

PRAGMA

Surveys

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Download & Set-Up

[Mac/Linux](#)

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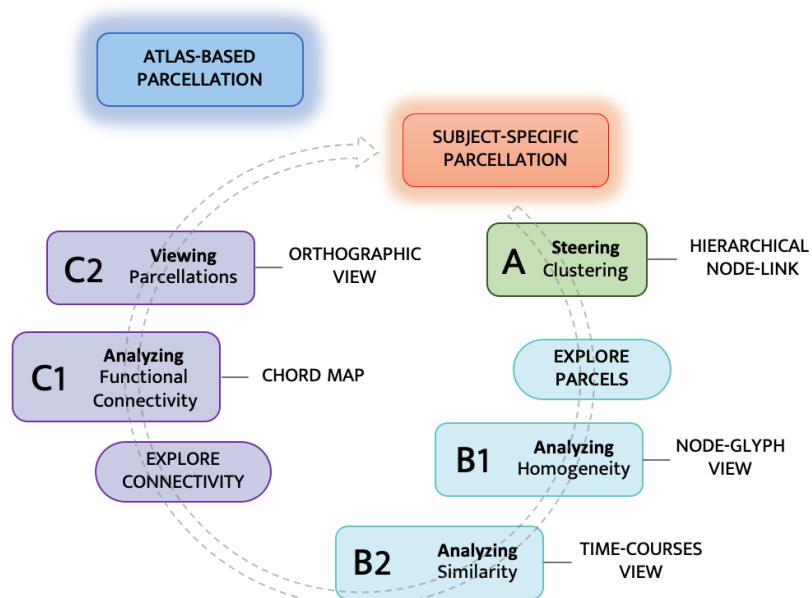
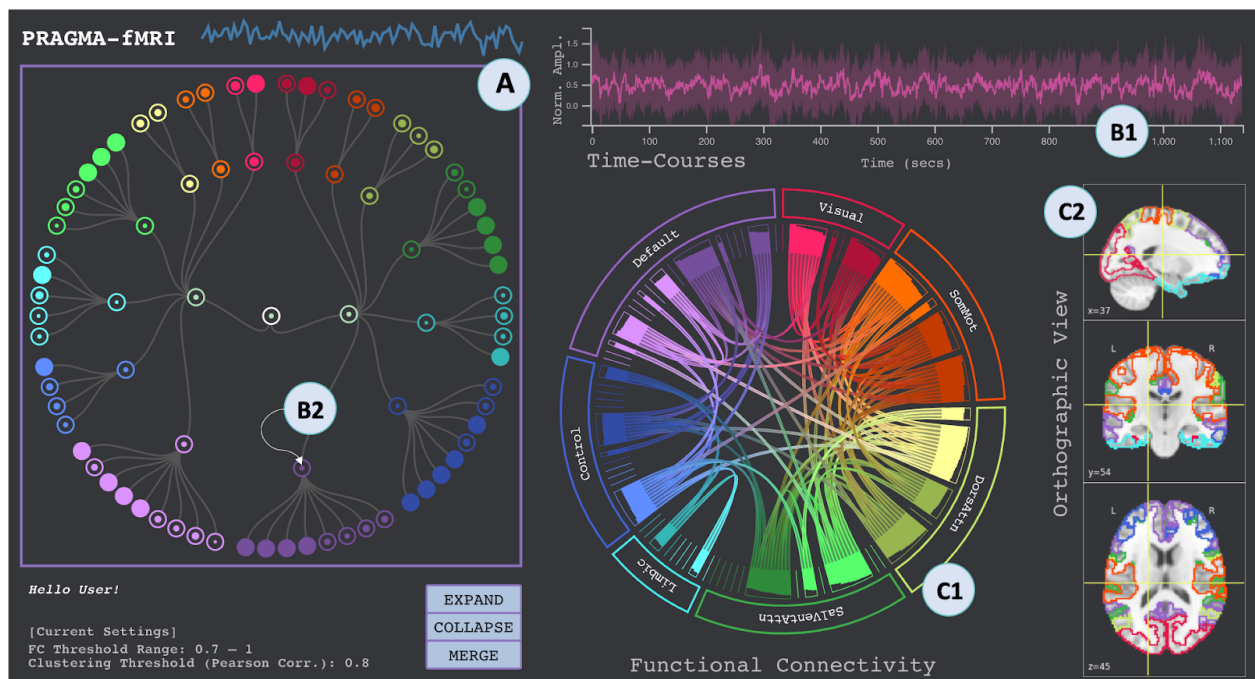
Glossary

