fMRI Course, Day 12: Introduction to Open Science and BIDS

August 10th, 2023

Review of Kriegeskorte Supplementary Material

Questions

What are three types of multiple comparisons correction?

What is the summary statistic approach?

What is an example of a circular analysis?

Why is it widely recommended to use a CDT of p=0.001?

Questions

What does permutation thresholding do
for parametric (i.e., continuous) regressors?

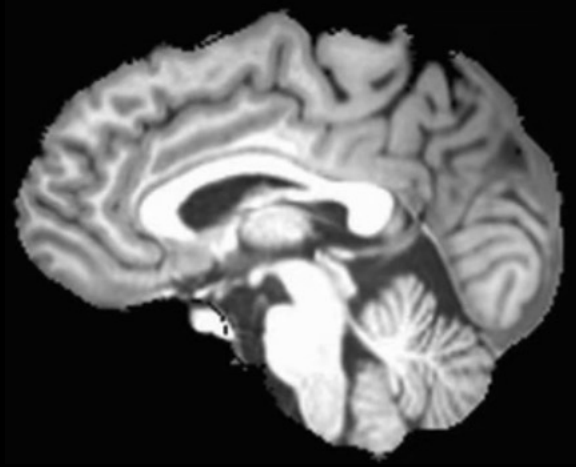
What can we do to improve between-subjects inferences
(brain-individual differences associations)?
Are mass univariate analyses potentially less appropriate than previously thought?

How to address large, contiguous, undifferentiated clusters,
even after you have increased alpha to break them up?

Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level					mm	mm	mm
p	c	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	k_E	p_{uncorr}	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	T	(Z_E)	p_{uncorr}			
0.846	**5**	**0.026**	**0.024**	**198**	**0.000**	**0.716**	**0.996**	**4.00**	**3.94**	**0.000**	**-39**	**-73**	**-22**
						1.000	0.996	3.26	3.23	0.001	-42	-52	-19
						1.000	0.996	3.24	3.20	0.001	-27	-70	-16
		0.537	**0.175**	**85**	**0.011**	**0.912**	**0.996**	**3.79**	**3.74**	**0.000**	**42**	**-40**	**-19**
						1.000	0.996	3.12	3.09	0.001	48	-52	-25
		0.999	**0.794**	**31**	**0.102**	**0.998**	**0.996**	**3.48**	**3.44**	**0.000**	**-66**	**-43**	**11**
		0.489	**0.175**	**89**	**0.010**	**1.000**	**0.996**	**3.26**	**3.22**	**0.001**	**24**	**-1**	**65**
						1.000	0.996	2.91	2.89	0.002	33	2	50
						1.000	0.996	2.89	2.86	0.002	30	-7	50
		0.105	**0.050**	**146**	**0.002**	**1.000**	**0.996**	**3.24**	**3.20**	**0.001**	**9**	**14**	**32**
						1.000	0.996	3.11	3.08	0.001	0	29	26
						1.000	0.996	3.04	3.01	0.001	-3	20	71

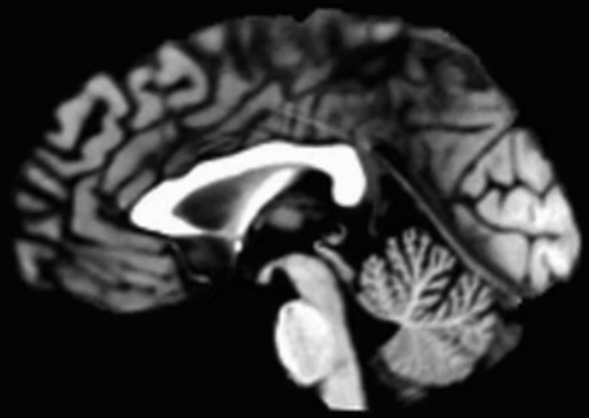
Andy's Brain



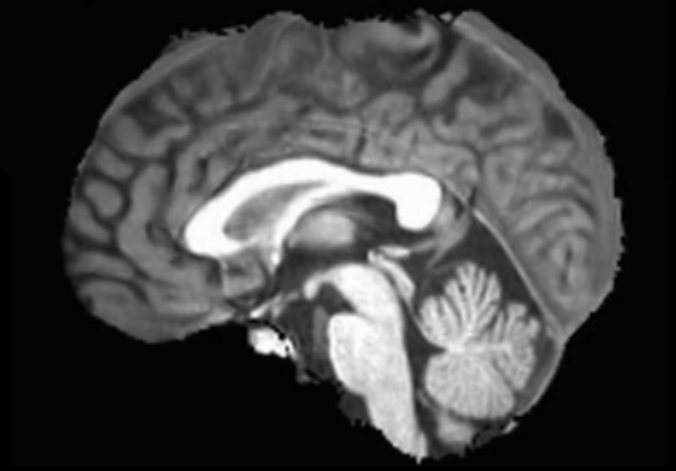
Warped to

=

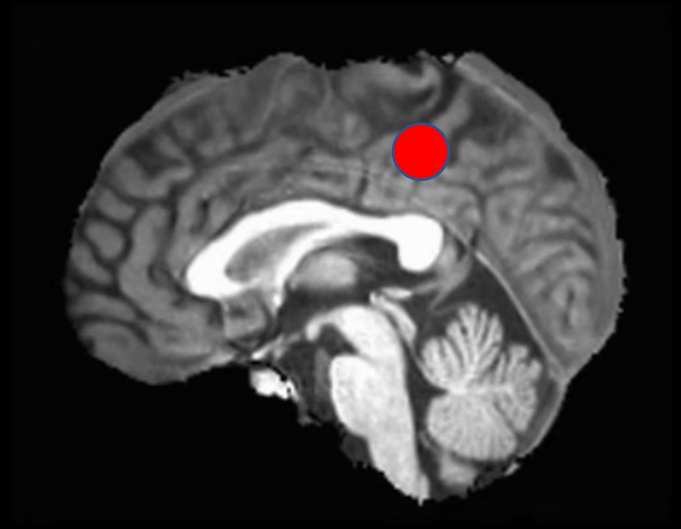
Template Brain



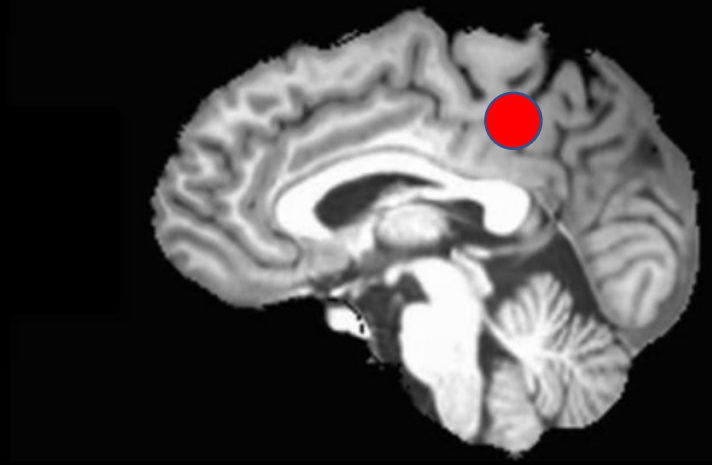
Andy's Warped Brain



Andy's Warped Brain
(Standardized space)



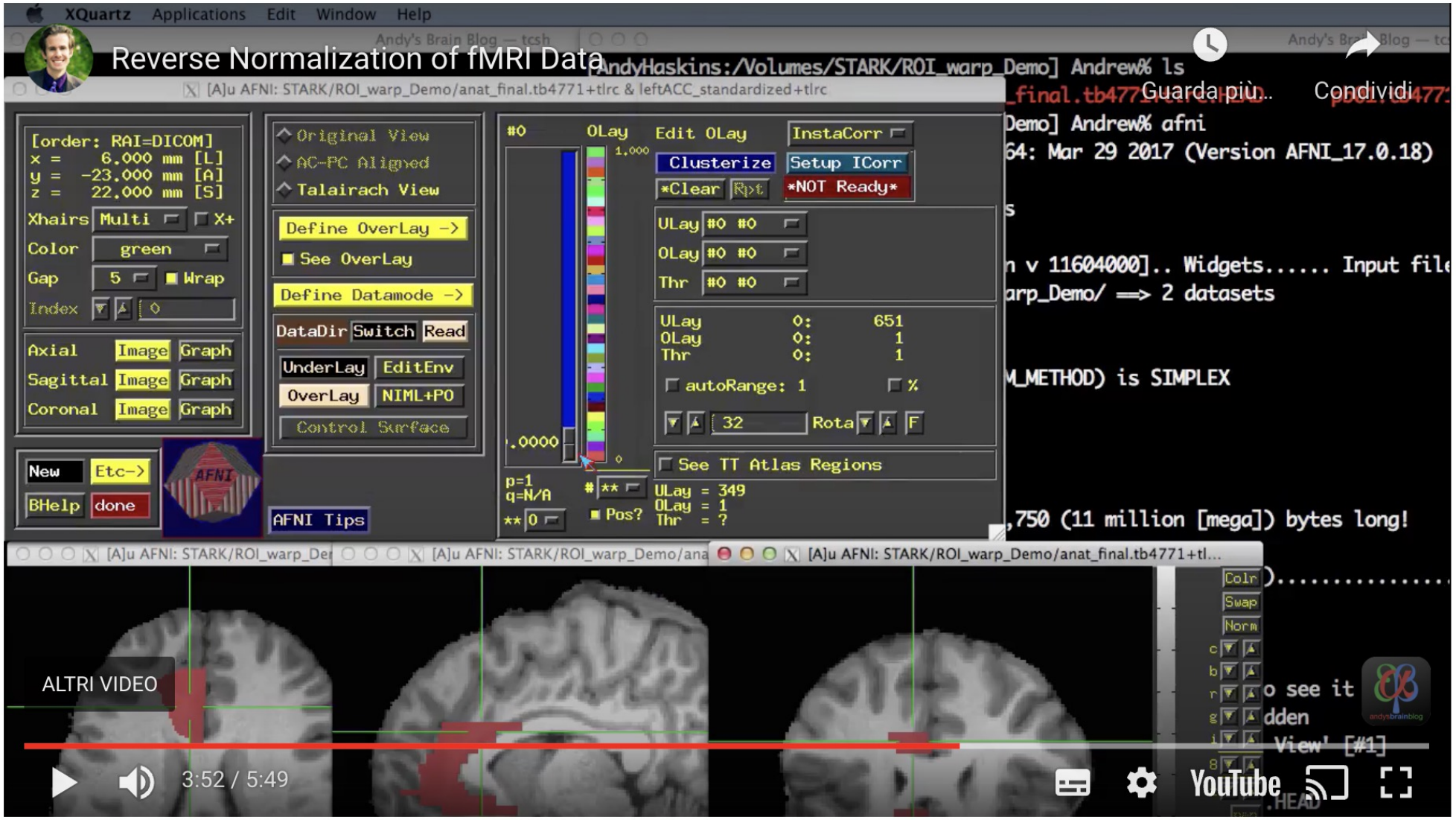
Andy's Unwarped Brain
(Native space)



Reverse Normalization

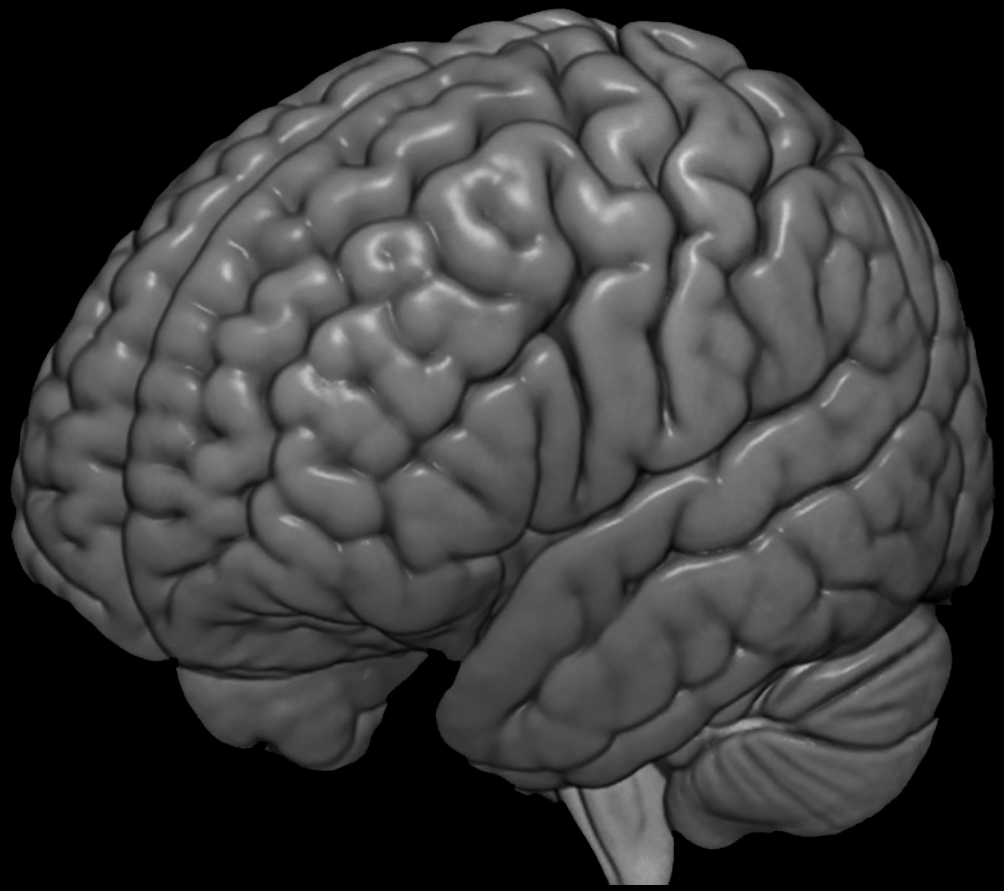
Reverse Normalization of fMRI Data

May 13, 2017

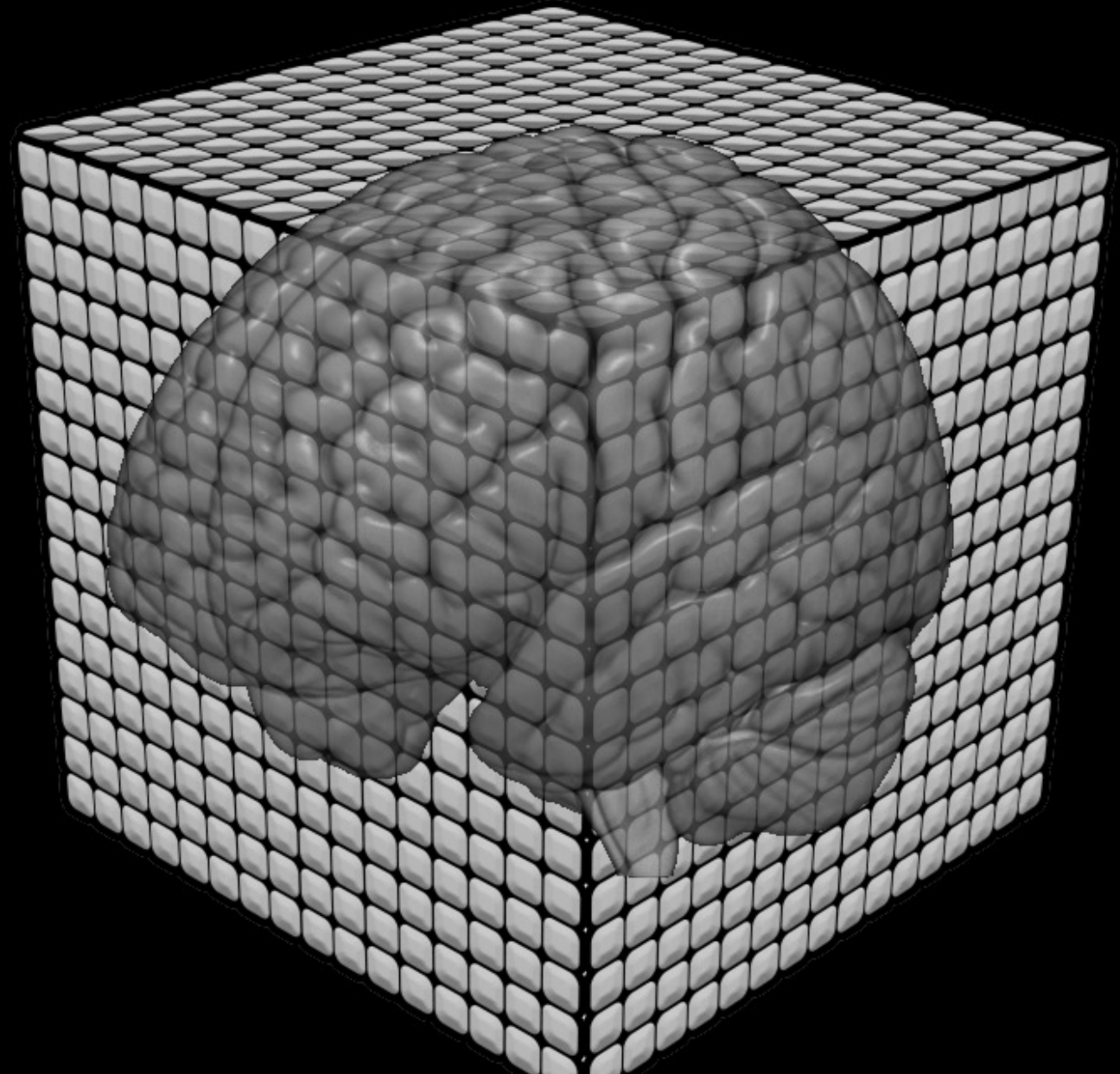


Surface-based analysis with FreeSurfer

Why use it?



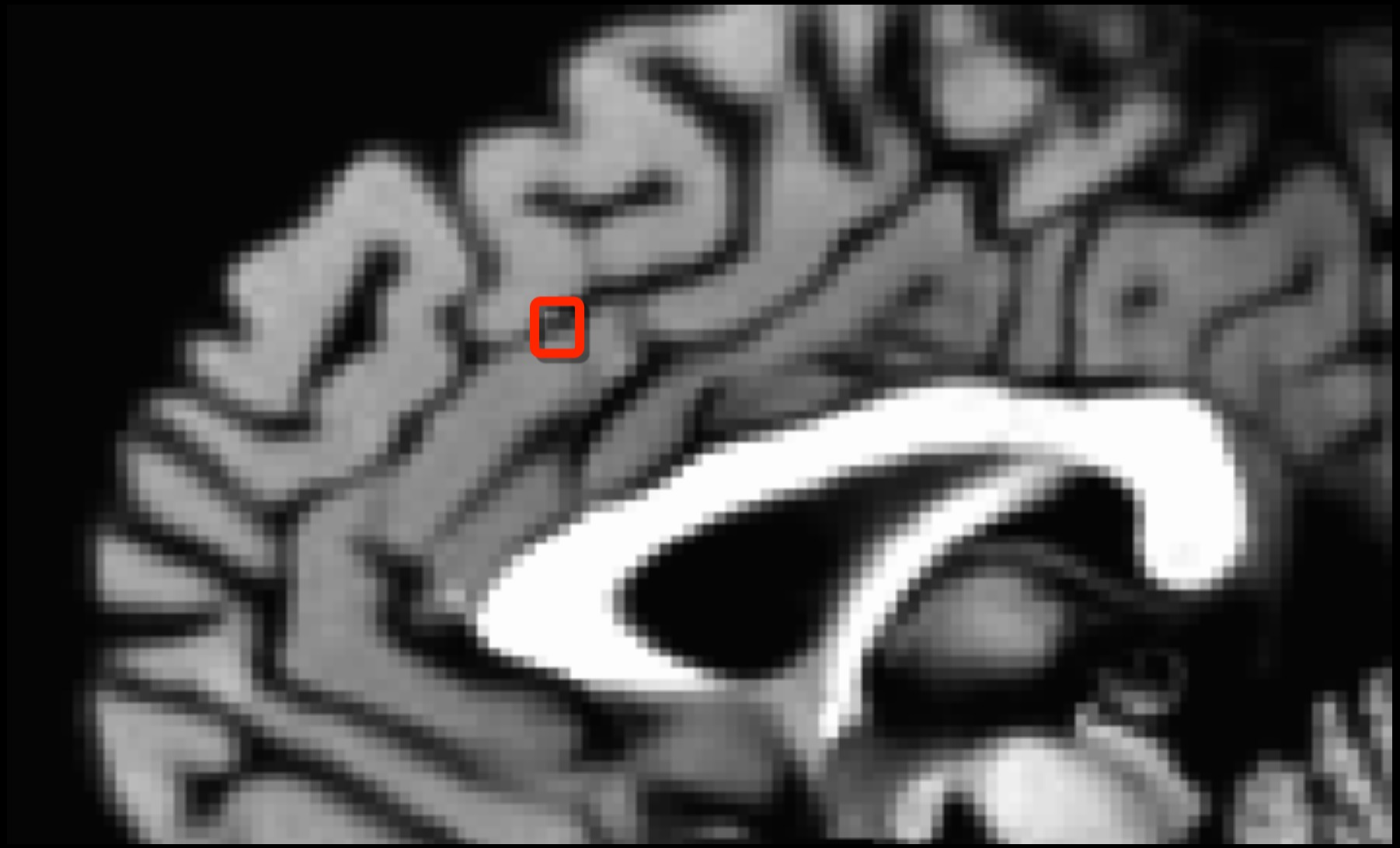
Why use it?



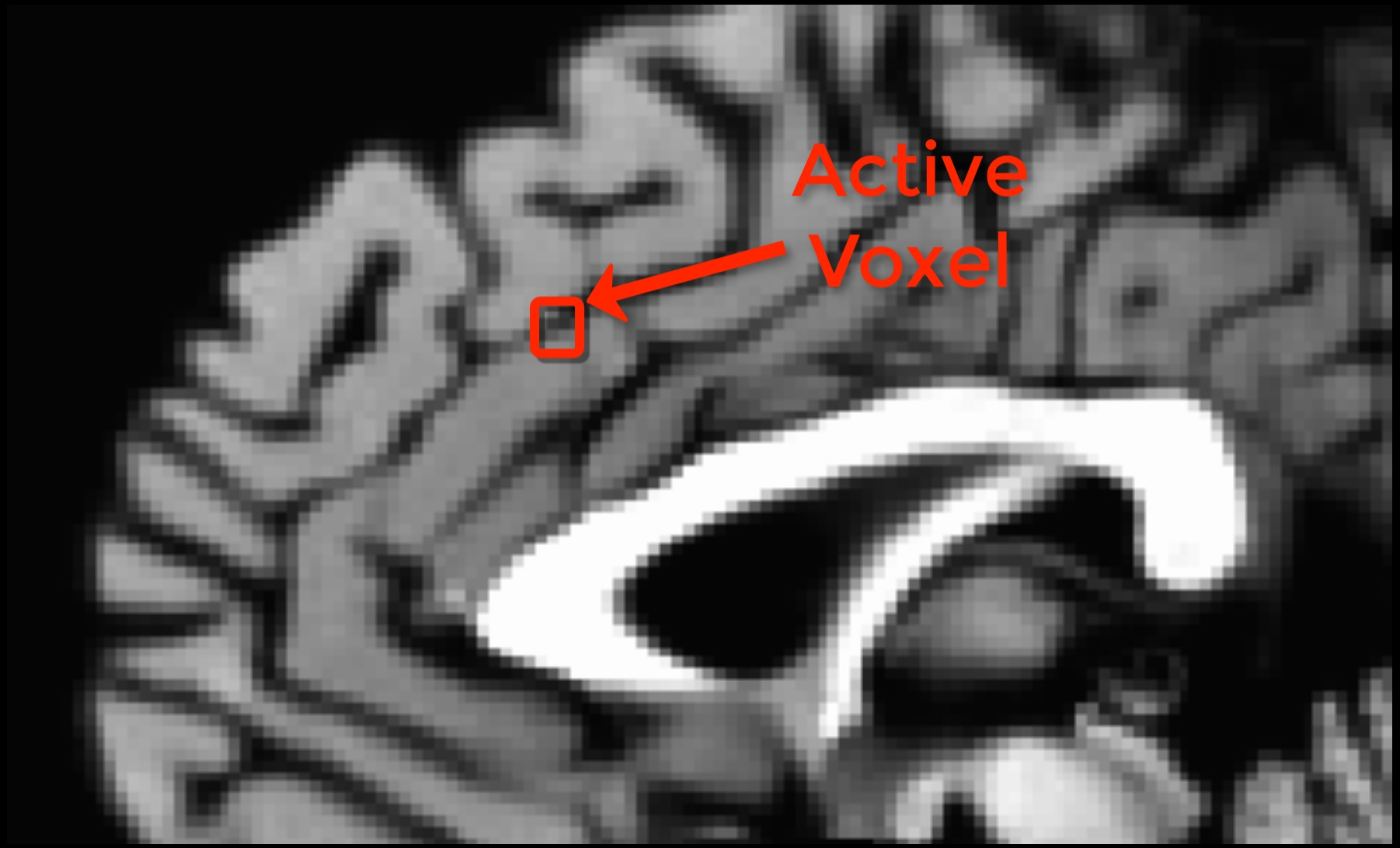
Why use it?

