a correlation matrix for the data.

The processing command window shows the execution of the `tcsh -xsf proc.FT / & tee output.proc.FT` command, which is used to process the data. The output includes a list of jobs and their status, as well as a correlation matrix for the data.

Single-Subject RS-fMRI Processing

Generate Analysis Pipeline with *afni_proc.py*

```
afni_proc.py -subj_id subj123  
-dsets epi_run1+orig.HEAD  
-copy_anat anat+orig  
-blocks despike ricor tshift align  
          volreg blur regress  
-regress_anaticor  
-regress_censor_motion 0.2  
-regress_bandpass 0.01 0.1  
-ricor_regs RICOR/r*.slibase.1D
```

See *afni_proc.py -h_view* for more detailed examples,

Single-Subject RS-fMRI Processing

Generate Analysis Pipeline with *afni_proc.py*

```
afni_proc.py -subj_id subj123 ← Subject ID \
  -dsets epi_run1+orig.HEAD ← EPI timeseries \
  -copy_anat anat+orig ← Anatomical \
  -blocks despike ricor tshift align \
  volreg blur regress \
  -regress_anaticor \
  -regress_censor_motion 0.2 \
  -regress_bandpass 0.01 0.1 \
  -ricor_regs RICOR/r*.slibase.1D \
```

See *afni_proc.py -h_view* for more detailed examples,

Single-Subject RS-FMRI Processing

Generate Analysis Pipeline with *afni_proc.py*

```
afni_proc.py -subj_id subj123  
-dsets epi_run1+orig.HEAD  
-copy_anat anat+orig  
-blocks despike ricor tshift align  
           volreg blur regress ← Processing blocks  
-regress_anaticor           Use defaults or specify sequence  
-regress_censor_motion 0.2  
-regress_bandpass 0.01 0.1  
-ricor_regs RICOR/r*.slibase.1D
```

See *afni_proc.py -h_view* for more detailed examples,

Single-Subject RS-fMRI Processing

Generate Analysis Pipeline with *afni_proc.py*

```
afni_proc.py -subj_id subj123  
-dsets epi_run1+orig.HEAD  
-copy_anat anat+orig  
-blocks despike ricor tshift align  
          volreg blur regress  
-regress_anaticor ← Use Local Eroded White Matter  
-regress_censor_motion for2denoising. (Joel et al. 2010)  
-regress_bandpass 0.01 0.1  
-ricor_regs RICOR/r*.slibase.1D
```

See *afni_proc.py -h_view* for more detailed examples,

Single-Subject RS-fMRI Processing

Generate Analysis Pipeline with *afni_proc.py*

```
afni_proc.py -subj_id subj123  
-dsets epi_run1+orig.HEAD  
-copy_anat anat+orig  
-blocks despike ricor tshift align  
          volreg blur regress  
-regress_anaticor  
-regress_censor_motion 0.2    ← Motion censoring  
-regress_bandpass 0.01 0.1    and bandpass filter  
-ricor_regs RICOR/r*.slibase.1D
```

See *afni_proc.py -h_view* for more detailed examples,

Single-Subject RS-fMRI Processing

Generate Analysis Pipeline with *afni_proc.py*

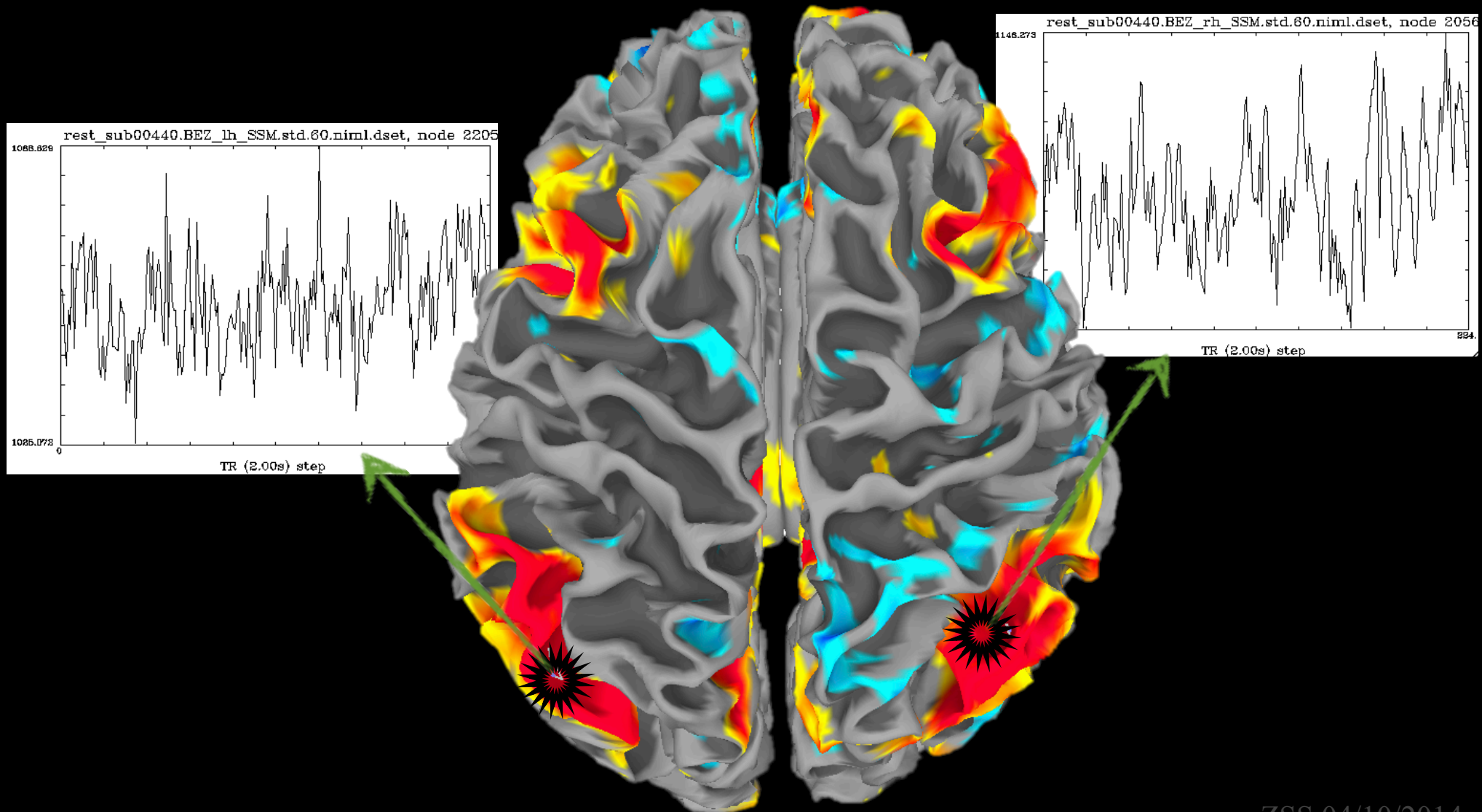
```
afni_proc.py -subj_id subj123  
-dsets epi_run1+orig.HEAD  
-copy_anat anat+orig  
-blocks despike ricor tshift align  
          volreg blur regress  
-regress_anaticor  
-regress_censor_motion 0.2  
-regress_bandpass 0.01 0.1  
-ricor_regs RICOR/r*.slibase.1D ← RICOR+RVT for  
respiration & cardiac denoising (Glover 2002, Birn 2006)
```

See *afni_proc.py -h_view* for more detailed examples,

AFNI in 1 minute

Surface-based analysis: SUMA

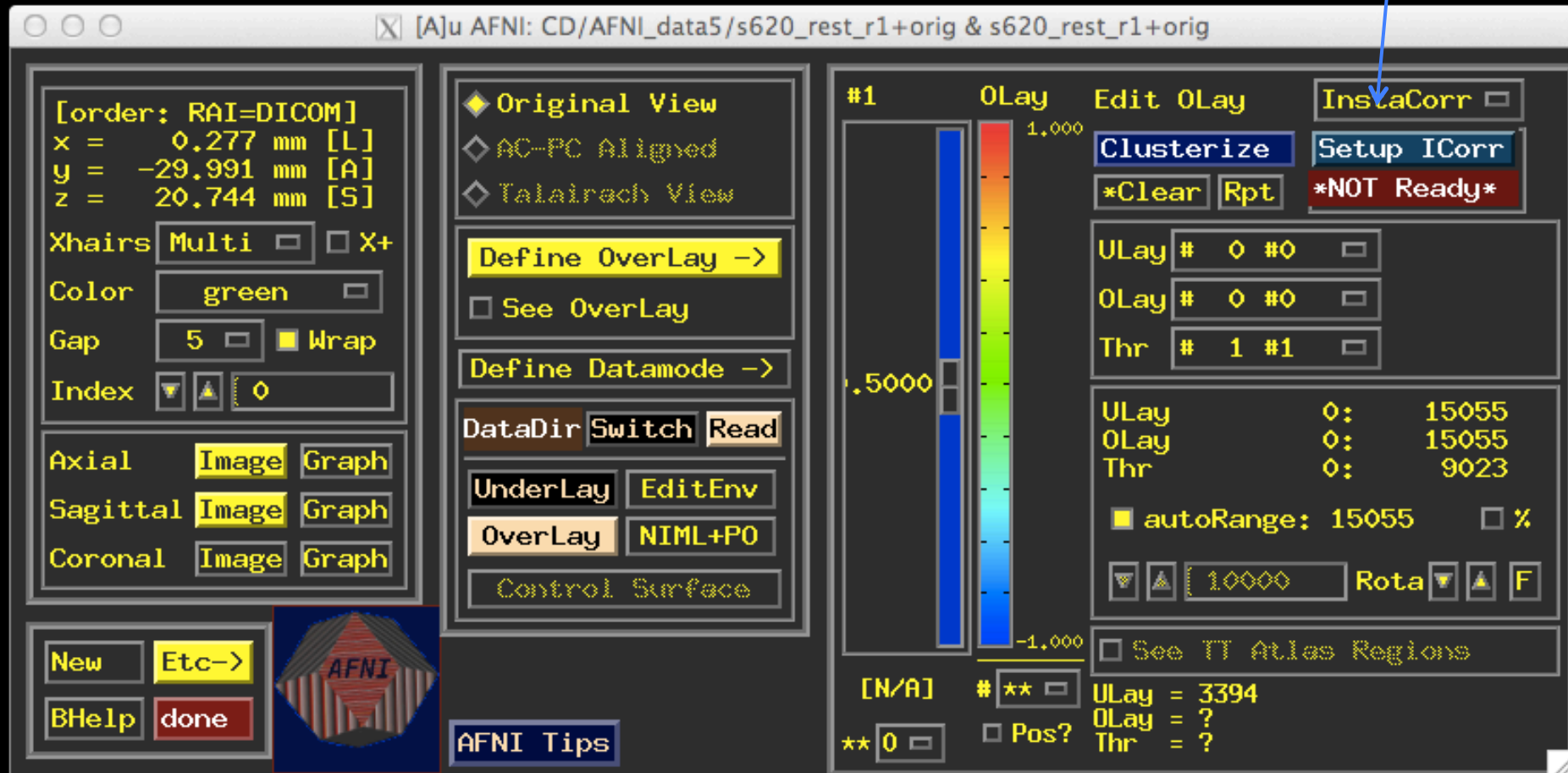
Pipeline also created with `afni_proc.py`



InstaCorr, Single-Subject

cd AFNI_data5/
afni &

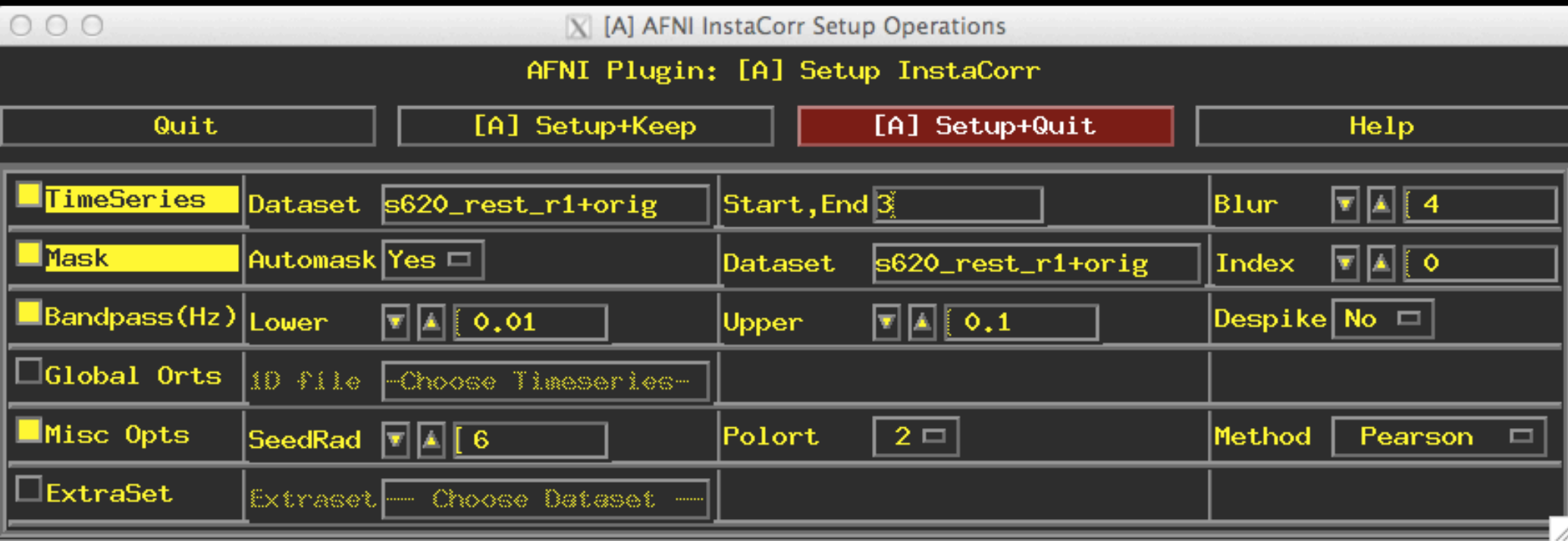
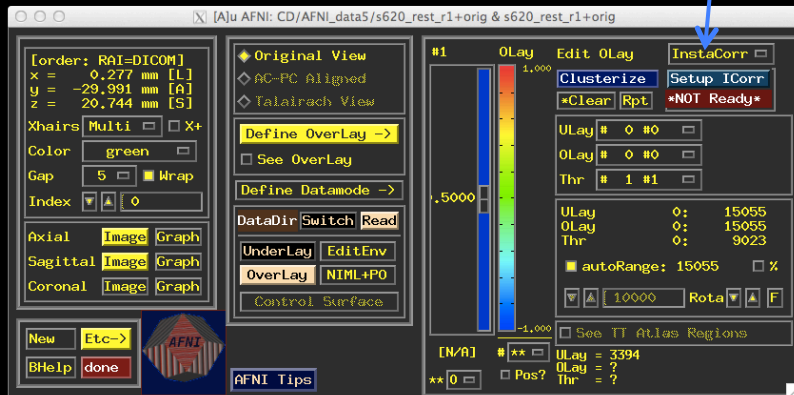
Setup ICorr



InstaCorr, Single-Subject

```
cd AFNI_data5/  
afni &
```

Setup ICorr



InstaCorr, Single-Subject

```
cd AFNI_data5/  
afni &
```

Choose EPI time series
S620_rest_r1

Start at time point 3

Blur by 4mm

[X] [A] AFNI InstaCorr Setup Operations

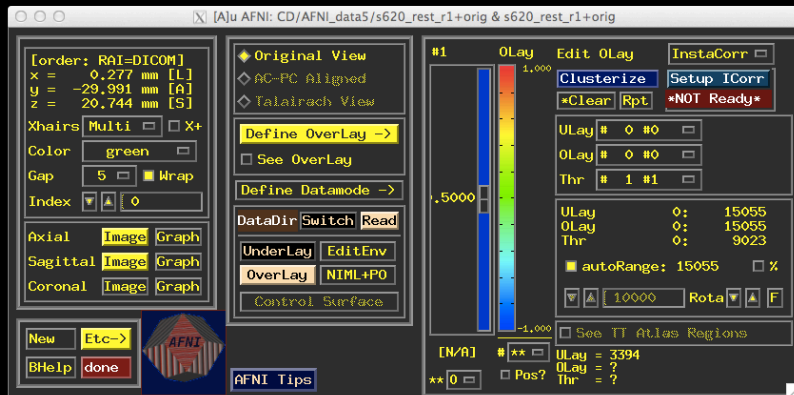
AFNI Plugin: [A] Setup InstaCorr

Quit [A] Setup+Keep [A] Setup+Quit Help

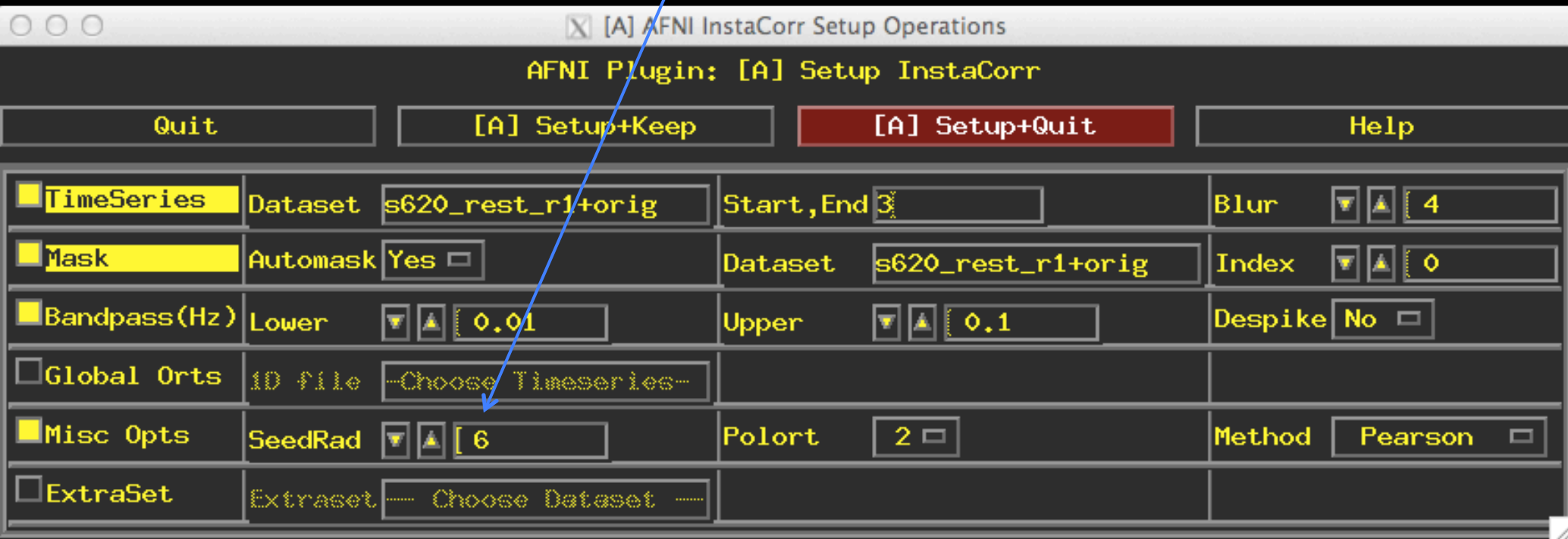
☒ TimeSeries	Dataset	s620_rest_r1+orig	Start,End	3	Blur	▼ ▲	4	
☒ Mask	Automask	Yes ☐	Dataset	s620_rest_r1+orig	Index	▼ ▲	0	
☒ Bandpass(Hz)	Lower	▼ ▲	0.01	Upper	▼ ▲	0.1	Despike	No ☐
☐ Global Orts	ID file	--Choose Timeseries--						
☒ Misc Opts	SeedRad	▼ ▲	6	Polort	2 ☐	Method	Pearson ☐	
☐ ExtraSet	Extrasets	-- Choose Dataset --						

InstaCorr, Single-Subject

```
cd AFNI_data5/  
afni &
```

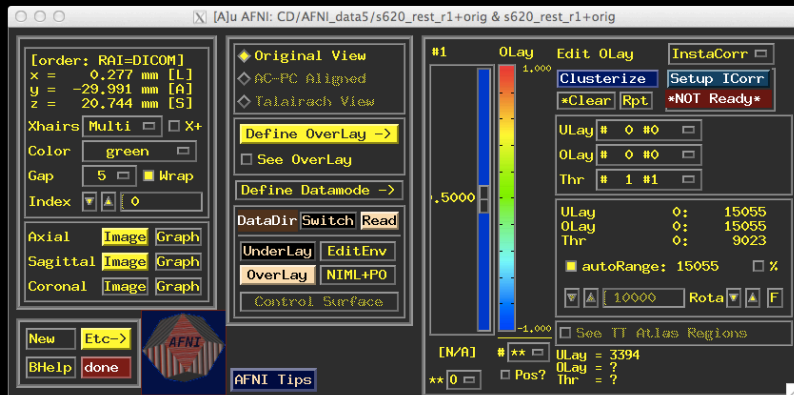


Set seed radius
to 6mm

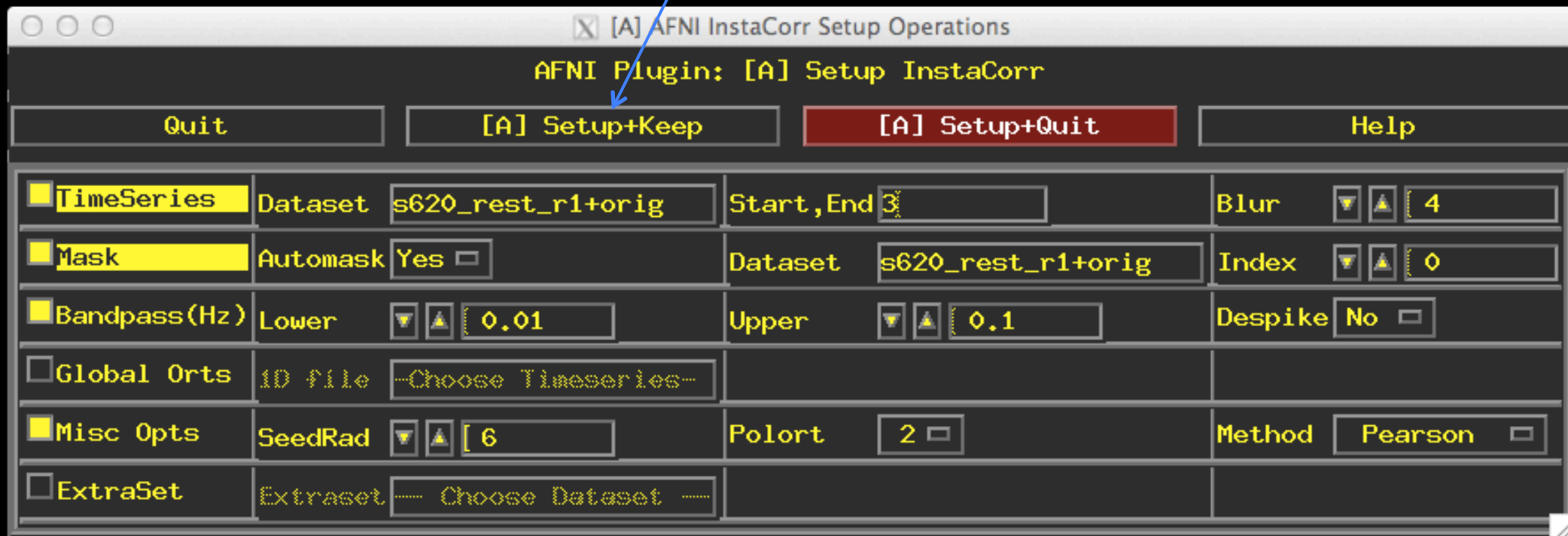


InstaCorr, Single-Subject

```
cd AFNI_data5/  
afni &
```



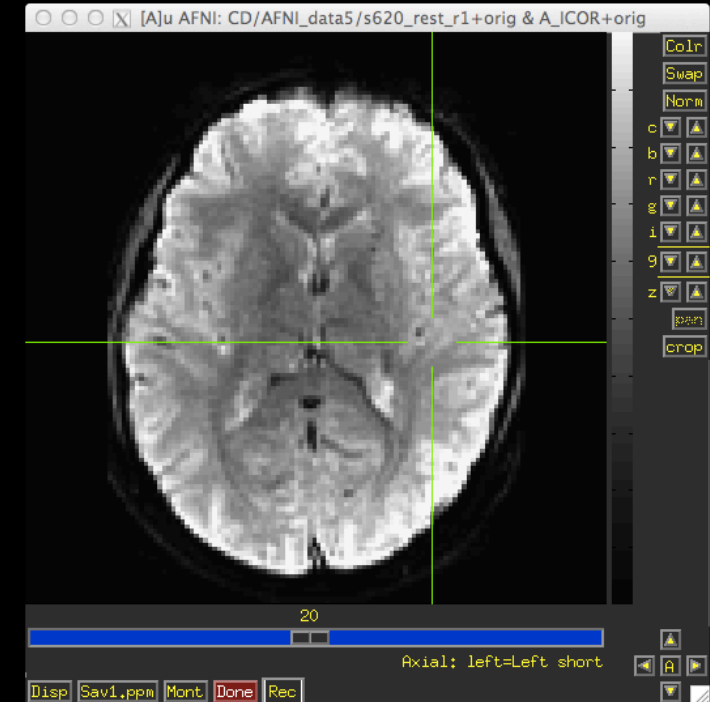
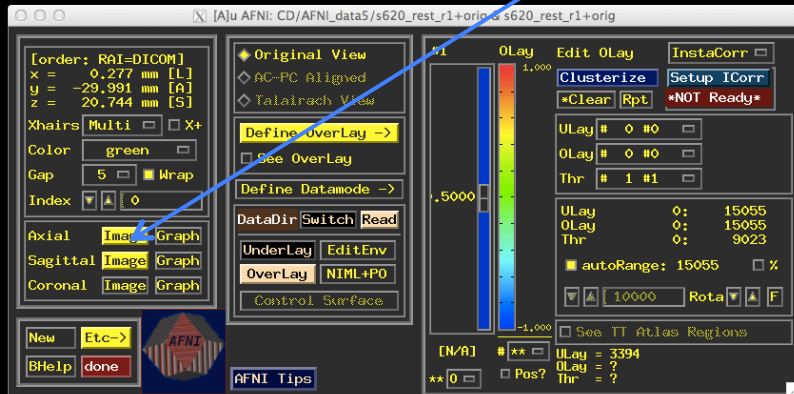
Setup & Keep



