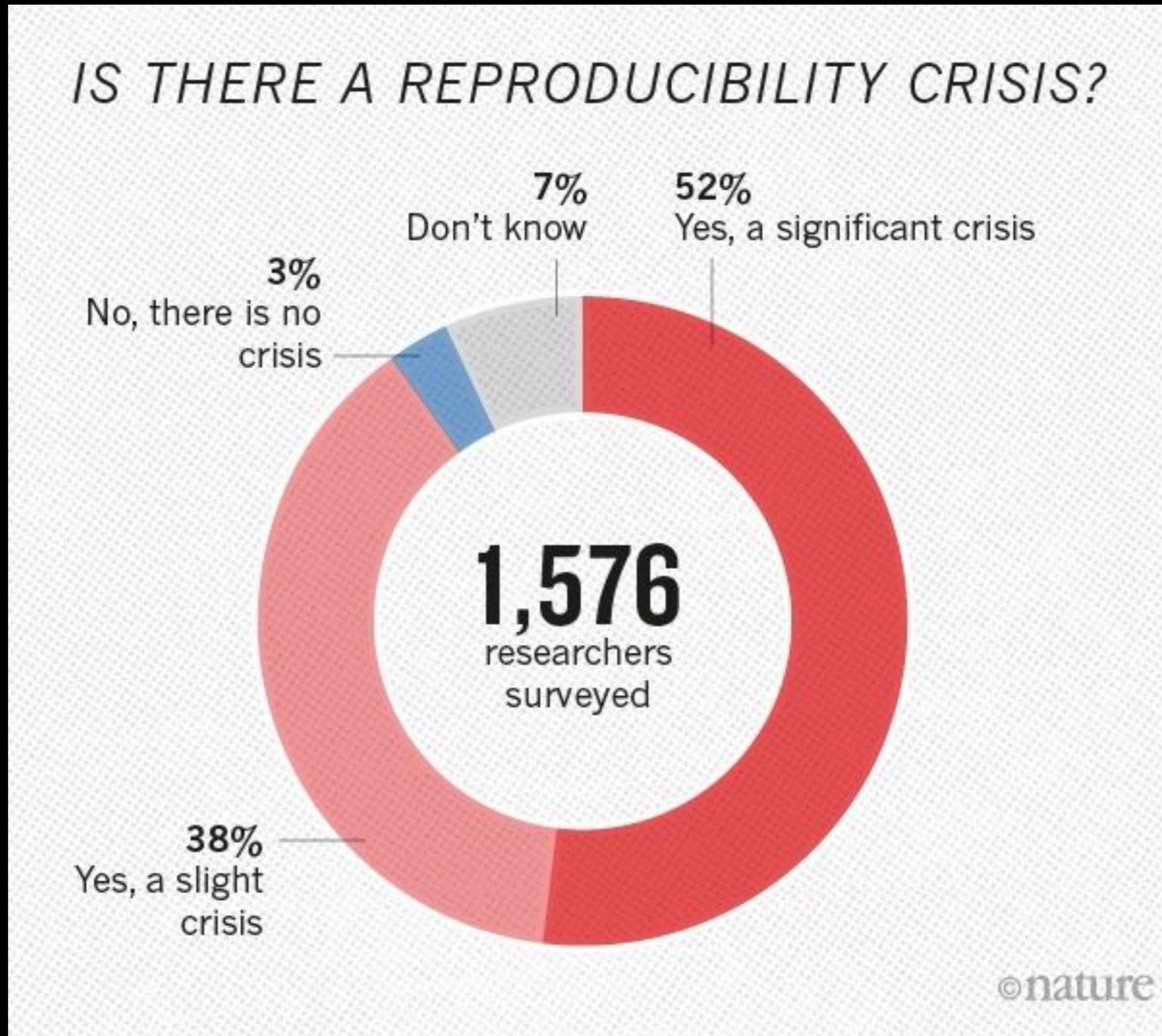




# USER-FRIENDLY WEB APPS TO FACILITATE FMRI STUDY DESIGN AND ANALYSIS

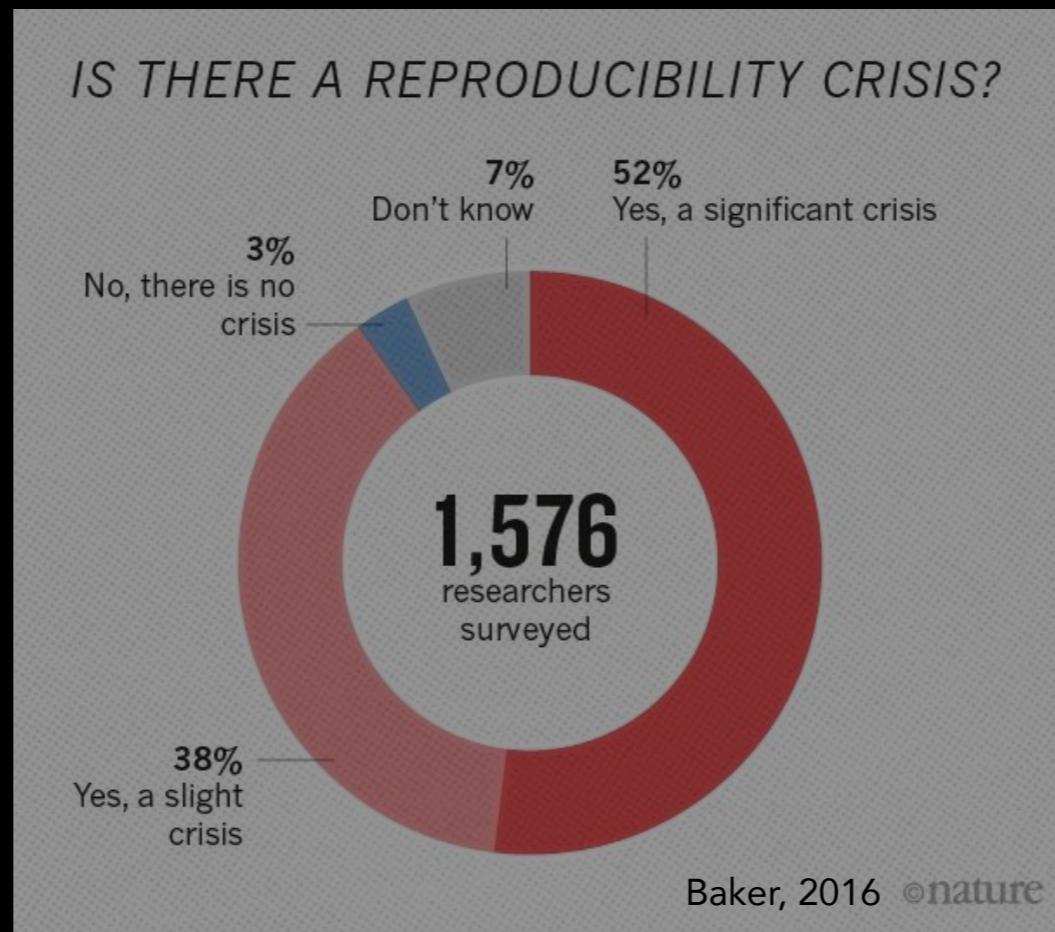
STEPHANIE NOBLE  
NEUROPRISM LAB  
DEPARTMENT OF PSYCHOLOGY  
DEPARTMENT OF BIOENGINEERING  
CENTER FOR COGNITIVE & BRAIN HEALTH  
NORTHEASTERN UNIVERSITY

# MOTIVATION



Baker, 2016

# MOTIVATION



## NIH plans to enhance reproducibility

Francis S. Collins and Lawrence A. Tabak discuss initiatives that the US National Institutes of Health is exploring to restore the self-correcting nature of preclinical research.

A growing chorus of concern, from scientists and laypeople, contends that the complex system for ensuring

shorter term, however, the checks and balances that once ensured scientific fidelity have been hobbled. This has compromised

## Raise standards for preclinical cancer research

C. Glenn Begley and Lee M. Ellis propose how methods, publications and incentives must change if patients are to benefit.

Efforts over the past decade to characterize the genetic alterations in human cancers have led to a better understanding of molecular drivers of this complex set of diseases. Although we in the cancer field hoped that this would lead to more effective drugs, historically, our ability to translate cancer research to clinical success has been remarkably low<sup>1</sup>. Sadly, clinical

trials in oncology have the highest failure rate compared with other therapeutic areas. Given the high unmet need in oncology, it is understandable that barriers to clinical development may be lower than for other disease areas, and a larger number of drugs with suboptimal preclinical validation will enter oncology trials. However, this low success rate is not sustainable or acceptable, and

investigators must reassess their approach to translating discovery research into greater clinical success and impact.

Many factors are responsible for the high failure rate, notwithstanding the inherently difficult nature of this disease. Certainly, the limitations of preclinical tools such as inadequate cancer-cell line and mouse models make it difficult for even

## Power failure: why small sample size undermines the reliability of neuroscience

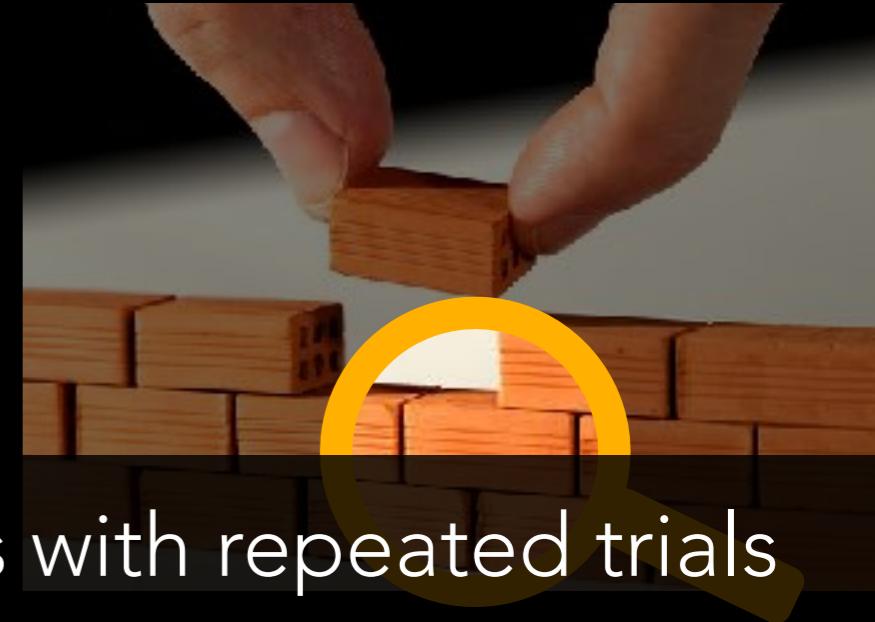
Katherine S. Button<sup>1,2</sup>, John P. A. Ioannidis<sup>3</sup>, Claire Mokrysz<sup>4</sup>, Brian A. Nosek<sup>4</sup>, Jonathan Flint<sup>5</sup>, Emma S. J. Robinson<sup>6</sup> and Marcus R. Munafò<sup>1</sup>

**Abstract** | A study with low statistical power has a reduced chance of detecting a true effect, but it is less well appreciated that low power also reduces the likelihood that a statistically significant result reflects a true effect. Here, we show that the average statistical power of studies in the neurosciences is very low. The consequences of this include overestimates of effect size and low reproducibility of results. There are also ethical dimensions to this problem, as unreliable research is inefficient and wasteful. Improving reproducibility in

Need for more precise analytical methods

# MOTIVATION

- **Accuracy:** reliability & validity
  - **Reliability:** ability to get similar results with repeated trials
  - **Validity:** correspondence with desired outcome