Problems with Voxels

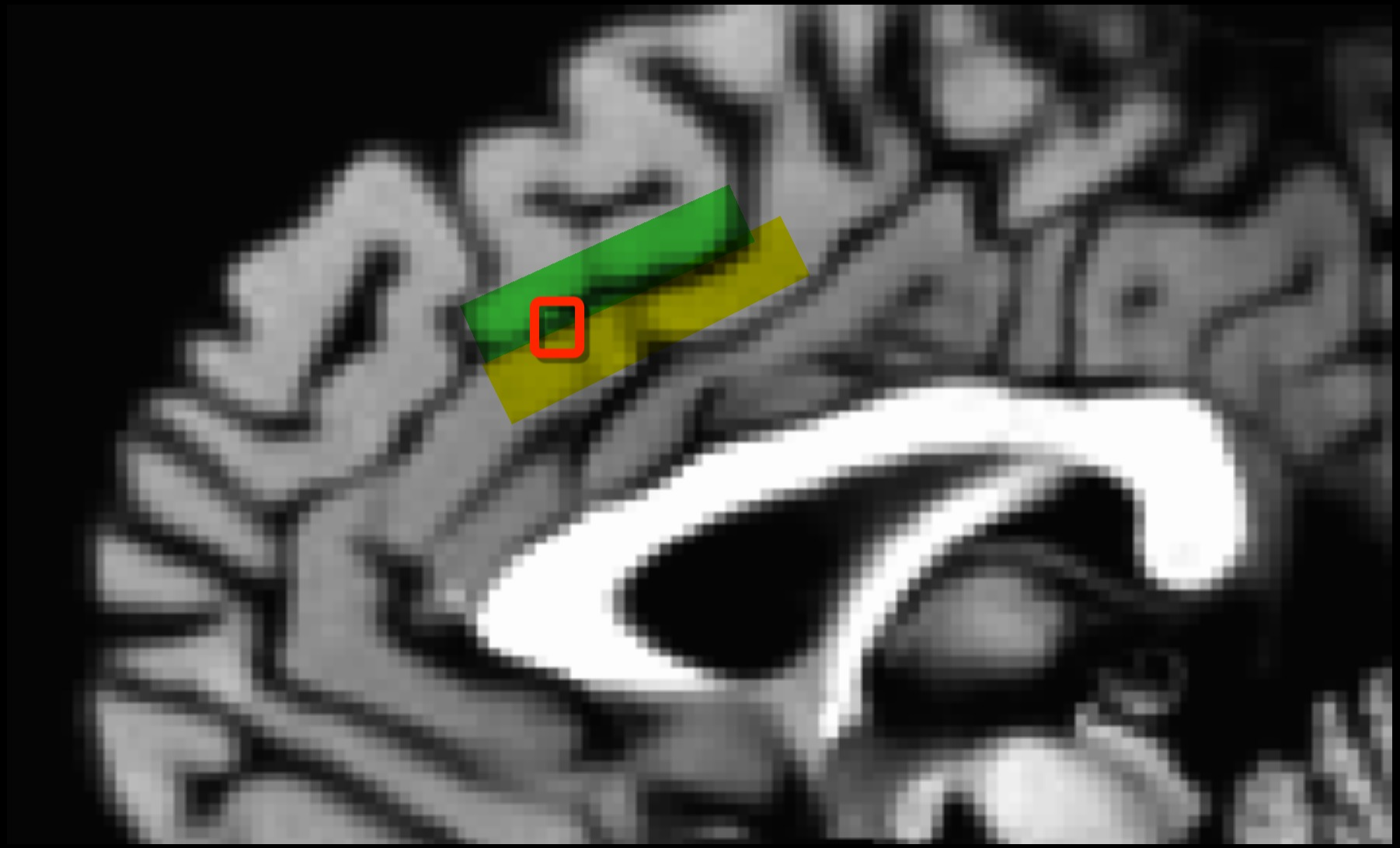
Problems with voxels



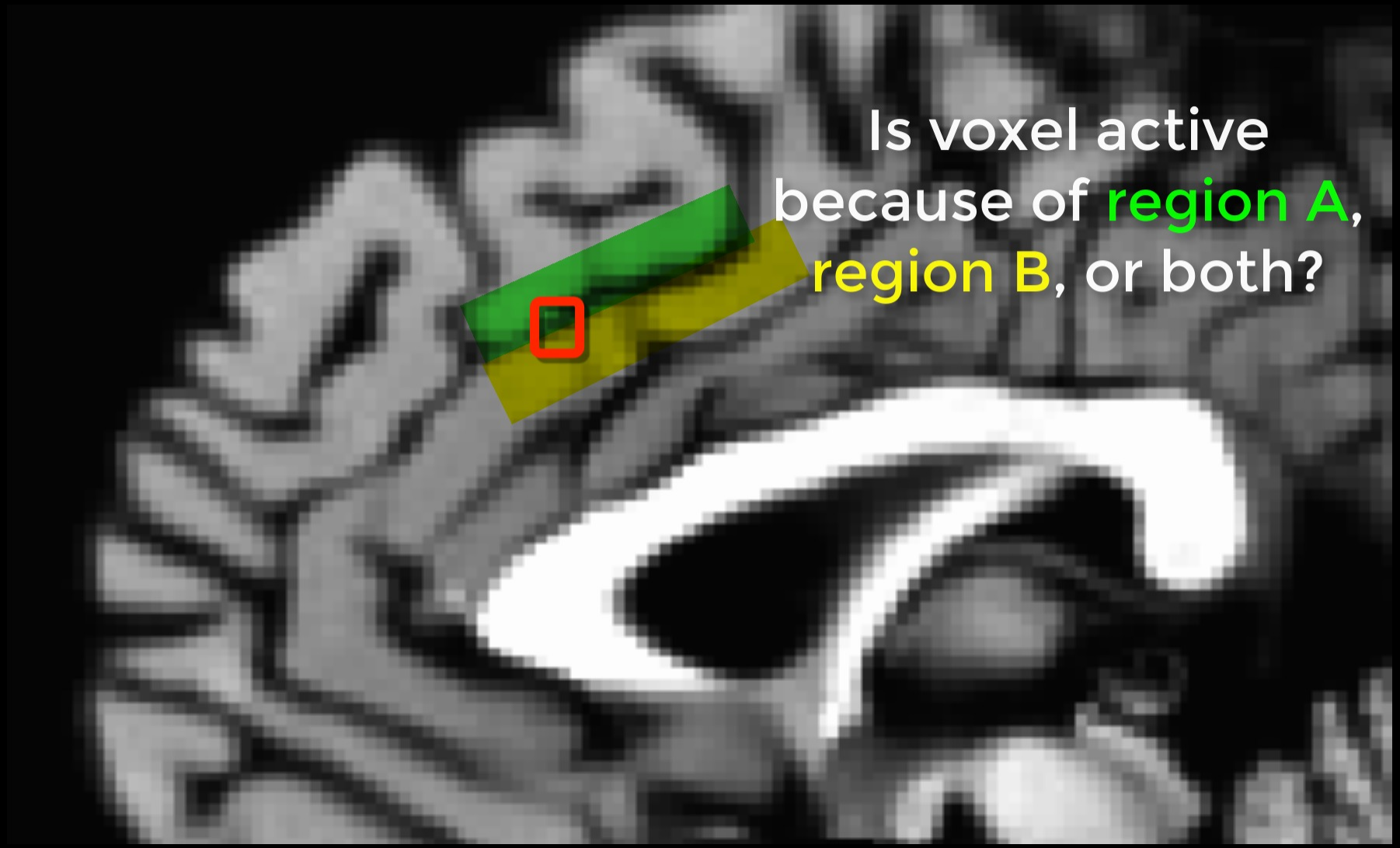
Problems with voxels



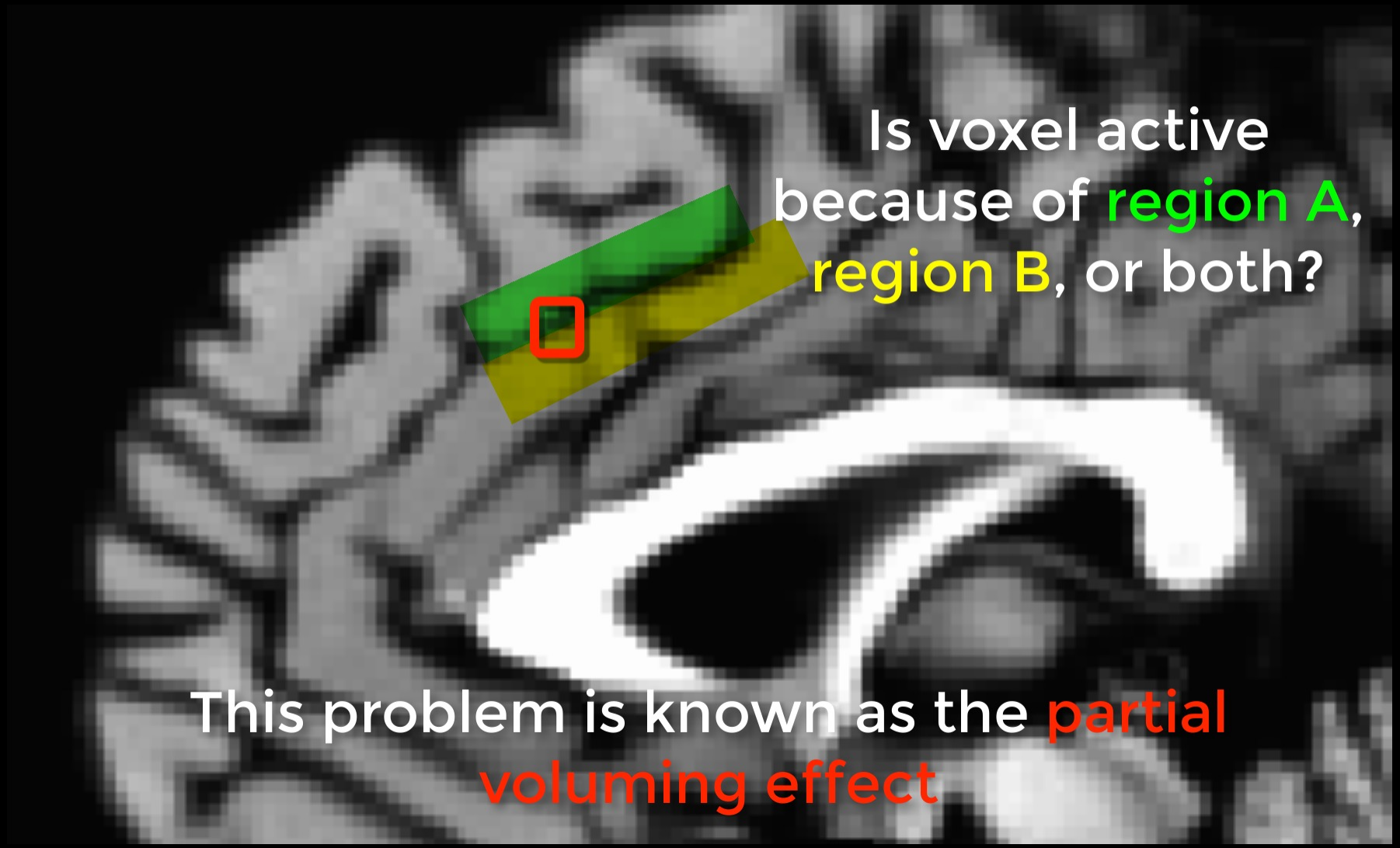
Problems with voxels



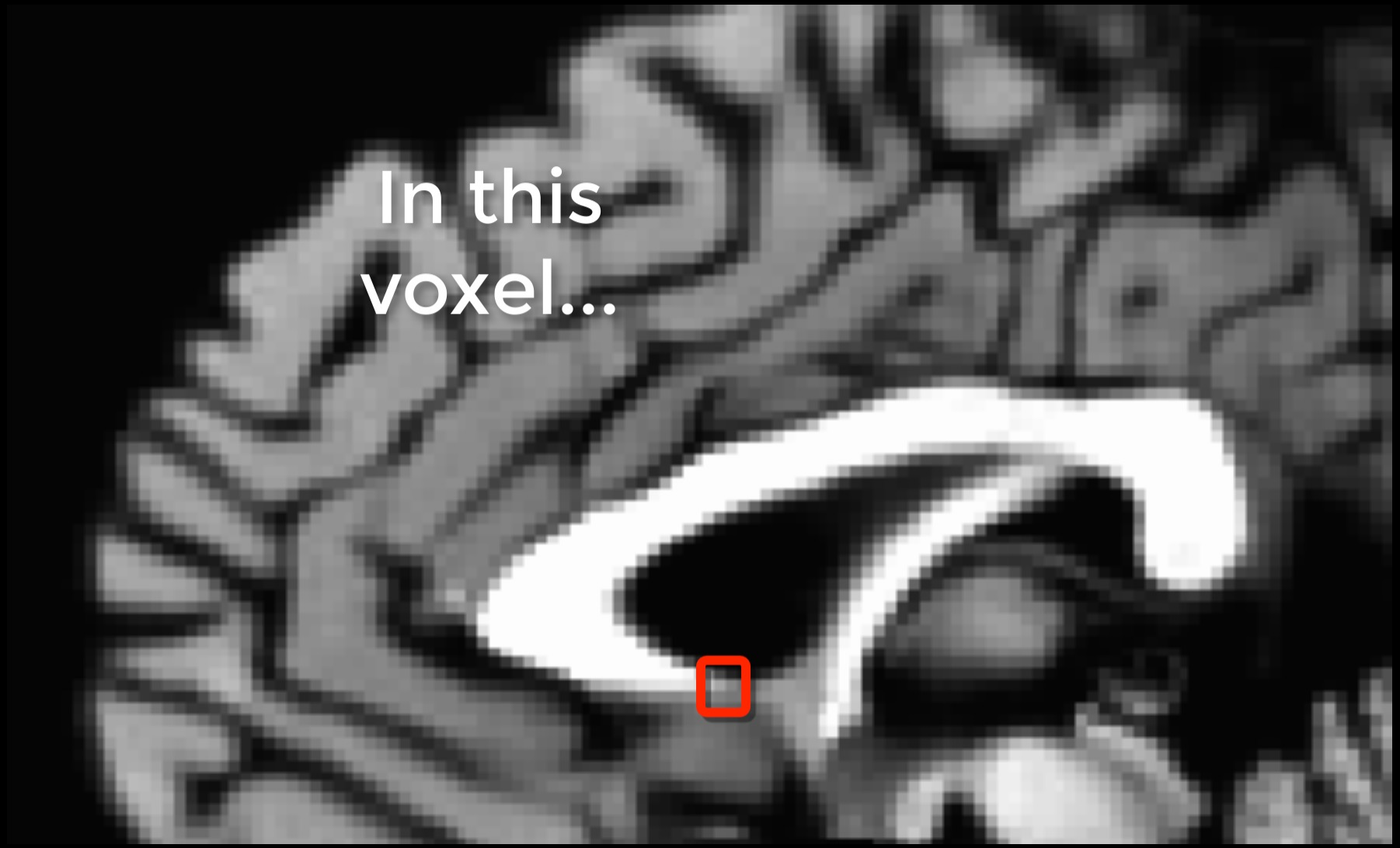
Problems with voxels



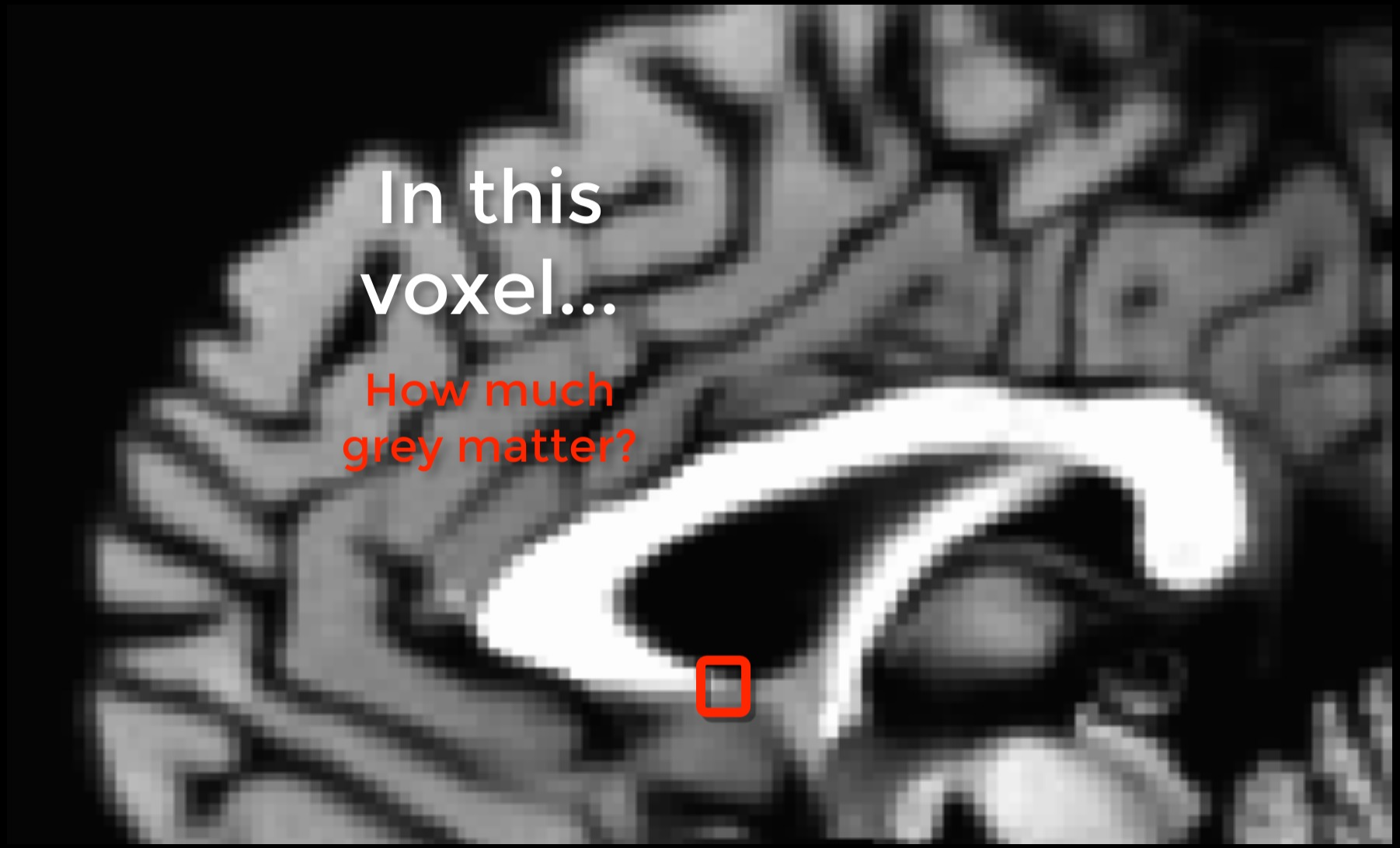
Problems with voxels



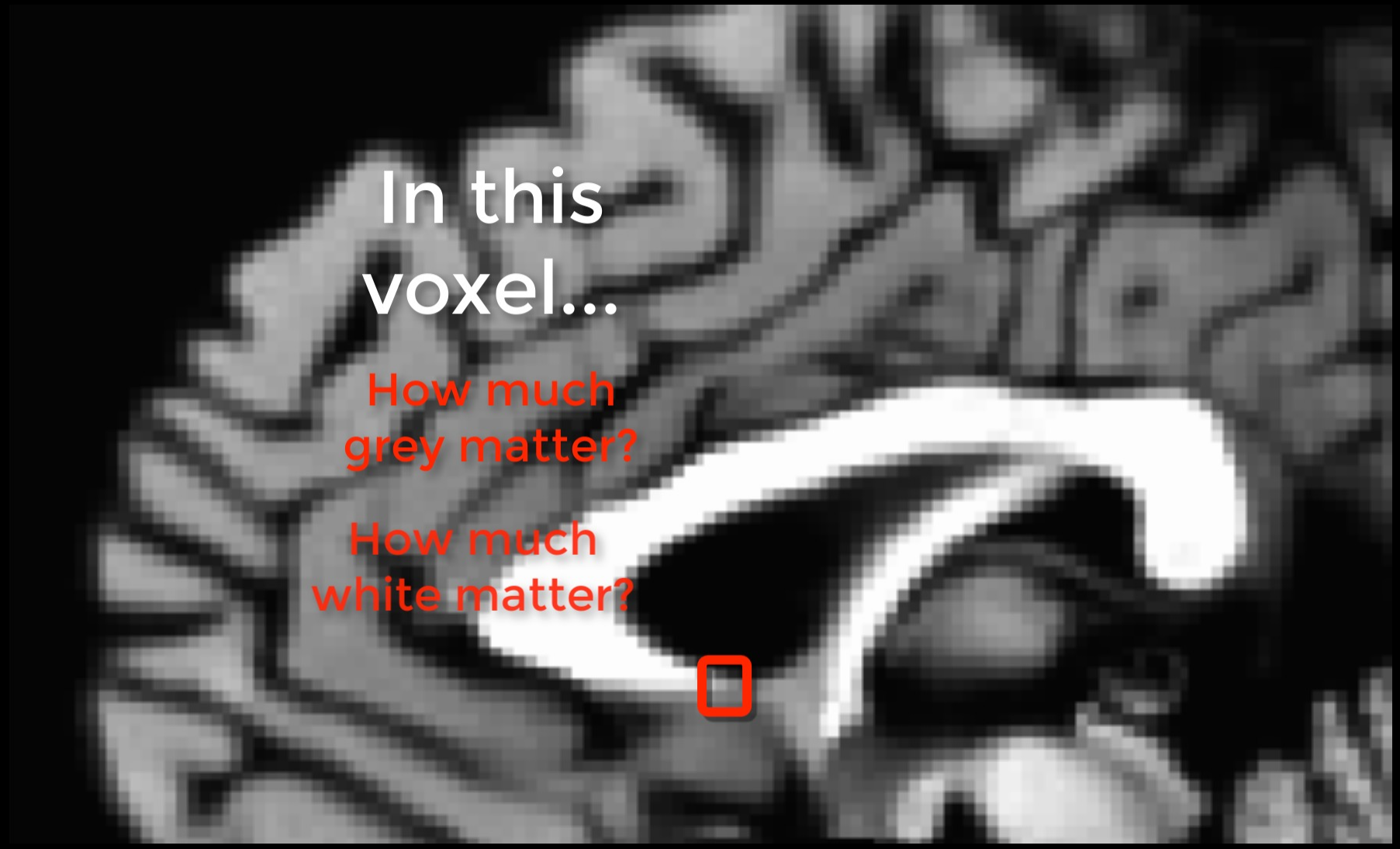
Problems with voxels



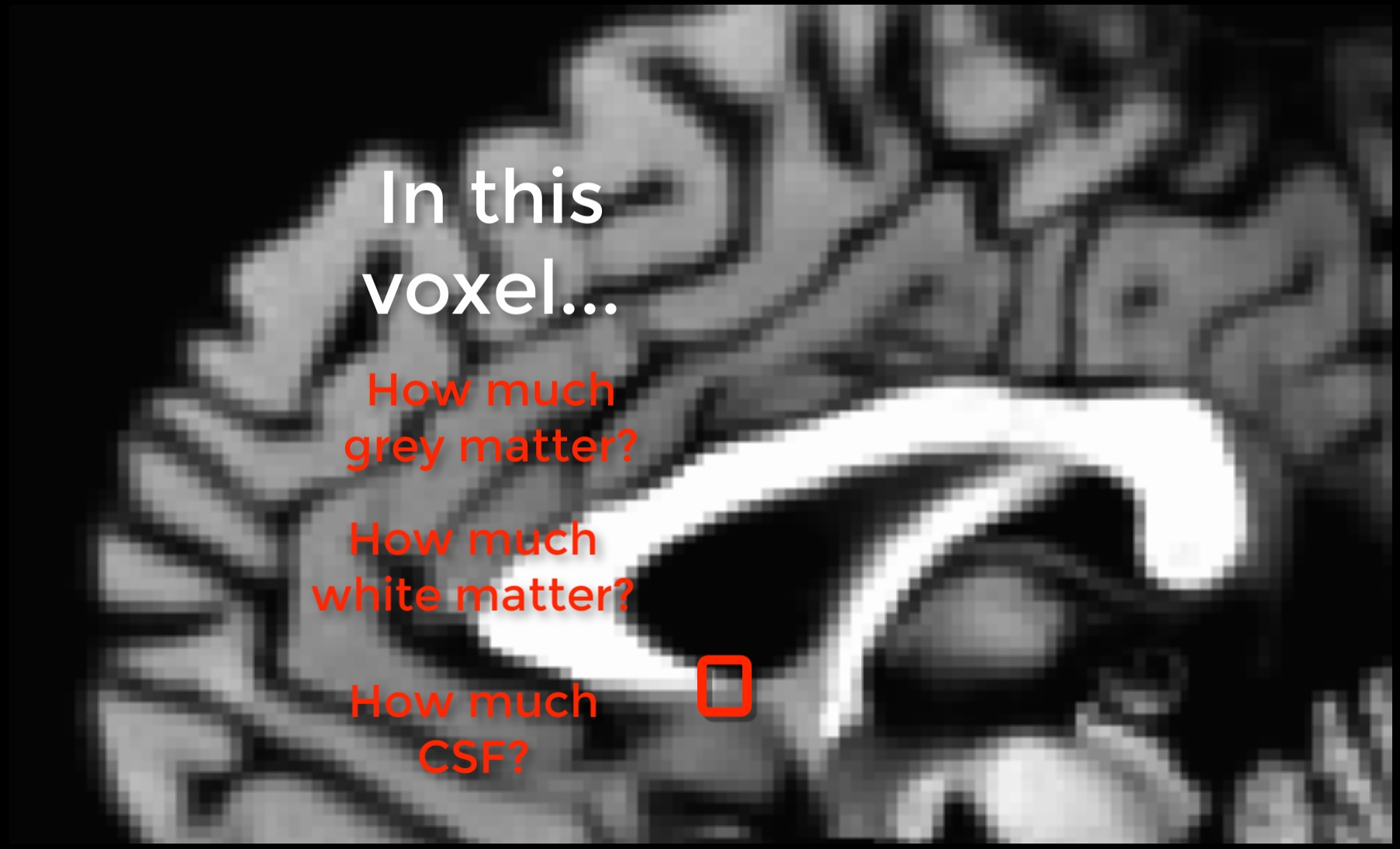
Problems with voxels



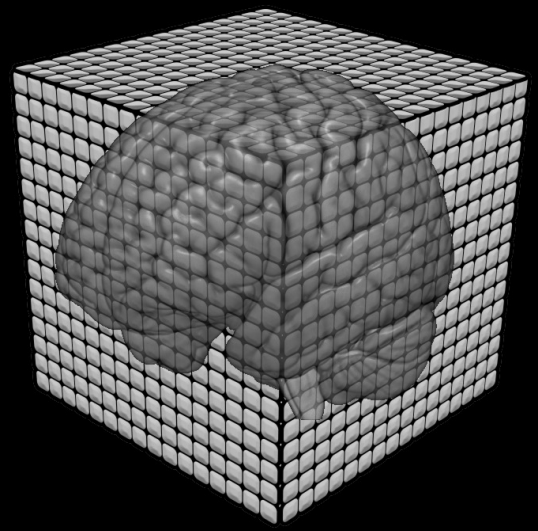
Problems with voxels

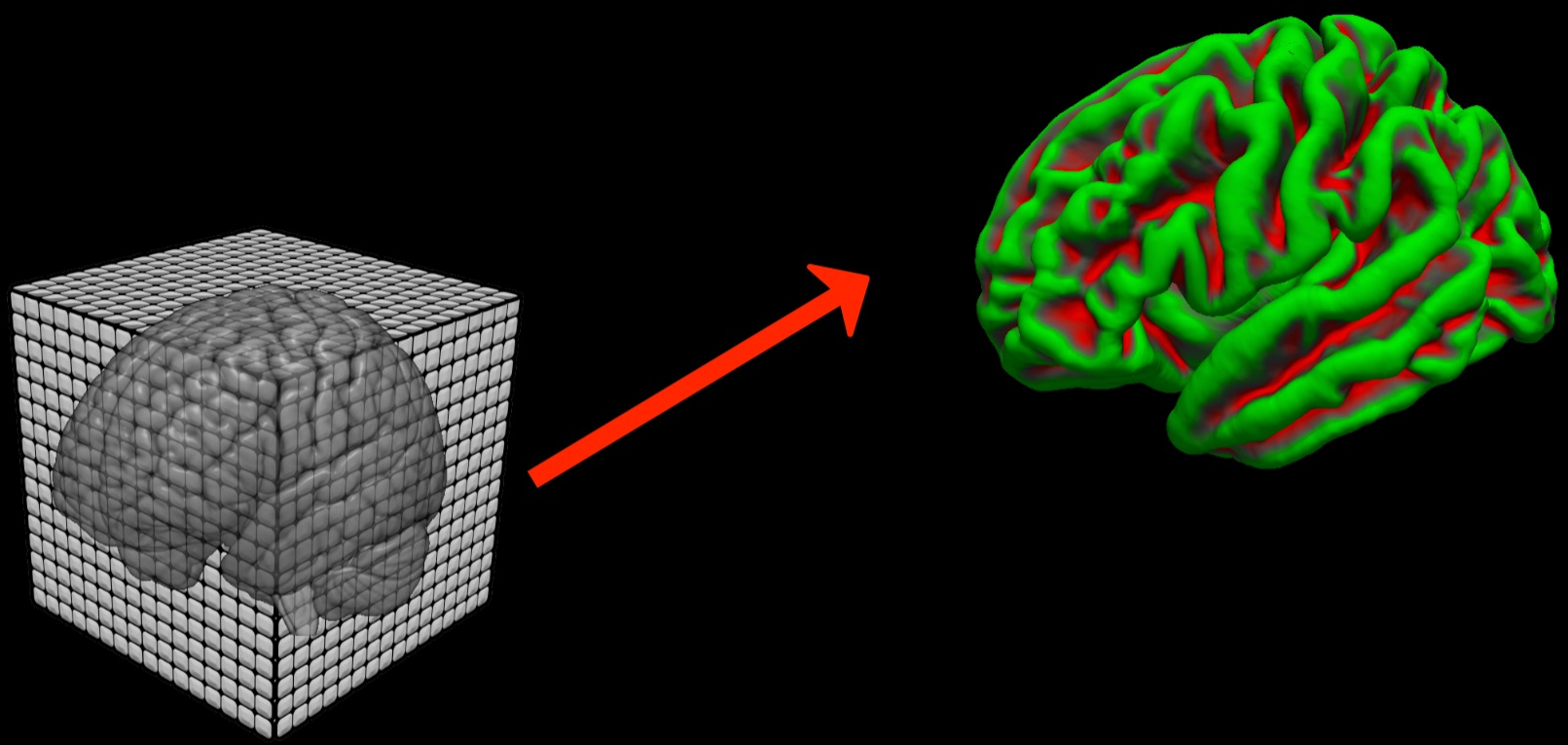


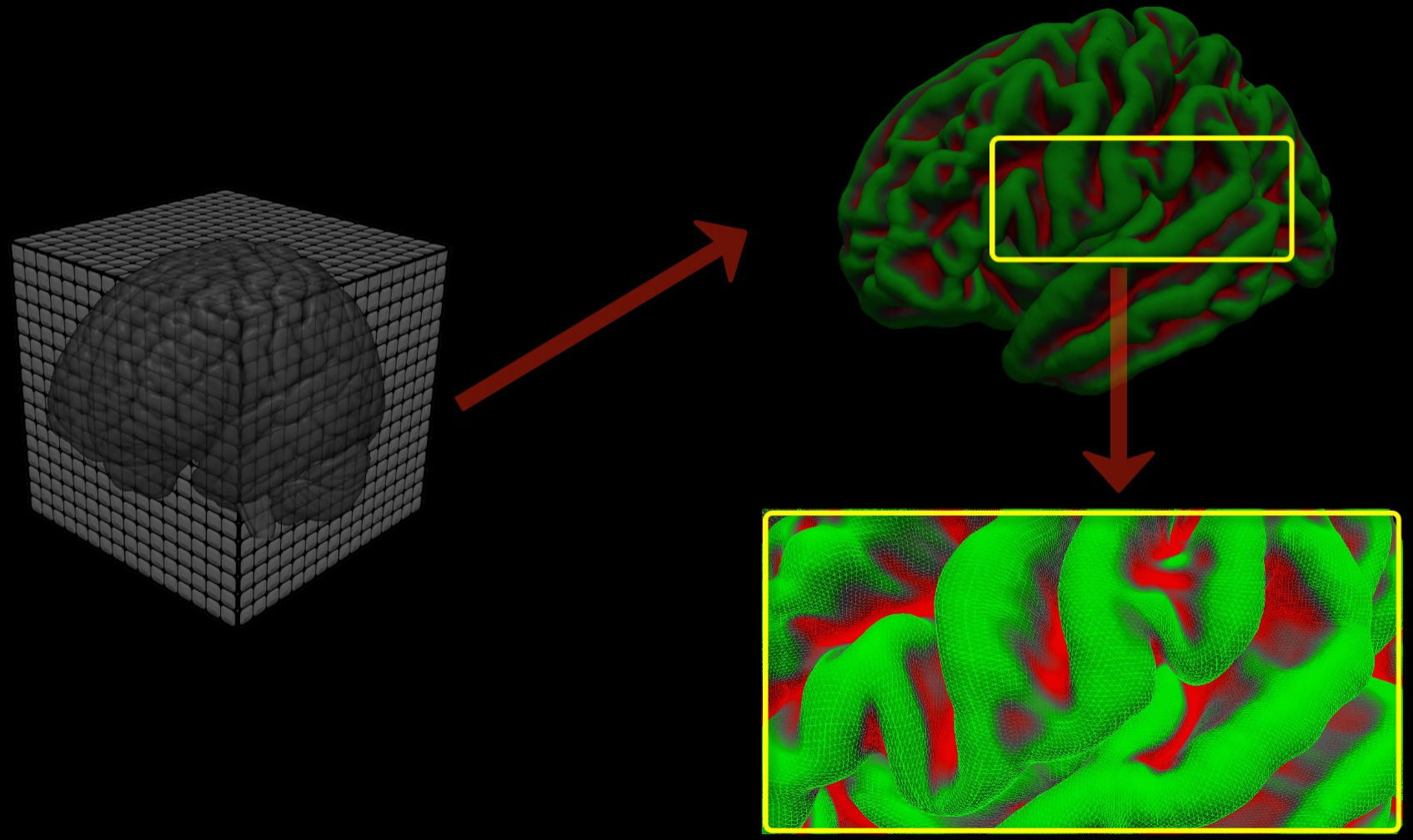
Problems with voxels

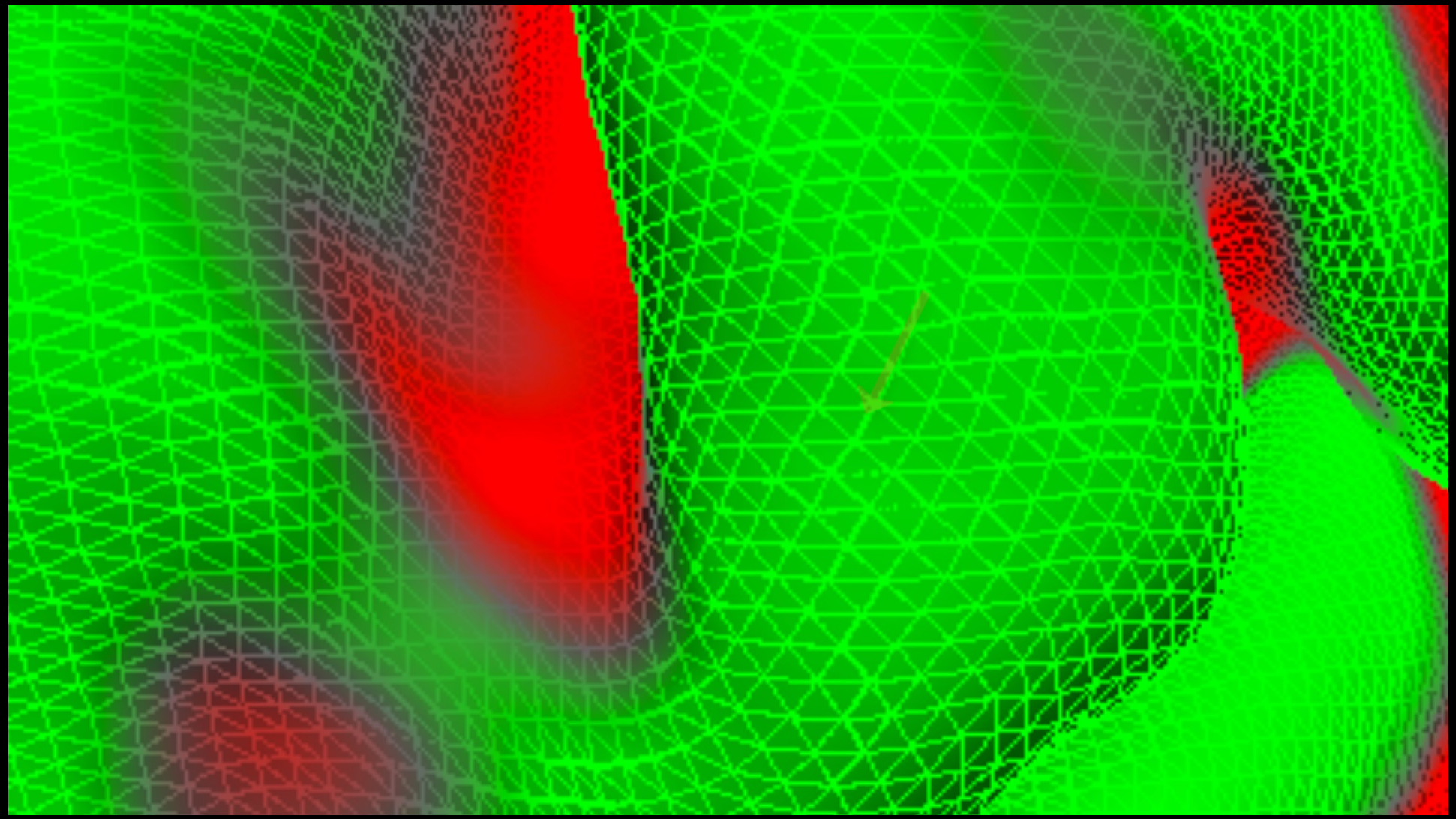


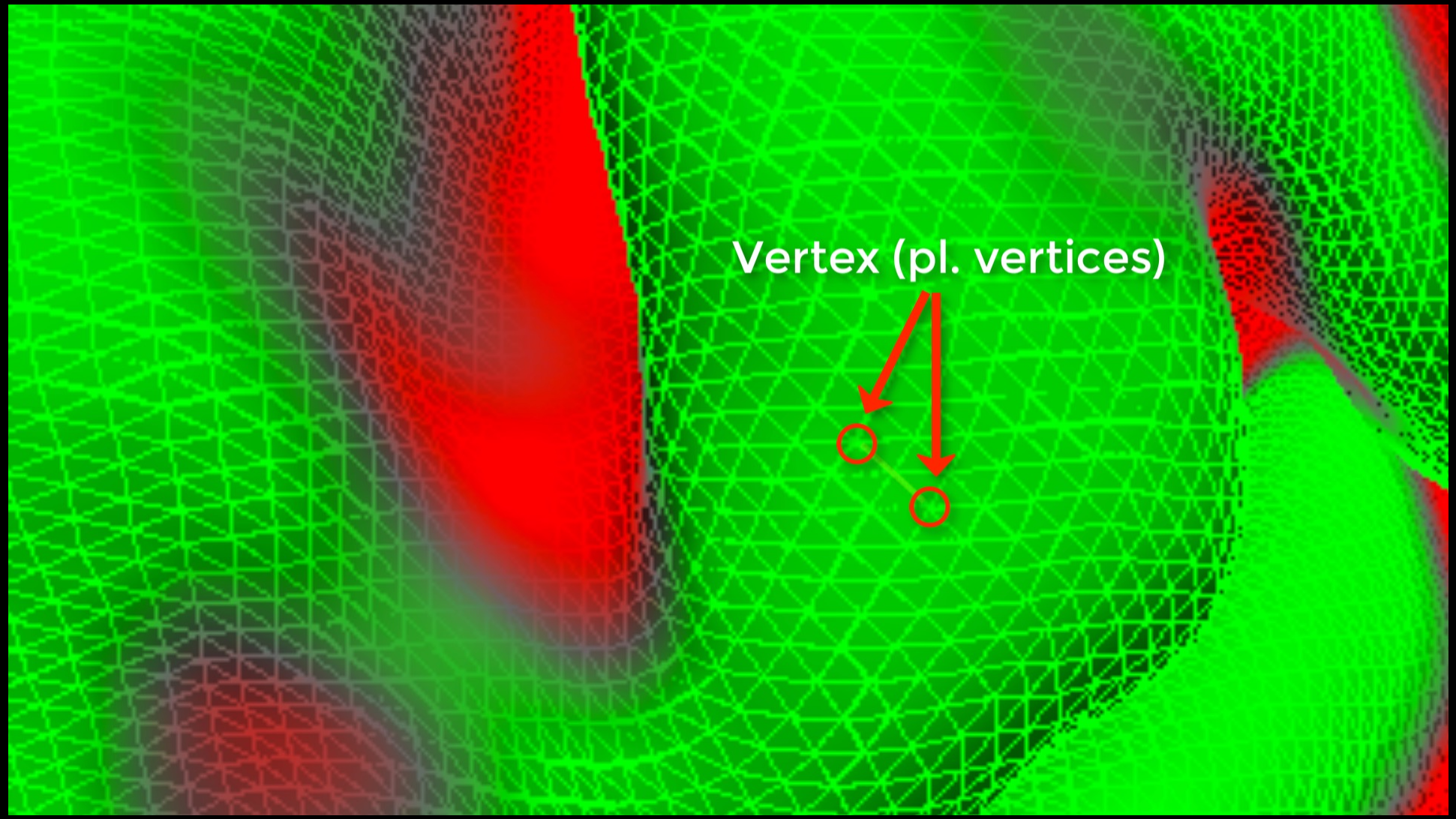
Overview of FreeSurfer

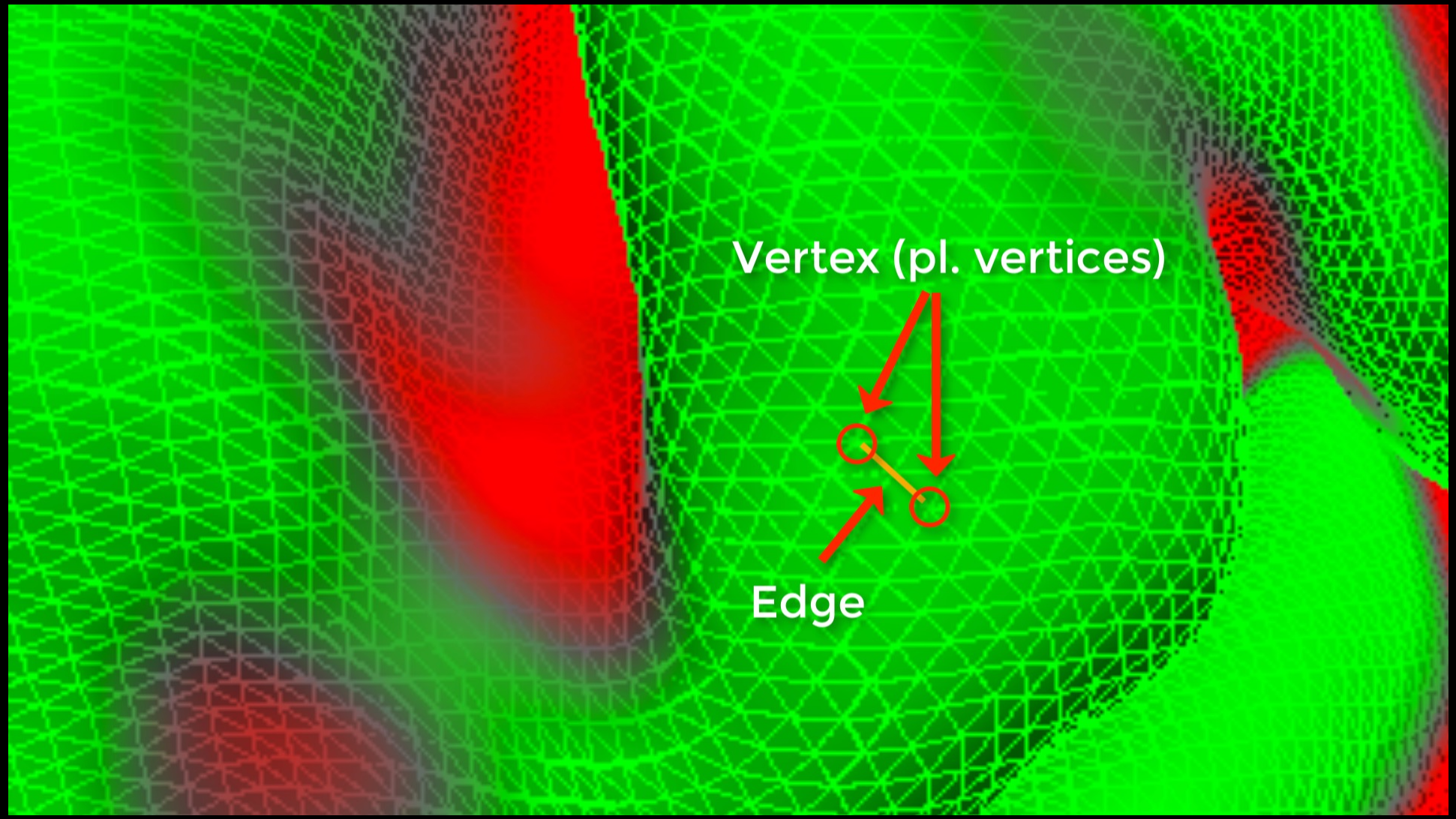


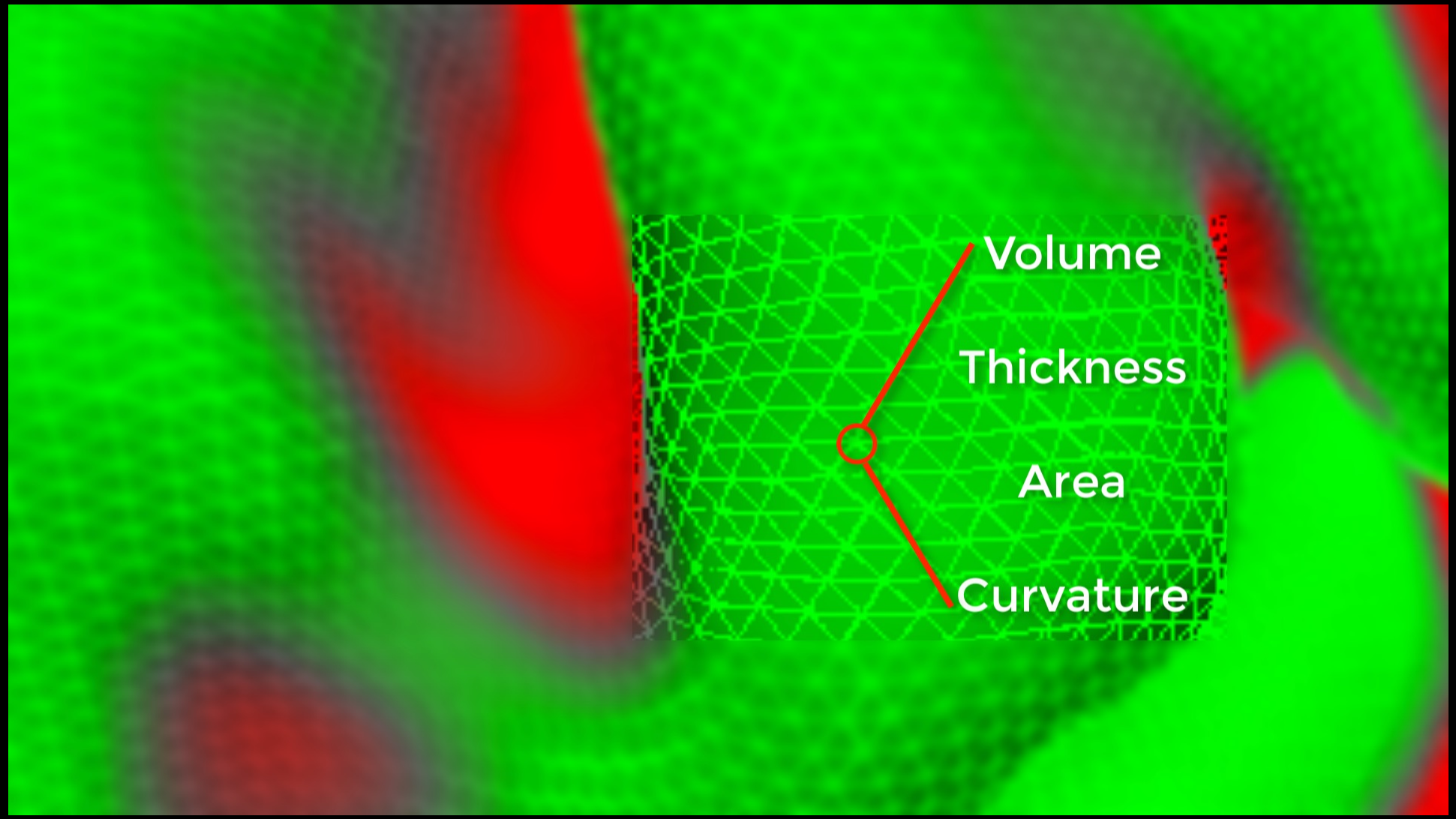


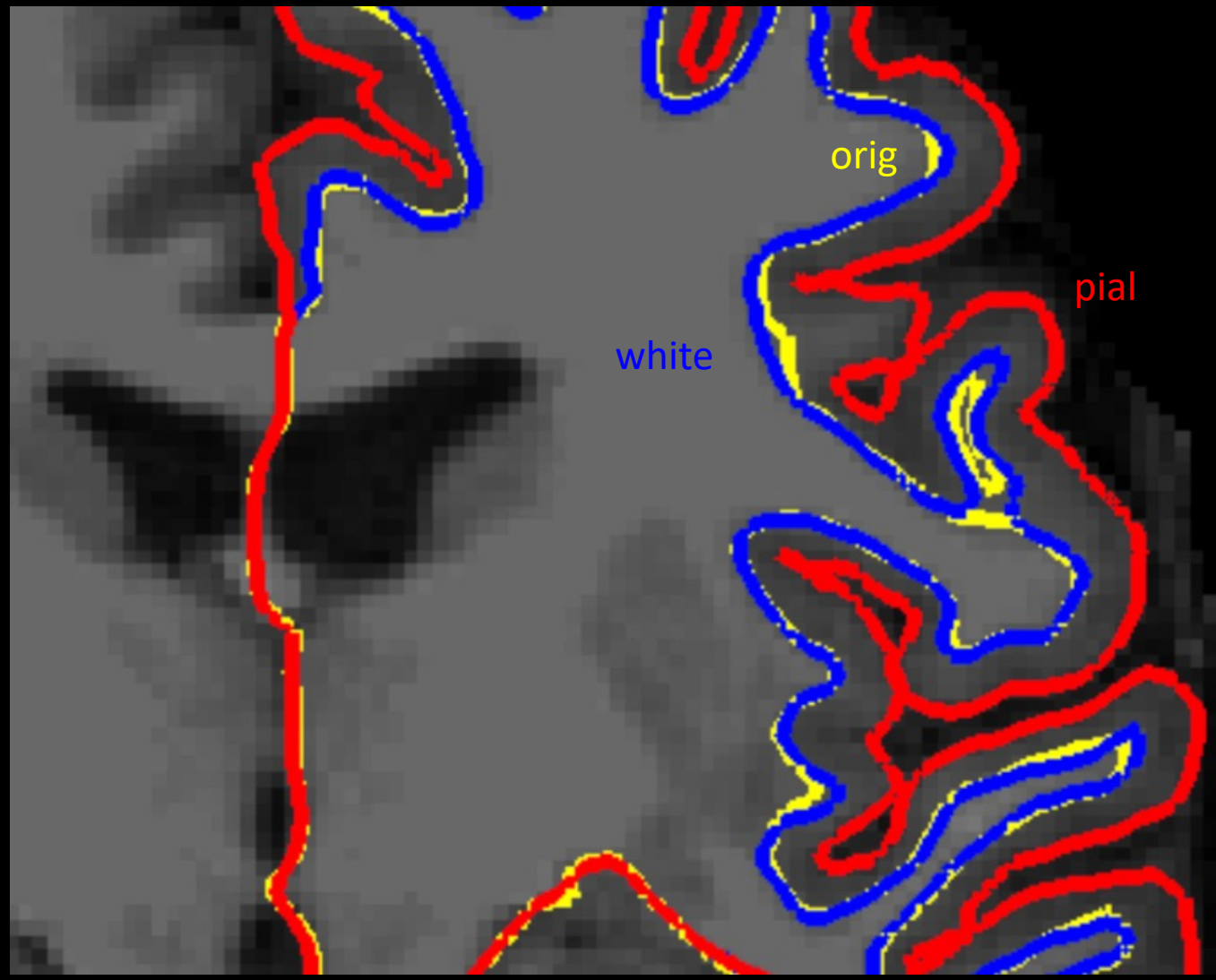





Vertex (pl. vertices)


Vertex (pl. vertices)
Edge

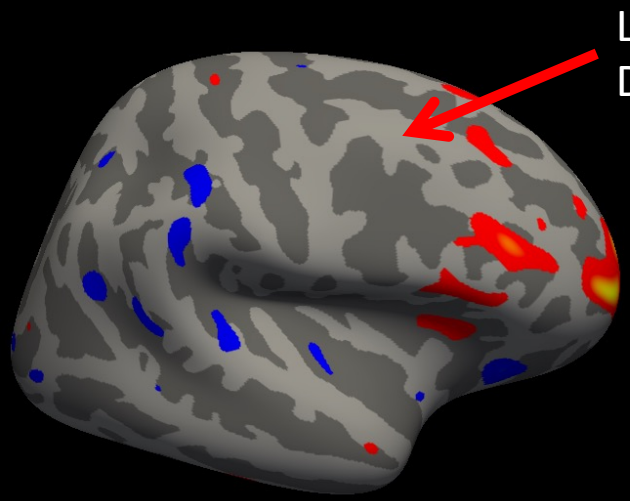

Volume
Thickness
Area
Curvature

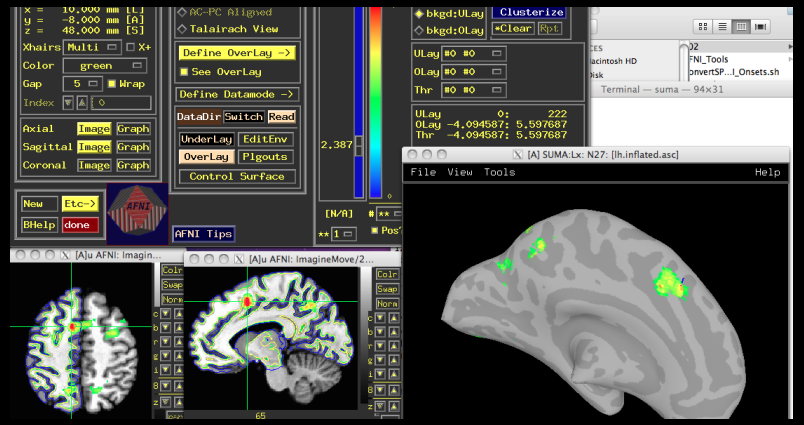

orig
pial
white

Why use it?

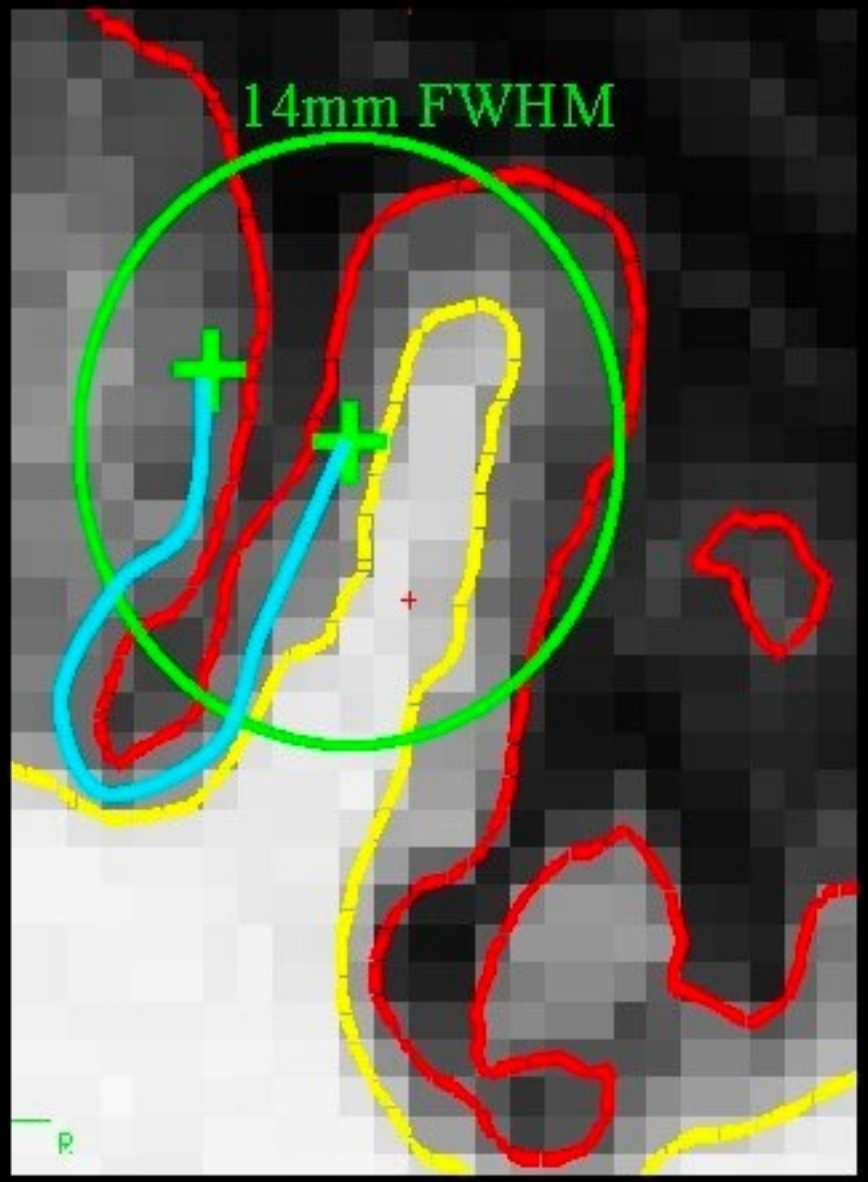
Most sophisticated and widely-used morphometry software available

fMRI activation follows cortical surface





Volume-based Smoothing

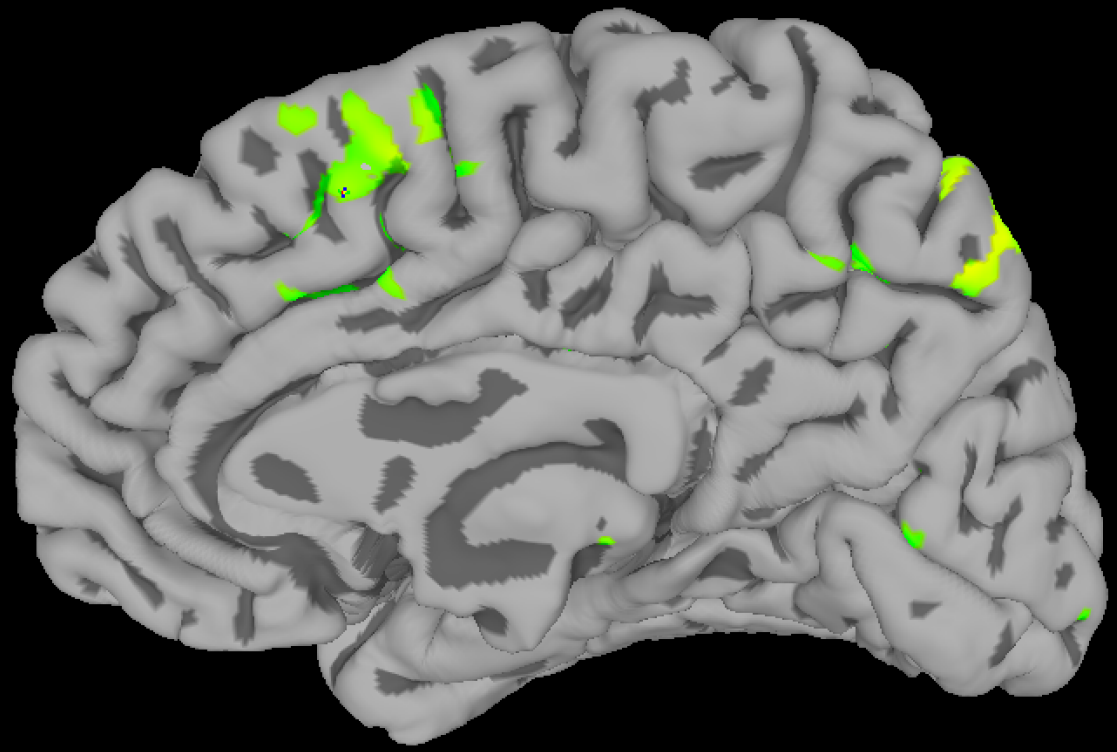


- 5 mm apart in 3D
- 25 mm apart on surface!
- Kernel much larger
- Averaging with other tissue types (WM, CSF)
- Averaging with other functional areas

Slide from FreeSurfer

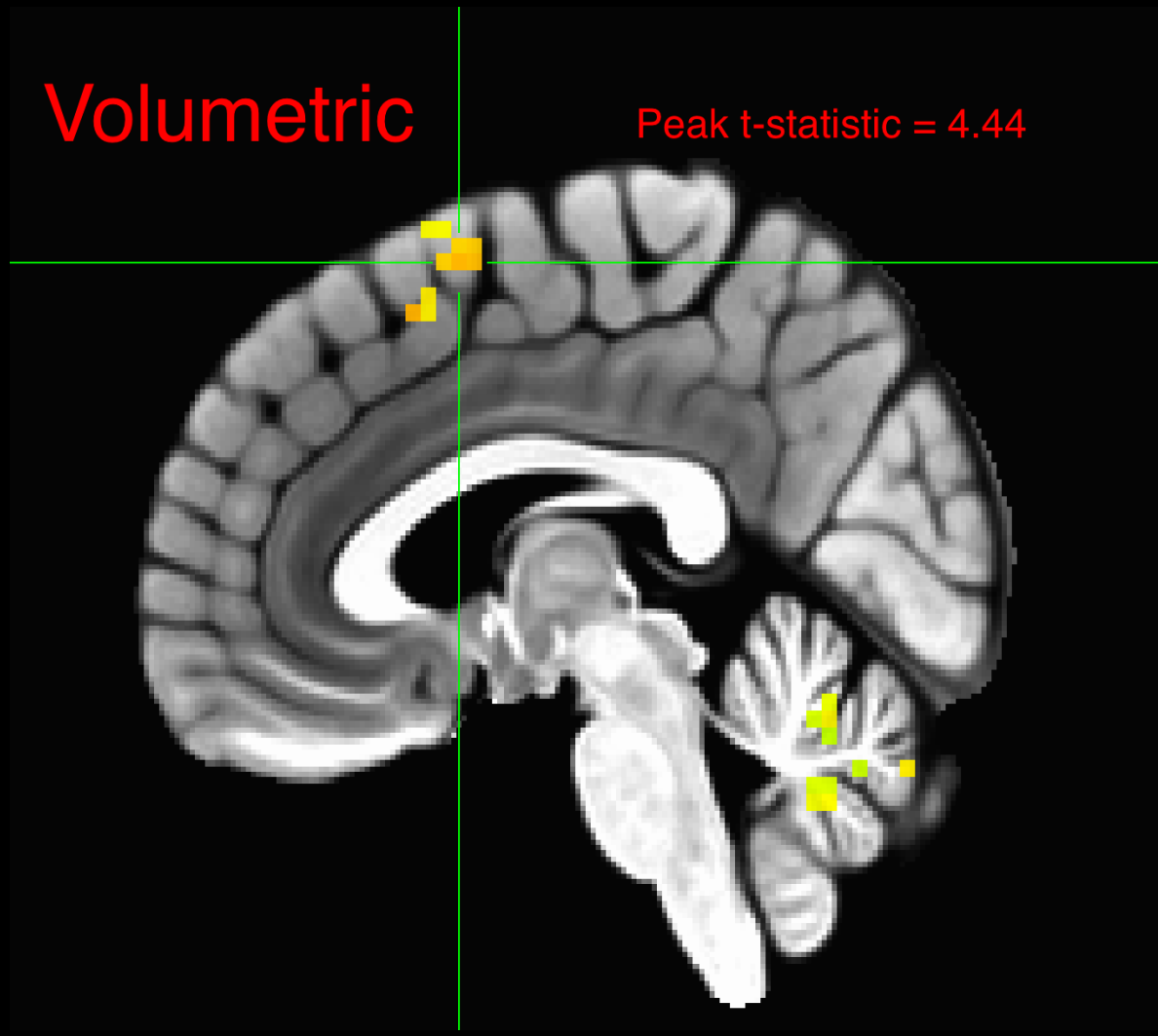
wm_rh_G_front_sup
(I,B)Inc-Con_mean=0.204 (T)Inc-Con_Tstat=5.079

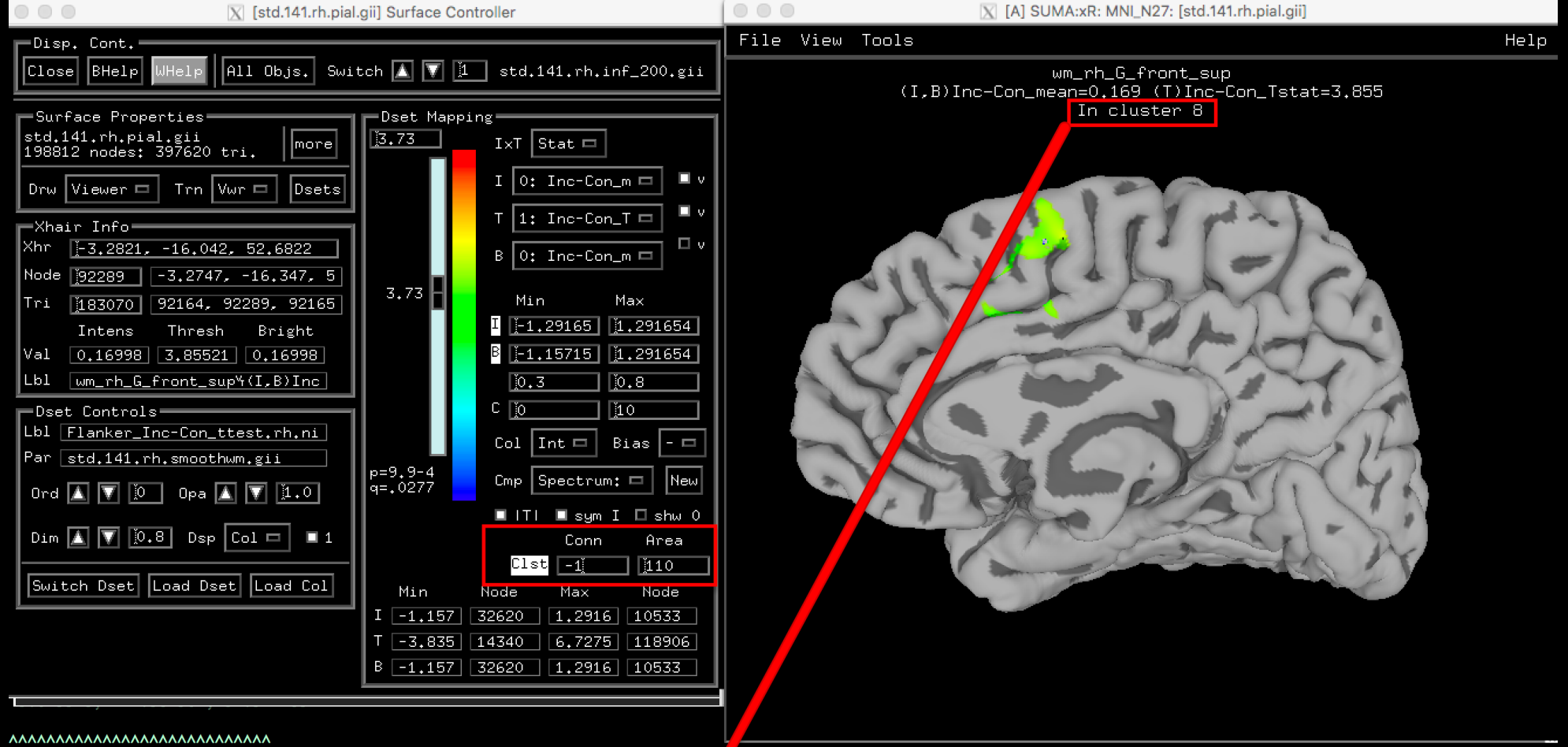
Surface



Volumetric

Peak t-statistic = 4.44

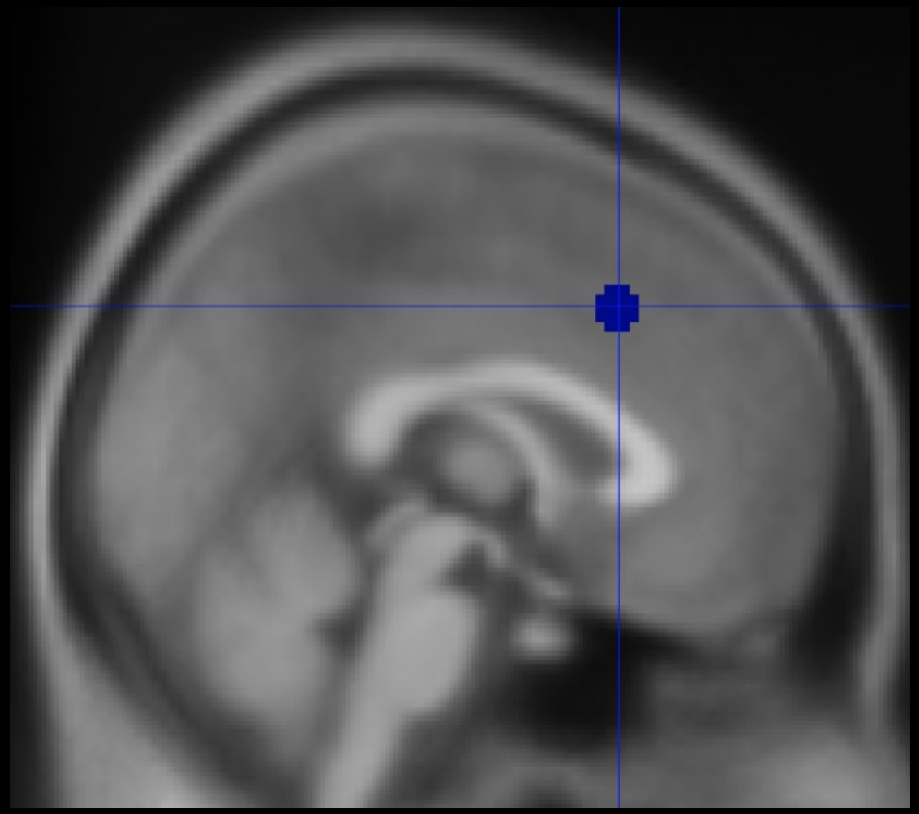





```
^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
SUMA_FindClusters: Have 5403 nodes to work with. 0 nodes have 0 value.

Interactive Clustering Output:
#Command history:
#SurfClust -i suma_MNI_N27/./std.141.rh.smoothwm.gii -input ./Flanker_Inc-Con_ttest.rh.niml.dset 0 -rmm -1.000000 -thresh_col 1 -athresh 3.730000 -amm2 110.000000 -sc
# Rank    num Nd        Area        Mean       |Mean|       Cent    W Cent       Min V   Min Nd       Max V   Max Nd         Var         SEM     Min |V|   |Min| Nd      Max
     1       593      302.64       0.248       0.248          0         0       0.156   119194       0.332   118443       0.002       0.002       0.156   119194       (
     2       276      177.56       0.243       0.243          0         0       0.181    66554       0.319    67697       0.001       0.002       0.181    66554       (
     3       310      168.21       0.210       0.210          0         0       0.142    81881       0.301    73563       0.001       0.002       0.142    81881       (
     4       313      145.33       0.173       0.173          0         0       0.110    95944       0.237    95932       0.001       0.001       0.110    95944       (
     5       181      134.99       0.241       0.241          0         0       0.160   163637       0.291   162612       0.001       0.002       0.160   163637       (
     6       345      130.80       0.210       0.210          0         0       0.130      785       0.290    47993       0.001       0.002       0.130      785       (
     7       216      130.64       0.230       0.230          0         0       0.134   151374       0.345   152365       0.002       0.003       0.134   151374       (
     8       197      118.21       0.197       0.197          0         0       0.128    92036       0.289    91660       0.001       0.003       0.128    92036       (

vvvvvvvvvvvvvvvvvvvvvvvvvvvv
Selected surface std.141.rh.pial.gii (Focus_DO_ID # 2).
FaceSet 183070, Closest Node 92289
```



Getting Started with FreeSurfer

Docs » AFNI Overview Edit on GitHub

AFNI Overview

What is AFNI?

