Network Theory and Analysis:

Understanding Macaque Brains

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May 4, 2023

Executive Summary

This paper and presentation aim to investigate the graph models of the macaque monkey's brain areas and connections. The dataset comprises 45 areas and 463 directed connections, which are presented in the form of a directed graph object. This information was sourced from the Creative Commons Attribution-Share Alike 2.0 UK: England & Wales License, and the dataset itself was originally introduced by Negysessy et al. (2006). The goal of this exploration is to leverage network analysis techniques to gain a better understanding of the macaque's brain and the connections involved in tactile function. To achieve this, multiple techniques to analyze the network we employed, including centralization metrics, clustering, and an exponential random graph model (ERGM). These analyses helped us identify critical areas and connections involved in the function of the visual cortex. Our results showed that the FEF, VIP, 46, V4, and LIP regions of the macaque brain exhibited significant connectivity patterns.

Introduction

The Macaque brain has been a significant model for scientific research for its similarity to the human brain. It's network offers tons of information as macaque brain is structurally and functionally similar to the human brain and studying macaque brain networks can provide valuable insights into how the human brain works. Understanding the organization of brain networks in the macaque can help us understand how information is processed and integrated across different regions of the brain. This, in turn, can help us understand how the brain mediates behavior and cognition. The macaque brain is also a common model organism used in neuroscience research. Therefore, a better understanding of the macaque brain networks can help improve our understanding of neurological disorders and brain-related diseases. In this paper and presentation, we aim to provide a comprehensive overview of our network analysis of the macaque brain and highlight the key findings of our study. By leveraging network analysis techniques such as centralization, clustering methods, and exponential random graph models.

Methods

Centralization

The first method employed was analyzing the degree, betweenness, closeness, and eigenvector centrality. We wanted to observe the brain areas that held higher importance in this network. The first metric we calculated was the degree of centralization; this value came out to be 0.226 (Figure 1). Degree centrality with this network indicates that the macaque brain network is somewhat centralized in terms of degree, meaning that some brain areas have a relatively large number of connections compared to the rest of the areas. However, this value is not extremely high suggesting that there is some degree of equality in connectivity across the

network. The second metric we calculated was the closeness centralization; this value came out to be 0.281 (Figure 2). This value indicates that the macaque brain network is moderately centralized in terms of closeness, meaning that some brain areas can more quickly transmit information to other areas compared to the rest. The third metric we calculated was the betweenness centralization; this value came out to be 0.16 (Figure 3). This value indicates that the macaque brain network is relatively decentralized in terms of betweenness, meaning that many brain areas have similar levels of importance in terms of routing information between different parts of the network. However, there are still some areas that are more important than others in this regard. Lastly, we examined the eigenvector closeness that had a value of 0.565 (Figure 4). This value of 0.565 indicates that the macaque brain network is fairly centralized in terms of eigenvector centrality, meaning that a few highly connected brain areas have a large influence over the rest of the network. This suggests that information processing in the network may be strongly influenced by these highly connected areas.

Community Detection

To identify clusters of the brain region that work closely together we employed several community cluster algorithms such as fluid, eigen, walktrap, spinglass, label, optimal, fastgreedy, infomap, and louvain. Louvain and Optimal had the highest modularity with with around 0.37 to 0.38. Both models almost gave the same communities, but one big difference was that the Louvain method had 4 communities while optimal method had 3 communities (See figure 5 and 7). The first 2 communities in both algorithms consisted of visual areas, which are involved in visual processing (V1, V2, V3, V3A, V4t, VP, MT, MSTd/p, MST, etc), and (V4, VOT, PITd, PITv, CITd, CITv, AITd, etc.). The third community in both algorithms include (IP, 3a, 3b, 1, 2, 5, Ri, SII, etc), these are for more cognitive functions, decision making, and motor

functions. The fourth community that is only in the louvain method consists of (Ig, Id, 35, 36) which are also motor processing (see figures 6 and 8).

