Poster ID 1977

The Configurable Pipeline for the Analysis of Connectomes (C-PAC) 2020-21: Transitioning Out of Beta

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Introduction

The Configurable Pipeline for the Analysis of Connectomes (C-PAC) is a configurable, open-source, Nipype(Gorgolewski et al., 2011)-based, automated processing pipeline for resting state functional MRI (R-fMRI) data, for use by both novice and expert users. C-PAC is designed to bring the power, flexibility and elegance of the Nipype platform to users in a plug and play fashion—without requiring the ability to program. Using an easy to read, text-editable configuration file or a graphical user interface, C-PAC users can rapidly orchestrate automated R-fMRI processing procedures, including: quality assessment measurements, image preprocessing based upon user specified preferences, generation of functional connectivity maps (e.g., seed-based correlation analysis), customizable extraction of time-series data, generation of graphical representations of the connectomes at various scales (e.g., voxel, parcellation unit), generation of local R-fMRI measures (e.g., regional homogeneity, voxel-matched homotopic connectivity, frequency amplitude measures). At the group level, C-PAC features Connectome-Wide Association Studies, Bootstrap Analysis of Stable Clusters, Intersubject Correlation Analysis (based on BrainIAK (Kumar et al., 2020)), and integrated group statistics using FSL/FEAT (Smith et al., 2004). Users can easily extract preprocessed time-series data and connectivity matrices for analysis with other packages.

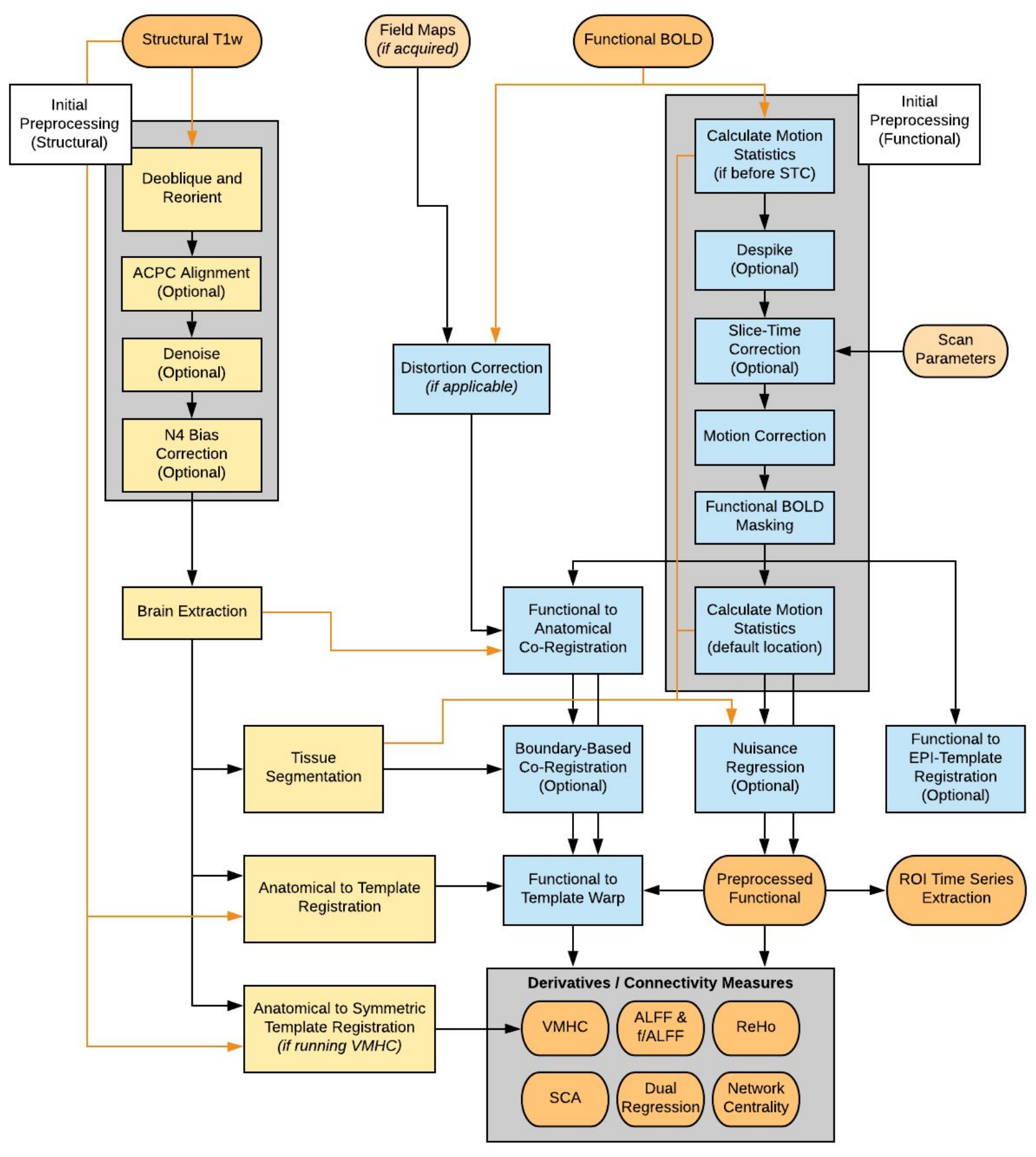
Methods

Launched in 2012, C-PAC is implemented in Python using the Nipype pipelining library, which provides mechanisms to automatically detect and exploit parallelism in a pipeline, maintain provenance, iterate over parameter settings, and restart a pipeline without re-executing previously completed steps.

