

# Characterizing the Stability of Neuroimaging Analyses Through Perturbations in Experimental Design

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# Outline

- Background & Overview
- Chapter 1: Scalable and Provenance Rich Pipeline Deployment (Clowdr)
- Chapter 2: Evaluating the Stability of Neuroimaging Pipelines & Analyses
- Chapter 3: Exploring Sources of Instability & Dependence Within Pipelines
- Conclusion

# Background & Overview

# Reproducibility in Neuroscience

- Noisy data and incomplete statistics can lead to spurious results (Bennett et al., 2011) (fMRI)
- Operating system differences have led to different results (Glatard et al., 2015) (sMRI)
- Dominant software libraries have inflated false-positive rates (Eklund et al., 2016) (fMRI)
- 1-voxel perturbations to inputs result in significantly different outputs (Lewis et al., 2016) (sMRI)
- Similar tools performing similar operations give different results (Bowring et al., 2018) (fMRI)

# Currently missing in neuroimaging:

1. Infrastructure for easily running and capturing “repro-analyses” at scale  
→ I have created an infrastructure for this purpose
  
2. A consistent method for evaluating the stability of results and tools  
→ I will develop a metric for evaluating stability of neuroimaging analyses
  
3. Methods for identifying sources of instability within pipelines  
→ I will use the metric above to explore the impact of individual processes on pipeline stability

(and, applications of “repro-analyses” to diffusion neuroimaging, which I will focus on)

# Chapter 1: Scalable and Provenance Rich Pipeline Deployment (Clowdr)

1 year; complete

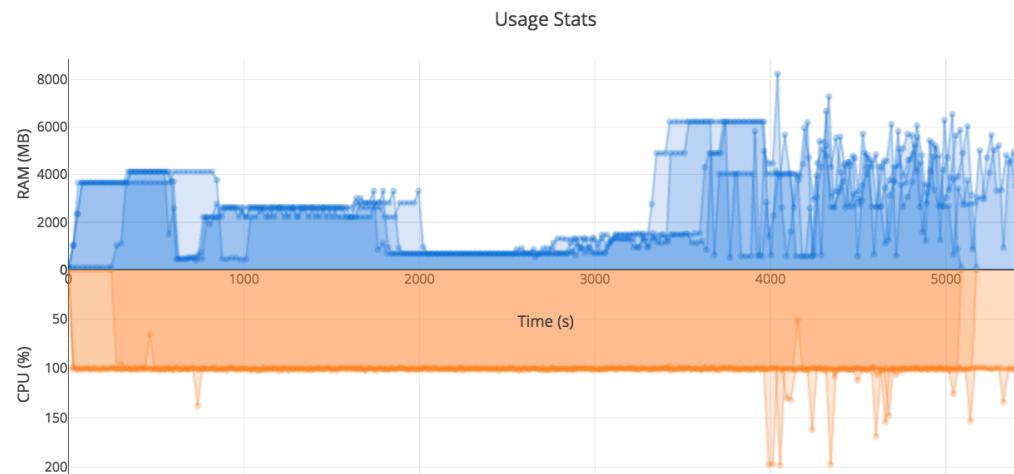
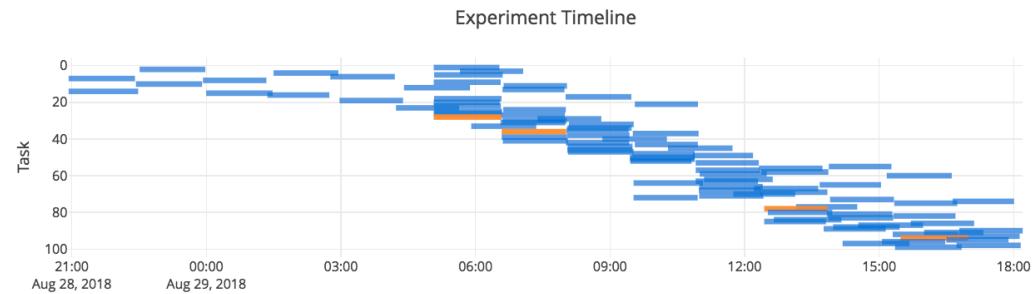
# Clowdr is...

- Server-less microtool for running pipelines at scale on HPC and cloud systems
- Captures system-level provenance information (i.e. CPU/RAM usage) and Reprozip
- Provides an interactive web-report for exploring and sharing experiments.

# Clowdr Experiment Explorer

Statistics			Invocations			
	▲Task	analysis_level	bids_dir	modality	output_dir	participant_label
0	0	participant	/data/hcp1200_mir	func	/data/hcp1200_mir	100206
1	1	participant	/data/hcp1200_mir	func	/data/hcp1200_mir	100307
2	2	participant	/data/hcp1200_mir	func	/data/hcp1200_mir	100408
3	3	participant	/data/hcp1200_mir	func	/data/hcp1200_mir	100610
4	4	participant	/data/hcp1200_mir	func	/data/hcp1200_mir	101006
5	5	participant	/data/hcp1200_mir	func	/data/hcp1200_mir	101107

FILTER ROWS



(Kiar, 2018; in review)

# Analysis with Clowndr

```
$ # Installable on Python3...
$ pip install clowndr
$
$ # Run locally/on clusters, the cloud, and share results
$ clowndr local {tool} {invocation} {dataset} {output loc}
$ clowndr cloud {tool} {invocation} {dataset} {output loc} {cloud} {keys}
$ clowndr share {task loc} # {task loc} returned by any of the above
$
```

# Chapter 2: Evaluating the Stability of Neuroimaging Pipelines & Analyses

1.5 years (total: 2.5 years)

# In linear systems, this has been solved

Condition number of  $\mathbf{A}\mathbf{f} = \mathbf{x}$  can be evaluated as:

$$\kappa(\mathbf{A}) = \|A\| \|A^{-1}\| \geq \max_{x, f(x) \neq 0} \frac{|\delta f(x)| / |f(x)|}{|\delta x| / |x|}$$

”  $\delta f(x) = f(x + \delta x) - f(x)$

maximum ratio of change in output,  $f$ ,  
with respect to change in input,  $x$ .