AFNI (Analysis of Functional NeuroImages) is a suite of programs designed to analyze fMRI data. Created in the mid-1990's by Bob Cox, AFNI is now used by hundreds of imaging labs around the world.

The following tutorials will show you how to analyze a sample dataset with AFNI. You will begin by learning the fundamentals of fMRI preprocessing, and then proceed to create a model of your data with AFNI's 3dDeconvolve command. We will finish by learning about different types of group analyses, and how to do region of interest (ROI) analyses.

Start to Finish Analysis with AFNI

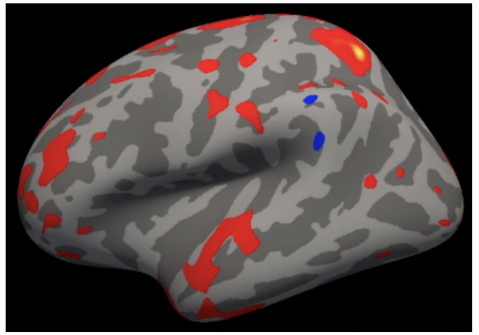
- Introduction to AFNI
- AFNI Tutorial #1: Downloading the Data
- AFNI Tutorial #2: The Flanker Experiment
- AFNI Tutorial #3: Looking at the Data
- AFNI Tutorial #4: AFNI Commands and Preprocessing
- AFNI Tutorial #5: Statistics and Modeling
- AFNI Tutorial #6: Scripting
- AFNI Tutorial #7: Group Analysis
- AFNI Tutorial #8: ROI Analysis
- AFNI Tutorial #9: Surface-Based Analysis with SUMA
- Appendix A: Parametric Modulation in AFNI

Docs » FreeSurfer Short Course Edit on GitHub

FreeSurfer Short Course

Overview

FreeSurfer is a software package that enables you to analyze **structural MRI** images - in other words, you can use FreeSurfer to quantify the amount of grey matter and white matter in specific regions of the brain. You will also be able to calculate measurements such as the thickness, curvature, and volume of the different tissue types, and be able to correlate these with covariates; or, you can contrast these structural measurements between groups.



An example of a typical group-level map created by FreeSurfer. This is from a group-level contrast between two groups, with the red and blue colors indicating where there are differences in cortical thickness between the groups. Typically these results are depicted on inflated brains; darker grey represents sulci, and lighter grey represents gyri.

This course will show you how to download and install FreeSurfer, and how to analyze a dataset from start to finish. Along the way you'll learn the basic FreeSurfer vocabulary and how to do preprocessing, volume editing, and region of interest analysis.

Start to Finish Analysis with FreeSurfer

- FreeSurfer Tutorial #1: Basic Terms
- FreeSurfer Tutorial #2: How to Download and Install
- FreeSurfer Tutorial #3: Recon-all

Questions?

Introduction to Meta-Analysis

Combining Results from Different Studies

Karl Pearson (1904)

REPORT ON CERTAIN ENTERIC FEVER INOCULATION STATISTICS.

PROVIDED BY LIEUTENANT-COLONEL R. J. S. SIMPSON, C.M.G., R.A.M.C.

BY KARL PEARSON, F.R.S.,
Professor of Applied Mathematics, University College, London.

The following table gives the results of calculating the correlation coefficients of the tables in Appendix B:

INOCULATION AGAINST ENTERIC FEVER:

Correlation between Immunity and Inoculation.		
I. Hospital Staffs	+ 0.373	± 0.021
II. Ladysmith Garrison	+ 0.445	± 0.017
III. Methuen's Column	+ 0.191	± 0.026
IV. Single Regiments	+ 0.021	± 0.053
V. Army in India	+ 0.100	± 0.013
Mean value	+ 0.226	
Correlation between Mortality and Inoculation.		
VI. Hospital Staffs	+ 0.307	± 0.128
VII. Ladysmith Garrison	− 0.010	± 0.081
VIII. Single Regiments	+ 0.300	± 0.093
IX. Special Hospitals	+ 0.119	± 0.022
X. Various military Hospitals ...	+ 0.194	± 0.022
XI. Army in India	+ 0.248	± 0.050
Mean value	+ 0.193	

If we except IV and VII, the values of the correlations are at least twice (in the very sparse data of VI) and generally four, five, or more times their probable errors. From this standpoint we might say that they are all significant, but we are at once struck with the extreme irregularity and the lowness of the values reached. They are absolutely incomparable with the fairly steady and large values of the vaccination correlations obtained for different epidemics and towns. The effect of enteric inoculation is evidently largely influenced by difference of environment or of treatment.

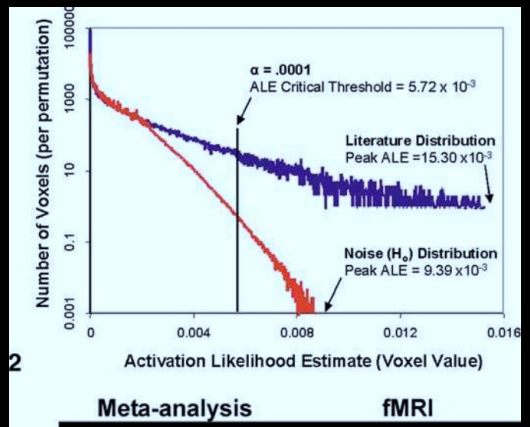
For example, taking the relation between deaths and recoveries, and presence and absence of vaccination scar in cases of small-pox, we have:[2]

	Correlation.
Metropolitan Asylums Board Returns,	
Epidemic 1893	0.595 ± 0.027
Epidemics for six towns	0.656 ± 0.009
Sheffield, 1887-8	0.769 ± 0.012
Homerton and Fulham, 1873-85 ...	0.576 ± 0.009
London: Epidemic 1901	0.578 ± 0.031
Glasgow: Epidemic 1900-1	0.629 ± 0.030

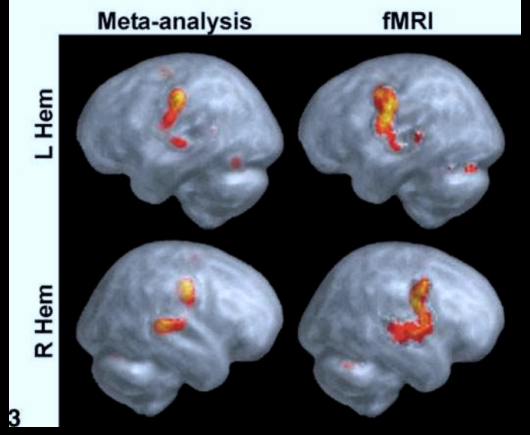
We may safely say that the protective character of vaccination as against mortality after incurring small-pox is very substantial, and numerically it is represented by the value 0.6, which is fairly closely the actual result for the various epidemics which have at present been dealt with.

Meta-analysis and Neuroimaging Studies

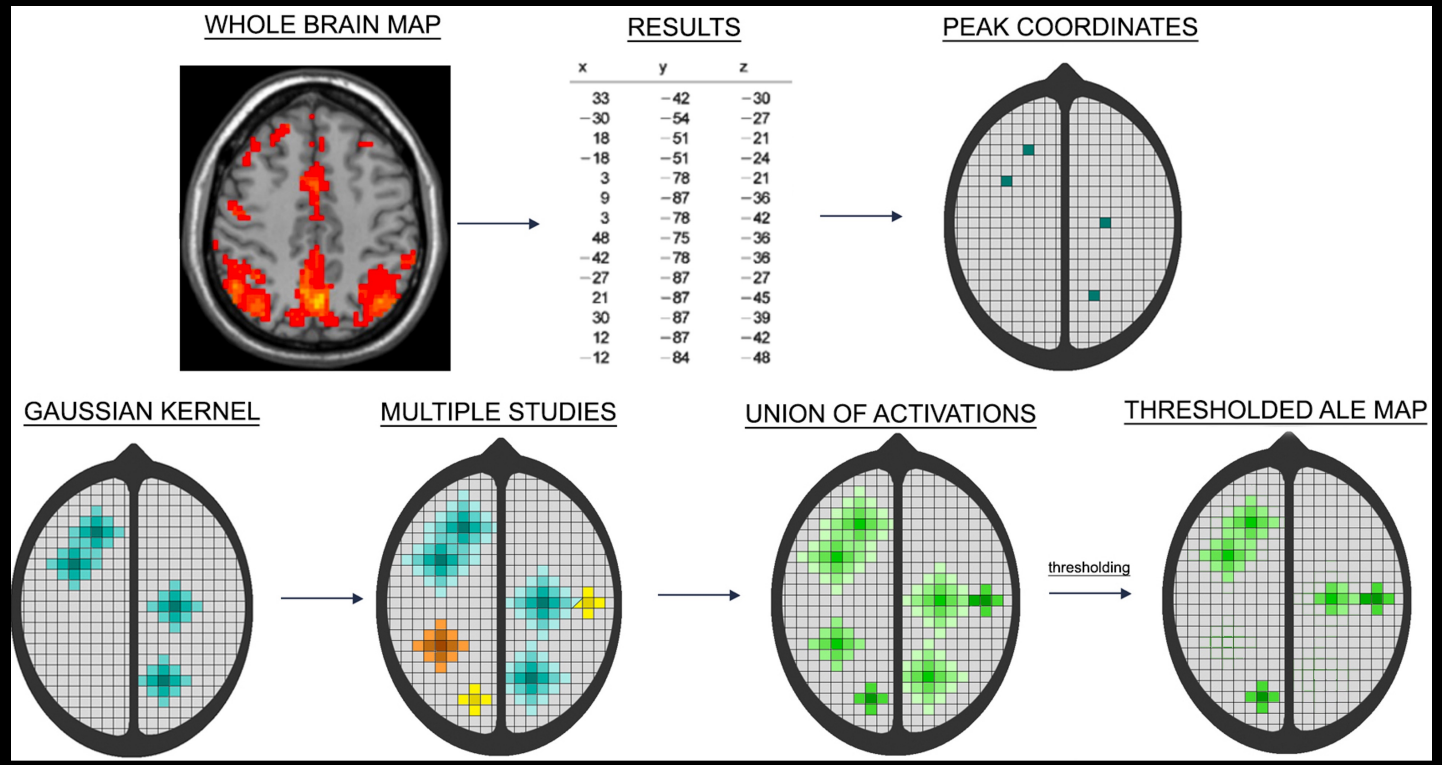
Activation Likelihood Estimation (ALE), Turkeltaub et al., 2002)



2



3



How to use this?

One option: BrainMap

Contains links to Sleuth and GingerALE software

Can also enter coordinates to see where other papers also report activation

brainmap.org

Announcements

March 4, 2021: The BrainMap database is now back up after maintenance this morning. Thank you for your patience.

What is BrainMap?

BrainMap is a database of published functional and structural neuroimaging experiments with coordinate-based results (x,y,z) in Talairach or MNI space. The goal of BrainMap is to develop software and tools to share neuroimaging results and enable meta-analysis of studies of human brain function and structure in healthy and diseased subjects.

The BrainMap Project is developed at the Research Imaging Institute of the University of Texas Health Science Center San Antonio. BrainMap was conceived in 1988 and originally developed as a web-based interface. After more than 20 years of development, BrainMap has evolved into a much broader project whose software and data have been utilized in numerous publications. BrainMap provides not only data for meta-analyses and data mining, but also distributes software and concepts for quantitative integration of neuroimaging data.

Collaborations

The BrainMap development team welcomes collaborations. We will provide guidance and assistance in the execution of meta-analyses upon request. We encourage collaborations that develop new tools for meta-analysis or use BrainMap data to develop or validate other neuroinformatics tools and strategies.

BrainMap ICA Results

Networks resulting from an ICA decomposition of modeled activation images archived in BrainMap strongly correspond to resting state networks, as shown by Smith et al., 2009. Given the vast amount of metadata archived in BrainMap, the functional significance of these intrinsic connectivity networks was quantitatively assessed by Laird et al. (2011). For more details, and the associated network images and metadata at a model order of 20, please click here.

Citing BrainMap

If you have used the BrainMap database in your research, please cite one or more of the following papers in your references.

For citations concerning Sleuth, Scribe, and BrainMap meta-data:

Fox PT, Lancaster JL. Mapping context and content: The BrainMap model. Nature Rev Neurosci 3, 319-321, 2002. [pdf] [PubMed]

and

Fox PT, Laird AR, Fox SP, Fox PM, Uecker AM, Crank M, Koenig SF, Lancaster JL. BrainMap taxonomy of experimental design: Description and evaluation. Hum Brain Mapp 25, 185-198, 2005. [pdf] [PubMed]

BrainMap Forums

Have a question? Check our forums!

- brainmap.org/forum

Find a previous answer or ask the experts yourself

Quick Author Search

Want to check if a paper is already in the BrainMap database? Just type in the author's last name below:

Search

Activation Coordinate Experiment-wise Search (ACES)

Upload a tab-delimited file of locations to find which BrainMap experiments are most similar:

Choose File myCoords

Reference space: Talairach MNI

Find similar experiments: Search

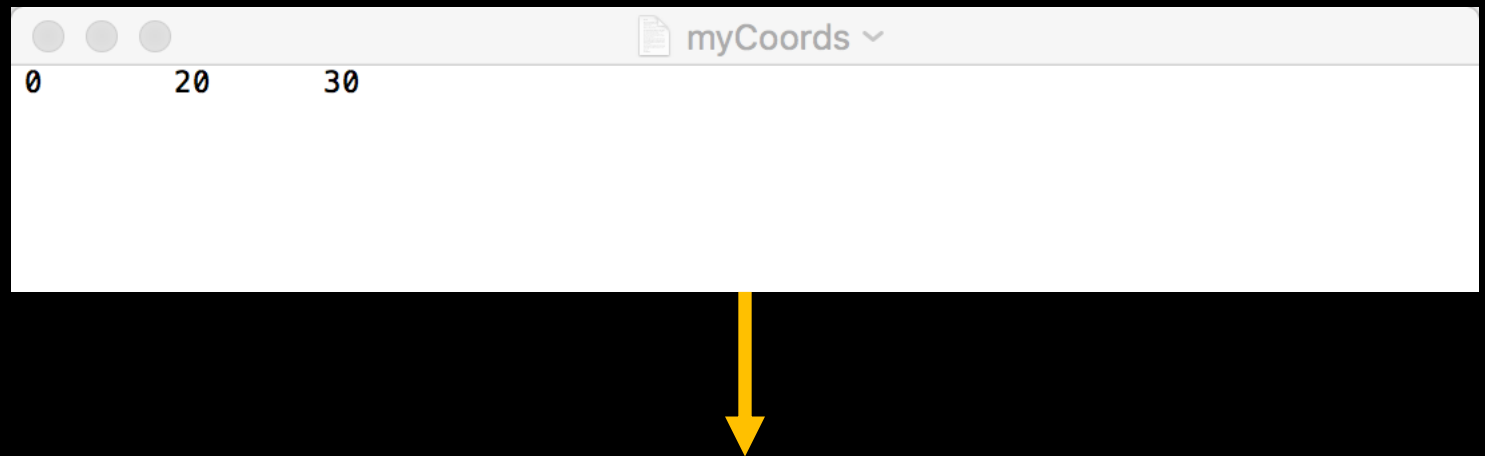
Functional Database Status

Papers: 3783
Experiments: 19137
Paradigm Classes: 115
Subjects: 89644
Locations: 147765

VBM Database Status

Papers: 1130
Experiments: 3661
Subjects: 99098
Locations: 24979

Current Software Versions



Activation Coordinate Experiment-wise Search (ACES)

Searching for experiments similar to 1 coordinates...

Top 10 experiments:

BrainMap ID	Exp. Size	Coordinates Matching	Coordinate Similarity
10010002 5	2	1	100%
Name: Healthy Controls > Major Depression			
10010003 5	2	1	100%
Name: Healthy Controls > Depressed Patients			
10080202 2	8	1	100%
Name: Errors > Successful Inhibitions			
7120389 2	14	.9	92%
Name: Allodynia vs. Contralateral Touch, Right-Sided Allodynia Patients			
8050127 4	19	.9	92%
Name: Win $4.00 > Win $0.50, All Subjects			
9020032 3	10	.9	92%
Name: Regions Positively Associated with Speechreading Skill, Deaf Patients			
10080181 4	13	.9	92%
Name: Tics in Tourette's > Normals at Rest, Random Effect Analysis			
7090249 1	6	.9	88%
Name: CS+ > CS-, Acquisition			
14050049 5	9	.8	84%
Name: STROOP, Autism Group			
5080219 1	9	.8	81%
Name: Pathological Gamblers, Incongruent vs. Congruent, Activations			

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GingerALE

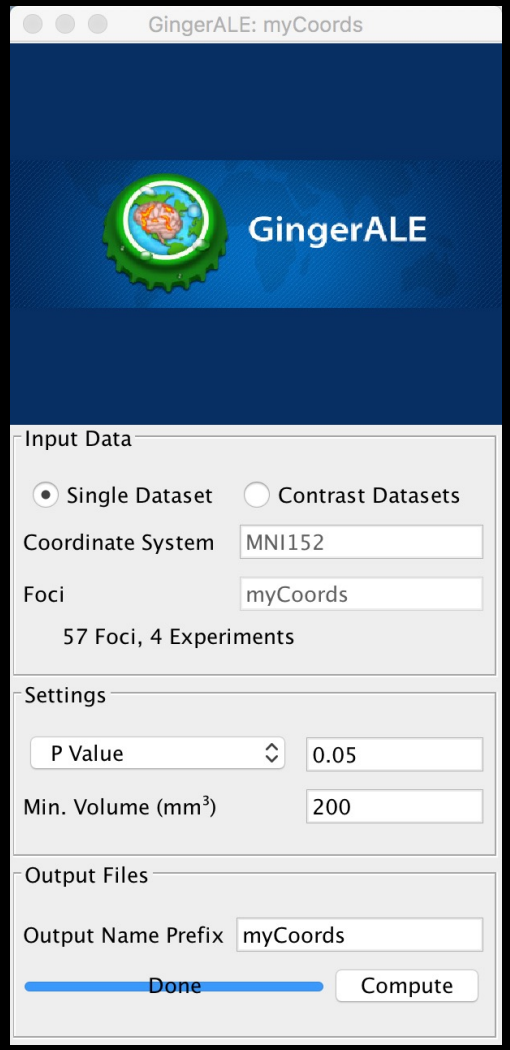
Enter set of coordinates

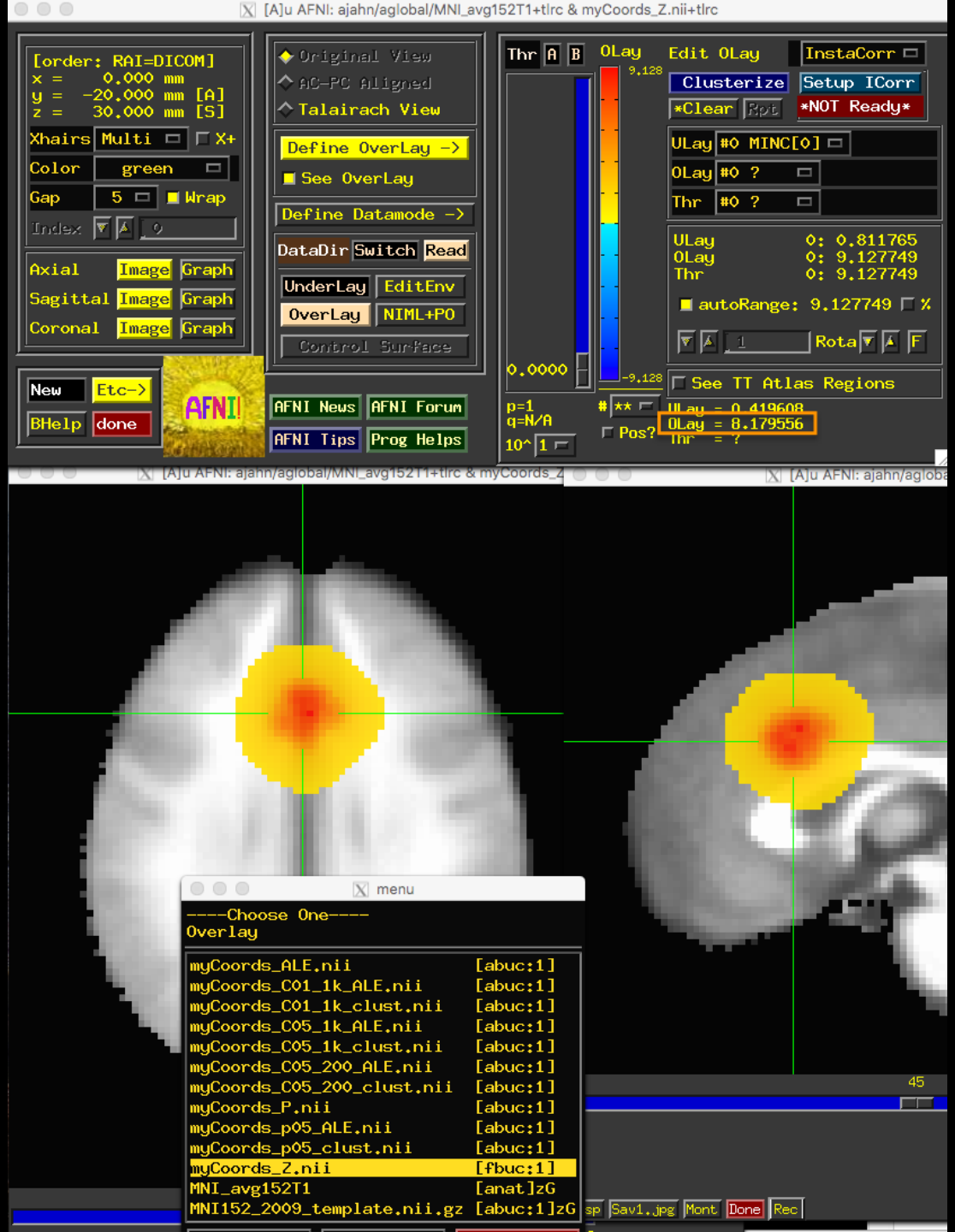
Uses Clustering to find significant overlap between foci

myCoords

```
// Reference=Talairach
// Hui, 2000: Acupuncture vs. Tactile Stimulation, Increases
// Subjects=13
0       20      30
56      -15     50
-50     -18     43
59      -21     21
-50     -18     18
```

GingerALE


GingerALE: myCoords
GingerALE
Input Data
Single Dataset
Contrast Datasets
Coordinate System
MNI152
Foci
myCoords
57 Foci, 4 Experiments
Settings
P Value
0.05
Min. Volume (mm3)
200
Output Files
Output Name Prefix
myCoords
Done
Compute

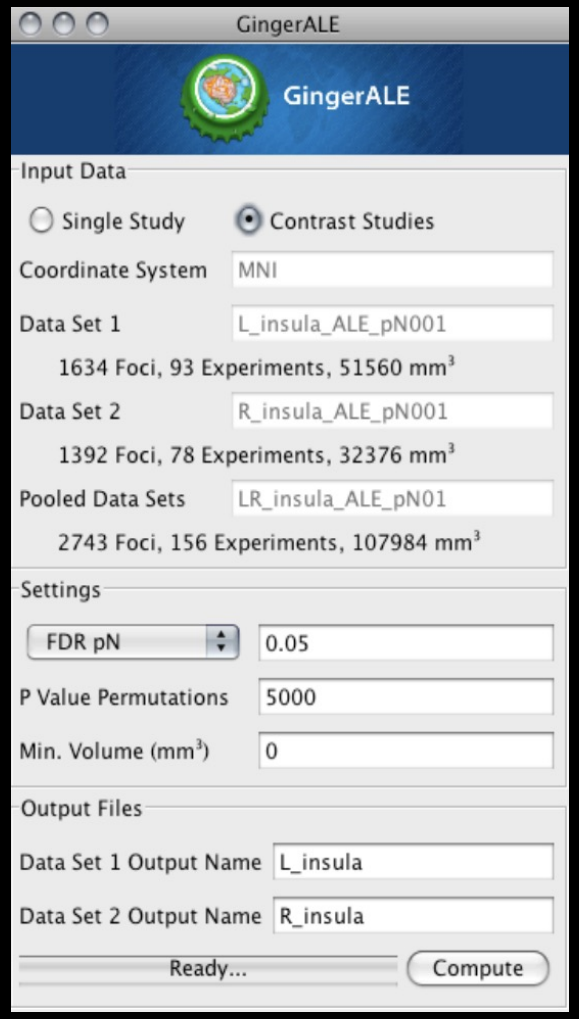

[A]u AFNI: ajahn/aglobal/MNI_avg152T1+tlrc & myCoords_Z.nii+tlrc
[order: RAI=DICOM]
x = 0.000 mm
y = -20.000 mm [A]
z = 30.000 mm [S]
Xhairs Multi X+
Color green
Gap 5 Wrap
Index 0
Axial Image Graph
Sagittal Image Graph
Coronal Image Graph
Original View
AC-PC Aligned
Talairach View
Define OverLay ->
See OverLay
Define Datamode ->
DataDir Switch Read
UnderLay EditEnv
OverLay NIML+PO
Control Surface
New Etc->
BHelp done
AFNI
AFNI News AFNI Forum
AFNI Tips Prog Helps
Thr A B
OLay
9.128
-9.128
0.0000
p=1
q=N/A
10^ 1
Edit OLay
InstaCorr
Clusterize
Setup ICorr
*Clear Rpt
NOT Ready
ULay #0 MINC[0]
OLay #0 ?
Thr #0 ?
ULay 0: 0.811765
OLay 0: 9.127749
Thr 0: 9.127749
autoRange: 9.127749 %
Rota F
See TT Atlas Regions
ULay = 0.419608
OLay = 8.179556
Thr = ?
Pos?
menu
----Choose One----
Overlay
myCoords_ALE.nii [abuc:1]
myCoords_C01_1k_ALE.nii [abuc:1]
myCoords_C01_1k_clust.nii [abuc:1]
myCoords_C05_1k_ALE.nii [abuc:1]
myCoords_C05_1k_clust.nii [abuc:1]
myCoords_C05_200_ALE.nii [abuc:1]
myCoords_C05_200_clust.nii [abuc:1]
myCoords_P.nii [abuc:1]
myCoords_p05_ALE.nii [abuc:1]
myCoords_p05_clust.nii [abuc:1]
myCoords_Z.nii [fbuc:1]
MNI_avg152T1 [anat]zG
MNI152_2009_template.nii.gz [abuc:1]zG
45
Sav1.jpg Mont Done Rec

GingerALE

You can also create contrast maps to visualize the overlap and divergence of two meta-analyses

Requires performing two separate ALE analyses, as well as a pooled analysis (i.e., merging the two)

GingerALE


GingerALE
GingerALE
Input Data
Single Study
Contrast Studies
Coordinate System
MNI
Data Set 1
L_insula_ALE_pN001
1634 Foci, 93 Experiments, 51560 mm³
Data Set 2
R_insula_ALE_pN001
1392 Foci, 78 Experiments, 32376 mm³
Pooled Data Sets
LR_insula_ALE_pN01
2743 Foci, 156 Experiments, 107984 mm³
Settings
FDR pN
0.05
P Value Permutations
5000
Min. Volume (mm³)
0
Output Files
Data Set 1 Output Name
L_insula
Data Set 2 Output Name
R_insula
Ready...
Compute

GingerALE

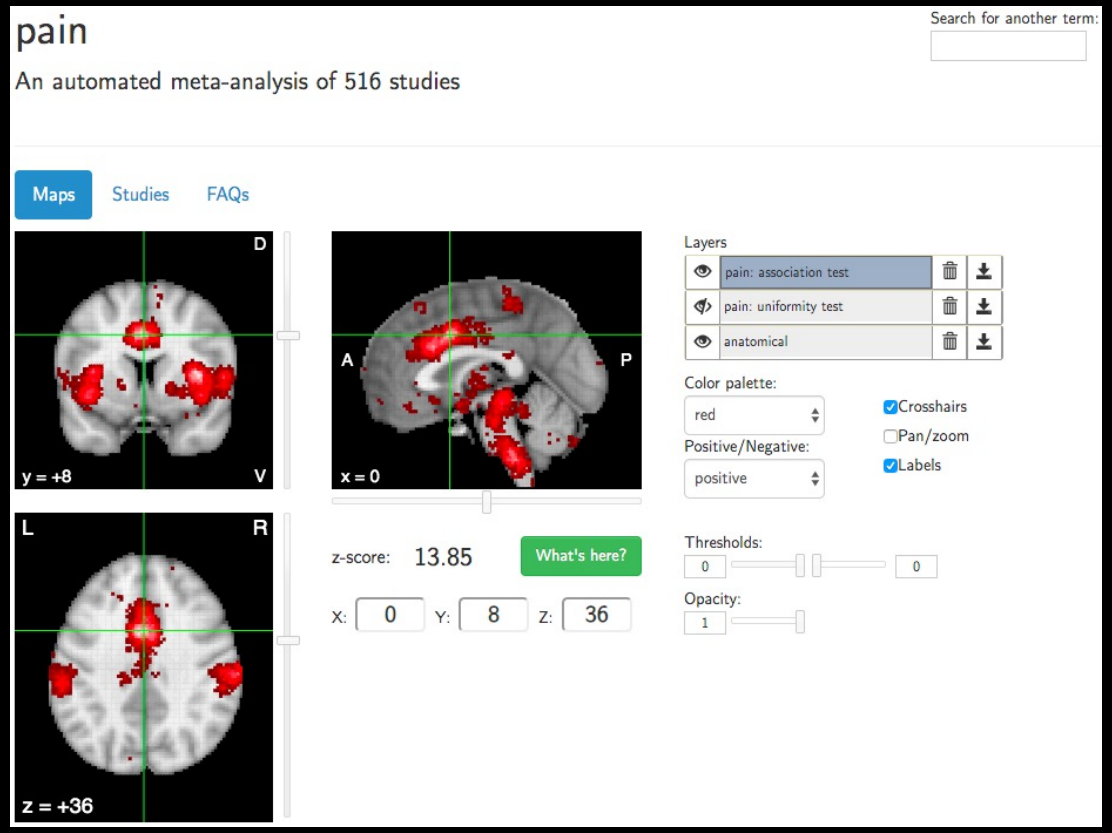
Advantages: Helps build intuition about how meta-analyses are conducted

Disadvantages: Can be tedious, even with auxiliary software (e.g., Sleuth)

Is there any way to automate this?

