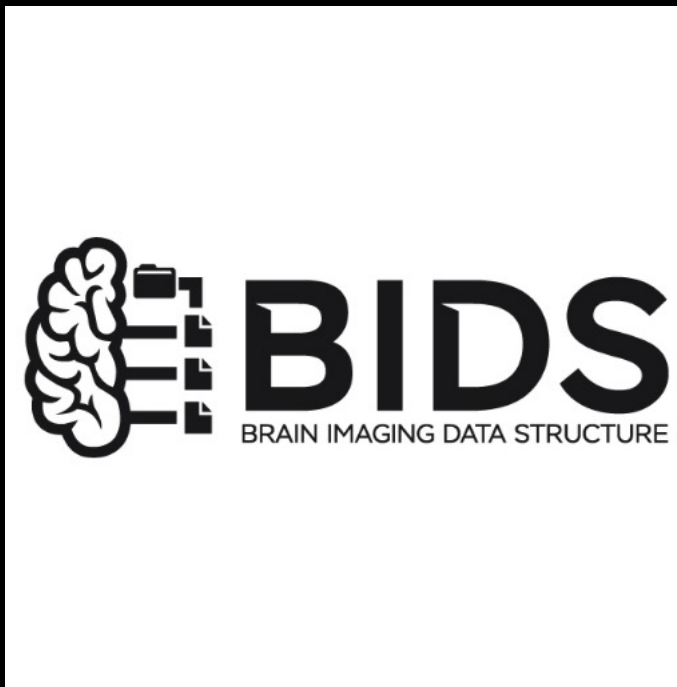


# fMRI Course, Day 12: Reproducibility

August 13<sup>th</sup>, 2022

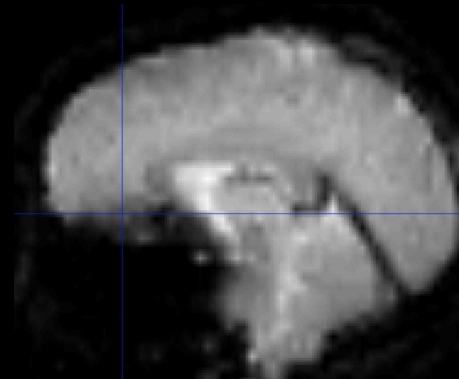
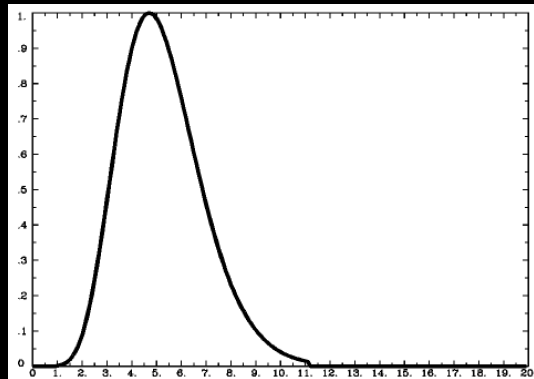


# Review So Far

From stimulus to the BOLD response

How tissue properties, blood flow, and magnetic properties interact

Creating contrast images from T1- and T2-weightings

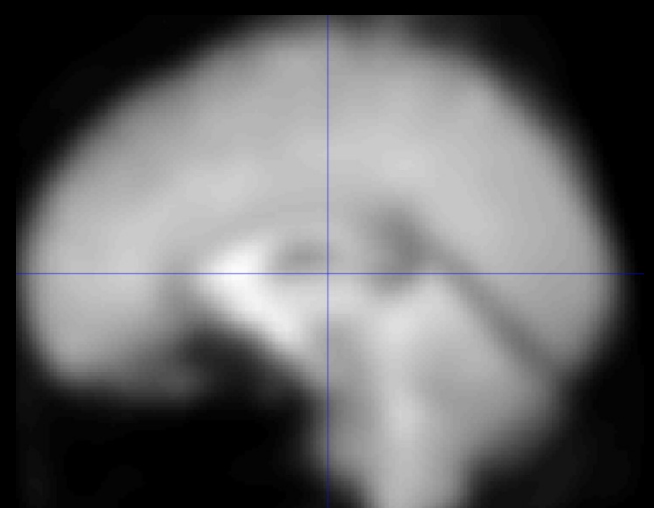
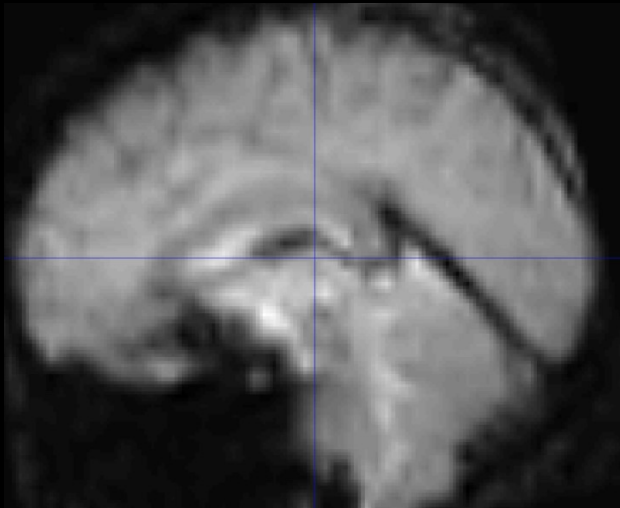


## Review So Far

Image artifacts: How to preprocess and why

Quality assurance checks after each step

Parameters that stay the same, versus those you can modify



## **Review So Far**

**When would you want to use a smaller smoothing kernel?**

**A larger smoothing kernel? Why?**

**When would you not want to use slice-timing correction?**

**Or should it always be used, no matter what?**

**What is the argument for using the mean functional image as the Reference and the anatomical image as the Source?**

**Would you ever want to swap them?**



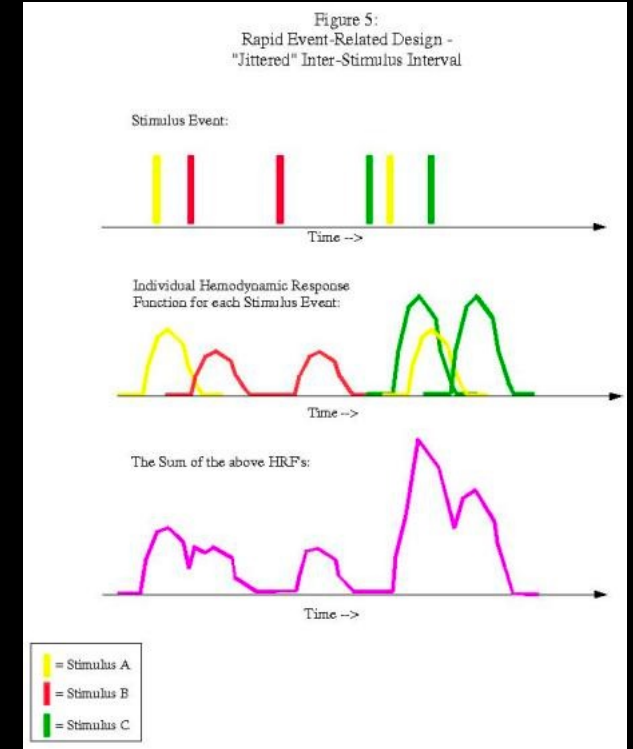
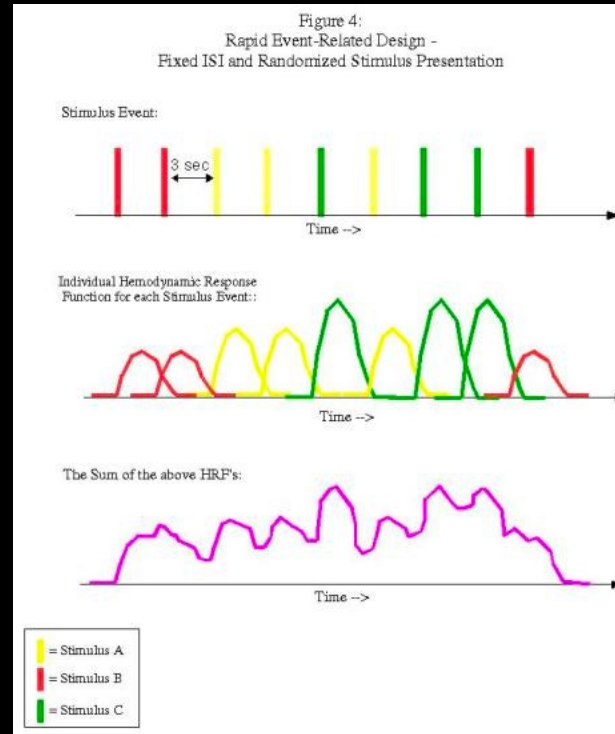
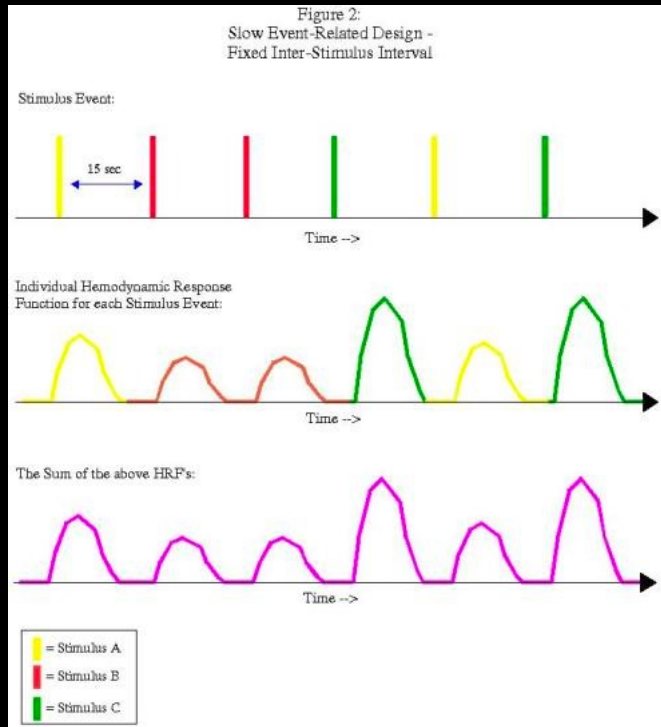
# **Review So Far**

**Experimental Design: Block vs. event-related**

**Slow vs. fast event-related**

**Jitter, collinearity, and power**

# Review So Far



What are the main advantages and disadvantages of each?

# What is Reproducibility?

**Replication: Arriving at the same result,  
using an independent dataset**

**Reproducibility: Ability to obtain the same result,  
using the same data and methods**

**Today: Use an open-access website to reproduce  
the results of that study**

# **What is Reproducibility?**

**Replication and reproducibility have become more talked about in the past decade**

**Methods such as pre-registration can help to increase the likelihood of a successful replication**

**In other words: Minimize the researcher degrees of freedom**

# **Theory-driven vs. Data-driven**

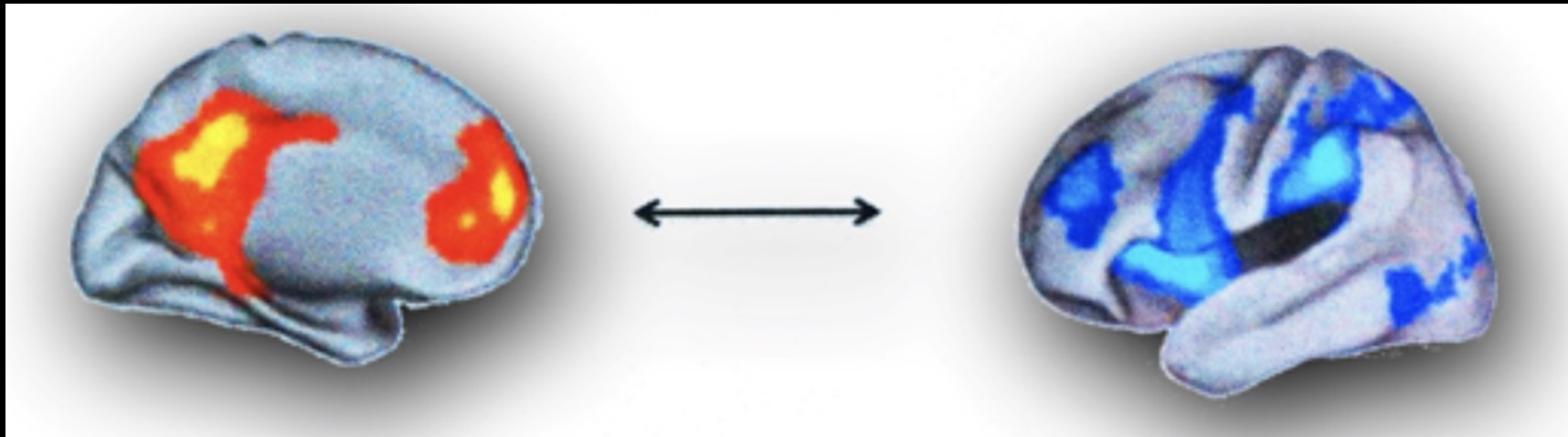
**Theory-driven: Based on previous studies, reasonable predictions about what a region does**

**Data-driven: Uses the data itself to identify patterns, and then possibly create theories**

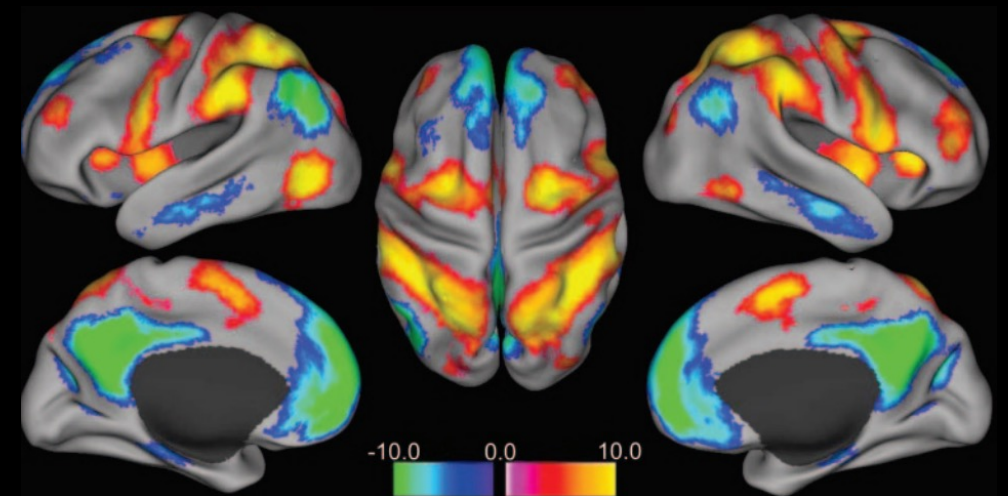
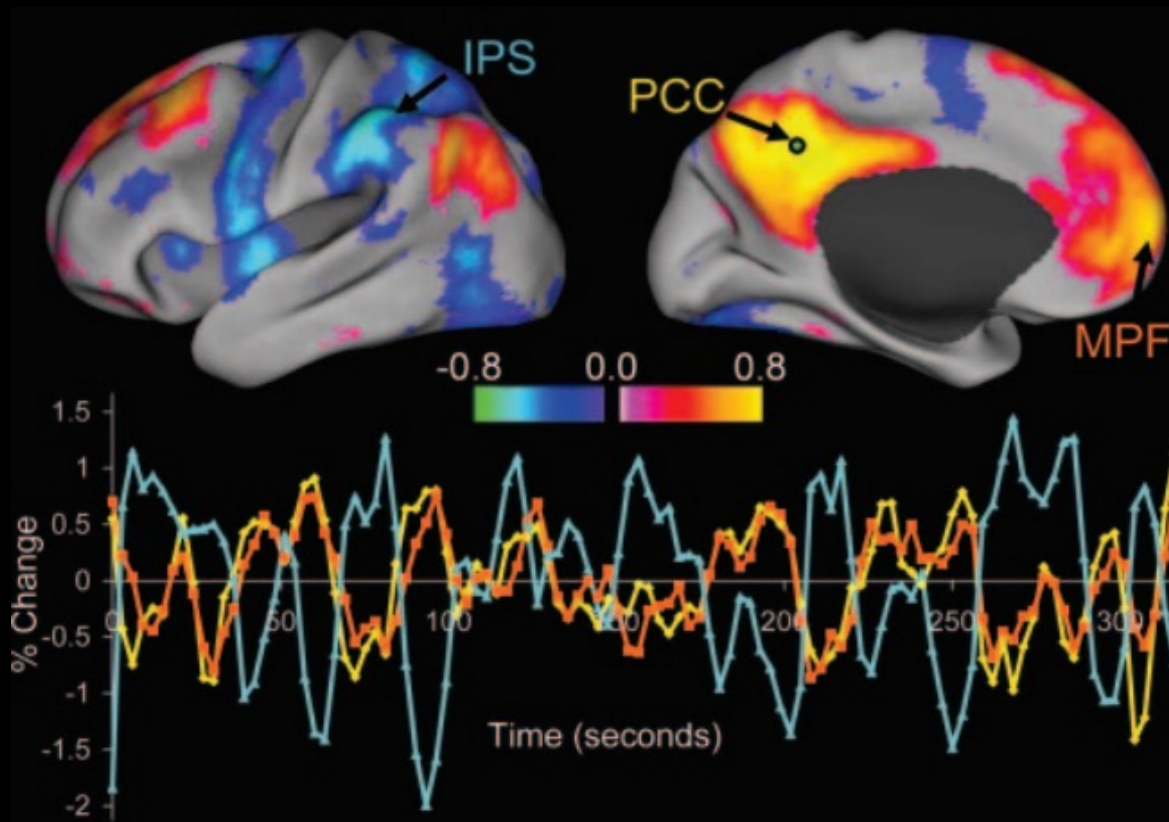
# Theory-driven vs. Data-driven