”

(Davidson, 1981)

# Applications in Diffusion Tensor Imaging

DWI tensor model:  $S_i = S_0 e^{-b\mathbf{g}_i^T \cdot \mathbf{D} \cdot \mathbf{g}}$

We can rearrange this with a couple clever substitutions...

# Applications in Diffusion Tensor Imaging

DWI tensor model:  $S_i = S_0 e^{-b \mathbf{g}_i^T \cdot \mathbf{D} \cdot \mathbf{g}}$

We can rearrange this with a couple clever substitutions...

$$\mathbf{X} = (D_{xx}, D_{yy}, D_{zz}, D_{xy}, D_{xz}, D_{yz})^T$$

$$a_i = (g_{ix}^2, g_{iy}^2, g_{iz}^2, 2g_{ix}g_{iy}, 2g_{ix}g_{iz}, 2g_{iy}g_{iz})$$

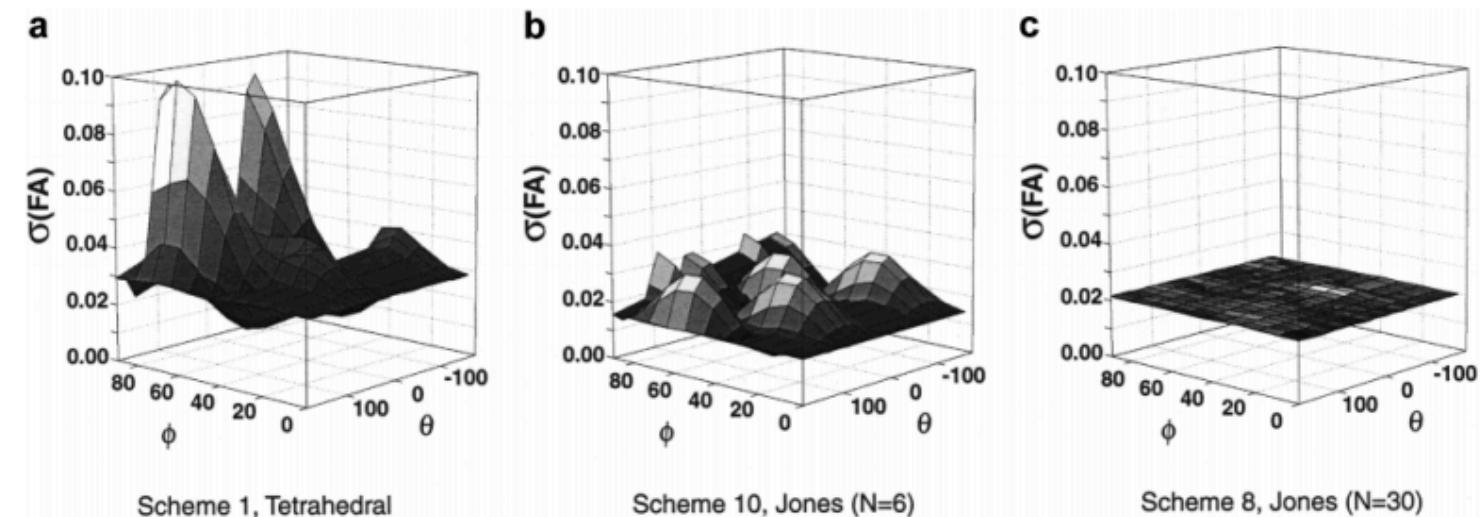
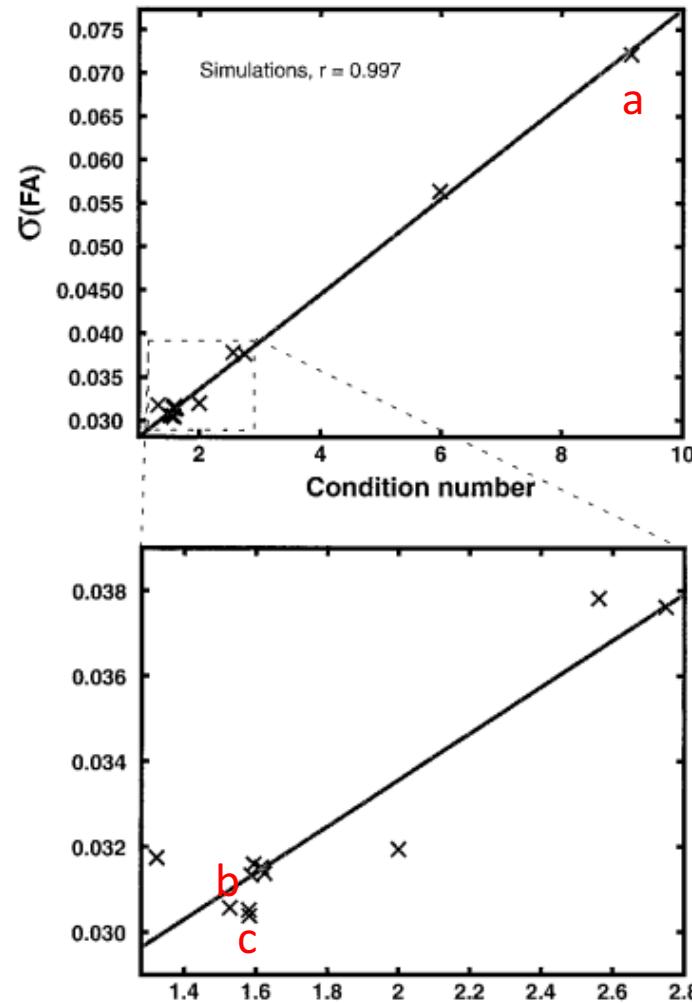
$$a_i^T \mathbf{X} = \ln(S_0/S_i)/b = ADC_i$$

