Week 2 Part 2 Assignment:

Identifying a network data set

by Gabrielle Bartomeo, Zach Dravis, Peter Lombardo, and Hovig Ohannessian

The open source platform “NeuroData” hosts a wealth of online neuro-imaging data. One of their available data forms are “Biologically Derived Graphs” available in graphML format. One data set they provide is the fly brain with 1781 nodes and 33,641 edges. Each node is also associated with a region (also known as an ROI—Region of Interest). This could be looked at as a categorically attribute for each node as well as a localizer (nodes of the same ROI will be near each other).

These data have some interesting findings we could identify using network analysis. For starters, neuroscience has recently begun to look at brains in terms of “pathways” or “networks.” This means that the connectivity of certain regions to other regions is of paramount interest. Take for example the corpus collosum in the human brain—a bundle of fibers and neurons responsible for linking the left and right hemispheres. This would clearly be a well-connected region with high centrality.

In terms of degree centrality, an initial analysis would consist of finding individual nodes that are the most connected to other nodes. This could lead to identifying which regions of interest have nodes with the most connectivity. Understanding which regions are connected can help explain functions of different brain regions. Furthermore, a closeness centrality analysis can determine which regions are related directly to other regions.

**Source:**

* https://neurodata.io/project/connectomes/