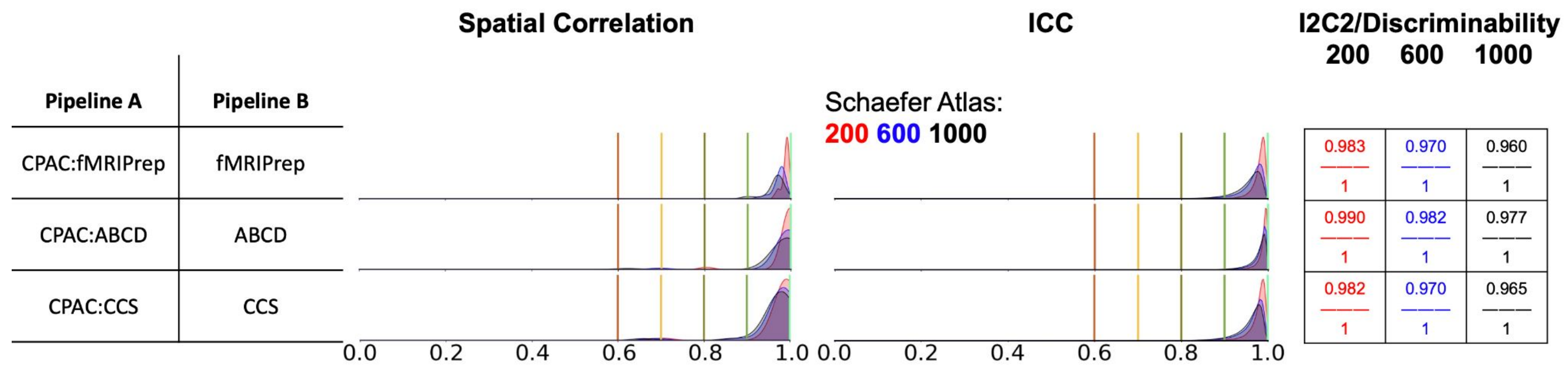
C-PAC extends Nipype functionality by providing workflows specific to connectivity analyses, functional connectivity derivatives and analyses not present in other neuroimaging packages. The C-PAC workflows are built from AFNI (Cox, 1996) and FSL (Smith et al., 2004) tools, as well as algorithms coded in Python using SciPy (Virtanen et al., 2020), NumPy (Harris et al., 2020) and scikit-learn (Pedregosa et al., 2011). C-PAC is designed to seamlessly interact with shared memory (multi-core) and cluster-based (e.g. Slurm, Sun Grid Engine) high performance computing environments to minimize computation time. Over the past two years, inspired by the needs of the BRAIN Initiative, the C-PAC team has placed an increased emphasis on implementing customizations to support nonhuman primate, rodent and longitudinal (including pre/post) studies.

Results

Comprehensive Pipeline



Harmonized Minimal Preprocessing Configurations



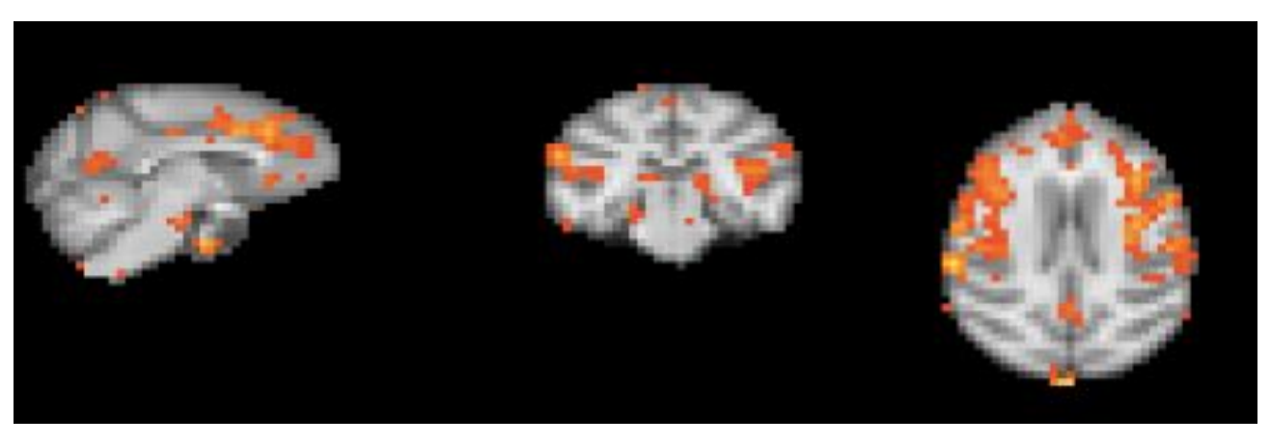
Pipeline A	Pipeline B
CPAC:fMRIPrep	fMRIPrep
CPAC:ABCD	ABCD
CPAC:CCS	CCS

I2C2/Discriminability

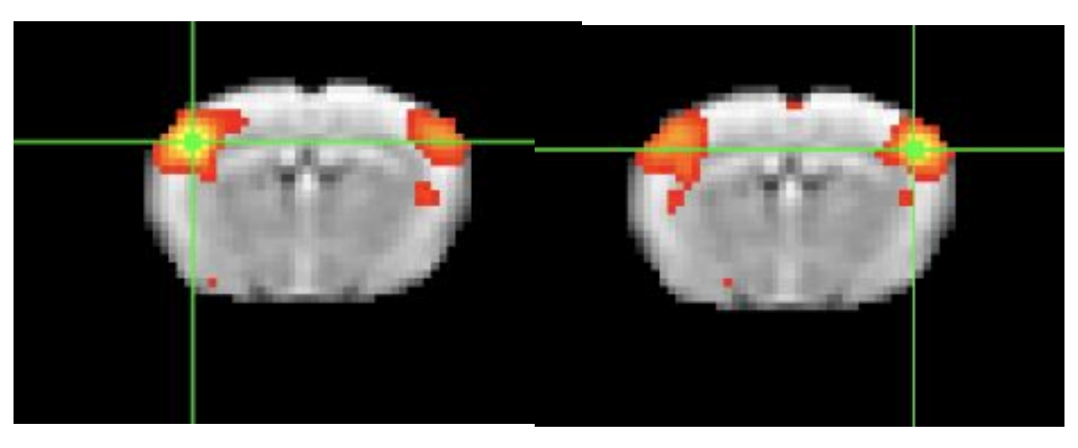
200	600	1000
0.983 / 1	0.970 / 1	0.960 / 1
0.990 / 1	0.982 / 1	0.977 / 1
0.982 / 1	0.970 / 1	0.965 / 1