$$\mathbf{ADC} = (ADC_1, ADC_2, \dots, ADC_N)^T \quad \mathbf{A} = (a_1, a_2, \dots, a_N)^T$$

**A**X = **ADC** ... which is the same form as earlier

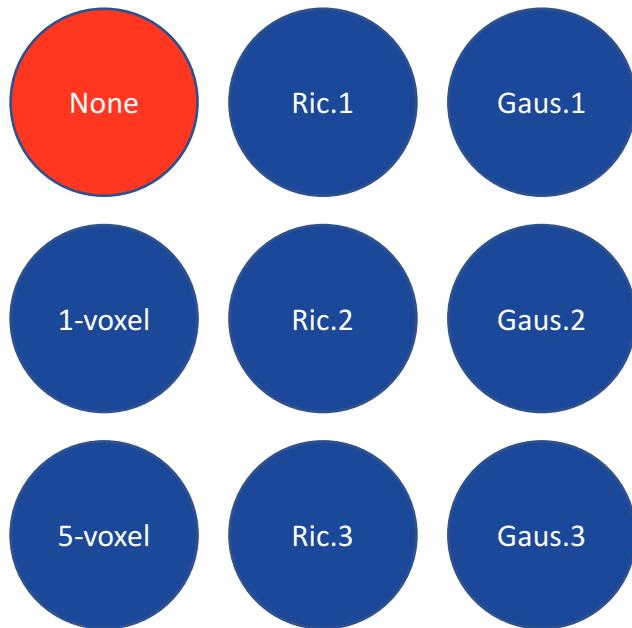
(Skare, 2000)

# Stability of Tensor Estimation



(Skare, 2000)

# Example comparison: noise effects



$\mathcal{A}$  : None, N-voxel, Ric., Gaus.

$\mathcal{D}$  : None

$\mathcal{A} - \mathcal{D}$  : Rician, N-voxel, Gaussian

"

*How similar are connectomes with no noise to those with Rician-, N-voxel- and Gaussian-noise?*

"

$$\kappa(\mathbf{A}) \geq \max_{x, f(x) \neq 0} \frac{|\delta f(x)|/|f(x)|}{|\delta x|/|x|}$$

# Evaluating stability with respect to data

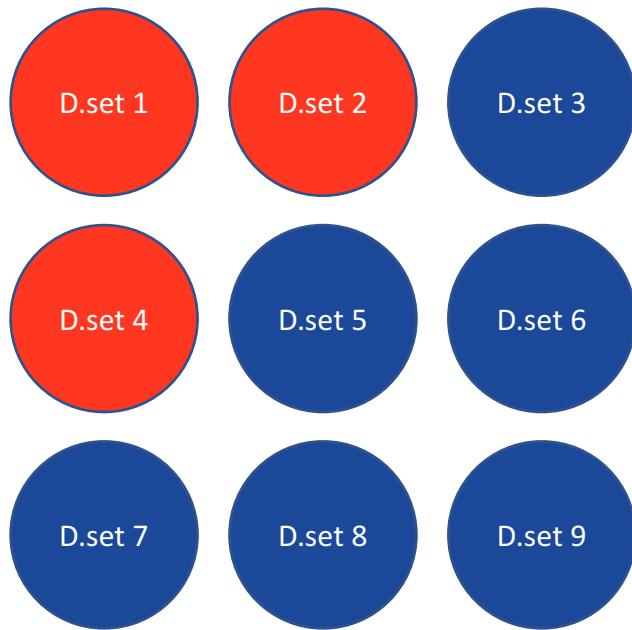
In this case,  $\mathcal{A}$  describes {datasets, subjects, noise, etc.}.

$$\hat{\kappa}(\mathcal{A}, \mathcal{D}) \geq \max_{x, x_d} \frac{\|f(x_d) - f(x)\|_R / \sigma_{f(x)}}{\|x_d - x\|_I / \sigma_x}$$

$$x_d \in \mathcal{D}$$

$$x = x_d - \delta x \in \mathcal{A} - \mathcal{D}$$

# Example: Evaluating dataset effects



$\mathcal{A}$  : D.set {1,2,3,4,5,6,7,8,9}

$\mathcal{D}$  : D.set {1,2,4}

$\mathcal{A} - \mathcal{D}$  : D.set {3,5,6,7,8,9}

"

How similar are connectomes from datasets {1,2,4} to those from datasets {3,5,6,7,8,9}?