- Parcellation Scheme: An atlas dividing the whole brain or a particular region in the brain to subregions.
- Parcel: A region of selected number of voxels that is represented by the average time-courses of these voxels.
- Node: An abstract representation of a group of parcels (represented as circles in the hierarchical node-link graph).
- Region of Interest (ROI): A spatial representation of a group of parcels.

Overview

There are five components in the main interface:

- (A) An interactive hierarchical node-link diagram
- (B1) An interactive aggregated time-series of a selected ROI
- (B2) Homogeneity glyph within each node (larger radius means more homogenous)
- (C1) An interactive functional connectivity chord map of the current ROIs (outermost nodes)
- (C2) Orthographic view of the current parcellation scheme

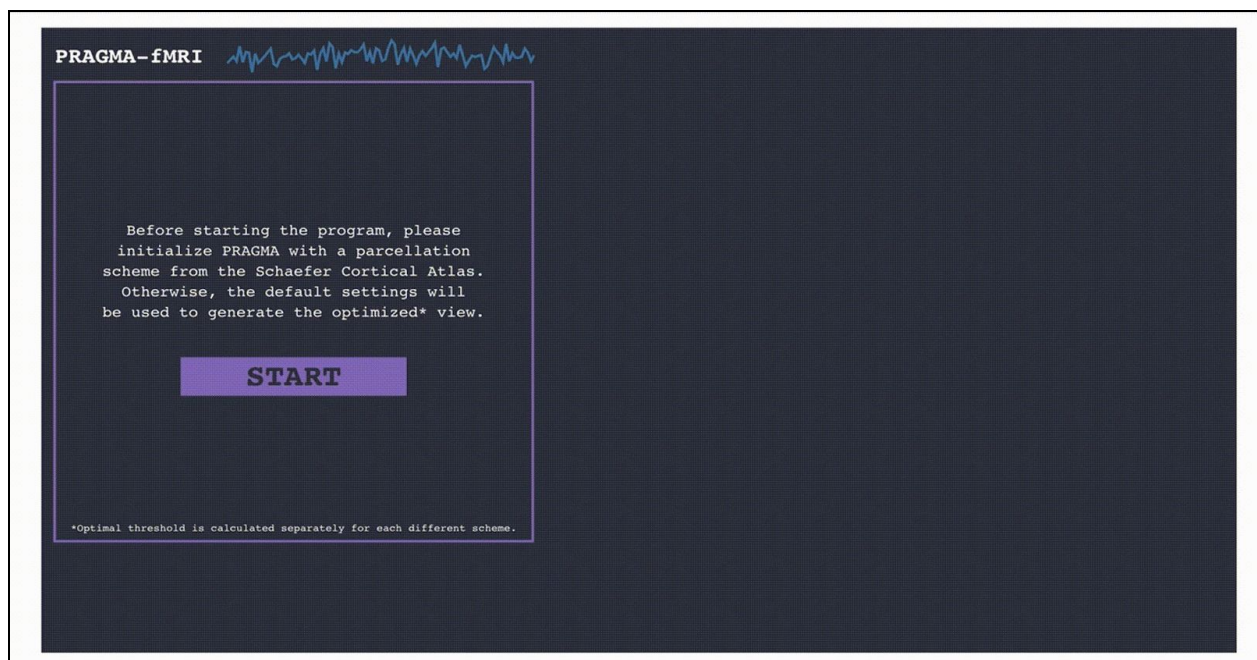


Initialization

Before clicking **START** in the interface, you can select a parcellation scheme from the **INITIAL SET-UP** section (located below the interface).