Poster # 2405 (Li et al., Milham)
Xu et al., 2015; Esteban et al., 2018; Sturgeon et al., 2019

Optimized Nonhuman Pipelines

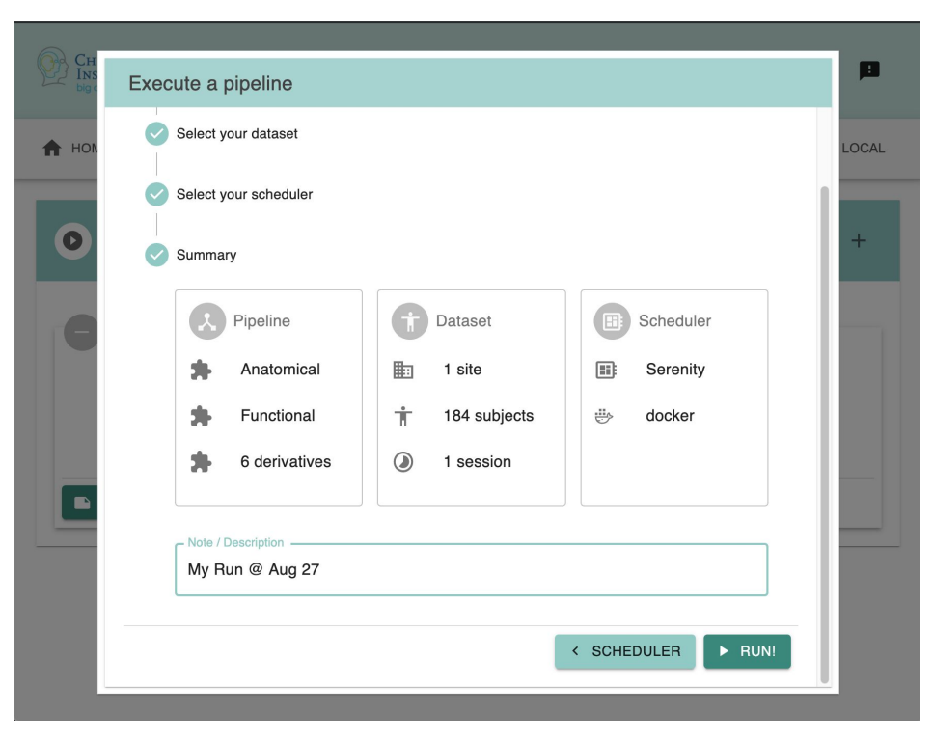