Theory-driven approaches have usually been more popular

Example: Fox et al., 2005

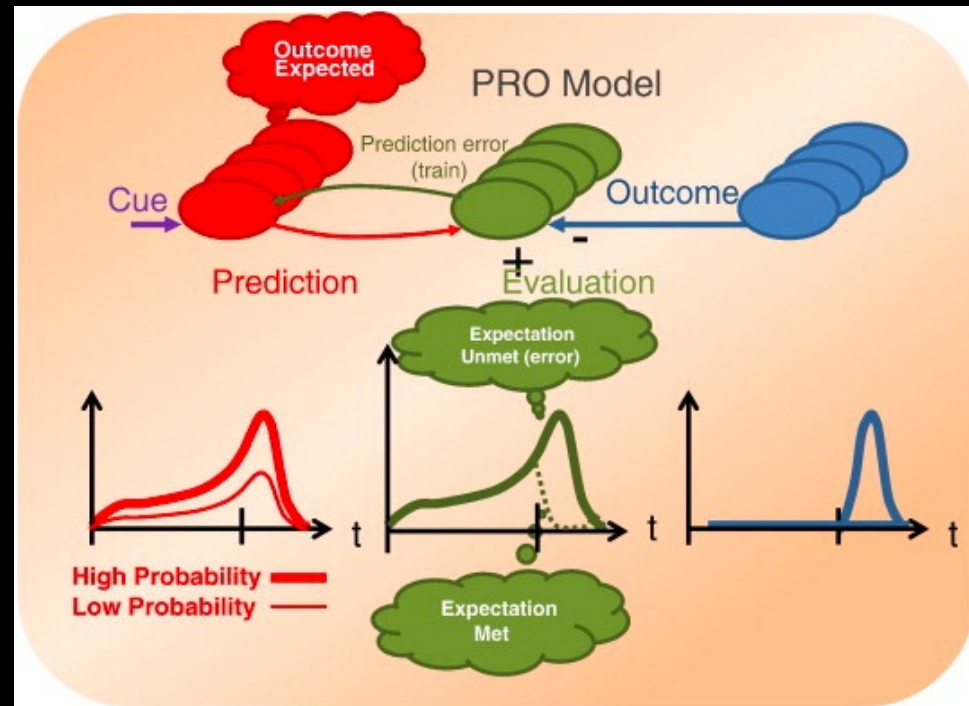


# Theory-driven vs. Data-driven



# Theory-driven vs. Data-driven

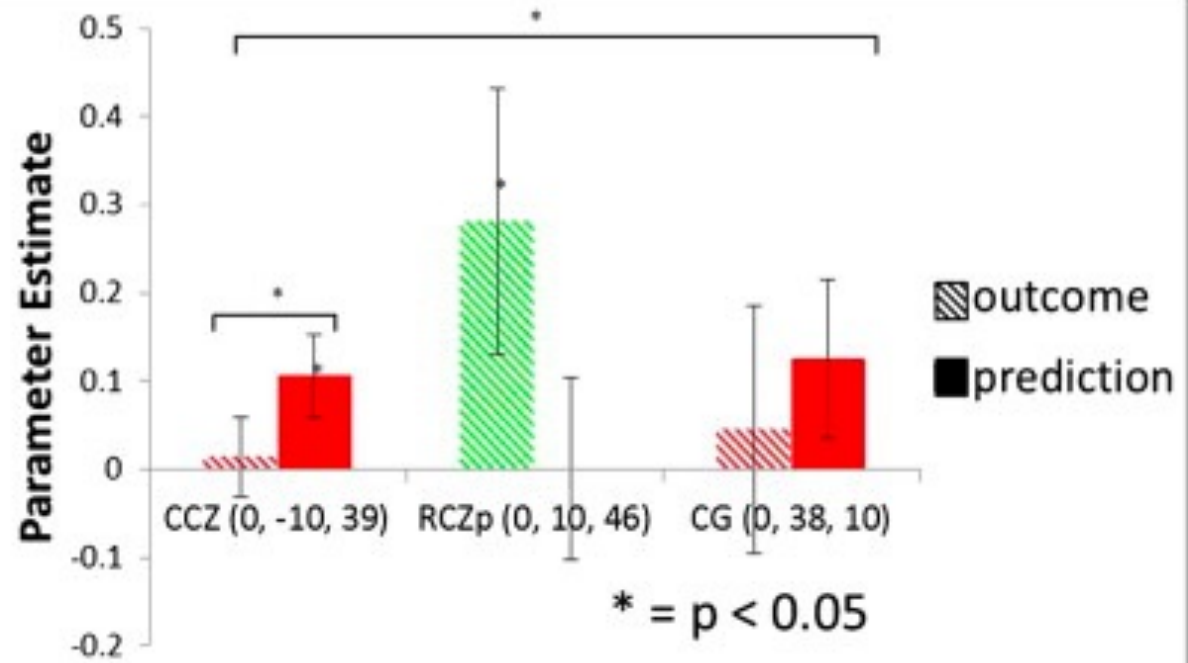
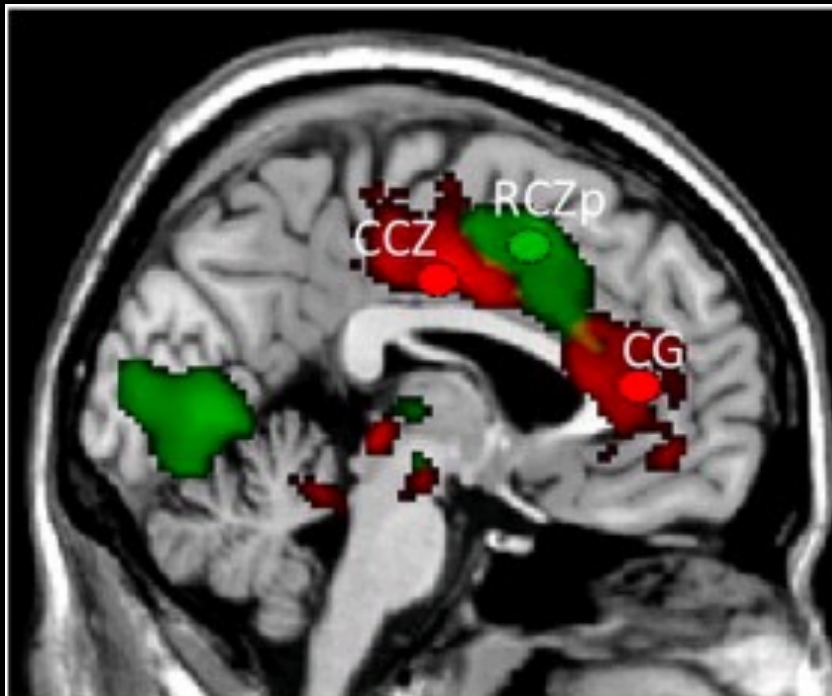
Can also use a theoretical framework to create regressors





# Theory-driven vs. Data-driven

$$Activity\ y_t = \sum_i [Predicted\ Outcome\ e_{i,t} - Actual\ Outcome\ e_{i,t}]^+$$



# **Data-driven**

**Useful results can be generated from the data itself**

**Usually requires a large number of observations or subjects**

**Popular data-driven method: Multivariate Pattern Analysis**

**Other methods can be used: e.g., clustering**

# MVPA

Training data vs. Testing data

Example: Height and hair length in males and females



# MVPA

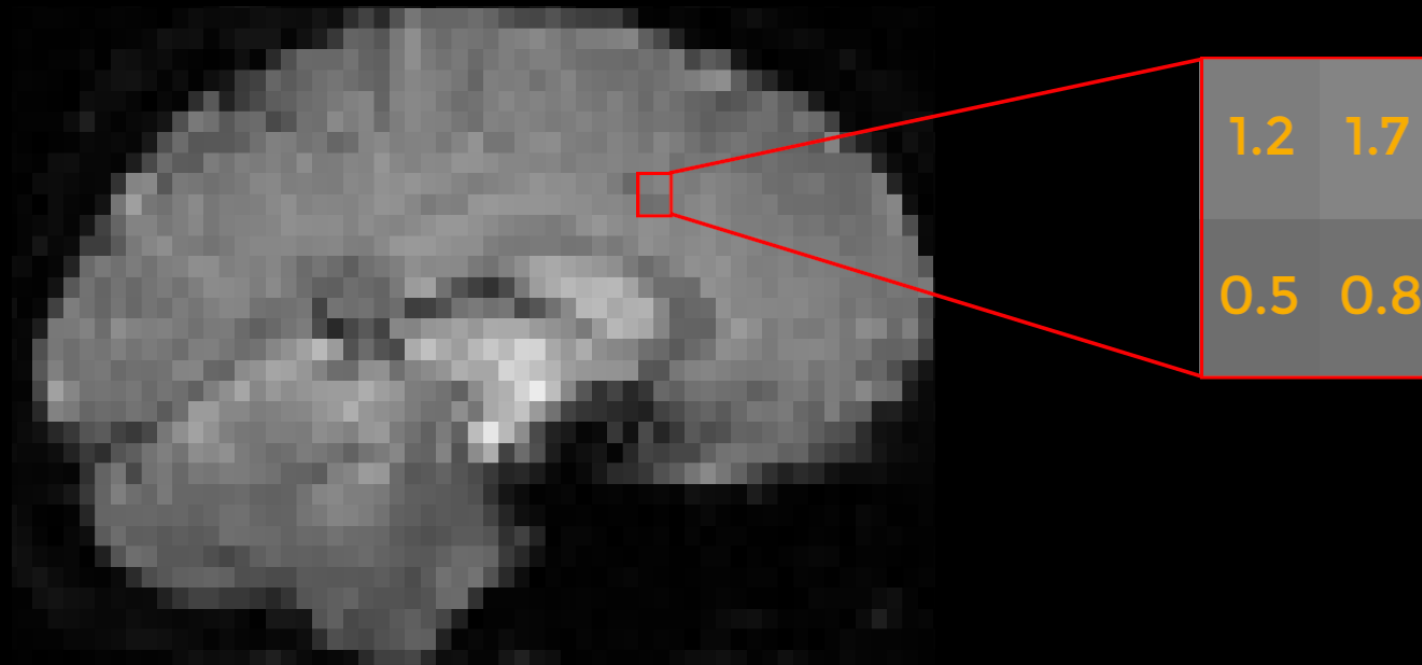
Someone is 6'4" with hair length of 3 inches

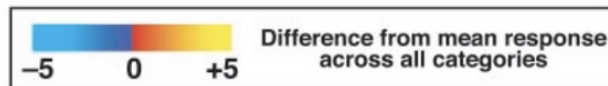
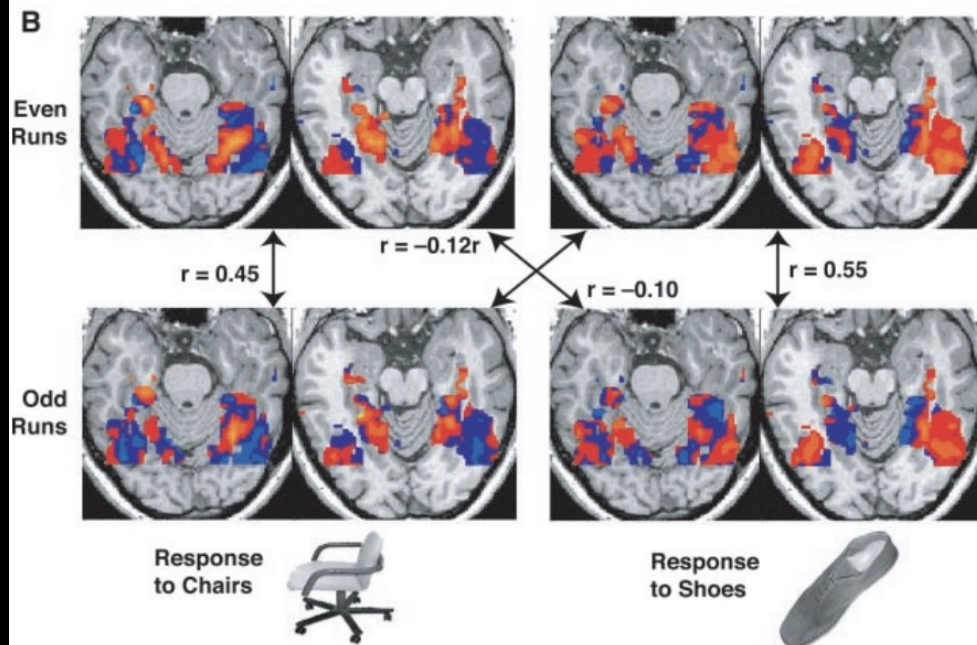
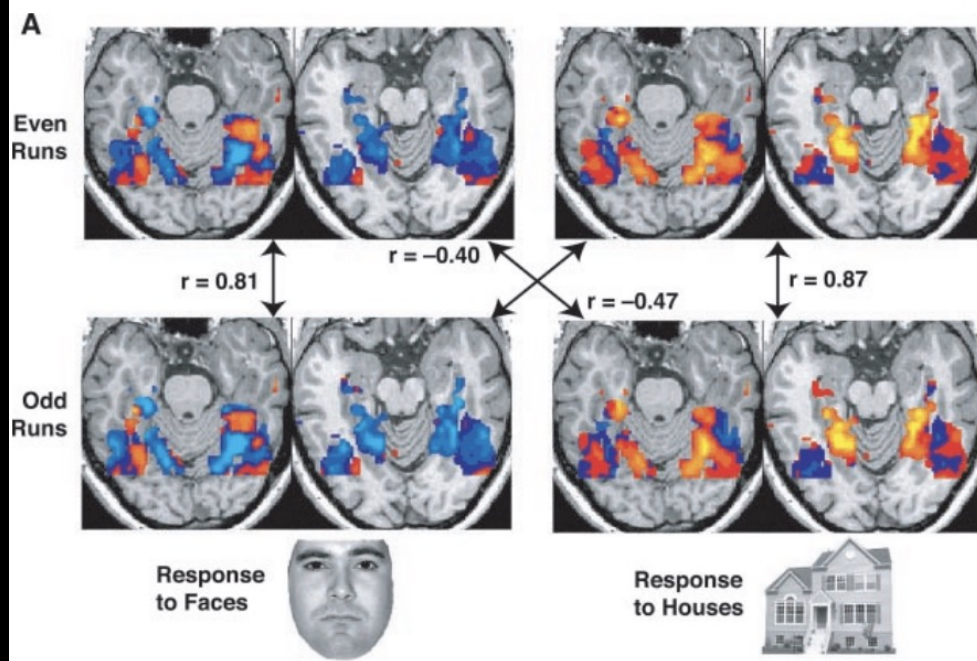
Someone is 5'7" with hair length of 8 inches

**Hits/#Observations = Accuracy**

# MVPA

Applied to fMRI Data

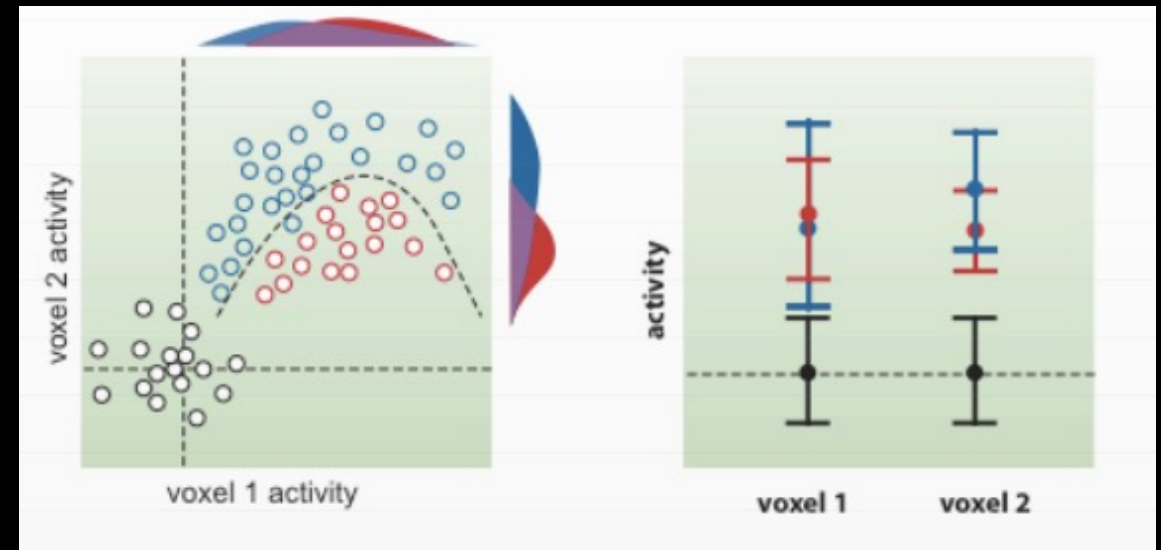
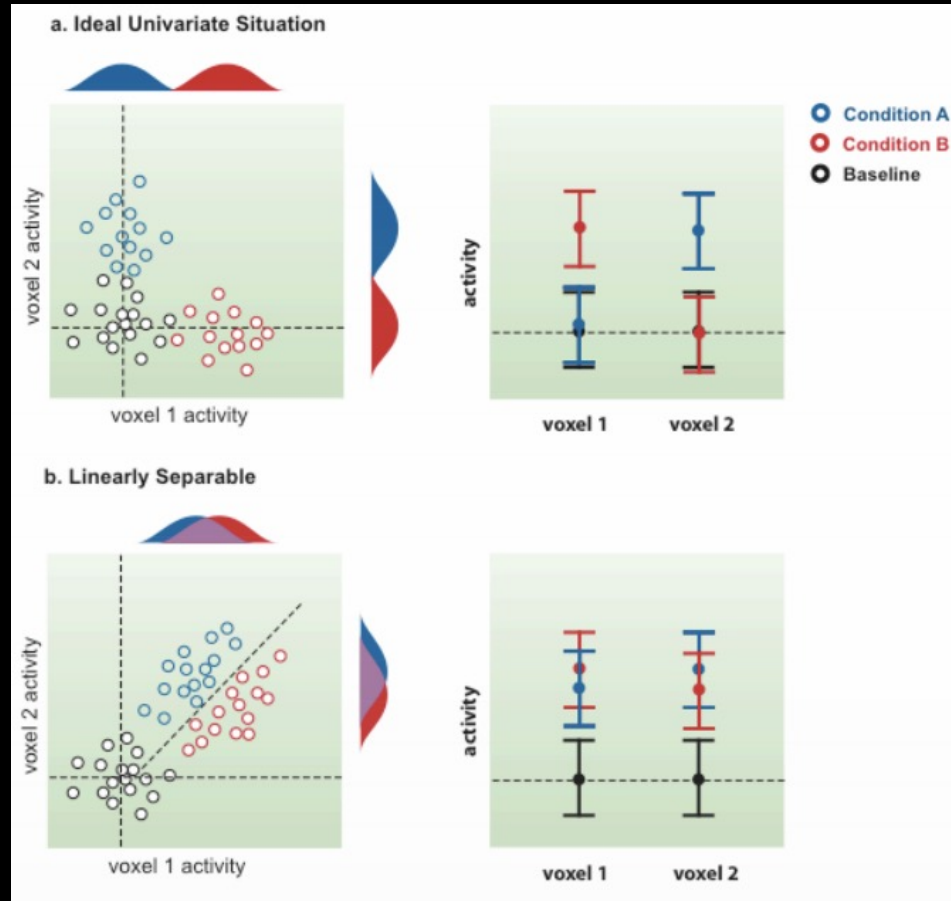






# MVPA

Use Support Vector Machines to classify beta maps



## Versions



580166c2cce88d000aa33631 2018-07-13

00001 2018-07-13

# Visual object recognition

uploaded by Chris Gorgolewski on 2016-10-14 - almost 4 years ago

last modified on 2018-07-14 - about 2 years ago

authored by Haxby, J.V., Gobbini, M.I., Furey, M.L., Ishai, A., Schouten, J.L., Pietrini, P.