An initial hierarchical parcellation representation (node-link diagram) will be generated using the farthest neighbor agglomerative clustering algorithm using a predefined threshold.

You can choose to change the default **Pearson's Correlation Threshold**. This threshold is used as a stopping criteria for the clustering algorithm. It represents the minimum correlation requirement for a cluster to allow a new parcel to be grouped together.



Basic actions:

- Click on a node to view its properties
 - Click on the root node to see the whole-brain properties
- Double-click on a node to keep its time-series and functional connectivity in view
 - Single-click on other nodes to directly compare the two nodes' properties
 - Double-click anywhere within box A to release the node(s)
- Brush over the time-series plot to zoom into the signal
 - Double-click anywhere on the plot to reset the view
- Hover over an ROI in the functional connectivity chord map to see its corresponding node in the hierarchical tree.

Parcellation (A)

The node-link diagram is an abstract view of the hierarchical parcellations. Each node represents a group of parcels. The root node contains all of the parcels provided by the atlas (representing the whole brain). The second layer of nodes represents the left and right hemispheres. The third layer of nodes shows regions clustered by functional networks.

Past this layer, the user has options for how regions can be clustered together, using the **EXPAND**, **COLLAPSE**, and **MERGE** buttons.

ROIs (outermost nodes) are the clusters that make up the current parcellation scheme. The functional connectivity chord diagram (C1) and orthographic view (C2) are based on these leaf nodes.

Message Board

Below the node-link diagram and to the left of the buttons is the message board, which is reactive to your actions. For example, when you click on a node, the message board will tell you the number of parcels that are contained in this node and its regional homogeneity. The message board will warn you of invalid actions or notify you of completed actions.

Node Selection

Click on a node to view its properties:

- Regional homogeneity and number of parcels contained in it
- Time-series plot (mean and standard error of ROI time-series)
- Location on orthographic view (ROI(s) that belong to this cluster are outlined in black)
- Connectivity of the selected ROI to the other ROIs on the functional connectivity chord diagram within the selected **Functional Connectivity Threshold**