InstaCorr, Single-Subject

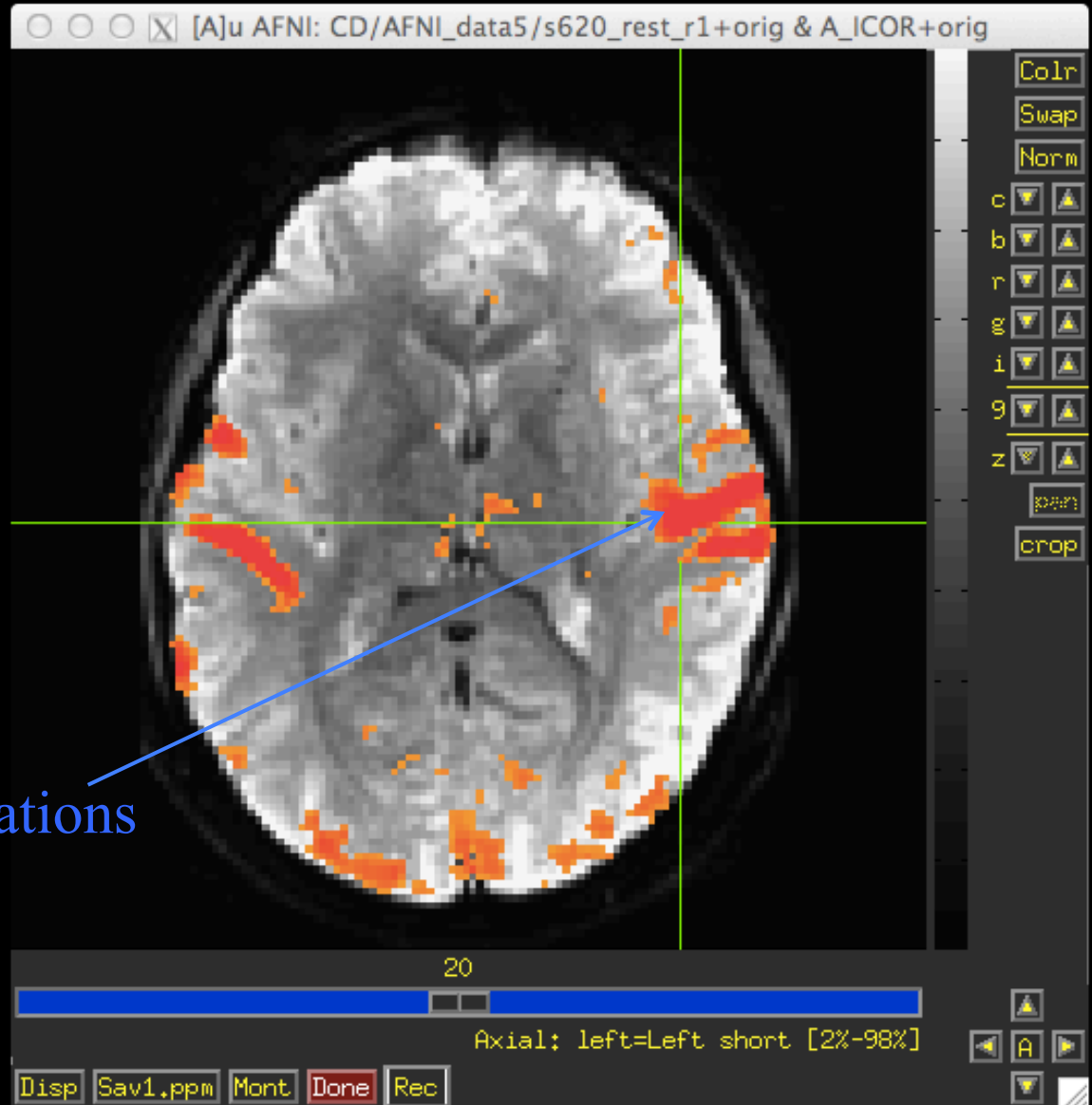
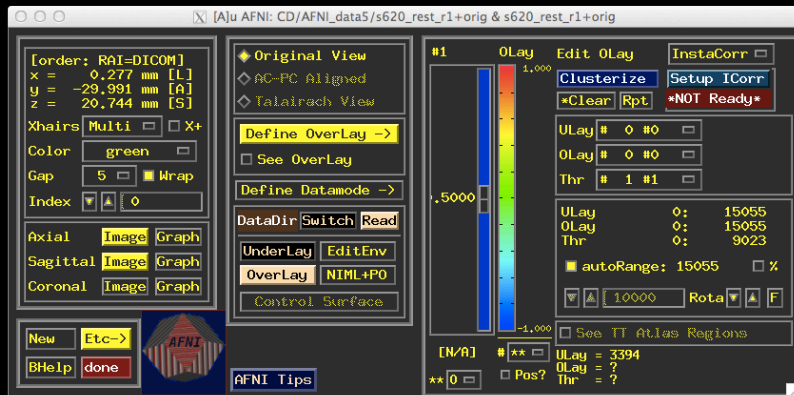
cd AFNI_data5/
afni &

Get an axial image



InstaCorr, Single-Subject

cd AFNI_data5/
afni &



To get **Single-Subject** seed correlations

Click in image

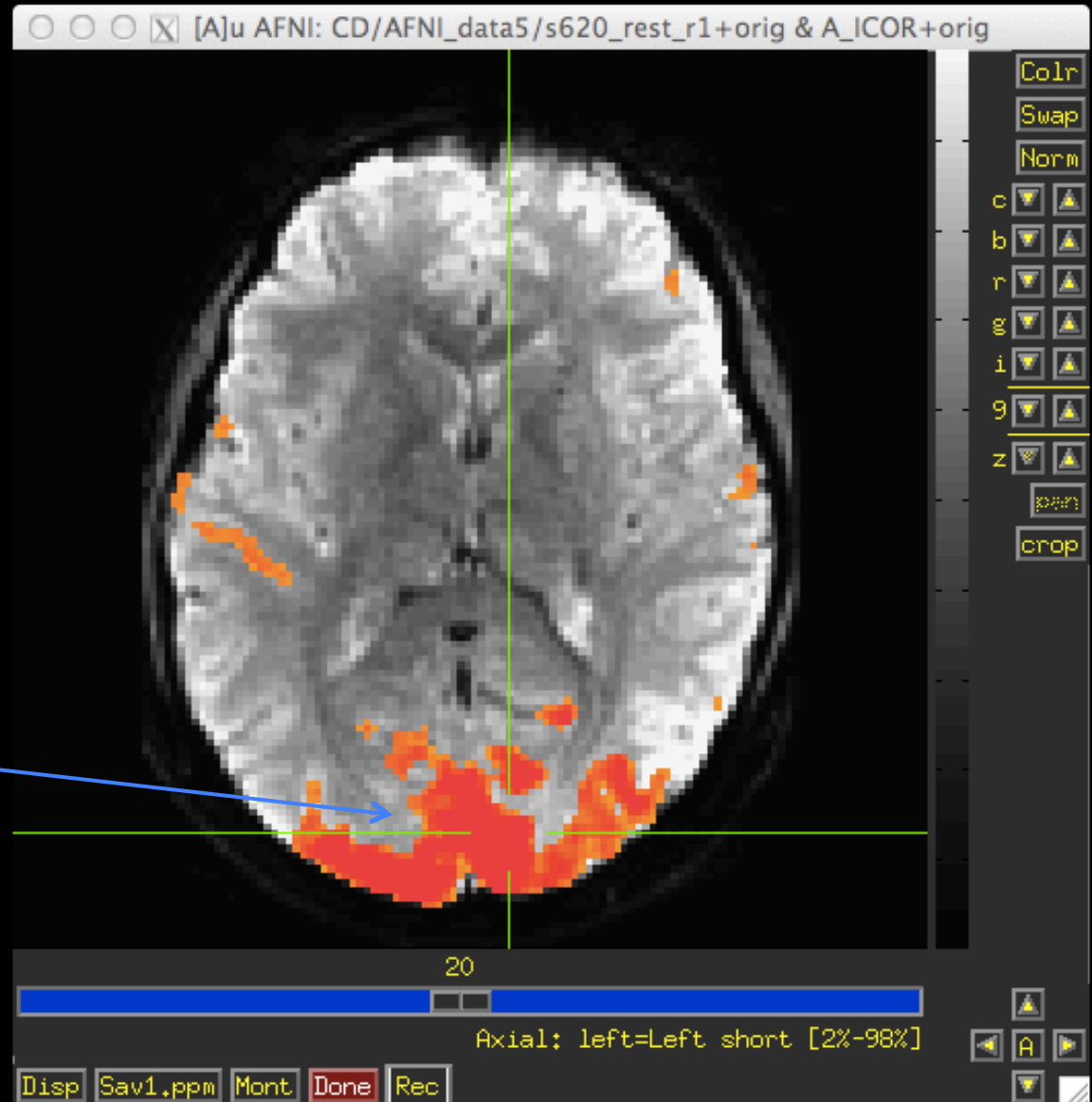
Right-click → InstaCorr Set

Or

Shift+Ctrl+Click & Drag

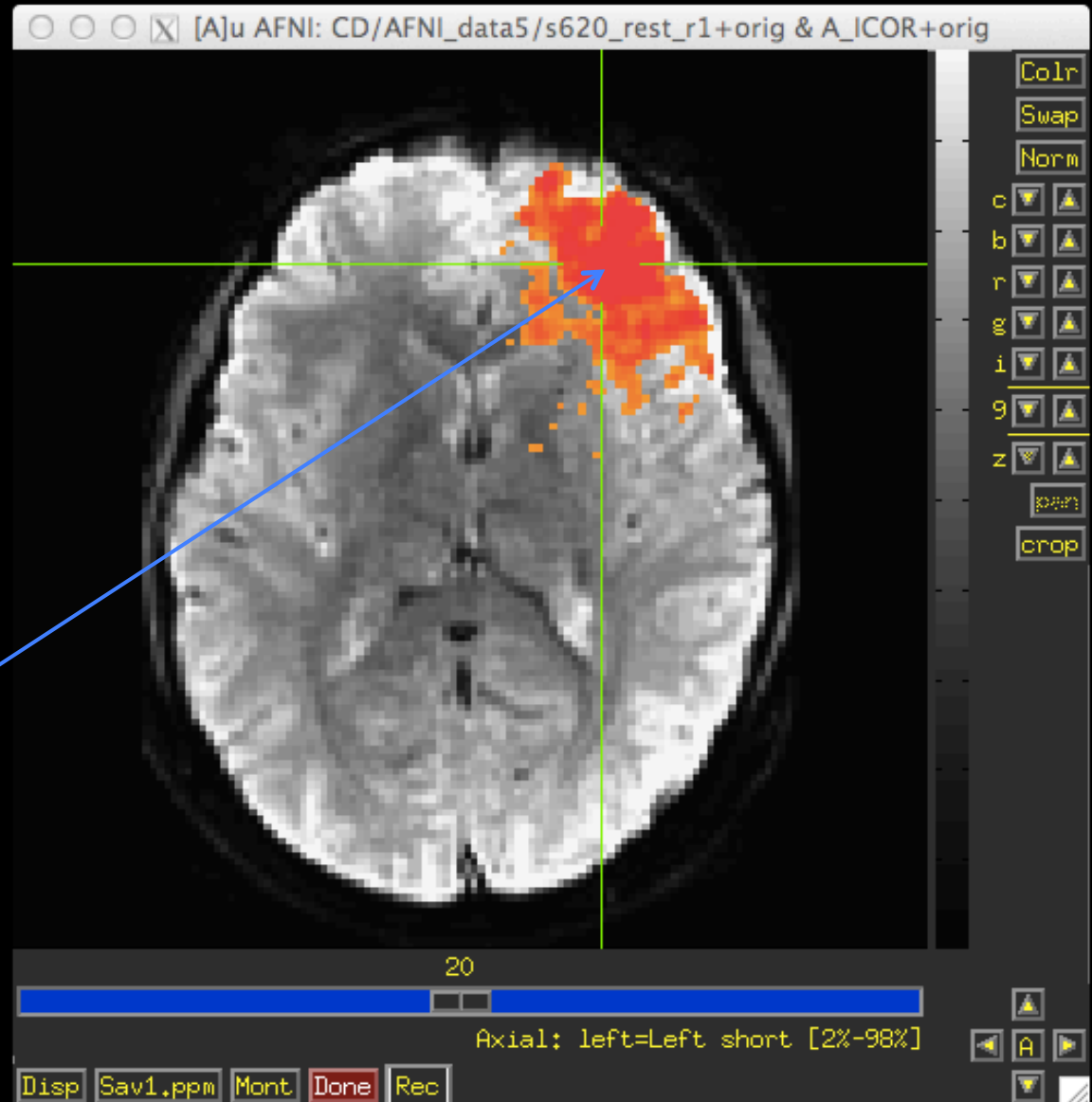
InstaCorr, Single-Subject

Still looking good
with seed in occipital
cortex



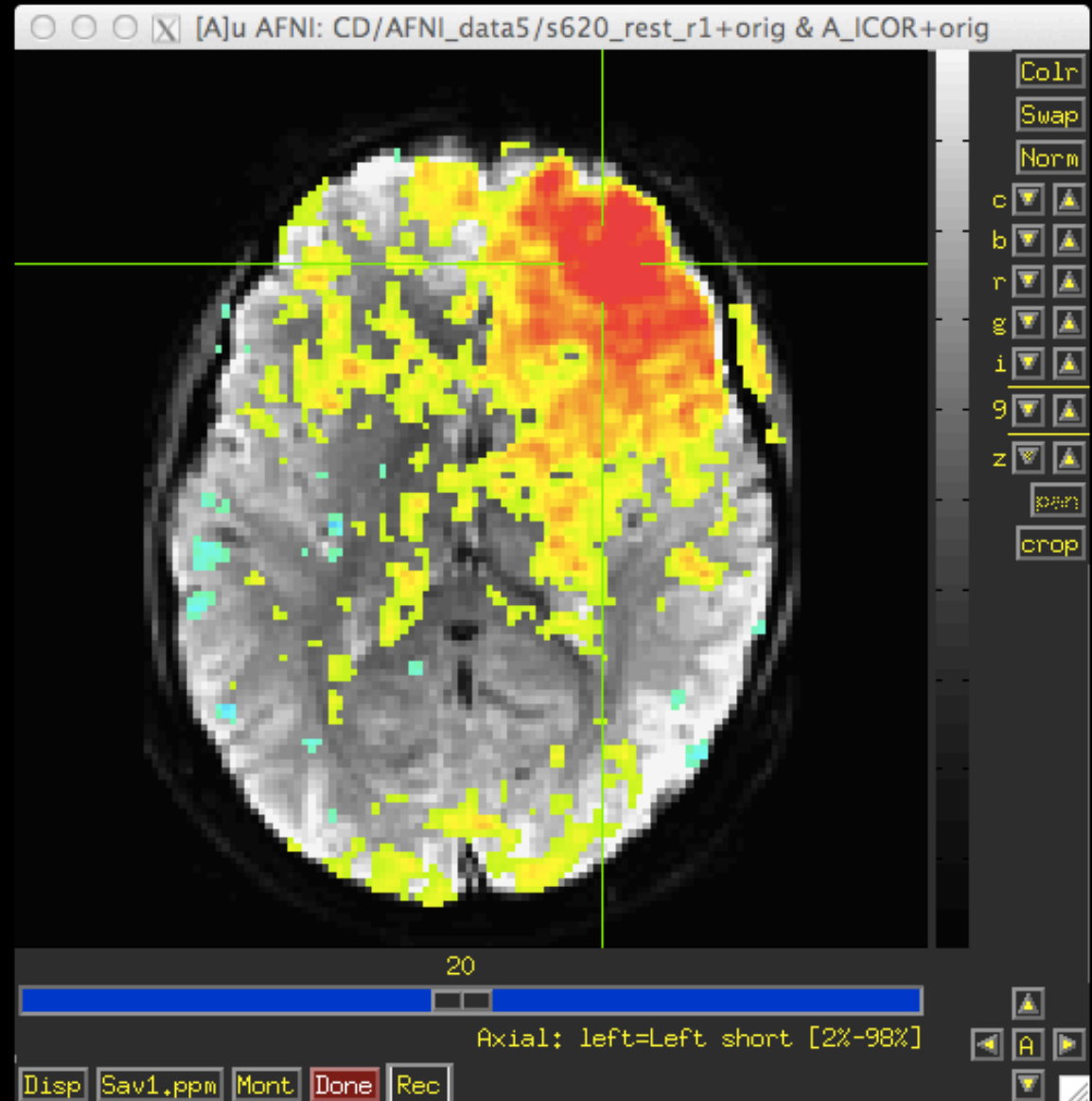
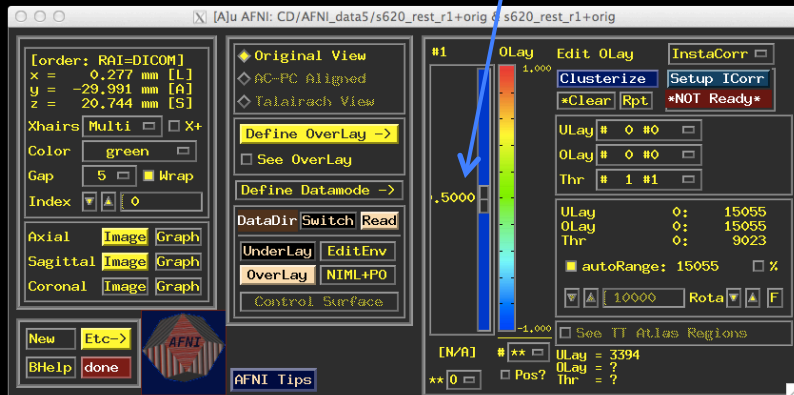
InstaCorr, Single-Subject

NOT looking good
with seed in frontal
lobe

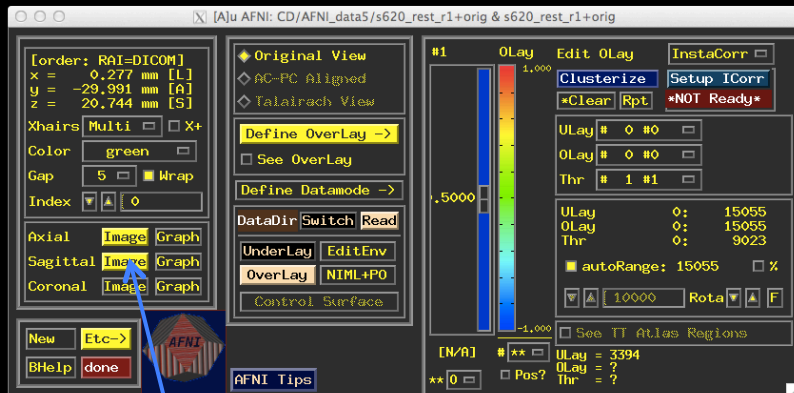


Investigate trouble

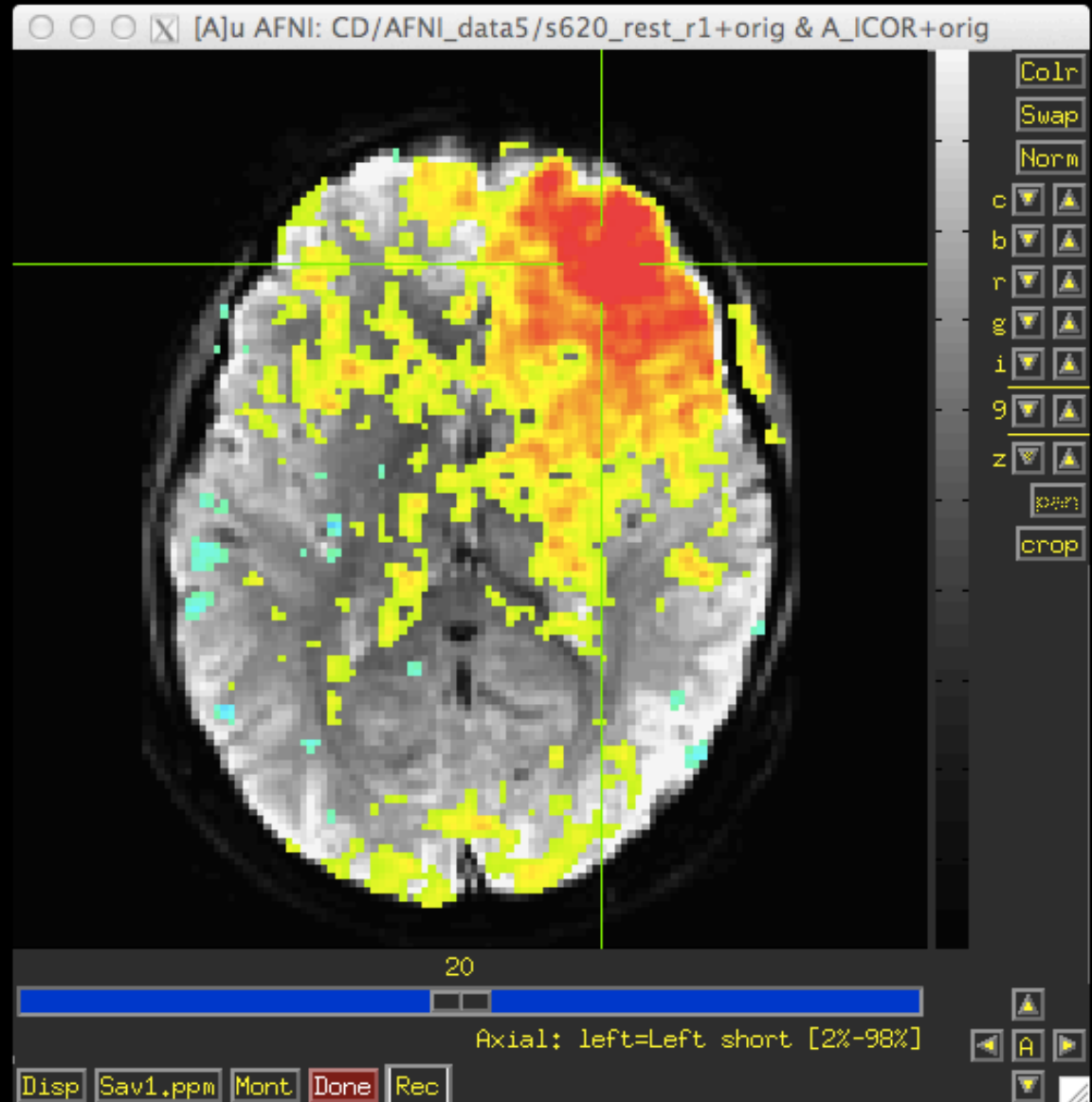
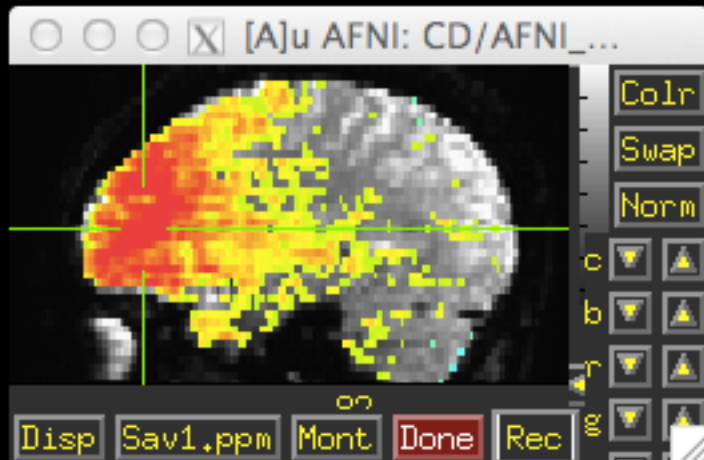
Drop threshold



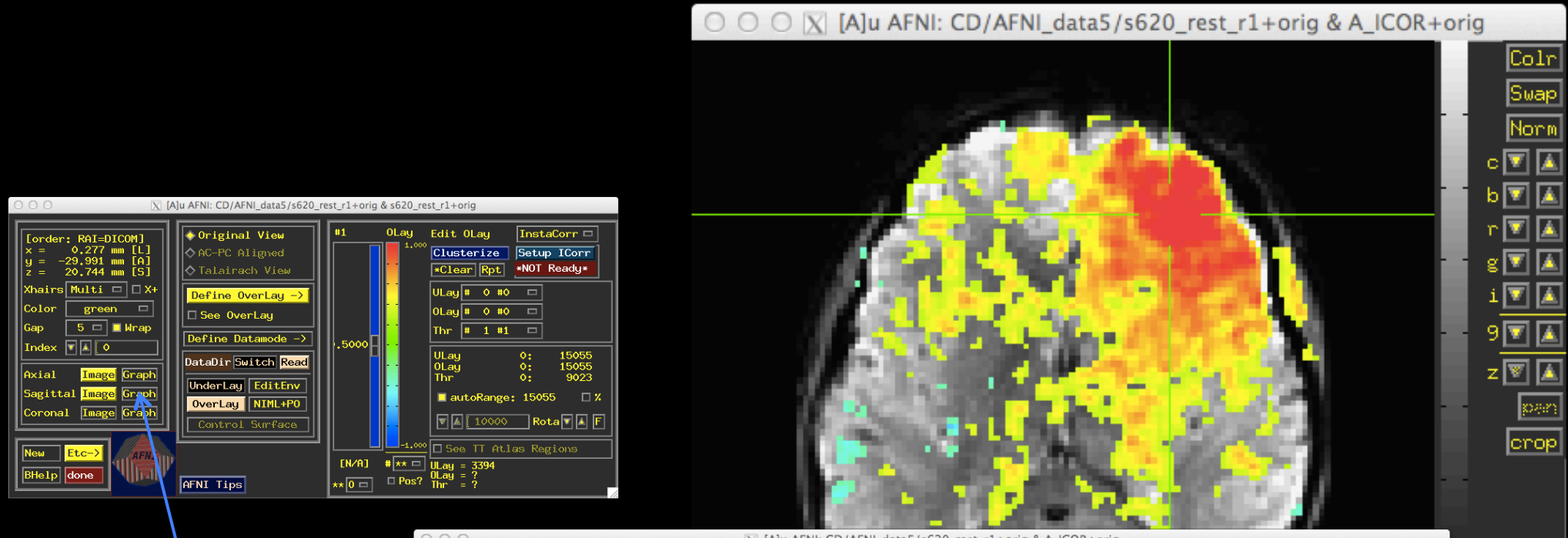
Investigate trouble



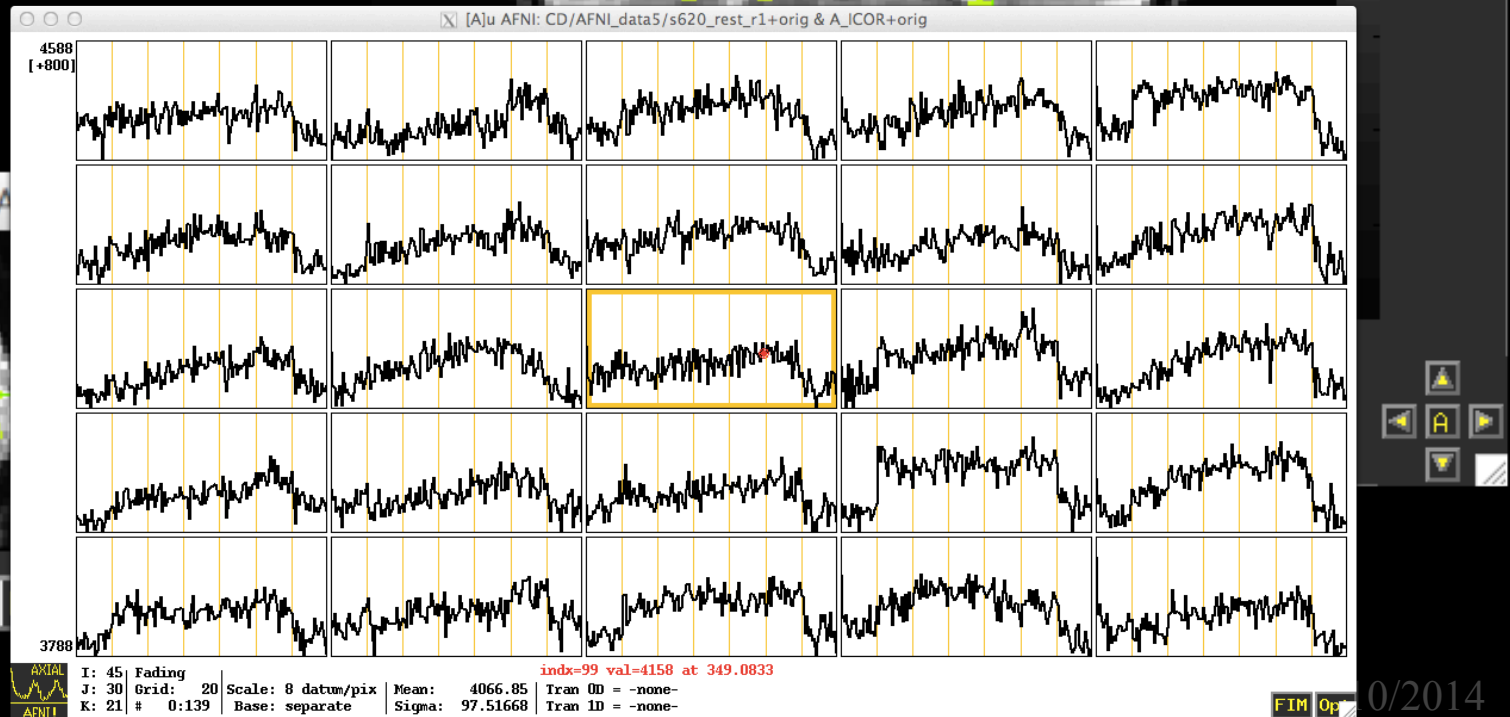
Other planes



Investigate trouble



Graph Timeseries



AFNI in 1 minute

Functional Connectivity

InstaCorr, 3dTcorrMap, 3dAutoTcorrelate

SEM, PPI, SVAR

3dReHo, 3dNetCorr, 3dRSFC

part of FATCAT, by Paul Taylor

Live demos follow.