📄 807 👁 15359

Download Analyze on [brainlife.io](https://brainlife.io)**OpenNeuro Accession Number:** ds000105**Files:** 1095, **Size:** 1.75GB, **Subjects:** 6, **Session:** 1**Available Tasks:** object viewing**Available Modalities:** T1w, bold

## README

This dataset was obtained from the OpenfMRI project (<http://www.openfmri.org>).

Accession #: ds105

Description: Visual object recognition

Please cite the following references if you use these data:

Haxby, J.V., Gobbini, M.I., Furey, M.L., Ishai, A., Schouten, J.L., Pietrini, P. (2001). Distributed and overlapping representations of faces and objects in ventral temporal cortex. *Science*, 293(5539):2425-30

Hanson, S.J., Matsuka, T., Haxby, J.V. (2004). Combinatorial codes in ventral temporal lobe for object recognition: Haxby (2001) revisited: is there a "face" area? *Neuroimage*. 23(1):156-66

O'Toole, A.J., Jiang, F., Abdi, H., Haxby, J.V. (2005). Partially distributed representations of objects and faces in ventral temporal cortex. *J Cogn Neurosci*, 17(4):580-90

Release history:

10/12/2011: initial release

## BIDS Validation

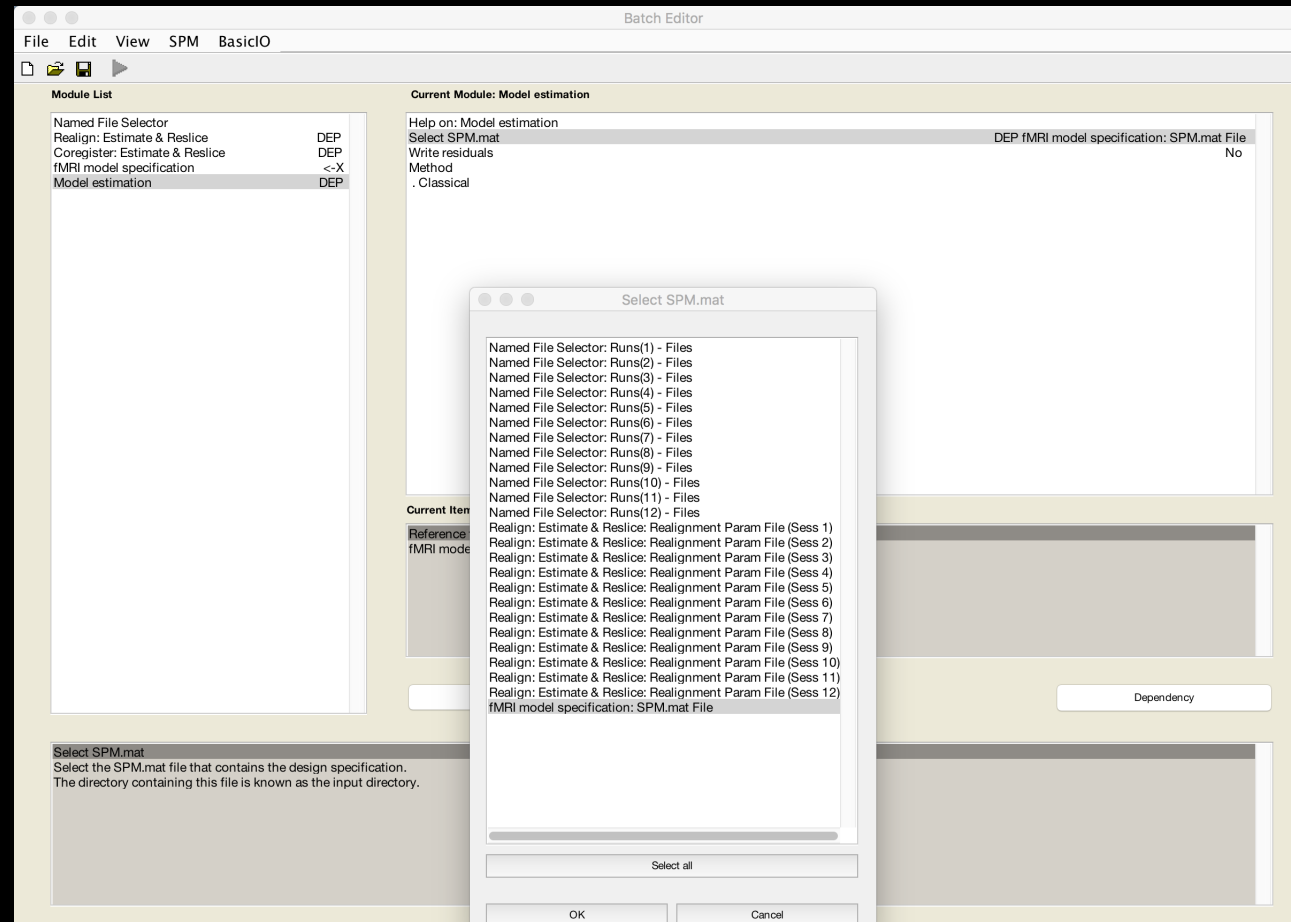
 Invalid

## Dataset File Tree

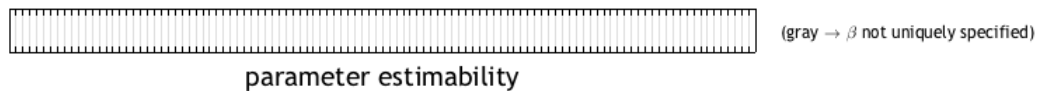
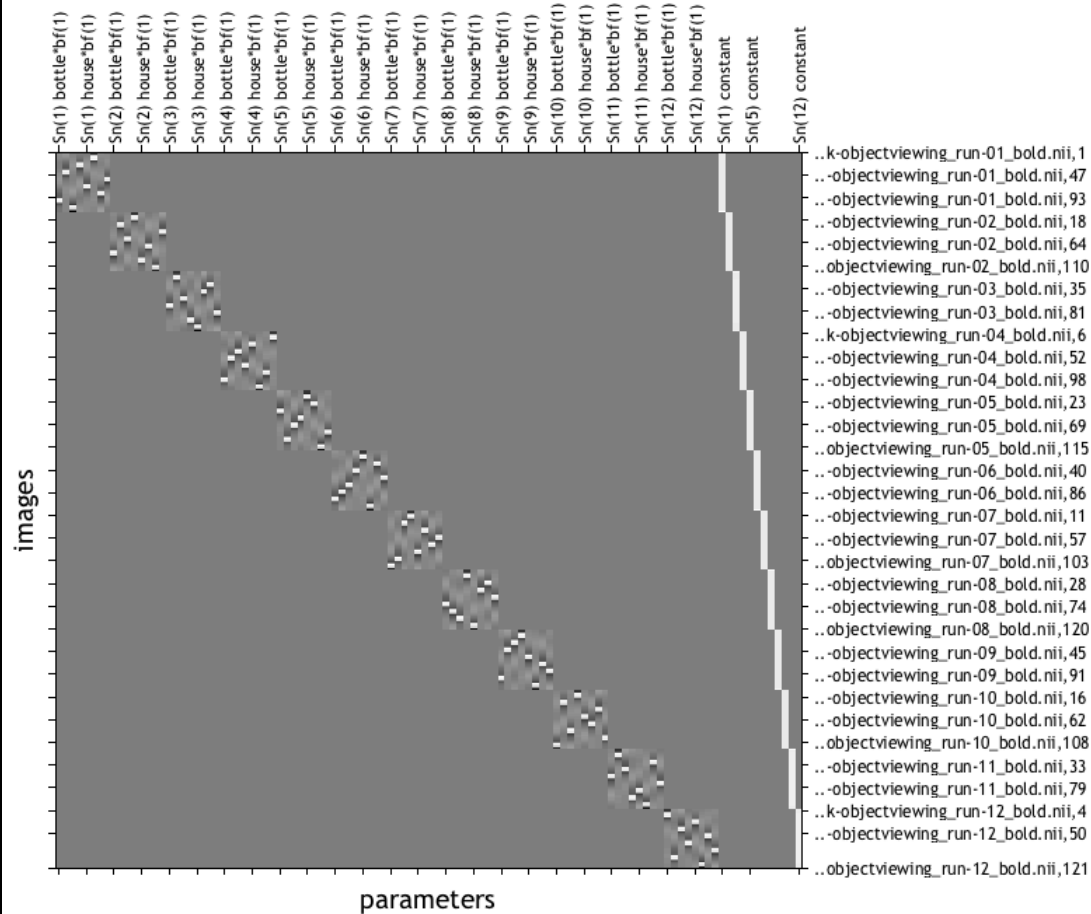
- Visual object recognition
  - CHANGES
    - DOWNLOAD
    - VIEW
  - dataset\_description.json
    - DOWNLOAD
    - VIEW
  - README
    - DOWNLOAD
    - VIEW
  - task-objectviewing\_bold.json
    - DOWNLOAD
    - VIEW
  - derivatives
    - sub-1
    - sub-2
    - sub-3
    - sub-4
    - sub-5
    - sub-6



# Preprocessing an MVPA experiment is similar to fMRI, with the exception of smoothing



# Statistical analysis: Design



## Design description...

Basis functions : hrf  
 Number of sessions : 12  
 Trials per session : 8 8 8 8 8 8 8 8 8 8 8 8  
 Interscan interval : 2.50 {s}  
 High pass Filter : [min] Cutoff: 128 {s}  
 Global calculation : mean voxel value  
 Grand mean scaling : session specific  
 Global normalisation : None

```
labelname1 = 'bottle';
labelname2 = 'cat';
labelname3 = 'chair';
labelname4 = 'face';
labelname5 = 'house';
labelname6 = 'scissors';
labelname7 = 'scrambledpix';
labelname8 = 'shoe';
```

```
8 % Make sure the decoding toolbox and your favorite software (SPM or AFNI)
9 % are on the Matlab path (e.g. addpath('/home/decoding_toolbox') )
10 % addpath('$ADD FULL PATH TO TOOLBOX AS STRING OR MAKE THIS LINE A COMMENT IF IT IS ALREADY$')
11 % addpath('$ADD FULL PATH TO TOOLBOX AS STRING OR MAKE THIS LINE A COMMENT IF IT IS ALREADY$')
12
13 % Set defaults
14 cfg = decoding_defaults;
15 cfg.results.overwrite = 1;
16
17 % Set the analysis that should be performed (default is 'searchlight')
18 cfg.analysis = 'ROI';
19 cfg.searchlight.radius = 3; % use searchlight of radius 3 (by default in voxels), see more details below
20
21 % Set the output directory where data will be saved, e.g. 'c:\exp\results\buttonpress'
22 cfg.results.dir = [pwd '/SPM_Results_1'];
23
24 % Set the filepath where your SPM.mat and all related betas are, e.g. 'c:\exp\glm\model_button'
25 beta_loc = [pwd '/SPM_Results_1'];
26
27 % Set the filename of your brain mask (or your ROI masks as cell matrix)
28 % for searchlight or wholebrain e.g. 'c:\exp\glm\model_button\mask.img' OR
29 % for ROI e.g. {'c:\exp\roi\roimaskleft.img', 'c:\exp\roi\roimaskright.img'}
30 % You can also use a mask file with multiple masks inside that are
31 % separated by different integer values (a "multi-mask")
32 cfg.files.mask = [pwd '/Haxby_Masks/sub-1_mask4_vt.nii'];
33
34 % Set the label names to the regressor names which you want to use for
35 % decoding, e.g. 'button left' and 'button right'
36 % don't remember the names? -> run display_regressor_names(beta_loc)
37 labelname1 = 'bottle';
38 labelname2 = 'cat';
39 labelname3 = 'chair';
40 labelname4 = 'face';
41 labelname5 = 'house';
42 labelname6 = 'scissors';
43 labelname7 = 'scrambledpix';
```

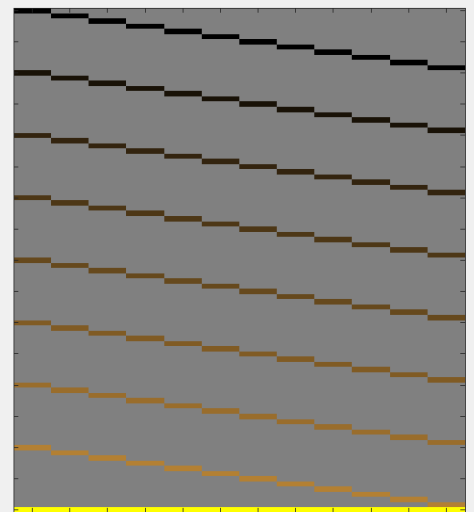
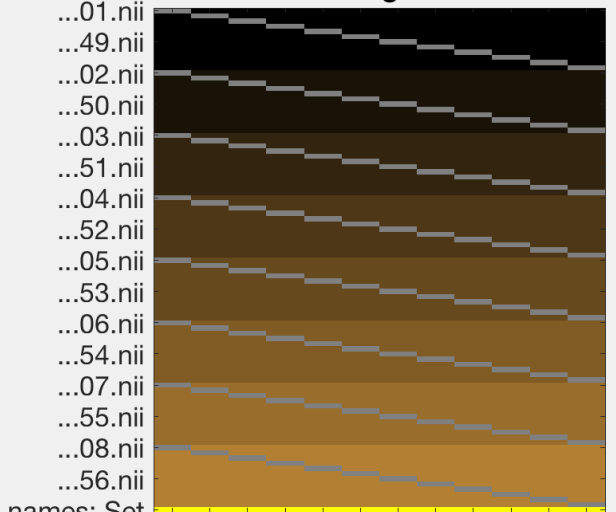
Figure 1: eoding Design



TDT - Decoding details  
 Filestart: /Users/ajahn/Desktop/Haxby\_Data/SPM\_Results\_1/beta\_00  
 Results: /Users/ajahn/Desktop/Haxby\_Data/SPM\_Results\_1  
 Start: 28-Sep-2020 15:36:29, End: 28-Sep-2020 15:36:32