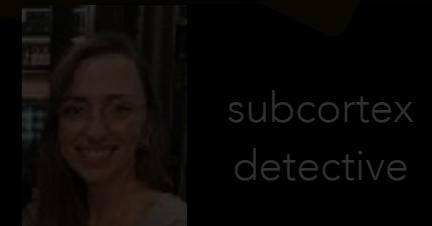
# MOTIVATION

- **Accuracy:** reliability & validity



- **Reliability:** ability to get similar results with repeated trials

- For "A guide to the measurement and interpretation of fMRI test-retest reliability", cf. Noble, Scheinost, & Constable, 2021, COBEHA



- **Validity:** correspondence with desired outcome

- Inferential methods
- Standard goal: find true positives, limit false positives



# MOTIVATION



(often to improve reproducibility)

Much discussion about improving power in fMRI  
...but there are many open questions

Adequate sample sizes

Power failure: why small sample size undermines the reliability of neuroscience

Katherine S. Button<sup>1,2</sup>, John P. A. Ioannidis<sup>3</sup>, Claire Mokrysz<sup>4</sup>, Brian A. Nosek<sup>4</sup>, Jonathan Flint<sup>5</sup>, Emma S. J. Robinson<sup>6</sup> and Marcus R. Munafò<sup>1</sup>

NATURE REVIEWS | NEUROSCIENCE VOLUME 14 | MAY 2013 | 265

bioRxiv preprint doi: <https://doi.org/10.1101/2024.02.16.680448>; this version posted February 18, 2024.  
**MRI economics: Balancing sample size and scan duration in brain wide association studies**

Leon Qi Rong Qoi<sup>1-5</sup>, Csaba Orban<sup>2-5</sup>, Thomas E Nichols<sup>6</sup>, Shaoshi Zhang<sup>1-5</sup>, Trevor Wei Kiat Tan<sup>1-5</sup>, Ru Kong<sup>2-5</sup>, Scott Marek<sup>7</sup>, Nico U.F. Dosenbach<sup>7-10</sup>, Timothy Laumann<sup>9</sup>, Evan M Gordon<sup>7</sup>, Juan Helen Zhou<sup>1-4</sup>, Danilo Bzdok<sup>11-13</sup>, Simon B Eickhoff<sup>14,15</sup>, Avram J Holmes<sup>16</sup>, B. T. Thomas Yeo<sup>1-5\*</sup>

Reproducible brain-wide association studies require thousands of individuals

Scott Marek<sup>1,2,3</sup>, Brenden Terro-Clemmens<sup>2,3,4,5</sup>, Finnegan J. Calabro<sup>4,5</sup>, David F. Montez<sup>2</sup>, Benjamin P. Kay<sup>6</sup>, Alexander S. Hatzius<sup>1</sup>, Meghan Rose Denonieu<sup>1</sup>, William Foran<sup>4</sup>, Ryland L. Miller<sup>1,8</sup>, Timothy J. Hendrickson<sup>1</sup>, Stephen M. Malone<sup>6</sup>, Sridhar Kandula<sup>7</sup>, Eric Fecchio<sup>3,10</sup>, Oscar Miranda-Dominguez<sup>8,9</sup>, Alice M. Graham<sup>11</sup>, Eric A. Earl<sup>1,7</sup>, Anders J. Perrone<sup>1,7</sup>, Michaela Cordova<sup>11</sup>, Olivia Doyle<sup>7</sup>, Lucille A. Moore<sup>7</sup>, Gregory M. Corieri<sup>1,11</sup>, Johnny Uriarte<sup>7</sup>, Kathy Snider<sup>1</sup>, Benjamin J. Lynch<sup>1,7</sup>, James G. Wilgenbusch<sup>1,5</sup>, Thomas Pengo<sup>7</sup>, Angela Tam<sup>12,13,14,15,16</sup>, Jianzhong Chan<sup>13,14,15,16</sup>, Dillon J. Newbold<sup>6</sup>, Annie Zheng<sup>6</sup>, Nicole A. Seider<sup>6</sup>, Andrew N. Van<sup>1,2,7</sup>, Athanasia Metoki<sup>6</sup>, Roselyne J. Chauvin<sup>1</sup>, Timothy O. Laumann<sup>1</sup>, Deanna J. Greene<sup>19</sup>, Steven E. Petersen<sup>1,20,21</sup>, Hugh Corriveau<sup>22</sup>, Wesley K. Thompson<sup>23</sup>, Thomas E. Nichols<sup>24</sup>, B. T. Thomas Yeo<sup>1,2,3,15,25,26</sup>, Deanna M. Barch<sup>1,21</sup>, Beatriz Luna<sup>1,24</sup>, Daniela A. Fair<sup>1,20,21,23,25</sup> & Nico U. F. Dosenbach<sup>1,2,3,15,25,26</sup>

654 | Nature | Vol 603 | 24 March 2022

What Is the Test-Retest Reliability of Common Task-Functional MRI Measures? New Empirical Evidence and a Meta-Analysis

Maxwell L. Elliott<sup>1</sup>, Annchen R. Knodt<sup>1</sup>, David Ireland<sup>2</sup>, Meriwether L. Morris<sup>1</sup>, Richie Poulton<sup>2</sup>, Sandhya Ramrakha<sup>2</sup>, Maria L. Sison<sup>1</sup>, Terrie E. Moffitt<sup>1,3,4,5</sup>, Avshalom Caspi<sup>1,3,4,5</sup>, and Ahmad R. Hariri<sup>1</sup>

Psychological Science © The Author(s) 2020

More reliable & valid measures

Influences on the Test-Retest Reliability of Functional Connectivity MRI and its Relationship with Behavioral Utility

Stephanie Noble<sup>1</sup>, Marisa N. Spann<sup>2</sup>, Fuyuze Tokoglu<sup>3</sup>, Xilin Shen<sup>3</sup>, R. Todd Constable<sup>1,3,4</sup> and Dustin Scheinost<sup>3</sup>

Cerebral Cortex, 2017, Vol. 27, No. 11

Improving power in functional magnetic resonance imaging by moving beyond cluster-level inference

Stephanie Noble<sup>1,2</sup>, Amanda F. Mejia<sup>3,4</sup>, Andrew Zalesky<sup>2,4</sup>, and Dustin Scheinost<sup>1,2,3,5,6</sup>

PNAS 2022 Vol. 119 No. 32 e2203020119

Beyond Increasing Sample Sizes: Optimizing Effect Sizes in Neuroimaging Research

on Individual Differences

Colin G. DeYoung<sup>1,7</sup>, Kirsten Hilger<sup>2,1</sup>, Jamie L. Hanson<sup>3</sup>, Rany Abend<sup>4</sup>, Timothy A. Allen<sup>5</sup>, Roger E. Beary<sup>6</sup>, Scott D. Blain<sup>7</sup>, Robert S. Chavez<sup>8</sup>, Stephen A. Engel<sup>9</sup>, Ma Feilong<sup>10</sup>, Alex Fornito<sup>11</sup>, Erhan Genç<sup>12</sup>, Vina Goghari<sup>13</sup>, Rachael G. Grazioplene<sup>14</sup>, Philipp Homan<sup>15</sup>, Kearan Joyner<sup>16</sup>, Antonia N. Kaczkurkin<sup>17</sup>, Robert D. Latzman<sup>18</sup>, Elizabeth A. Martin<sup>19</sup>, Aki Nikolaidis<sup>20</sup>, Alan D. Pickering<sup>21</sup>, Adam Safron<sup>22</sup>, Tyler A. Sassenberg<sup>1</sup>, Michelle N. Servaas<sup>23</sup>, Luke D. Smillie<sup>24</sup>, R. Nathan Spreng<sup>25</sup>, Essi Viding<sup>26</sup>, Jan Wacker<sup>27</sup> 2024 OSF-PREPRINTS

More powerful inferential procedures

More powerful study design

Answering these questions requires power estimator tailored for fMRI—  
**deceptively difficult!**

# MOTIVATION



**Path towards better estimation of effects & power for fMRI study planning**

1. Understand expected effects for typical study designs
2. Develop tailored power estimation procedures for typical studies

# “TYPICAL” STUDIES



- Here, **study** = analysis to estimate the effect of a unique phenomenon in a given dataset
- Criteria:  $n > 400$ , reflect typical study designs

## 6 Datasets



45 “studies” → 45 effect maps

# MEASURING & COMPARING EFFECTS

## Conversion to Cohen's d

$$\text{1-sample } t: d_s = \frac{t}{\sqrt{n}}$$

$$\text{2-sample } t: d_s = t\sqrt{\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$$

$$r: d_s = d = \frac{r}{\sqrt{(1 - r^2)}} \quad \Delta y \text{ for } \Delta x = 2\sigma$$

## Sample size needed to detect

	Cohen's d	n within	n between (per group)
small	0.2	198	393
medium	0.5	33	64
large	0.8	14	26

Lakens, 2013

Mathur & VanderWeele, 2021

Starting place for comparison and interpretation across studies

although within- and between-sample  $d$  have different implications

# EFFECT SIZES

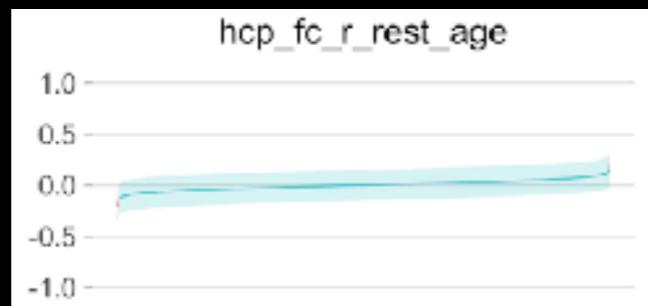
95% Simultaneous Confidence Intervals for  $d$ , by edge/voxel



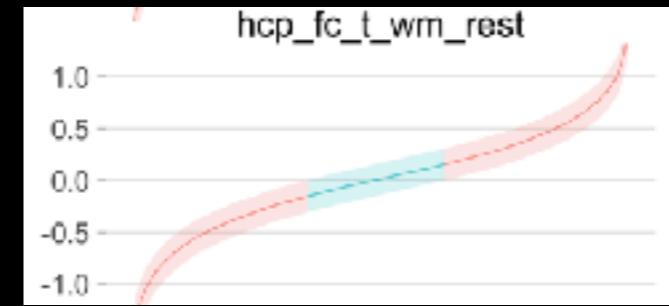
95% of experiments will contain the true value for all edges/voxels

## Representative studies (HCP)

Between-subject  
 $r$  (FC)



Within-subject (task)  
 $t$  (FC)



"Task-vs-rest FC"

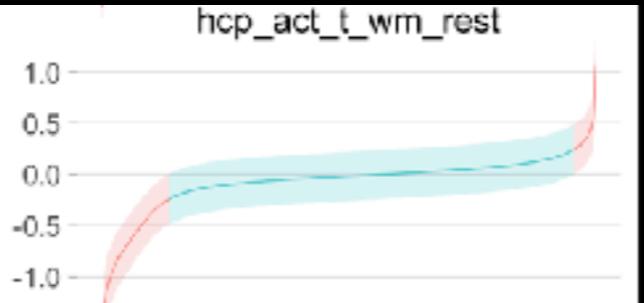
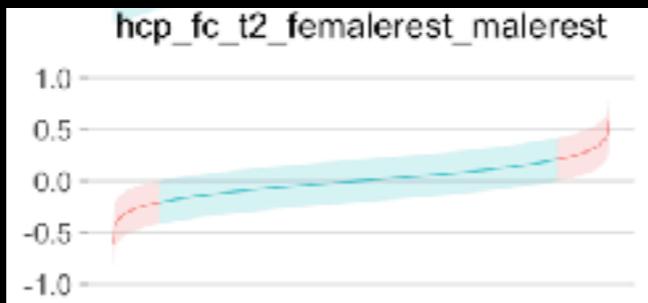
30% of effects could be 0