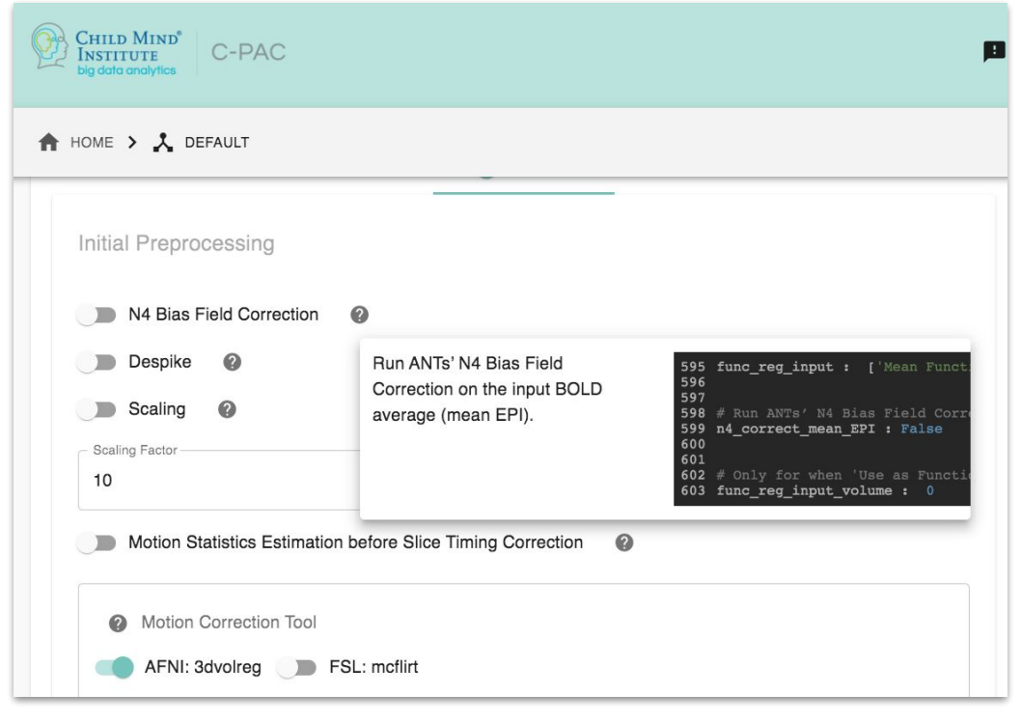
Nonhuman Primate$^{v1.8.2}$

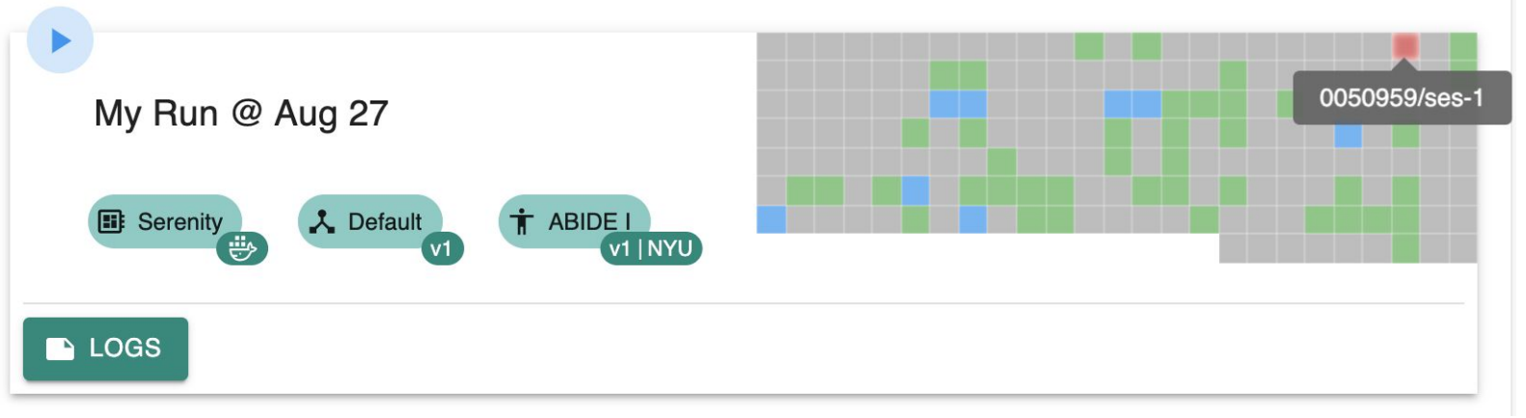


Rodent$^{v1.8.2}$

Graphical User Interface & Dashboard$^{v2.0}$