"

# Example: Evaluating tool effects



$\mathcal{A}$  : FSL, MRtrix, Dipy

$\mathcal{D}$  : FSL

$\mathcal{A} - \mathcal{D}$  : MRtrix, Dipy

"

*How similar are connectomes from FSL to those from MRtrix/Dipy?*

"

$$\hat{\kappa}(\mathcal{A}, \mathcal{D}) \geq \max_{x, x_d} \frac{\|f(x_d) - f(x)\|_R / \sigma_{f(x)}}{\|x_d - x\|_I / \sigma_x}$$

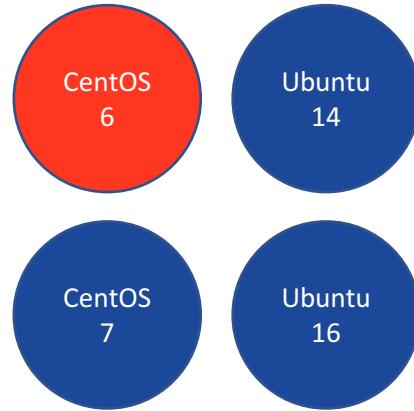
# Evaluating stability with respect to tool

In this case,  $\mathcal{A}$  describes {tool, operating system, etc.}.

$$\hat{\kappa}_t(\mathcal{A}, \mathcal{D}, \mathbf{x}) \geq \max_{x \in \mathbf{x}} \|f_d(x) - f(x)\|_R / \sigma_{f_d}$$

$$f \in \mathcal{A} - \mathcal{D} \quad f_d \in \mathcal{D}$$

# Example: Evaluating OS effects



$\mathcal{A}$  : CentOS, Ubuntu

$\mathcal{D}$  : CentOS 6

$\mathcal{A} - \mathcal{D}$  : CentOS 7, Ubuntu

"

*How similar are connectomes generated on CentOS 6 to those generated on CentOS 7 and Ubuntu?*

"

# Experiment: Estimating Stability

<b>Purpose</b>	Characterizing the instability and variability of analyses		
<b>Outcomes</b>	<ul style="list-style-type: none"><li><input type="checkbox"/> Metric for evaluating the stability of analyses with respect to dependent experimental variables</li><li><input type="checkbox"/> Exploration of the variability introduced in Diffusion MRI experiments by dataset, noise, and tool selection</li></ul>		
<b>Datasets</b>	<b>Modality</b>	<b>Derivatives</b>	<b>Tools</b>
Consortium of Reproducibility and Reliability	Diffusion MRI, Structural MRI (Functional MRI)*	Structural Connectomes (Functional Activation Maps)*	Dipy, FSL, MRtrix (SPM, AFNI, FSL)*
<b>Experiment</b>	<ul style="list-style-type: none"><li><input type="checkbox"/> Partial replication of [27] comparing conditioning to observed variance</li><li><input type="checkbox"/> Determine a space-independent proxy for conditioning</li><li><input type="checkbox"/> Process CoRR datasets using default Dipy, FSL, and MRtrix pipelines</li><li><input type="checkbox"/> Reprocess CoRR datasets with:<ul style="list-style-type: none"><li><input type="checkbox"/> 1-voxel perturbation</li><li><input type="checkbox"/> Rician noise</li><li><input type="checkbox"/> Gaussian noise</li></ul></li><li><input type="checkbox"/> Calculate conditioning across:<ul style="list-style-type: none"><li><input type="checkbox"/> Noise (fixed tool and dataset)</li><li><input type="checkbox"/> Datasets (fixed tool)</li><li><input type="checkbox"/> Tool (fixed datasets)</li></ul></li><li><input type="checkbox"/> Compare each setting, and identify axes and regions of instability</li></ul>		
<b>Notes</b>	<ul style="list-style-type: none"><li><input type="checkbox"/> *Based on collaboration with Dr. Camille Maumet, this work may be extended to cover functional MRI applications. This will leverage her experience with fMRI evaluation, and will require the development of theory similar to that presented in [27] on algorithms used in fMRI.</li></ul>		