ERGM

In order to analyze the macaque network, we chose to run an ERGM model. We decided to run it to test hypotheses about the structural properties of a network and the processes that generate those structures. Two fundamental structural characteristics of the network are edges and mutual. Node factor and nodematch represent the names of the nodes in our network. The initial analysis of the model showed that density and mutual, as well as multiple different vertex names turned out to be highly significant in the model. We will explain the highest significant independent variables in the results section of this paper.

In order to evaluate the model, we run goodness of fit. Dyad-wise shared partners, degree, indegree showed a really good fit. Based on the findings of the GoF test, the model closely matches the observed data. It specifically contends that the degree, indegree, and dyad-wise shared partners of the simulated networks produced by the ERGM model correspond to those of the observed network. This might be a sign that the ERGM model is successfully capturing crucial network characteristics and yielding accurate predictions of the structural characteristics of the network.

Another way to check the degree to which the model is performing well was to run MCMC chains diagnostics. All of the variables showed bell shaped and equal distribution around zero. The bell-shaped distribution is a characteristic of the normal or Gaussian distribution, which is a common distribution in statistics. The normal distribution is symmetric about its mean, which in this case is zero. When MCMC chains produce a normal distribution of

parameter values, it indicates that the posterior distribution works normally and the MCMC algorithm has successfully investigated it.

In addition, the equal density on either side of zero implies that there is no bias towards positive or negative parameter values in the MCMC algorithm. This is important because errors in the algorithm can lead to inaccurate parameter estimates and erroneous statistical conclusions.

Finally, we've created the network plots(Figure 9) of both simulated and original networks to see how they are similar or different. The plots look similar, yet the simulated plot doesn't perfectly depict the network. Moreover, reciprocity and edge densities of both networks are similar in numbers, while transitivity in the original network is much higher than in the simulated one. A high transitivity score means that triangular connections between network nodes are more common than they would be through chance in the original network.

Results

Through our initial discovery we analyzed the centrality of brain areas in the macaque brain network using four metrics: degree, closeness, betweenness, and eigenvector. The network was somewhat centralized in terms of degree and moderately centralized in terms of closeness. In terms of betweenness, the network was relatively decentralized, although some areas were still more important than others. Finally, the network was fairly centralized in terms of eigenvector centrality, suggesting that a few highly connected brain areas have a large influence over the rest of the network and may strongly influence information processing.

Based on the results from the community detection model we can study the optimal and louvain methods since they had the highest modularity with the most well defined communities. Optimal had three clusters, and louvain had four clusters, and as mentioned before we can see

how some of the nodes which are used for similar or different functions in the brain work together. As mentioned before, the nodes in the first two communities were mainly visual processing, and the nodes in the third communities were cognitive and motor functions. Conclusively this provides more information about the framework of the connectedness and clusters in the macaque brain structure.

Based on the ergm model, the increase in edges in the network leads to a significant decrease of 3.80504 log-odds of forming a tie at random in a network. Whearease, an increase in mutual ties leads to an increase of 5.37555 log-odds of reciprocating a tie in a network. Increase in vertex names 46, FEF, LIP, V4, VIP are all associated with positive effect on the creation of a tie in a network.

Discussion

Getting an in-depth look at the highly significant vertex names, we learned that all of them are different brain areas responsible for different functions. Since it is not a biological class we will give just one example. VIP area receives input from the visual, somatosensory, and motor areas. Moreover, the degree of VIP in the original network is very high. After running a model and looking at the structural data of the network, we can say that such variables as VIP play a big role in creating the ties within the network. Moreover, based on the results of centralization, all of the variables(46, FEF, LIP, V4, VIP) have a high degree of centralization in the network, which makes us conclude that they are playing a central role in the overall network function.