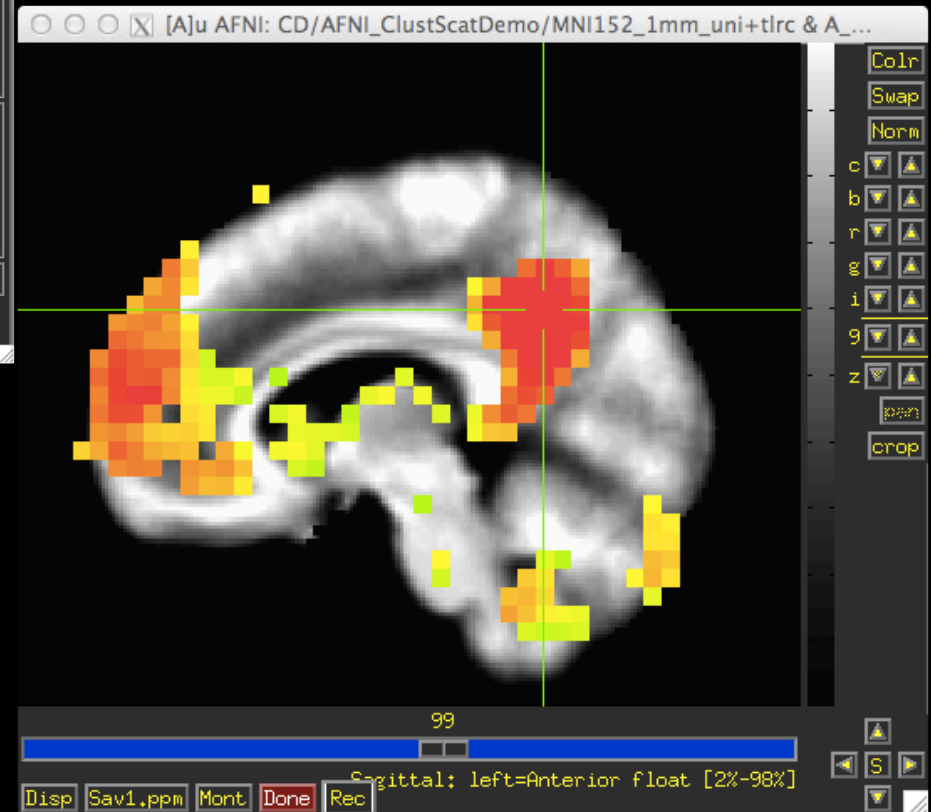
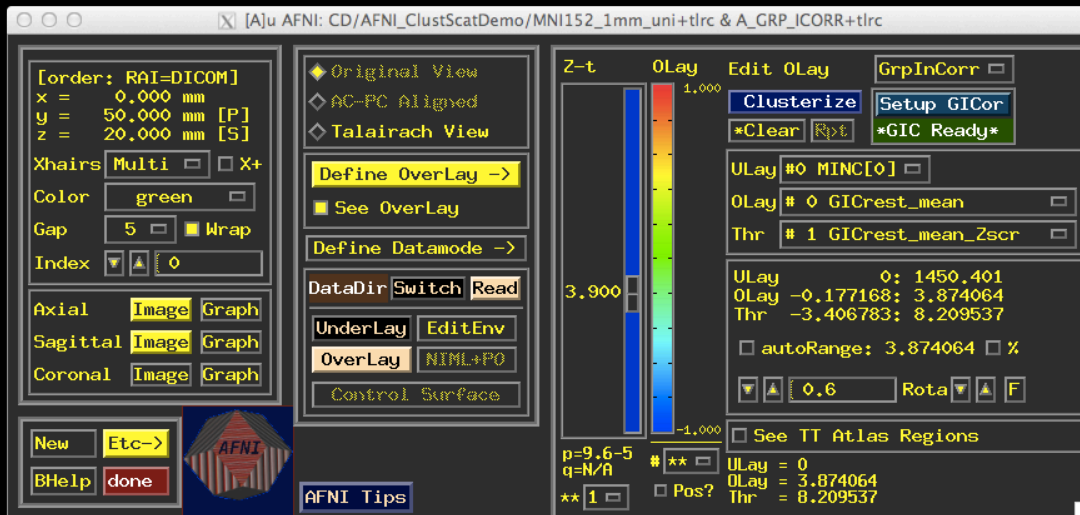
Run *@Install_InstaCorr_Demo* to get data and demo scripts.

Just run the script and follow the instructions.

See also http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/afni_handouts/instastuff.pdf
Slide 6 onwards.

InstaCorr, Group-Level

```
cd ~/AFNI_ClustScatDemo/  
tcsch @Run_GIC
```



InstaCorr, Group-Level

```
cd ~/AFNI_ClustScatDemo/  
tcsch @Run_GIC
```

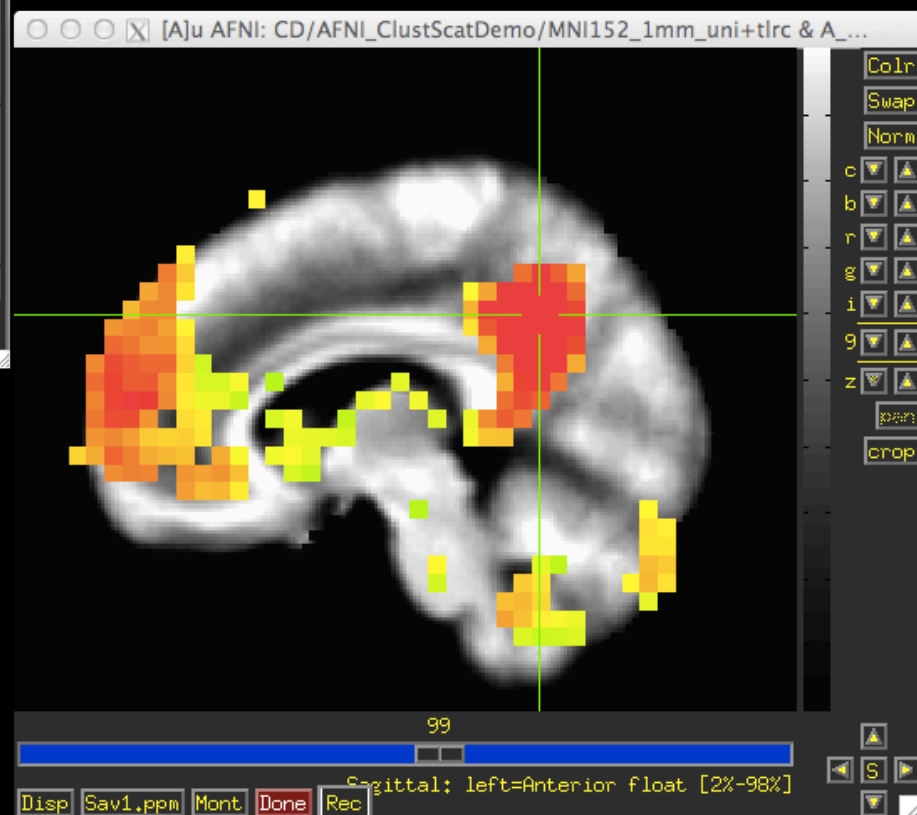
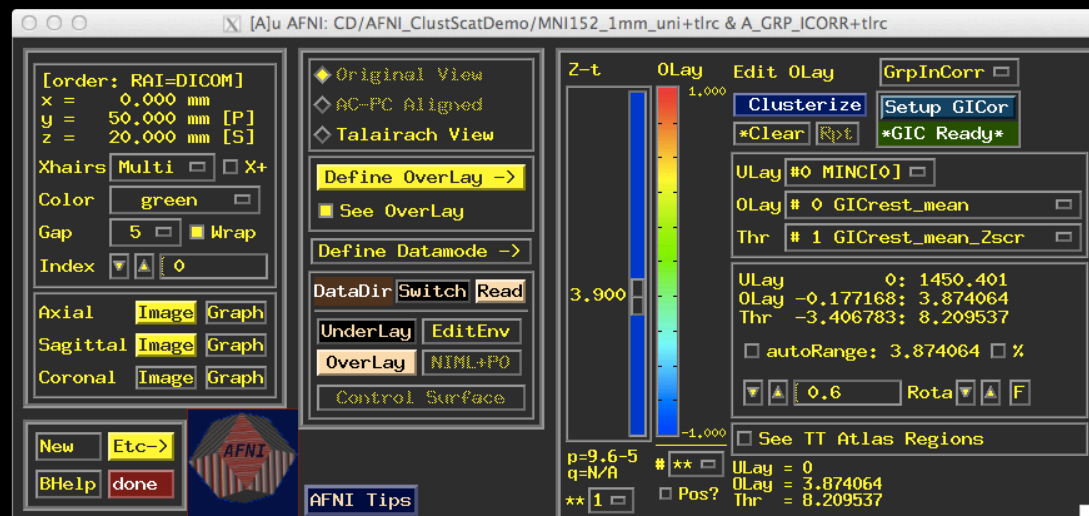
To get **GROUP** seed correlation results

Click in image

Right-click → InstaCorr Set

Or

Shift+Ctrl+Click & Drag



InstaCorr, Group-Level

```
cd ~/AFNI_ClustScatDemo/  
tcsh @Run_GIC
```

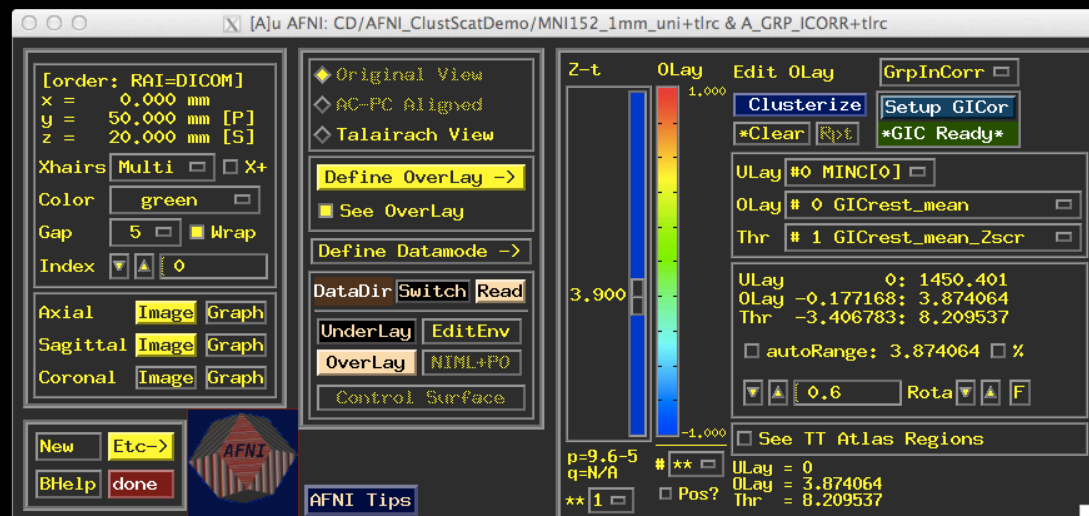
To get **GROUP** seed correlation results

Click in image

Right-click → InstaCorr Set

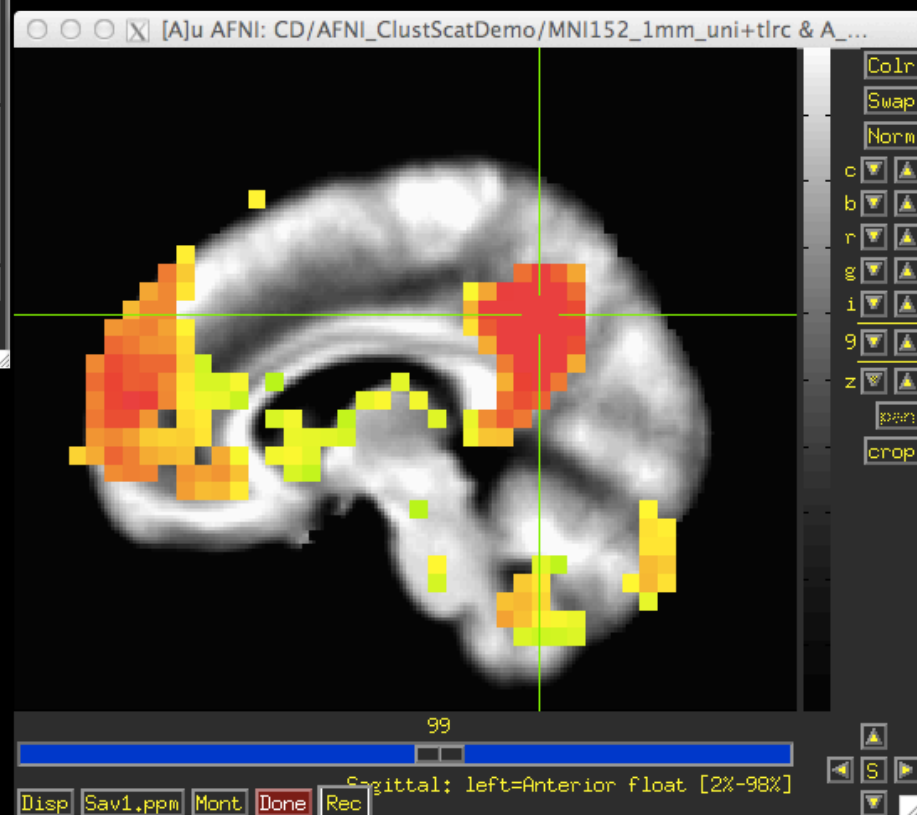
Or

Shift+Ctrl+Click & Drag



With each click you are performing one-/two-/paired-T-Tests, with covariates if desired.

Can also be run in batch mode



AFNI in 1 minute

Advanced group level analysis tools Chen Gang

Group Analysis Program List

- **3dttest++** (one-sample, two-sample and paired t) + covariates (voxel-wise)
- **3dMEMA** (R package for mixed-effects analysis, t-tests plus covariates)
- **3ddot** (correlation between two sets)
- **3dANOVA** (one-way between-subject)
- **3dANOVA2** (one-way within-subject, 2-way between-subjects)
- **3dANOVA3** (2-way within-subject and mixed, 3-way between-subjects)
- **3dMVM** (ANOVA and ANCOVA)
- **3dLME** (R package for sophisticated cases)

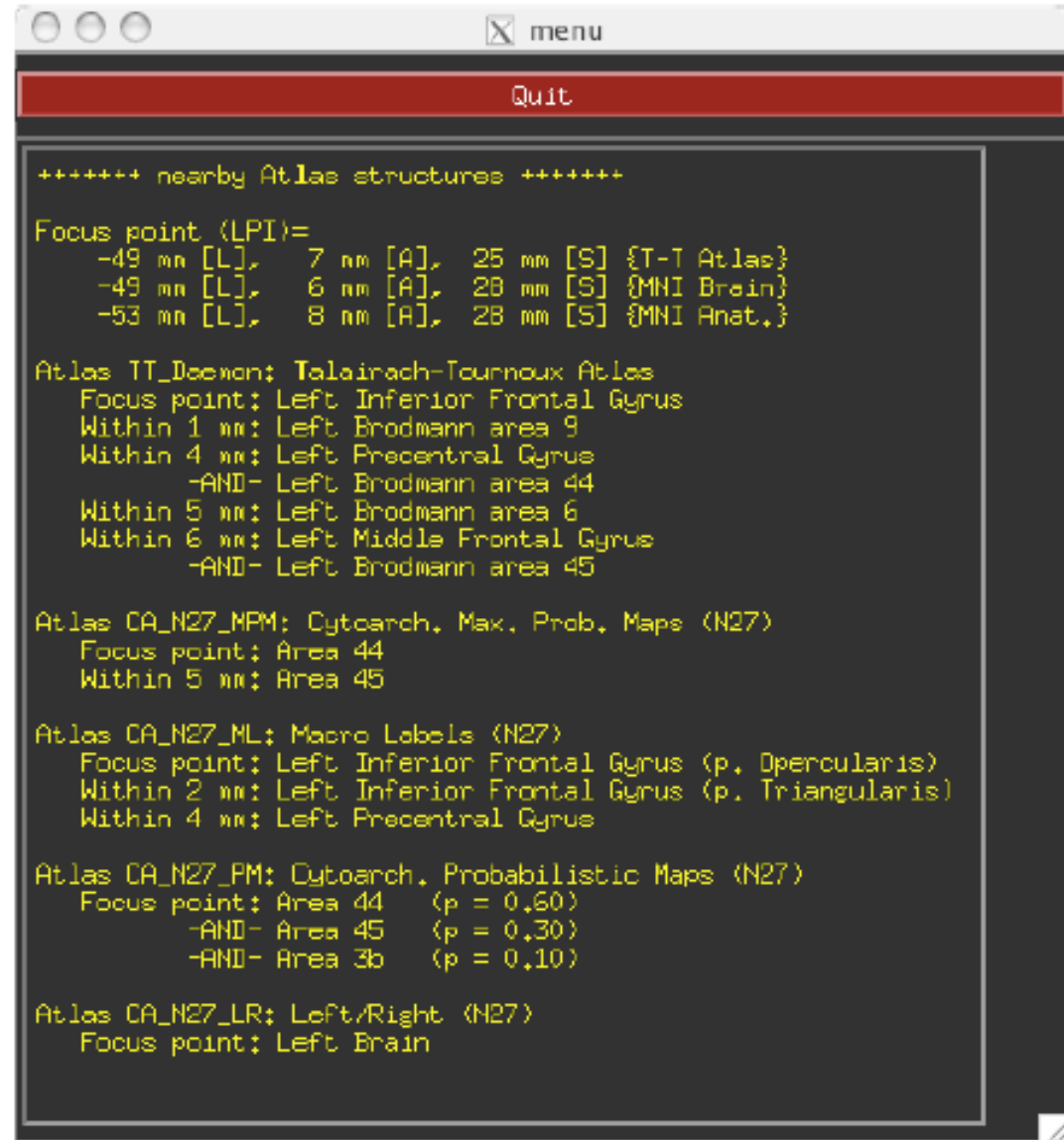
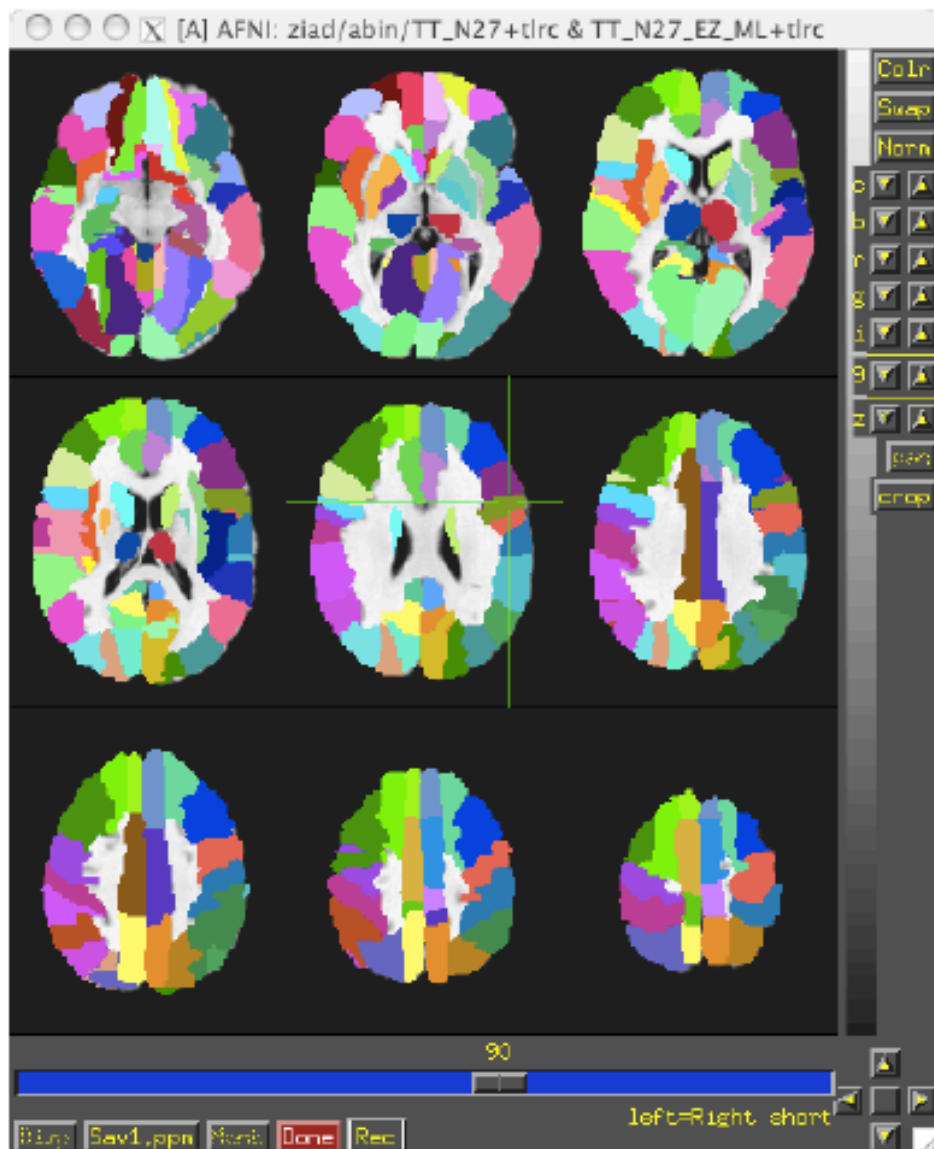
See http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/afni_handouts/GroupAna.pdf
and http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/afni_handouts/GroupAna_HO.pdf

ZSS 04/10/2014

AFNI in 1 minute

Atlas functions

Daniel Glen



See http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/afni_handouts/afni11_roi.pdf

AFNI in 1 minute

Anatomical Connectivity: FATCAT

FATCAT: Functional And Tractographic Connectivity Analysis Toolbox (Taylor & Saad, 2013), now available in AFNI with demo data.