"BWAS"

>99% of effects could be 0

"Group-contrast (FC)"

80% of effects could be 0



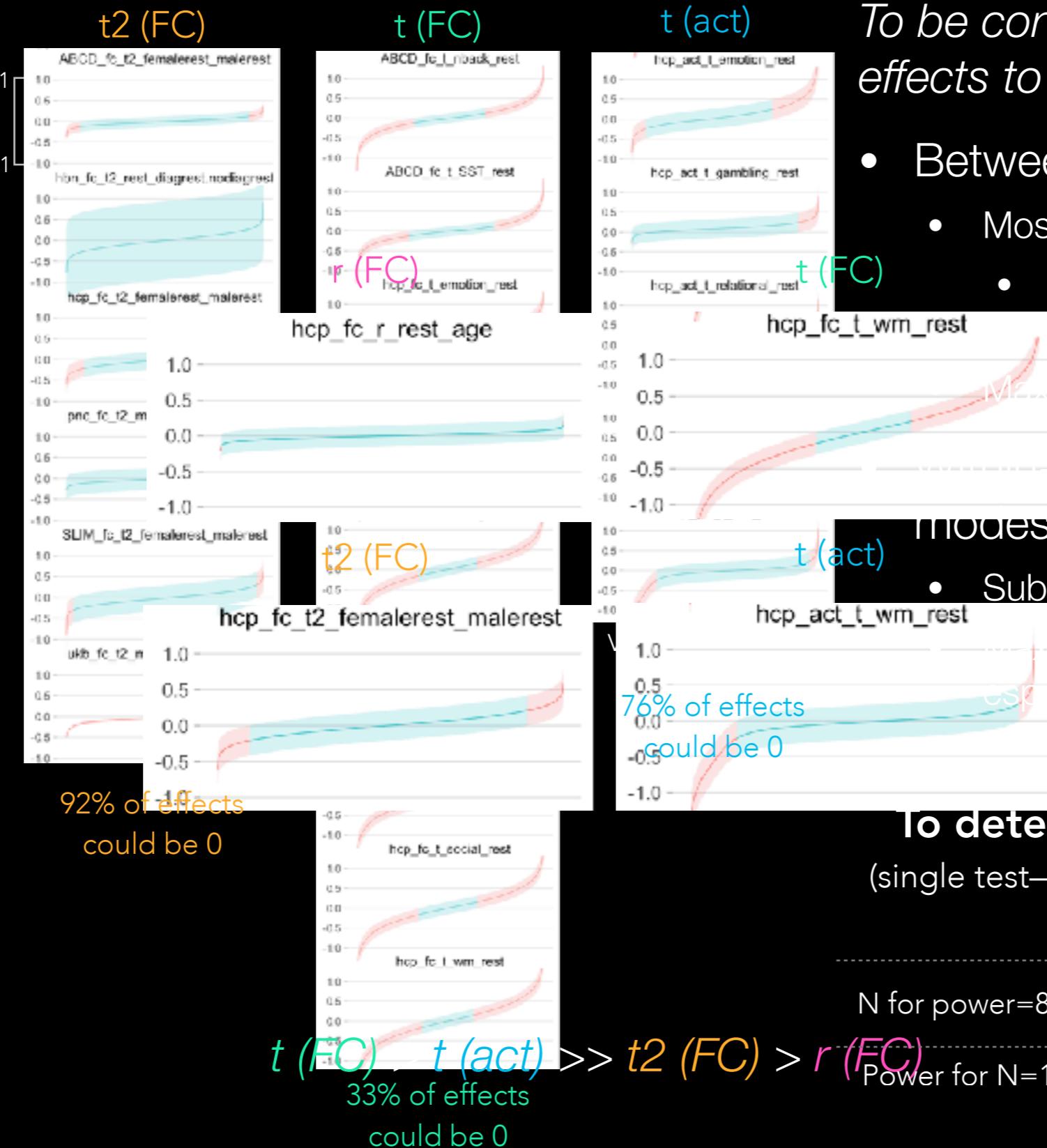
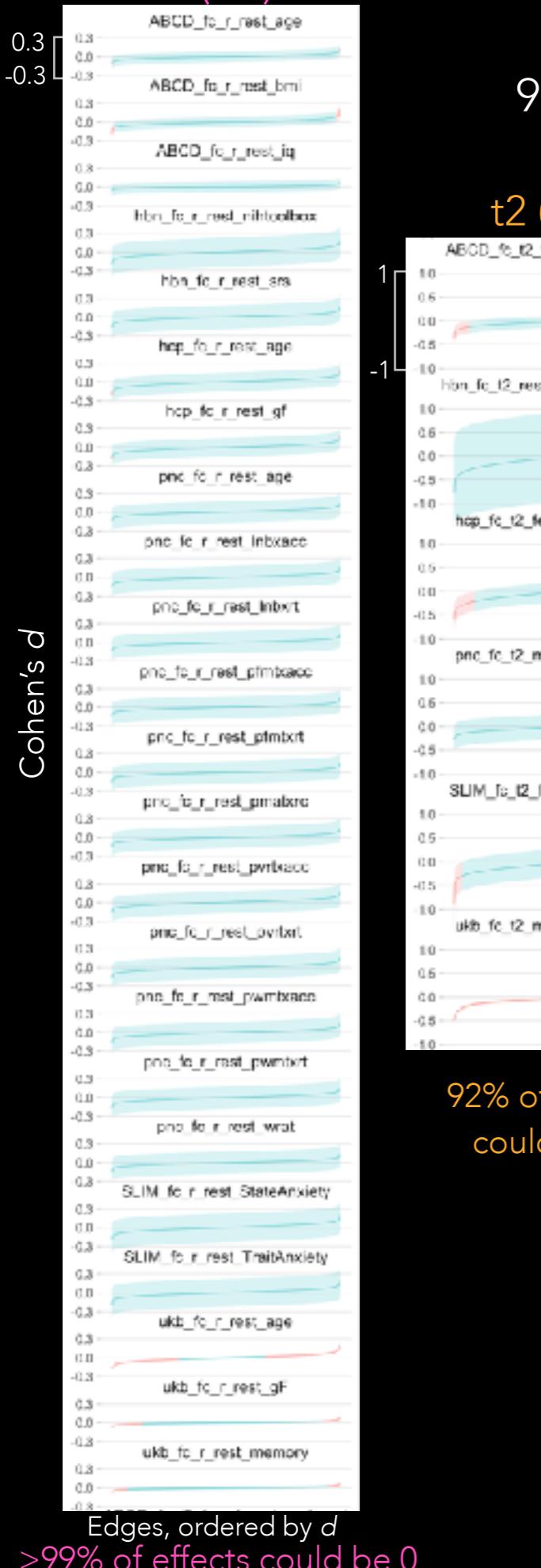
"Task-based activation"

50% of effects could be 0

$t$  (FC) >  $t$  (act) >>  $t2$  (FC) >  $r$  (FC)

# EFFECT SIZES

95% Simultaneous Confidence Intervals, by edge/voxel



To be conservative, plan for most effects to be:

- Between-sub: very small
  - Most edges could be  $\sim 0$
  - Psychological constructs most difficult to detect

conservative  $d \leq$  medium

sub task-contrast:  
modest to medium

- Substantial # of nonzero effects  
conservative  $d >$  large,  
especially for FC

To detect **max conservative  $d$**

(single test—no multiple testing correction)

	$r$ (FC)	$t2$ (FC)	$t$ (FC)	$t$ (act)
N for power=80%	419 per group	68 per group	4	5
Power for N=100	30%	90%	100%	100%

# SHINY APP!



The image shows a screenshot of a Shiny web application titled "BrainEffeX". The application is designed to explore effect sizes in typical neuroimaging study designs. It features a sidebar with various filters and a main panel displaying four plots and two heatmap matrices.

**Filters:**

- Dataset:** All
- Map Type:** All
- Task:** All
- Test Type:** All
- Spatial scale:** Univariate
- What do you want to group by?**: None

**Download Data:** A button to download the data used in the plots.

**Plot Area:**

The plots below visualize all edges or voxels in each study.

Simultaneous confidence Intervals (95% CI across all edges/voxels). Red indicates simultaneous CIs overlapping with 0, green indicates no overlap.

Four plots are shown, each with parameters:

- Plot 1:** Dataset: ABCD, Map Type: FC, Test type: t, Var1: rest, Var2: age, Sample Size: n = 3261. Maximum conservative effect size: 0.28.
- Plot 2:** Dataset: ABCD, Map Type: FC, Test type: t, Var1: rest, Var2: bmi, Sample Size: n = 3261. Maximum conservative effect size: 0.25.
- Plot 3:** Dataset: ABCD, Map Type: FC, Test type: t, Var1: rest, Var2: sex, Sample Size: n = 3381. Maximum conservative effect size: 0.
- Plot 4:** Dataset: ABCD, Map Type: FC, Test type: t, Var1: rest, Var2: sex, Sample Size: n = 3574. Maximum conservative effect size: 0.01.

**Heatmaps:**

**Effect size matrices:** These matrices show the average effect sizes across all studies that fit the selected parameters.

**Studies with Shen 268 node atlas:** A heatmap showing effect sizes across 268 nodes. Nodes are listed on the left, and regions are listed at the bottom. A color scale from -0.5 to 0.5 is provided.

**Studies with UKB 55 nodes:** A heatmap showing effect sizes across 55 nodes. Nodes are listed on the left, and regions are listed at the bottom. A color scale from -0.5 to 0.5 is provided.

**Activation Maps (Cohen's d):** A large heatmap showing activation maps for the UKB 55 nodes. A color scale from -0.5 to 0.5 is provided.

**Text Box:**

For correlation studies (r), Var1 is the scanning condition, and Var2 is the behaviour.

For task vs. rest studies (t), Var1 is the task, and Var2 is rest.

For between-group studies (t2), Var1 and Var2 are the two groups.

The maximum conservative effect size is the largest of: 1) the absolute value of the largest lower bound across confidence intervals, 2) the absolute value of the smallest upper bound across confidence intervals.

Version 1.3; Last updated 2024-june-08



# Filter, Visualize, Download, & Contribute\*

## 1. Filter the available studies by parameters of interest

Select from the following options to visualize effect sizes:

Dataset

Map Type

Task

Test Type

Spatial scale

What do you want to group by?

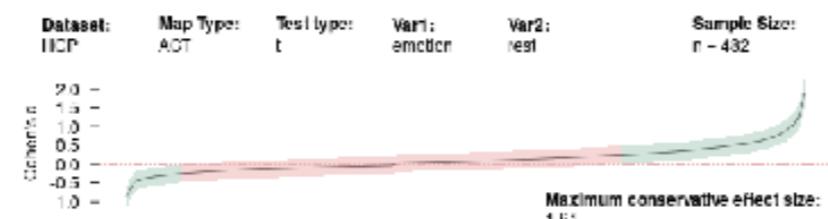
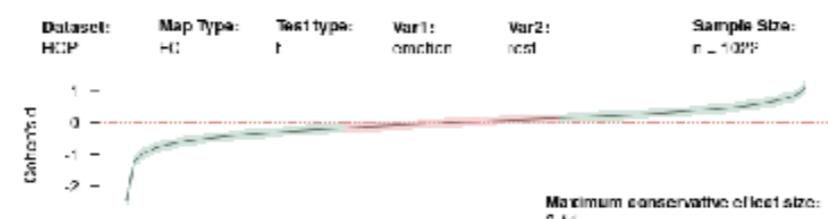
Download Data

## 3. Download the effect maps of the matching studies

## 2A. Visualize the effect sizes and simultaneous confidence intervals of all studies that match the parameters selected

The plots below visualize all edges or voxels in each study.