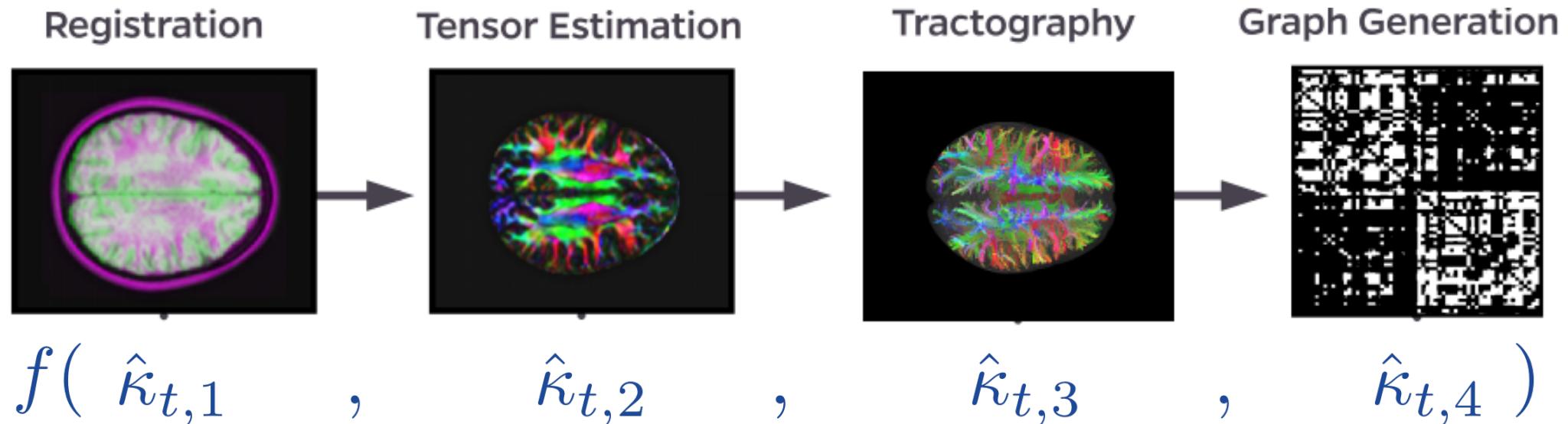
Paper 1

Paper 2

# **Chapter 3: Exploring Sources of Instability & Dependence Within Pipelines**

1 year (total: 3.5 years)

# Evaluating pipeline components



(Kiar, 2018)

# Experiment: Sources of Instability

Purpose	Explaining sources of instability and variability in tools		
Outcomes	<ul style="list-style-type: none"><li><input type="checkbox"/> Comparison of the stability of individual pipeline components with the overall tool stability</li><li><input type="checkbox"/> Identification of sources of instability in pipelines</li><li><input type="checkbox"/> Principled method for reconstructing pipelines with stable algorithms</li></ul>		
Datasets	Modality	Derivatives	Tools
Consortium of Reproducibility and Reliability	Diffusion MRI, Structural MRI	Structural Connectomes	Dipy, FSL, MRtrix
Experiment	<ul style="list-style-type: none"><li><input type="checkbox"/> Dissect structural pipelines into independently runnable components</li><li><input type="checkbox"/> For each pipeline component, beginning with the first:<ul style="list-style-type: none"><li><input type="checkbox"/> Process CoRR datasets (or derivatives of previous step) with:<ul style="list-style-type: none"><li><input type="checkbox"/> 1-voxel perturbation</li><li><input type="checkbox"/> Rician noise*</li><li><input type="checkbox"/> Gaussian noise</li></ul></li><li><input type="checkbox"/> Calculate conditioning for each component across:<ul style="list-style-type: none"><li><input type="checkbox"/> Noise (fixed tool and dataset)</li><li><input type="checkbox"/> Datasets (fixed tool)</li><li><input type="checkbox"/> Tool (fixed datasets)</li></ul></li><li><input type="checkbox"/> Compare each algorithm for each setting</li></ul></li></ul>		
Notes	<ul style="list-style-type: none"><li><input type="checkbox"/> *Rician noise will only be added to either raw MR images or minimally preprocessed MR images, since it is unexpected in other contexts.</li></ul>		

# Conclusion

# Expected collaborations

- Boutiques (Glatard)
- Enhancing data discovery and querying (Poline)

Tool Development

- Evaluating the stability of functional MRI software (Maumet)

Stability Analysis

- Mapping structural and functional connectivity (Suarez, Misic)
- Network evolution in development (Khundrakpam)
- Heritability of structural connectomes (Vogelstein, Priebe)

Connectomics

# In summary

- Replicability can be difficult to achieve and assess in neuroimaging
- I have developed a tool increasing the ease with which scientists can perform repro-analyses
- I will develop a metric for evaluating the stability of results and identify their dependence on various variables such as tool, dataset, and noise

# Acknowledgements



Fondation  
Brain Canada  
Foundation



HEALTHY BRAINS  
FOR **HEALTHY LIVES**



**NSERC**  
**CRSNG**



CANADA  
FIRST  
RESEARCH  
EXCELLENCE  
FUND

APOGÉE  
CANADA  
FONDS  
D'EXCELLENCE  
EN RECHERCHE



...

All code mentioned in this presentation is publicly available on GitHub.