### Training Data

### Test Data



1[1][1][1][1][1][1][1][1][1][1][1][1][1]  
 Training - Step [Set] nr

1[1][1][1][1][1][1][1][1][1][1][1][1][1]  
 Test - Step [Set] nr

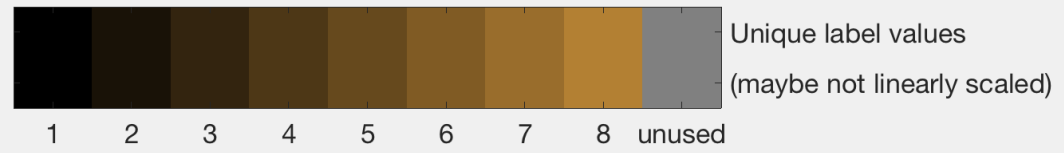
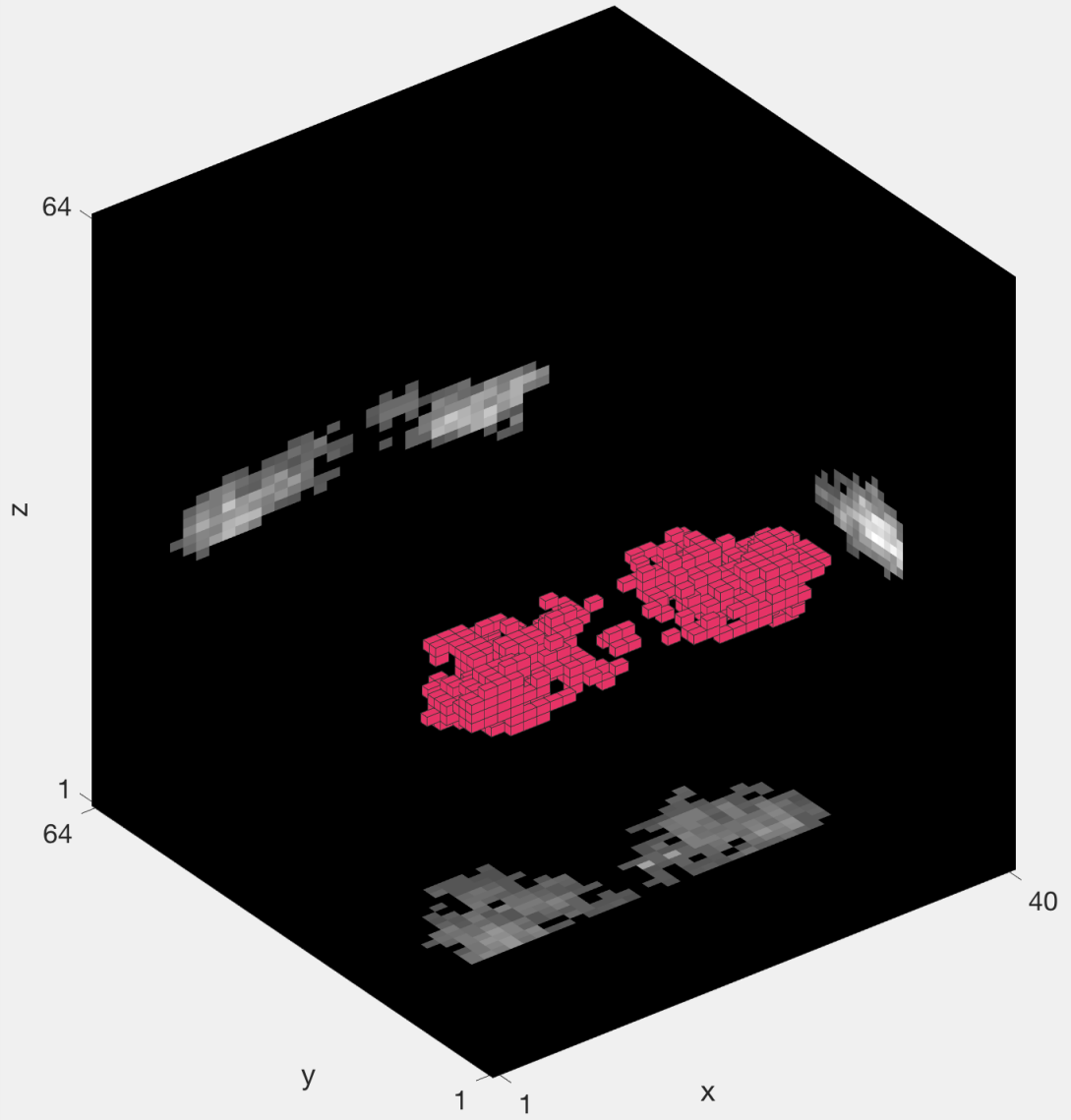
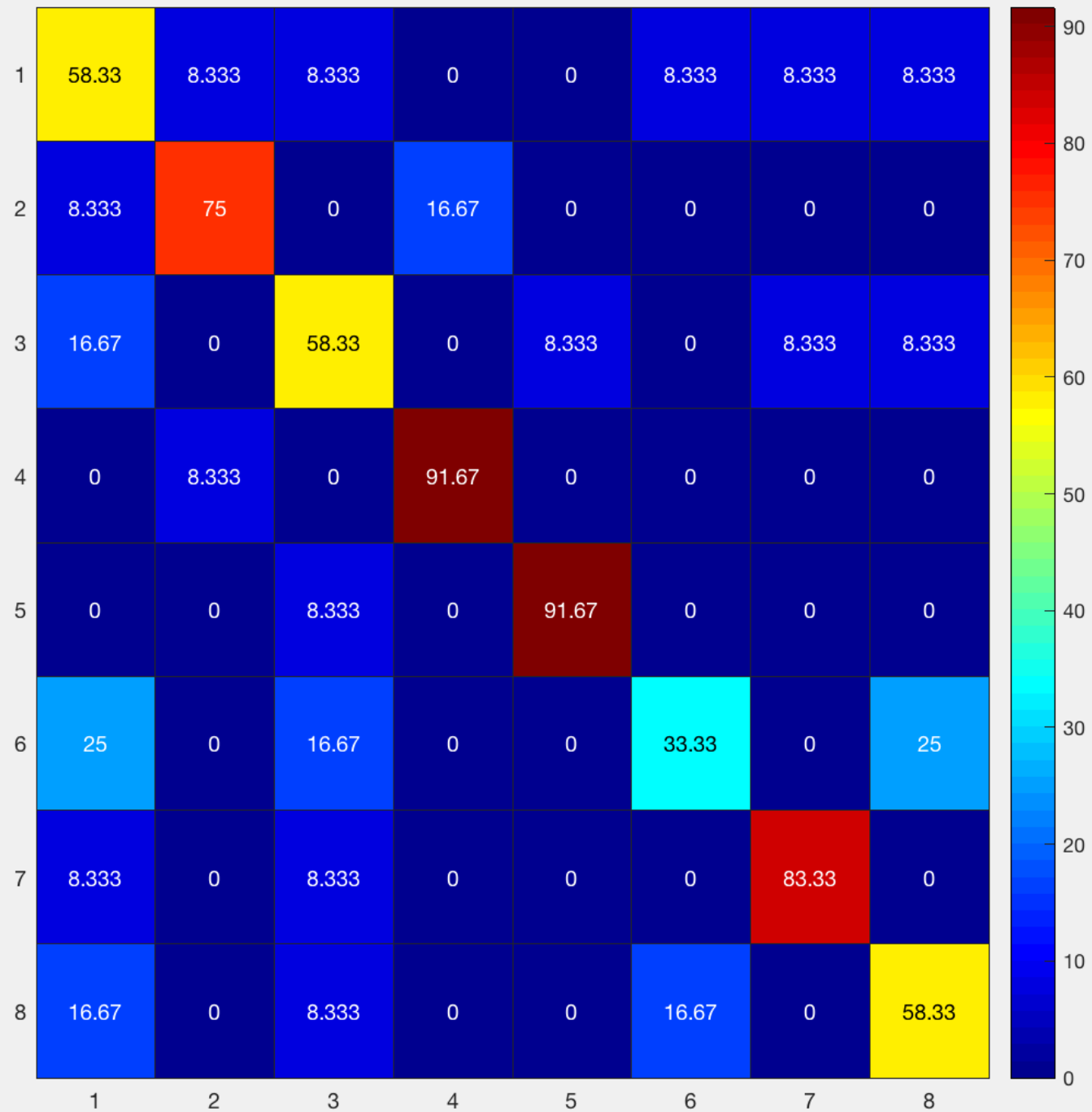
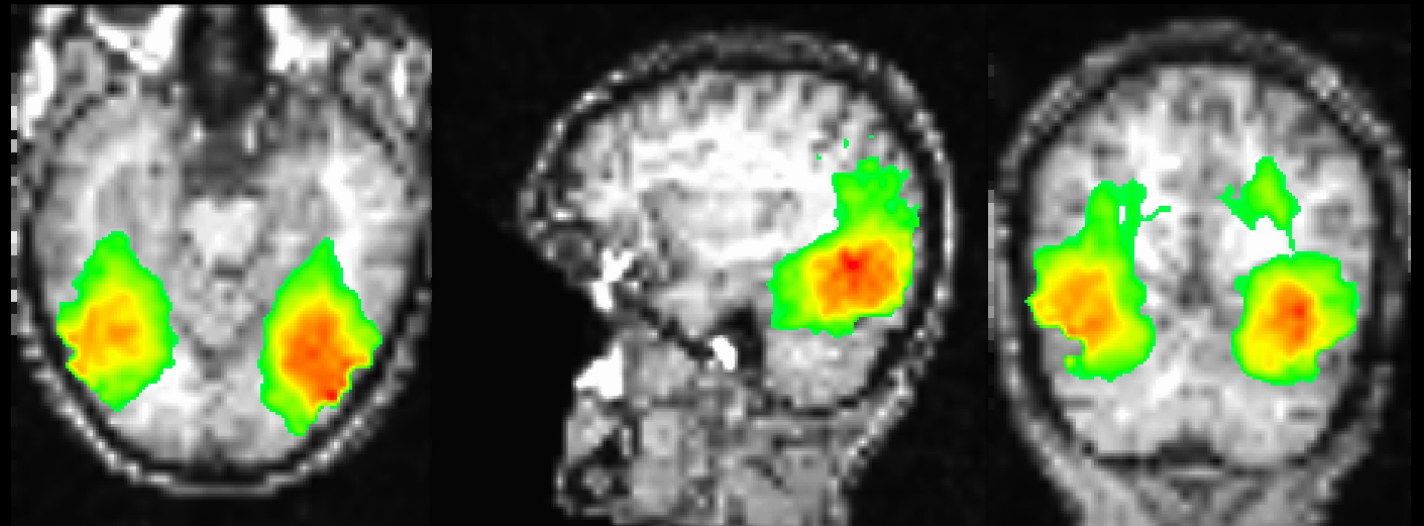
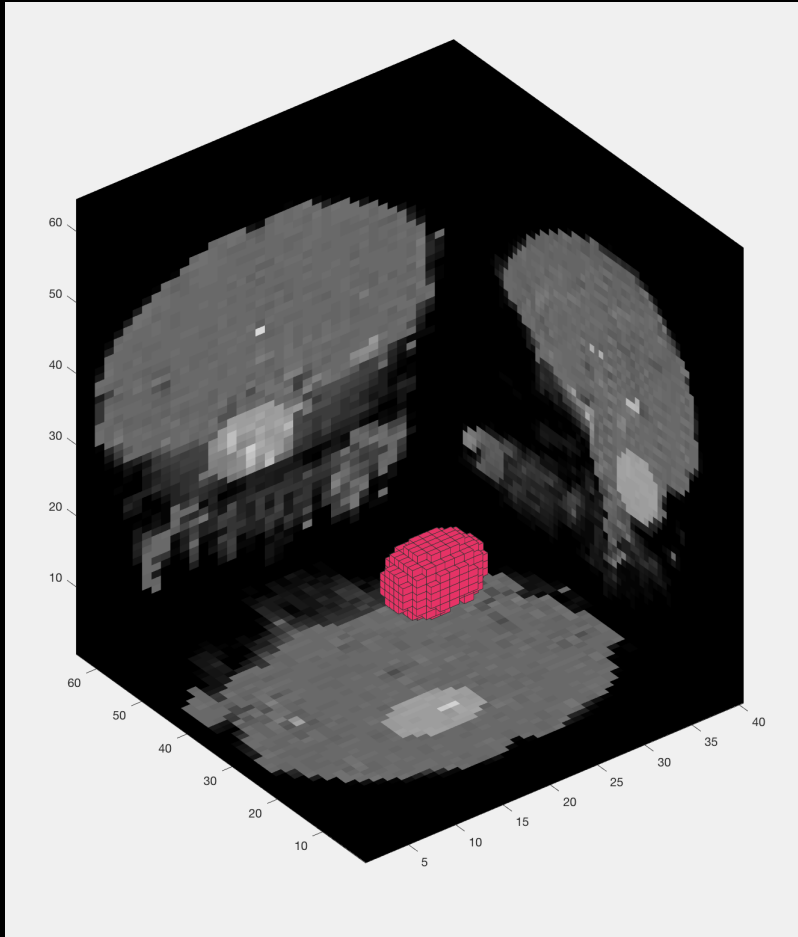


Figure 2: Online ROI, showing 1/500 steps (cfg.plot\_selected\_voxels=0 for more speed)





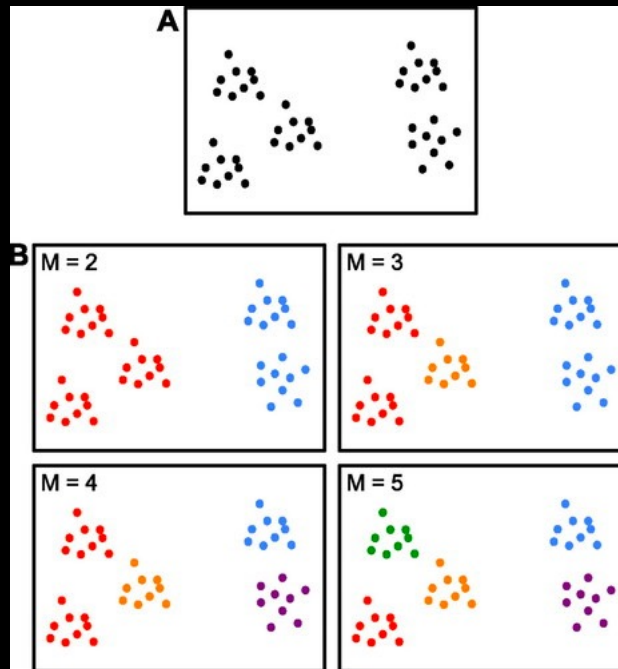
# Searchlight Analysis



# Data-driven

Example of Clustering: Yeo et al., 2011

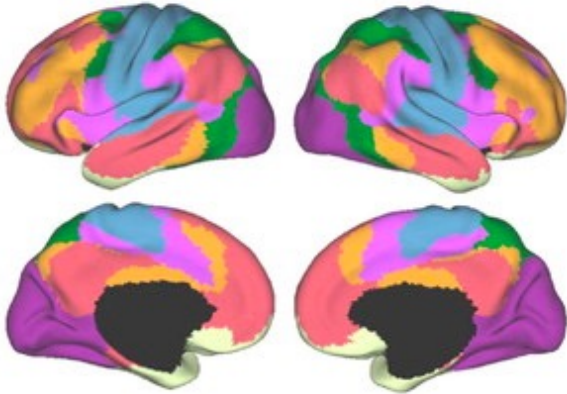
Used clustering to reveal intrinsic FC networks



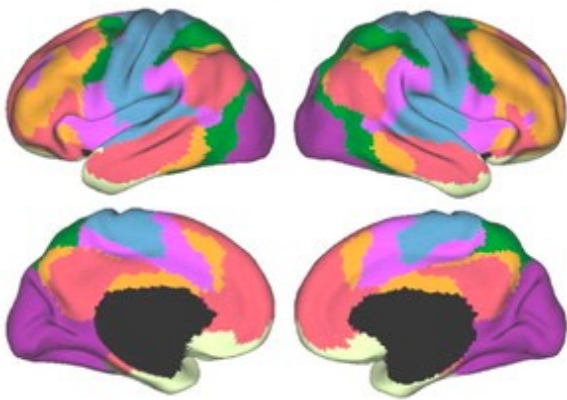


# Data-driven

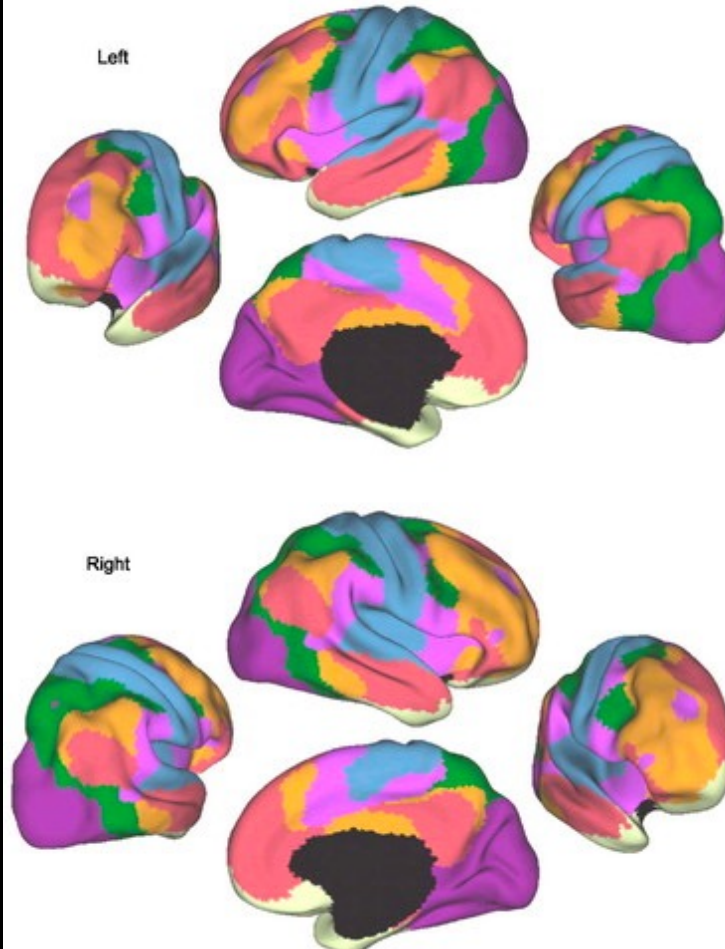
Discovery Sample (n = 500)



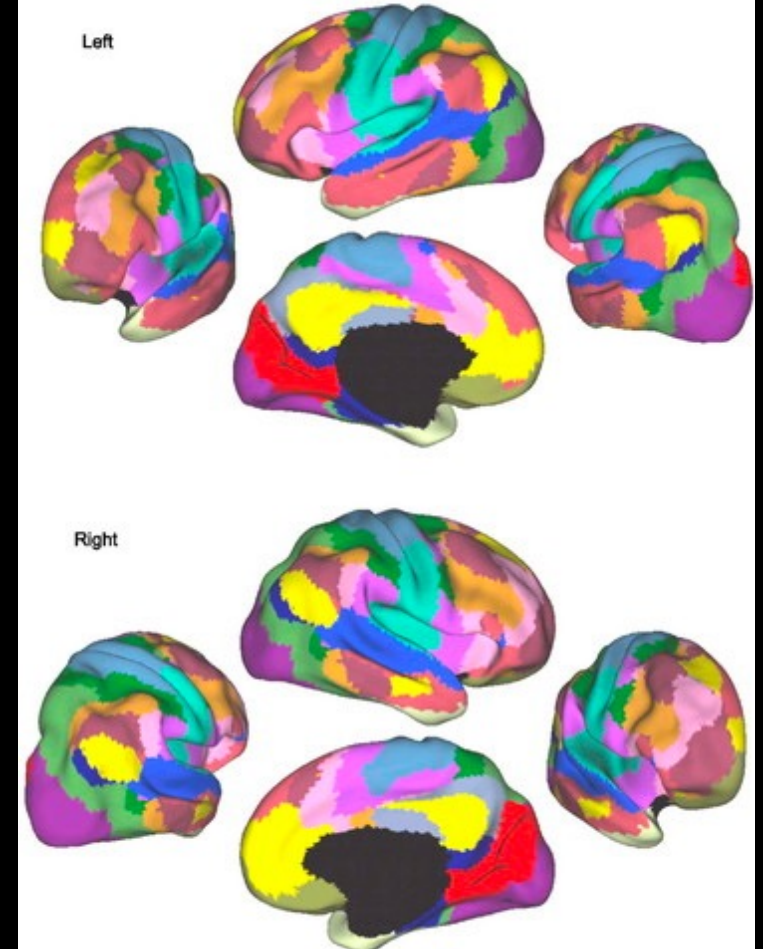
Replication Sample (n = 500)



7-Network Parcellation (N=1000)

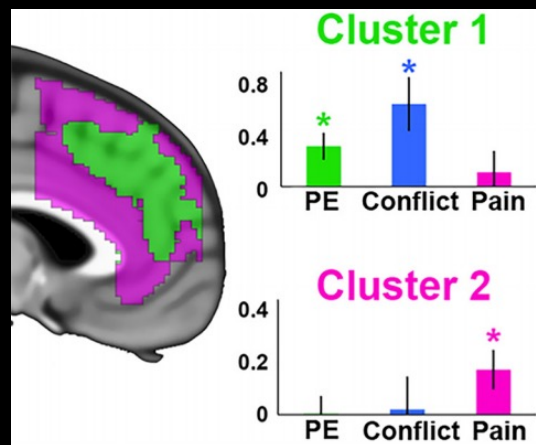
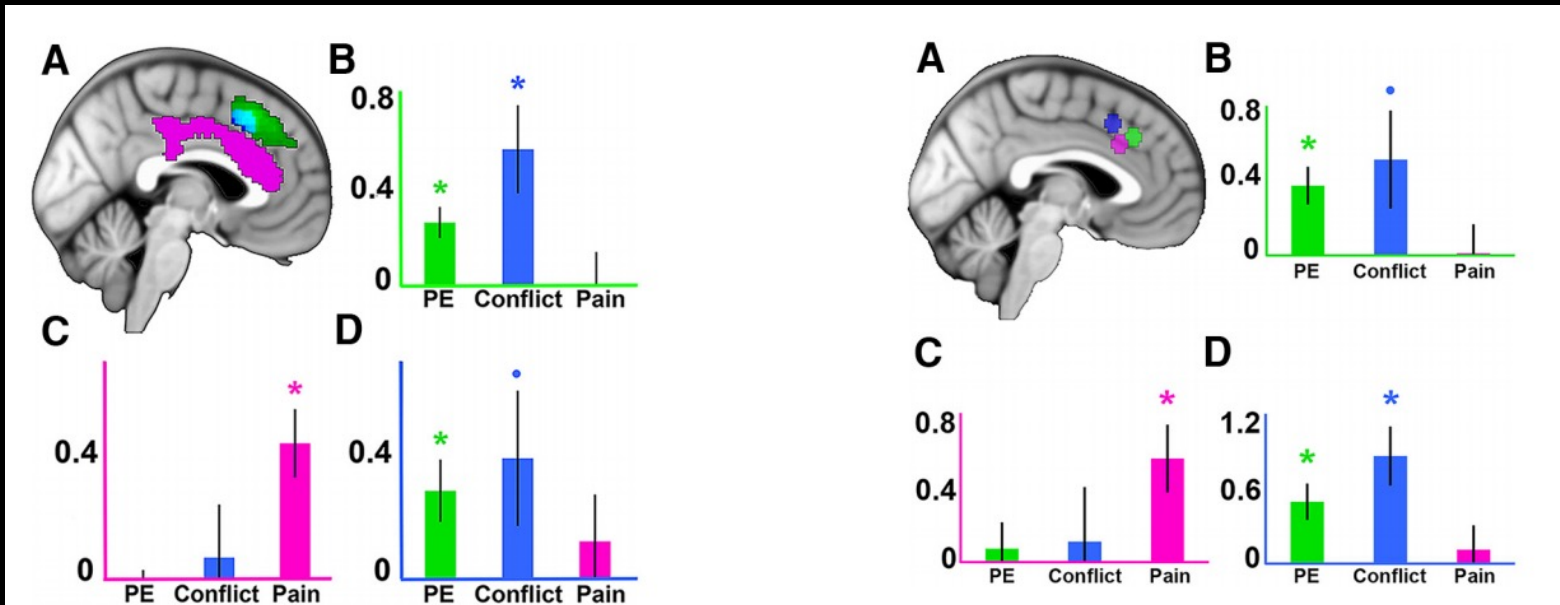