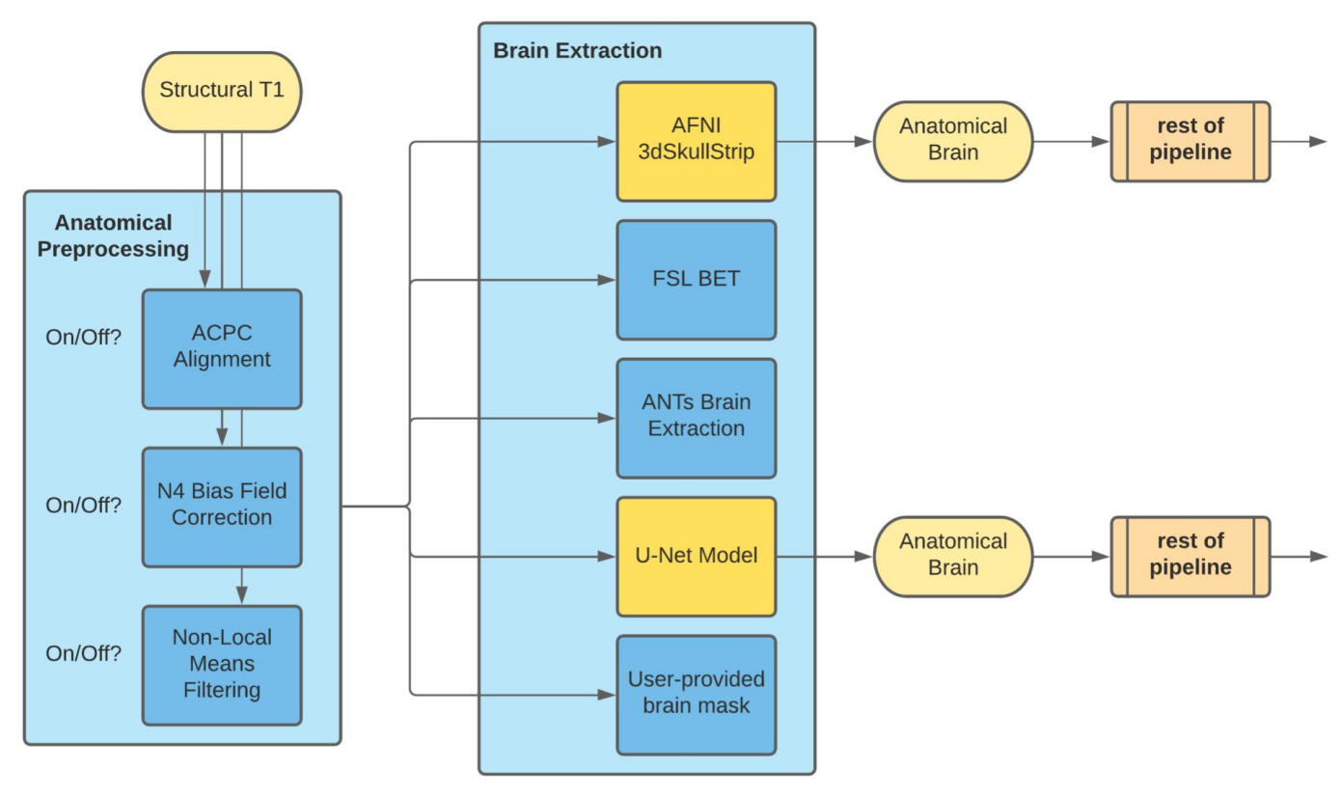


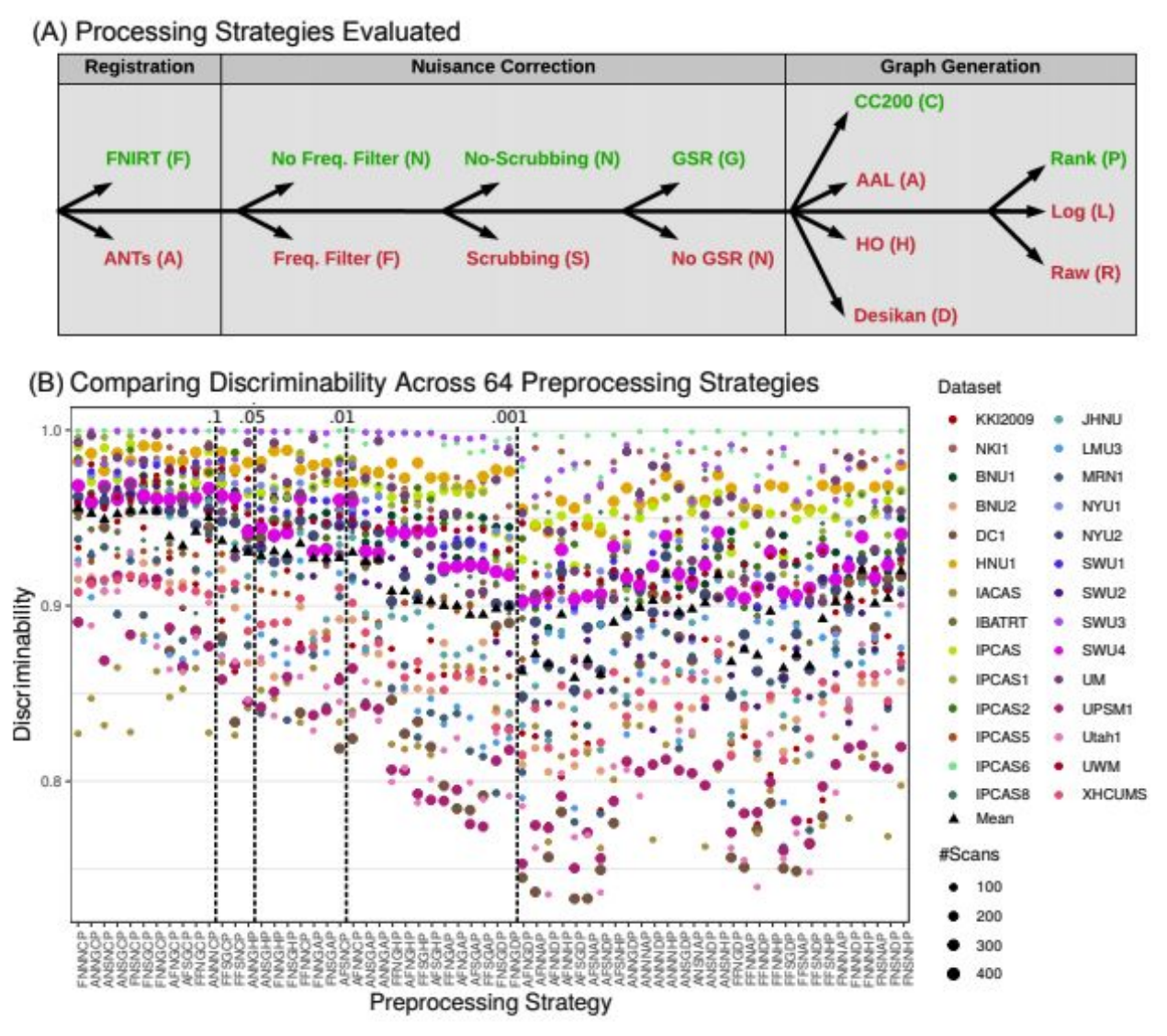




Innovative Analyses

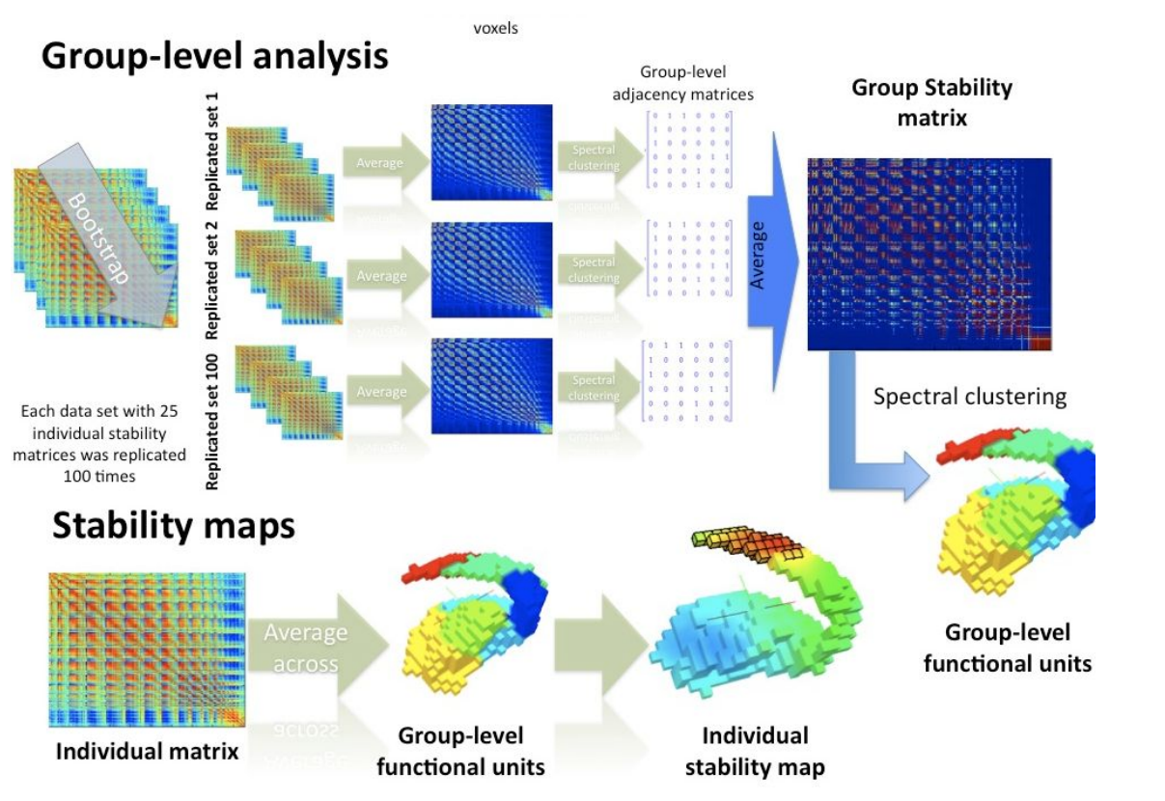
Pipeline Forking and Iterables