# Thanks!

Find me @



gkiar



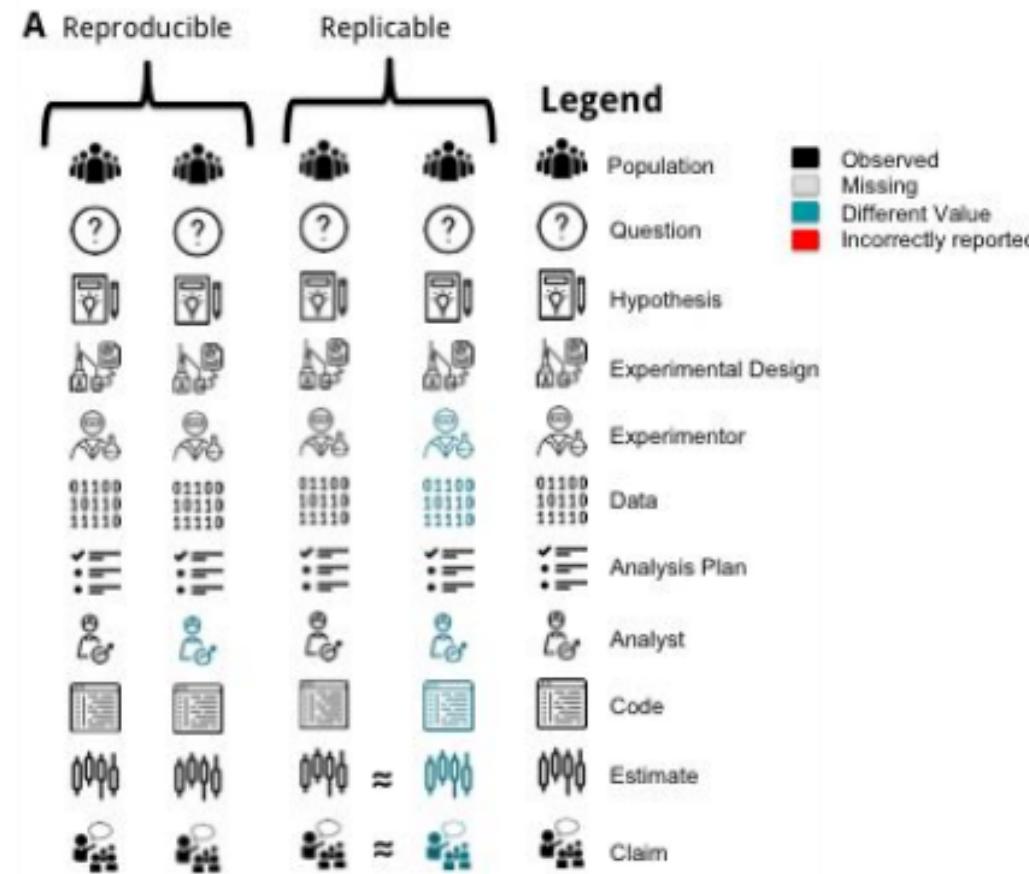
g\_kiar



greg.kiar@mcgill.ca

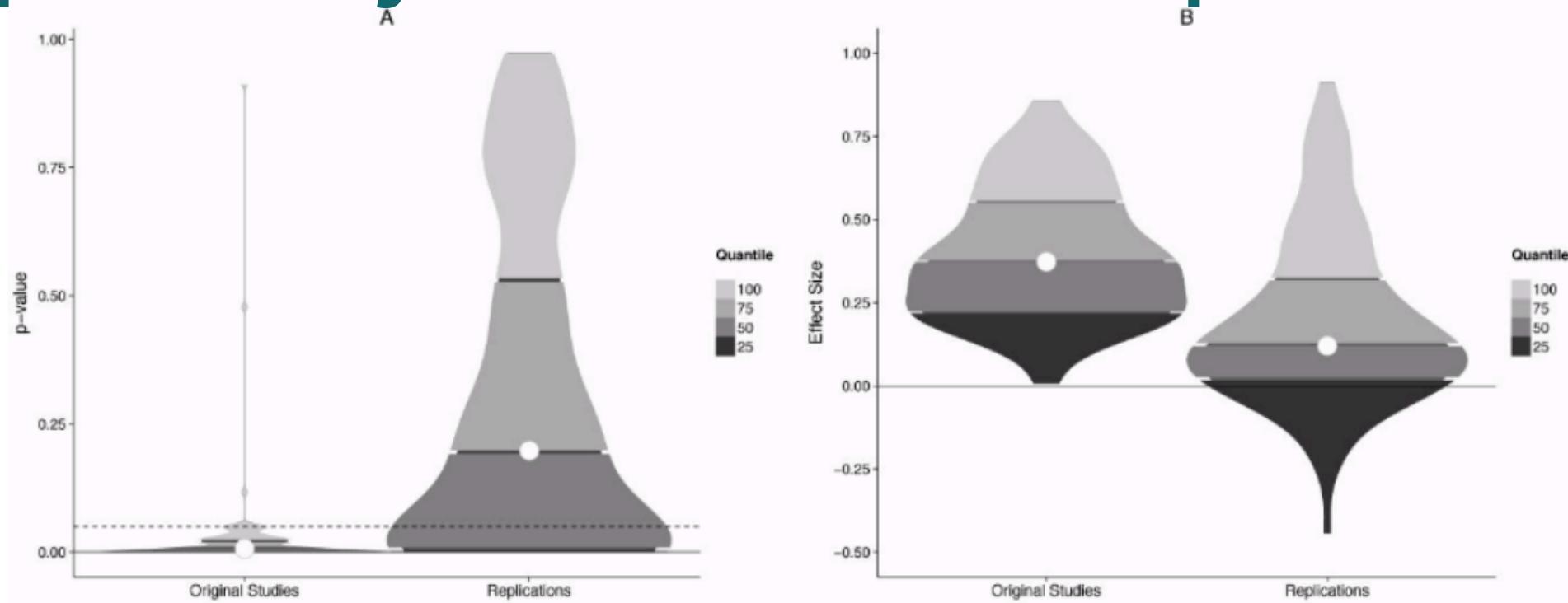
# Extras

# Reproducibility or Replicability?



(Patil, 2016)

# Replicability is a measurable problem



**Fig. 1. Density plots of original and replication *P* values and effect sizes. (A) *P* values. (B) Effect sizes (correlation coefficients).** Lowest quantiles for *P* values are not visible because they are clustered near zero.