*picture from google search, not from/of either author

Run **@Install_FATCAT_DEMO** to get data and demo scripts

Courtesy of P. Taylor
AFNI bootcamp 12/13

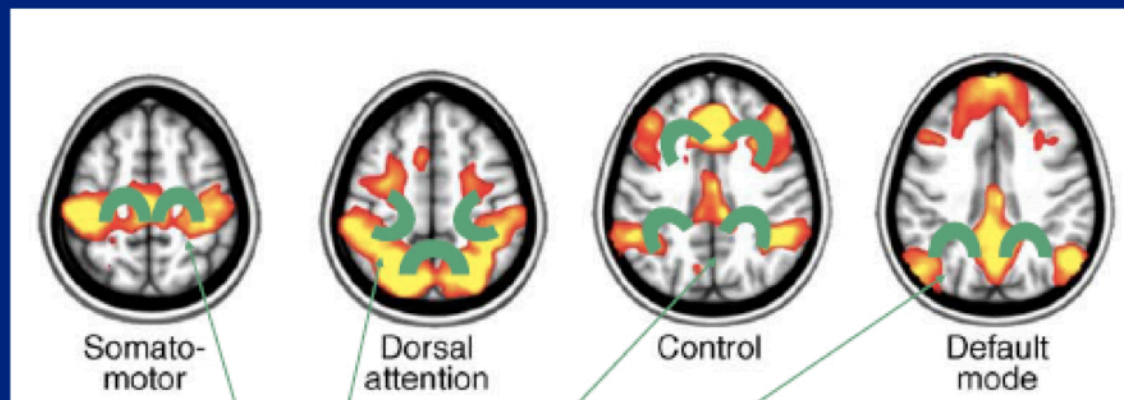
See http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/afni_handouts/FATCAT.pdf

ZSS 04/10/2014

Structure + Function

Simple example:

GM ROIs
network:



Raichle (2010, TiCS)

Associated WM ROIs

Courtesy of P. Taylor
AFNI bootcamp 12/13

Our goal for tractography->

*estimate likely/probable locations of WM associated with GM,
and relate ROI quantities with functional/GM properties*

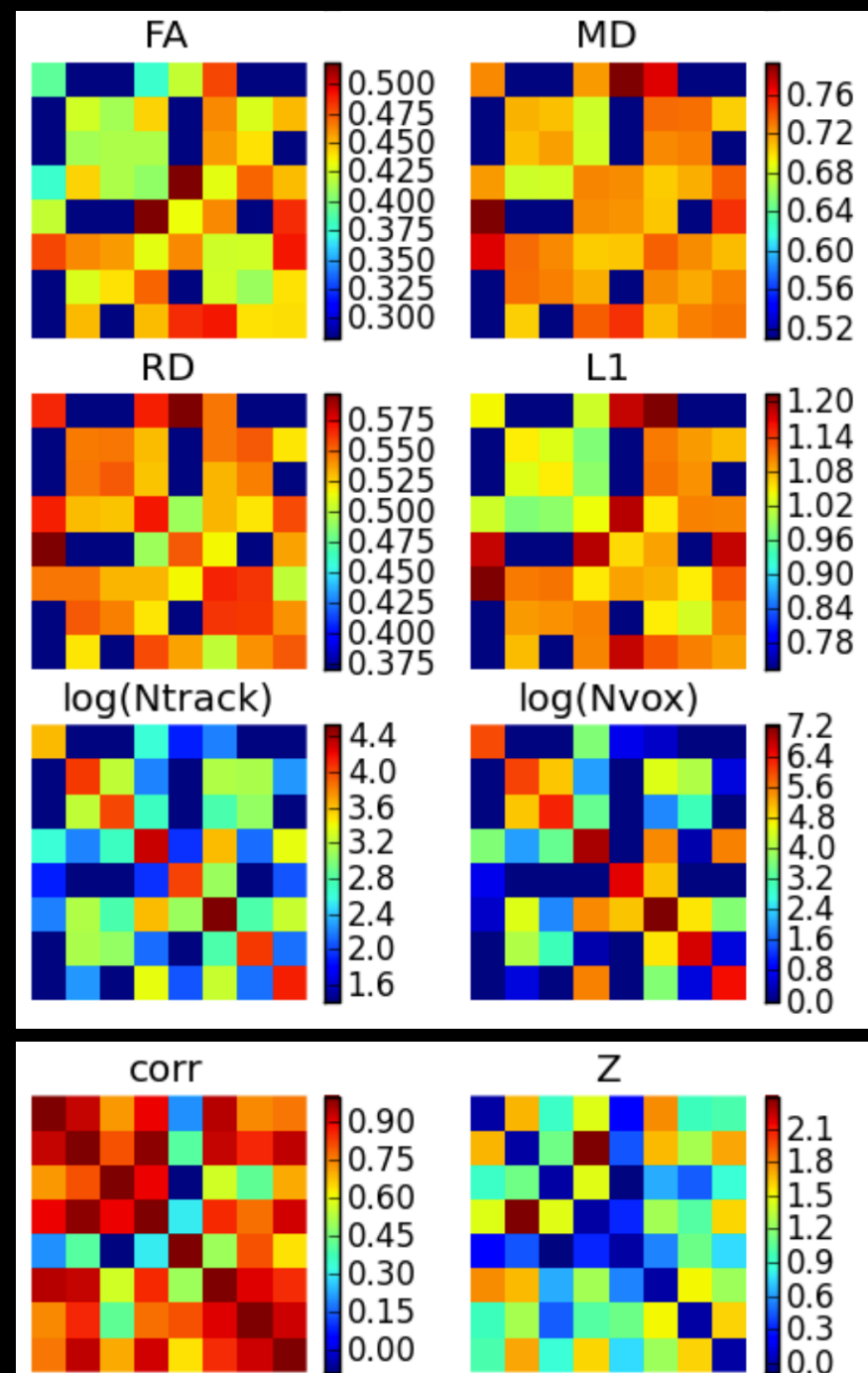
WM (ROI) Quantities

For connected pairs of GM ROIs in a network, have an average WM property (or can map to T1, PD...) →

Have produced sets of localized structural/anatomical quantities for comparison with functional values or behavioral scores, genetics, etc.

Can use for group or individual comparisons/regressions.

3dNetCorr: correlation matrices
Of average time series in ROIs
(e.g., uninflated GM ROIs from 3dROIMaker)

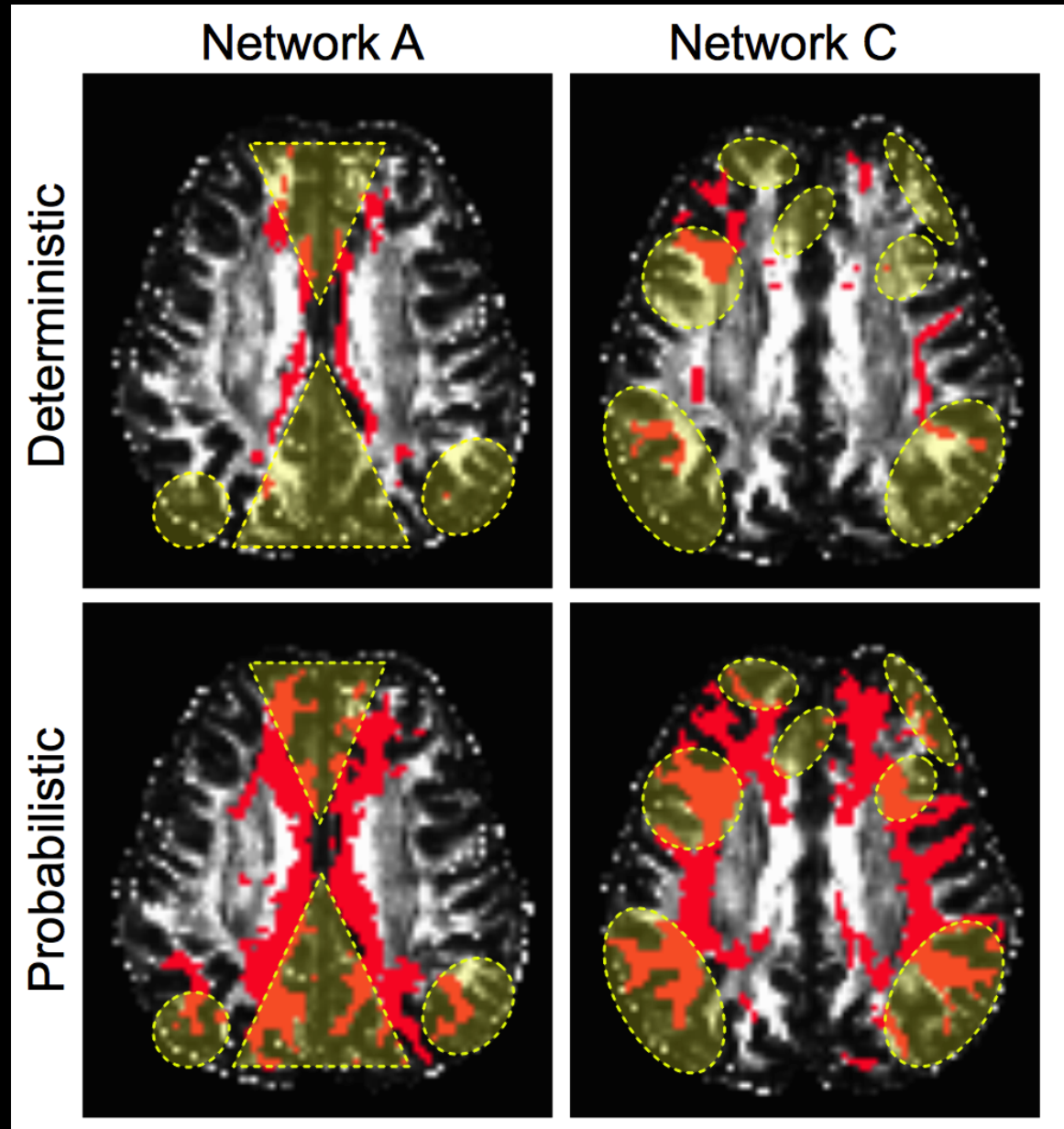


Courtesy of P. Taylor
AFNI bootcamp 12/13

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Deterministic vs Probabilistic

- + NB: coverage and connectivity differences between tractography types
- + Deterministic can be useful for initial investigations, but is more susceptible to noise/errors and truncation

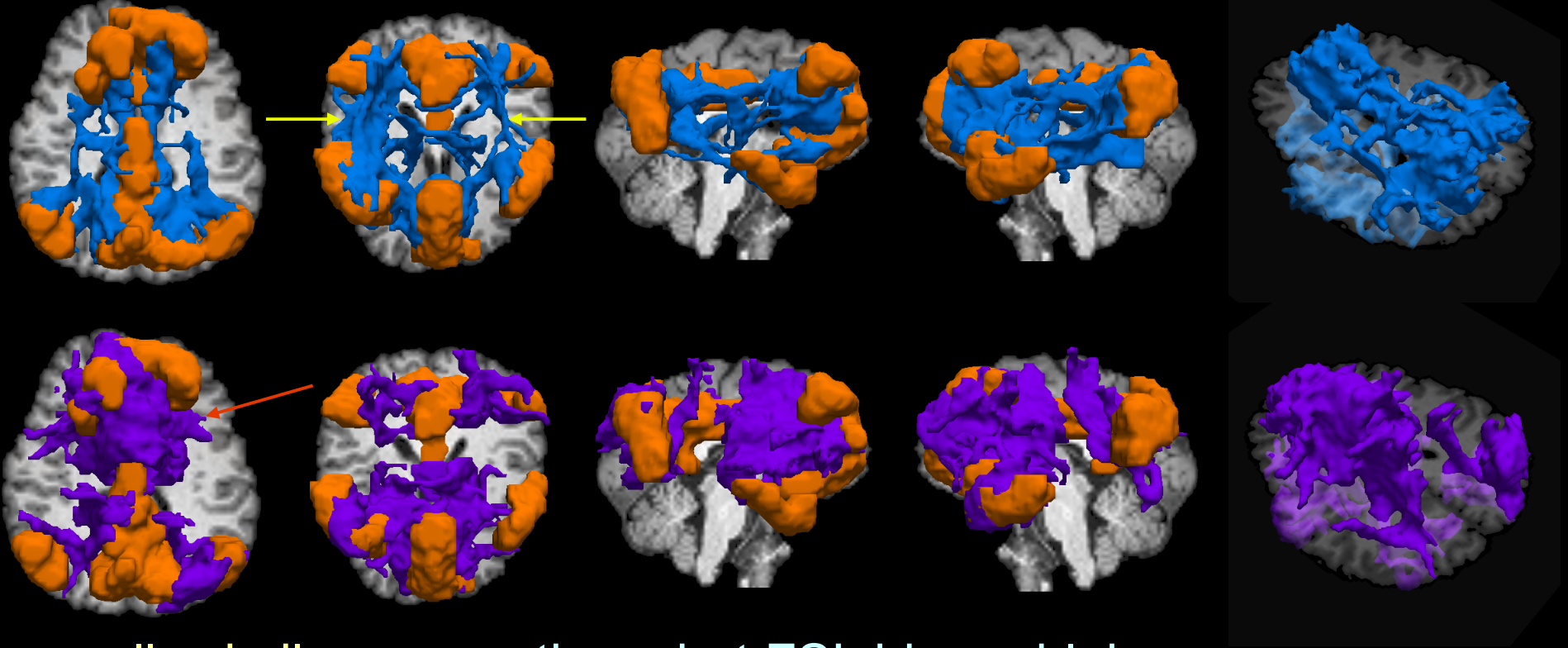


Courtesy of P. Taylor
AFNI bootcamp 12/13

3dProbTrackID: Probabilistic tractography

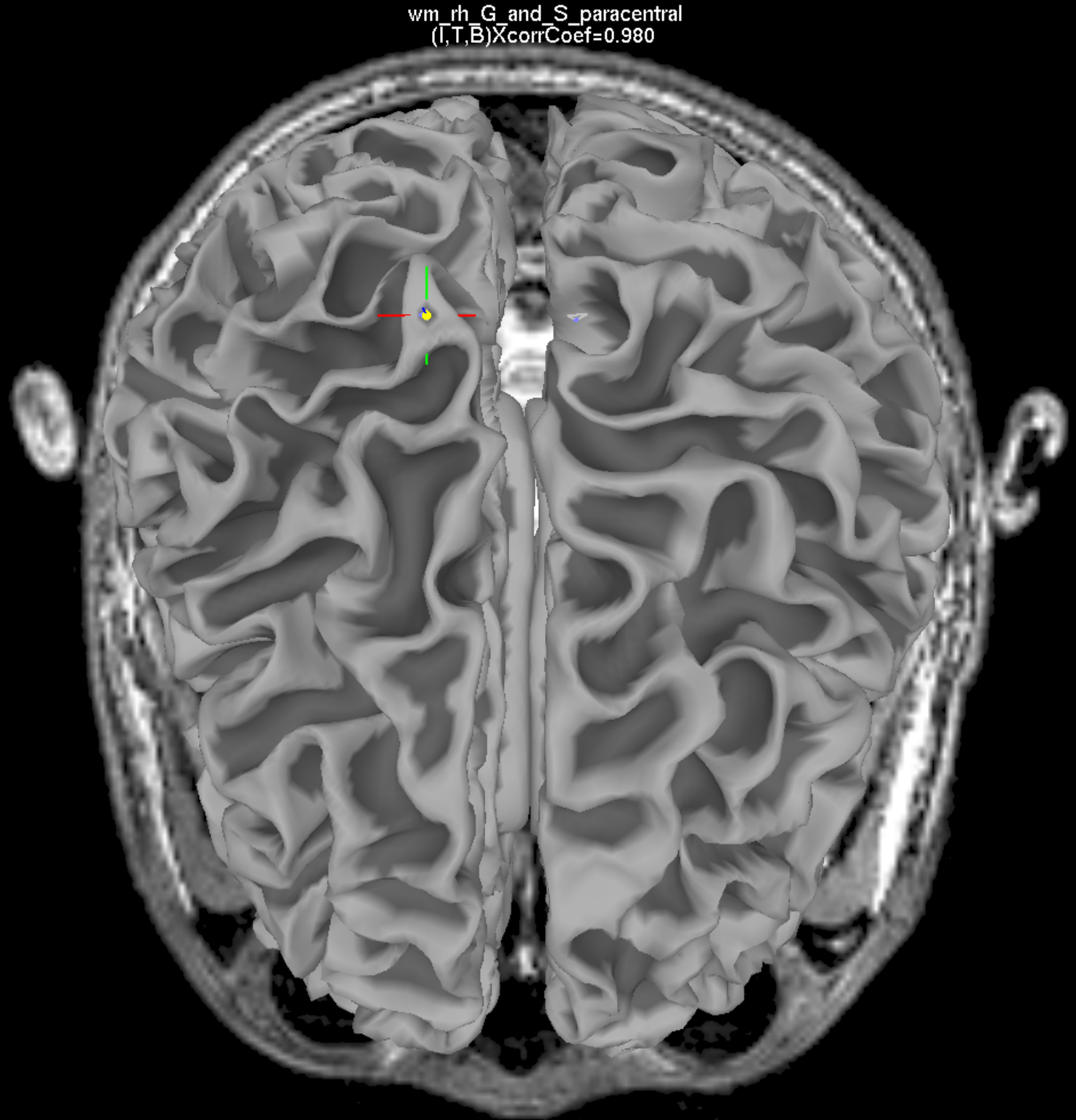
- + compare with existing algorithms:
 - purple: FSL-probtrackX (and FSL-bedpostX for uncertainty)
 - same parameters: $FA > 0.2$, max angle 60deg, 5000 Monte Carlo iterations; 1 tract direction/voxel

A



- + generally similar connections, but FSL bigger blobs
- + FSL took several hours for uncertainty, and then >24 hours for tracking this single network (and had to run 4 for this study)
- + 3dDWUncert took 7min; 3dProbTrackID took 25mins total for 4 netw.

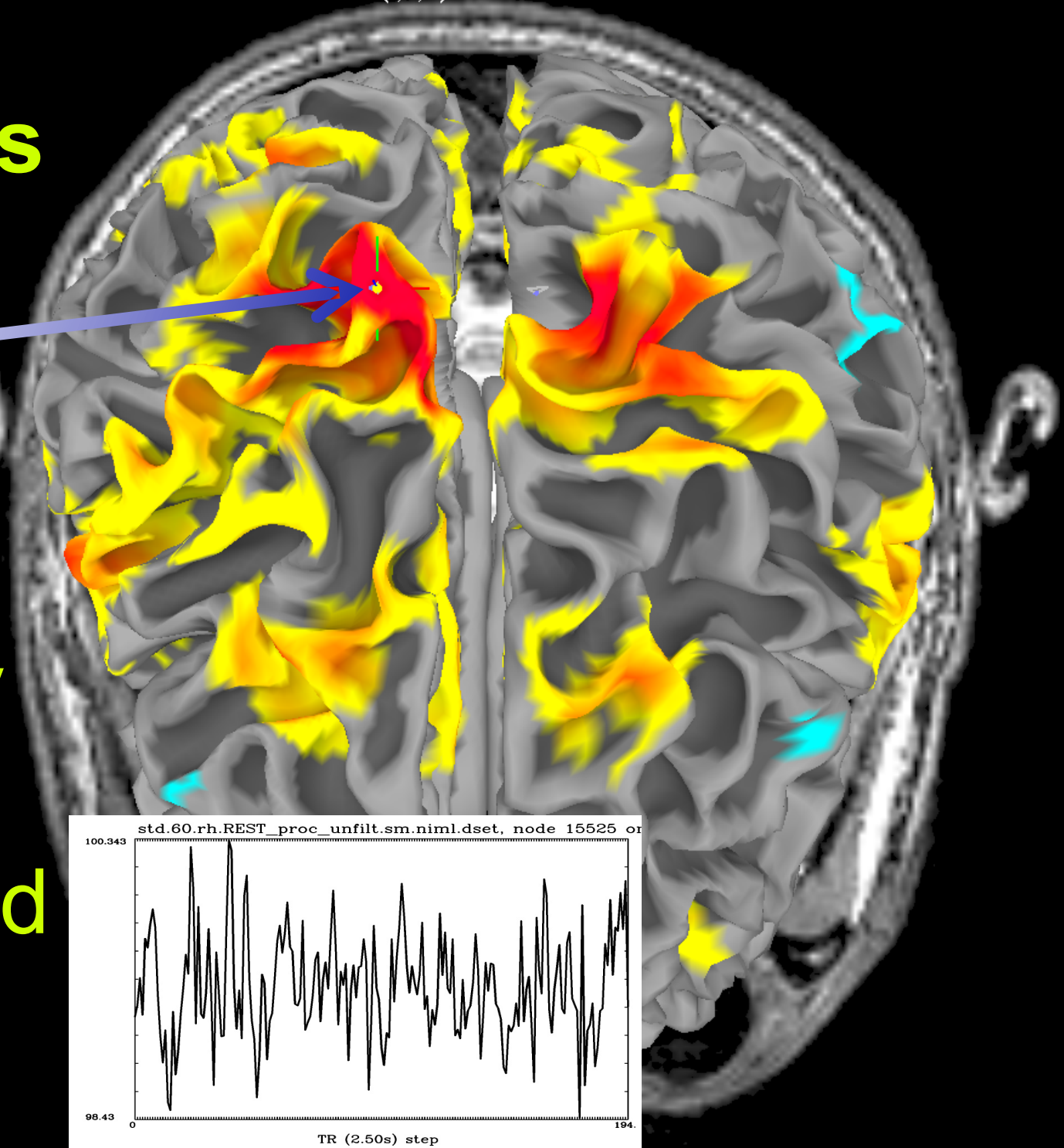
Naked brain surface



RS-FMRI correlations from seed voxel

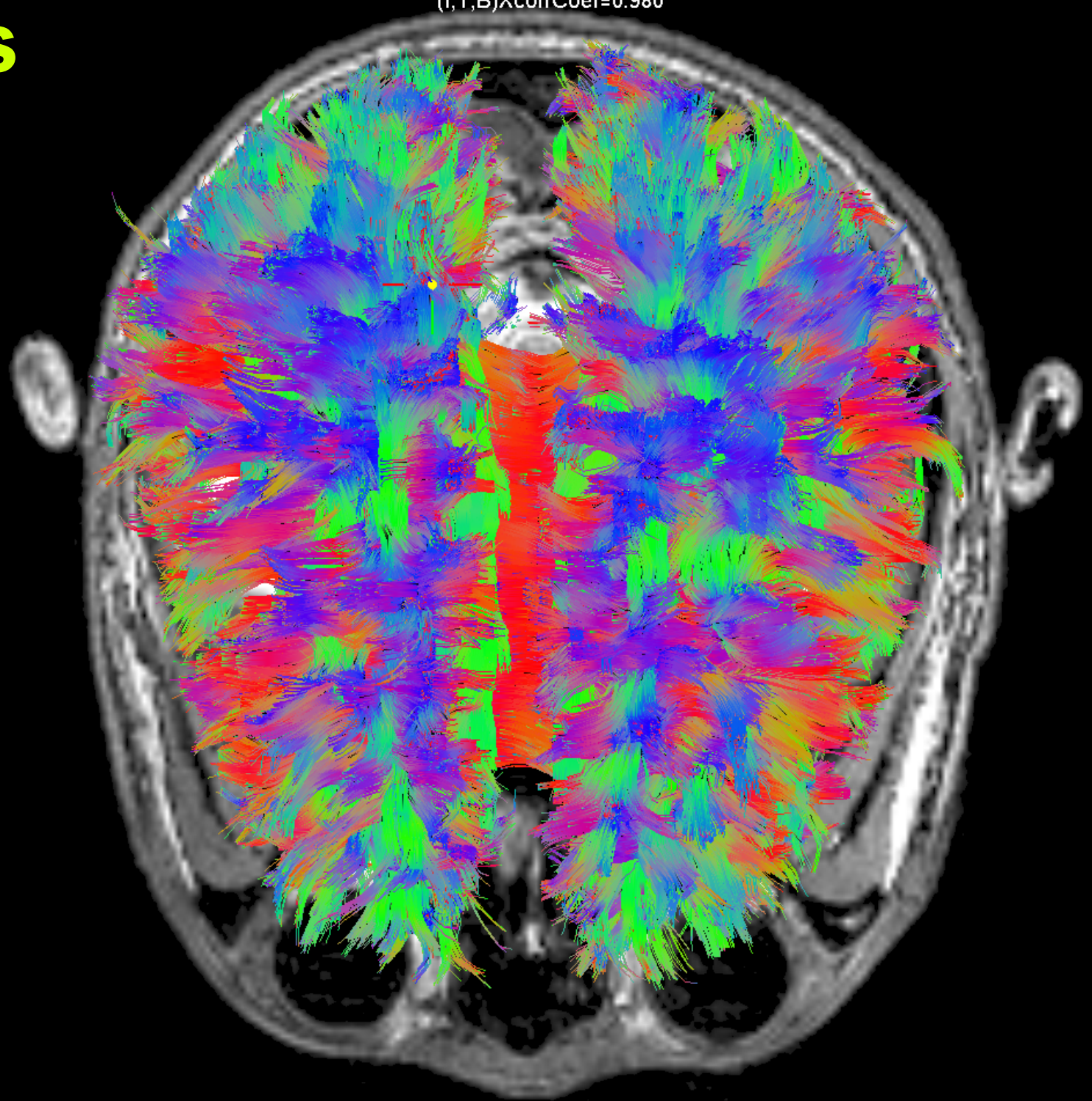
computed
interactively
with mouse
click on seed

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



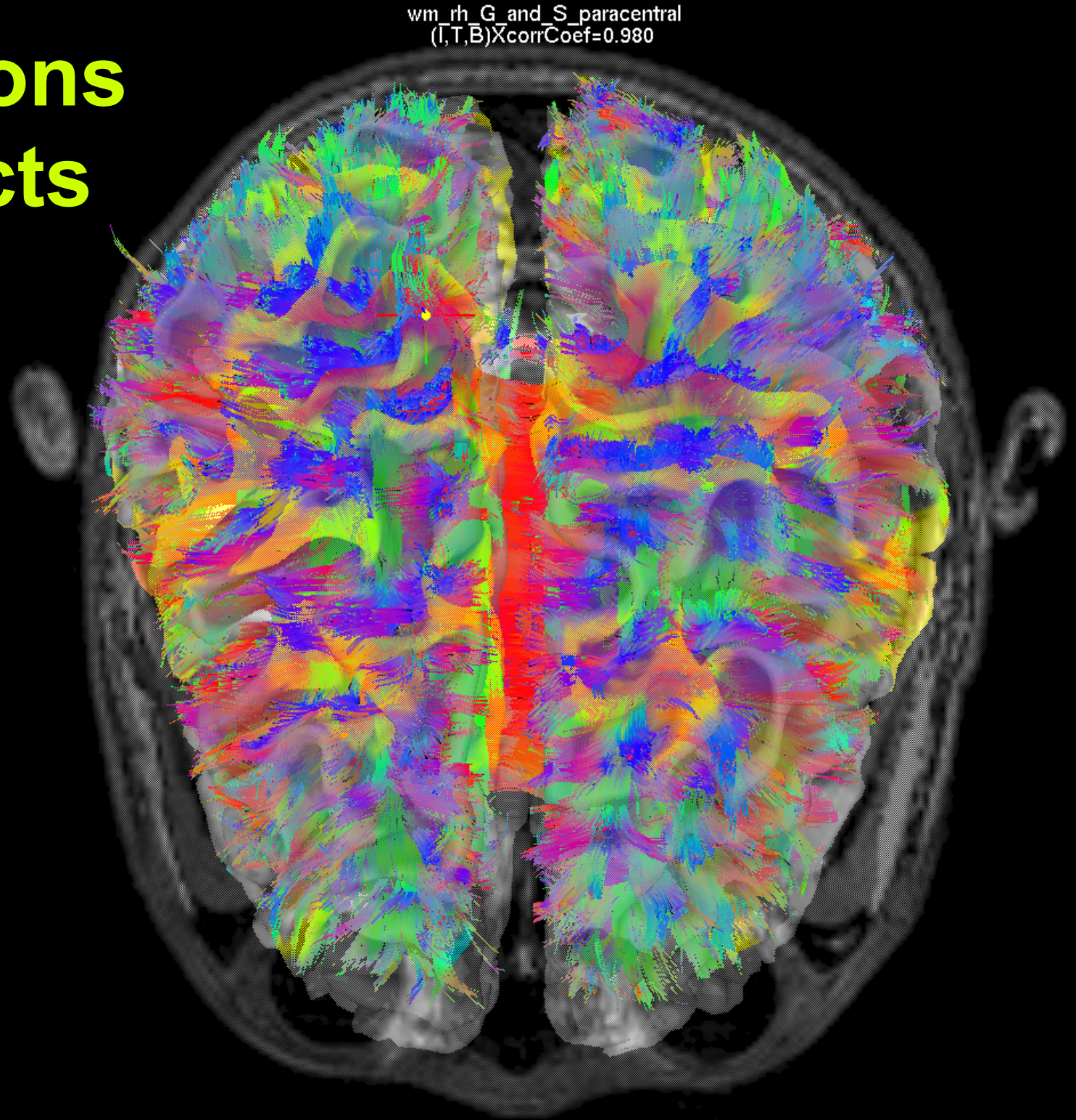
DTI tracts
[brain is
hidden]