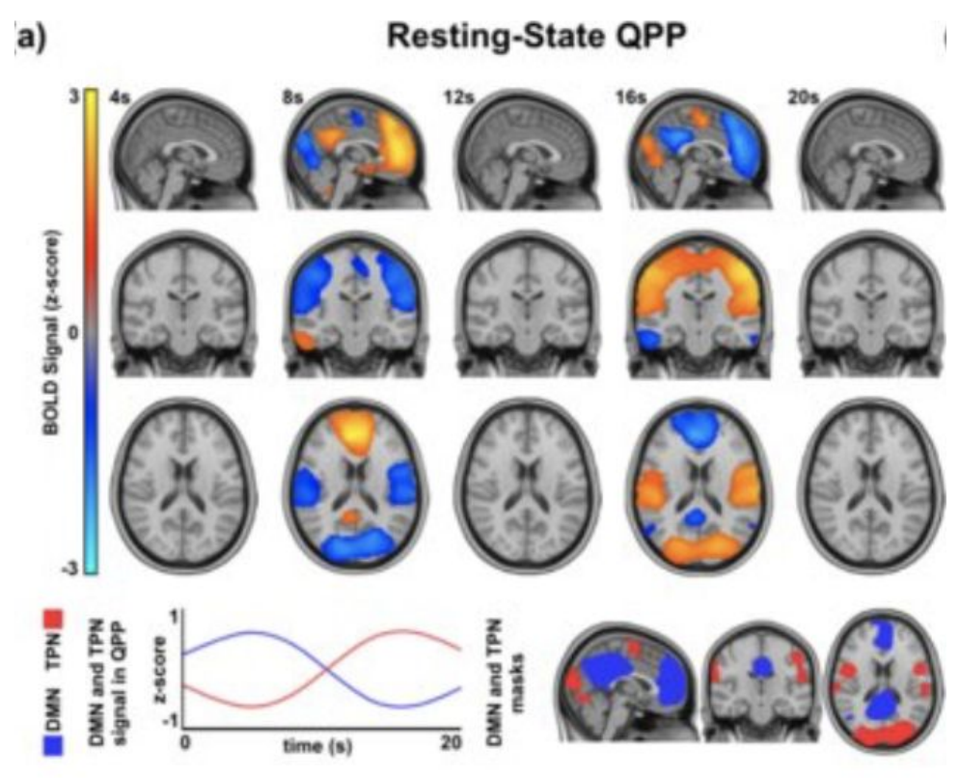
Bridgeford et al., in press

Bootstrap Analysis of Stable Clusters (BASC)



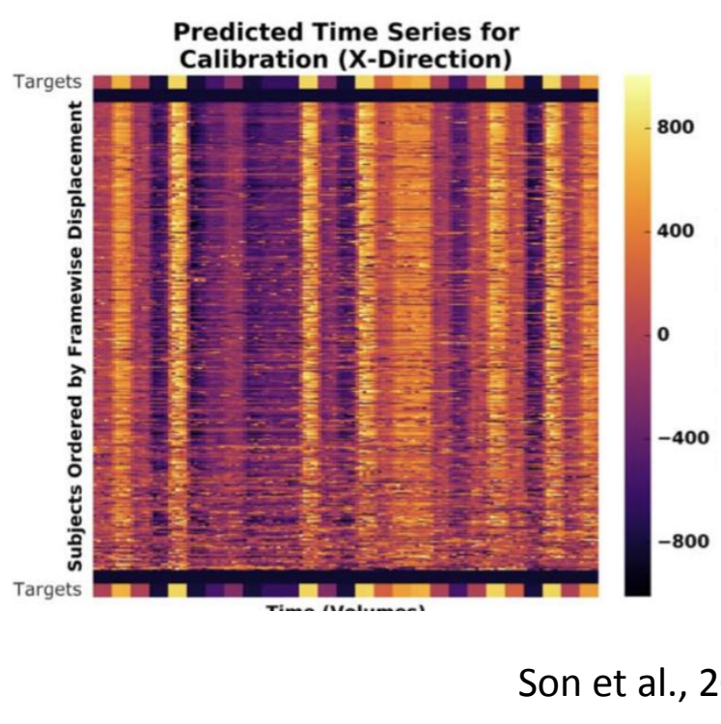
Bellec et al., 2010
pypi.org/project/PyBASC