Neurosynth

How it works: Search Terms



Neurosynth

Association vs. Uniformity Tests

Used to be called Forward vs. Reverse Inference

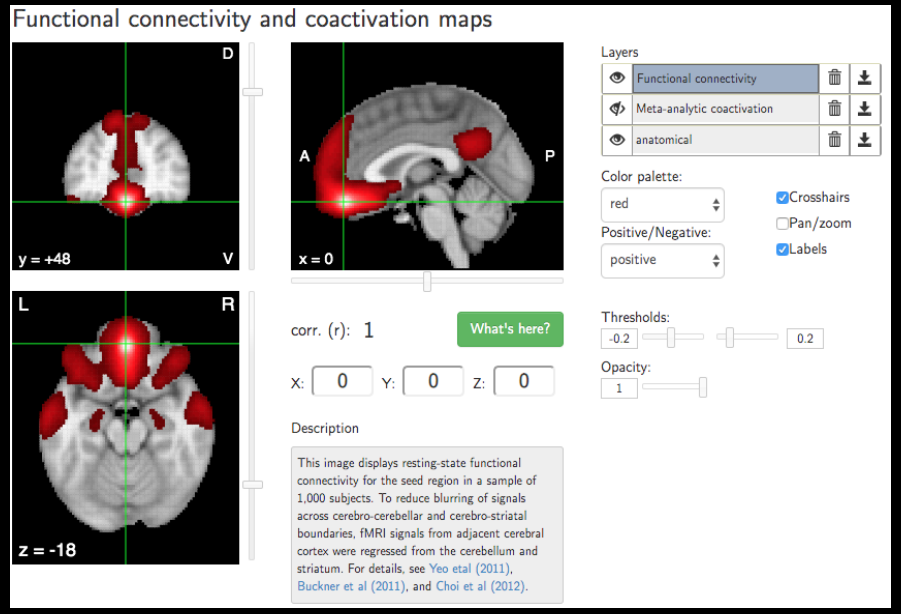
Uses: Downloading the Maps to use for ROI analysis

Comparing your results to other studies

Neurosynth

Other uses of Neurosynth

Functional Connectivity Analysis



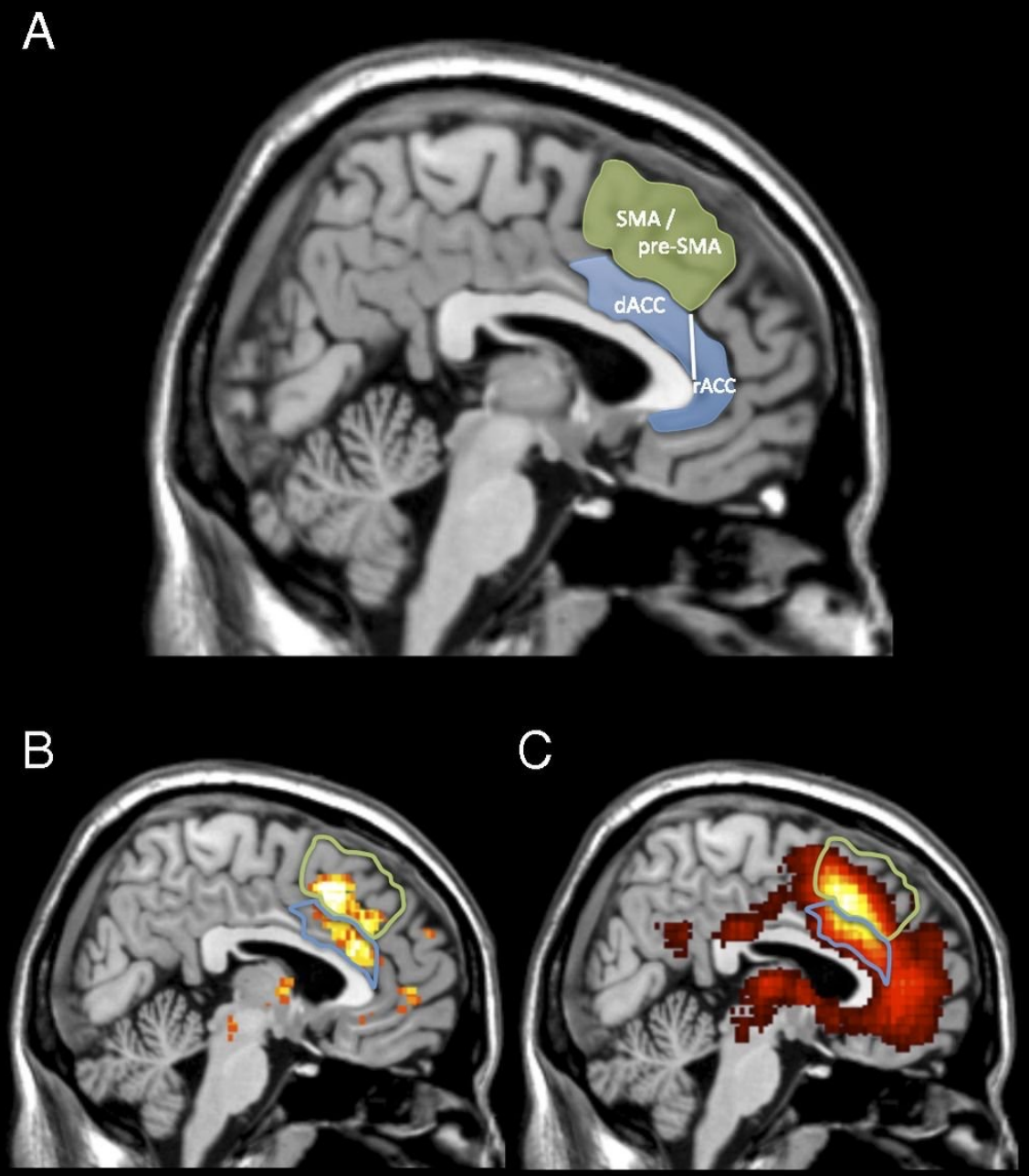
Neurosynth

Demonstration

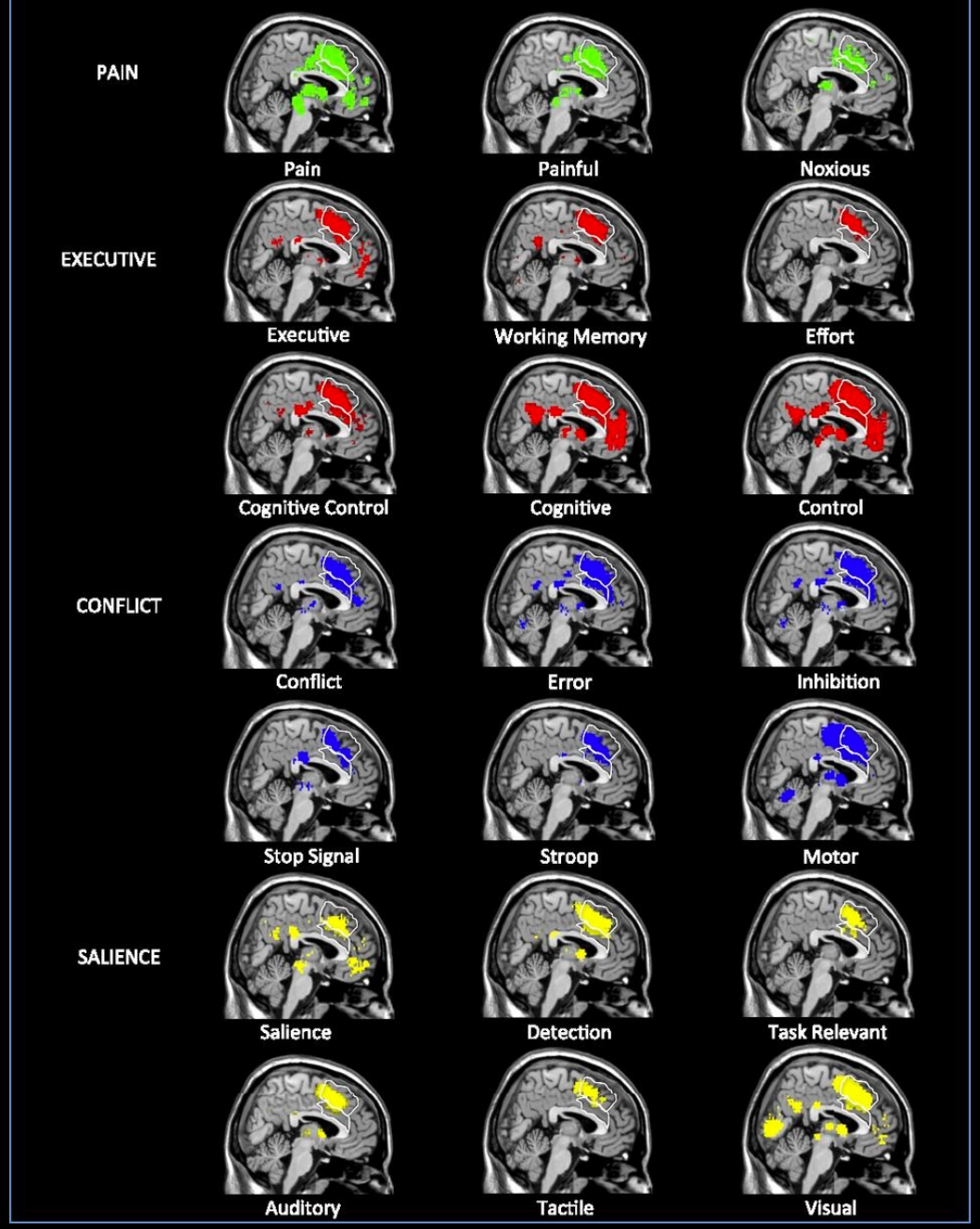
Neurosynth

Proper ways for using Neurosynth

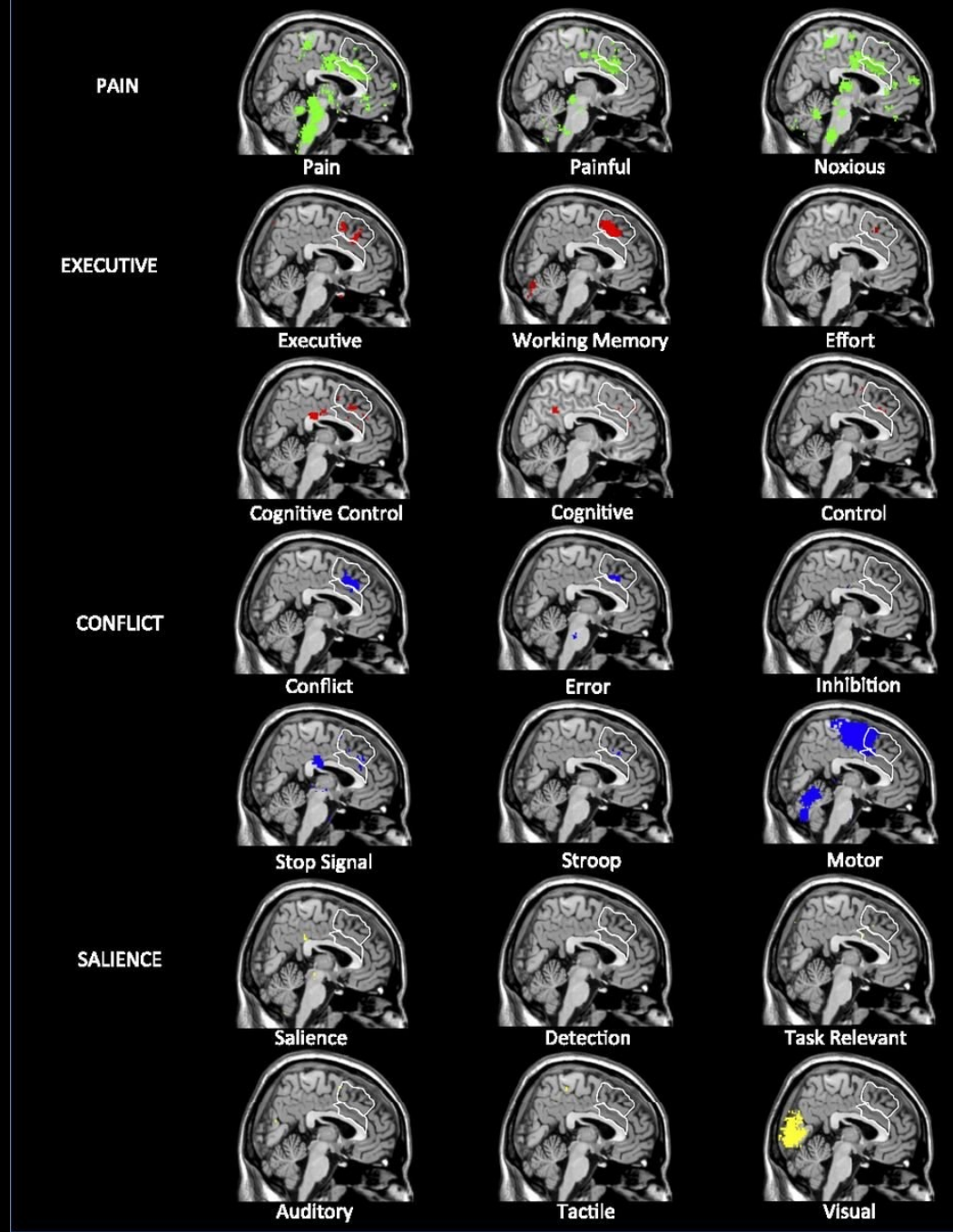
Lieberman & Eisenberger 2015


A
SMA /
pre-SMA
dACC
rACC
B
C
Search Term:
dACC
Search Term:
Anterior Cingulate

Forward Inference

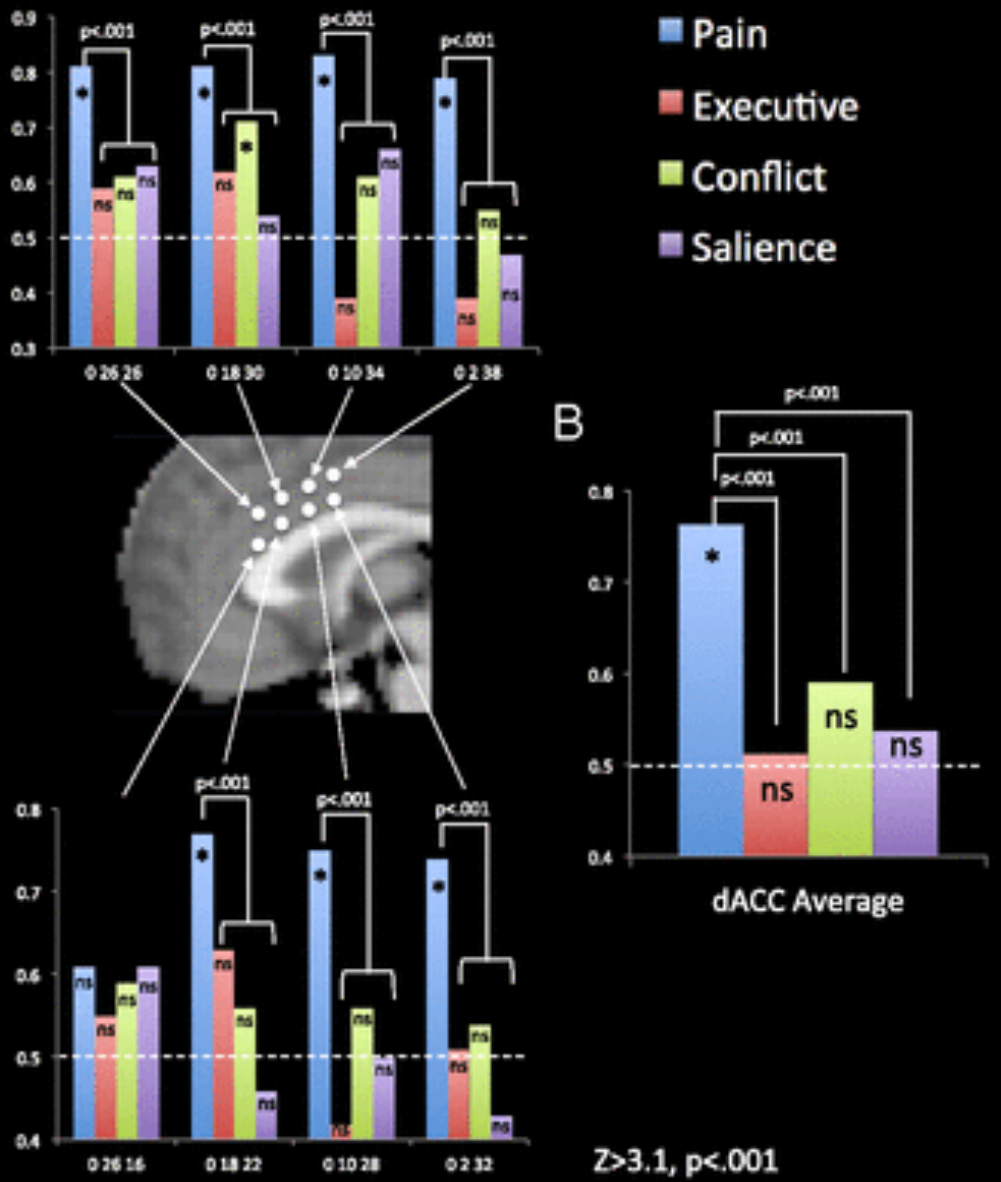


Reverse Inference



A

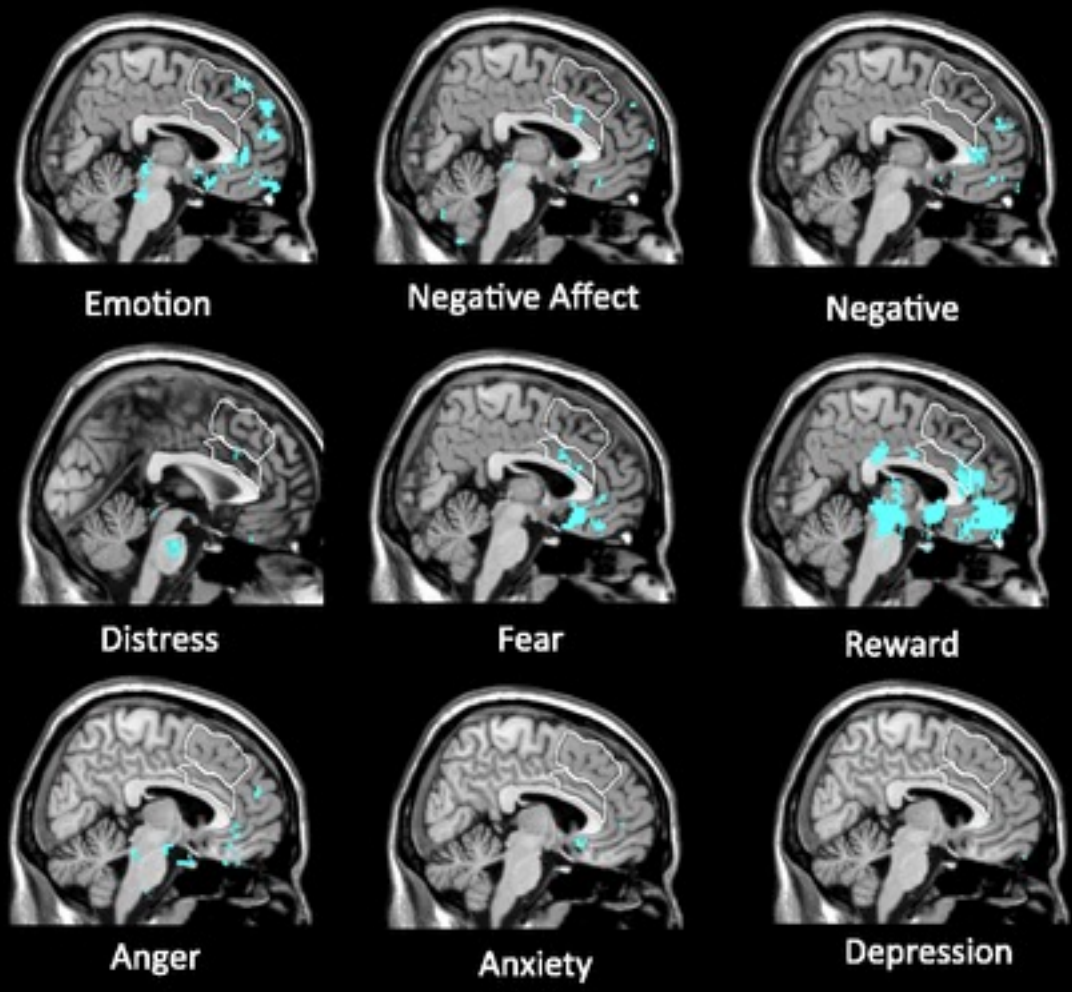
dACC Reverse Inference



B

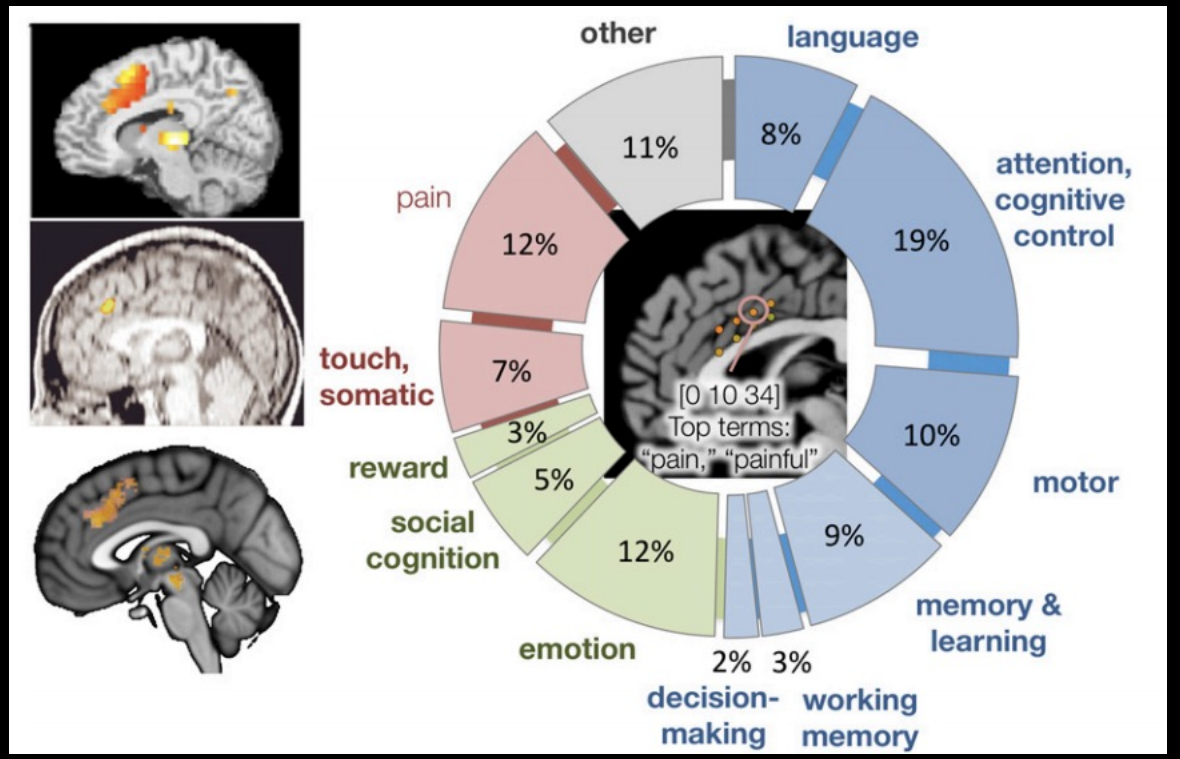
Z>3.1, p<.001

Reverse Inference

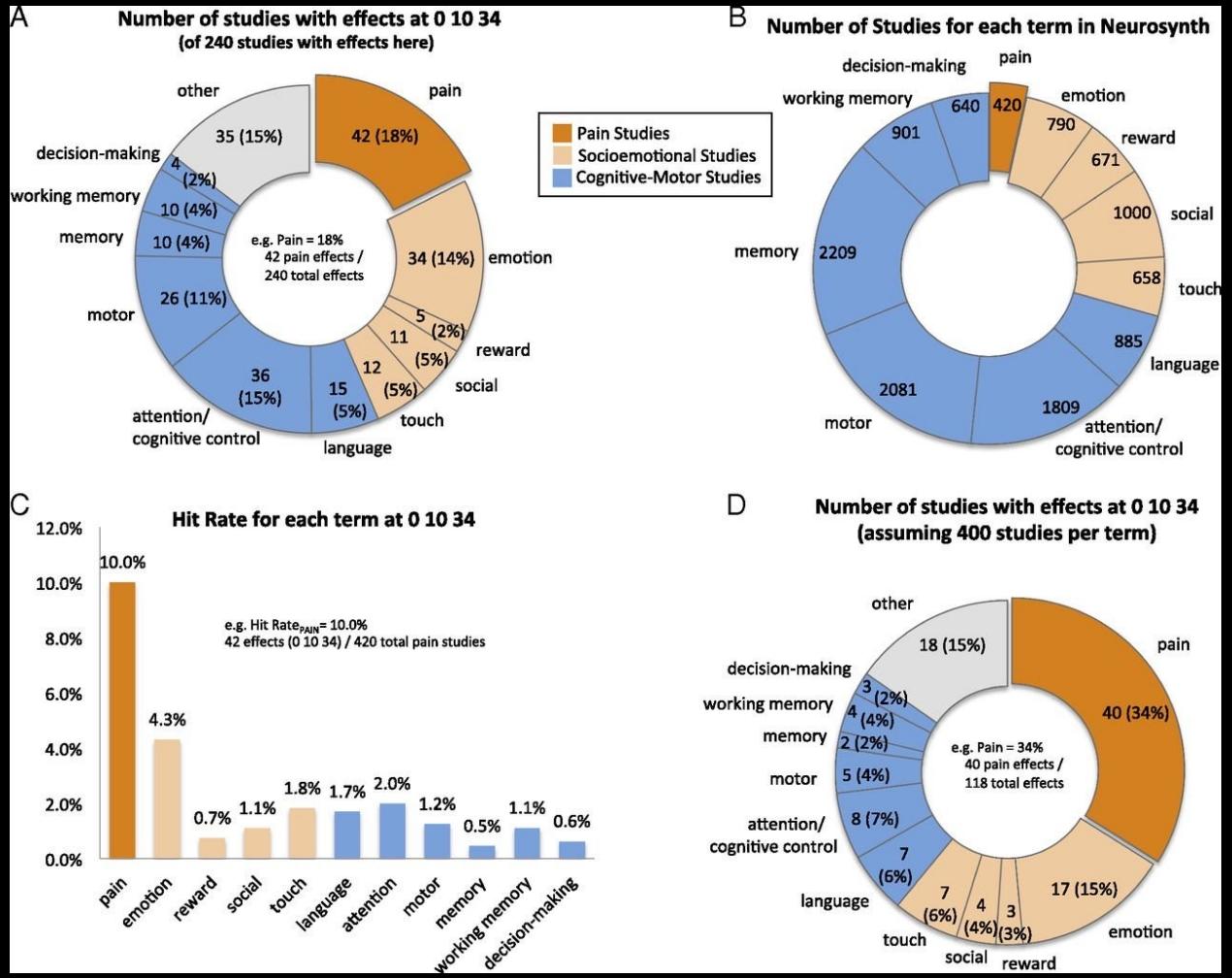


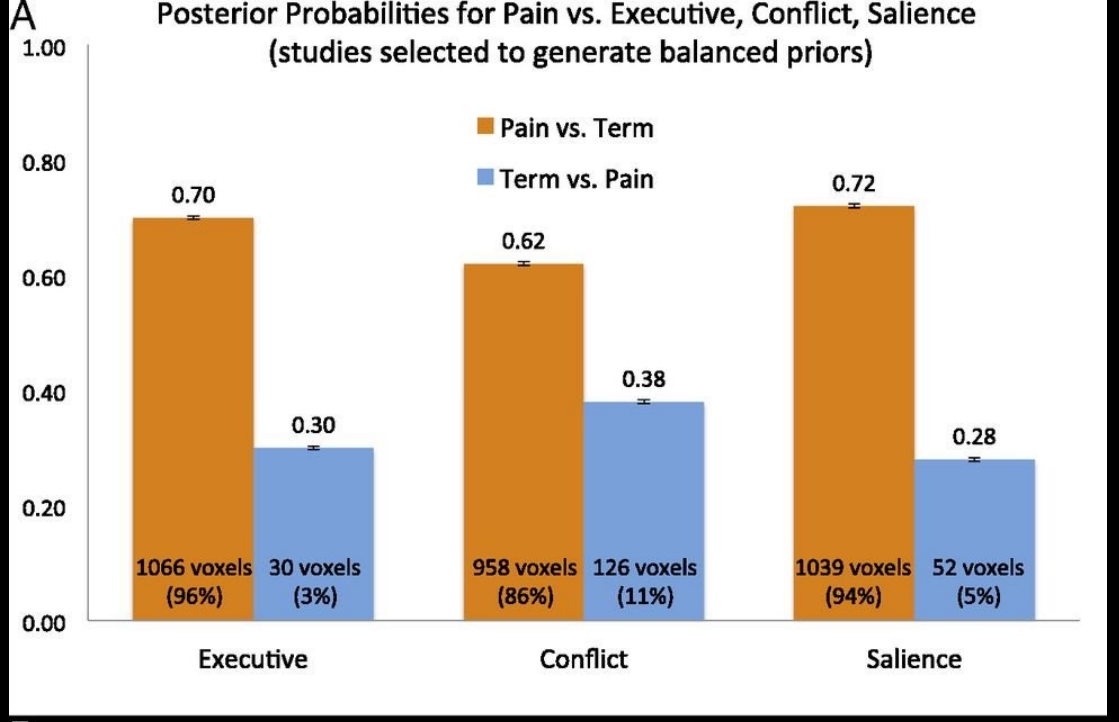
Wager et al. Rebuttal

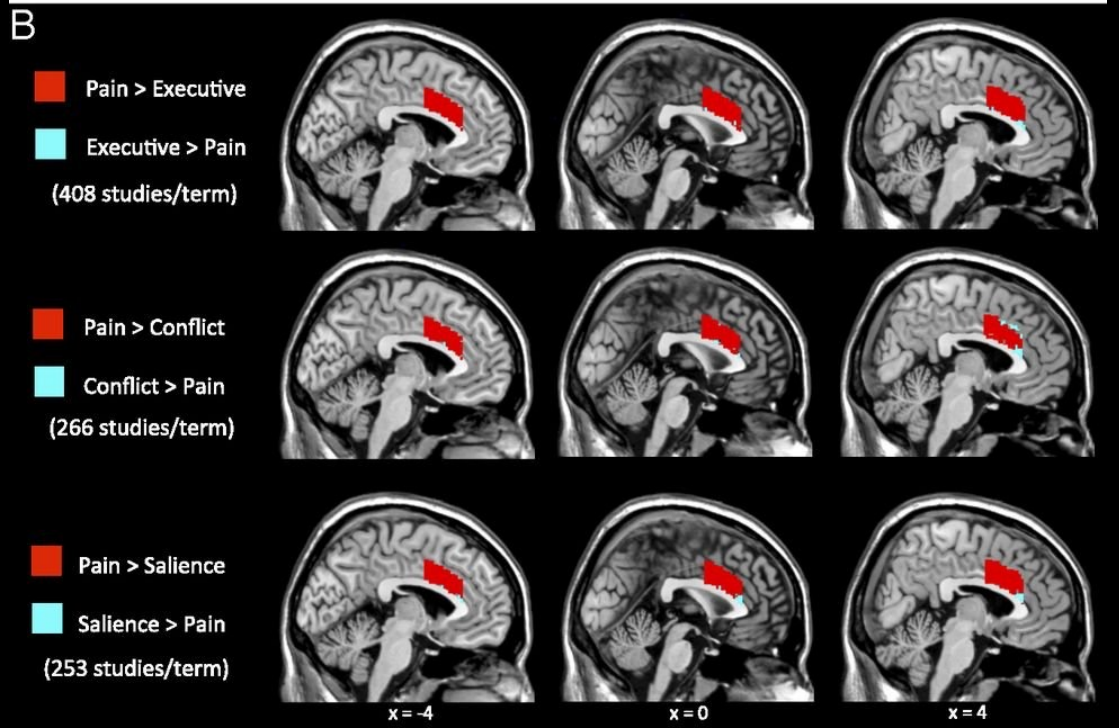
Lieberman and Eisenberger's (1) conclusions are based on Neurosynth.org (7), a database of activation coordinates and words used in >11,000 neuroimaging studies. The claim of pain selectivity is based on a statistical preference in dACC activation studies for the use of pain-related words, compared with a modest number of alternatives (e.g., "salience"). Neurosynth analyses are based on word frequencies in published papers. They may not reflect the actual processes studied, and are not linked specifically to particular brain locations. They are subject to biases in how different literatures use words and label brain areas (e.g., "salience" has multiple meanings, and dACC is also called anterior mid-cingulate cortex). Neurosynth is useful for exploring structure-to-function mappings across a large literature, but it cannot provide definitive inferences about specific brain regions.