17-Network Parcellation (N=1000)





# Data-driven



## **Summary: Comparison of each Approach**

**Theory-driven: Builds upon previous research; logically coherent; consecutive results; can be done with relatively few subjects**

**Data-driven: Can leverage large open-access datasets to answer new questions; depending on number of subjects and trials, has huge power**


## Word of Caution

Does not protect you from statistical fallacies discussed earlier



Large datasets provide more power; also,  
more opportunities for fishing and p-hacking


# Tools for Reproducibility

## Open-access repositories



**OpenNEURO**  
A free and open platform for sharing MRI, MEG, EEG, iEEG, ECoG, ASL, and PET data

 Sign in with Google  Sign in with ORCID

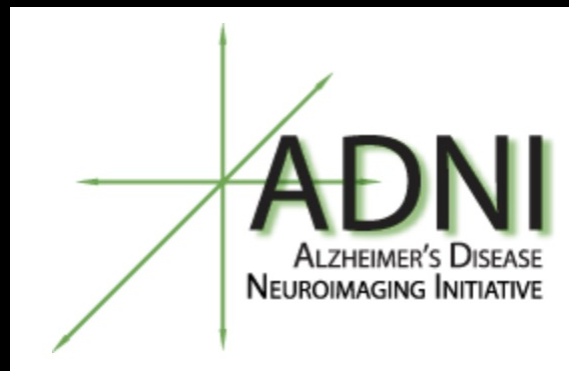
Search Datasets 

[Browse All Public Datasets](#)

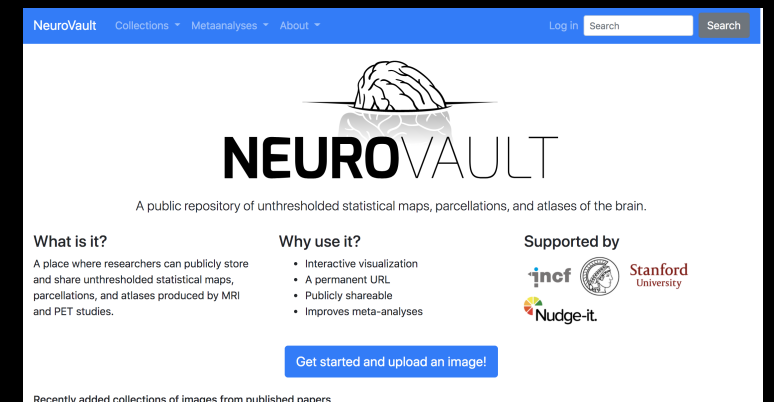


Human **Connectome** Project


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**ADNI**  
ALZHEIMER'S DISEASE  
NEUROIMAGING INITIATIVE



NeuroVault Collections Metaanalyses About Log In Search Search




  
**NEUROVAULT**  
A public repository of unthresholded statistical maps, parcellations, and atlases of the brain.

**What is it?**  
A place where researchers can publicly store and share unthresholded statistical maps, parcellations, and atlases produced by MRI and PET studies.

**Why use it?**

- Interactive visualization
- A permanent URL
- Publicly shareable
- Improves meta-analyses

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[Get started and upload an image!](#)

Recently added collections of images from published papers

# Overview of Openneuro

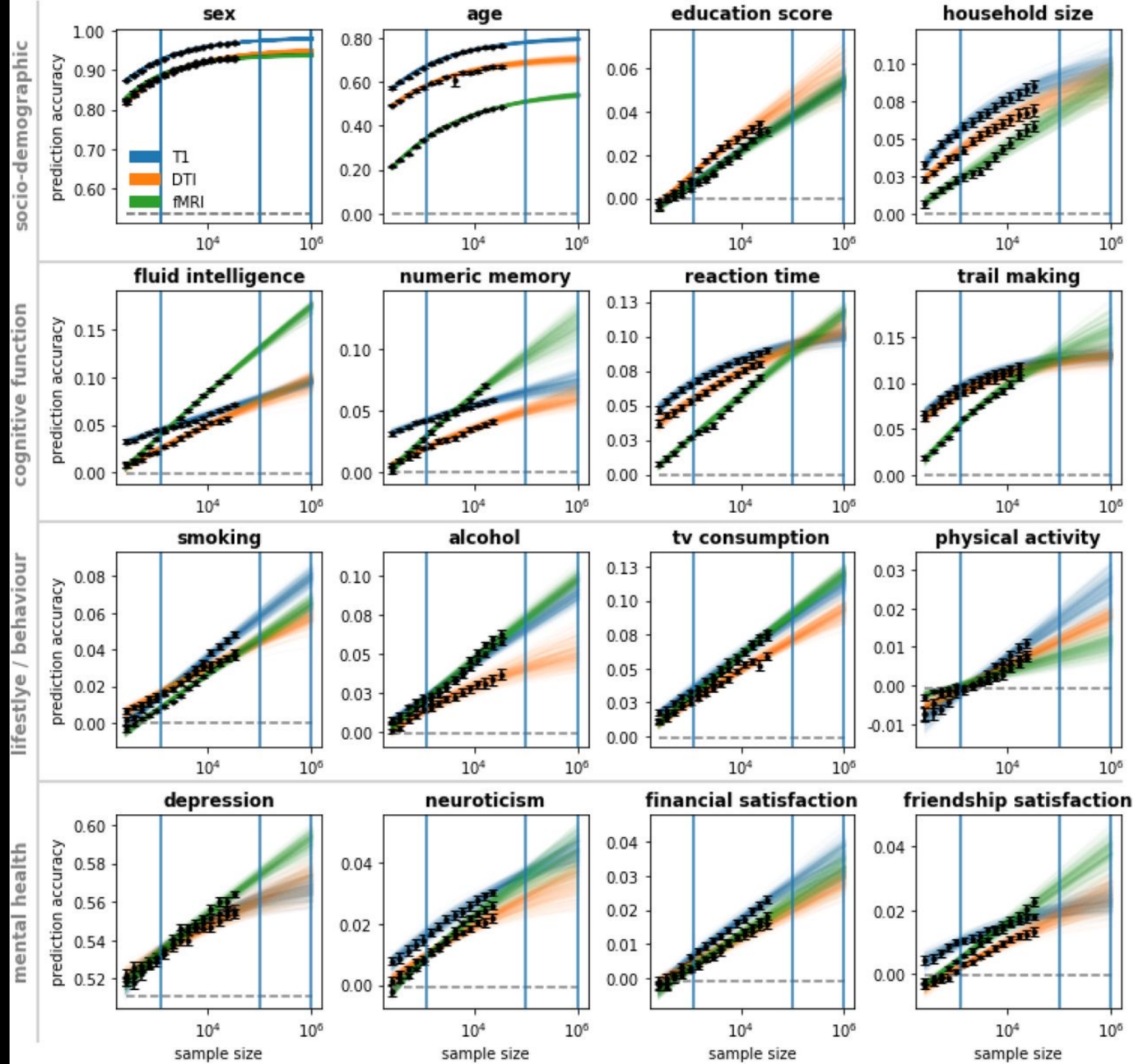
# Growing use of large databases

**ABCD (n=11,874)**

**Human Connectome Project (n=1,200)**

**UK Biobank (n=36,735)**

**Typical fMRI study n = ~25**



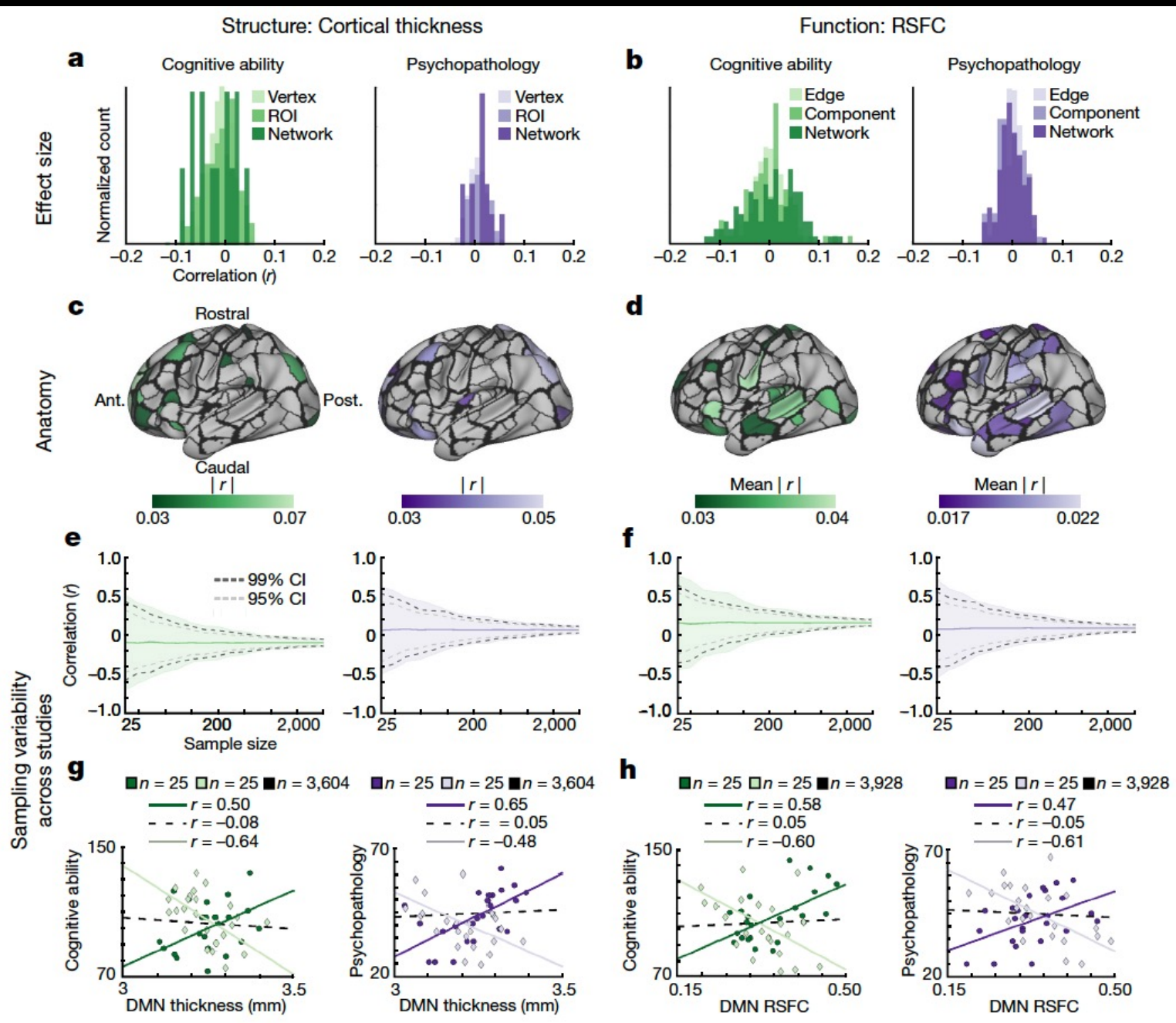
# Large database issues

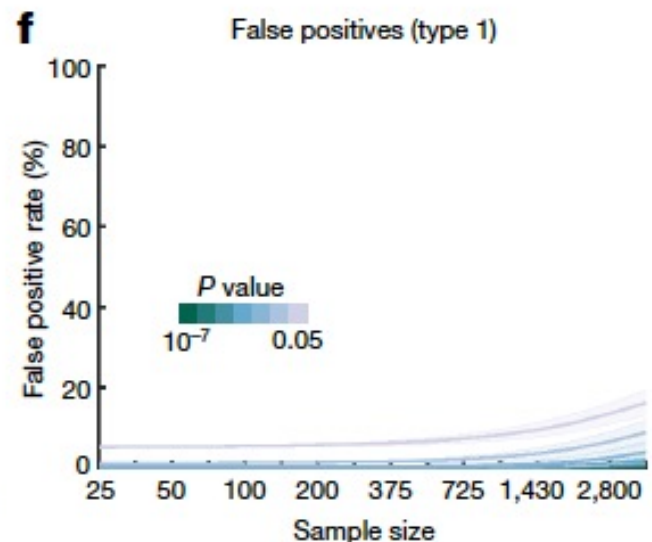
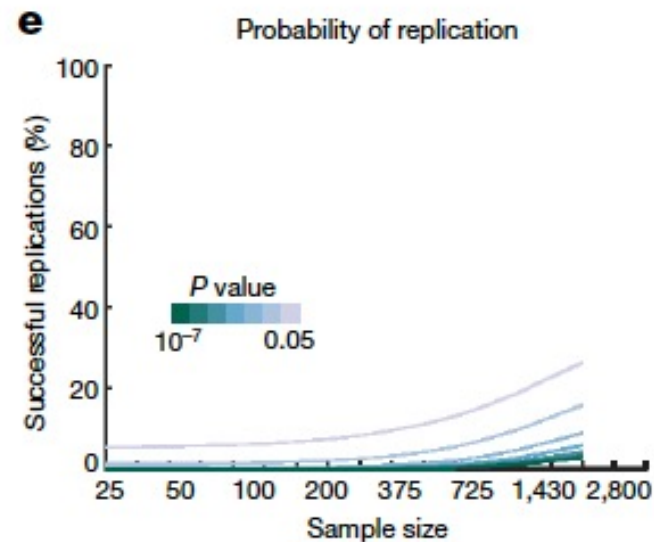
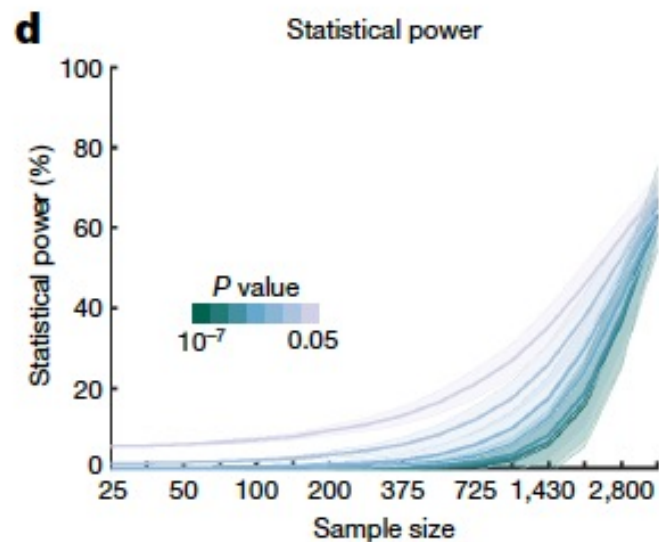
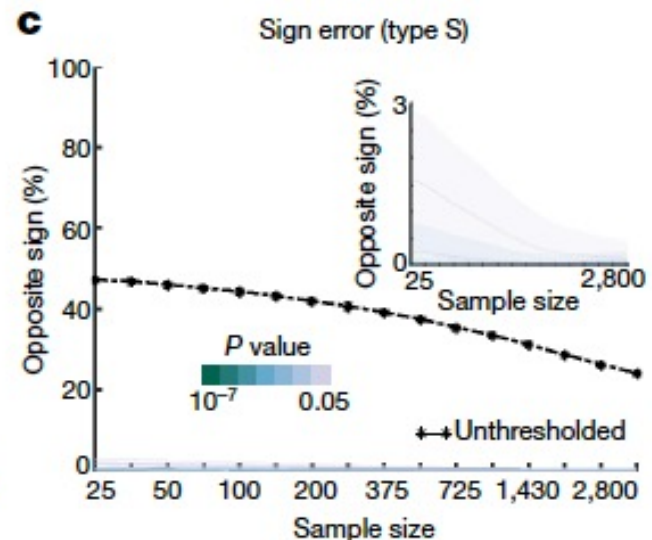
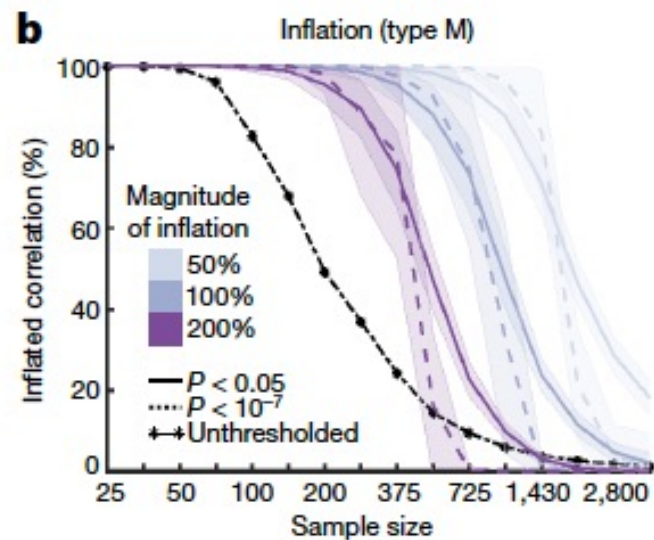
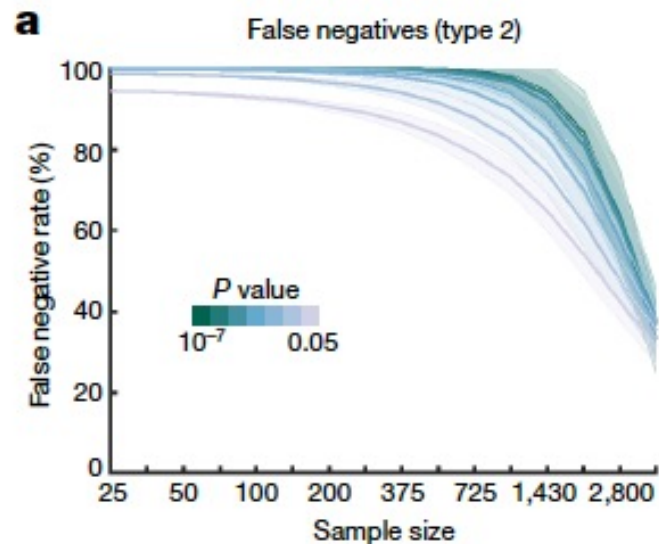
Can be collected from different sites