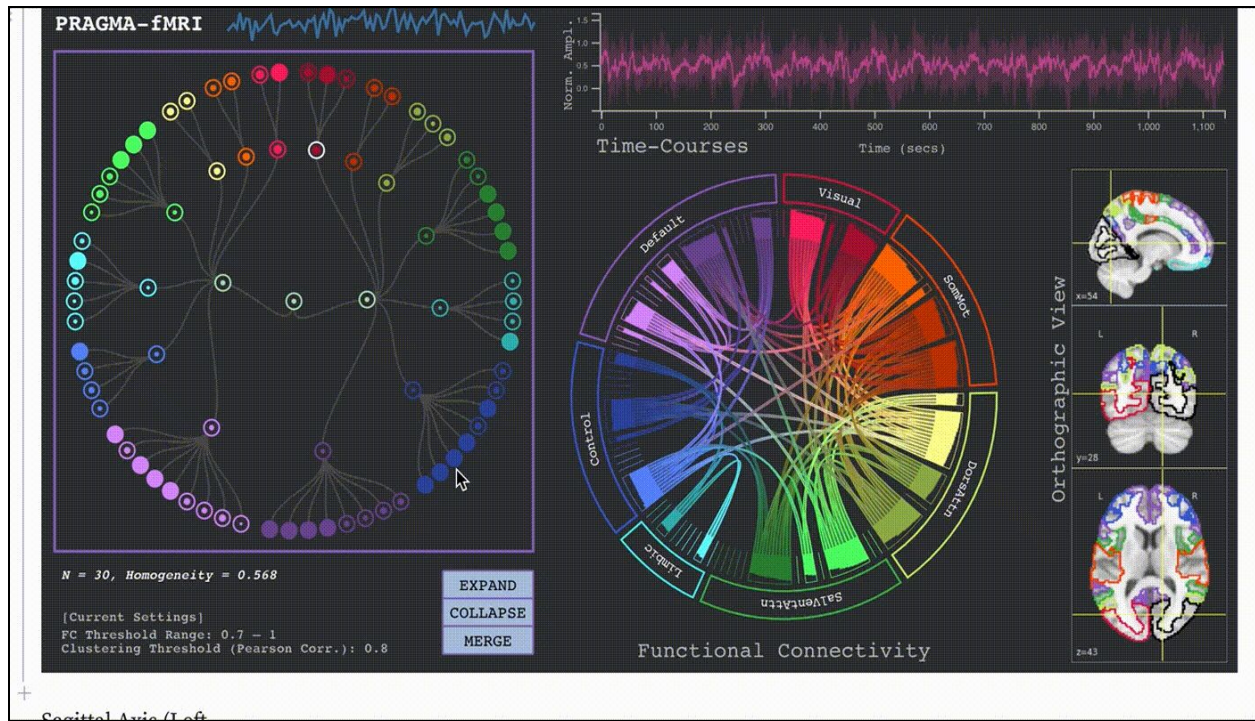
The selected node is marked with a white outline. Selecting the root node will reset the views to be at-large.

Within-cluster Homogeneity (B2)

The radius of the inner circle within each node represents the homogeneity of the parcels within that node. I.e. the inner circle covers the entire node in the situation where there is only a single parcel, therefore homogeneity is 1.

Collapse Node

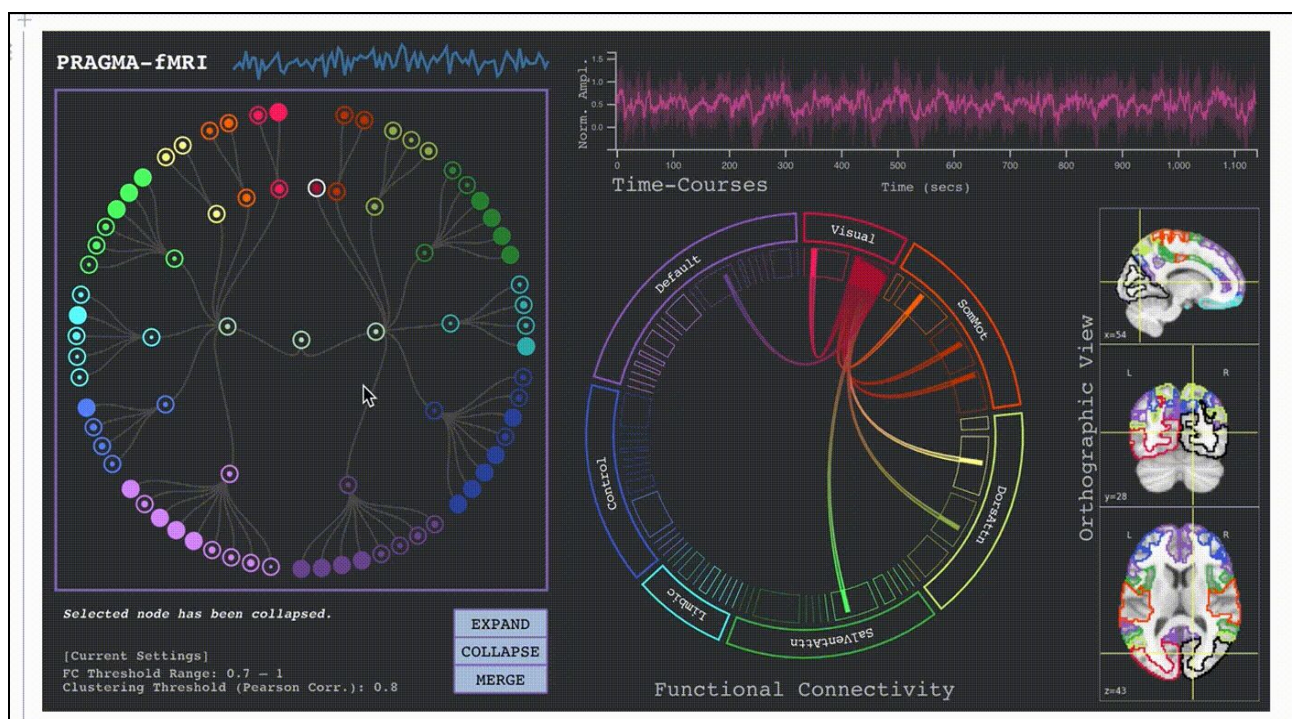
Select a node and click **COLLAPSE** to discard the children nodes (this action turns the selected node to an ROI). It is useful in the case where you deem the node's subregions to be too narrowly defined.