Lieberman et al. Response



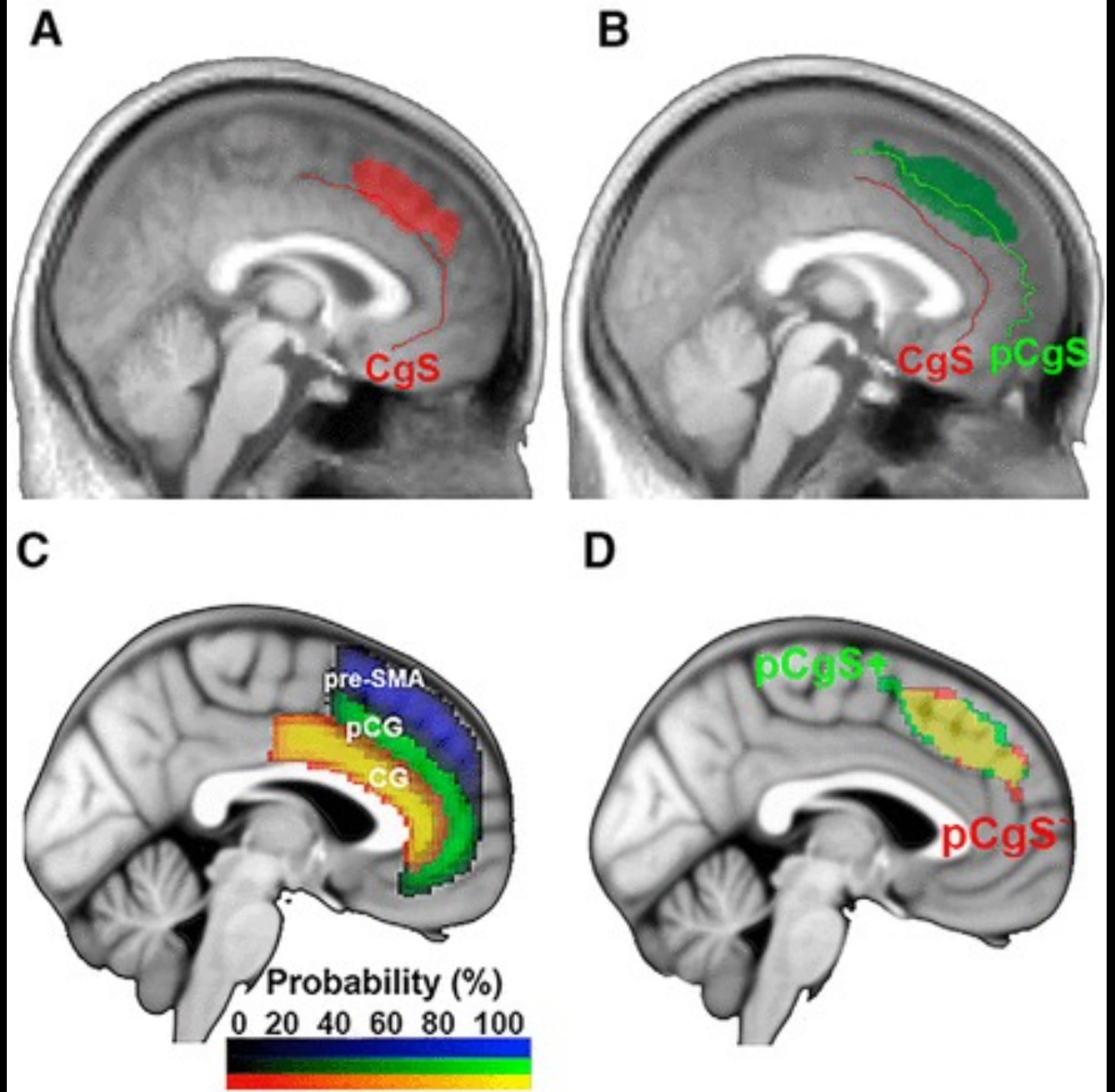

A
Posterior Probabilities for Pain vs. Executive, Conflict, Salience
(studies selected to generate balanced priors)
1.00
0.80
0.60
0.40
0.20
0.00
Pain vs. Term
Term vs. Pain
0.70
0.30
0.62
0.38
0.72
0.28
1066 voxels (96%)
30 voxels (3%)
958 voxels (86%)
126 voxels (11%)
1039 voxels (94%)
52 voxels (5%)
Executive
Conflict
Salience


B
Pain > Executive
Executive > Pain
(408 studies/term)
Pain > Conflict
Conflict > Pain
(266 studies/term)
Pain > Salience
Salience > Pain
(253 studies/term)
x = -4
x = 0
x = 4

Thoughts?

What about a within-subjects study comparing pain and cognitive effects?

This should be the preferred method for making region-specific claims


A
CgS
B
CgS
pCgS
C
pre-SMA
pCG
CG
Probability (%)
0 20 40 60 80 100
D
pCgS+
pCgS-

Neuroquery demo

Reproducing Results from Psychology Studies

Present Day

RESEARCH ARTICLE

Estimating the reproducibility of psychological science

Open Science Collaboration*,†

+ See all authors and affiliations

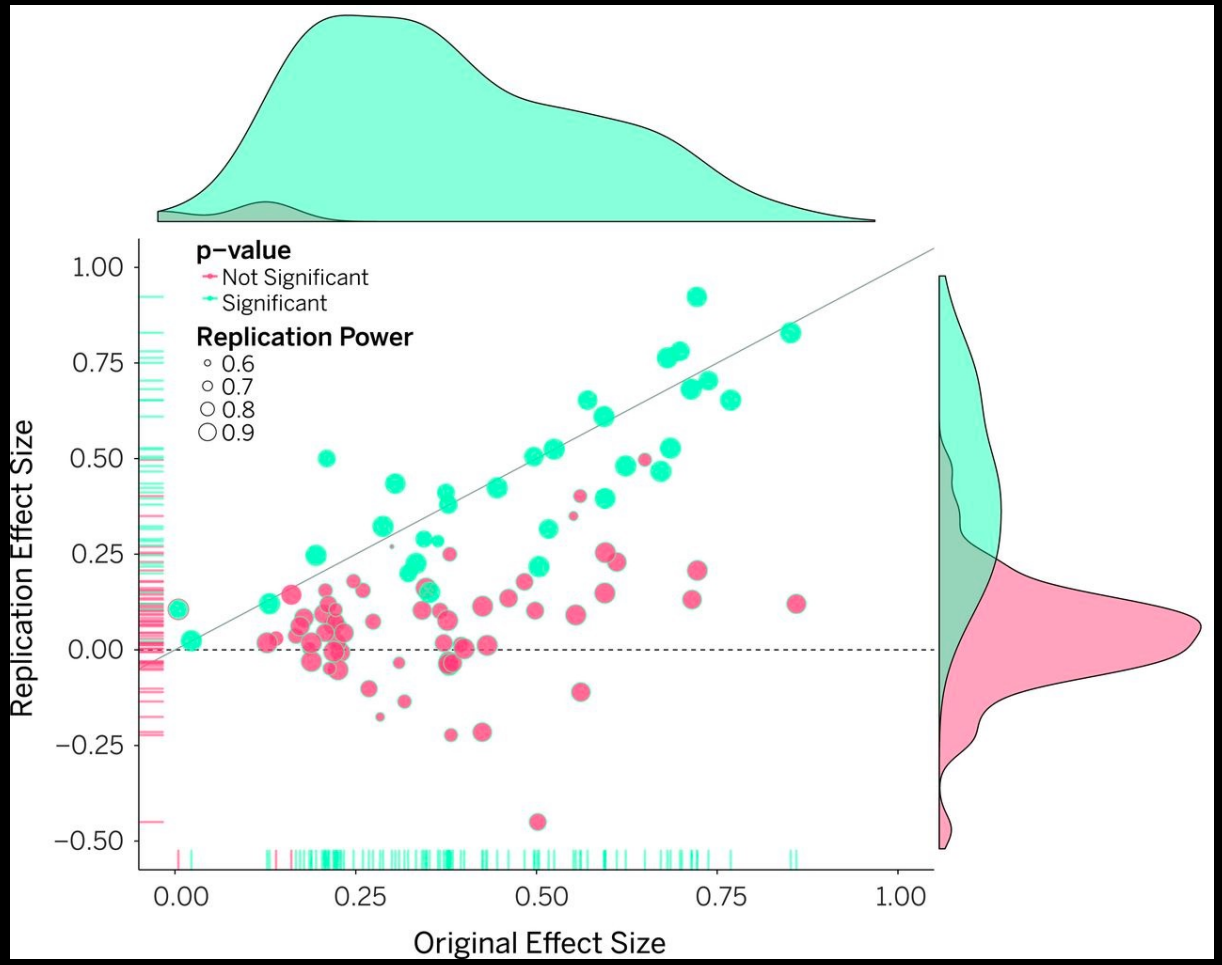
Science 28 Aug 2015:
Vol. 349, Issue 6251, aac4716
DOI: 10.1126/science.aac4716

This should be great, right?

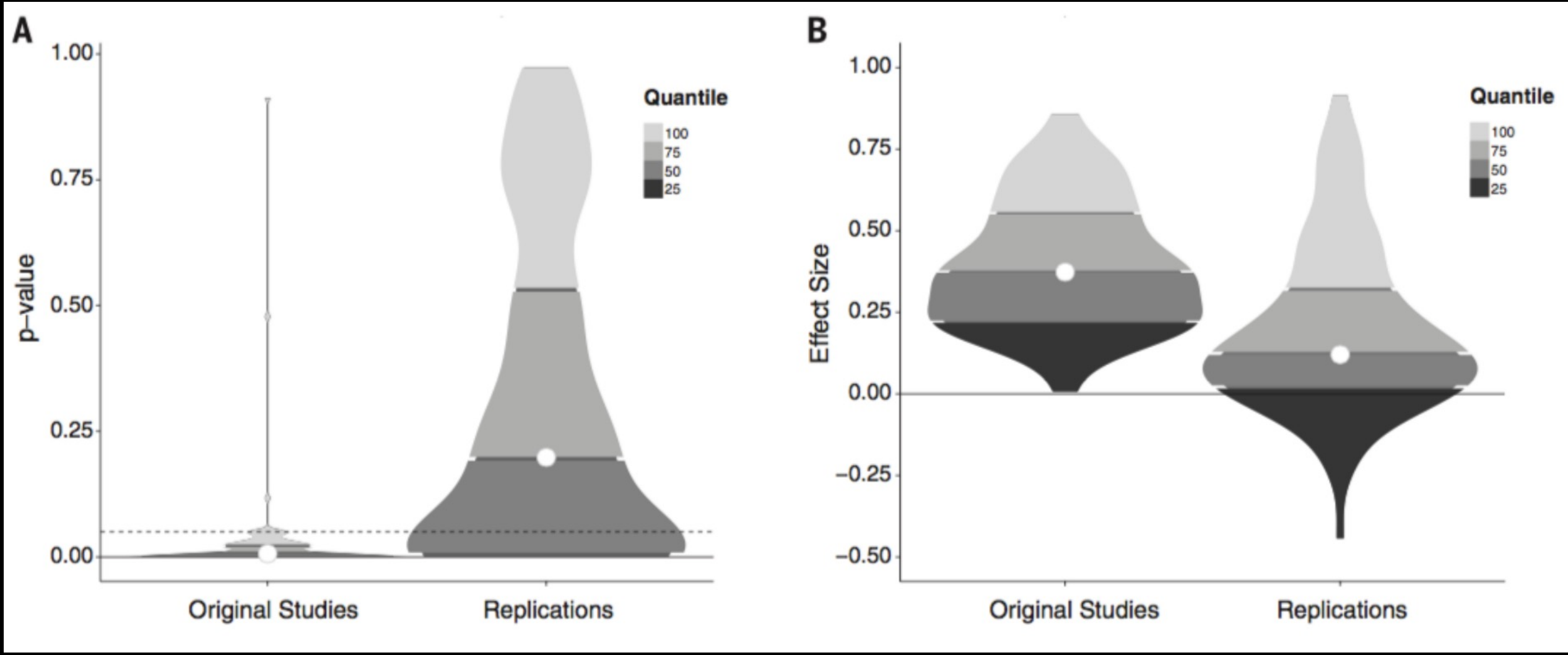
RESULTS

We conducted replications of 100 experimental and correlational studies published in three psychology journals using high-powered designs and original materials when available. There is no single standard for evaluating replication success. Here, we evaluated reproducibility using significance and *P* values, effect sizes, subjective assessments of replication teams, and meta-analysis of effect sizes. The mean effect size (r) of the replication effects (M_r = 0.197, SD = 0.257) was half the magnitude of the mean effect size of the original effects (M_r = 0.403, SD = 0.188), representing a substantial decline. Ninety-seven percent of original studies had significant results (*P* < .05). Thirty-six percent of replications had significant results; 47% of

Reproducing Results from Psychology Studies



Reproducing Results from Psychology Studies



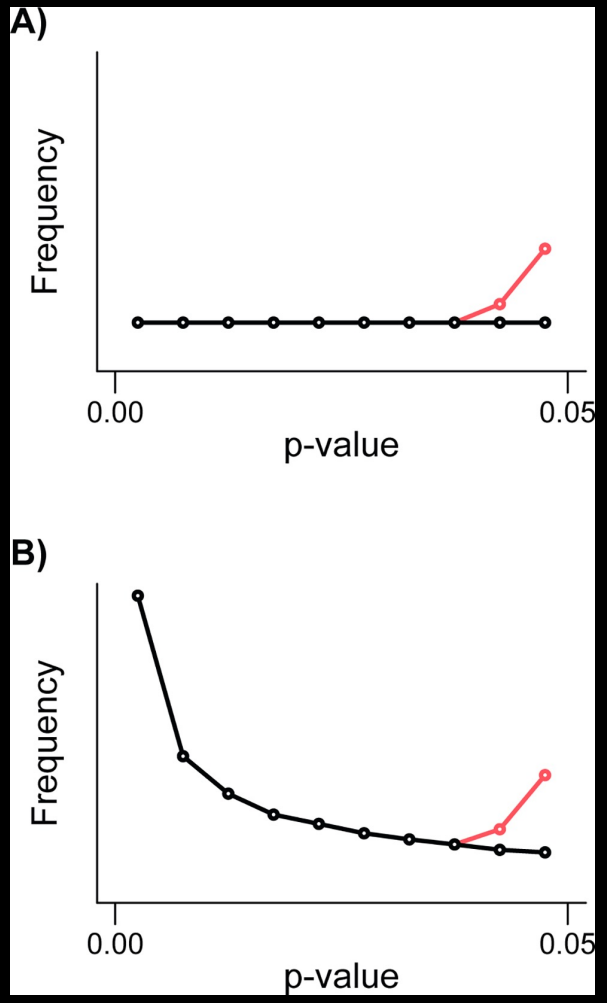
Reproducing Results from Psychology Studies

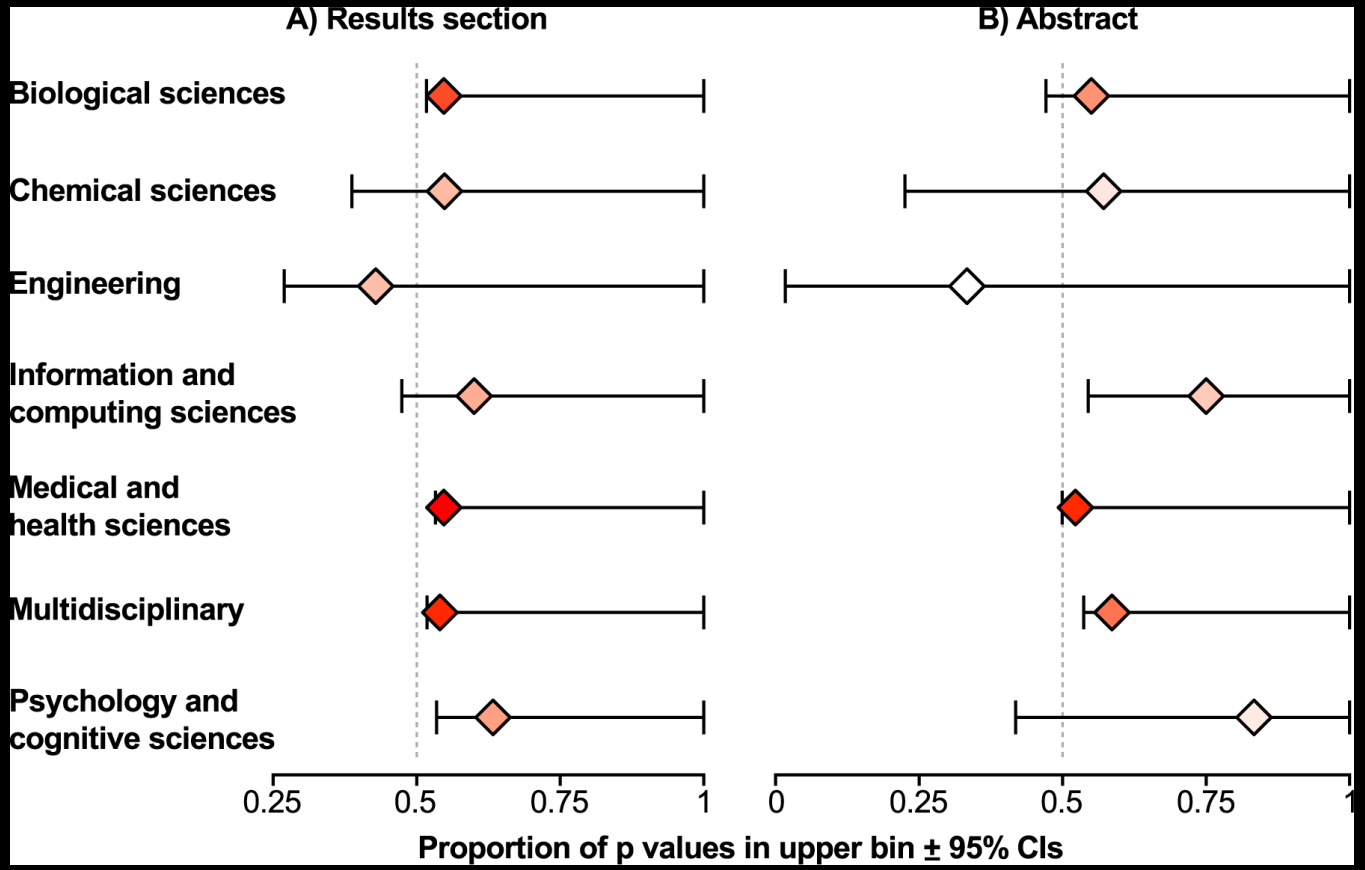
Why does this happen?

We discussed some of this on Tuesday
(circular analyses, file-drawer problem, etc.)

Another issue is “p-hacking”, trying to obtain a significant result by continuing to run analyses

Reproducing Results from Psychology Studies





Head et al., 2015

John Ioannides' 2005 Paper

PLOS MEDICINE

OPEN ACCESS

ESSAY

Why Most Published Research Findings Are False

John P. A. Ioannidis

Published: August 30, 2005 • https://doi.org/10.1371/journal.pmed.0020124

Like we discussed previously, controlling for Type I Error rates isn't enough to guarantee that results are real

John Ioannides' 2005 Paper

The crux of the paper rests on a formula called Positive Predictive Value (PPV)

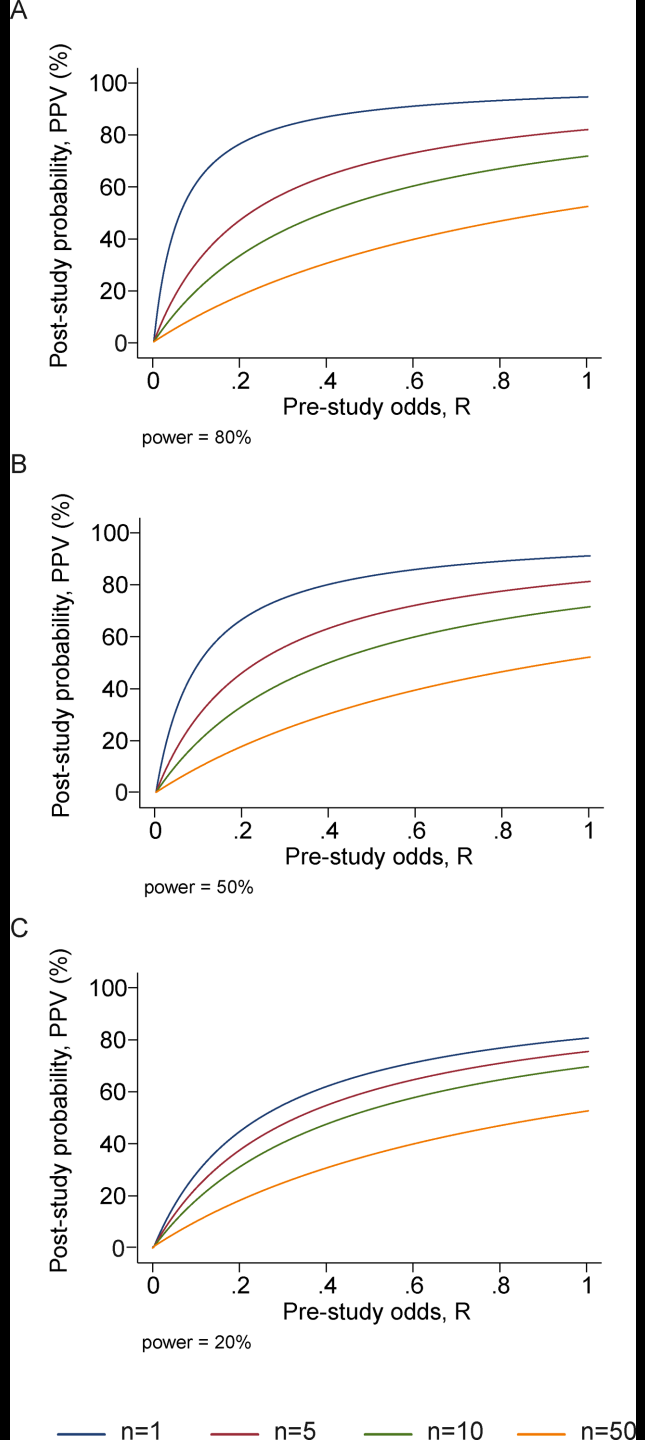
PPV is the number of true positives, divided by the number of rejected tests

John Ioannides' 2005 Paper

Let R be the ratio of the number of "true relationships" to "no relationships" (i.e., #HA/#H0)

Let α=alpha level, and (1-β)=Power

$$PPV = \frac{R(1-\beta)}{\alpha + R(1-\beta)}$$


A
Post-study probability, PPV (%)
100
80
60
40
20
0
0
.2
.4
.6
.8
1
Pre-study odds, R
power = 80%
B
Post-study probability, PPV (%)
100
80
60
40
20
0
0
.2
.4
.6
.8
1
Pre-study odds, R
power = 50%
C
Post-study probability, PPV (%)
100
80
60
40
20
0
0
.2
.4
.6
.8
1
Pre-study odds, R
power = 20%
n=1
n=5
n=10
n=50

John Ioannides' 2005 Paper

Lastly, let u=bias, the amount that a study is affected by biased practices (e.g., p-hacking); anything that tends to generate a positive results when it shouldn't

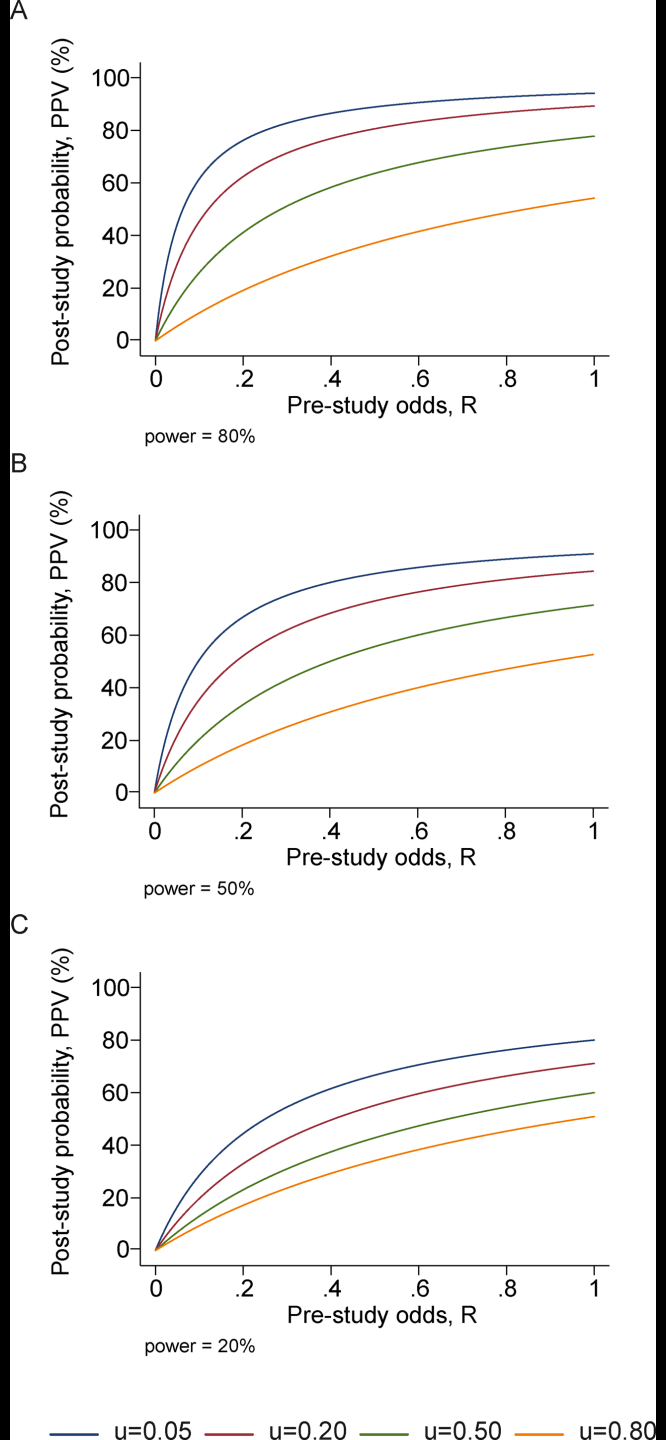

A
Post-study probability, PPV (%)
100
80
60
40
20
0
0
.2
.4
.6
.8
1
Pre-study odds, R
power = 80%
B
Post-study probability, PPV (%)
100
80
60
40
20
0
0
.2
.4
.6
.8
1
Pre-study odds, R
power = 50%
C
Post-study probability, PPV (%)
100
80
60
40
20
0
0
.2
.4
.6
.8
1
Pre-study odds, R
power = 20%
u=0.05
u=0.20
u=0.50
u=0.80

Table 4. PPV of Research Findings for Various Combinations of Power (1 – β), Ratio of True to Not-True Relationships *(R)*, and Bias *(u)*

1 – β	*R*	*u*	Practical Example	PPV
0.80	1:1	0.10	Adequately powered RCT with little bias and 1:1 pre-study odds	0.85
0.95	2:1	0.30	Confirmatory meta-analysis of good-quality RCTs	0.85
0.80	1:3	0.40	Meta-analysis of small inconclusive studies	0.41
0.20	1:5	0.20	Underpowered, but well-performed phase I/II RCT	0.23
0.20	1:5	0.80	Underpowered, poorly performed phase I/II RCT	0.17
0.80	1:10	0.30	Adequately powered exploratory epidemiological study	0.20
0.20	1:10	0.30	Underpowered exploratory epidemiological study	0.12
0.20	1:1,000	0.80	Discovery-oriented exploratory research with massive testing	0.0010
0.20	1:1,000	0.20	As in previous example, but with more limited bias (more standardized)	0.0015

Corollaries

What can be done?

Follow COBIDAS guidelines (Nichols et al., 2016)

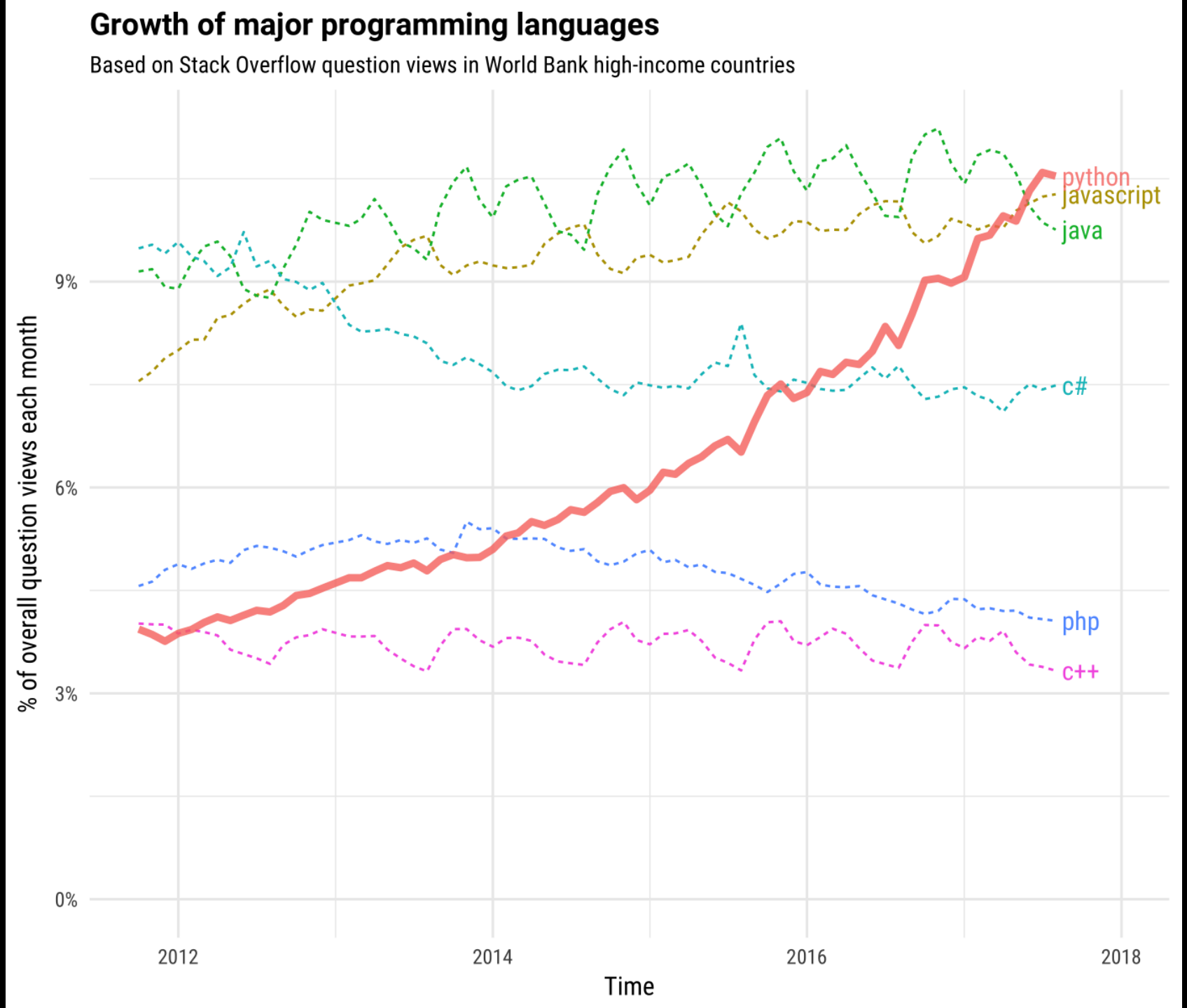
Run appropriate power analyses (discussed on Monday)

Pre-register your experiment (to be discussed on Friday)

Standardize your analyses (to be discussed right now!)