(Open Science Collaboration, 2015)

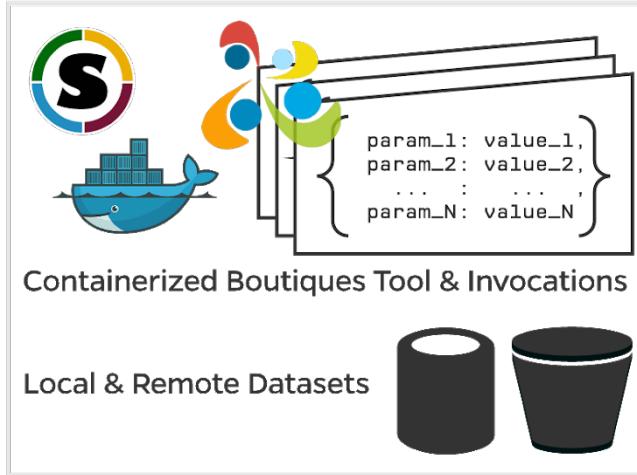
# Many tools make analyses accessible

- Standards for **data and code interoperability** increase re-usability
    - ... but, require in depth knowledge of the data/code in question
  - **Software virtualization** allows for portable code deployment
    - ... but, different virtualizations are required for different systems
  - **Workflow engines** enable constructing graphs between processing steps
    - ... but, are tied to specific programming languages and constructs
  - Capturing **provenance** records informs analysis and future experiments
    - ... but, provenance tools and standards are typically complex and unintuitive
  - Navigating through **web platforms** is user-friendly and intuitive
    - ... but, they are bulky and don't allow for the development or prototyping of tools and analyses
-

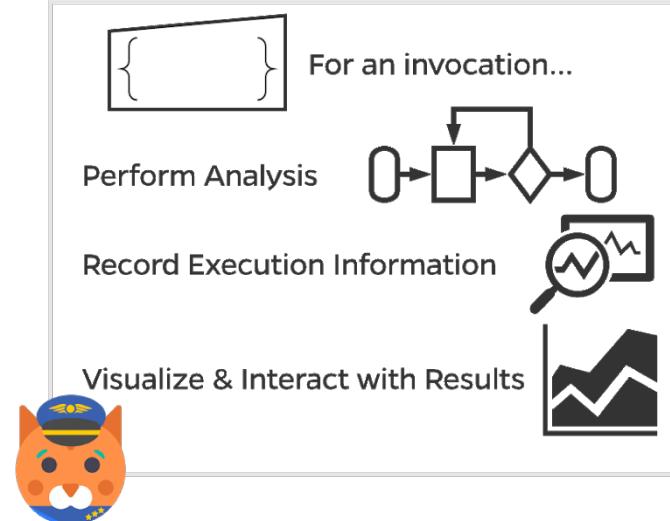
# Clowdr ...

- is based on **Boutiques** and is **BIDS-aware**
- runs bare-metal and **Docker/Singularity** virtualized tools on **HPC** systems and **clouds**
- supports the **batch deployment** of pipelines constructed with **workflow-engines**
- captures system-level provenance information (i.e. **CPU** and **RAM** usage) and **Reprozip**
- supports both **development-** and **production-level** tools without an active server, and provides a **web-report** for exploring and sharing experiments.