Expand Node

The parcels contained in a node are subdivided into smaller clusters using the farthest neighbour agglomerative clustering algorithm. The stopping criteria for this clustering is based on the **Pearson's Correlation Threshold**, which is decided by the user. This threshold is the minimum pairwise correlation that a parcel's time-series data must have to all the other parcels in the cluster.

To further divide a node into smaller clusters, set a **Pearson's Correlation Threshold** and then click **EXPAND**. Note that you'll need to set lower thresholds to expand nodes that are a result of a higher clustering threshold.



Merge Nodes

The merge-related features of PRAGMA allow direct comparisons of two nodes. This action allows users to merge the regions of two nodes (the nodes can be from two different functional networks).

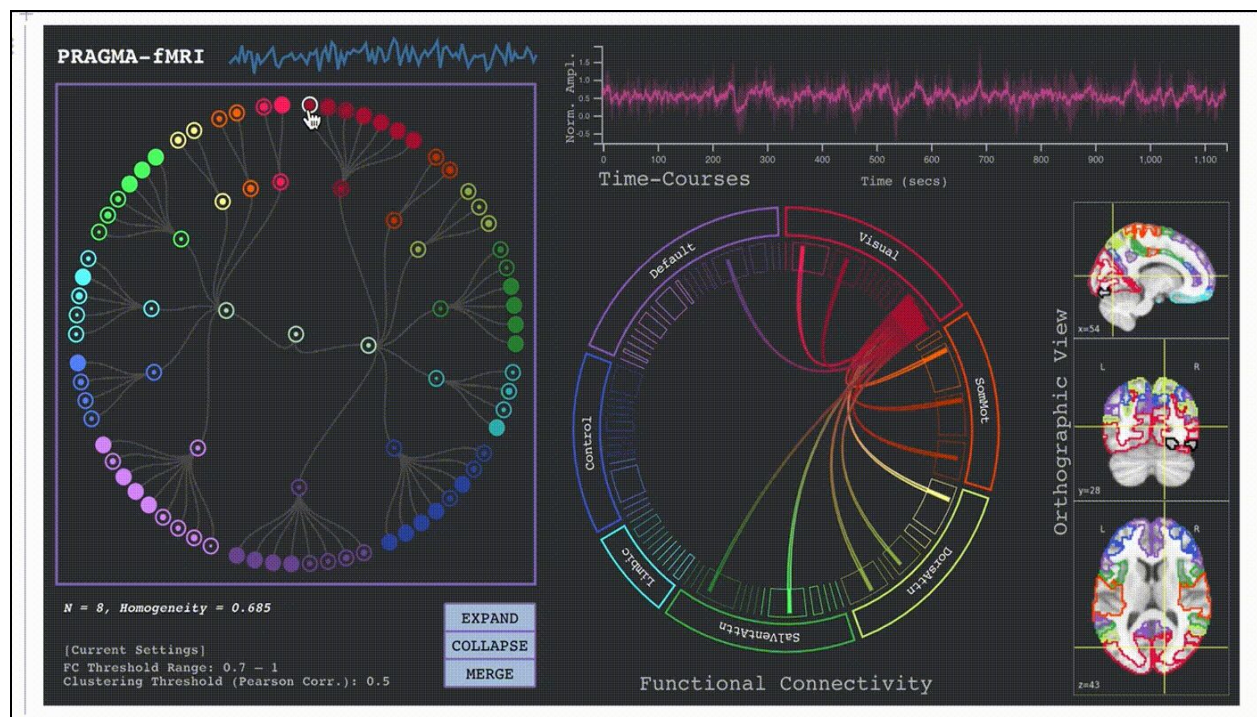
Double-clicking on a node marks it as the first merge node— the regions of the second merge node will be moved to this node. The first merge node and its time-series signal are marked with a pink fill. Its functional connectivity position persists on the chord diagram, as does its time-series signal.

