Data Science Project
On Brain Distance: Measured and Connectome-Generated

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January 26, 2023

Abstract

This project aims to compare the node distances generated by a connectome-based graph network and real measured between-area distances in the marmoset brain. The goal is to establish similarities between the marmoset brain and a marmoset brain-based graph network in order to assess the feasibility of using networks in brain research. The assumption is that brain areas with stronger connections will wire close together in the network graph, and therefore network distances should be comparable to brain distances. The project discovers several dissimilarities between the two distances, indicating that networks tend to prefer functionality over topology.

1 Introduction

The study of brain connectivity has flourished with the development of new techniques and technologies that allow for the mapping of the brain's connections at an unprecedented level of resolution. The marmoset brain, especially, has proven to be a powerful model for understanding the organization and function of the primate brain, and by extrapolation, the human brain. In-vivo studies of the marmoset connectome through MRI recordings have produced complex atlases, which can be studied and used to extract important information of brain function and topology. Two important projects, The Marmoset Brain Mapping and The Marmoset Brain Connectivity Atlas are important resources of this project.

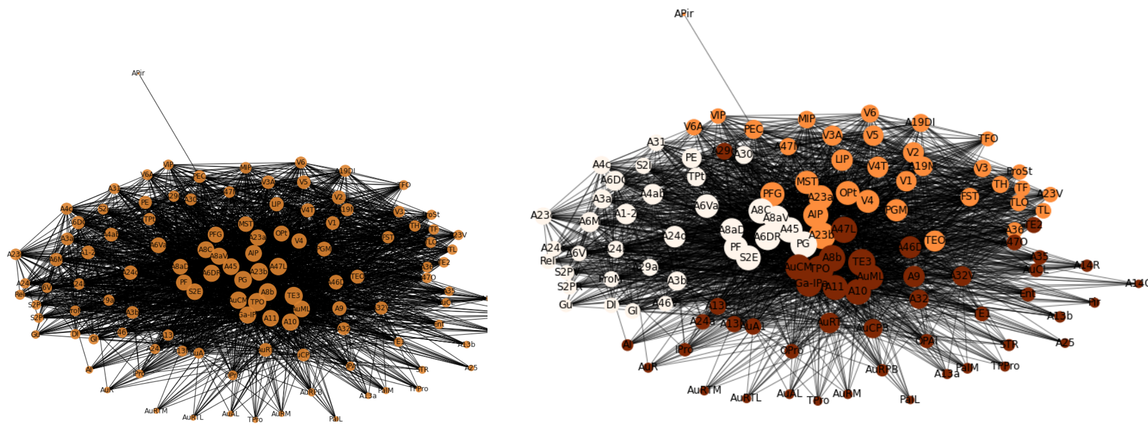
The aim of the project is to compare the node distances generated by a connectome-based graph network and the real measured between-area distances in the marmoset brain. The goal is to establish similarities between the marmoset brain and a marmoset brain-based graph network in order to assess the feasibility of using networks in brain research. This could be a powerful resource, especially when considering the potential of Graph Neural Networks to simulate experiments that otherwise would need preparing time, extensive resources, including the use of animal subjects.

The connectome, the comprehensive map of neural connections within the brain, can be represented as a complex network. It is assumed that brain areas with stronger connections will wire close together in the network graph, and therefore network distances should be comparable to brain distances. By comparing the node distances in the connectome-based graph network with the real measured between-area distances in the marmoset brain, we aim to better understand the relationship between brain connectivity and brain structure. This will provide valuable insights into the organization of the marmoset brain and the usefulness of network-based approaches in brain research.

1.1 Data

The first raw dataset contains pairwise physical distance information for all 116 marmoset brain areas. These distances are measured in micrometers and have been established by sectioning and computationally reconstructing the marmoset brain, across several specimens.

The second dataset, on pairwise connectome strength, was measured through neuroanatomical tracers. The strength is measured in the fraction of extrinsically labeled neurons, log_{10}(FLNe). This data is the one used to create the network graph (Figure 1a, 1b).



(a) Network of Brain Connectome

(b) The 3 Communities Generated by Louvain Modularity

Figure 1: A Peak at How Nodes Arrange By Connectivity Strength
Each node is a brain area, each edge an existing connection strength

The data was uploaded and processed using Pandas and Numpy libraries. To achieve a common measurement unit, both distances were normalized using the MinMaxScaler in the scikit-learn library. The edges of weight zero in the network graph were deleted.