Simultaneous confidence intervals (95% CI across all edges/voxels). Red indicates simultaneous CIs overlapping with 0, green indicates no overlap.



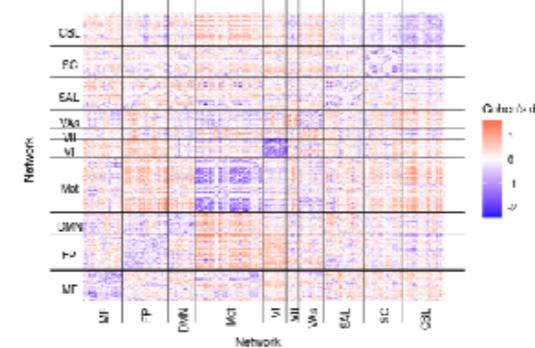
## 2C. Visualize effect sizes of activation studies on the brain

## 2B. Visualize effect sizes of FC studies as matrices

### Effect size matrices

These matrices show the average effect sizes across all studies that fit the selected parameters.

#### Studies with Shen 268 node atlas



### Activation Maps (Cohen's d)



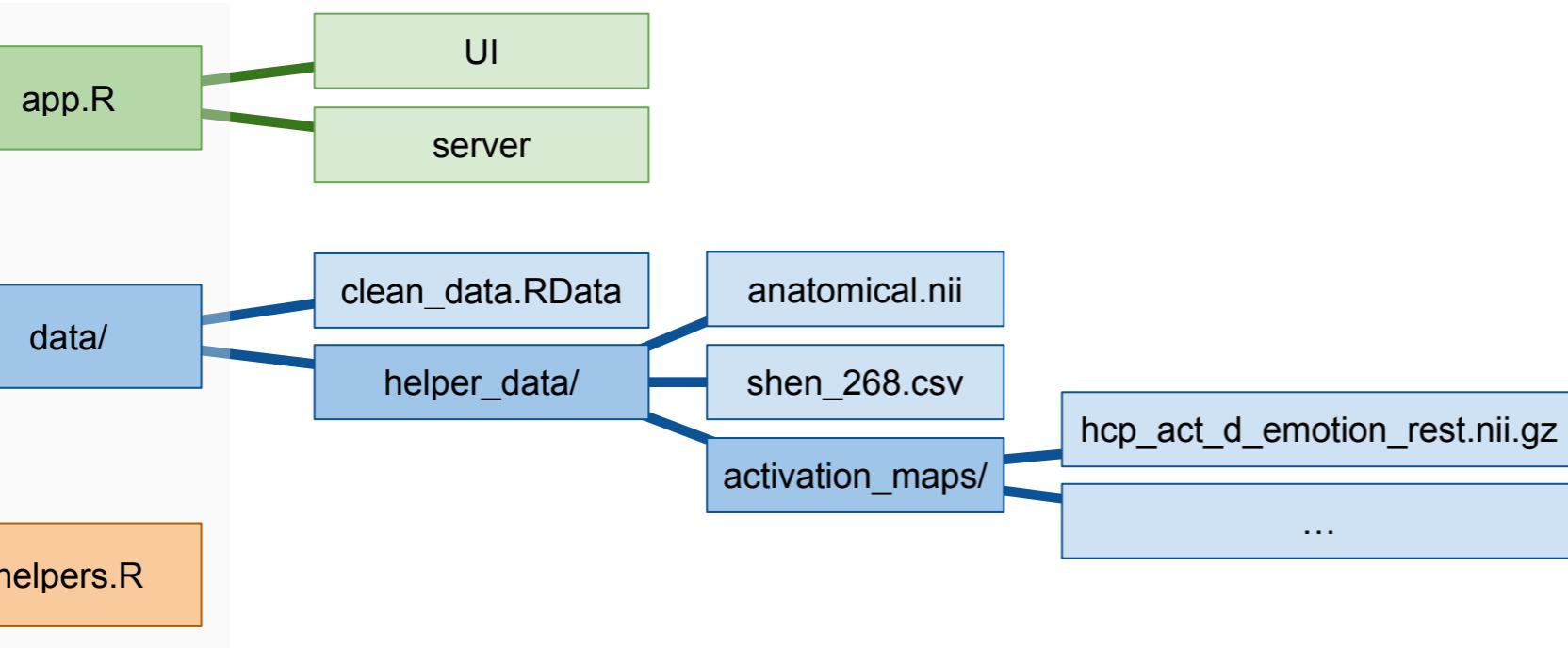
Let's walk through an example





prep\_subject\_level (Matlab)  
do\_group\_level (R)  
app (R)

## [Contributed data format](#)



----- last dim is n\_sub long

----- continuous/ordinal, binary (for t-test), or strings/factors (categorical)

----- IF doing test='r', score label(s) (if binary score, provide {score\_label0, score\_label1}), e.g., 'gF' or {'male', 'female'}

----- IF doing test='r', brain condition label

----- IF doing test='t' | 't2': 1D (t) or 2D (t or t2) cell array of condition label(s)

----- demographic, biometric, cognitive, psychiatric



# MOTIVATION



**Path towards better estimation of effects & power for fMRI study planning**

1. Understand expected effects for typical study designs
2. Develop tailored power estimation procedures for typical studies

# MOTIVATION



## Path towards better estimation of effects & power for fMRI study planning

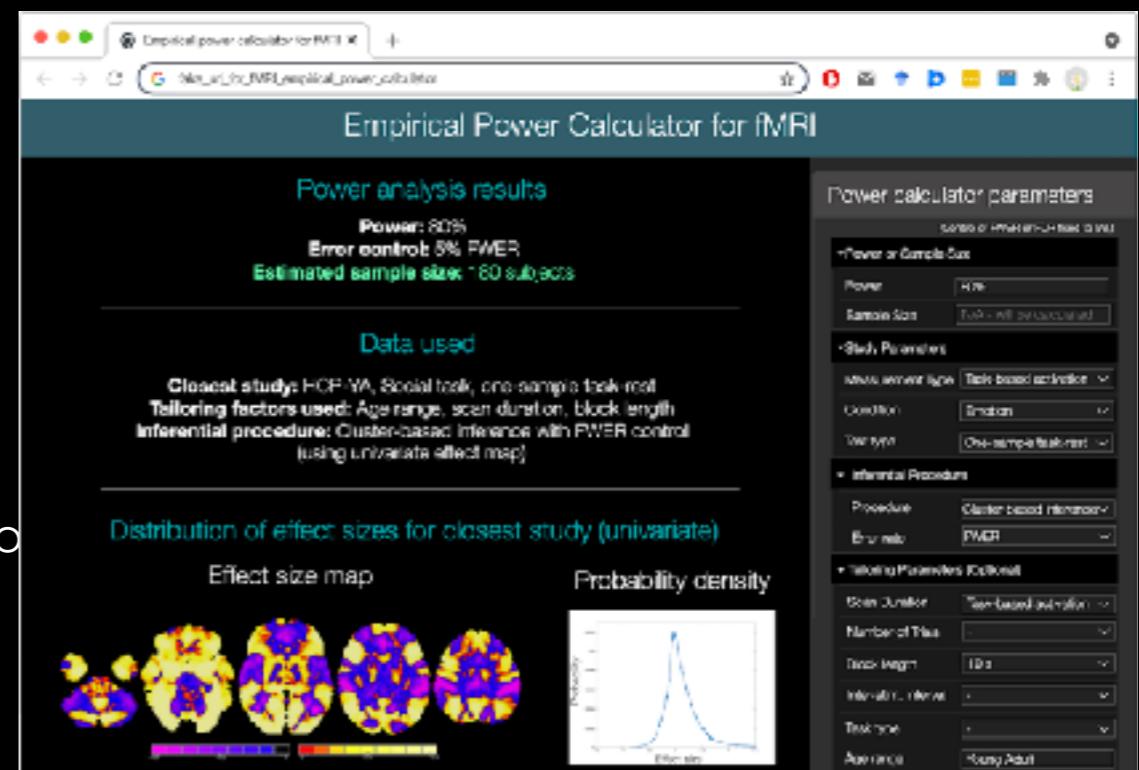
1. Understand expected effects for typical study designs
2. Develop tailored power estimation procedures for typical studies

### Historical (no longer available)

- fMRIPower (ROI; Mumford, Poldrack, & Nichols, 2008)
- NeuroPower (peak+RFT; Durnez et al., 2015)
- PowerMap (voxel+RFT; Joyce & Hayasaka, 2012)

### A New Approach: Empirical Benchmarking

- Pros
  - No requirement for user-defined effects (often small n, pilot)
  - Adaptable for arbitrarily complex inferential procedures
  - Easy-to-use—user provides information readily on hand
- Cons
  - Limited generalizability



# MOTIVATION



## Path towards better estimation of effects & power for fMRI study planning

1. Understand expected effects for typical study designs
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### Historical (no longer available)

- fMRIPower (ROI; Mumford, Poldrack, & Nichols, 2008)
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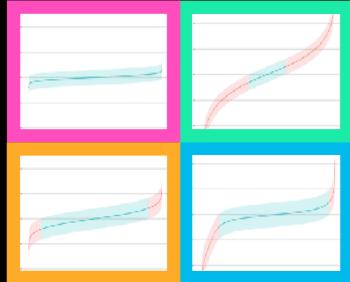
### A New Approach: Empirical Benchmarking

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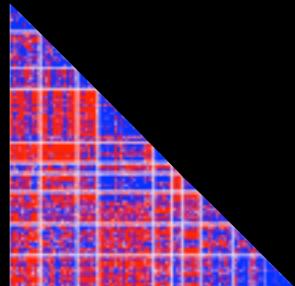
The screenshot shows a web browser displaying an article titled "Sample Size Justification" from the journal "Cortex: Psychology". The article discusses the importance of justifying sample sizes in empirical studies. A yellow callout box highlights a section of the text: "An important step when designing an empirical study is to justify the sample size that will be collected. The key aim of a sample size justification for such studies is to explain how the collected data is expected to provide valuable information given the inferential goals of the researcher. In this overview article six approaches are discussed to justify the sample size in a quantitative empirical study: 1) collecting data from (nearly) the entire population, 2) choosing a sample size based on resource constraints, 3) performing an a priori power analysis, 4) planning for a desired accuracy, 5) using heuristics, or 6) explicitly acknowledging the absence of a justification. An important question to consider when justifying sample sizes is which effect sizes are deemed interesting, and the extent to which the data that is collected informs inferences about these effect sizes. Depending on the sample size justification chosen, researchers could consider 1) what the smallest effect size of interest is, 2) which minimal effect size will be statistically significant, 3) which effect sizes they expect (and what they base these expectations on), 4) which effect sizes would be rejected based on a confidence interval around the effect size, 5) which ranges of effect sizes a study has sufficient power to detect based on a sensitivity power analysis, and 6) which effect sizes are expected in a specific research area. Researchers should also consider the costs associated with different sample sizes, such as time, money, and resources, and how these factors may impact the feasibility and validity of their study design."