**Just too
much to
take in!**



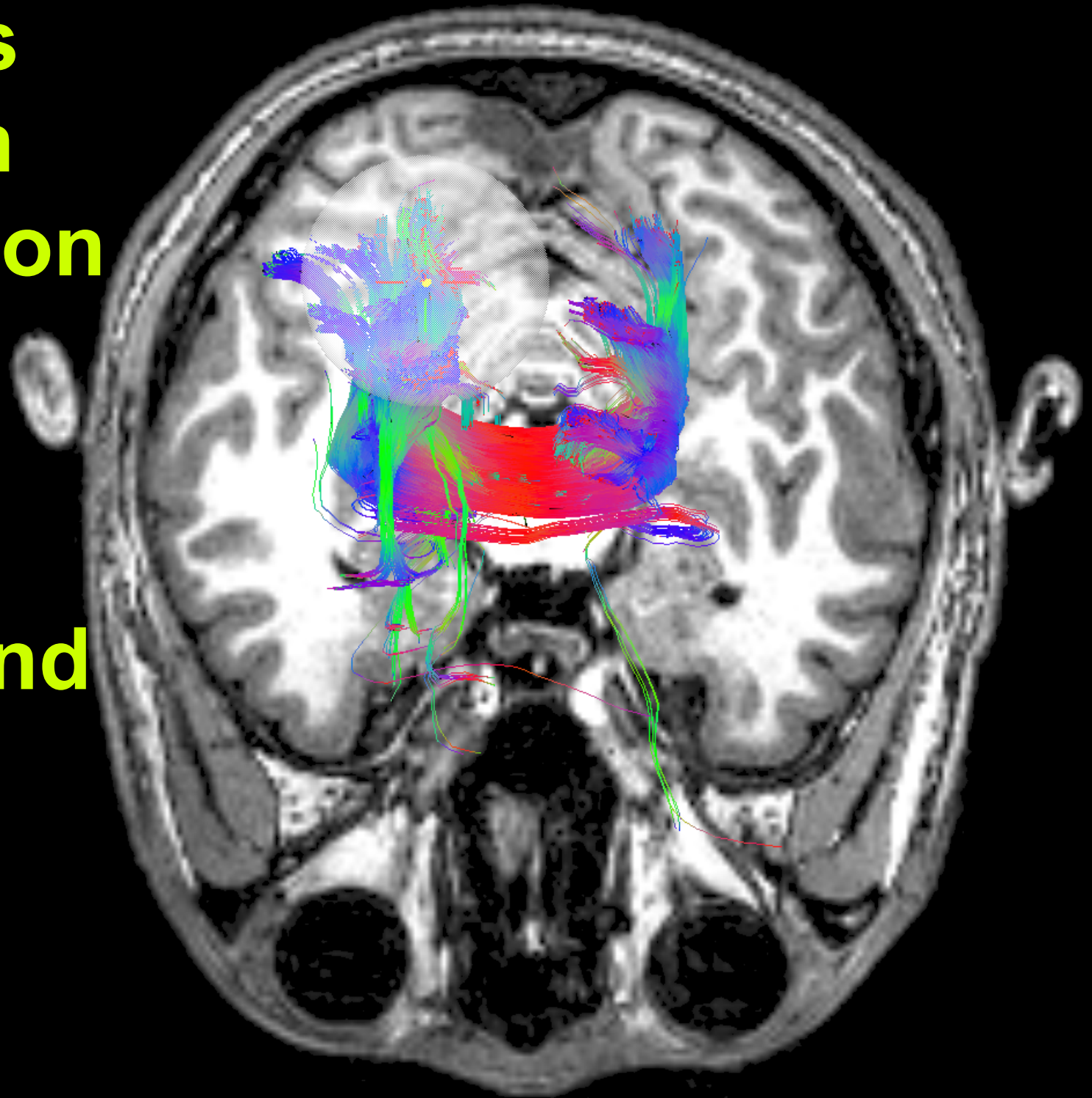
**Correlations
+ DTI tracts
+ Brain**

***Way too
much to
take in!***



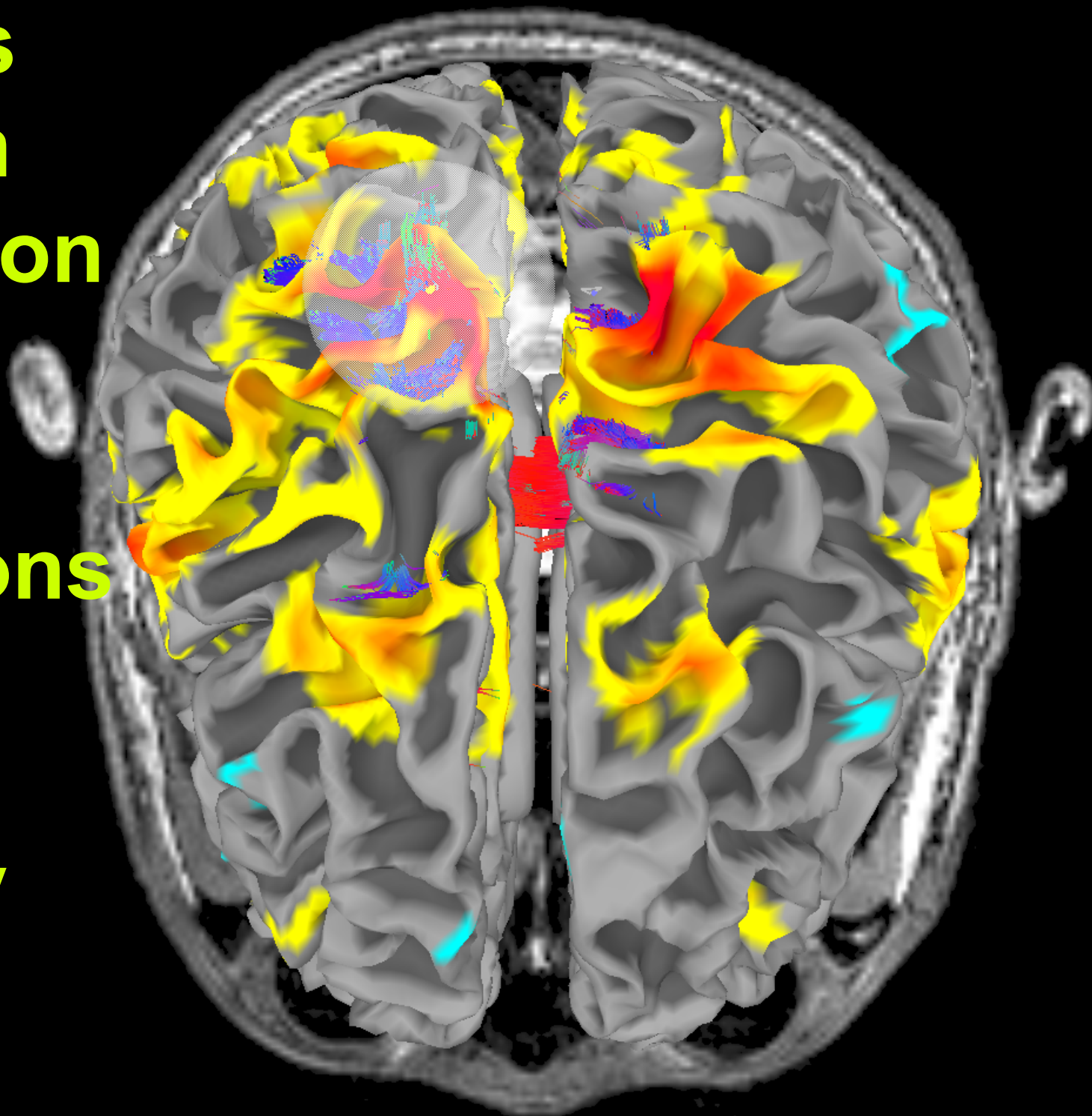
**DTI tracts
only from
seed region**

***Much
easier to
understand***



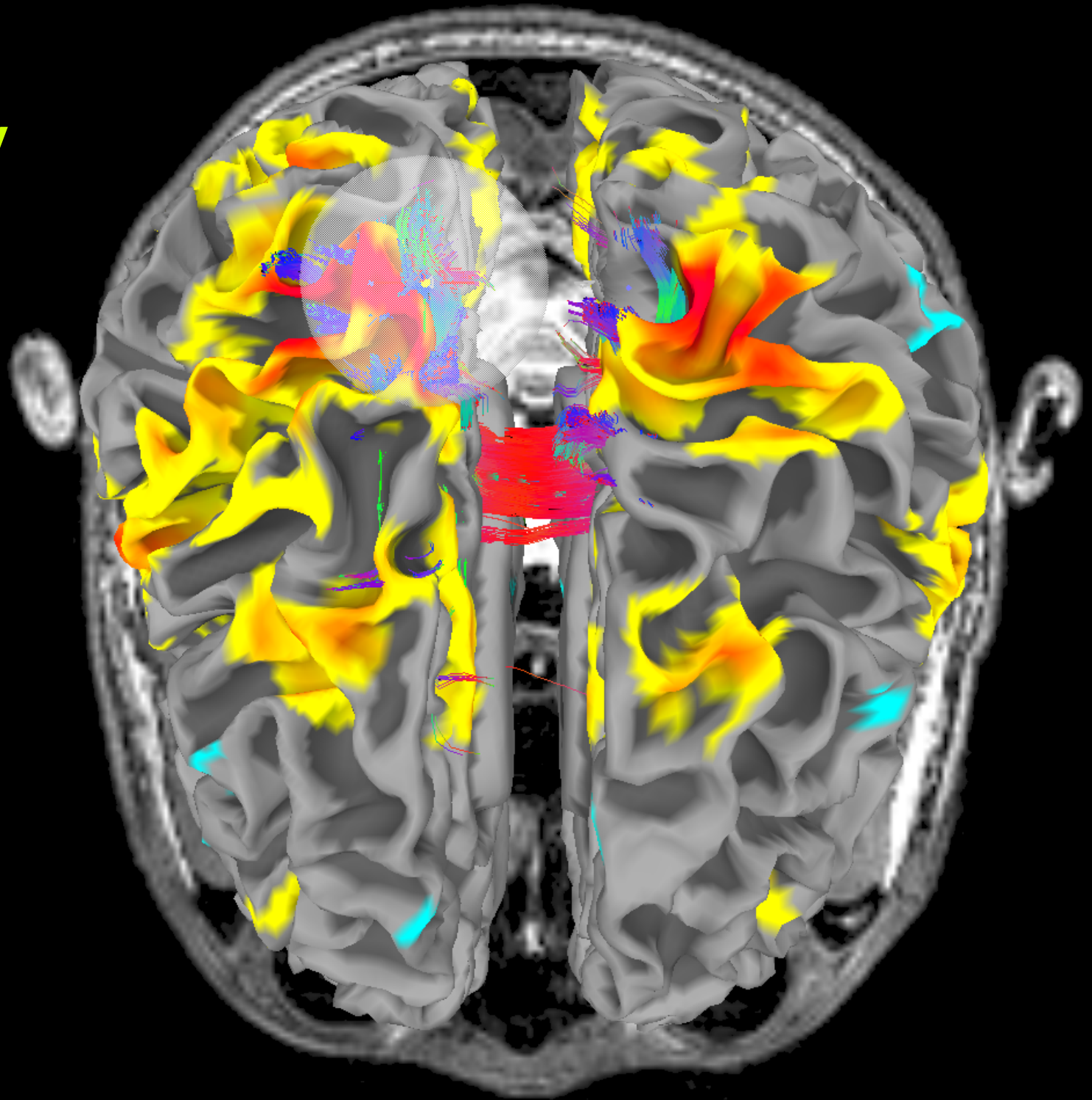
**DTI tracts
only from
seed region
+ time
series
correlations**

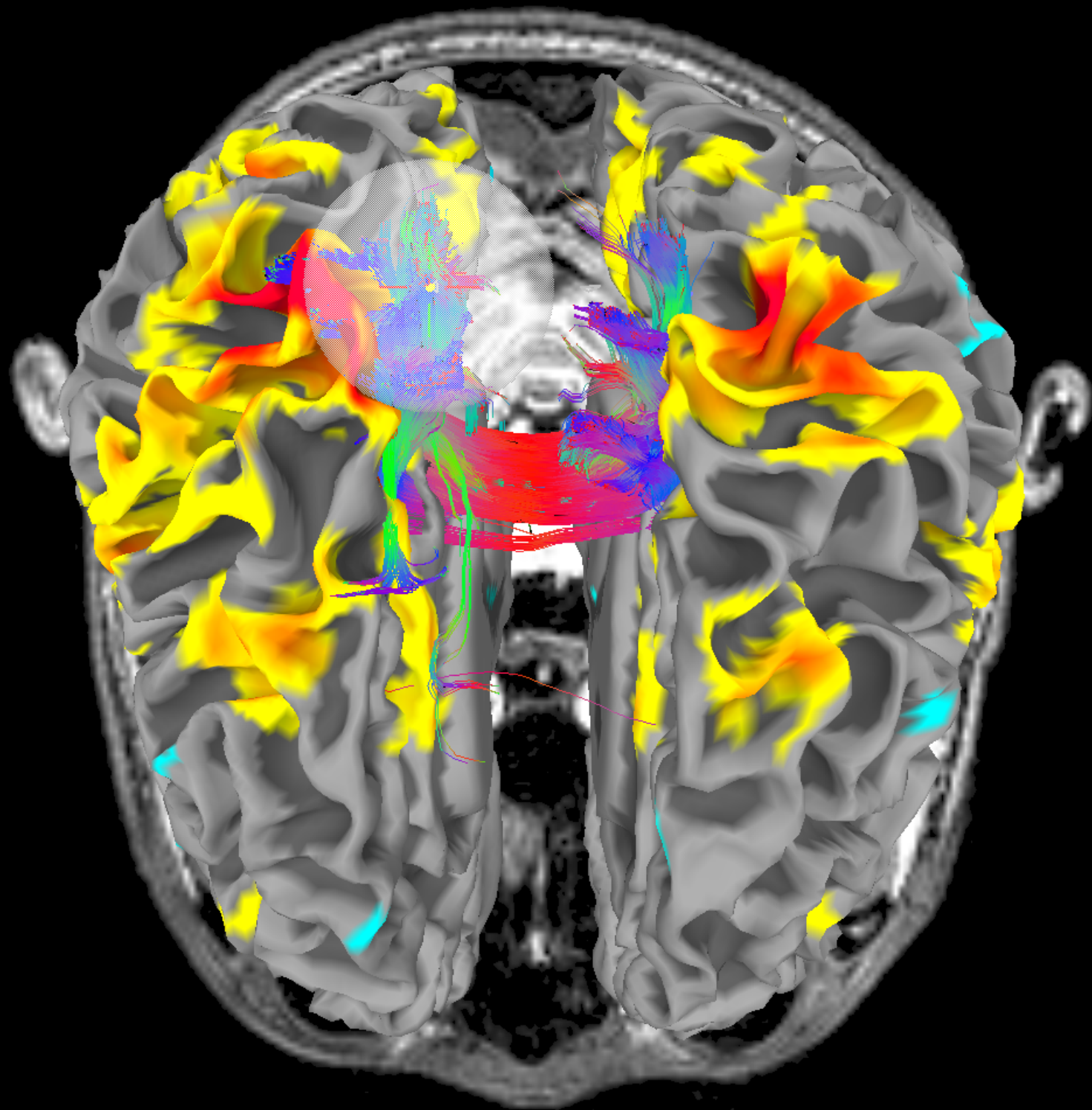
**Brain is
in the way**

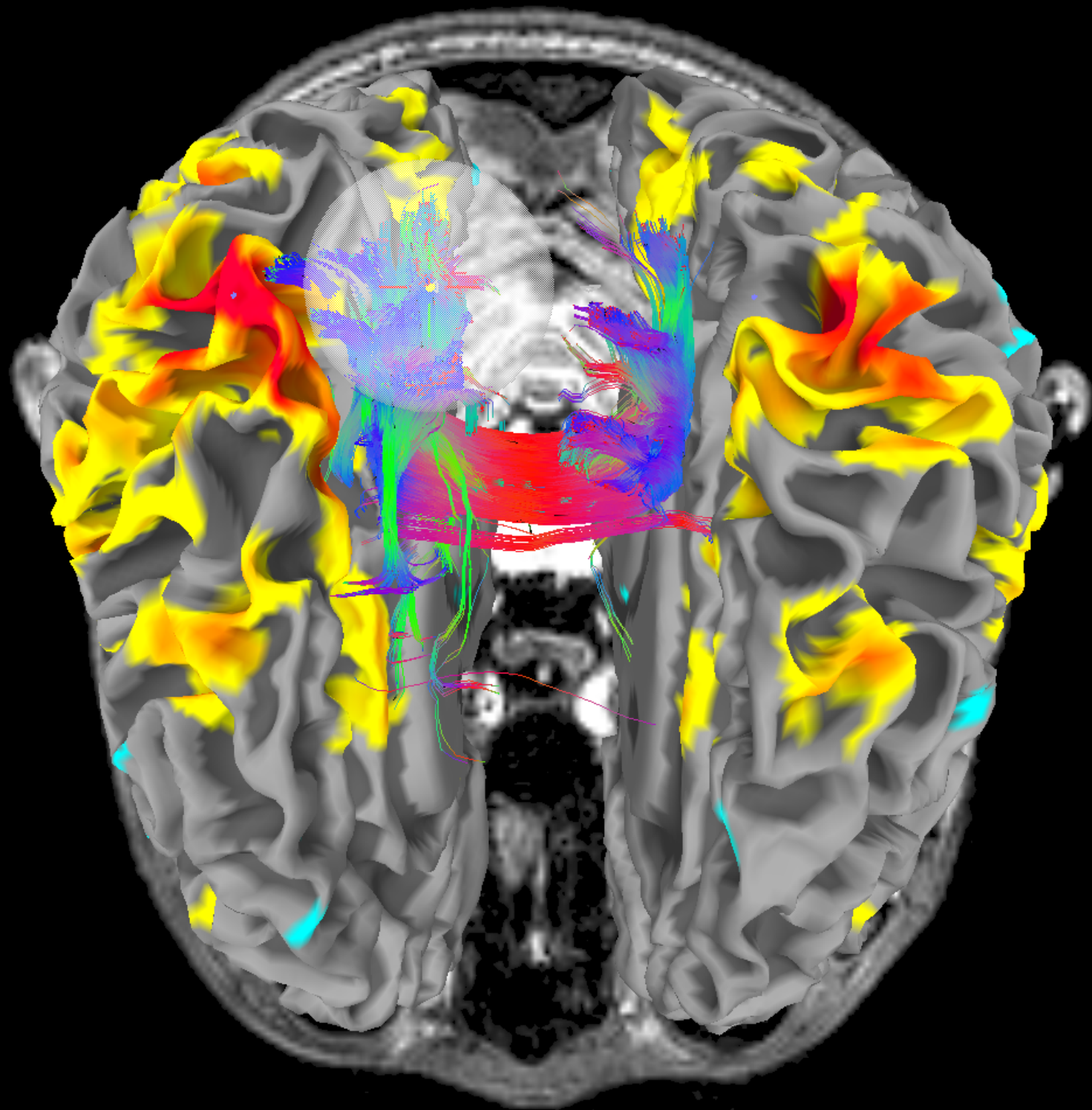


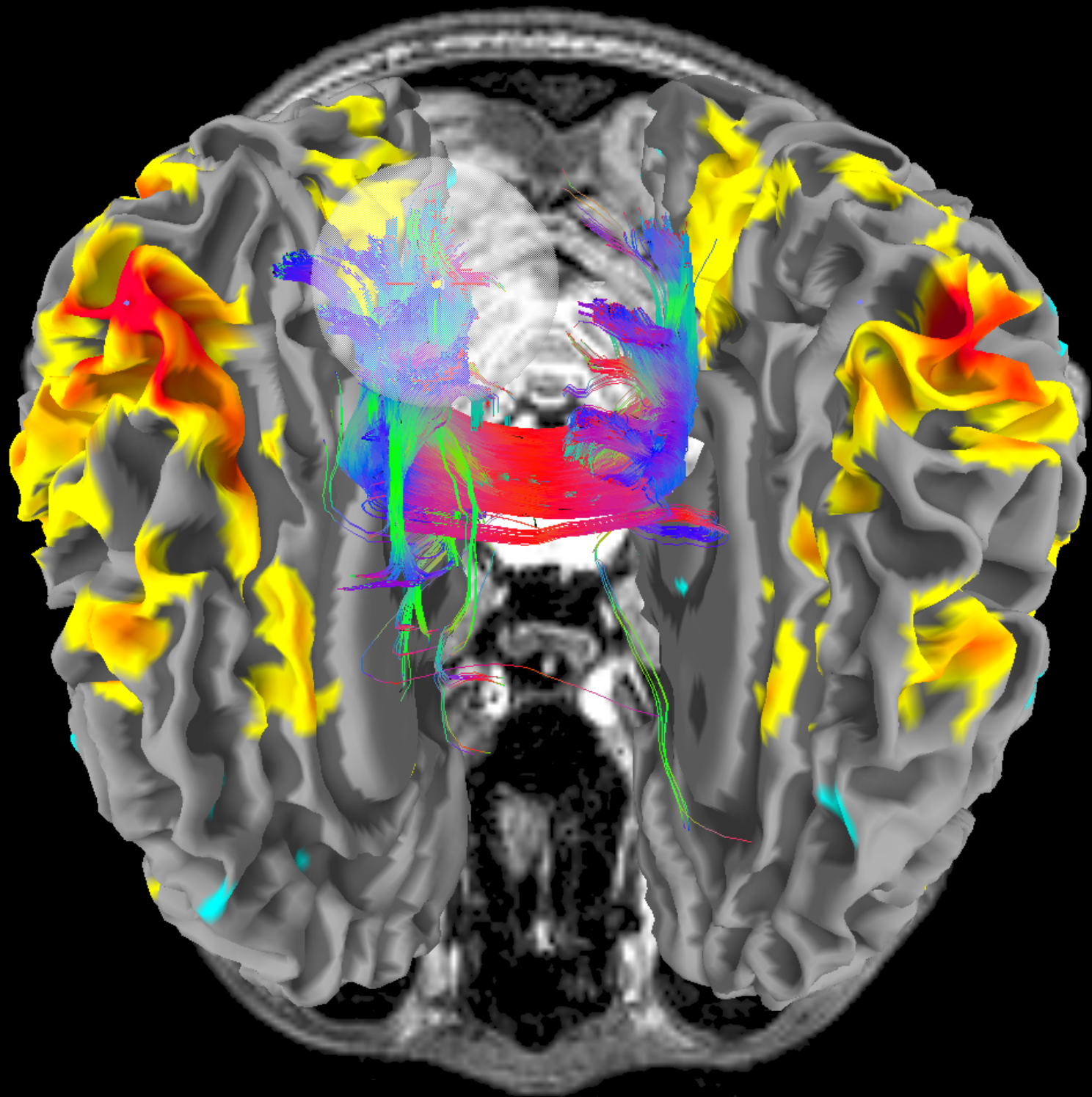
Brain is
in the way

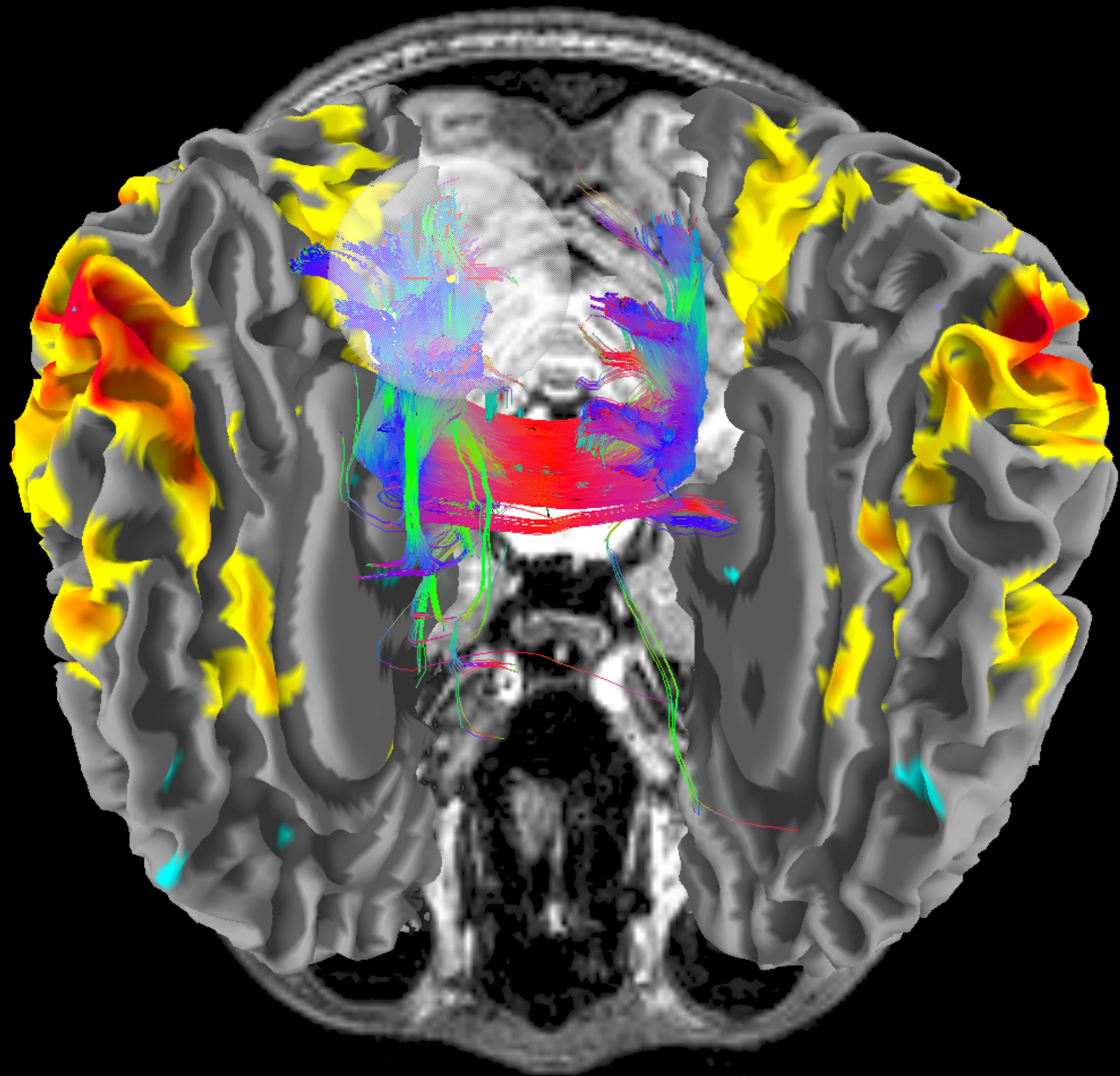
So move
it aside!

