BRAIN Platform

Manage, Share, and Validate Data Analysis Workflows

Fraunhofer CMA & University of Maryland

Main Features (as of version 0.6):

Workflow creation/setup

- Setup workflows from existing modules within the BRAIN platform
- Mix-and-match modules of different programming languages
- Use pre-processing data stored in the NWB file

Workflow sharing

- Share your configured workflows with a click of a button
- Download workflows created by others

Workflow execution history

- Track workflow execution configurations and results
- Compare multiple executions' inputs and outputs side-by-side

Module creation, edit, and sharing

- Create and share your own module with other BRAIN users
- Extend existing/other users' modules

Available Modules

- Image registration (corrects for motion artifacts)
 - Particle-tracking-based [Based on the work of "Motion Correction based on trackable landmarks in the image sequence" (Aghayee 2017)]
 - DFT registration [Customized based on the work of "Efficient subpixel image registration by cross-correlation" (Guizar 2016)]
- Cell segmentation (identifies regions of interests)
 - Manual cell clicking [UMD Losert Lab]
 - Automatic cell segmentation [CaImAn]
- Fluorescence extraction and processing
 - o Fluorescent time series extraction from ROIs
 - o dF/F calculation [Based on algorithm that utilize sliding window to estimate baseline fluorescence]
- Fluorescent signal analysis
 - Spike deconvolution [suite2p Matlab]

Fraunhofer can help integrate your own analysis written in Matlab or Python!

For questions or access to BRAIN platform, please contact:

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Web-based GUI - runs on Windows, Mac, and Linux

HDF5-based file system (enable NWB format)

Capable of ingesting NWB file and images produced by Prairie and Thor microscopes