Quasi-Periodic Pattern Analysis (QPP)



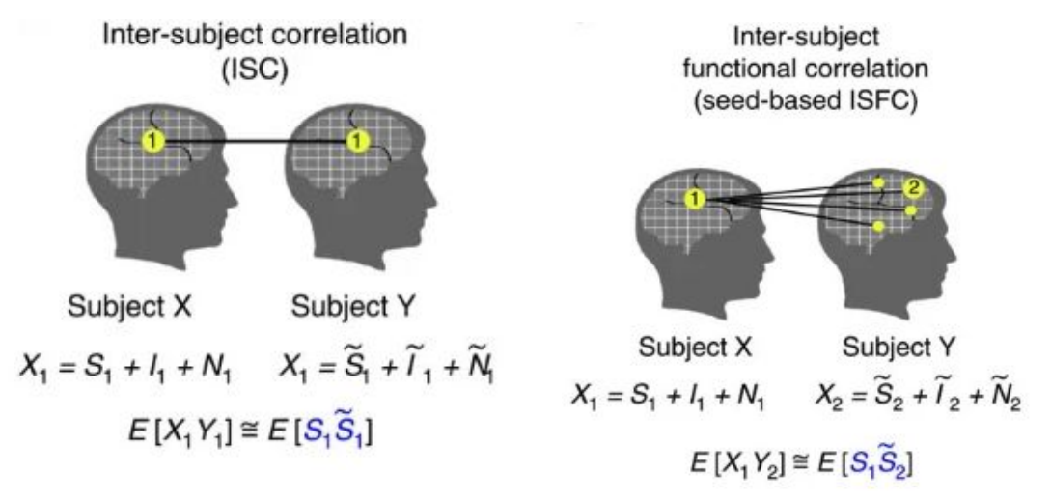
Abbas et al., 2019

Predictive Eye Estimate Regression (PEER)