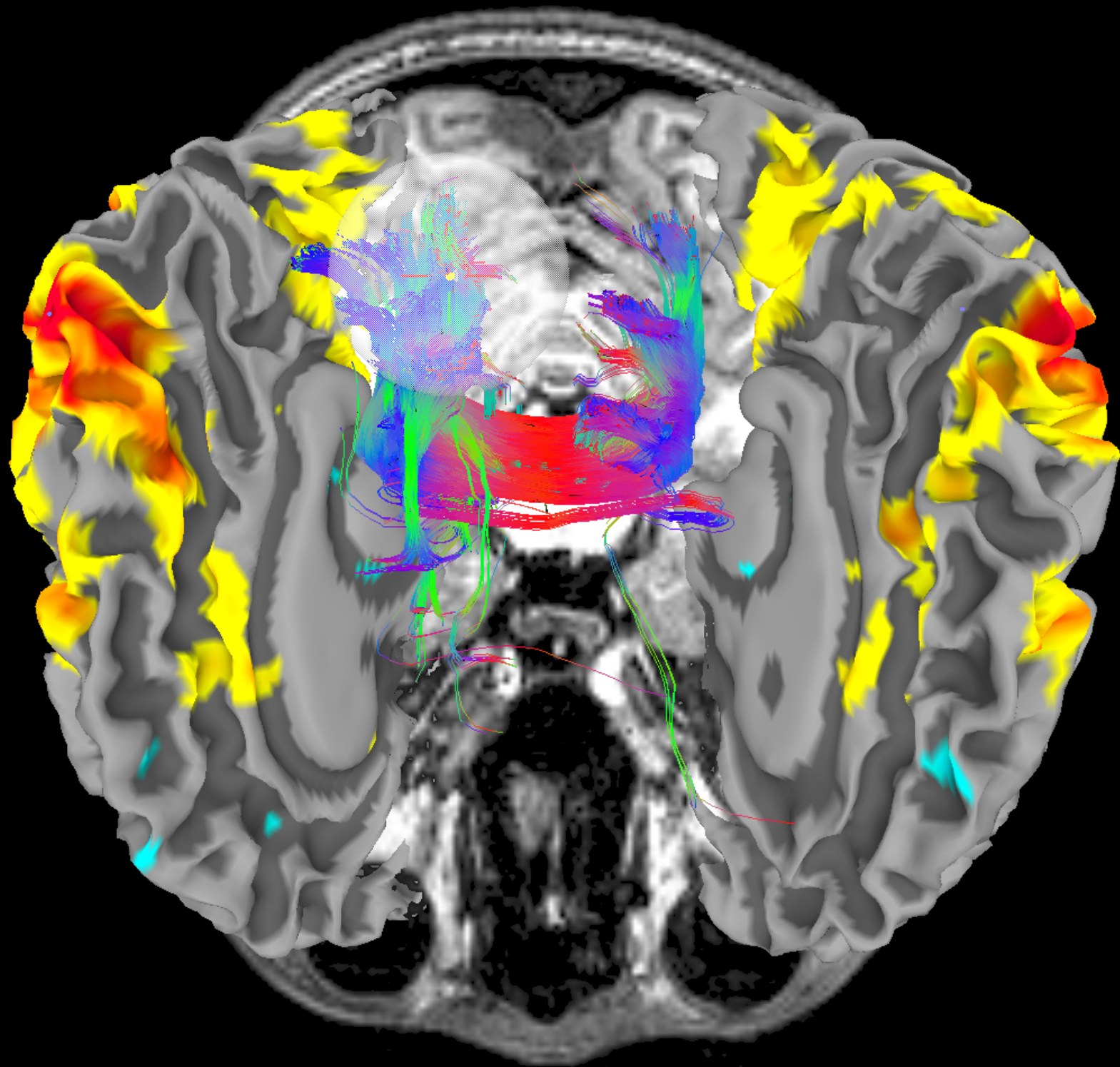




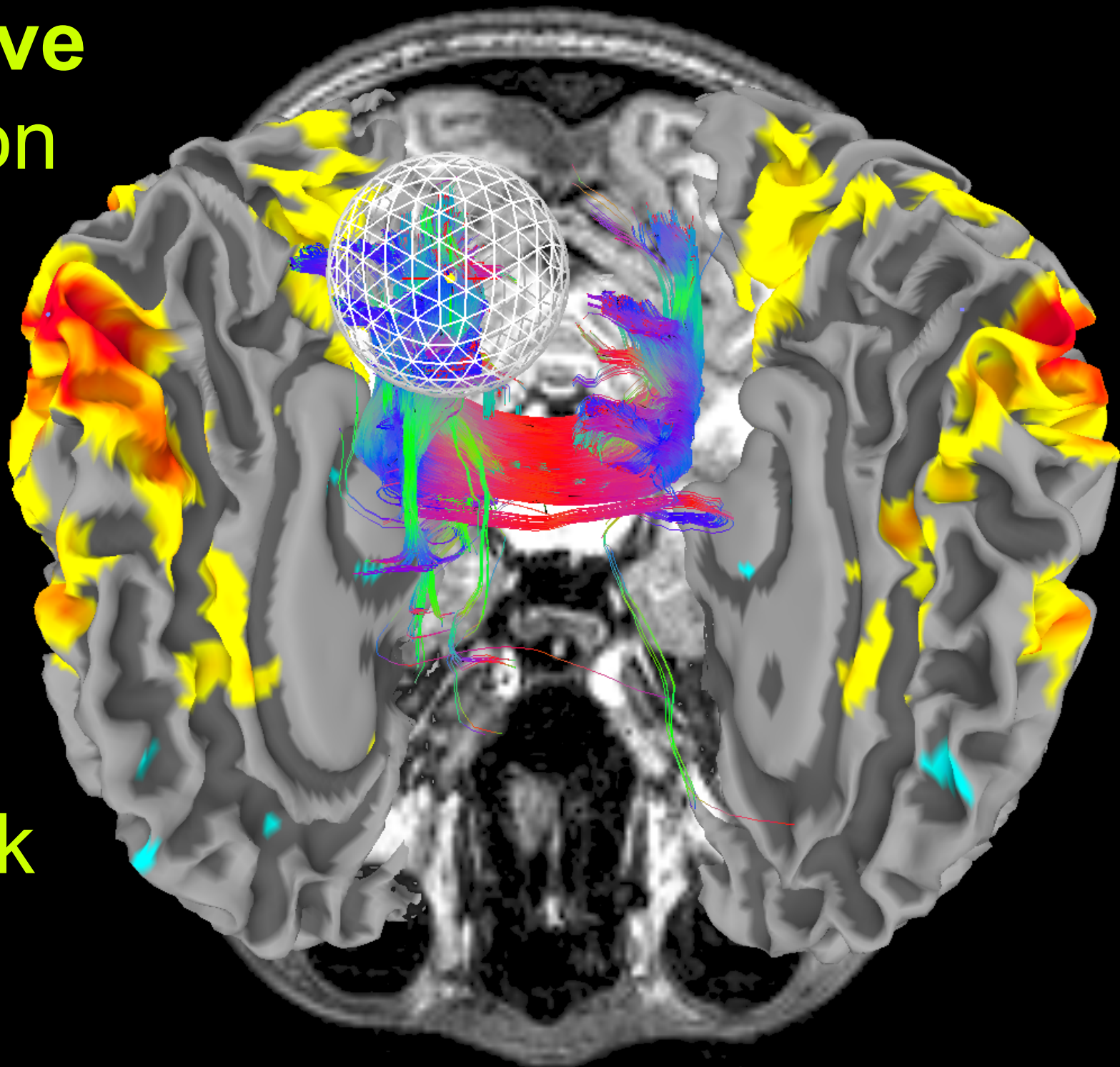




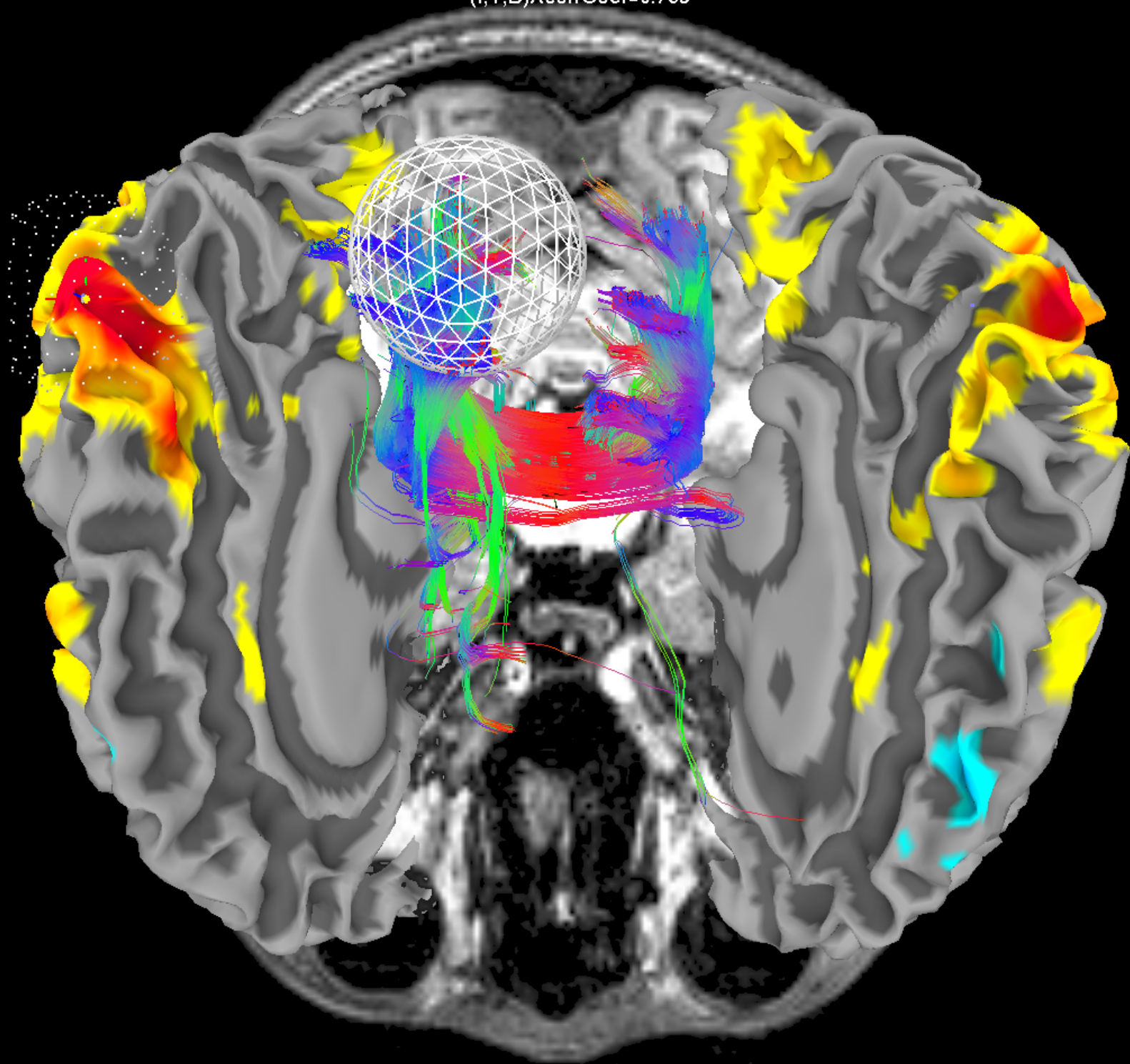




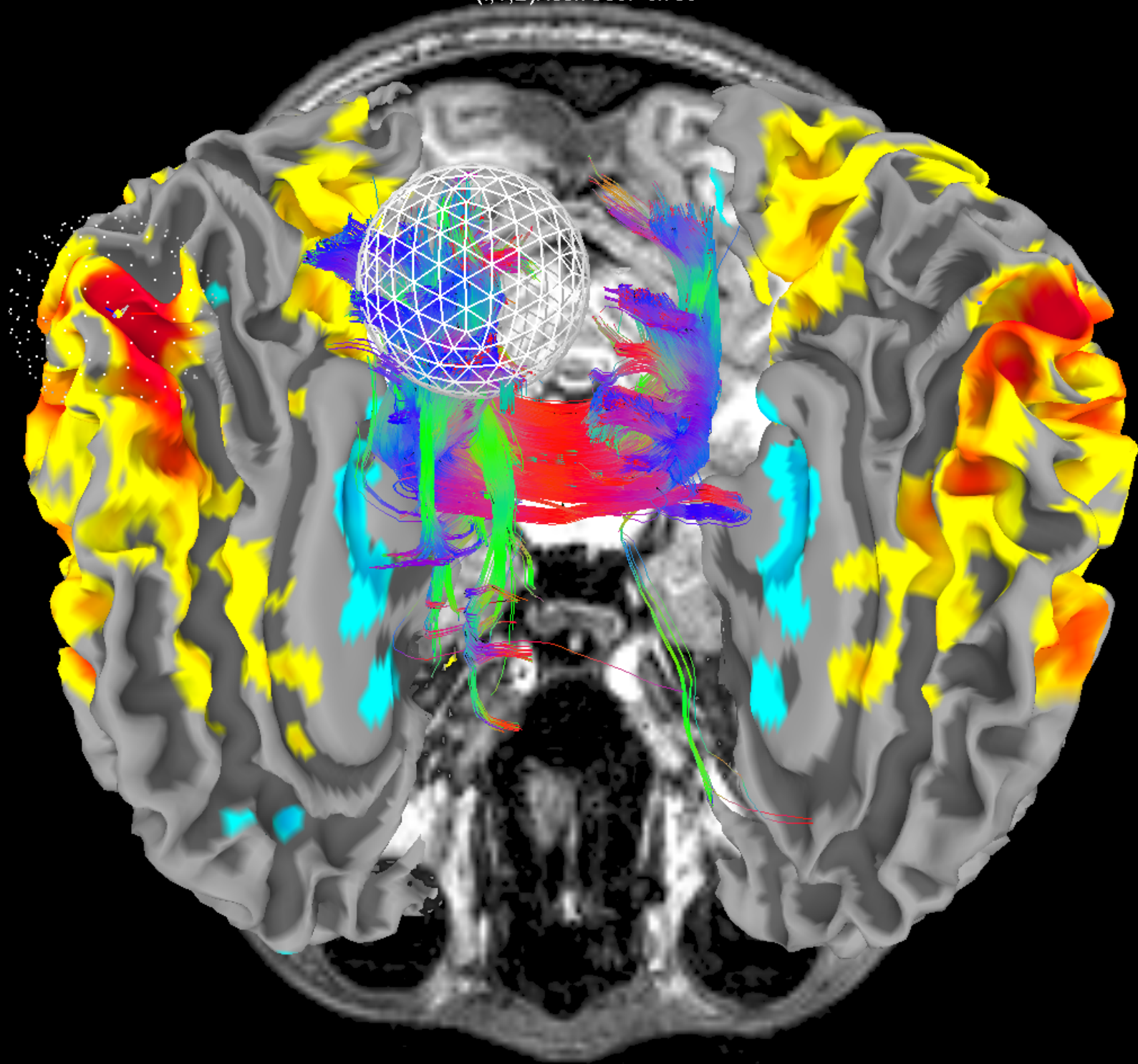
**Now move
correlation
and
tract
seed
along
the
sulcus
from back
to front**



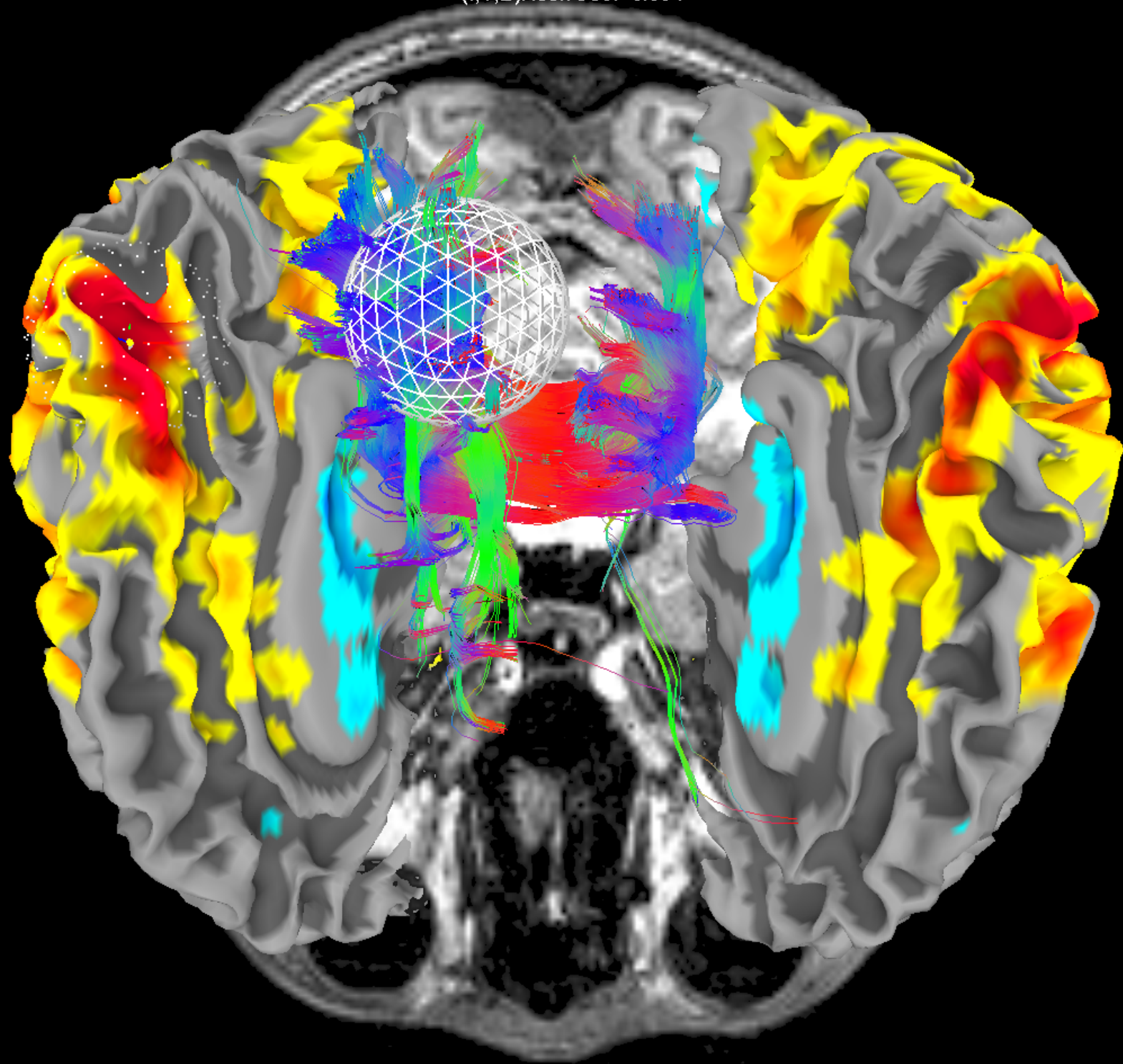
wm rh G and S paracentral
(I,T,B)XcorrCoef=0.765



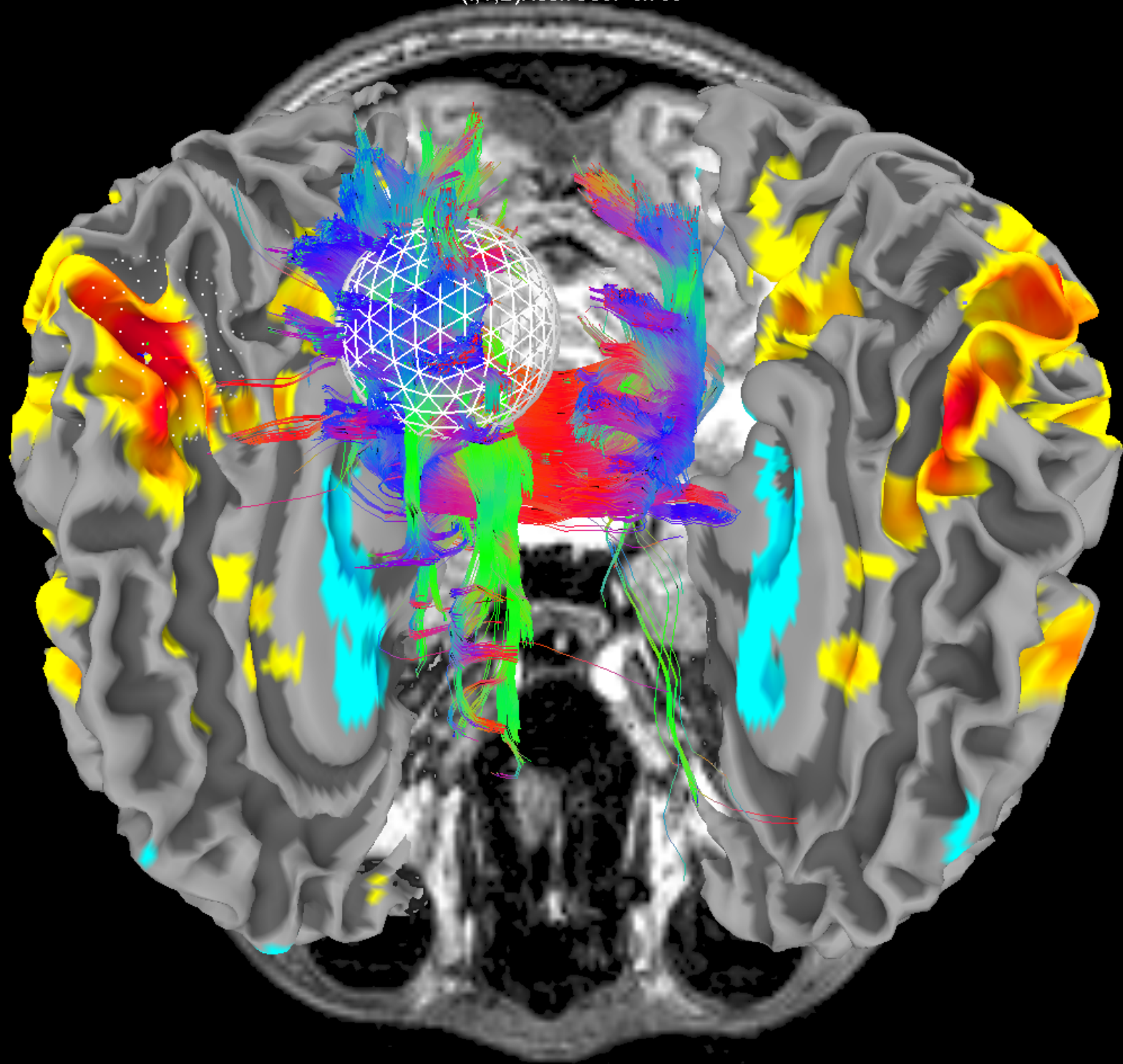
wm rh G and S paracentral
(I,T,B)XcorrCoef=0.753



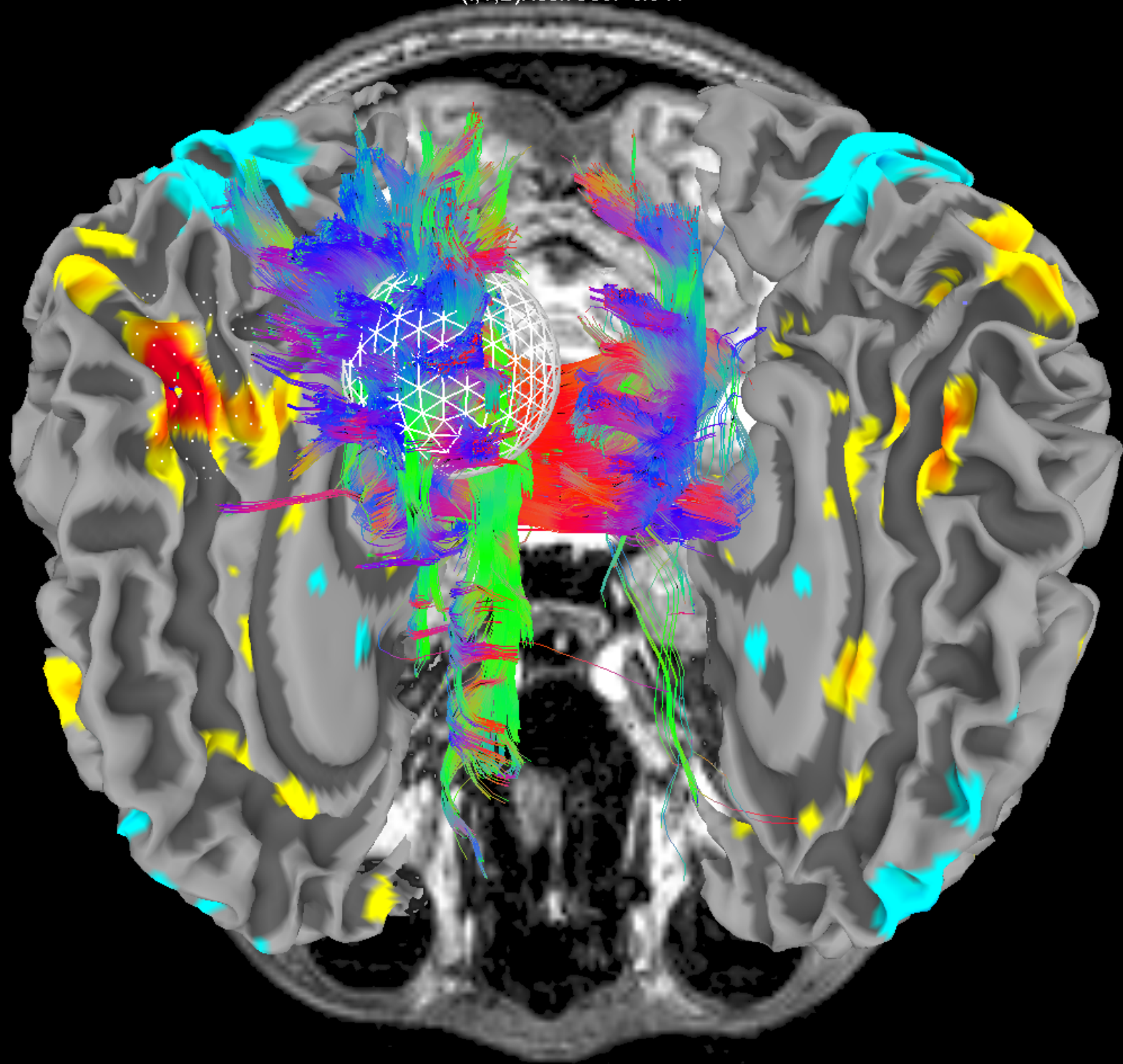
wm rh S_cingul-Marginalis
(l,T,B)XcorrCoef=0.884