Questions?

Brief Overview of Python


Growth of major programming languages
Based on Stack Overflow question views in World Bank high-income countries
% of overall question views each month
9%
6%
3%
0%
2012
2014
2016
2018
Time
python
javascript
java
c#
php
c++

Advantages of Python

Popular, lots of support (e.g., Stack Overflow)

Intuitive Syntax

Widely used for open-source projects, and especially for the latest neuroimaging methods

Easy to transfer code through Jupyter notebooks

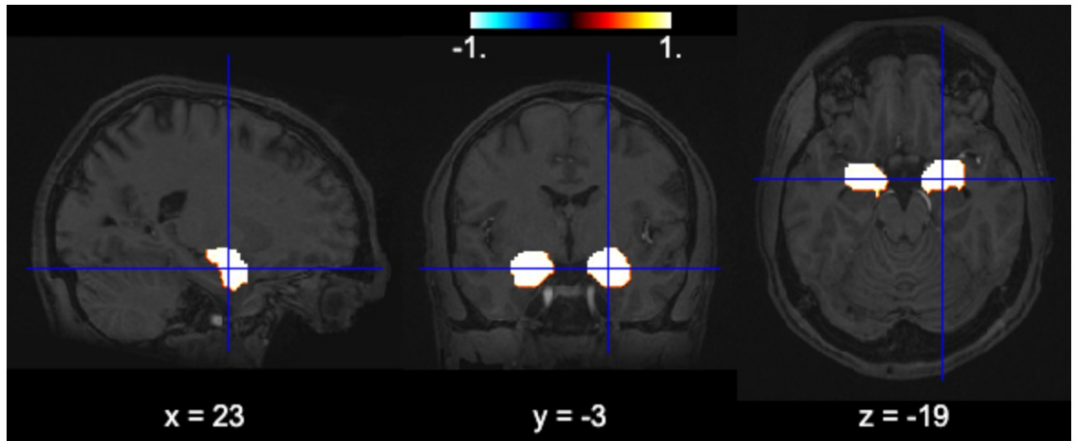
Python Terms

Similar to Matlab terms (variables, conditional statements, etc.)

Dictionaries, tuples, and sets are used to store data

Different packages can be downloaded to perform different functions

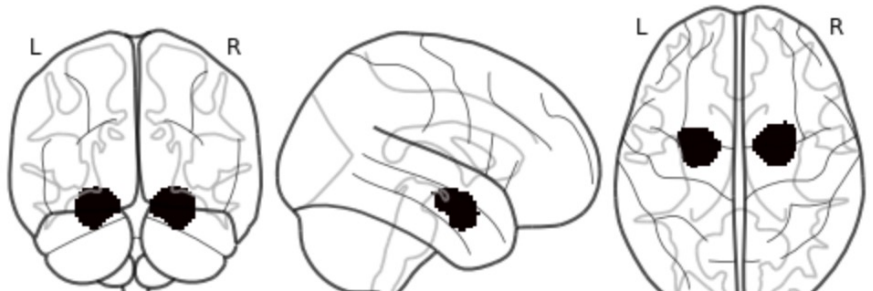
```
from nltools.data import Brain_Data
amygdala_mask = Brain_Data('https://neurovault.org/media/images/1290/FSL_BAmyg_thr0.nii

view_img(amygdala_mask, data)
```



We can also plot a glass brain which allows us to see through the brain from different slice orientations. In this example, we will plot the binary amygdala mask.

```
plot_glass_brain(amygdala_mask)
```

```
<nilearn.plotting.displays.OrthoProjector at 0x7fad29aa88d0>
```



jupyter Introduction_to_Neuroimaging_Data (unsaved changes)

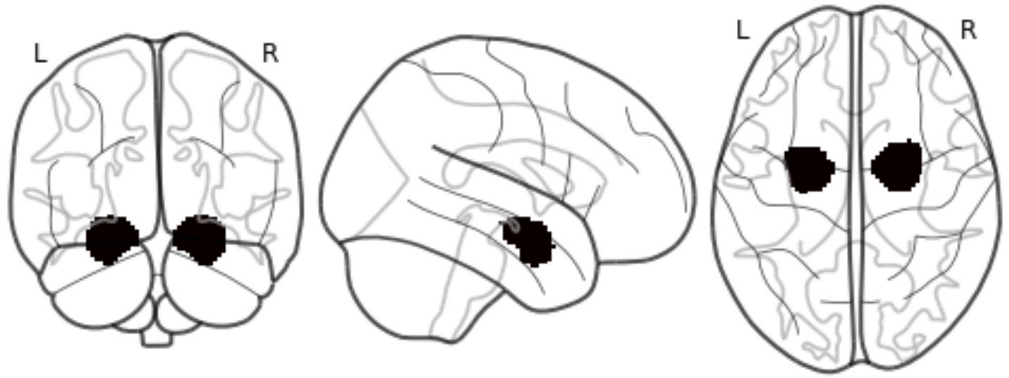
Logout

File Edit View Insert Cell Kernel Help Not Trusted Python 3 (ipykernel)

Run Markdown

In [42]:
```
plot_glass_brain(amygdala_mask)
```

Out[42]:
```
<nilearn.plotting.displays.OrthoProjector at 0x7fad29aa88d0>
```



Manipulating Data with Nltools

Ok, we've now learned how to use nibabel to load imaging data and nilearn to plot it.

Next we are going to learn how to use the `nltools` package that tries to make loading, plotting, and manipulating data easier. It uses many functions from nibabel, nilearn, and other python libraries. The bulk of the nltools toolbox is built around the `Brain_Data()` class. The

Jupyter Terms

Code cell: Code that you want to run

Preceded by “In”; an asterisk (”*”) means the cell is running

Markdown cell: Text that can be formatted for presentation purposes

Kernel: Version of Python you are running

Python distribution for package management

Comes with many packages pre-installed, but you can install more

Works well across operating systems

How to analyze data with Python?

Can use several different packages

e.g., nibabel for loading and aligning data, nipy for preprocessing, nilearn for machine learning

Lab today will use nibabel for loading and displaying images

Python Demonstration

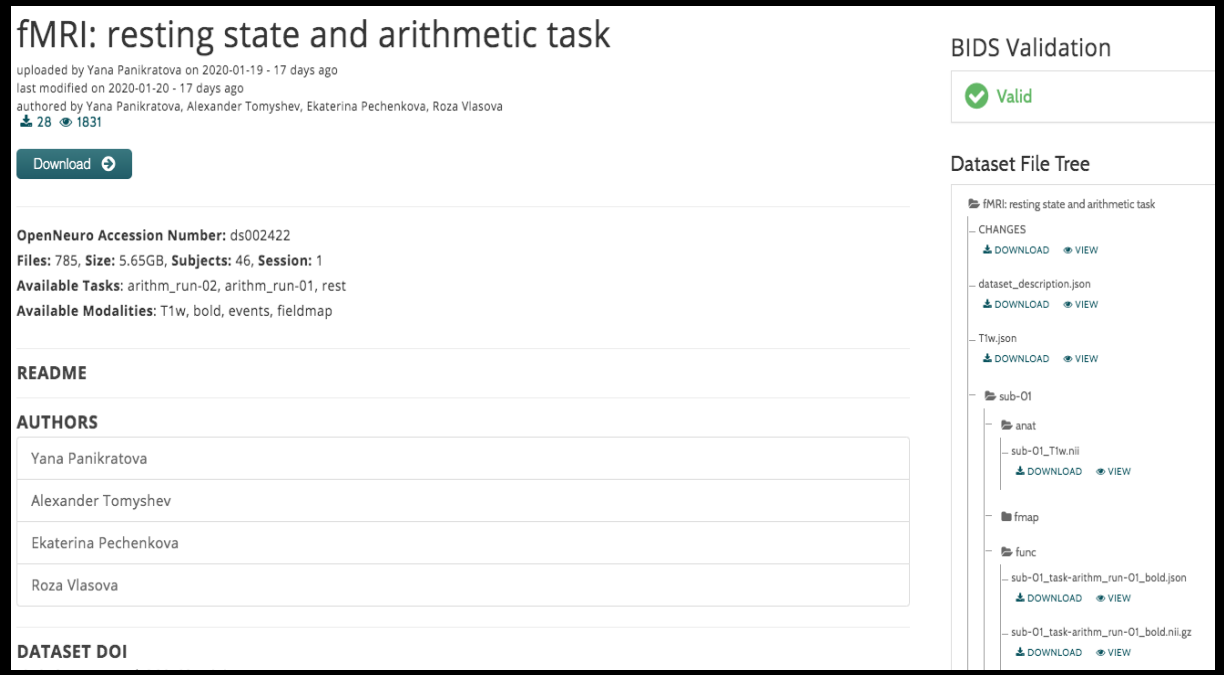
The Good Old Days

Idiosyncratic labeling for data and folders

```
ajahn:~/Desktop/myExp$ ls
1stAnalysis                     preproc_NoSmooth_Nonlinear
2ndAnalysis                     raw
FinalAnalysis                   timings
FinalAnalysis_FINAL             timings_ScannerOffset
preproc
```

What is BIDS?

Standard for organizing imaging data




```
ajahn:~/Desktop$ ls Flanker/
CHANGES                   sub-06                    sub-17
README                    sub-07                    sub-18
T1w.json                  sub-08                    sub-19
dataset_description.json  sub-09                    sub-20
derivatives               sub-10                    sub-21
participants.tsv          sub-11                    sub-22
sub-01                    sub-12                    sub-23
sub-02                    sub-13                    sub-24
sub-03                    sub-14                    sub-25
sub-04                    sub-15                    sub-26
sub-05                    sub-16                    task-flanker_bold.json
ajahn:~/Desktop$ ls Flanker/sub-01
anat  func
ajahn:~/Desktop$ ls Flanker/sub-01/func
sub-01_task-flanker_run-1_bold.nii.gz  sub-01_task-flanker_run-2_bold.nii.gz
sub-01_task-flanker_run-1_events.tsv   sub-01_task-flanker_run-2_events.tsv
ajahn:~/Desktop$ ls Flanker/sub-01/anat
sub-01_T1w.nii.gz
ajahn:~/Desktop$
```

Benefits of BIDS

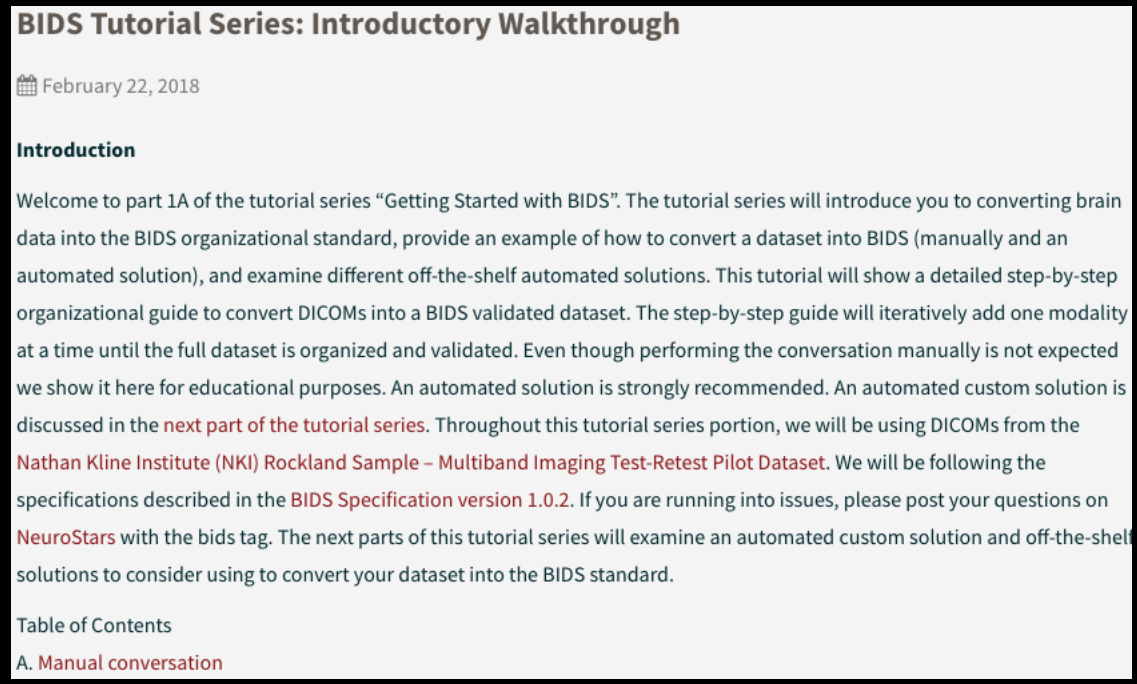
1. Reproducibility and Data Sharing

2. Access to BIDS-apps (e.g., MRIQC, fMRIPrep)

3. Ability to share your own BIDS-apps

How to convert to BIDS?

Stanford Center for Reproducible Neuroscience



BIDS Tutorial Series: Introductory Walkthrough

February 22, 2018

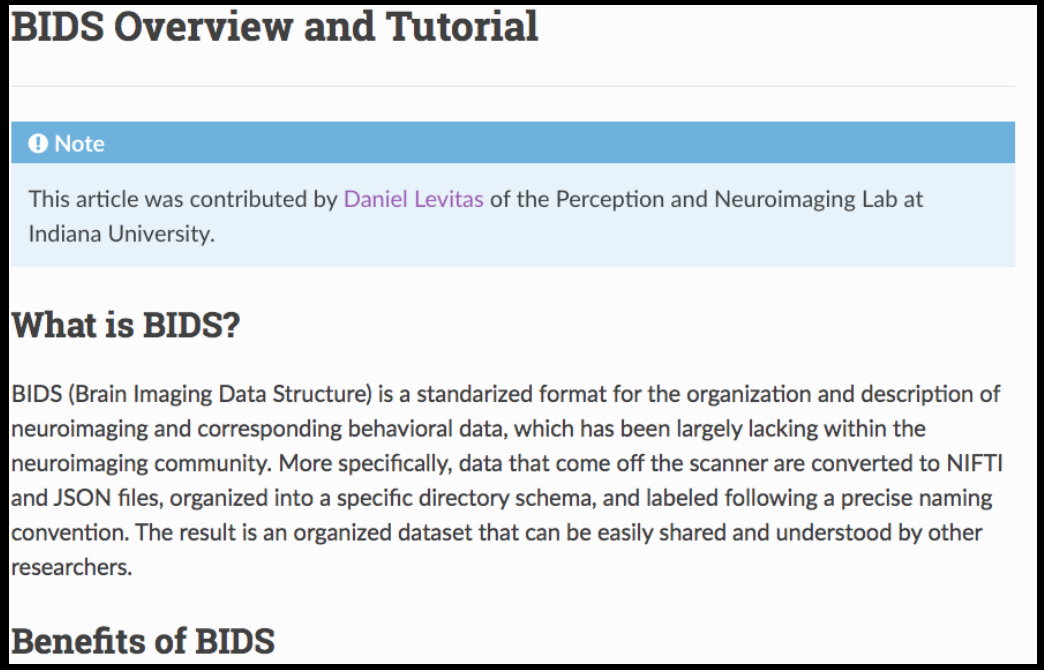
Introduction

Welcome to part 1A of the tutorial series "Getting Started with BIDS". The tutorial series will introduce you to converting brain data into the BIDS organizational standard, provide an example of how to convert a dataset into BIDS (manually and an automated solution), and examine different off-the-shelf automated solutions. This tutorial will show a detailed step-by-step organizational guide to convert DICOMs into a BIDS validated dataset. The step-by-step guide will iteratively add one modality at a time until the full dataset is organized and validated. Even though performing the conversation manually is not expected we show it here for educational purposes. An automated solution is strongly recommended. An automated custom solution is discussed in the next part of the tutorial series. Throughout this tutorial series portion, we will be using DICOMs from the Nathan Kline Institute (NKI) Rockland Sample – Multiband Imaging Test-Retest Pilot Dataset. We will be following the specifications described in the BIDS Specification version 1.0.2. If you are running into issues, please post your questions on NeuroStars with the bids tag. The next parts of this tutorial series will examine an automated custom solution and off-the-shelf solutions to consider using to convert your dataset into the BIDS standard.

Table of Contents

A. Manual conversation

How to convert to BIDS?



BIDS Overview and Tutorial

Note

This article was contributed by Daniel Levitas of the Perception and Neuroimaging Lab at Indiana University.

What is BIDS?

BIDS (Brain Imaging Data Structure) is a standarized format for the organization and description of neuroimaging and corresponding behavioral data, which has been largely lacking within the neuroimaging community. More specifically, data that come off the scanner are converted to NIFTI and JSON files, organized into a specific directory schema, and labeled following a precise naming convention. The result is an organized dataset that can be easily shared and understood by other researchers.

Benefits of BIDS

Requires certain commands (pigz, dcm2bids, etc.)

Should work with most Macintosh and Unix operating systems

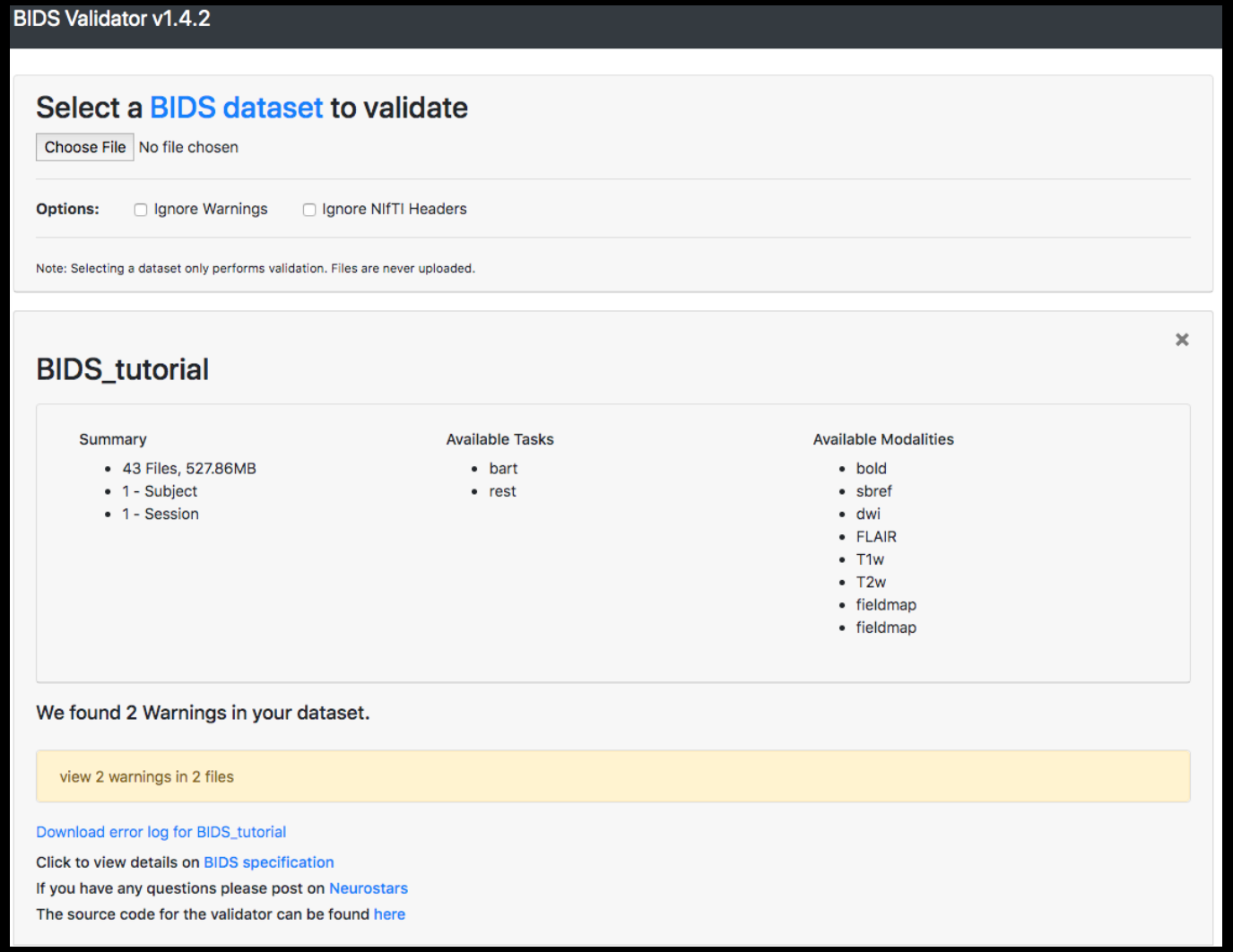
How to convert to BIDS?

```
{
 "descriptions": [
    {
       "dataType": "anat",
       "modalityLabel": "T1w",
       "criteria": {
          "SidecarFilename": "002*"
       }
    },
    {
       "dataType": "fmap",
       "modalityLabel": "epi",
       "customLabels": "dir-AP",
       "IntendedFor": [
          4,
          6
       ],
       "criteria": {
          "SidecarFilename": "003*"
       }
    },
    {
       "dataType": "fmap",
       "modalityLabel": "epi",
       "customLabels": "dir-PA",
       "IntendedFor": [
          4,
          6
       ],
       "criteria": {
          "SidecarFilename": "004*"
       }
```

Datasets require a BIDS configuration file in .json format

Each run that is collected requires a different section of javascript

BIDS Validation



One year ago…

Article | Published: 20 May 2020

Variability in the analysis of a single neuroimaging dataset by many teams

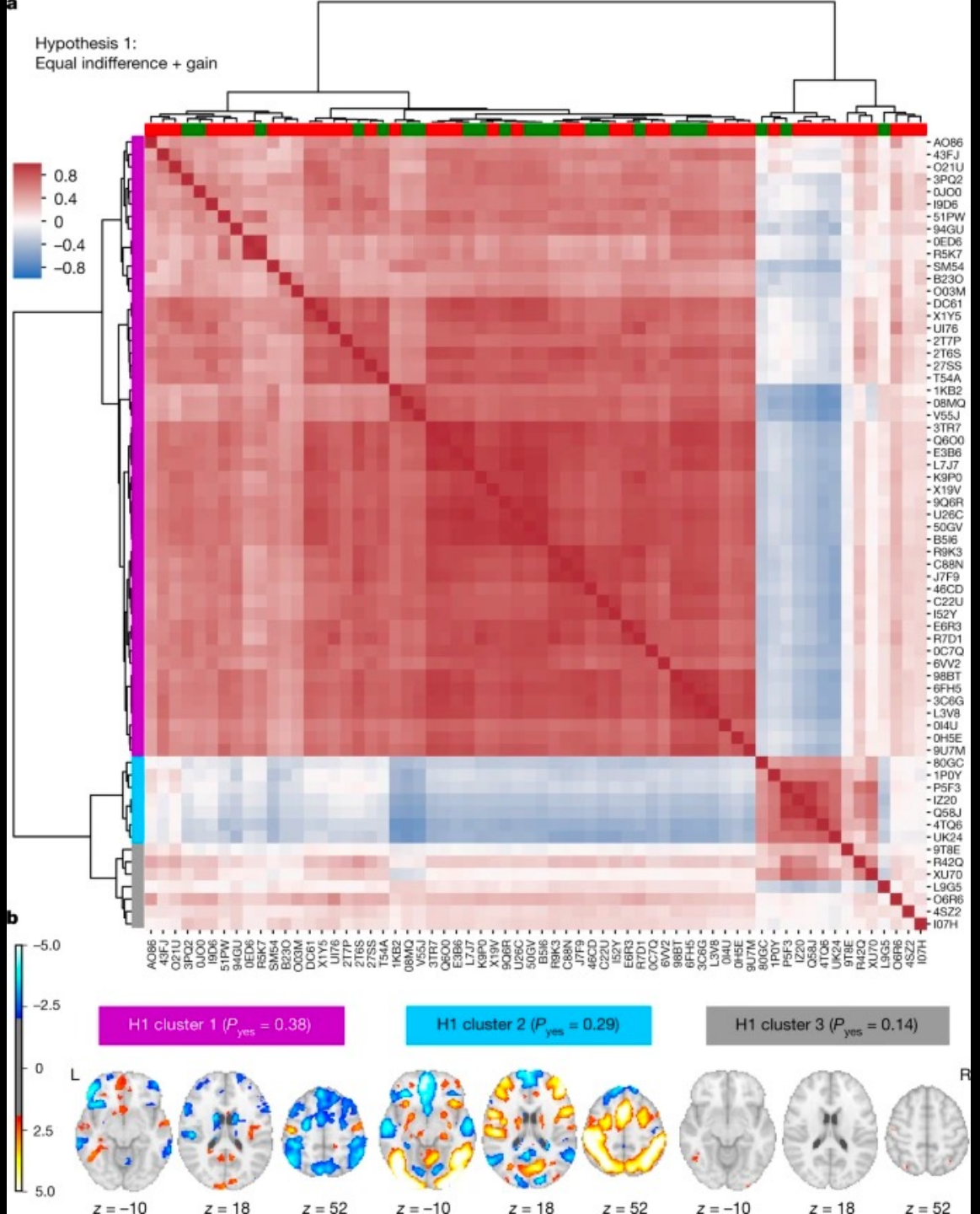
Rotem Botvinik-Nezer, Felix Holzmeister, […] Tom Schonberg ✉

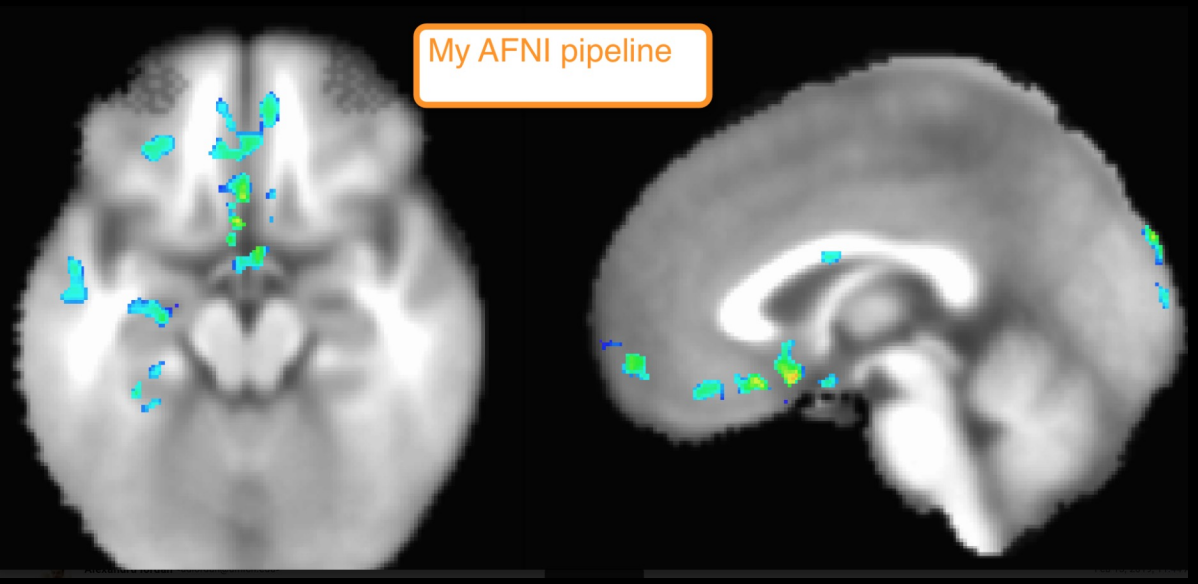
Nature **582**, 84–88(2020) | Cite this article

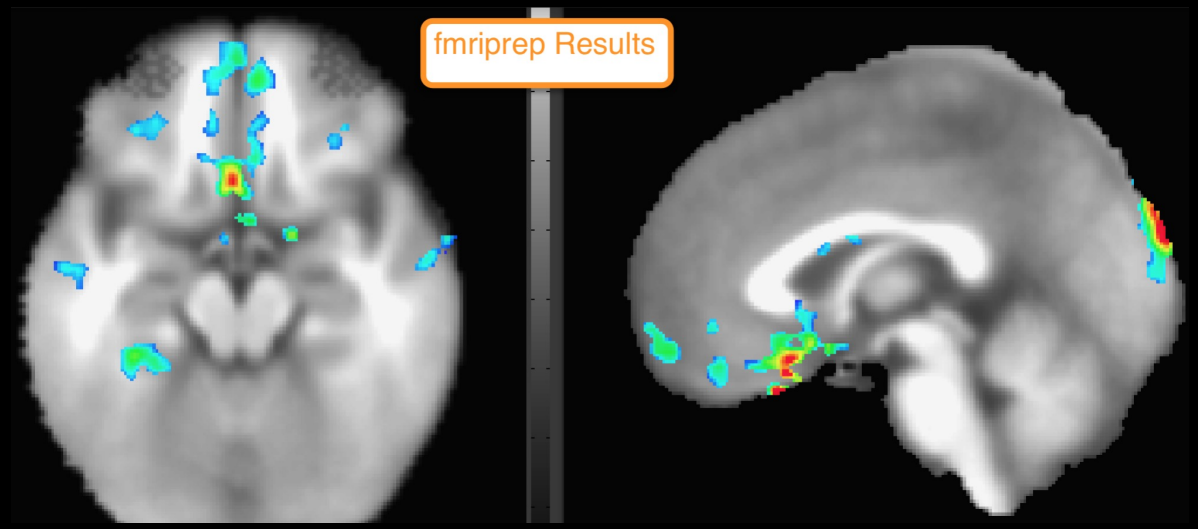
24k Accesses | **9** Citations | **874** Altmetric | Metrics