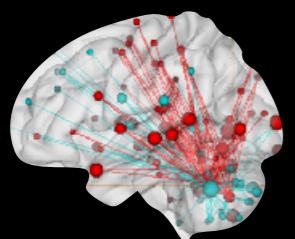
# BRAINEFFEX SUMMARY



- Plan for considerably smaller effects for between-subject designs
  - $t \text{ (FC)} > t \text{ (act)} >> t2 \text{ (FC)} > r \text{ (FC)}$  (matches some intuition)
  - Demographic, biometric > psychological



- Large open data + empirical benchmarking = practical guidelines
  - Starting place for what effects to expect
  - Practical consequences (e.g., where we need consortia-level studies)



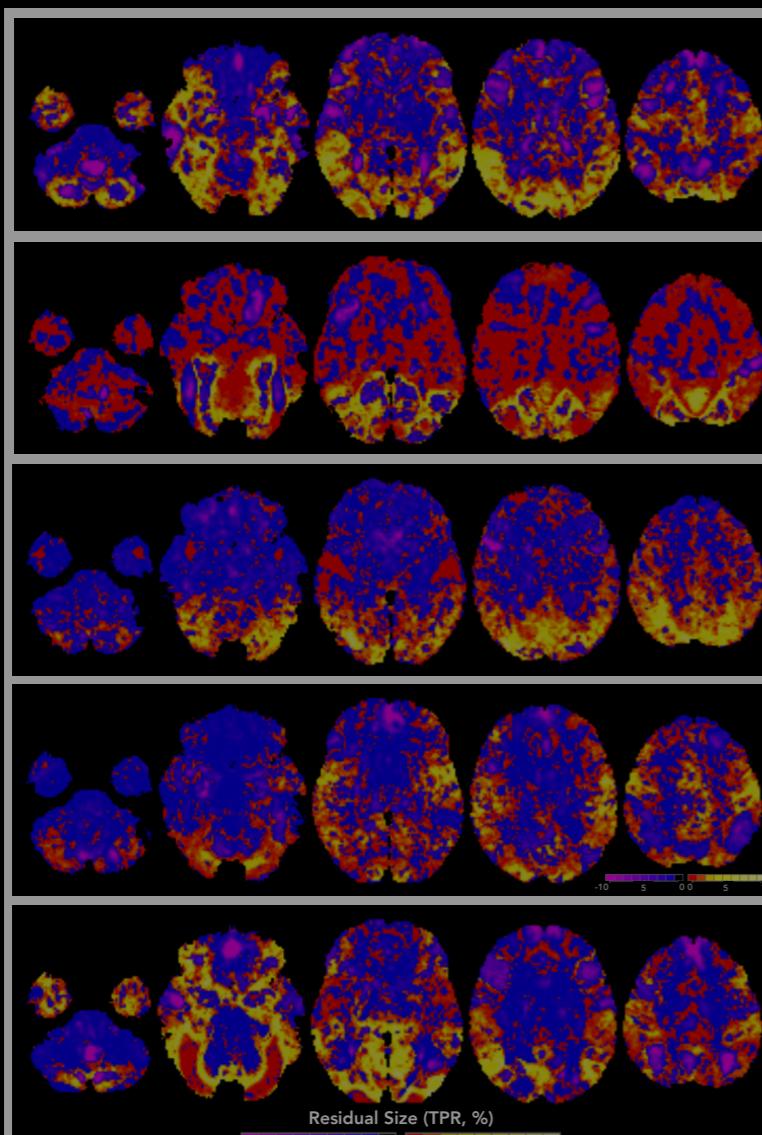
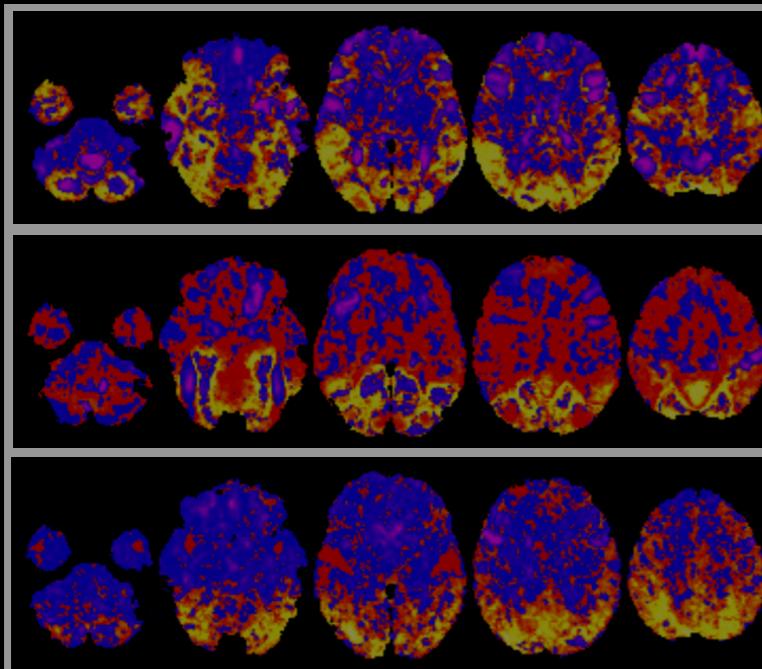
- Need for broader scale / multivariate inference
  - Effects can otherwise be too small for many studies to detect



- Check out the app! Stay tuned for contributions

So let's say you did a power analysis and collected some data...

**Time for analysis!**



# INTRODUCING BIOIMAGE SUITE WEB



**Dustin Scheinost (lead developer)**



**Xenophon Papademetris (lead developer)**

Stephanie Noble

Javid Dadashkarimi

Zachariah Saltzman



Cheryl Lacadie

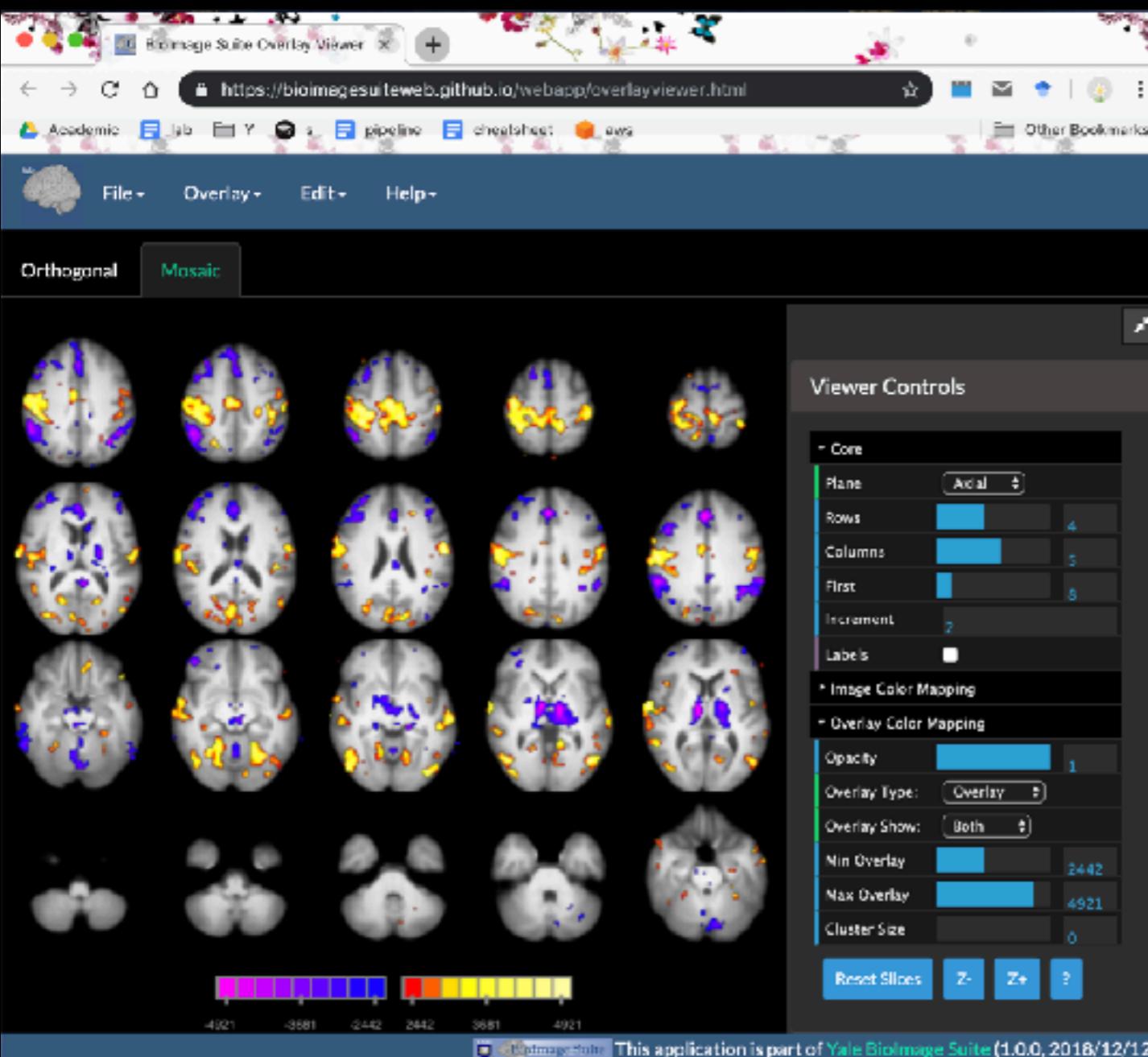
Haley Garbus

John Onofrey



R24MH114805 (PIs X.P. & D.S.)

# BISWEB OVERVIEW



- Web-based application
- Easy-to-use yet powerful
- No installation!
- No servers! All local processing
- Novel architecture & features

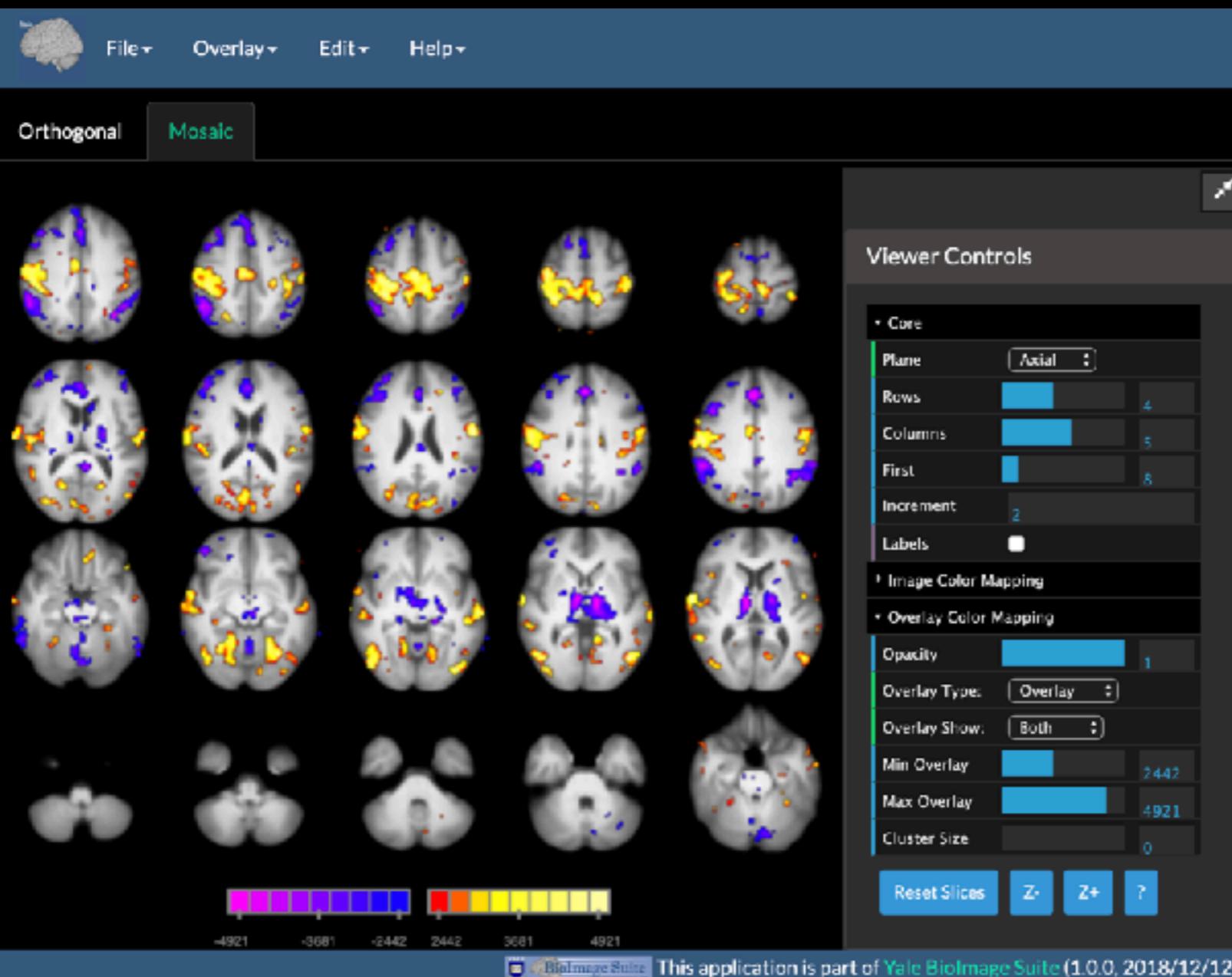
[Introduction video](#)





# OVERLAY VIEWER

## Overlay Viewer



## Directions

1. Applications > Overlay Viewer
2. Load Image and Overlay Data
  1. For Demo: Help > Load Sample Data
3. Play with Viewer Controls: Image Colors, Orthogonal v. Mosaic, etc.