Something we can take out of this network analysis is that there are specific brain areas, such as VIP, 46, FEF, LIP, and V4, that play a huge role in this network, and these are the central

networks for brain processing. Community detection also provided us insights into organizations and different clusters of brain regions that work together. Furthermore, the ERGM model helped understand the structure of the network.

Finally, our project gives a comprehensive overview of the macaque brain network structure and function, highlighting the key areas and connections involved in information processing. By the application of networks methods, such as structure analysis, clustering, exponential random graph models, we were able to gain new insights into the organization of the macaque brain network and its role in behavior and cognition.

Bibliography

Négyessy L, Nepusz T, Kocsis L, Bazsó F. Prediction of the main cortical areas and connections involved in the tactile function of the visual cortex by network analysis. Eur J Neurosci. 2006 Apr;23(7):1919-30. doi: 10.1111/j.1460-9568.2006.04678.x. PMID: 16623848.

Appendix

```
#degree centralization####
cent_deg <- centralization.degree(macaque, mode = "all")$centralization
round(cent_deg, digits = 3)
```
Figure 1

```
#closeness centralization####
cent_clo <- centralization.closeness(macaque, mode = "all")$centralization
round(cent_clo, digits = 3)
```
Figure 2

```
#betweenness centralization####
cent_bet <- centralization.betweenness(macaque)$centralization
round(cent_bet, digits = 3)
```
Figure 3

```
#eigenvector centralization####
cent_evc <- centralization.evcent(macaque)$centralization
round(cent_evc, digits = 3)
```
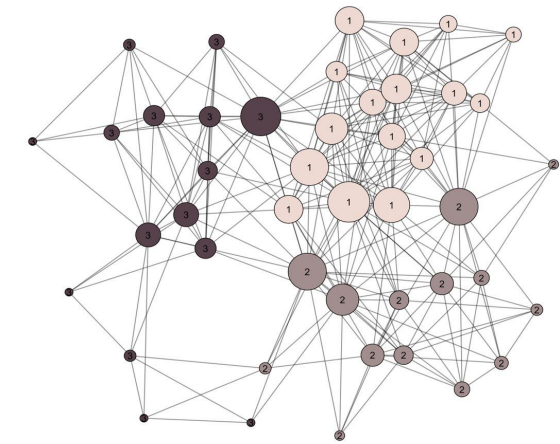Figure 4

Figure 5 (Optimal Cluster)

```
Vertices in community 1 : V1, V2, V3, V3A, V4t, VP, MT, MSTd/p, MSTl, PO, LI
P, PIP, DP, 7a, FST, FEF
Vertices in community 2 : V4, VOT, PITd, PITv, CITd, CITv, AITd, AITv, STPp,
STPa, TF, TH, 46, 36
Vertices in community 3 : VIP, 3a, 3b, 1, 2, 5, Ri, SII, 7b, 4, 6, SMA, Ig, I
d, 35
```
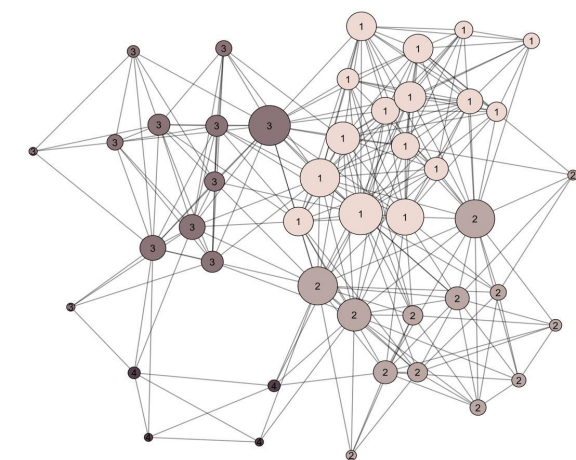
Figure 6 (Optimal Names)