Abstract

Data analysis workflows in many scientific domains have become increasingly complex and flexible. Here we assess the effect of this flexibility on the results of functional magnetic resonance imaging by asking 70 independent teams to analyse the same dataset, testing the same 9 ex-ante hypotheses[1]. The flexibility of analytical approaches is exemplified by the fact that no two teams chose identical workflows to analyse the data. This flexibility resulted in sizeable variation in the results of hypothesis tests, even for teams whose statistical maps were highly correlated at intermediate stages of the analysis pipeline. Variation in reported results was related to several aspects of analysis methodology. Notably, a meta-analytical approach that aggregated information across teams yielded a significant consensus in activated regions. Furthermore, prediction markets of researchers in the field revealed an overestimation of the likelihood of significant findings, even by researchers with direct knowledge of the dataset[2,3,4,5]. Our findings show that analytical flexibility can have substantial effects on scientific conclusions, and identify factors that may be related to variability in the analysis of functional magnetic resonance imaging. The results


a
Hypothesis 1:
Equal indifference + gain
0.8
0.4
0
−0.4
−0.8
AO86
43FJ
O21U
3PQ2
0JO0
I9D6
51PW
94GU
0ED6
R5K7
SM54
B23O
O03M
DC61
X1Y5
UI76
2T7P
2T6S
27SS
T54A
1KB2
08MQ
V55J
3TR7
Q6O0
E3B6
L7J7
K9P0
X19V
9Q6R
U26C
50GV
B5I6
R9K3
C88N
J7F9
46CD
C22U
I52Y
E6R3
R7D1
0C7Q
6VV2
98BT
6FH5
3C6G
L3V8
0I4U
0H5E
9U7M
80GC
1P0Y
P5F3
IZ20
Q58J
4TQ6
UK24
9T8E
R42Q
XU70
L9G5
O6R6
4SZ2
I07H
b
−5.0
−2.5
0
2.5
5.0
H1 cluster 1 (P_{yes} = 0.38)
H1 cluster 2 (P_{yes} = 0.29)
H1 cluster 3 (P_{yes} = 0.14)
L
R
z = −10
z = 18
z = 52
z = −10
z = 18
z = 52
z = −10
z = 18
z = 52

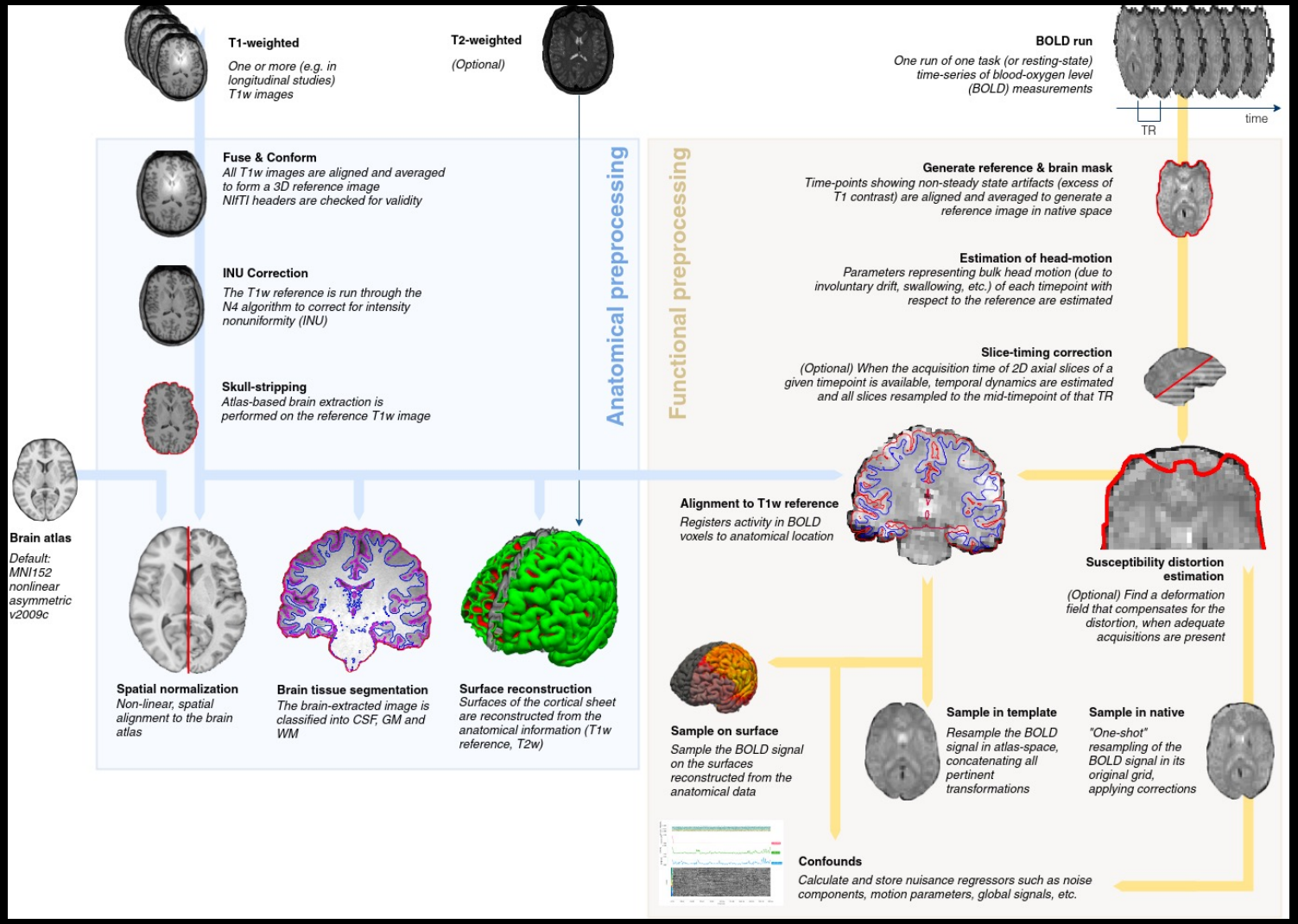




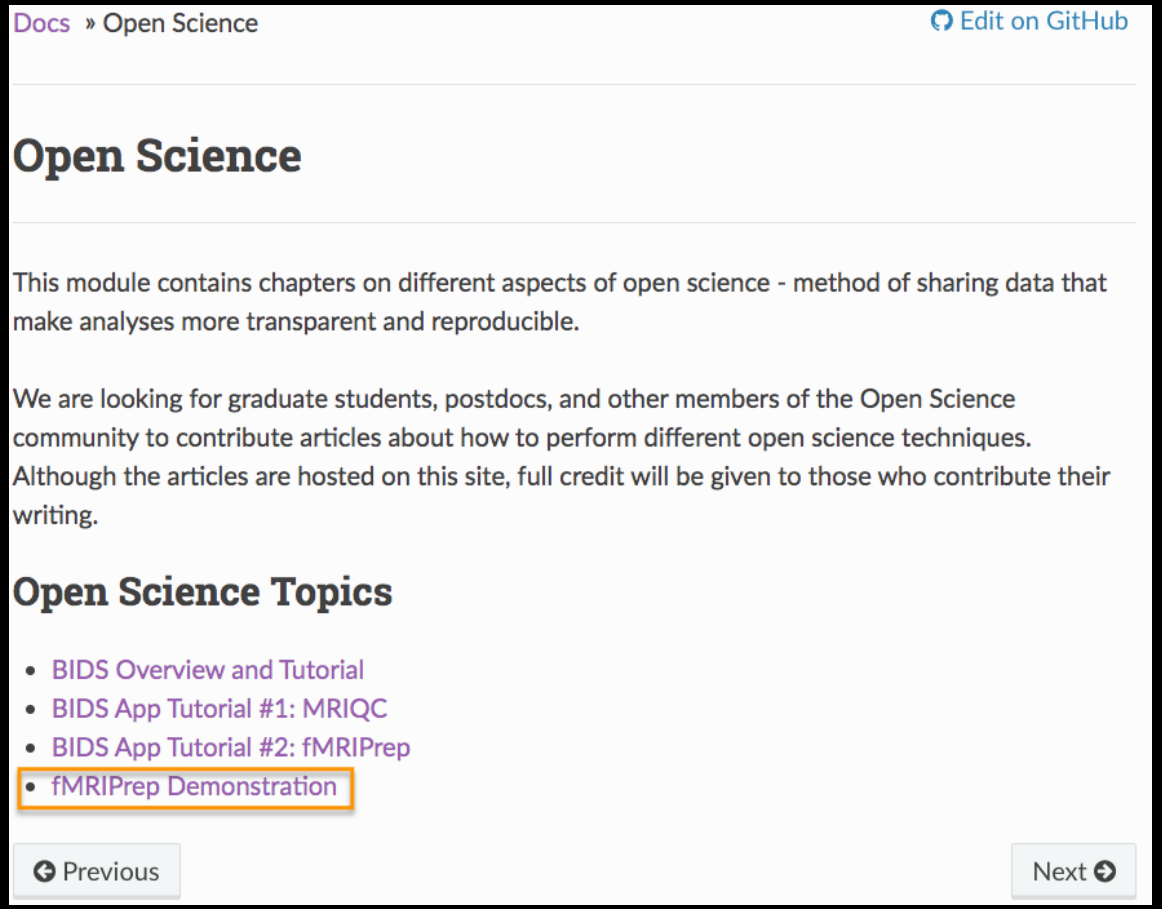
Peak t-statistic: 4.14

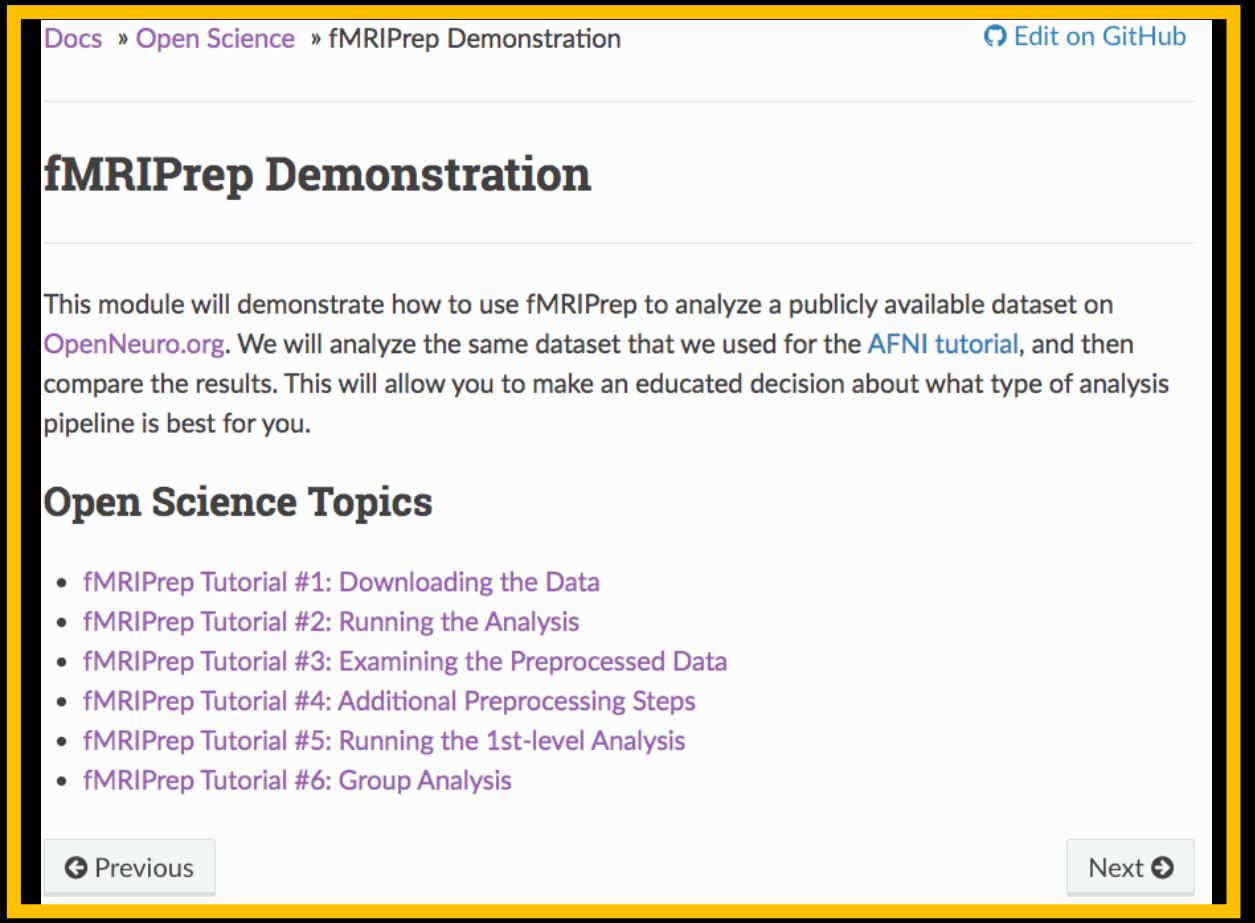
Peak t-statistic: 5.11

What is fMRIPrep?



The Module


Docs » Open Science
Edit on GitHub
Open Science
This module contains chapters on different aspects of open science - method of sharing data that make analyses more transparent and reproducible.
We are looking for graduate students, postdocs, and other members of the Open Science community to contribute articles about how to perform different open science techniques. Although the articles are hosted on this site, full credit will be given to those who contribute their writing.
Open Science Topics
BIDS Overview and Tutorial
BIDS App Tutorial #1: MRIQC
BIDS App Tutorial #2: fMRIPrep
fMRIPrep Demonstration
Previous
Next


Docs » Open Science » fMRIPrep Demonstration
Edit on GitHub
fMRIPrep Demonstration
This module will demonstrate how to use fMRIPrep to analyze a publicly available dataset on OpenNeuro.org. We will analyze the same dataset that we used for the AFNI tutorial, and then compare the results. This will allow you to make an educated decision about what type of analysis pipeline is best for you.
Open Science Topics
fMRIPrep Tutorial #1: Downloading the Data
fMRIPrep Tutorial #2: Running the Analysis
fMRIPrep Tutorial #3: Examining the Preprocessed Data
fMRIPrep Tutorial #4: Additional Preprocessing Steps
fMRIPrep Tutorial #5: Running the 1st-level Analysis
fMRIPrep Tutorial #6: Group Analysis
Previous
Next

fMRIPrep Analysis Prerequisites

Requires Docker (or Singularity, on a supercomputing cluster)

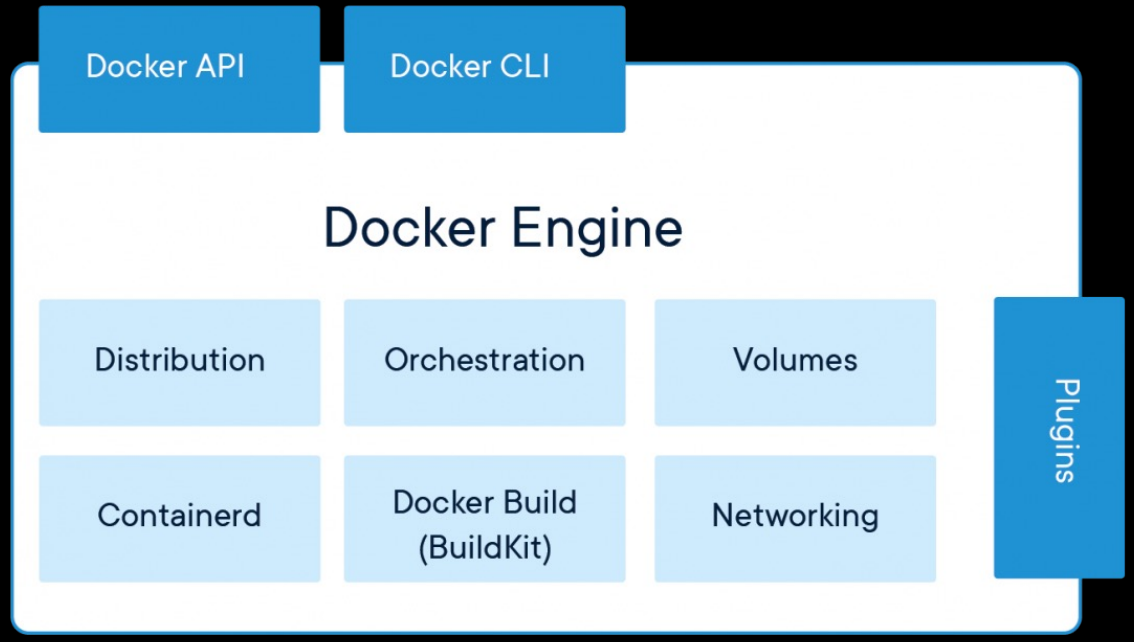
Data needs to be in BIDS format

fMRIPrep Analysis Prerequisites

Brief detour: What is a container?

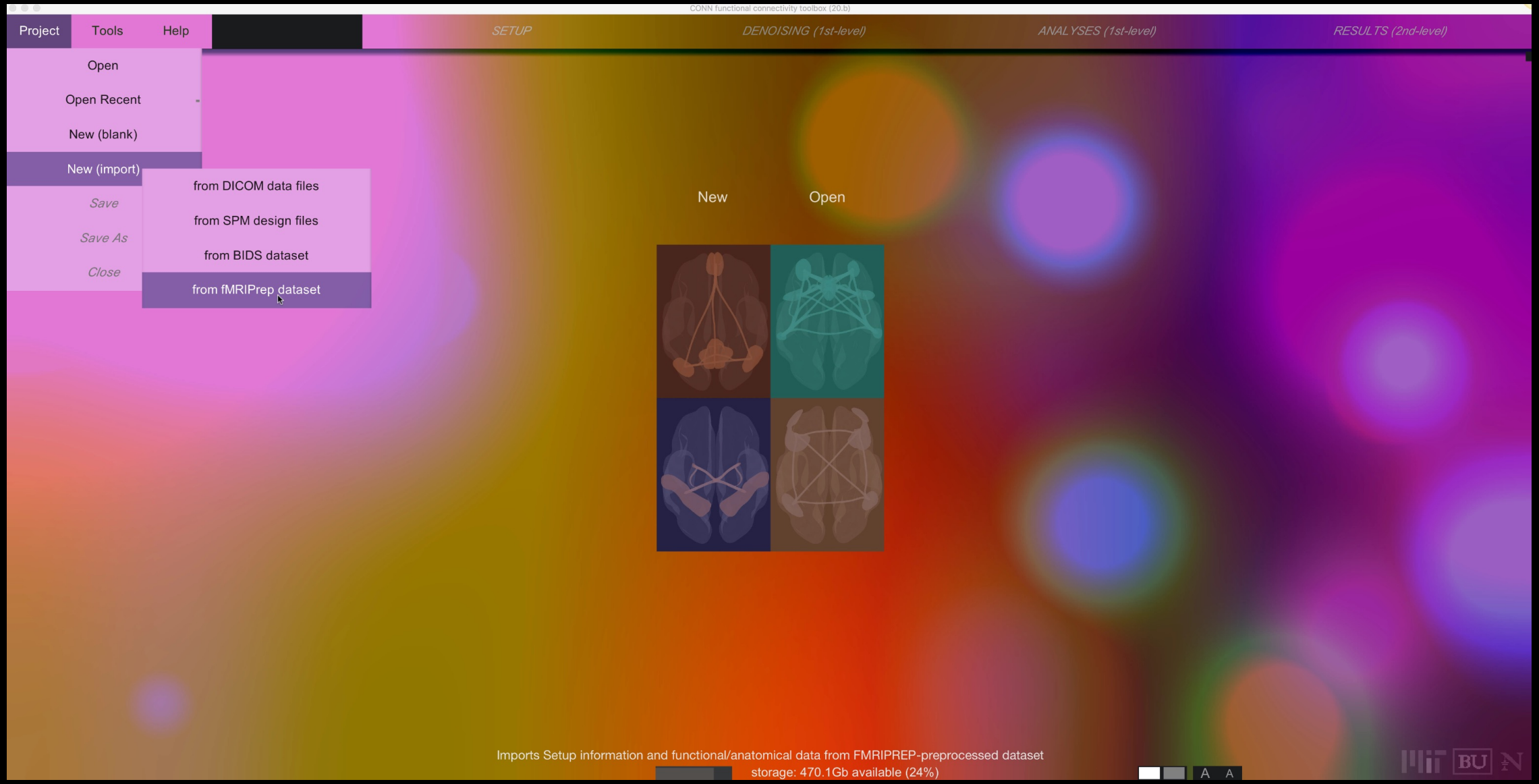
Docker

Environment in which containers are run

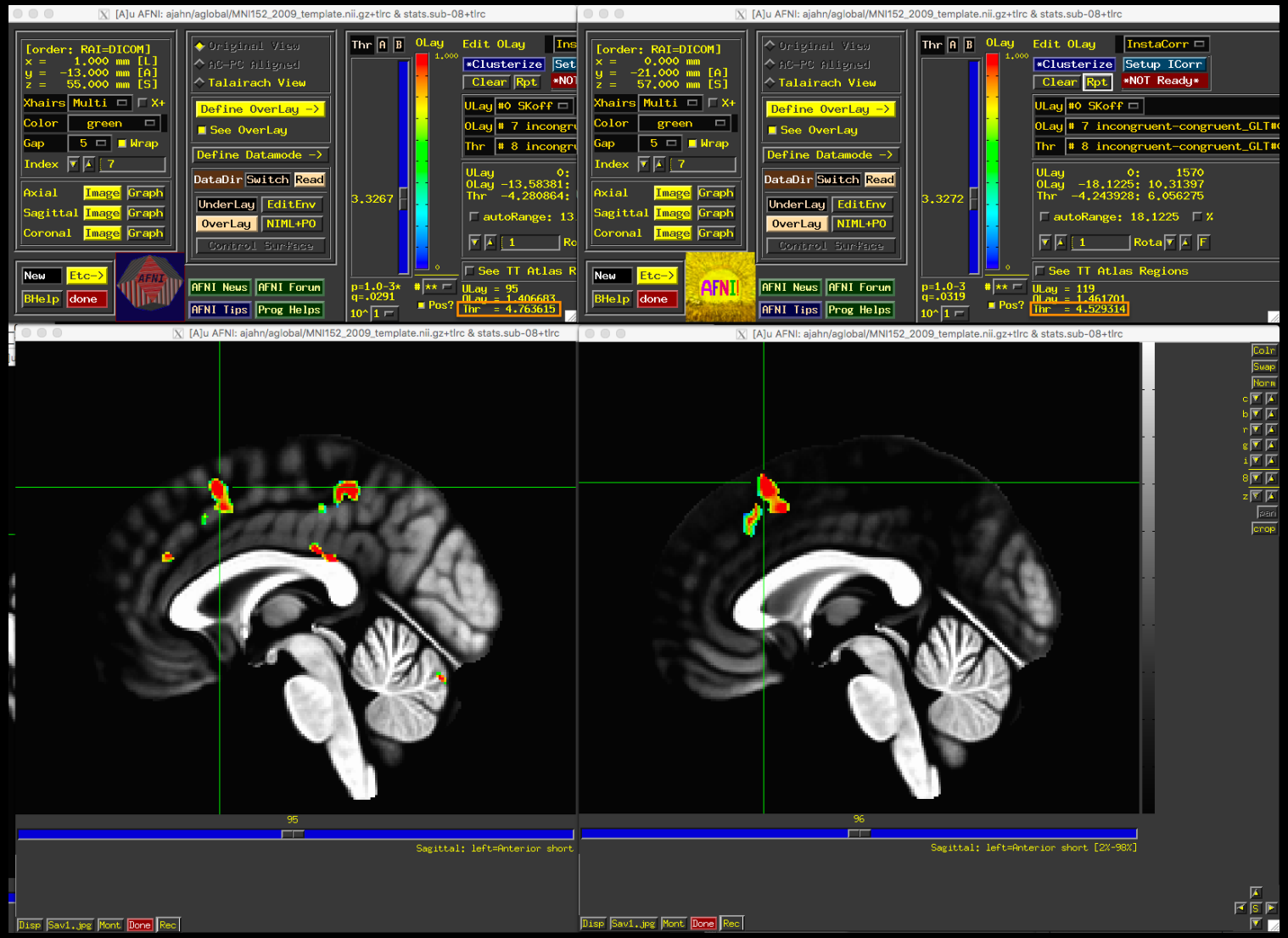


```
#User inputs:
bids_root_dir=$HOME/Desktop/Flanker
subj=08
nthreads=4
mem=20 #gb
container=docker #docker or singularity

#Begin:

#Convert virtual memory from gb to mb
mem=`echo "${mem//[!0-9]/}"` #remove gb at end
mem_mb=`echo $(((mem*1000)-5000))` #reduce some memory for buffer space during pre-processing

export FS_LICENSE=$HOME/Desktop/Flanker/derivatives/license.txt

#Run fmriprep
if [ $container == singularity ]; then
  unset PYTHONPATH; singularity run -B $HOME/.cache/templateflow:/opt/templateflow $HOME/fmrip
    $bids_root_dir $bids_root_dir/derivatives \
    participant \
    --participant-label $subj \
    --skip-bids-validation \
    --md-only-boilerplate \
    --fs-license-file $HOME/Desktop/Flanker/derivatives/license.txt \
    --fs-no-reconall \
    --output-spaces MNI152NLin2009cAsym:res-2 \
    --nthreads $nthreads \
    --stop-on-first-crash \
    --mem_mb $mem_mb \
    -w $HOME
else
  fmriprep-docker $bids_root_dir $bids_root_dir/derivatives \
    participant \
    --participant-label $subj \
    --skip-bids-validation \
    --md-only-boilerplate \
    --fs-license-file $HOME/Desktop/Flanker/derivatives/license.txt \
    --fs-no-reconall \
    --output-spaces MNI152NLin2009cAsym:res-2 \
    --nthreads $nthreads \
    --stop-on-first-crash \
    --mem_mb $mem_mb \
    -w $HOME
fi
```

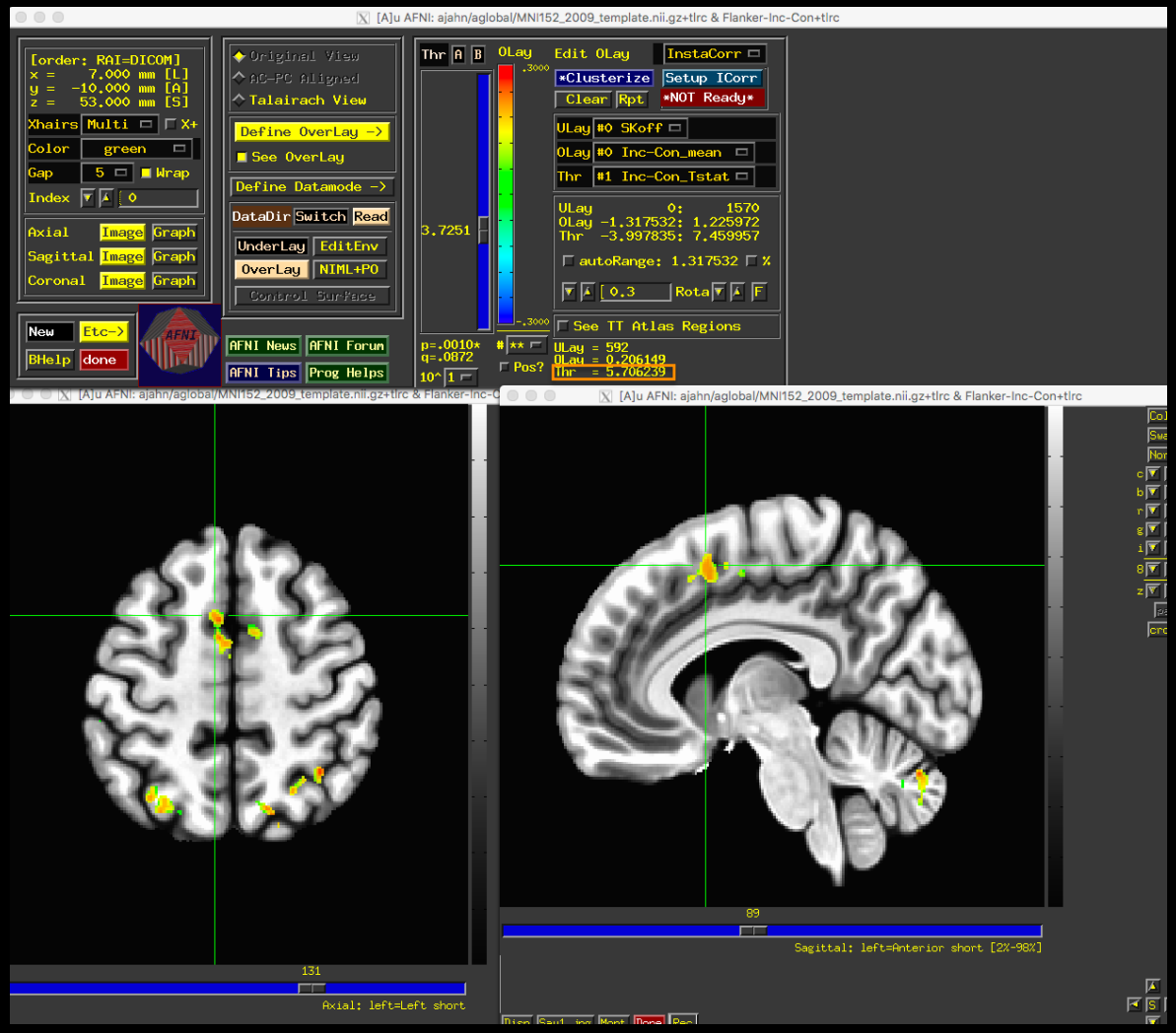
fMRIPrep with other software (e.g., CONN)

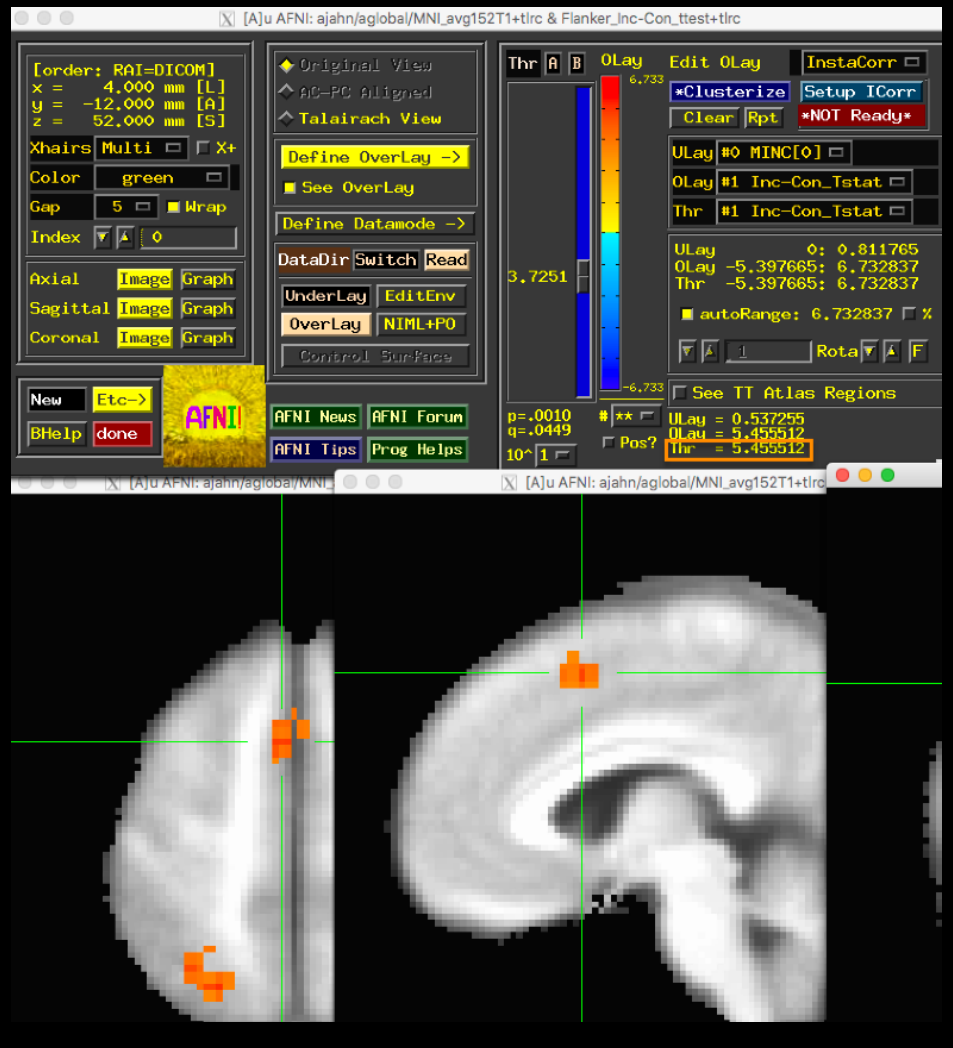


Comparing 1st-level Results



Comparing 2nd-level results





More Advanced BIDS Options

Surface-based analysis

Unwarping

Other BIDS extensions are being developed (e.g., ASL, TMS)

Scott will now walk you through the output of fMRIPrep

Questions?