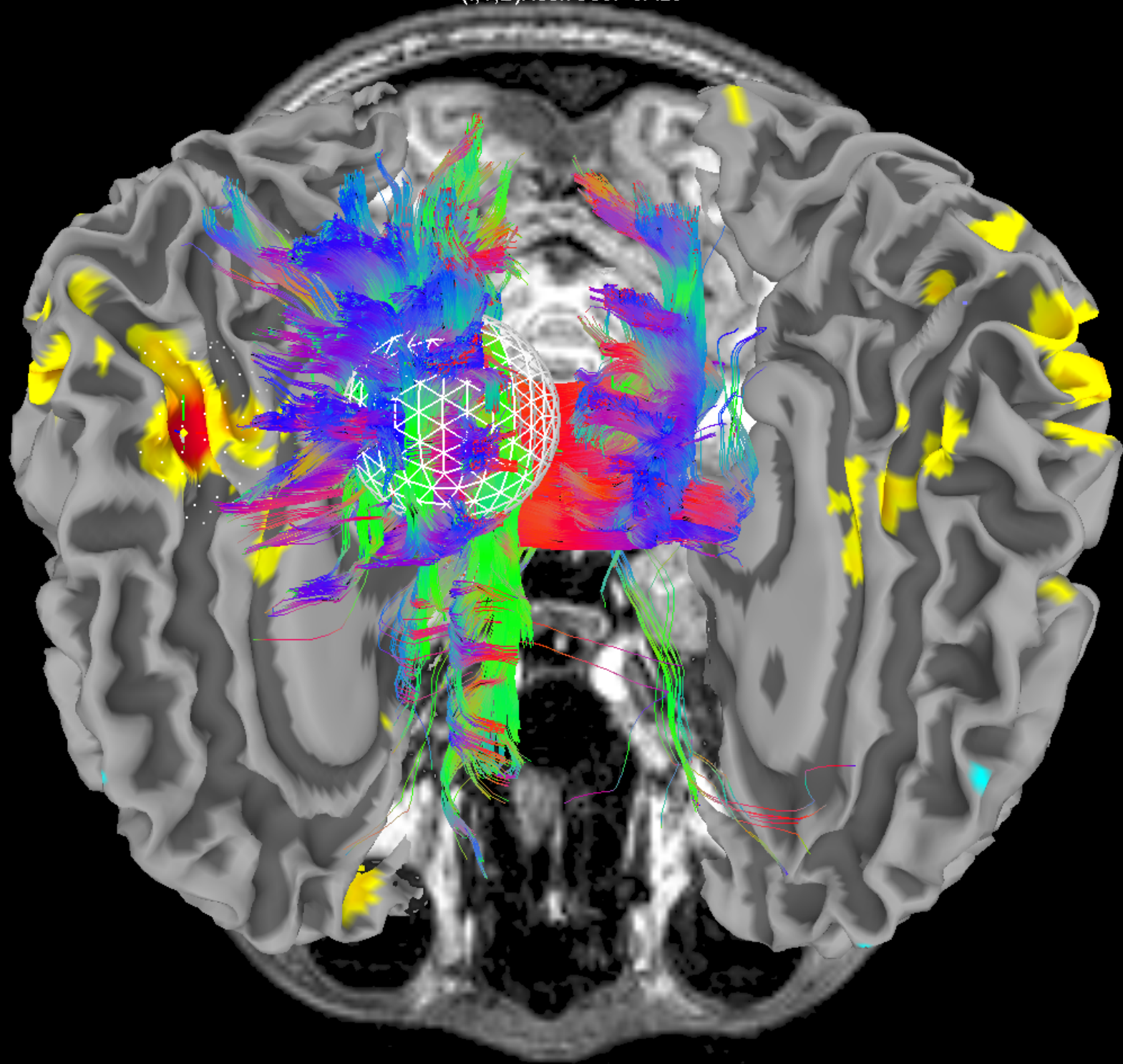
wm rh S_cingul-Marginalis
(l,T,B)XcorrCoef=0.780



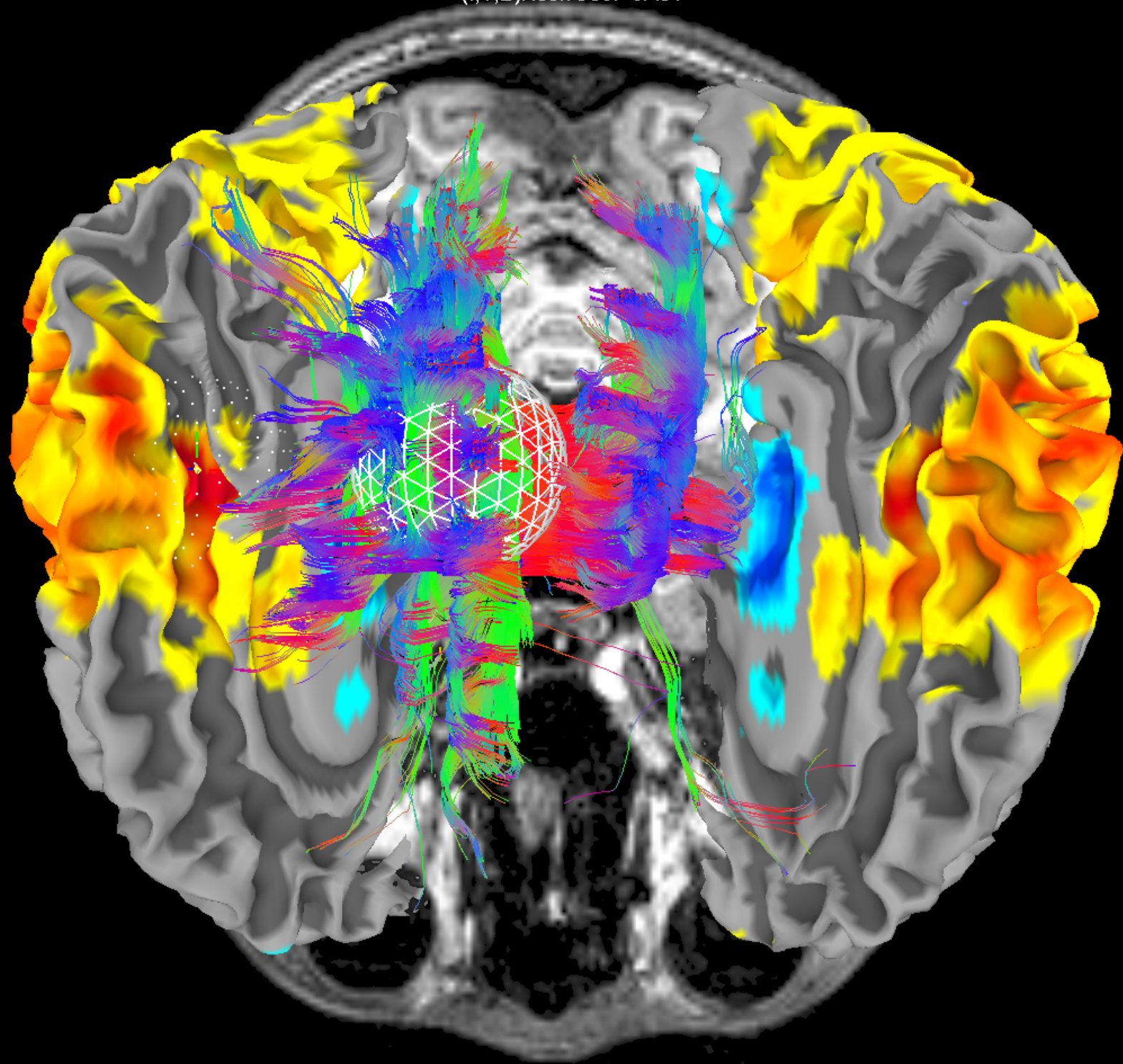
wm rh S_cingul-Marginalis
(I,T,B)XcorrCoef=0.644



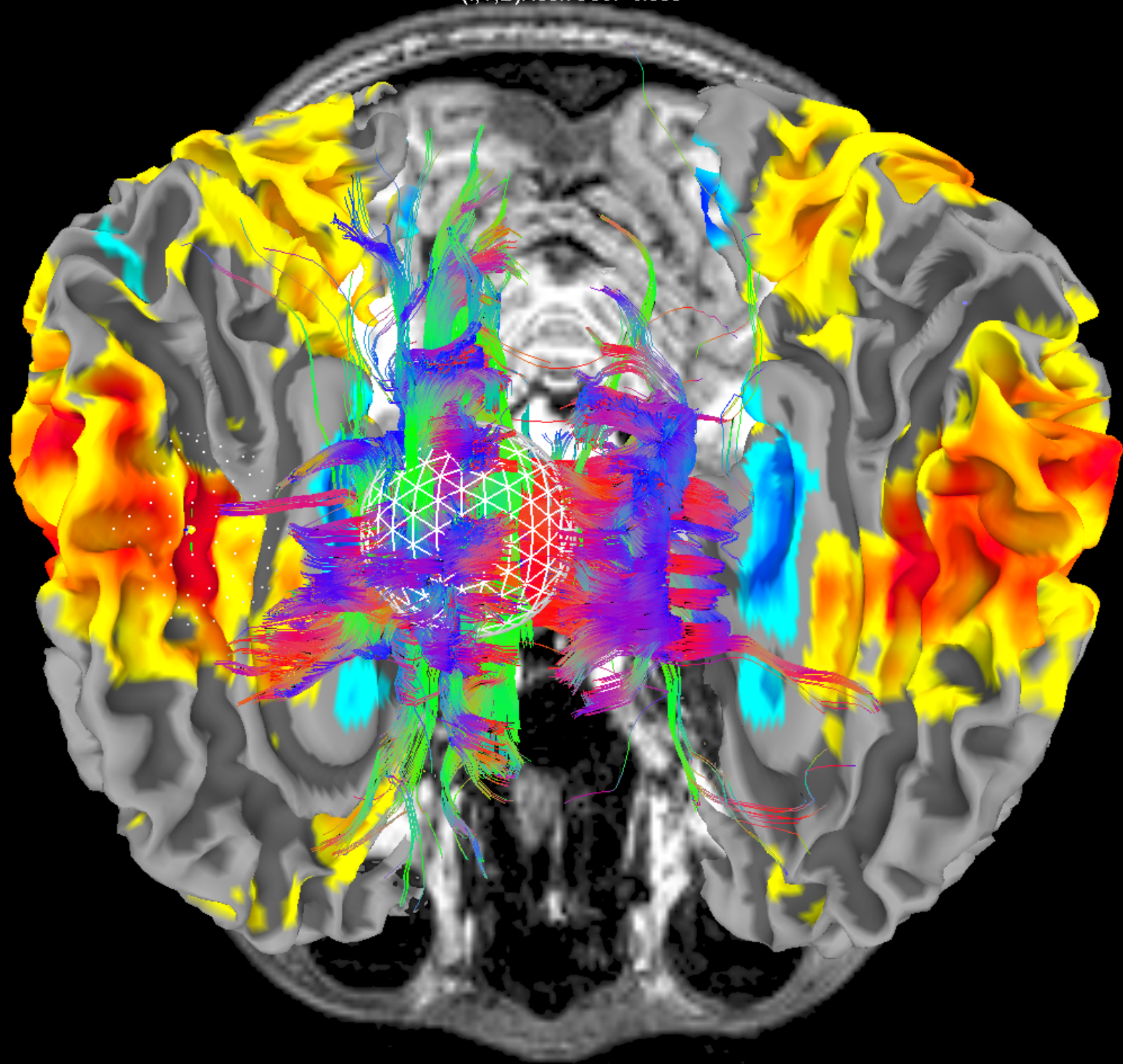
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.423



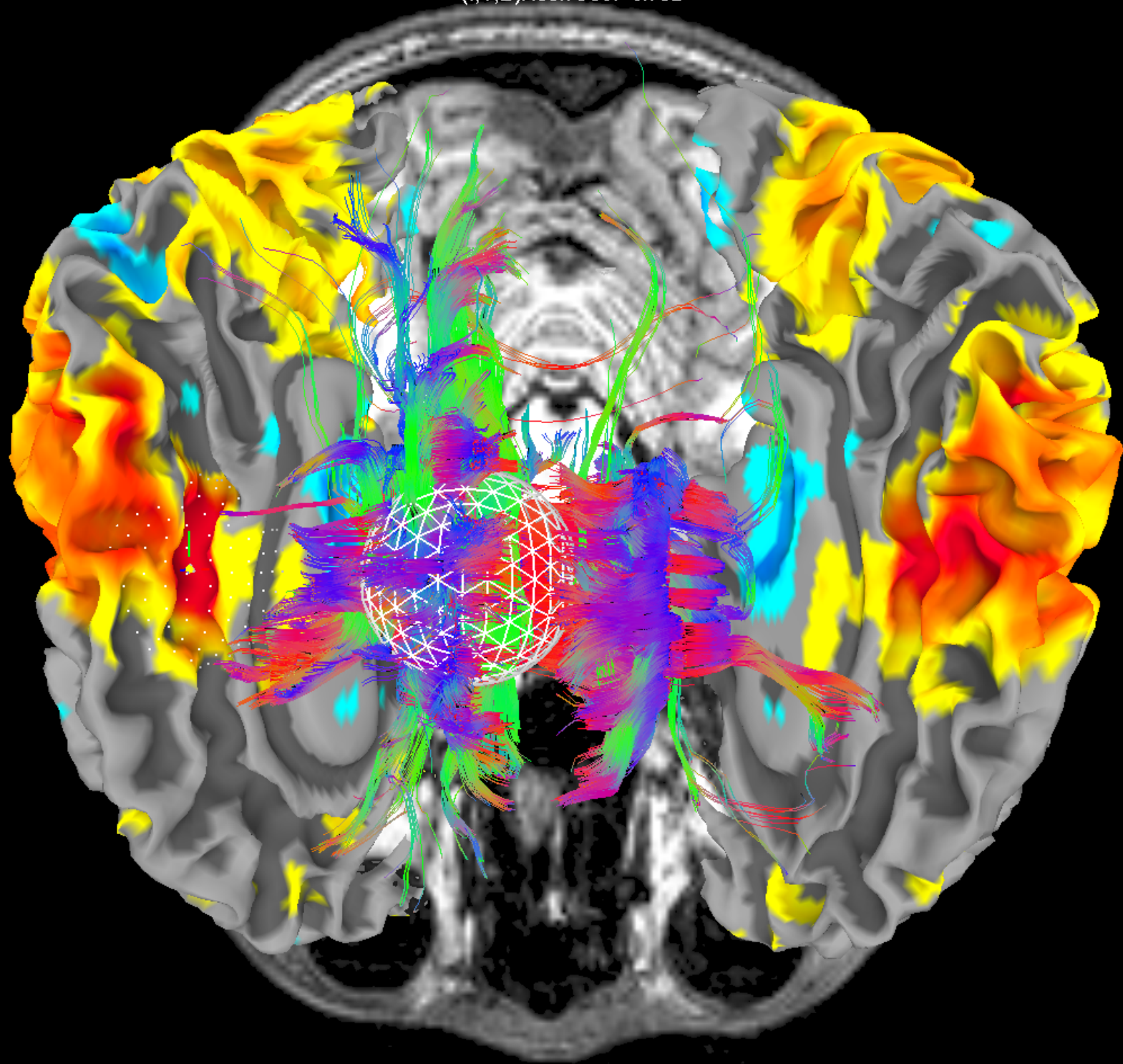
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(I,T,B)XcorrCoef=0.491



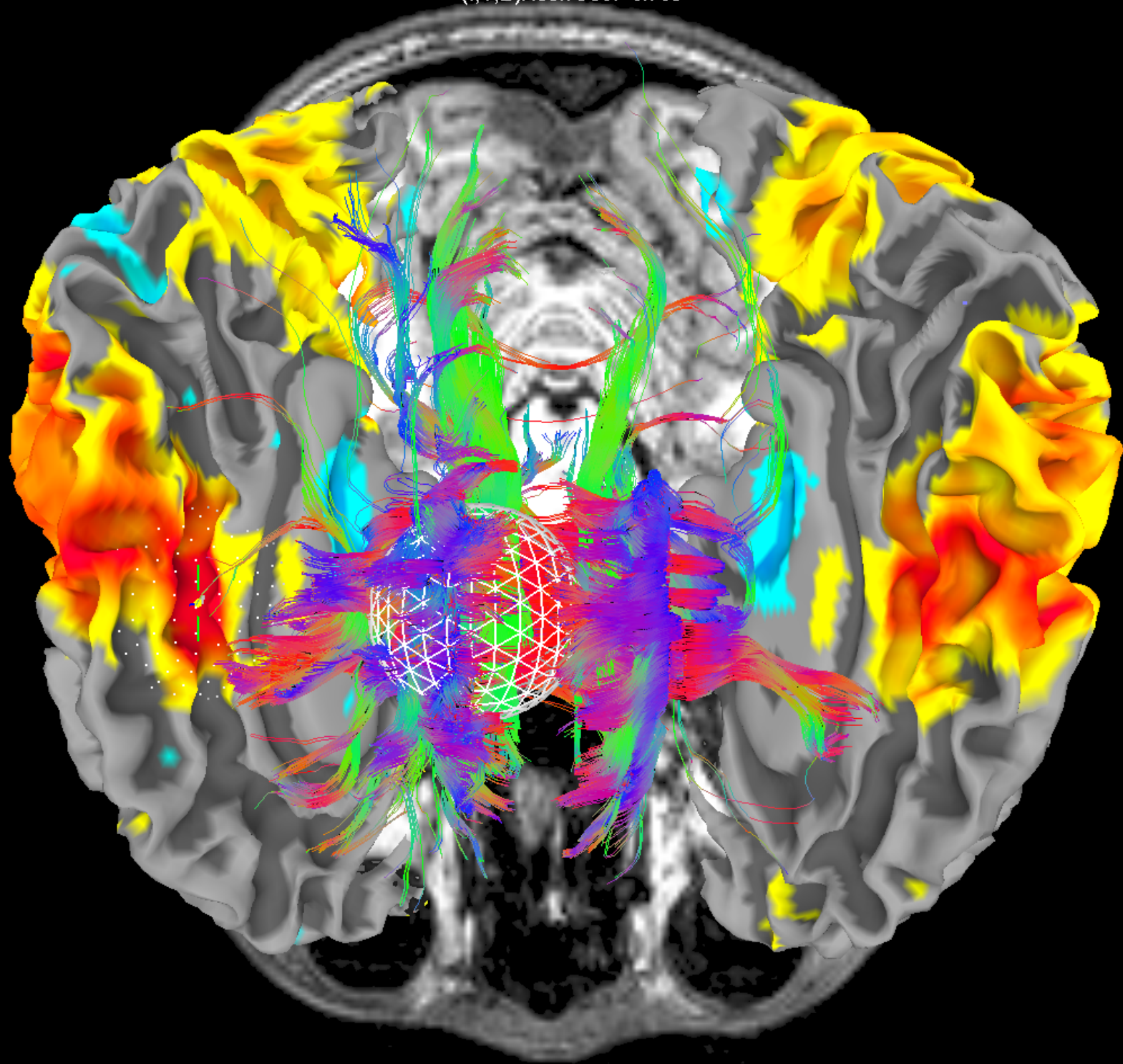
wm_rh_G and S_cingul-Mid-Post
(I,T,B)XcorrCoef=0.559



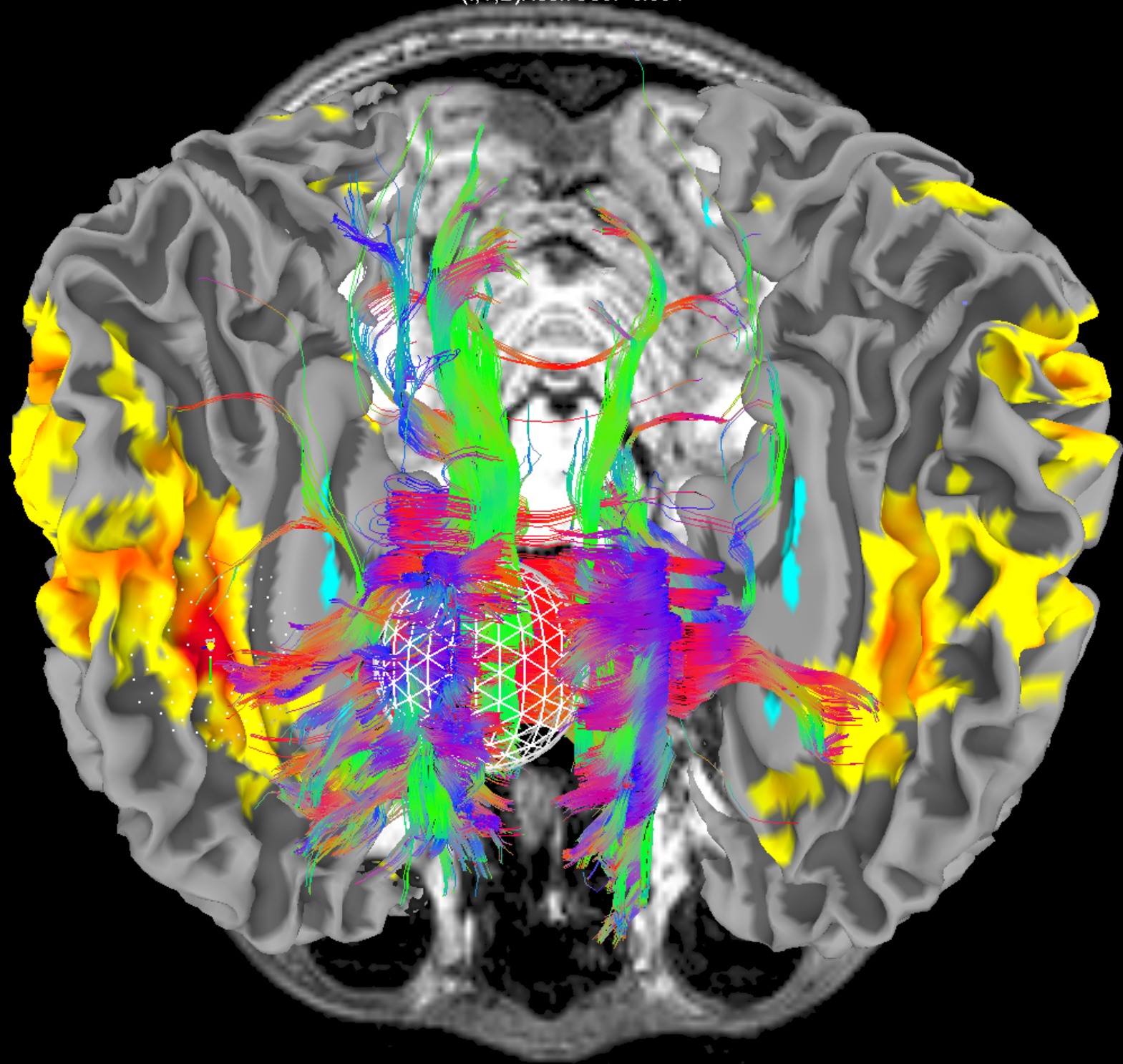
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(I,T,B)XcorrCoef=0.752



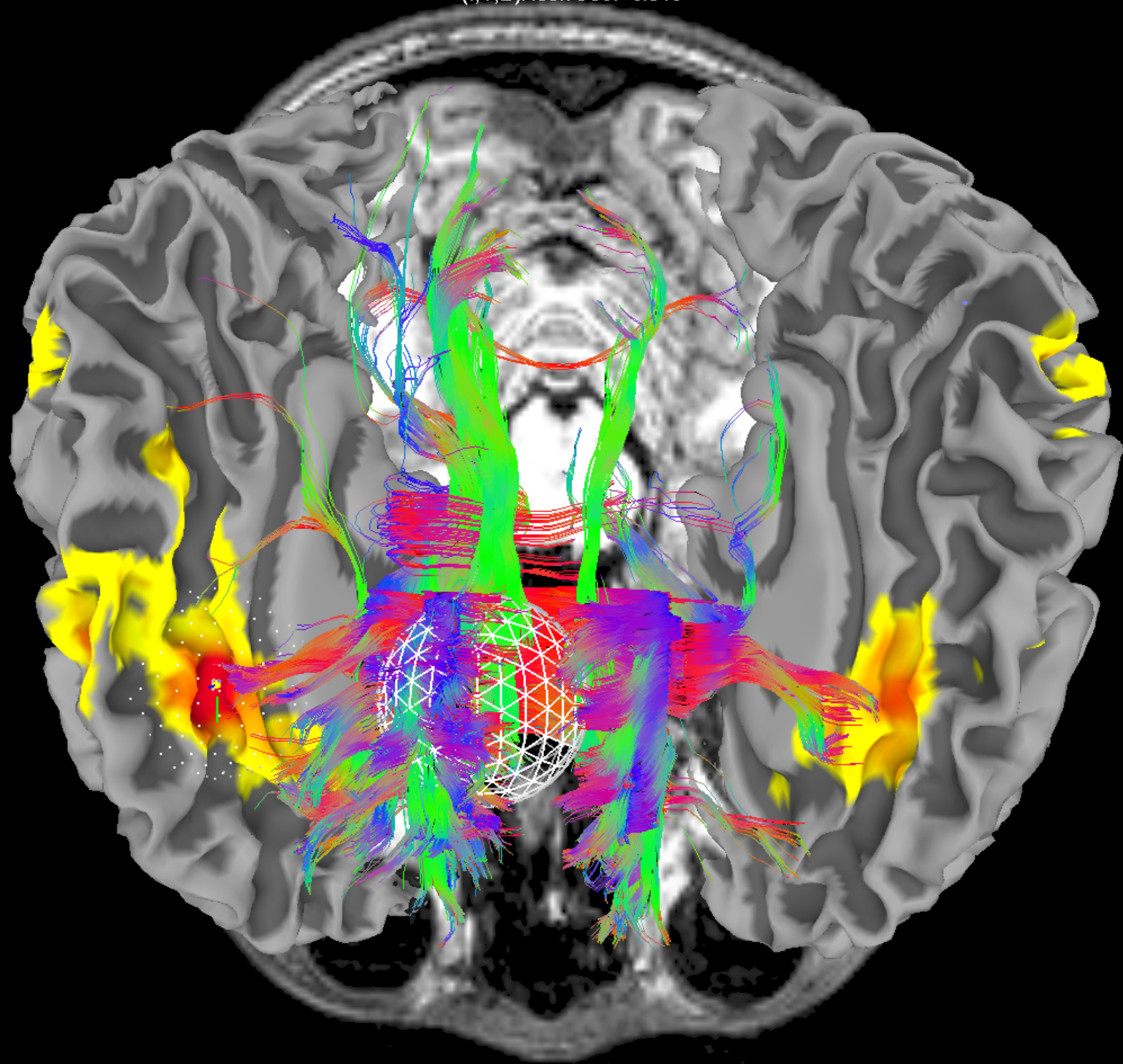
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(l,T,B)XcorrCoef=0.785