2 Methods

The problem at hand is tackled by creating a connectome-based network graph using the NetworkX Python library. The generated network then describes a node (brain area) organization based on the number of connections and their strengths between each pair of brain areas, data generated through injections. Therefore, if 2 regions share many connections, they would have a direct connection in the graph, and a high edge weight. The witin-graph distance would be calculated by multiplying the shortest path between two brain areas (nodes) with their connection strength (edge weight).

$$Distance(area_1, area_2) = ShortestPath(area_1, area_2) \times EdgeWeight(area_1, area_2)$$

This distance would then be compared with the measured between-area physical distance, measured in micrometers.

3 Results

To visualize the similarities and differences between the two distances, heatmaps were used to compare the node distances from the connectome-based graph network (Figure **??**) with the real measured between-area distances Figure(**??**) in the marmoset brain. The brain-distance heatmap shows a clear preference for areas in close proximity, such as those in the visual system. On the other hand, the graph shows little correlation between groups of areas. Interestingly, this pattern only appears when taking into account edge weights. Based on solely shortest paths, we can see similar (weak) clusters appear as in the brain distance heatmap.

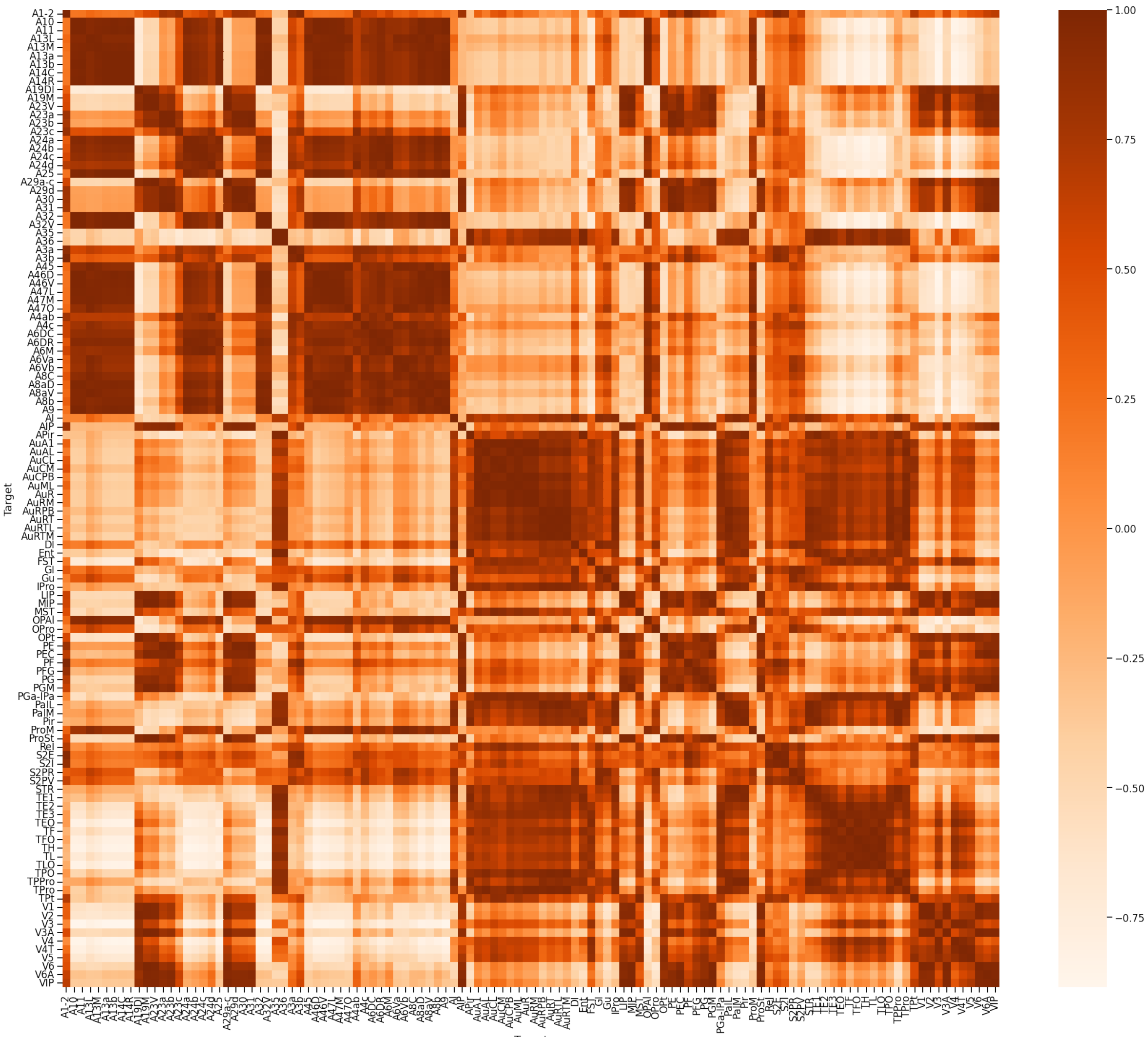


Figure 2: Brain Distances Heatmap.

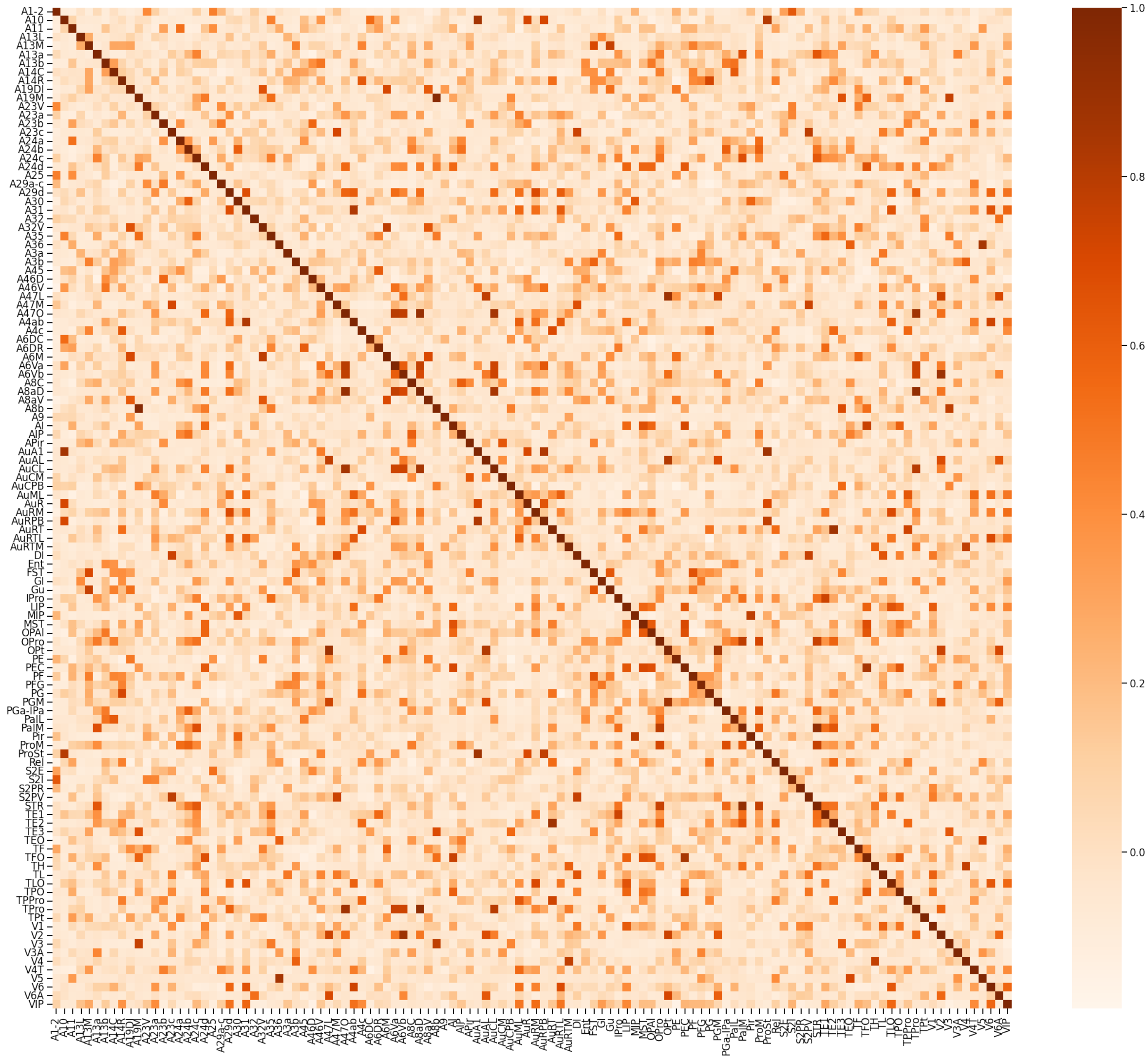


Figure 3: Graph Distances Heatmap.