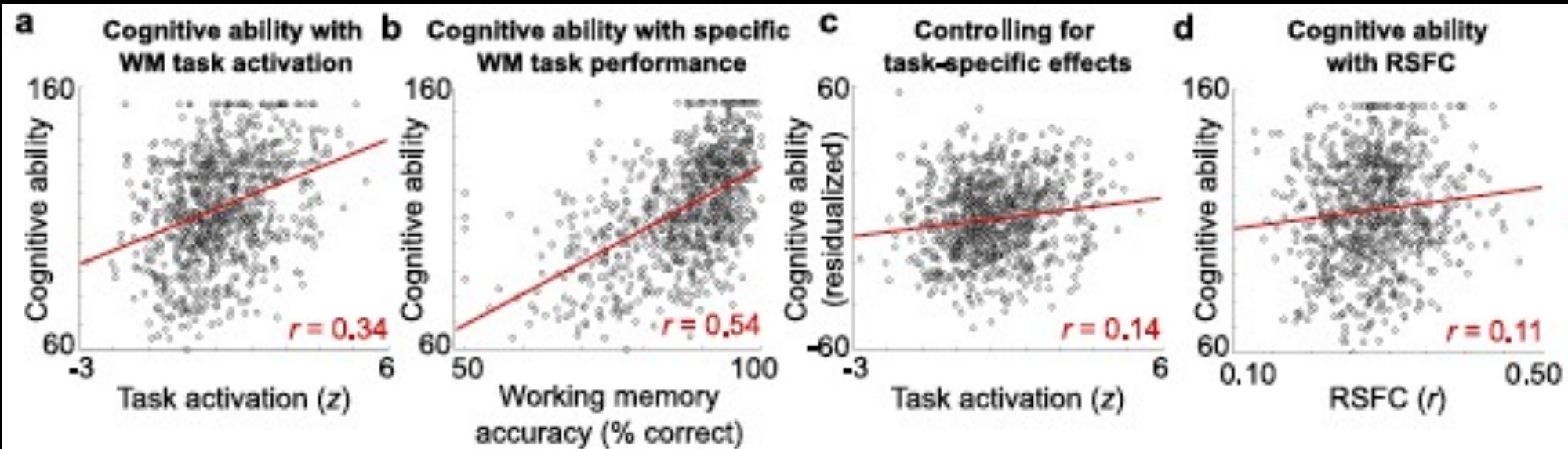
Changes in acquisition protocols over time  
(e.g., ADNI phases 1-3)

Current study: Look at ABCD, HCP, and UK Biobank









## Summary

**Although not all measures were studied, we can assume the effect sizes are similar (e.g., with EEG)**

**Compared to GWAS, BWAS requires fewer subjects**

**Ways to boost power: Within-study designs,  
Multivariate methods, interventions vs. observations**

## **Gratton's Response**

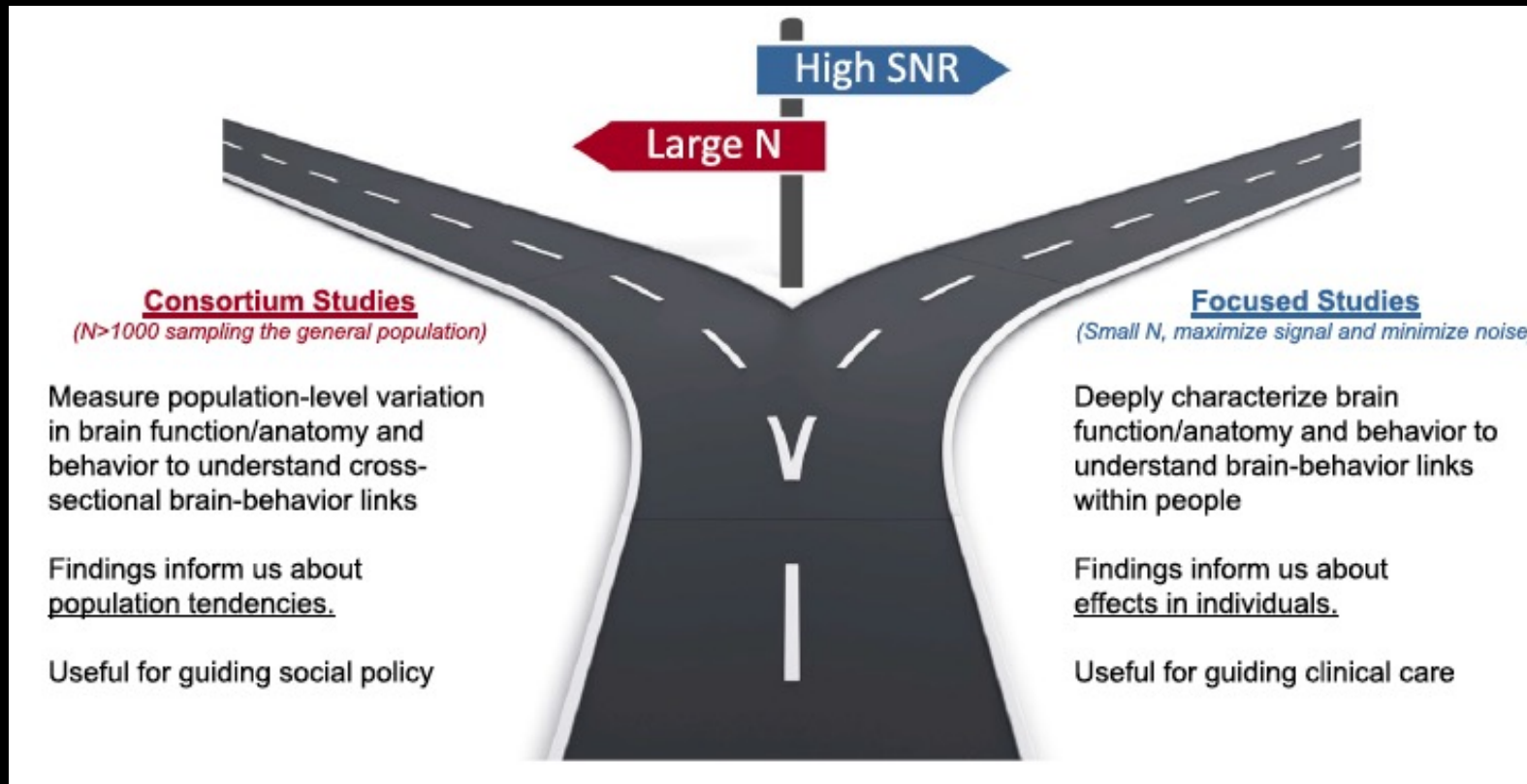
**Cross-sectional studies with small N are useless**

**Consortia studies may have small effect sizes, but they are comparable to others that are useful**

**Nevertheless, they usually avoid novel experimental questions and designs**



# Gratton's Response



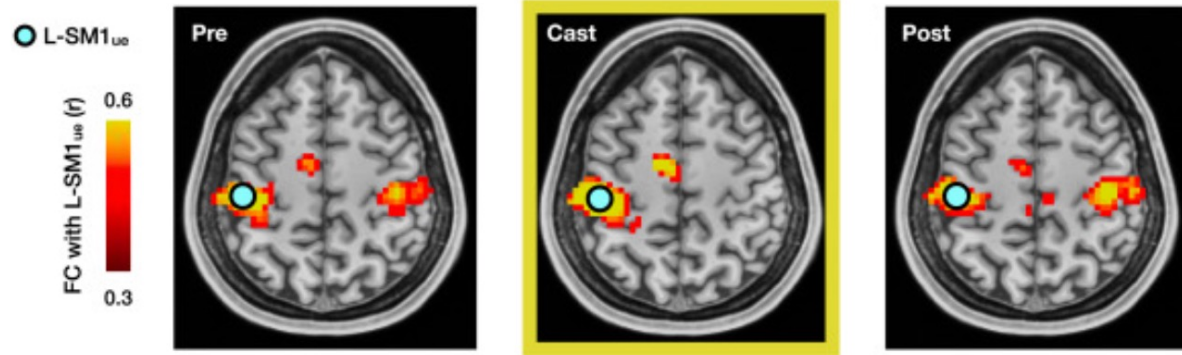
## **Other possibilities**

**Over-reliance on large-scale studies can limit funding opportunities for junior researchers**

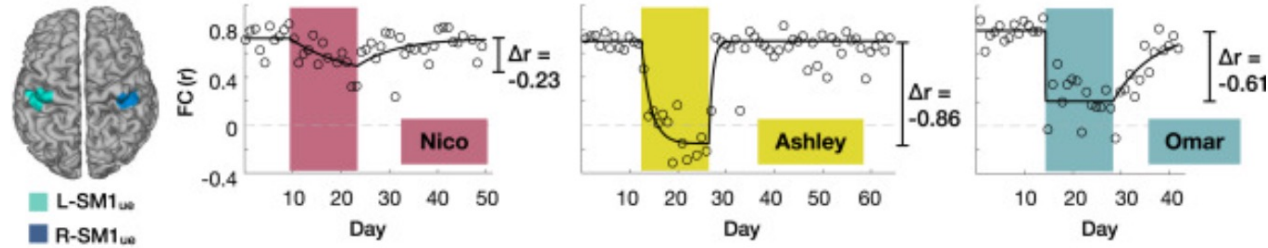
**Smaller studies can still yield useful results through higher signal and lower noise designs**

**e.g., within-subjects designs, using designs that induce large alterations in behavior**

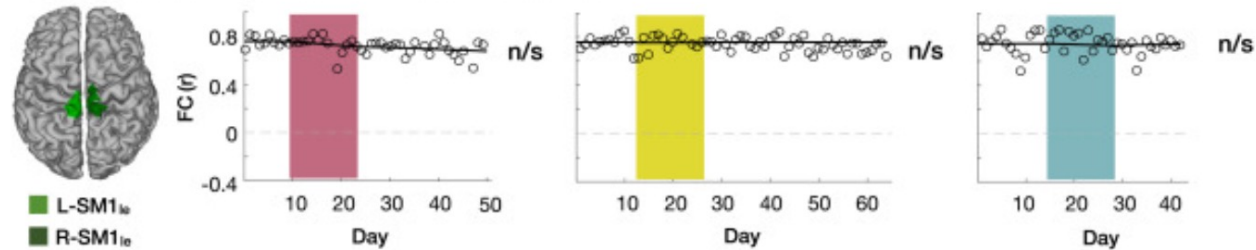
**A Functional connectivity (FC) seed maps**



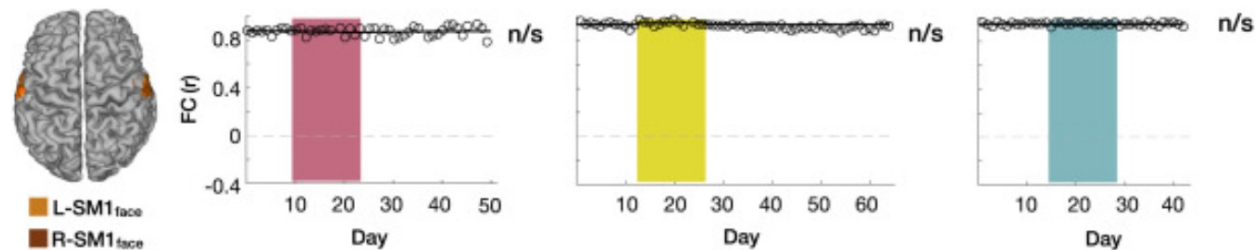
**B Daily time course of FC: upper extremity**



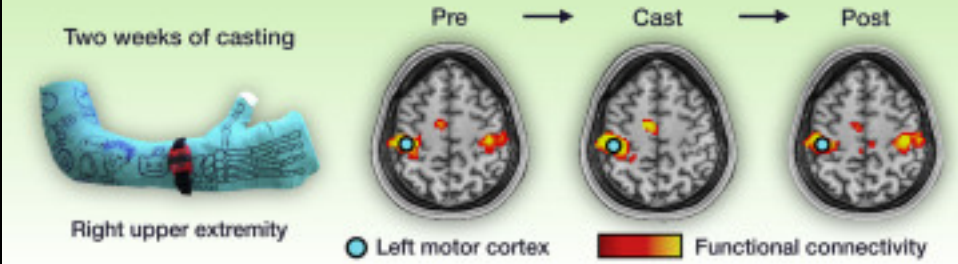
**C Daily time course of FC: lower extremity (negative control)**



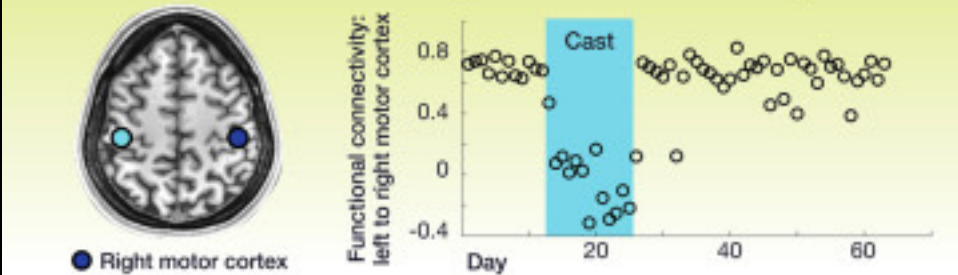
**D Daily time course of FC: face (negative control)**



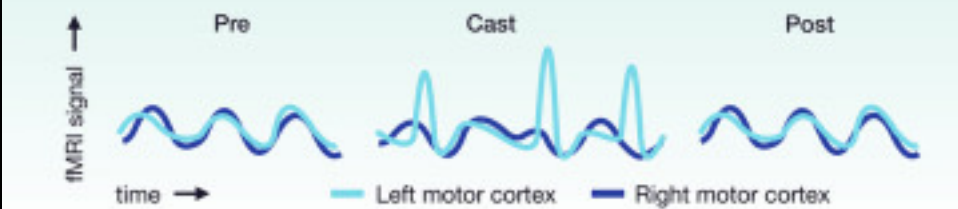
**Disuse of brain circuits causes functional disconnection**



**Functional disconnection begins within hours to days**



**Spontaneous activity pulses propagate through disused circuits**





# **Background to the IronTract Challenge**

**Historically, several issues with reconstructing pathways**

**Demands for higher spatial and angular resolution**

**Advanced acquisition parameters were developed  
by the Human Connectome Project (HCP)**

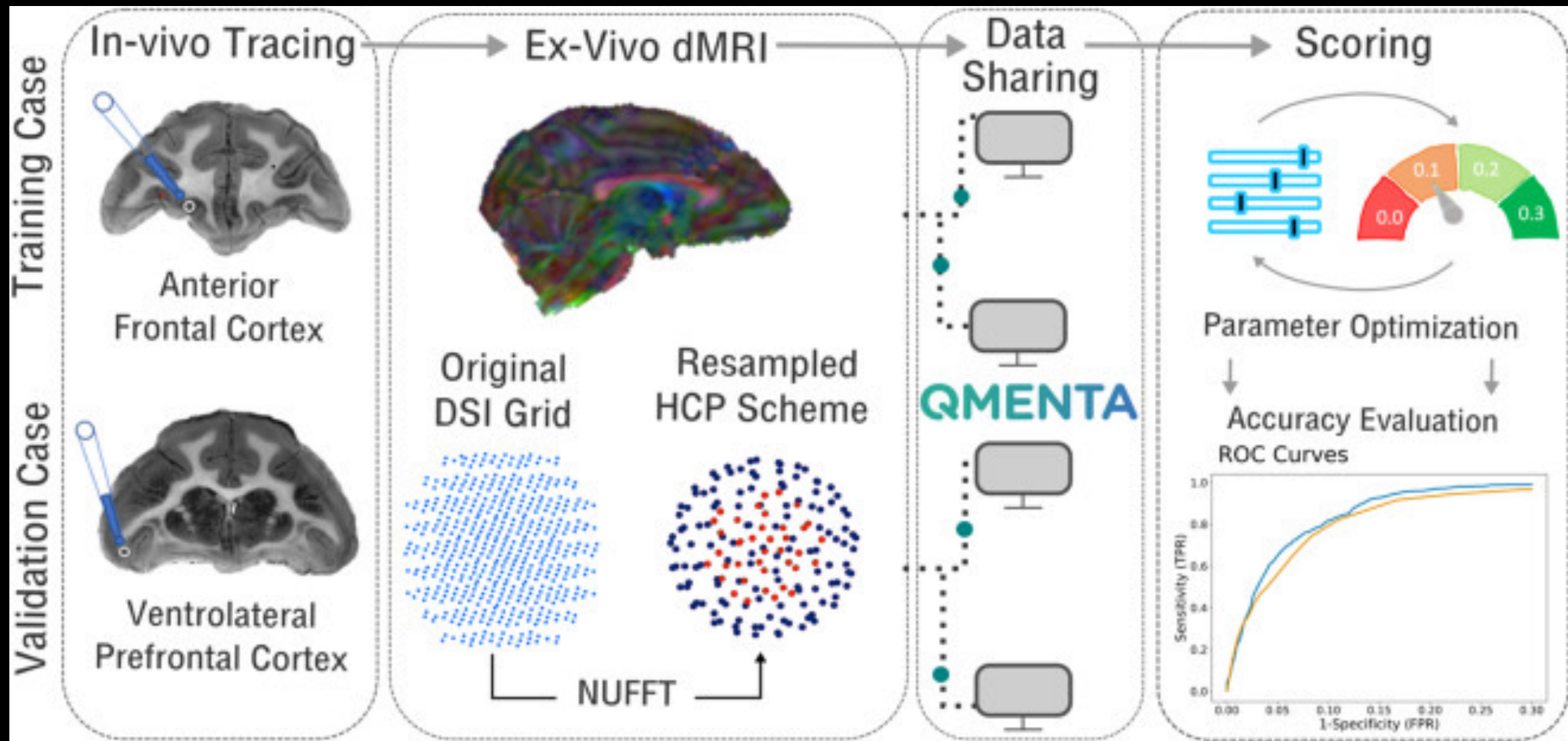
**Need for comparing different methods**