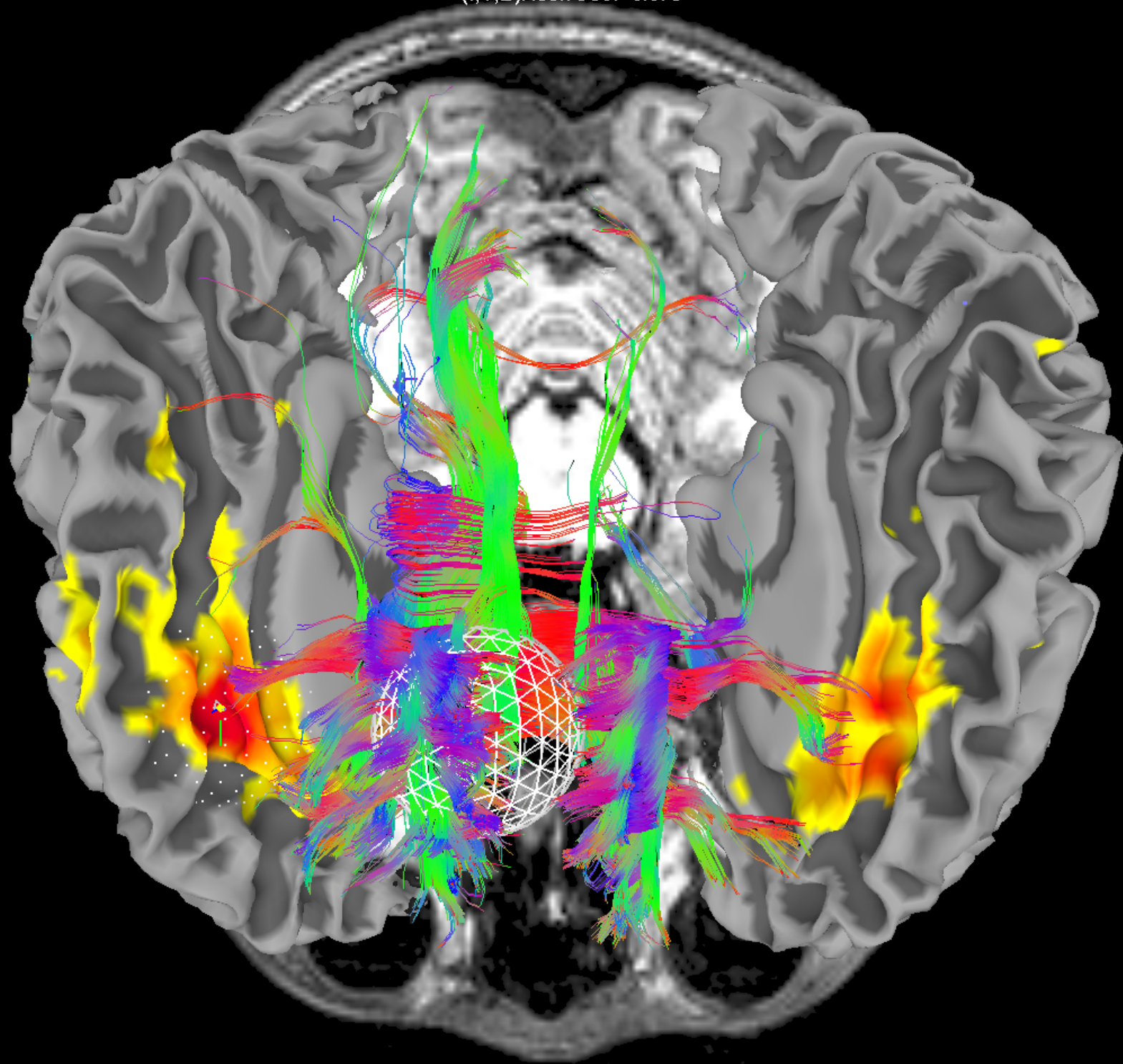
wm_rh_G and S_cingul-Mid-Ant
(l,T,B)XcorrCoef=0.604



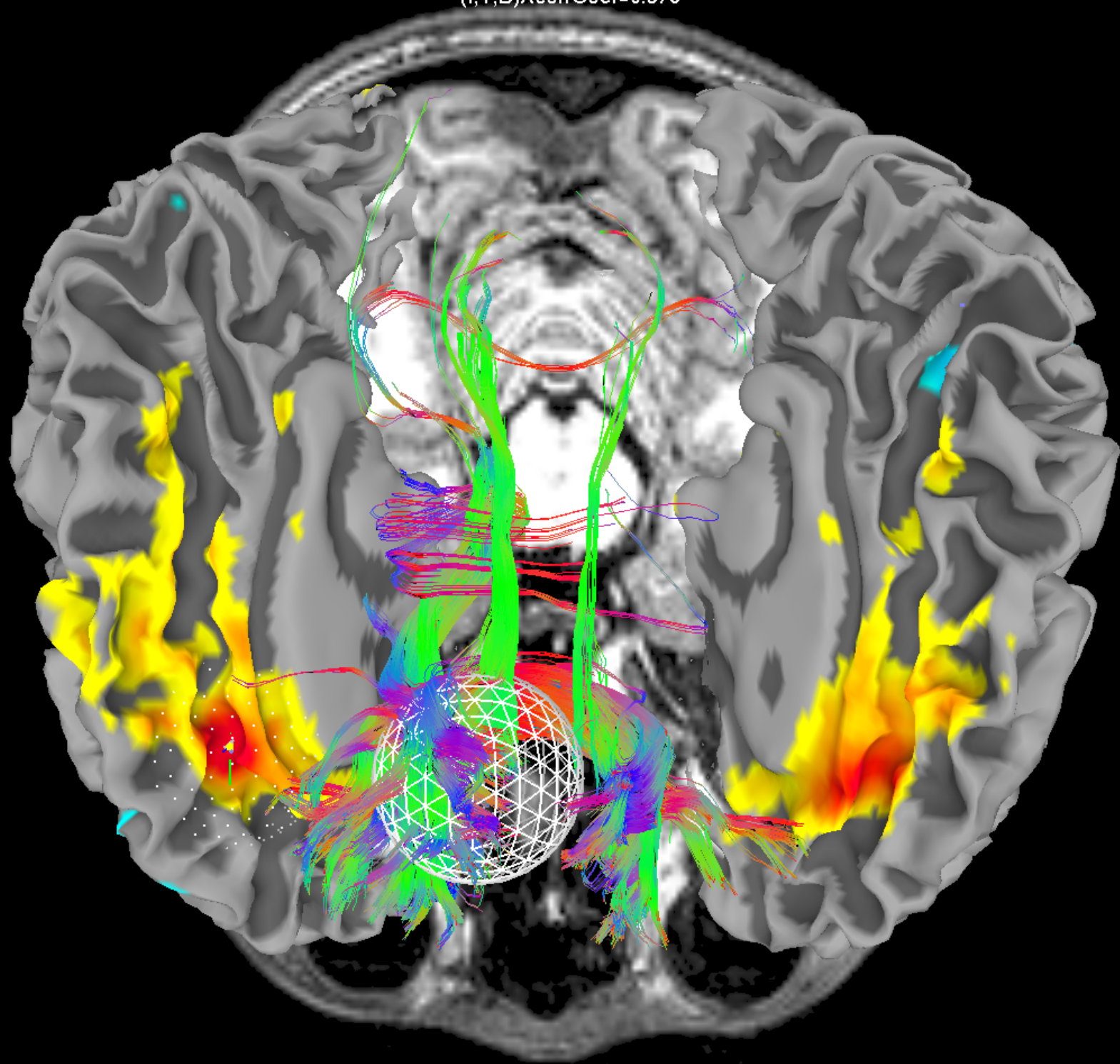
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(l,T,B)XcorrCoef=0.516



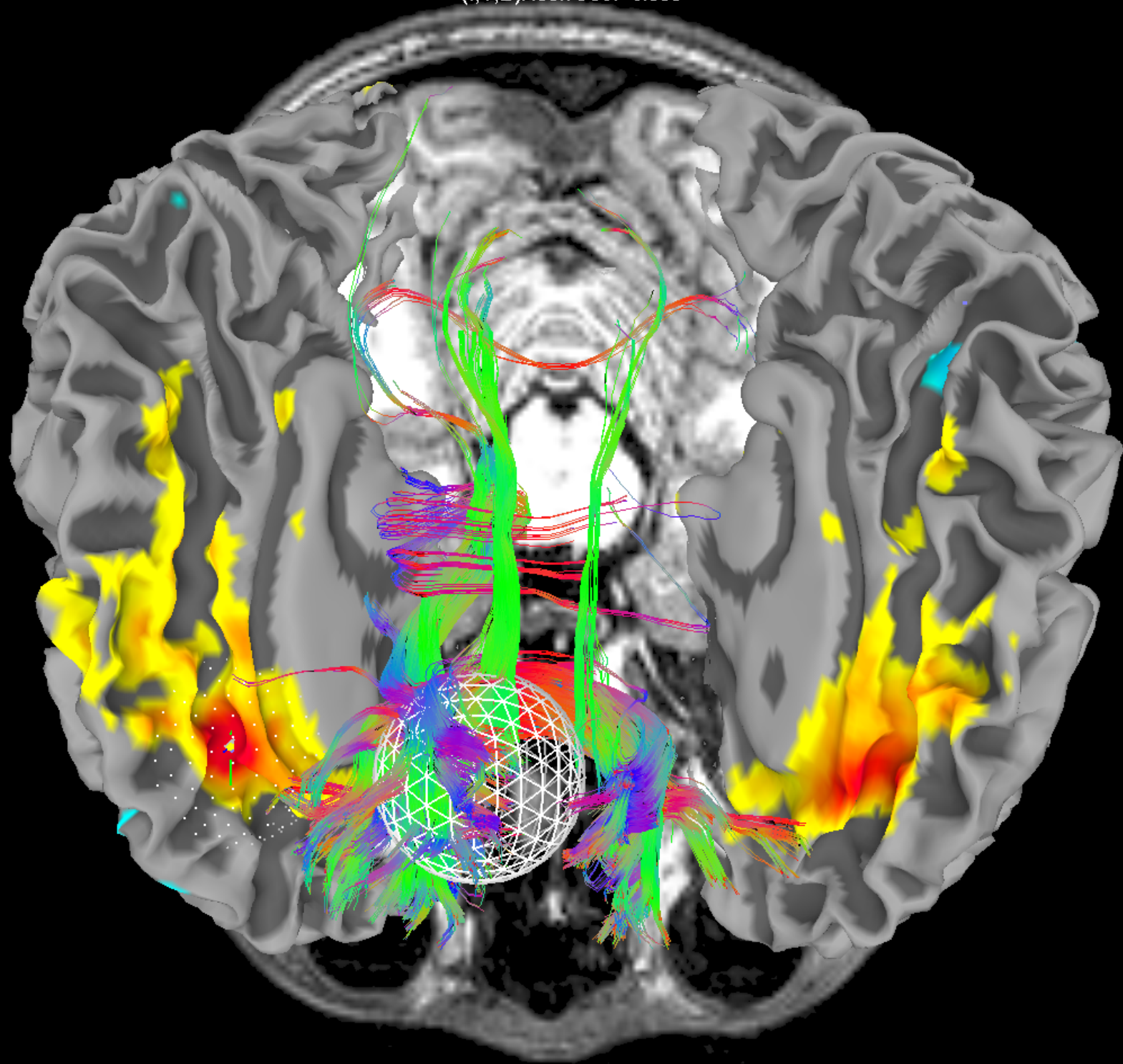
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(l,T,B)XcorrCoef=0.679



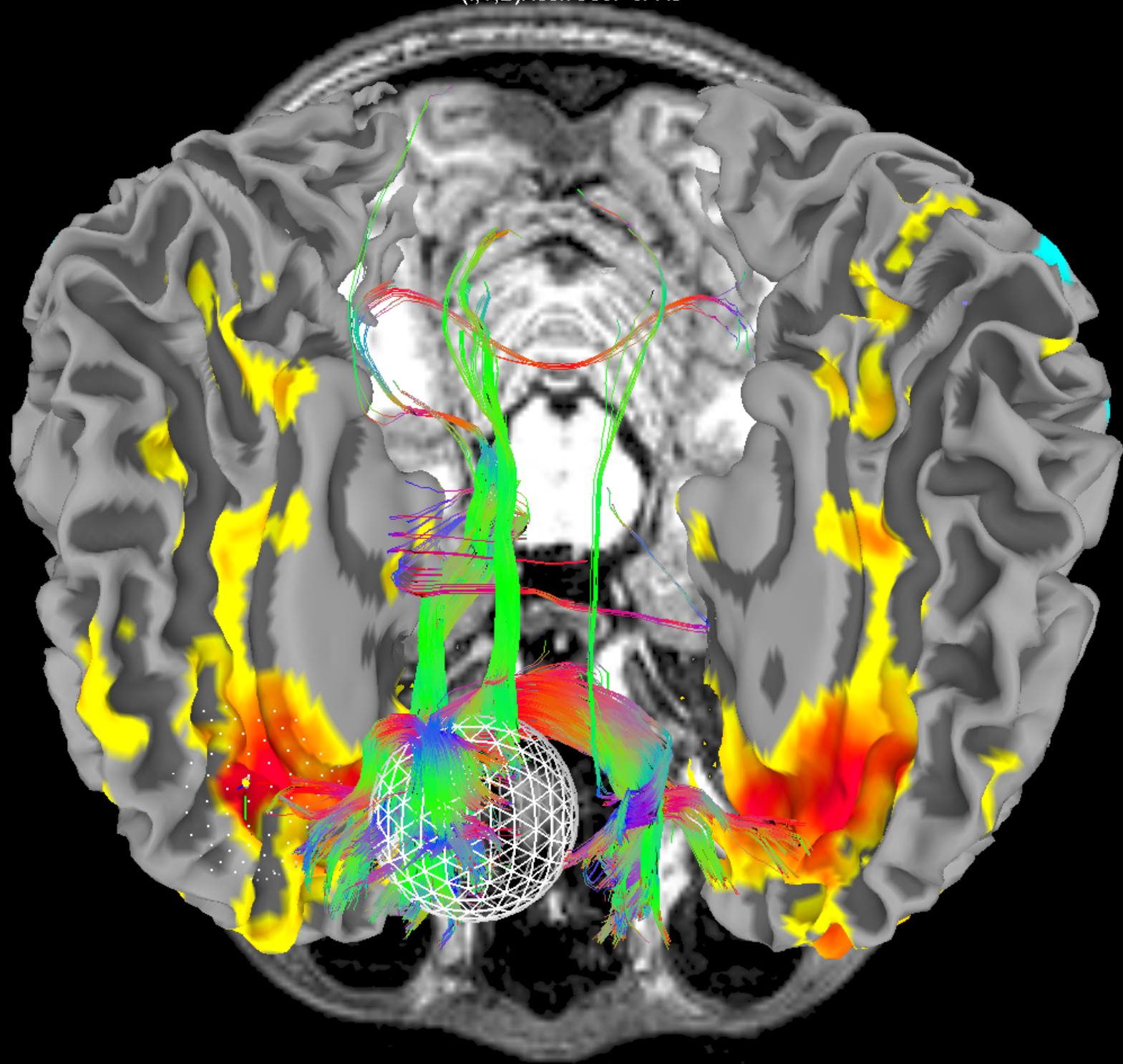
wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.578



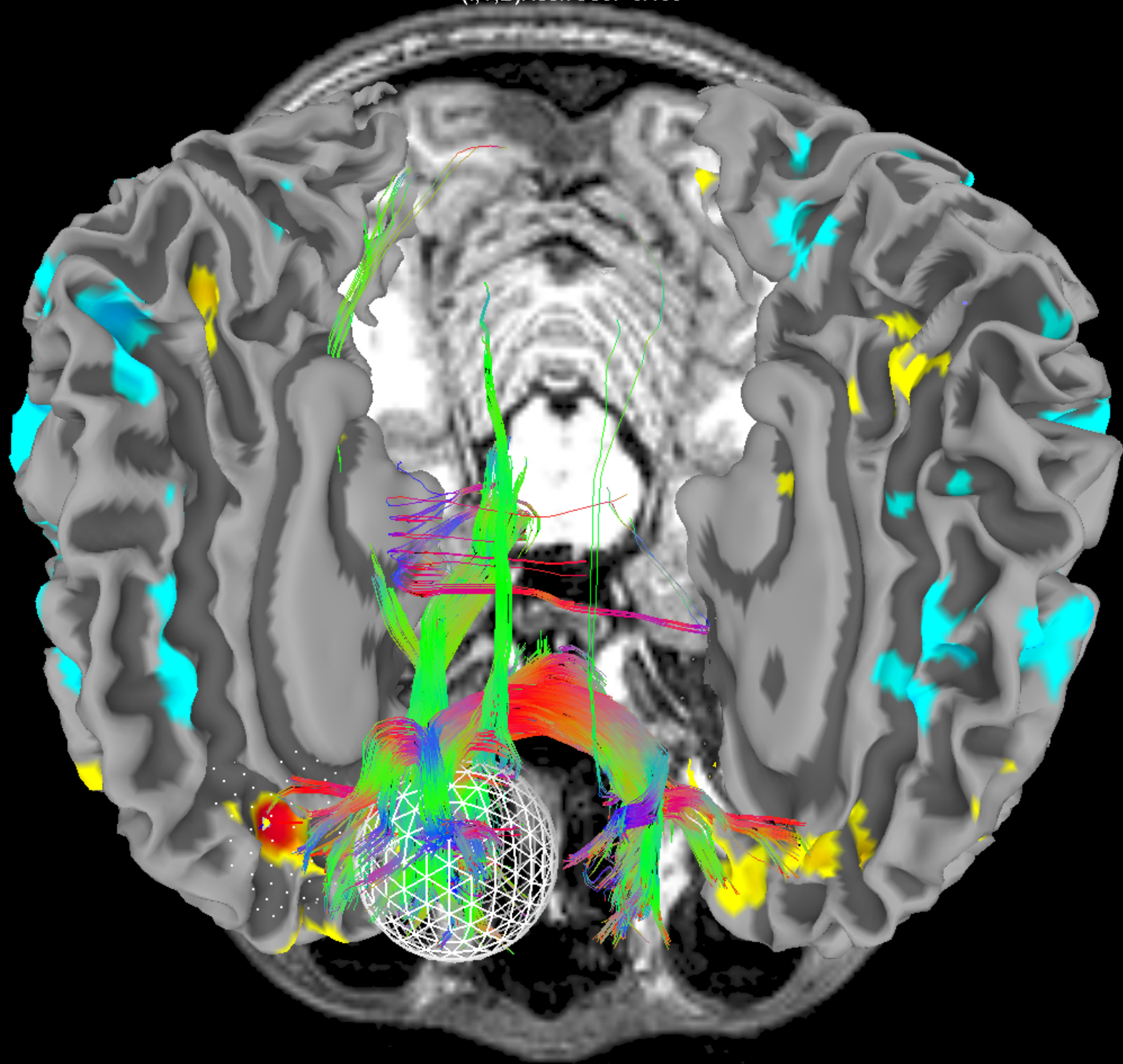
wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.999



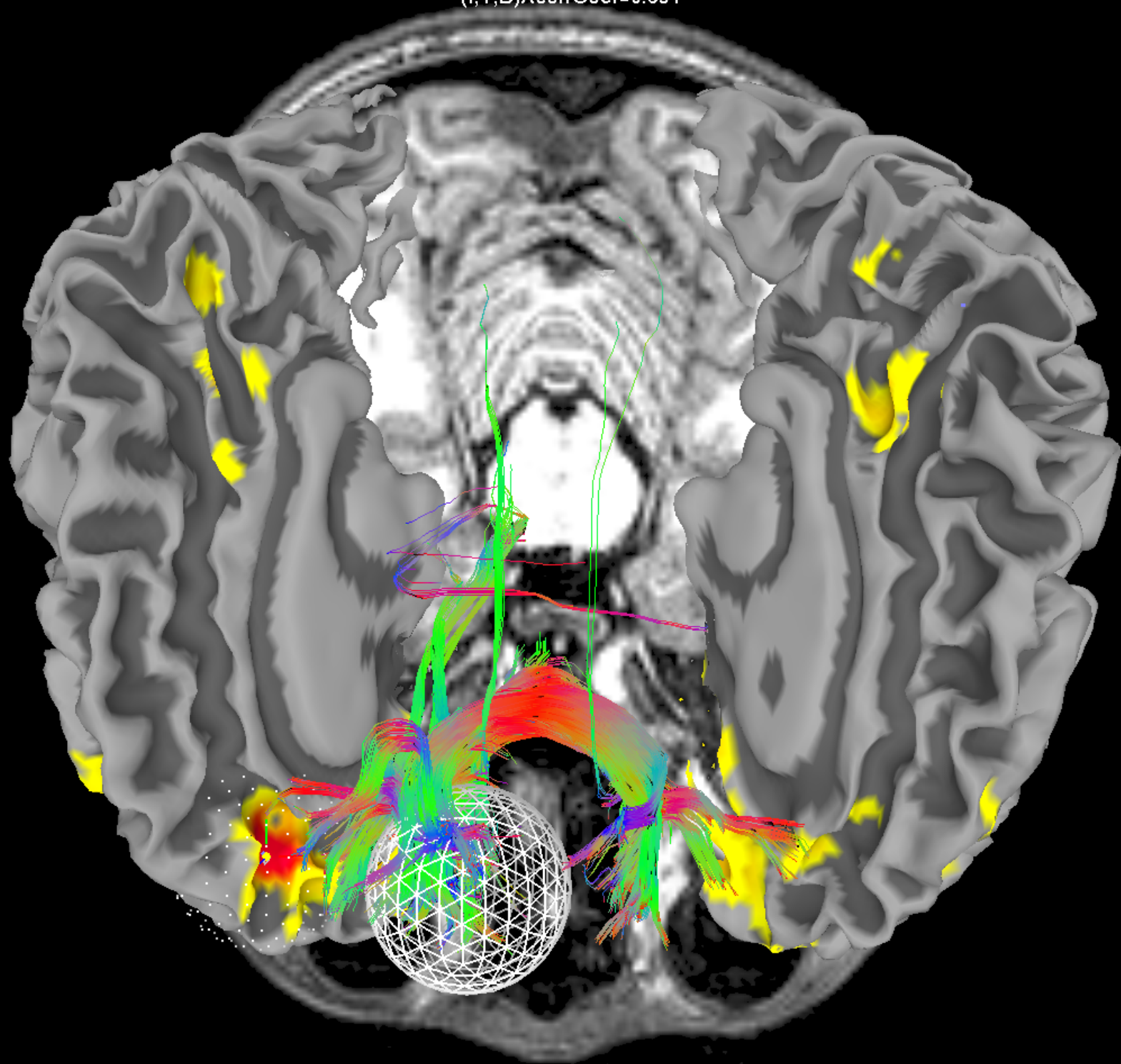
wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.445



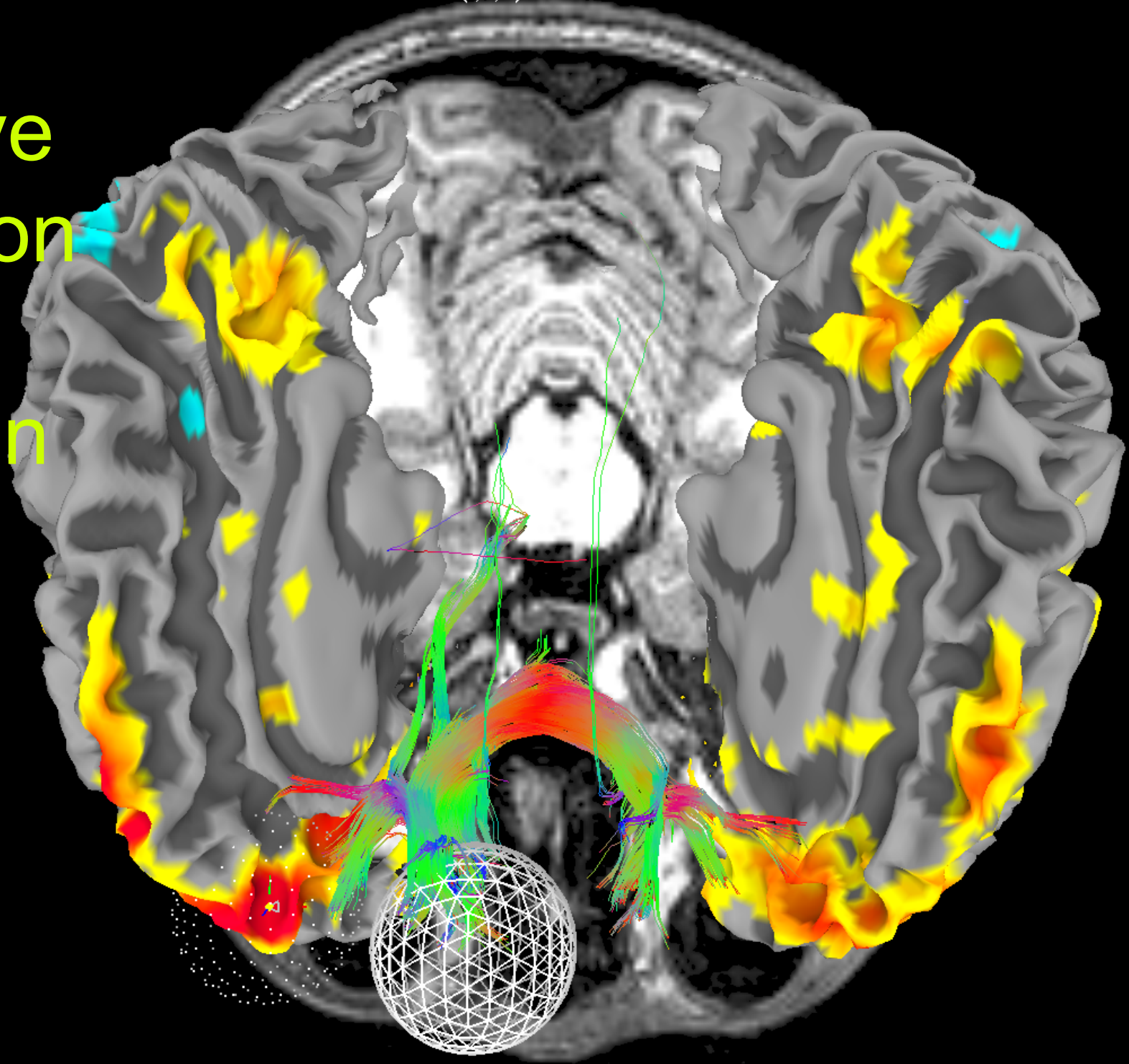
wm rh G and S cingul-Ant
(I,T,B)XcorrCoef=0.136



wm rh G and S_cingul-Ant
(I,T,B)XcorrCoef=0.391



Goal:
Interactive
exploration
of high
dimension
complex
datasets



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