[www.bioimagesuite.org](http://www.bioimagesuite.org)

# LIVE FIGURES! ↵..

Full application state + data

Overlay Viewer

Lets you...

- Continue where you left off
- Share with others (collaborators, publications, etc.)
  - now they too can dynamically change views, thresholds, etc.

Viewer Controls

- Plane: Axial
- Rows: 4
- Columns: 4
- First: 1
- Last: 4
- Labels
- Image Color Mapping
- Overlay Color Mapping
- Opacity
- Overlay Type: Overlay
- Overlay Show: Both
- Max Overlay: 2442
- Cluster Size: 4921
- Set S: Z+
- ?

This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)

## Directions

1. (Previous: open overlay app, load data, choose parameters)
2. File > Save Application State
3. File > Load Application State (can drag and drop)

Try a Live Figure from “Cluster failure or power failure” paper:

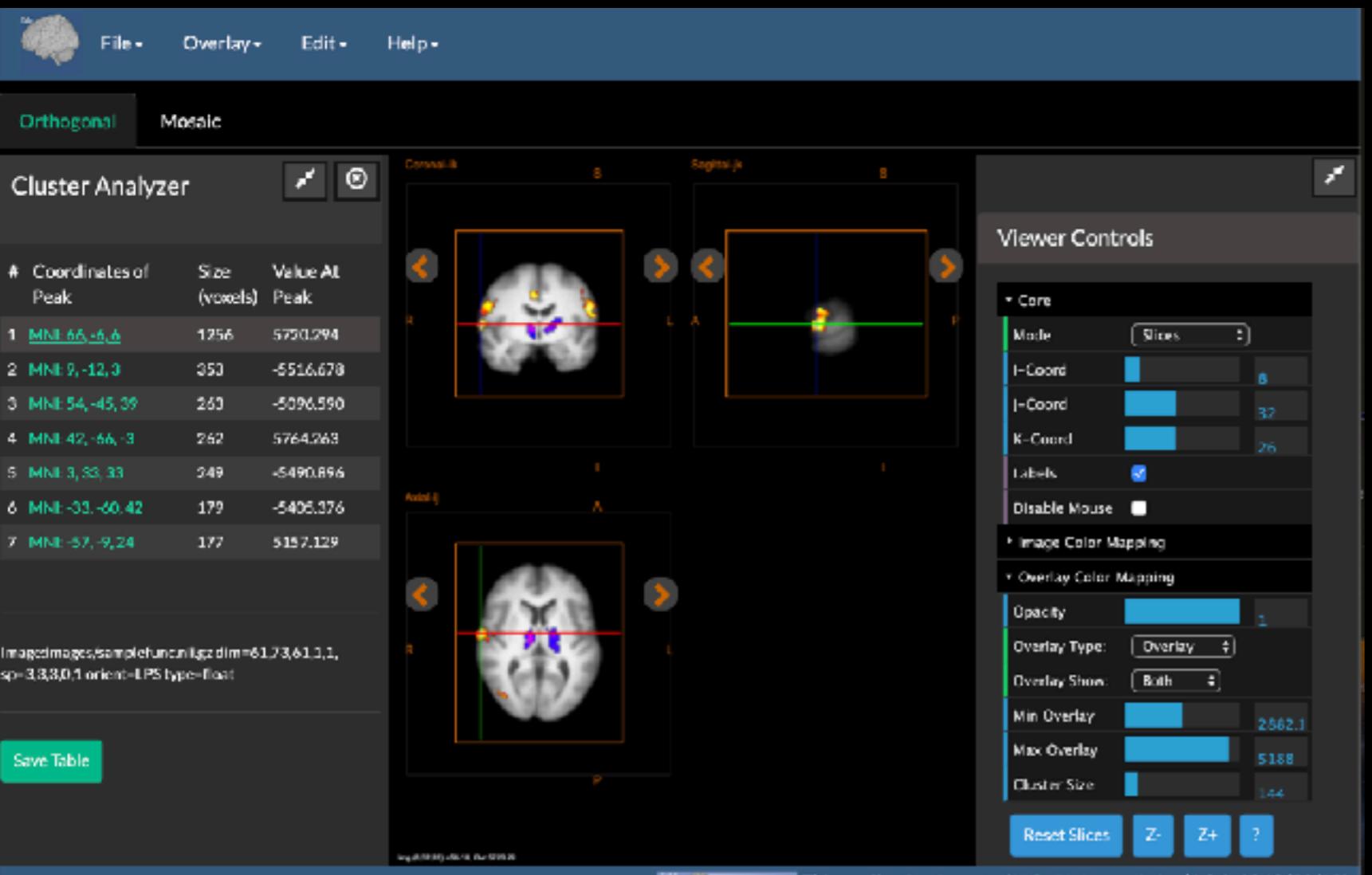
[https://github.com/SNeuroble/power\\_cluster\\_failure/tree/master/hcpTask/liveFigures](https://github.com/SNeuroble/power_cluster_failure/tree/master/hcpTask/liveFigures)




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# CLUSTER REPORTER

## Overlay Viewer



## Directions

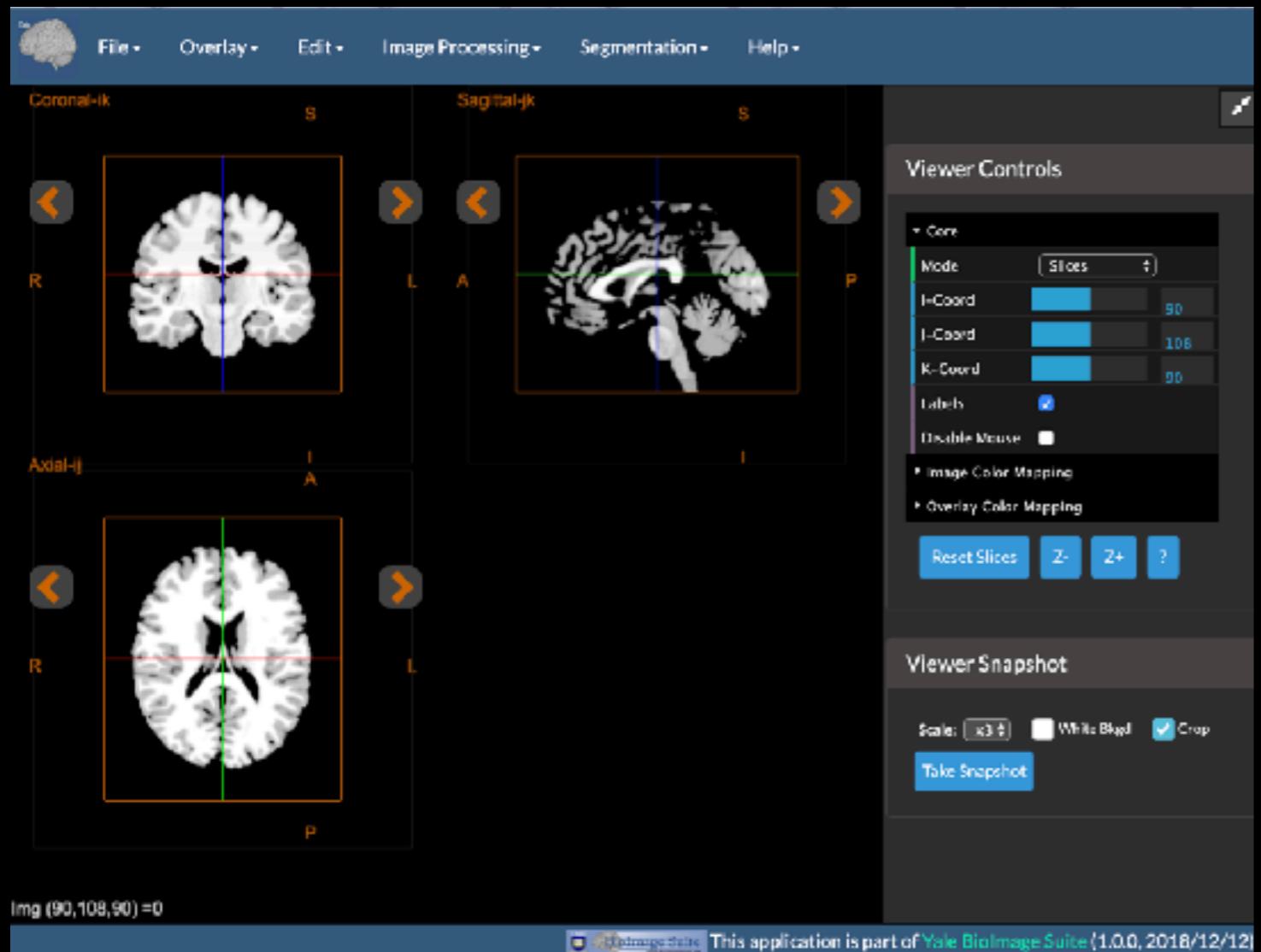
1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool
4. Play with this
  1. Go to Coordinates of Peak
  2. Automatically updates for new Min Overlay and Cluster Size
  3. Can click peak coordinates
5. Cluster Analyzer > Save Table