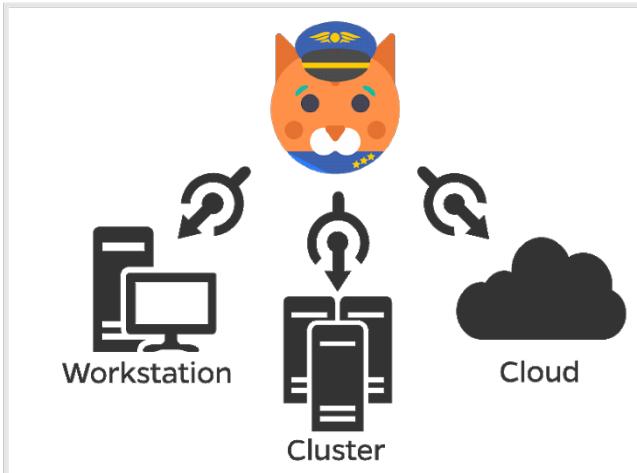
## 1. Curate experiment



## 2. Develop experiment locally



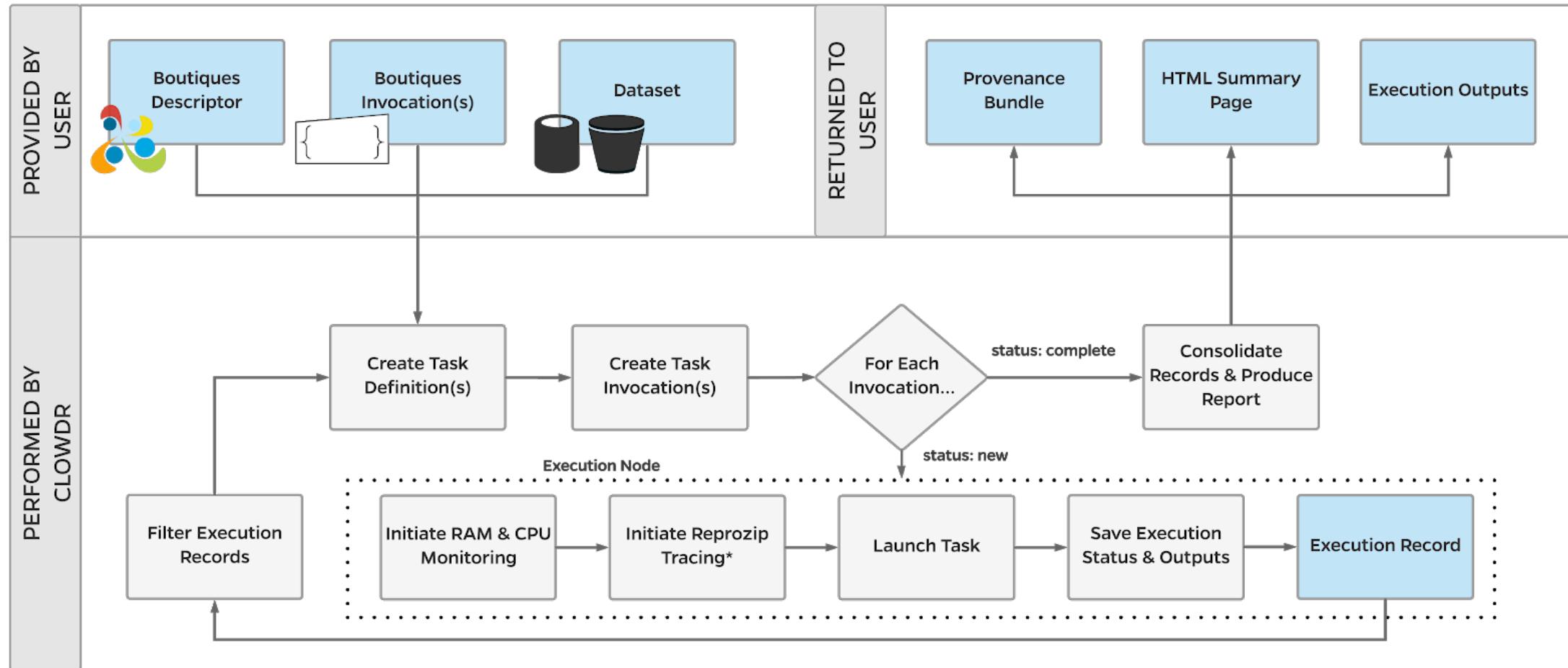
## 3. Deploy at scale



## 4. Share & re-run experiment



(Kiar, 2018; in review)

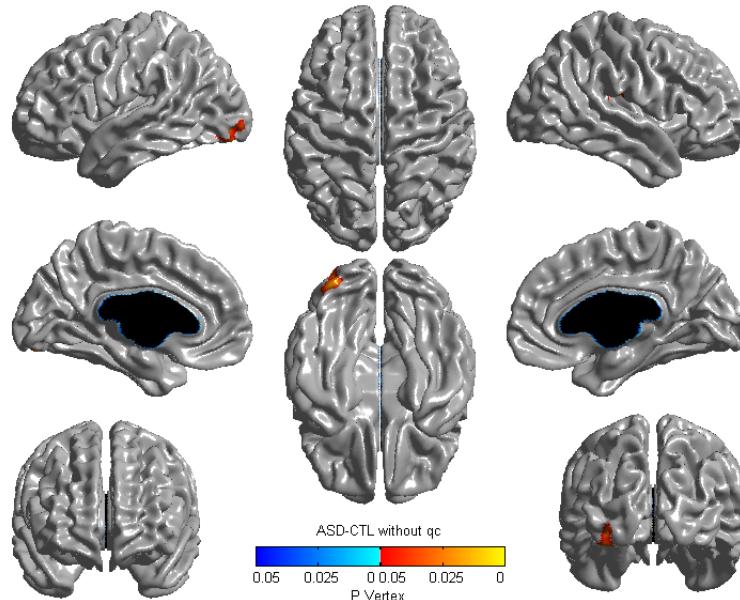


(Kiar, 2018; in review)

# Differences in ABIDE nulled with motion

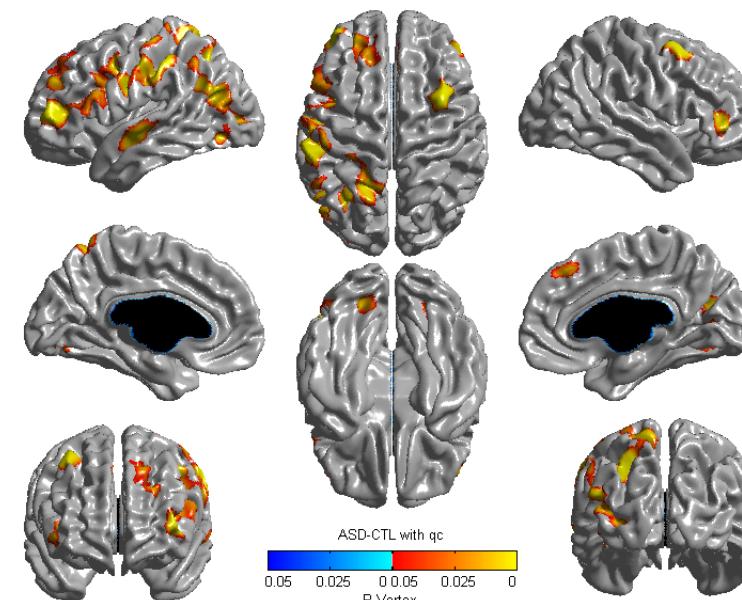
N ~ 1100

Data including subjects with motion



N ~ 400

Data with quality control



Stability of processing and strictness of quality control can meaningfully change resulting scientific claims (Khundrakpam et al., 2017)

# Expected Contributions to knowledge

- Accessible and portable tool for reproducible experiments
- Method for evaluating stability and tool-dependence in neuroimaging
- Method for identifying the sources of instability within pipelines