# Background to the IronTract Challenge

Based on data taken from *ex vivo* primate brains

Anatomic tracer injections show ground truth of  
the trajectory of brain tracts

This is compared to estimates by diffusion software



# Round 1

**Allowed to use analysis methods of choice**

**Both probabilistic and deterministic tractography were used**

**Training case: Could repeat analysis any number of times**

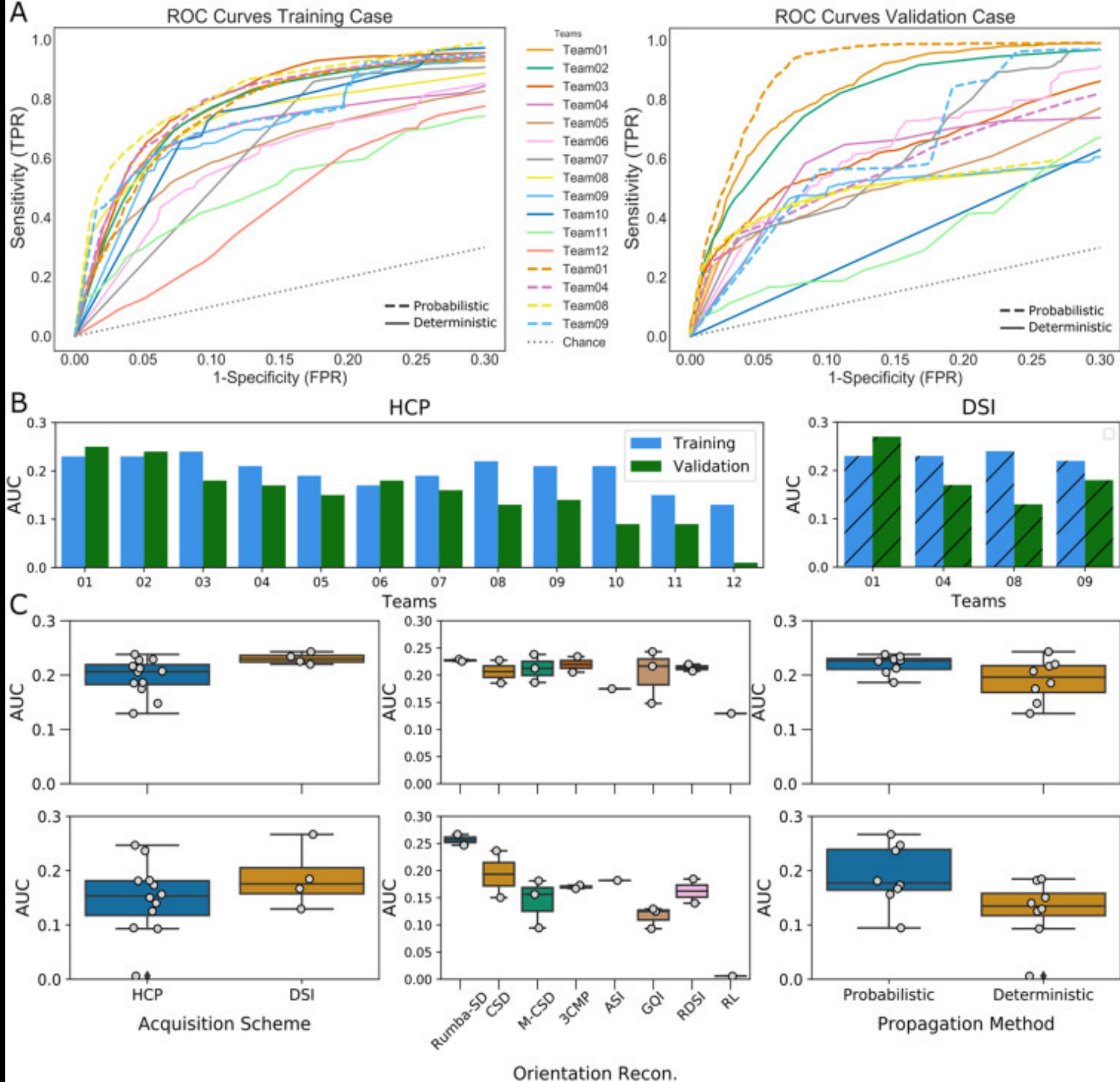
## Round 2

**Pre- and post-processing was standardized**

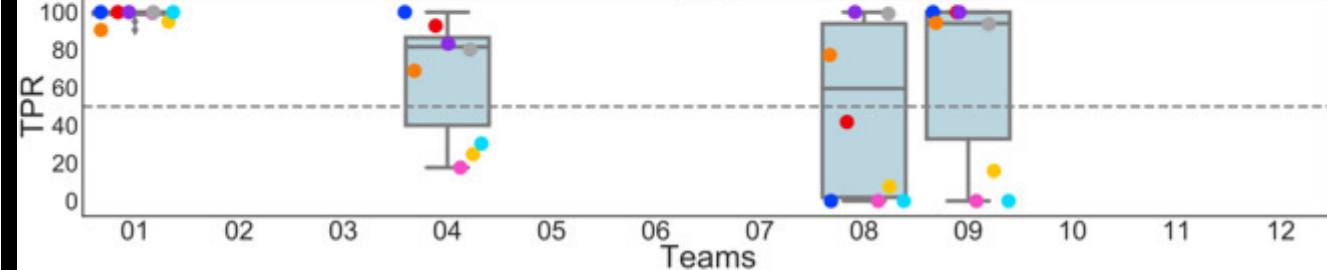
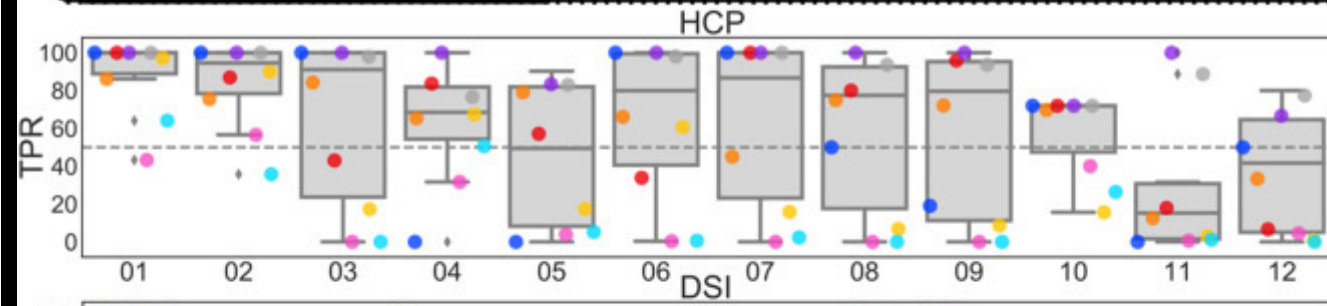
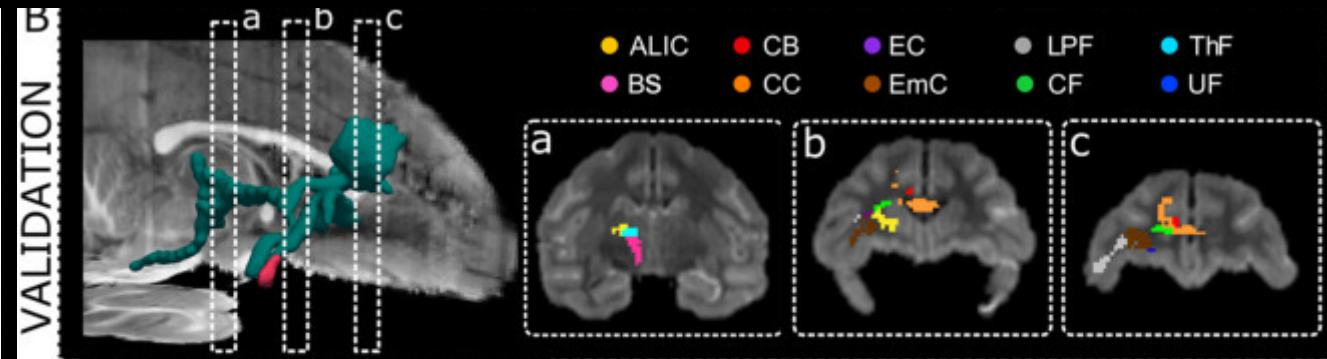
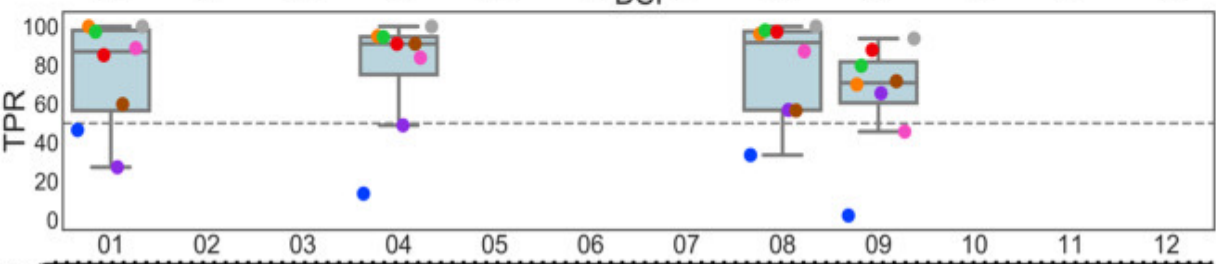
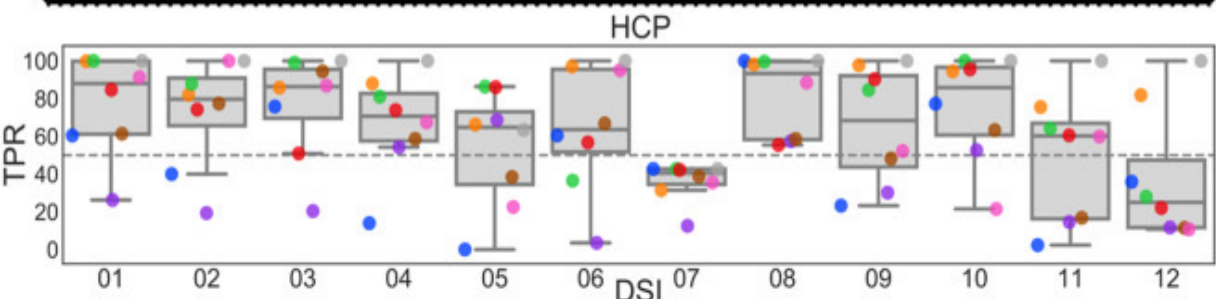
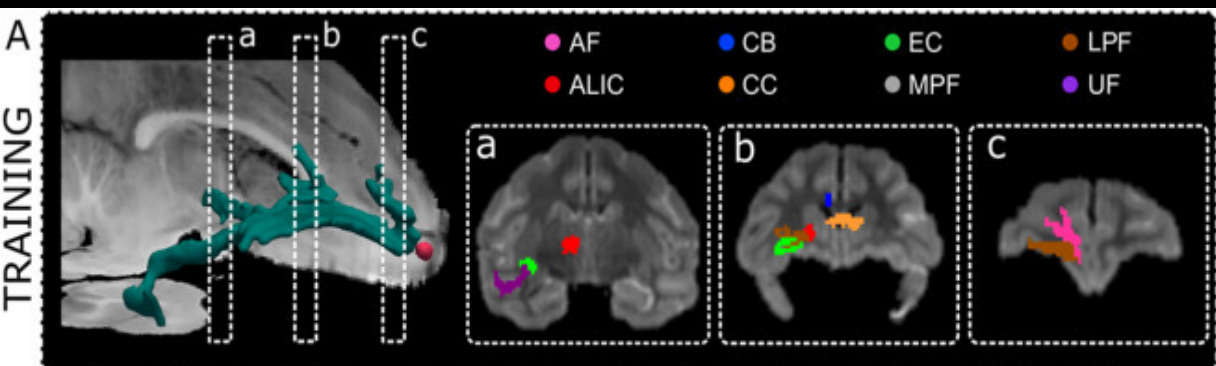
**Choice of orientation reconstruction and tractography**

**ROIs analyzed: Cingulum, CC genu, external capsule,  
internal capsule, and uncinate fasciculus**

# Round 1 Results







**Questions?**



# Pre-registration

**Posit hypotheses before collecting data**

**Specify parameters such as sample size, analysis options, dependent variables, and exclusion criteria**

# Pre-registration

## Example: Open Science Framework




Improve your research with [preregistration](#). By writing out specific details such as data collection methods, analysis plans, and rules for data exclusion, you can make important decisions early on and have a clear record of these choices. This can help reduce biases that occur once the data are in front of you.

# Pre-registration

## Alternative: AsPredicted.org

### Creating New AsPredicted

I am just trying things out. (Check the box and the submission will self destruct within 24 hours) 

#### Participating Authors (Up to 5)

Order	First	Last	email	Affiliation
1	Andrew	Jahn	ajahn@umich.edu	University of Michigan
2				
3				
4				
5				

#### AsPredicted Questions (version 2.00)

This [blog post](#) on how to answer pre-registration questions may be a useful resource.

**1) Data collection. Have any data been collected for this study already?**

Yes, we already collected the data.  
 No, no data have been collected for this study yet.  
 It's complicated. We have already collected some data but explain in Question 8 why readers may consider this a valid pre-registration nevertheless.  
(Note: "Yes" is not an accepted answer.)

**2) Hypothesis. What's the main question being asked or hypothesis being tested in this study?**

# Other Tools

## Github



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# Where the world builds software

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# Github



**Andrew Jahn**  
andrewjahn

Follow

Neuroimaging consultant, working primarily with AFNI, FSL, SPM, FreeSurfer, and MRtrix.

👤 108 followers · 1 following · ☆ 0

🏢 University of Michigan

📍 Ann Arbor, MI

🔗 <https://andysbrainbook.readthedocs.io...>

## Achievements



📄 Overview   📁 Repositories 15   📁 Projects   📦 Packages

## Popular repositories

### AndysBrainBook

This repository contains the files that generate Andy's Brain Book on ReadTheDocs.

☆ 55   🍴 23

### OpenScience\_Scripts

Scripts to use with Open Science materials such as fMRIPrep

● Shell   ☆ 6   🍴 7

### AFNI\_Scripts

Scripts used for fMRI data analysis in AFNI

● Shell   ☆ 5   🍴 5

### FSL\_Scripts

Scripts for analyzing fMRI data using FSL

● Shell   ☆ 4   🍴 8

### MRtrix\_Analysis\_Scripts

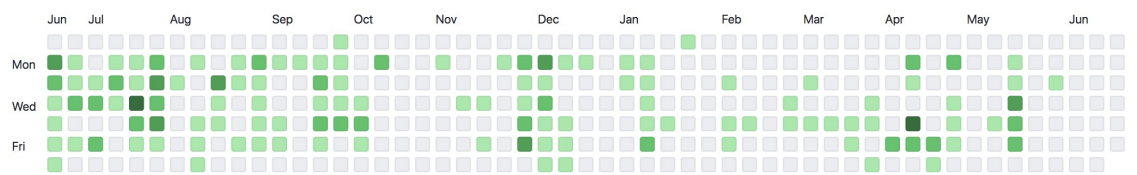
Scripts for analyzing diffusion data with MRtrix

● Shell   ☆ 3   🍴 3

### CONN\_Scripts

● MATLAB   ☆ 3   🍴 3

## 440 contributions in the last year



Learn how we count contributions

Less More

# Downloading the “git” command

**Installer for Macintosh:** <https://git-scm.com/download/mac>

**Installer for Windows:** <https://git-scm.com/download/win>

# Vocabulary

**Github has a technical (and sometimes confusing!) vocabulary**

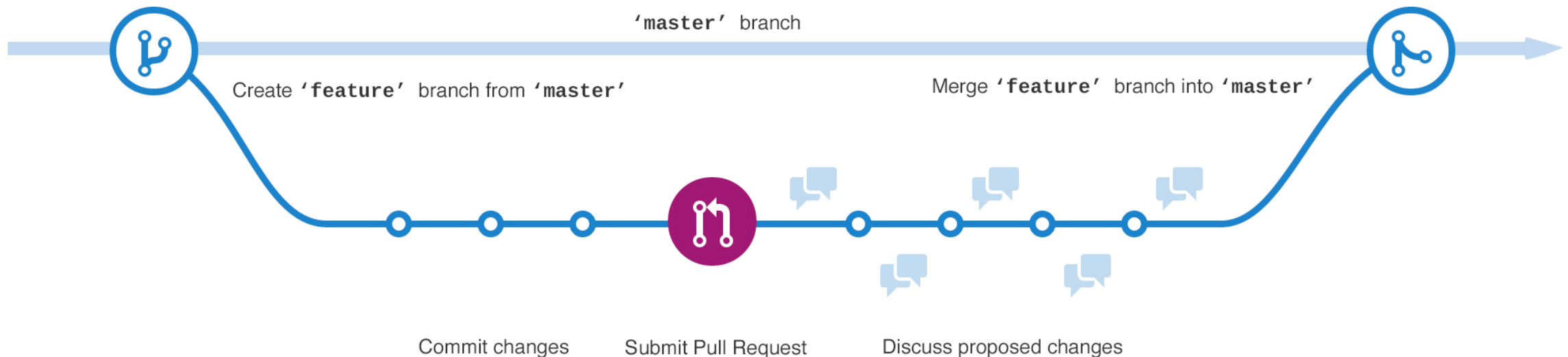
**Repository:**

**contains all of the project files (including documentation),  
and stores each file's revision history**

# Vocabulary

**Branch: Current copy of the finalized edits**

**Each repository by default has a “main” branch**





# Vocabulary

**Fork: Create a copy of a repository**

**Any edits made to this copy will not be seen by the public  
until the changes are merged**

# Vocabulary

**Commit: Snapshot of an edit that can be later merged into the main branch**

**Commits can be labeled with messages describing what the change was**

23 .. figure:: Github\_Repositories.png  
24  
25  
26 Example of repositories on a Github page.  
27  
28 \* Clone: Copying a repository to your local machine. For example, if I want to clone the repository ``SPM\_Scripts`` from Andy's Github page, I would need to know the link to the page (i.e., [https://github.com/andrewjahn/SPM\\_Scripts](https://github.com/andrewjahn/SPM_Scripts)), and then use it with the ``git`` command:  
29  
30 ..  
31  
32 `git clone https://github.com/andrewjahn/SPM_Scripts`  
33  
34 This will clone the SPM\_Scripts repository to my local machine, from where I ran the ``git`` command.  
35  
36 \* Branching: Each repository has a ``main`` branch, which contains all of the final edits that are seen by the public. A new branch is created to make edits, and can be called anything you like; when the edits are approved by whoever owns the repository, they are merged into the main branch.  
37  
38 .. figure:: Github\_Branch.png  
39



## Commit changes

Add Branching and Clone Definitions

This edit defines what Branching and Cloning mean in Github.

- Commit directly to the `master` branch.
- Create a **new branch** for this commit and start a pull request. [Learn more about pull requests.](#)

Commit changes

Cancel


# Vocabulary

## Push and pull

**Push: Send changes to your repository, even if they are created locally (need permissions)**


**Pull request: Ask for a review of your commits before they are merged into the main branch**


# Opening an Issue



 **TinasheMTapera** commented on Jul 30, 2020 😊 ⋮

Just wanted to let you know of an image that isn't rendered here:  
[https://github.com/andrewjahn/AndysBrainBook/blame/master/docs/fMRI\\_Short\\_Course/Preprocessing/Slice\\_Timing\\_Correction.rst#L10](https://github.com/andrewjahn/AndysBrainBook/blame/master/docs/fMRI_Short_Course/Preprocessing/Slice_Timing_Correction.rst#L10)


Great work on this book!

 **TinasheMTapera** added a commit to TinasheMTapera/AndysBrainBook that referenced this issue on Jul 30, 2020


 Update Slice\_Timing\_Correction.rst ⋮ Verified 9fcc702



  **TinasheMTapera** mentioned this issue on Jul 30, 2020

**Update Slice\_Timing\_Correction.rst #18** 🔗 Open

 **andrewjahn** commented on Oct 8, 2020 Owner 😊 ⋮




Fixed the link, it should be working now. Thanks!