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

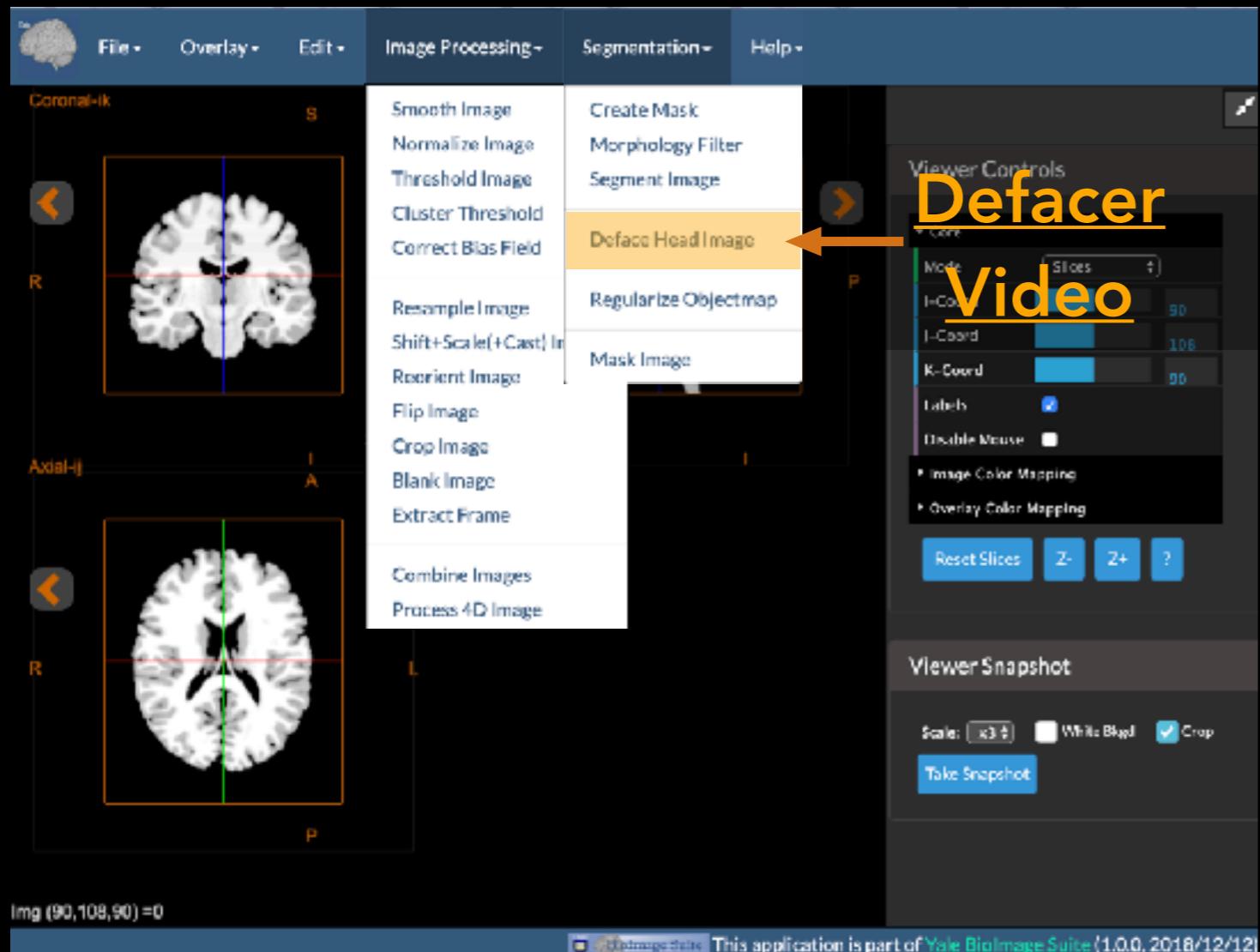
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"

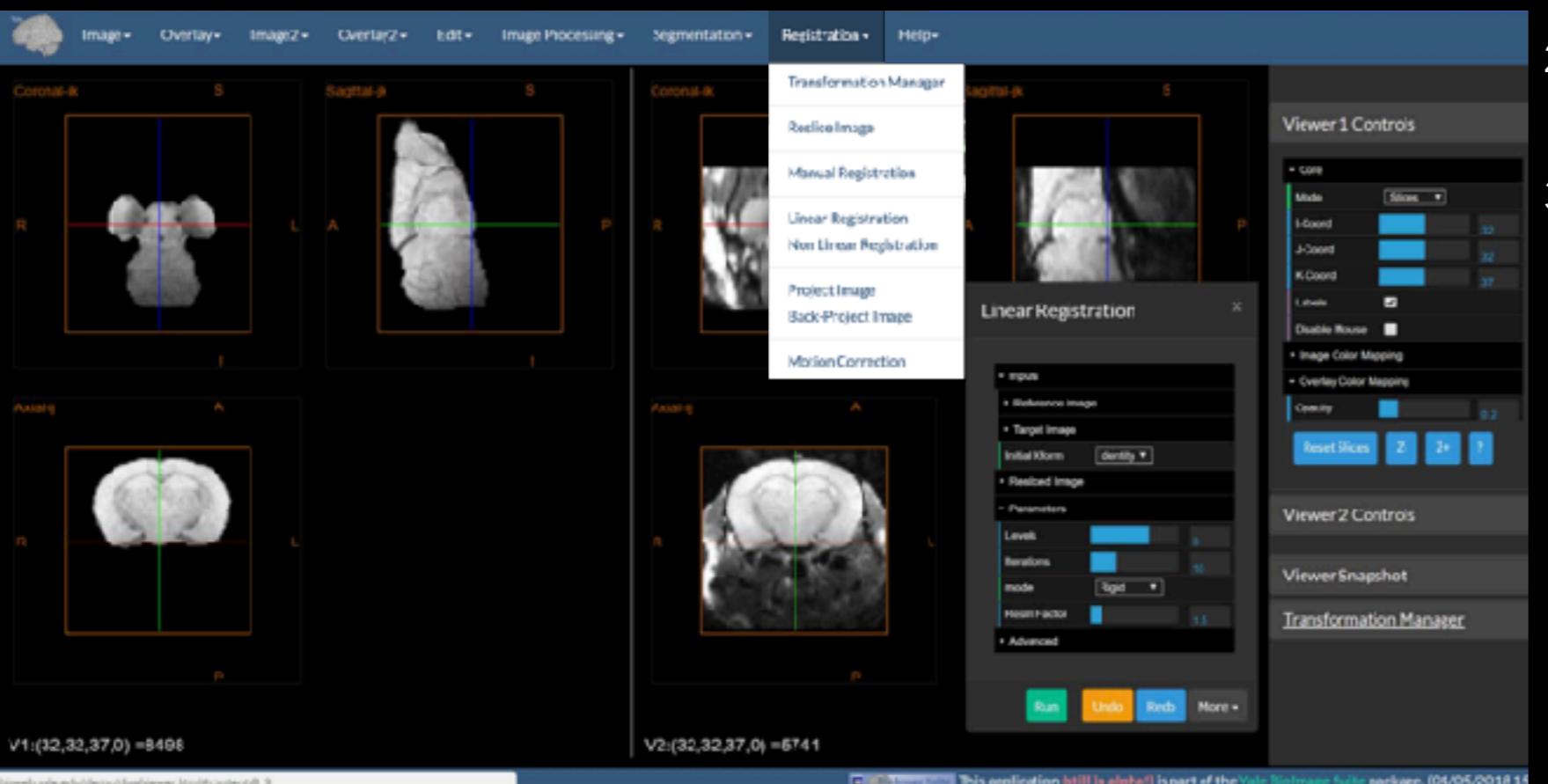




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# IMAGE PROCESSING

## Dual Viewer Tool



### Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo

#### 1. Image Processing > Smooth Image

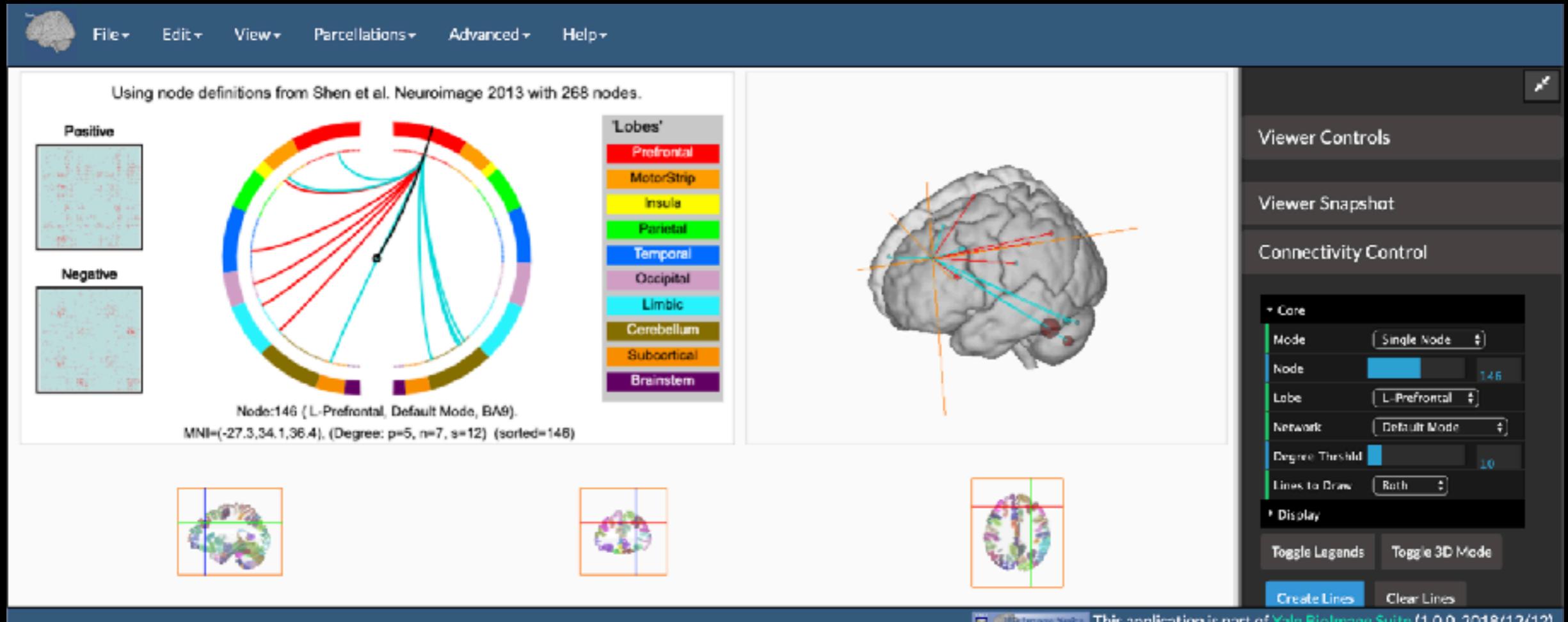
1. Sigma = 5mm
2. Click "Smooth"
3. File > Save Image (for next step)

#### 2. Image Processing > Combine Images

1. File > Load MNI T1 (1mm)
2. Overlay > Load Overlay (load smoothed image from above)
3. Input 1: Image, Input 2: Overlay
4. Operation: Subtract
5. Click "Execute"



# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices
3. Play with Viewer Controls
  1. Click around
  2. Connectivity Control > Mode: All
  3. Click "Chord Plot", "Summary Matrix"
  4. Click "Export as PNG"

Follow along in the app:



[www.bioimagesuite.org](http://www.bioimagesuite.org)





# REGRESSION TESTS

Biopsy your software!

[www.bioimagesuite.org](http://www.bioimagesuite.org)

BioImage Suite Web Display Regression Test Runner

First: 1 Last: 10 Run Single Test Run Multiple Tests

Orthogonal Mosaic

Viewer Controls

Score Mode Slices

i-Coord j-Coord k-Coord Labels

Test: 2 <= 1.000 PASSED

← → ⌛ ⌂ https://bioimagesuiteweb.github.io/webapp/biswebtest.html

BioImage Suite Web Regression Test Runner

First: 0 Last: 87 Testname: computeCorrelation WebWorker Run Tests

Running Tests

Executing tests 0:87 (Max index=87). Only running tests with name=computeCorrelation

**Test 3: computeCorrelation**

- Command: computeCorrelation -i testdata/ButterWorthOutput.csv --zscore false
- Test details: --test\_target testdata/newtests/goldcorrelation.matr --test\_type matrix --test\_comparision ssd --test\_threshold 0.01
- Should pass: true

... test execution time=0.21s  
... WASM memory size=16 MB.

Test completed, now checking results.