Figure 7 (Louvain Cluster)

```
Vertices in community 1 : V1, V2, V3, V3A, V4t, VP, MT, MSTd/p, MSTl, PO, LI
P, PIP, DP, 7a, FST, FEF
Vertices in community 2 : V4, VOT, PITd, PITv, CITd, CITv, AITd, AITv, STPp,
STPa, TF, TH, 46
Vertices in community 3 : VIP, 3a, 3b, 1, 2, 5, Ri, SII, 7b, 4, 6, SMA
Vertices in community 4 : Ig, Id, 35, 36
```
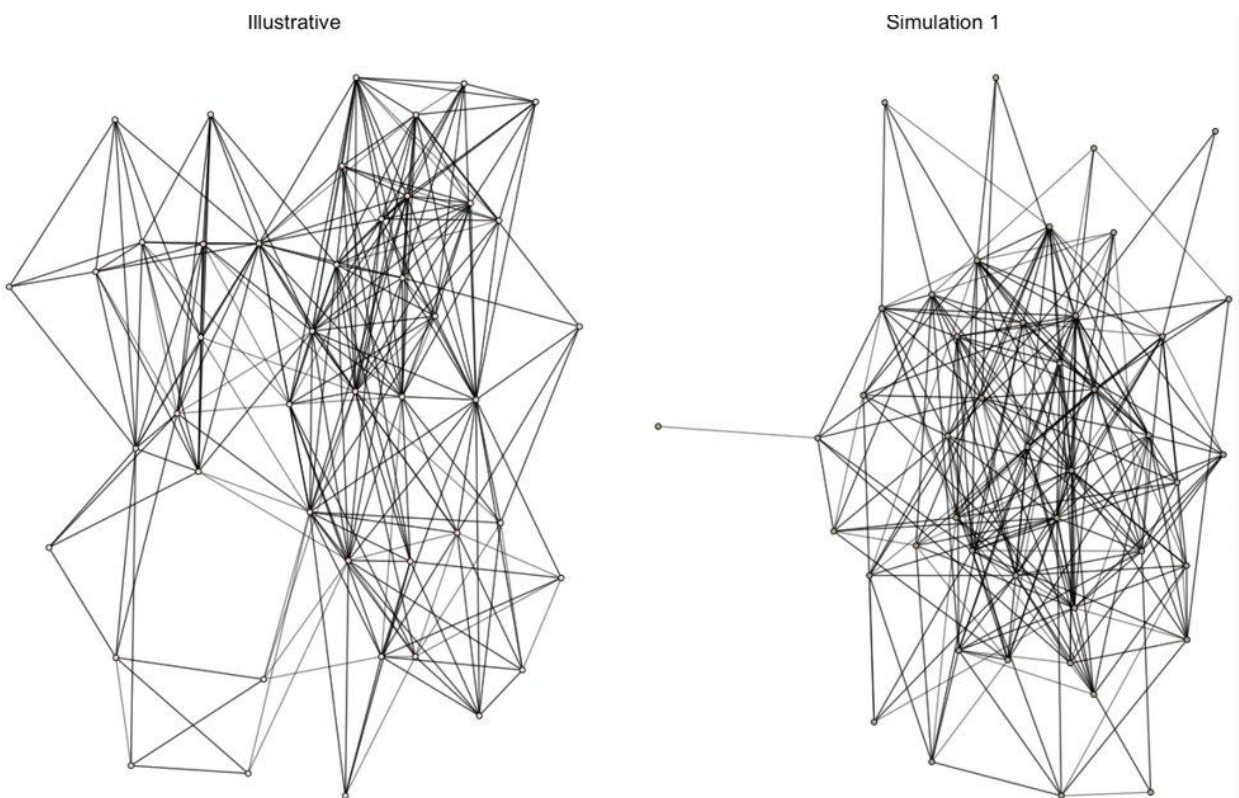
Figure 8 (Louvain Names)

Illustrative   Simulation 1

Figure 9(Simulated vs Original networks)