 1




  **andrewjahn** closed this on Oct 8, 2020

# Closing an Issue



Conversation 0   Commits 1   Checks 0   Files changed 1


 **TinasheMTapera** commented on Jul 30, 2020 First-time contributor  


#17

  Update Slice\_Timing\_Correction.rst  Verified 9fcc702

Add more commits by pushing to the **patch-1** branch on **TinasheMTapera/AndysBrainBook**.

  **Continuous integration has not been set up**  
GitHub Actions and several other apps can be used to automatically catch bugs and enforce style.

 **This branch has no conflicts with the base branch**  
Merging can be performed automatically.

**Merge pull request**  You can also open [this](#) in [GitHub Desktop](#) or view [command line instructions](#).

# Update Slice\_Timing\_Correction.rst #18

Edit

Open with ▾

Merged andrewjahn merged 1 commit into andrewjahn:master from TinasheMTapera:patch-1 now

Conversation 0

Commits 1

Checks 0

Files changed 1

+1 -1

Changes from all commits ▾ File filter ▾ Conversations ▾ Jump to ▾ ⚙ ▾

0 / 1 files viewed ⓘ

Review changes ▾

docs/fMRI\_Short\_Course/Preprocessing/Slice\_Timing\_Correction.rst

<> 📄 Viewed ⋮

@@ -7,7 +7,7 @@ Unlike a photograph, in which the entire picture is taken in a single moment, an

7 7

8 8 The two most commonly used methods for creating volumes are sequential and interleaved slice acquisition. Sequential slice acquisition acquires each adjacent slice consecutively, either bottom-to-top or top-to-bottom. Interleaved slice acquisition acquires every other slice, and then fills in the gaps on the second pass. Both of these methods are illustrated in the video below.

9 9

10 - .. figure:: SliceTimingCorrection\_Demo.gif

10 + .. figure:: SliceTimingCorrection\_Demo.gif

11 11

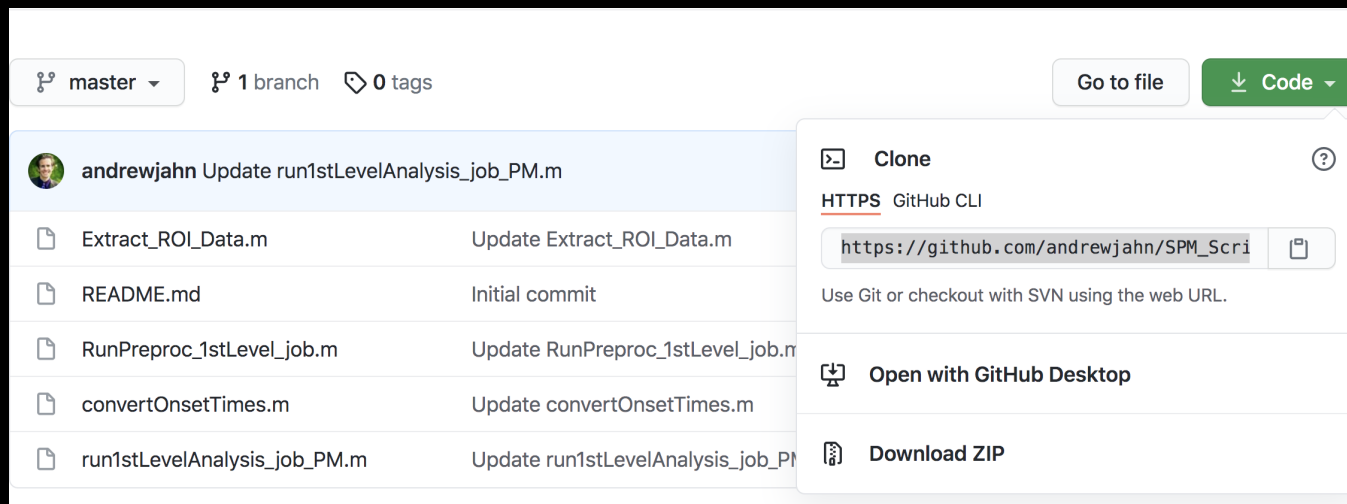
12 12 As you'll see later on, when we model the data at each voxel we assume that all of the slices were acquired simultaneously. To make this assumption valid, the `:ref:`time-series <Time_Series>` for each slice needs to be shifted back in time by the duration it took to acquire that slice. [`Sladky et al. \(2011\) <https://www.sciencedirect.com/science/article/pii/S1053811911007245>](#) also demonstrated that slice-timing correction can lead to significant increases in statistical power for studies with longer TRs (e.g., 2s or longer), and especially in the dorsal regions of the brain.

13 13

# Vocabulary

**Clone: Copy of a repository that lives on your computer**

**Sample usage: `git clone <repository address>`**



The screenshot shows a GitHub repository interface. At the top, it displays 'master' as the current branch, '1 branch', and '0 tags'. A 'Go to file' button and a 'Code' button with a dropdown arrow are visible. Below this, a commit by 'andrewjahn' is shown with the message 'Update run1stLevelAnalysis\_job\_PM.m'. A list of files follows, including 'Extract\_ROL\_Data.m', 'README.md', 'RunPreproc\_1stLevel\_job.m', 'convertOnsetTimes.m', and 'run1stLevelAnalysis\_job\_PM.m'. A 'Clone' dropdown menu is open, showing options: 'Clone' (with a question mark), 'HTTPS GitHub CLI' (with a text input field containing 'https://github.com/andrewjahn/SPM\_Scri' and a copy icon), 'Use Git or checkout with SVN using the web URL.', 'Open with GitHub Desktop', and 'Download ZIP'.



```
(base) ajahn:~/Desktop$ git clone https://github.com/andrewjahn/SPM_Scripts.git
Cloning into 'SPM_Scripts'...
remote: Enumerating objects: 40, done.
remote: Counting objects: 100% (40/40), done.
remote: Compressing objects: 100% (39/39), done.
remote: Total 40 (delta 19), reused 0 (delta 0), pack-reused 0
Unpacking objects: 100% (40/40), done.
(base) ajahn:~/Desktop$ ls
Archived                Flanker_fMRIprep      SPM_Scripts
BTC_preop              Gambles                ds002422-download
CONN_Demo              Haxby_Data            network_TDA_tutorial
FSL_Flanker            Haxby_Data_Umich
Flanker                NeuroNav
(base) ajahn:~/Desktop$ cd SPM_Scripts/
(base) ajahn:~/Desktop/SPM_Scripts$ ls
Extract_ROI_Data.m      convertOnsetTimes.m
README.md               run1stLevelAnalysis_job_PM.m
RunPreproc_1stLevel_job.m
(base) ajahn:~/Desktop/SPM_Scripts$ □
```

# Supercomputing

**What is a supercomputer?**

**Great Lakes is a supercomputing cluster,  
i.e., a large collection of computers**



# **Supercomputing at the University of Michigan**

**LSA students can apply for a supercomputing account through Michigan's Advanced Research Computing (ARC) center**

**Usually requires a shortcode from the PI**

**Can apply for a Umich Research Computing Package (UMRCP)**

**80,000 CPU hours and 10TB of storage per year,  
100TB archive storage**

# **Supercomputing at the University of Michigan**

**Uses Batch computing**

**i.e., you specify the resources for a job or several jobs**

**Jobs are run by a job manager, which is told  
when to run by a job scheduler**

**These are run with a computing language called  
SLURM**

```
#!/bin/bash
```

```
#-----
```

```
#----- HEADER -----#
```

```
#SBATCH --job-name=mri_prep_0000004_01_01_T1
```

```
#----- log file
```

```
#SBATCH -o /scratch/precisionhealth_project_root/precisionhealth_project1/shared_data/brainmri/slogs/mri_prep_0000004_01_01_T1.log
```

```
#----- Cancel job after d-hh:mm:ss
```

```
#SBATCH --time=09:00:00
```

```
#----- Number of cores
```

```
#SBATCH --nodes=1
```

```
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=5
```

```
#----- GB Memory
```

```
#SBATCH --mem=10g
```

```
#----- Account will pay job
```

```
#SBATCH --account=precisionhealth_project1
```

```
#----- Partition where job "lives"?
```

```
#SBATCH --partition=standard
```

```
#----- No e-mail notifications of job start/end/error
```

```
#SBATCH --mail-type=NONE
```

```
echo "Working in dir ${PWD}:"
```

```
#----- MODULES -----#
```

```
module purge
```

```
module load fsl/6.0.5.1
```

```
module load afni/18.0.27
```

```
module load freesurfer
```

## EXAMPLE JOBS AND THEIR CHARGES<sup>1</sup>

To help illustrate how the job charges work, here are some examples of differently-sized jobs.

Partition	Total CPU Cores Used	Total Memory Used	Total GPUs Used	Cost Per Minute
standard	1	1 GB	N/A	\$0.000250
standard	1	10 GB	N/A	\$0.000500
standard	36	5 GB	N/A	\$0.009000
standard	1	50 GB	N/A	\$0.002000
largemem	1	180 GB	N/A	\$0.003852
gpu	1	20 GB	1	\$0.002739

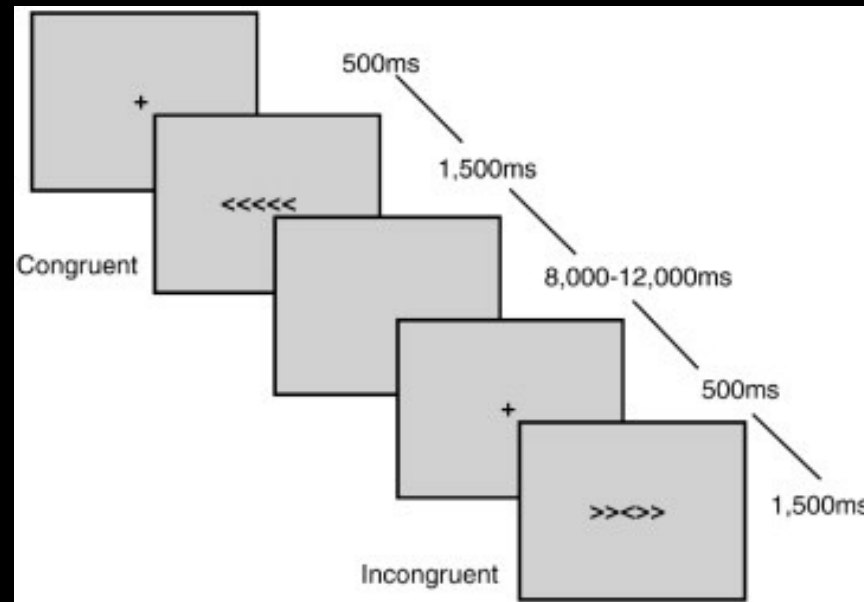
**Example: Analyzing a dataset from [openneuro.org](https://openneuro.org)**

# The Dataset

## Flanker Task (Kelly et al., 2008)

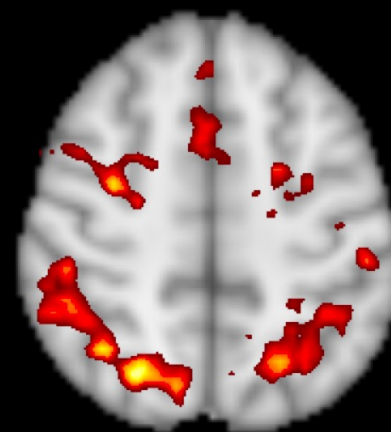
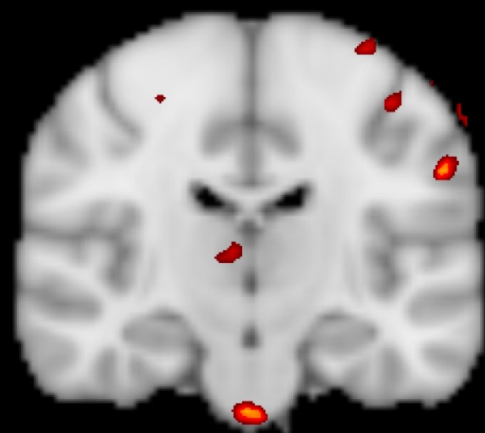
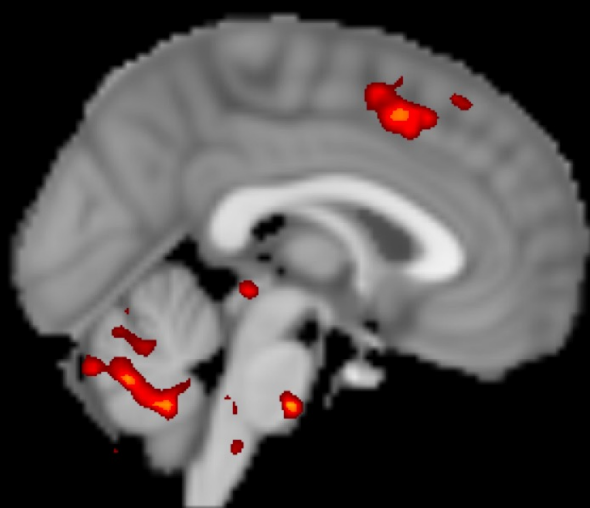
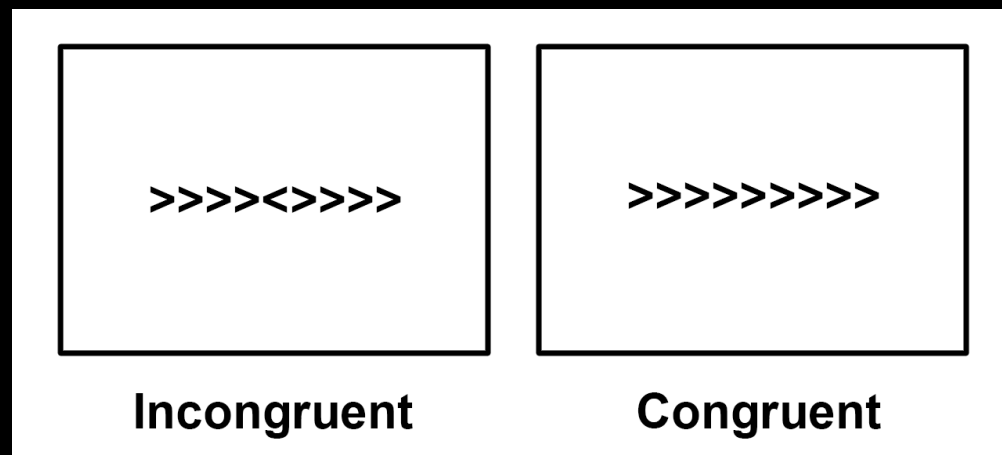
### Cognitive Control

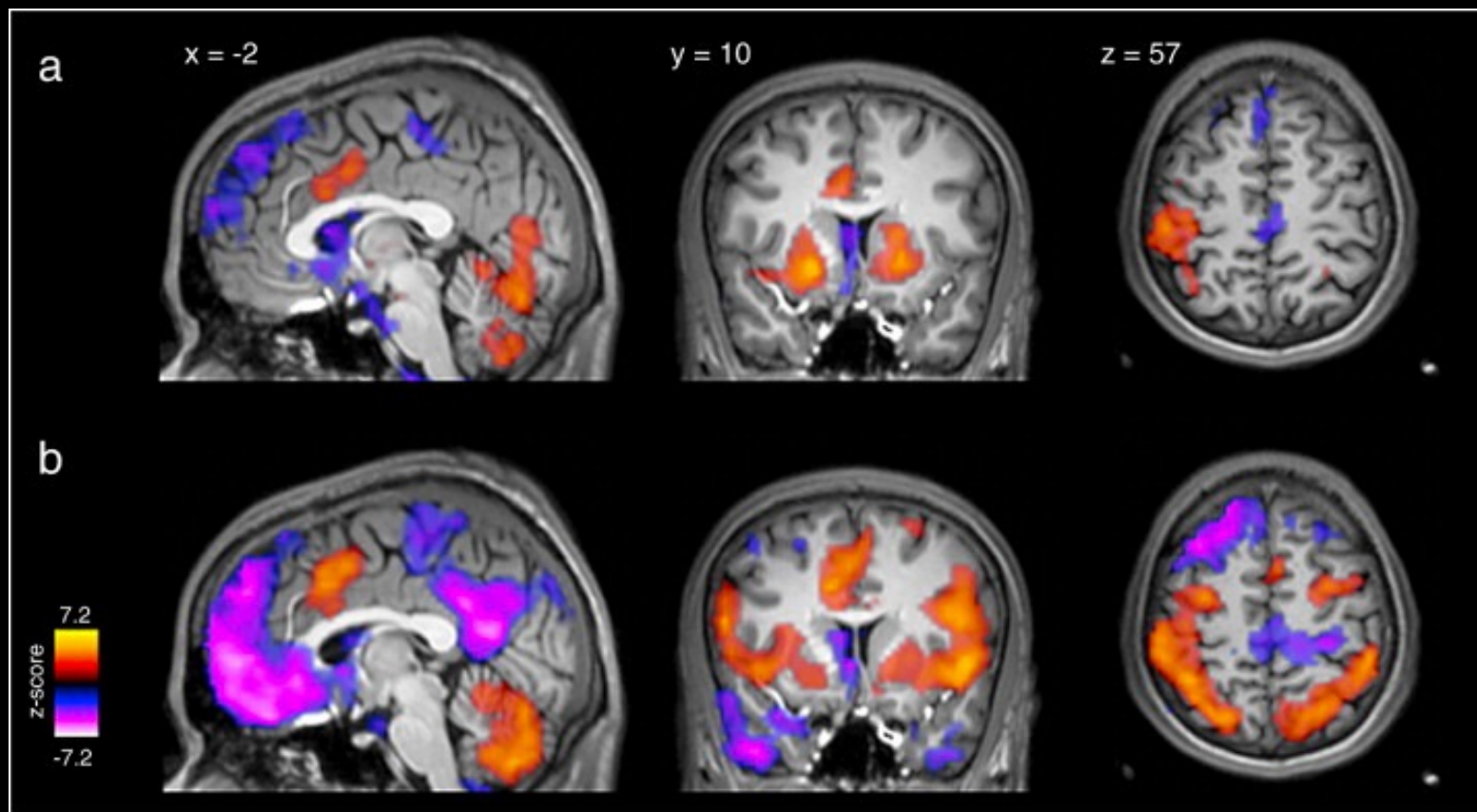
Filtering out irrelevant stimuli to perform a task



Kelly et al., 2008







**Demonstration: Download the data and analyze it**

# General Q & A Session

**Any questions about the material covered since last Friday?**

# **Future trends in neuroimaging analysis**

**Difficult to predict**

**What I think will happen:**

**Greater emphasis on standardized pipelines, software**

**More labs using large open-access datasets**

**Wider use of supercomputers**

# Concluding Remarks