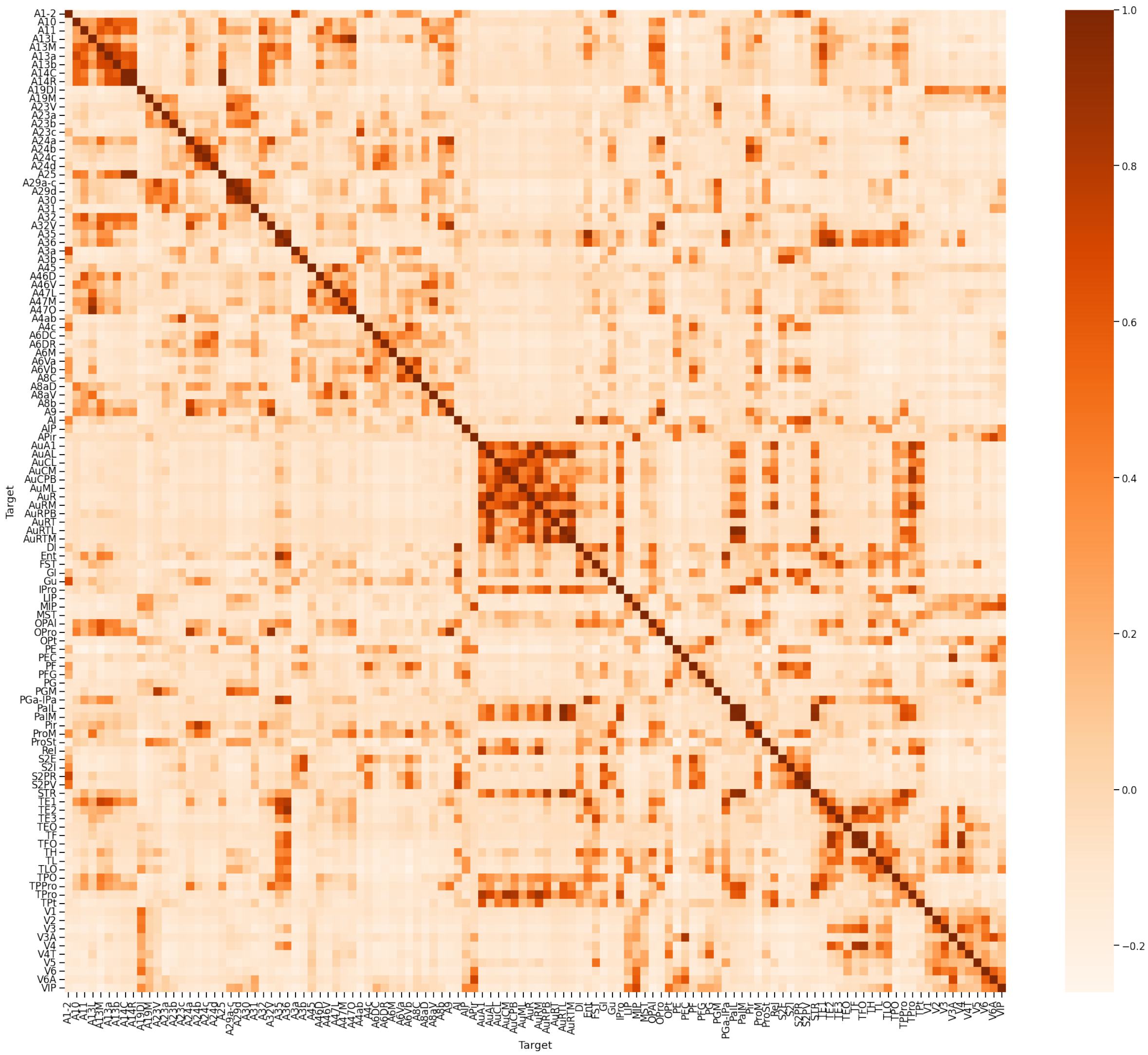


Figure 4: Graph Distances Heatmap, Without Edge Weights.

Plotting the two distributions of distances, it appeared that they mostly overlapped, with the brain distances being slightly larger than the graph ones (Figure 6). There was a slightly negative regression line between the distances (Figure 5). This suggests that there is some correlation between the two distances, but that they are not perfectly aligned.