Single-click on a second node to overlay its time-series signal onto the plot (in gray) and show its functional connectivity position on the chord diagram. Use this single-click feature to compare any/all other nodes to the first merge node.

Note that the orthographic view will only mark the region of the currently-selected node (with a black outline).

To merge a node's regions with the first merge node, double-click on this second node. This will mark the second merge node with a gray fill. Then click **MERGE**.

At any point, you can double-click within the box of the node-link diagram to release all merge nodes.



Functional Connectivity Chord Diagram (C1)

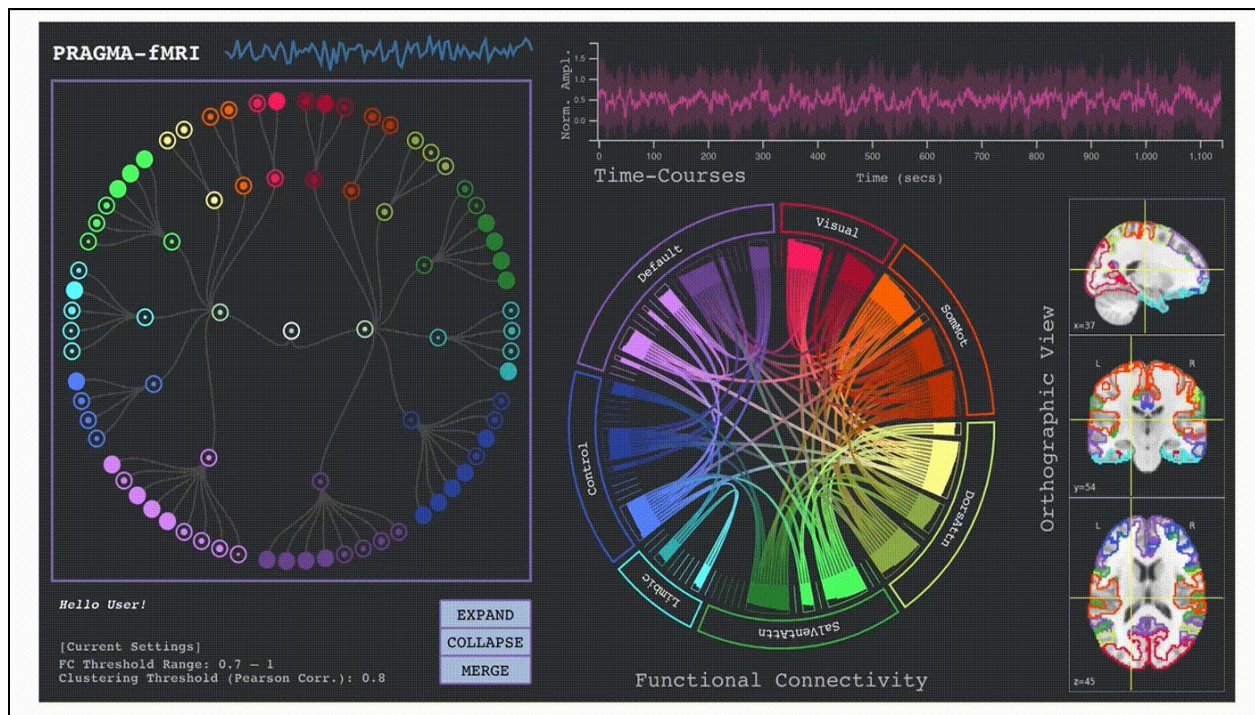
This diagram communicates the functional connectivity of the ROIs (the leaf nodes from the node-link diagram).