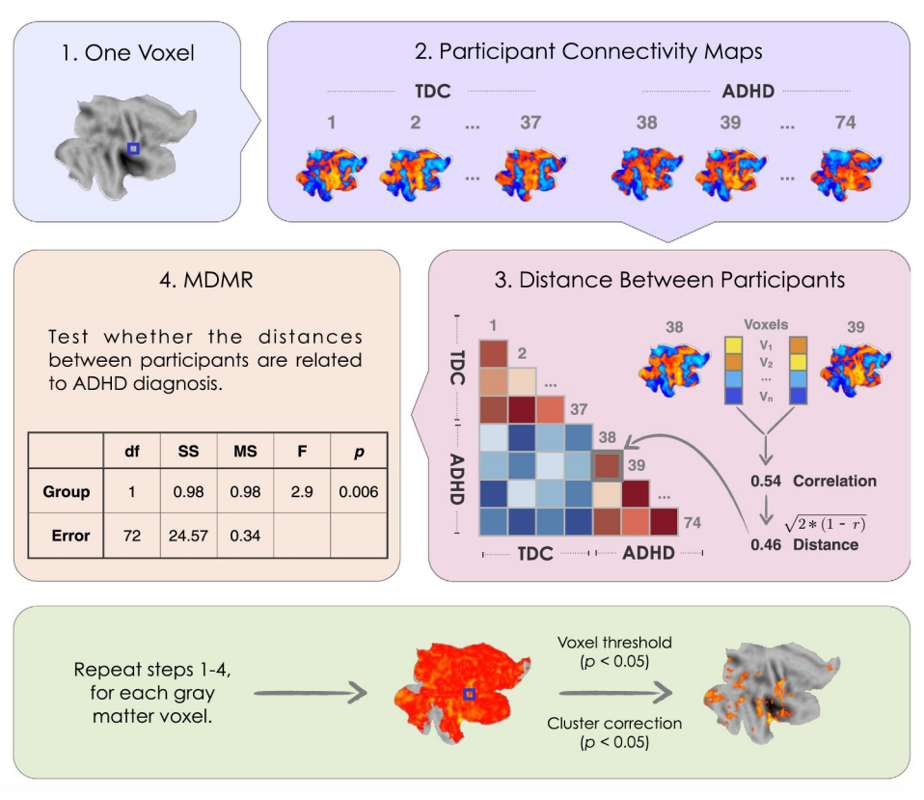
Son et al., 2019

Intersubject Correlation Analyses



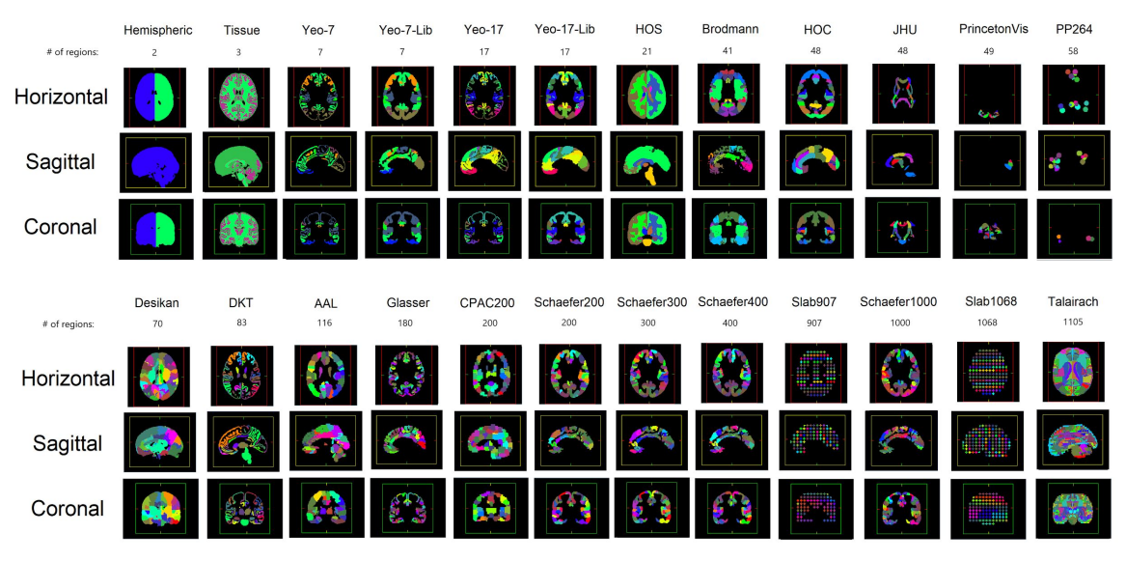
Simony et al., 2016
brainiak.org

Multivariate Distance Matrix Regression (MDMR)



Shehzad et al., 2014

Automated Atlas Extraction (Neuroparc Library)

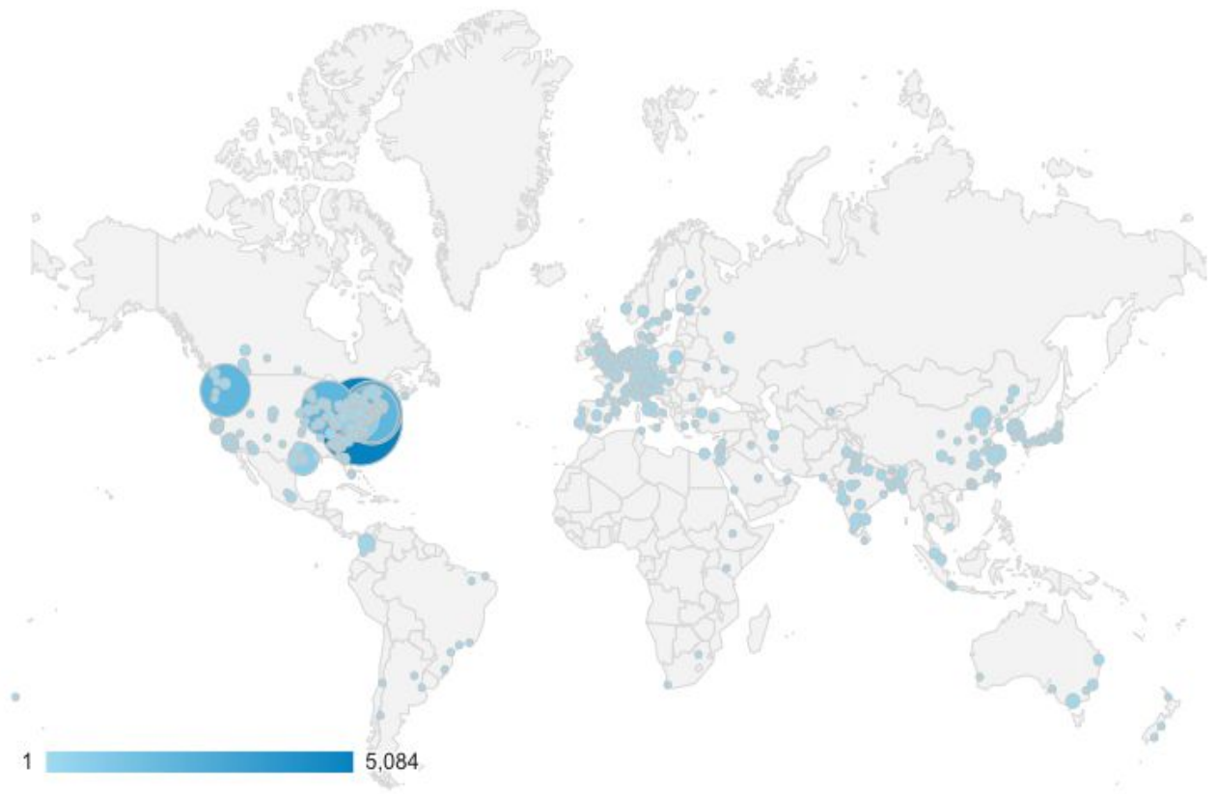


NeuroData, 2020

Simplified Access

docker
aws
Flywheel
brainlife.io

Broad Adoption



	30,340 % of Total: 100.00% (30,340)
1. United States	20,843 (68.18%)
2. Germany	1,102 (3.60%)
3. China	947 (3.10%)
4. United Kingdom	841 (2.75%)
5. India	763 (2.50%)
6. Canada	595 (1.95%)
7. Netherlands	589 (1.93%)
8. Japan	442 (1.45%)
9. Italy	349 (1.14%)
10. South Korea	342 (1.12%)

Google Analytics report for C-PAC runs by region.
Runs with `--tracking_opt-out` flag are not tracked.

Extensive Registration Options

- Unbiased longitudinal registration
- EPI-Template based registration
- Anatomical surface registration
- End-to-end surface registration$^{v1.82}$

BIDS Compatibility

- Inputs: BIDS Format
- Outputs: BIDS Derivatives
  - Gorgolewski et al., 2016
  - bids-specification.readthedocs.io

Conclusions

Following an iterative development process and multiple efforts to update the capabilities of the C-PAC project, the functional connectomics-focused pipeline configuration and execution platform is readying to exit its beta phase. We believe that the extended maturation process has allowed us to deliver the software needed to meet the ambitions and scale of cutting edge functional connectomics efforts.

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