To further investigate the relationship between the two distances, a T-Test was conducted to compare the means of the two distributions. The overall T-Test revealed that the means of the two distributions were statistically different (statistic = -23, pval = 0.0). When the T-Test was applied only to 10 brain areas at a time using bootstrapping, the average of the means was very different than the overall distribution mean (Figure 7).

	Distribution Mean	Mean of Bootstrap Means
Brain Distance	-2.87	0.02
Graph Distance	1.26	0.01

Table 1: Brain and Graph Distance Means: Distribution-wise and 10-sample-wise

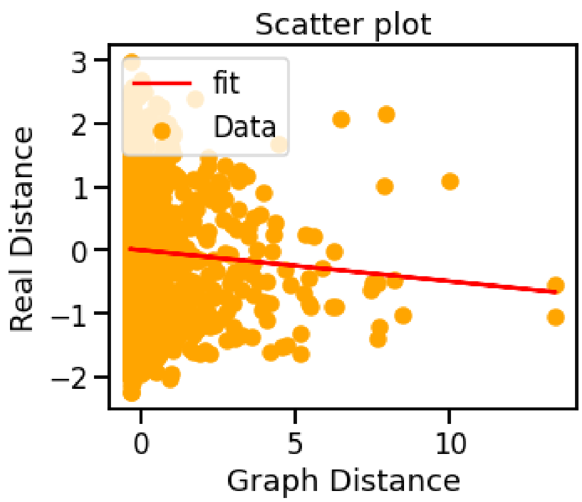


Figure 5: Scatter plot of brain and graph distances.

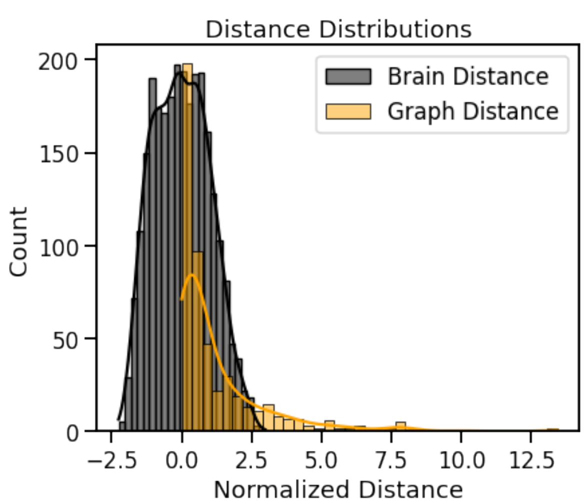


Figure 6: Distance Distributions

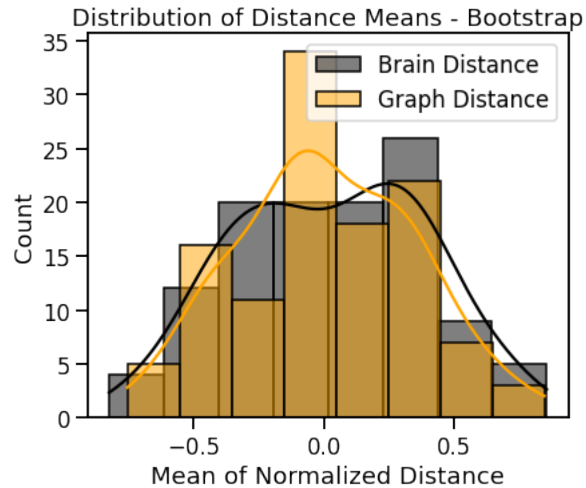


Figure 7: Mean Distance Distributions (Bootstrapped)

4 Discussion

While a useful representation, the connectome-based network distances showed some differences from the physical brain distances. The negative regression line between the two distances suggests that the node distances from the connectome-based graph network tend to be slightly smaller than the real measured between-area distances, pattern also mirrored as their distributions. This may suggest that the connectome-based graph network is not an exact replica of the marmoset brain and that there are there is more to unravel about how the brain is organized in the two systems.

In addition, The T-Test for 10-wise brain areas revealed that there are specific brain areas in which the relationship between the two distances is stronger or weaker. This suggests that the relationship between the two distances depends on the specific brain area being studied.

Overall, these results provide valuable insights into the organization of the marmoset brain and the usefulness of network-based approaches in brain research and suggest the need for further research to better understand the relationship between brain connectivity and brain structure in the marmoset brain.

5 References

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