The outermost ring denotes the functional network that each ROI currently belongs to.

The ribbons communicate the presence of functional connectivity between two ROIs. Adjust the range of functional connectivity to display using the **Functional Connectivity Threshold** slider located in the additional controls. (⚠ Sliders are communicating the changes to the server, so if you **slide** to change the range, please allow the server to finish computing. If you **CLICK** to move the slider this operation will be instant.)

The inner ring is composed of individual bar plots for each ROI, denoting the strength of connectivity between that ROI and the ROIs it connects to.

Single click on a node in the node-link diagram to display only its connectivity on the chord diagram. Conversely, hover over a region on the chord diagram to isolate the connectivity group. The corresponding node will be marked with a gray fill in the node-link diagram.



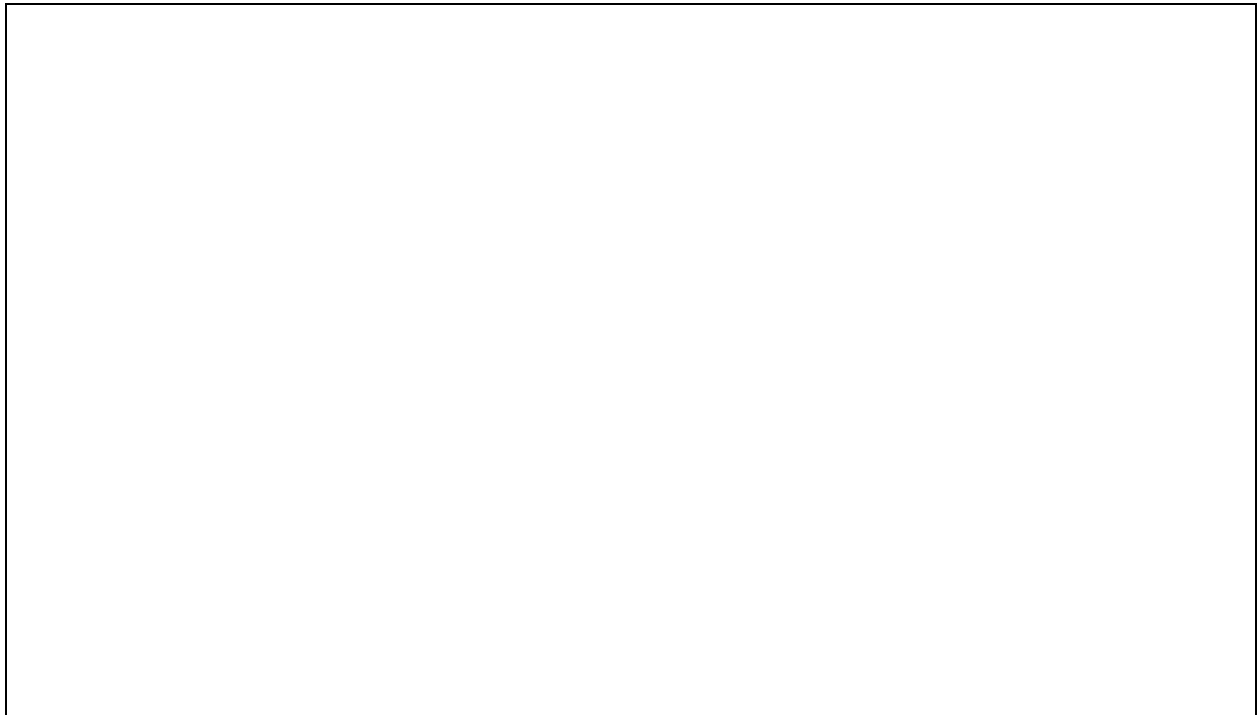
Orthographic Brain View of Parcellation (C2)