Comparing matrix using ssd and threshold=0.01 Module computeCorrelation test passed.  
deviation (ssd) from expected: 2.537576312709809e-7 < 0.01

► Details

Tests for version=2018/09/03: completed=1/88, passed=1/88, failed=0/88, skipped=87/88

```
{
  "command": "computeCorrelation -i testdata/ButterWorthOutput.csv --zscore false",
  "test": "--test_target testdata/newtests/goldcorrelation.matr --test_type matrix"
}
```

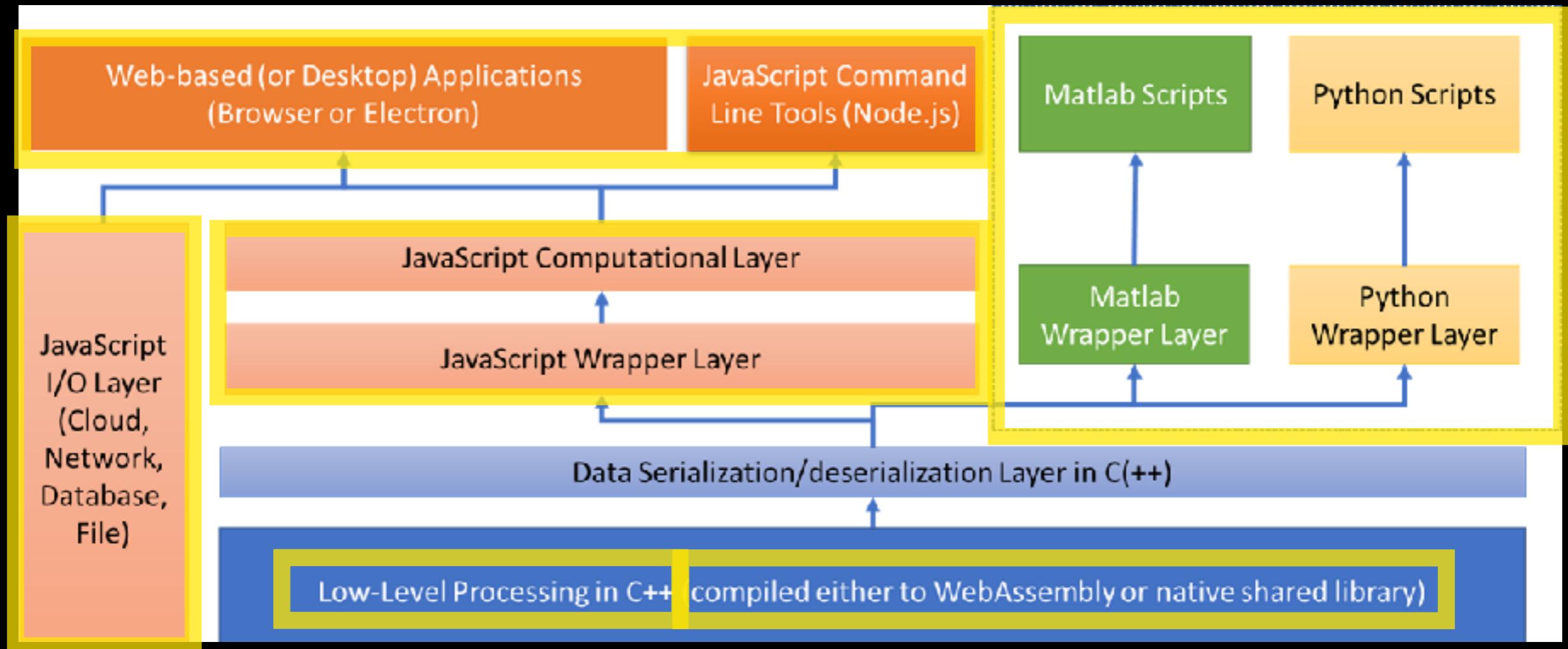
## Directions

1. Developer Info > Run Display Regression Tests
  1. Click "Run Multiple Tests"
  2. Can also run Module Regression Tests
  1. Specify module to test under "Testname"



# ARCHITECTURE

No installation!  
No servers!



Makes C++ usable in browser



Compared with native C++:

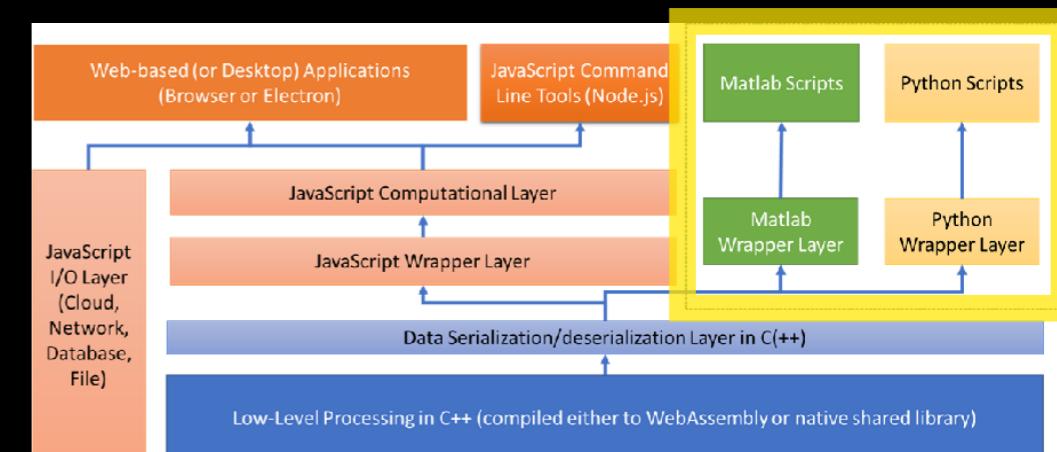
JavaScript 50% speed

WebAssembly 90% speed



# ARCHITECTURE

Example of **Individualized Parcellation** module called by Matlab, Python, and JavaScript (Salehi et al., 2018)



**JS** (js/modules/individualizedParcellation.js)

```
let paramobj= { 'numberofexemplars' : vals.numregions, "usefloat" : true , "saveexemplars": saveexemplars };
this.outputs['output']= await biswrap.individualizedParcellationWASM(fmri, group, paramobj, vals.debug);
```

**Python** (python/modules/individualizedParcellation.py)

```
paramobj= {
    'numberofexemplars' : vals['numregions'],
    'usefloat' : self.parseBoolean(vals['usefloat']),
    'saveexemplars' : self.parseBoolean(vals['saveexemplars']),
};

self.outputs['output']=libbis.individualizedParcellationWASM(fmri,group,paramobj,debug);
```

**Matlab** (matlab/test\_indiv.m)

```
paramobj.numexemplars=numexemplars;
paramobj.usefloat='true';
paramobj.saveexemplars='false';
indiv_ptr=lib.individualizedParcellationWASM(fmri_smoothed,resliced_group, paramobj,debug);
```



# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

1. Install node (<https://nodejs.org/en/download/>)
2. Install BISWeb tools: sudo npm install -g biswebnode

Done!

Example usage:

- Image processing: **biswebnode smoothImage -h**
- Regression tests: **biswebnode regressiontests --last 20 --run 1**



```
(steph@stephanies-MacBook-Pro data)$ biswebnode linearRegistration
+++++
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....
.... BioImage Suite Web user preferences loaded from /Users/steph/.bisweb
.... {"orientationOnLoad": "None", "snapshotScale": 2, "snapshotToWhite": true, "fileSource": "local", "showWelcome": true, "favoriteFolders": [], "internal": false, "darkMode": false}
+++++
+++++ Executing module linearRegistration
+++++
---- Not enough arguments passed to run this tool

Usage: biswebnode linearRegistration [options]

Options:
  -V, --version          output the version number
  --dorestlice [s]        If true also output a resliced targed image using the current transform
  --norm [s]              If true normalize input intensities by saturating using cumulative histogram
  --intscale [n]           Determines the intensity scaling post image normalization
  --numbins [n]            Number of bins in joint histogram
  --imagesmoothing [n]   Amount of image smoothing to perform
  --metric [s]             Metric to compare registration
  --optimization [s]      Optimization Method
  --steps[1..n]            Number of steps to run
  --levels[1..n]           Number of levels to run
  --iterat[1..n]           Number of iterations to run
  --resolu[n|m|p]          Resolution level (n), (m) or (p)
  --debug                Run in debug mode
  --steps[1..n]            Number of steps to run
  --mode [r|s|h]           Mode: registration (r), segmentation (s) or help (h)
  --usehead               Use headless mode
  --r --ref                Reference image
  --t --tar                Target image
  --initial               Initial transformation
  --o --out                Output directory
  --reslic[n|m|p]          Resolution level (n), (m) or (p)
  --param[1..n]             Parameters
  --silent                Run in silent mode
  -h, --he                Help

[steve@stephanies-MacBook-Pro data]$ biswebnode regressiontests --last 20 --run 1
+++++
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....
.... BioImage Suite Web user preferences loaded from /Users/steve/.bisweb
.... {"orientationOnLoad": "None", "snapshotScale": 2, "snapshotToWhite": true, "fileSource": "local", "showWelcome": true, "favoriteFolders": [], "internal": false, "darkMode": false}
+++++
+++++ Executing module regressiontests
+++++
---- Loaded all inputs.
0000
0000 Loaded all inputs.
0000
0000 Parsed : {"first":0, "last":20, "testname": "", "run": 1, "testlist": "", "testdir": "", "debug": false}
0000
0000 Invoking module RegressionTest ...
0000 invoking: testmodule with vals {"first":0, "last":20, "testname": "", "run": true, "testlist": "", "testdir": "", "debug": false}
[19:13:26] /usr/local/lib/node_modules/biswebnode/lib/mocha /usr/local/lib/node_modules/biswebnode/test/test.module.js --first 0 --last 20
+++++
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....
[19:13:26] Beginning module tests
[19:13:26]   Testscript: node /usr/local/lib/node_modules/biswebnode/lib/bisweb-test.js /usr/local/lib/node_modules/biswebnode/test
[19:13:26]   Reading: https://bioimagesuiteweb.github.io/test/module_tests.json
[19:13:26]   Running tests: 0 : 20 out a total of 98 tests. Filter name=all
    / (19:13:26)   This is a required placeholder to allow before() to work
[19:13:26] -----
[19:13:26] ----- test 0 -----
[19:13:26] /var/local/lib/node_modules/biswebnode/test/node /usr/local/lib/node_modules/biswebnode/lib/bisweb-test.js smoothImage -sigma 2.0 -radiusfactor 2.0
N1_2mm_resliced.nii.gz --test_target testdata/newtests/goldsmooth2sigma.nii.gz --test_base_directory https://bioimagesuiteweb.github.io/test/
[19:13:26] -----
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
```



# CONTRIBUTIONS WELCOME!

Find resources on the web app “Documentation” tab

- Youtube tutorials
- User docs
- Developer docs
- ...and more!

Repo: <https://github.com/bioimagesuiteweb/bisweb>



# ACKNOWLEDGMENTS



## NeuroPRISM Lab



Alex Fischbach  
**Hallee Shearer**

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Eric Bridgeford (Johns Hopkins)  
  
Argyris Stringaris (UCL) &  
Dylan Nielson (NIMH)  
  
Joshua Curtiss (Northeastern)  
  
Amanda Mejia (Indiana)  
  
Thomas Nichols (Oxford)  
  
Luiz Pessoa (Maryland)  
  
Marisa Spann (Columbia)  
  
Jia-Hong Gao (Peking) &  
Guoyuan Yang (SJTU)  
  
Daniel Barron (Yale)  
  
Karim Ibrahim (Yale)  
  
Chris Benjamin (Yale)



NAPLS



NSF GRFP  
DGE1122492

NIH DSPAN F99/K00  
F99NS108557  
K00MH122372

NIH BRAIN K99/R00  
K99MH130894  
R00MH130894



# THANK YOU! QUESTIONS?



 sNeuroble

 @sNeuroble

 sNeuroble