This view shows the color-coded location of all the ROIs (leaf nodes on the node-link diagram) on the brain.

Use the axis sliders located in the additional controls to adjust the orthographic views.

⚠ *Clicking on the slider -rather than dragging on it- will generate views faster.*

The location of the currently-selected node will be represented by a black outline on the orthographic view.



Aggregated Time-series (B1)

This plot shows the aggregated time-series of the regions for the selected node. The line plot is the mean amplitude, and the area plot is the standard error.

Brush over a section of the plot (hold down mouse and drag) to zoom into that section of the signal. Double-click anywhere on the plot to reset the view back to the full signal.

Additional Controls

The controls located directly under the visualization cell offer additional settings such as:

- Axis sliders for the orthographic view
- Functional connectivity threshold slider for the chord diagram
- Pearson's correlation threshold input for the expand node action
- Dropdown menu with atlas options

Sagittal Axis (Left to Right)37

Coronal Axis (Posterior to Anterior)54

Axial Axis (Inferior to Superior)45

Functional Connectivity Threshold0.7 ... 1

Pearson Correlation Threshold:

0.8

Update

Similarity Visual

MD, STD(+/-) ▼

INITIAL SET-UP

Initialize

Parcellation

Schaefer 2018 - 400 (default) ▼

Go fullscreen!

Installation — Mac/Linux

Download & Set-Up

Note: This requires python3, pip3, and venv.

At this [link](#), you will find a zipped project directory containing scripts for running PRAGMA. For this user study, we have also provided data: (a) a single-subject pre-processed resting-state fMRI scan from the Human Connectome Project and (b) a set of parcellation schemes from [Schaefer et al.](#). Unzipped, the directory is 42.9MB.

Within the project directory, run the following commands on your terminal to create a virtual environment and install the necessary dependencies. **You only need to do this once.**

```
python3 -m venv pragma_venv
source pragma_venv/bin/activate
pip3 install -r pragma_requirements.txt
```

Run PRAGMA

Activate your virtual environment if you haven't done so already:

```
source pragma_venv/bin/activate
```

Start the PRAGMA servers from your terminal, within the project directory:

```
source start_pragma.sh
```

Launch the Observable notebook from your browser:

```
https://observablehq.com/d/0a3780675484b524
```

To shut down PRAGMA, close the Observable browser window, and end the servers:

```
source end_pragma.sh
```


Installation — Windows

Note: This requires [docker](#).

The project repo contains scripts for running PRAGMA. For this user study, we have also provided data: (a) a single-subject pre-processed resting-state fMRI scan from the Human Connectome Project and (b) a set of parcellation schemes from [Schaefer et al.](#).

Pull the the PRAGMA docker image:

```
docker pull rgbayrak/pragma
```

To run PRAGMA, start the docker container's bash shell and then run the servers:

```
docker run --name pragma --rm -i -t -p 8000:8000 -p 5000:5000 rgbayrak/pragma bash  
cd /pragma && source start_pragma.sh
```

Launch the Observable Notebook in a web browser:

<https://observablehq.com/d/0a3780675484b524>

To shut down PRAGMA, close the Observable browser window, and end the servers with `exit()` on the terminal.