

A taxonomy of multifunctionality in connectome-constrained neuromorphic computers

Jacob Morra (jmorra6@uwo.ca)

Abstract

The relationship between biological neural network (BNN) structure and artificial neural network (ANN) function is poorly understood. In the brain, structure and function are positively correlated, but far from unity. And yet, structure acts as a guide for function, while disruptions in structure can lead to dysfunction. As a NeuroAI approach, finding topological rules can help us to curtail ANN behaviours. Thanks to recent efforts in connectomics, or the construction of brain wiring diagrams, this strategy is now viable. We are well-poised to begin to explore ‘what’ questions, before proceeding towards the ‘how’ or ‘why’. The ‘what’ in this paper builds on previous work constructing a taxonomy of mesoscale connectomes across species. We sample from this dataset, comparing 18 connectomes to their rewired counterparts within a neuromorphic machine learning framework (reservoir computing) on their capacity to exhibit multifunctionality (MF). We observe a dramatic difference between connectomes and their rewired variants, suggesting a link between BNN structure and MF. We furthermore identify shared features across ‘successful’ networks. Future work will ablate these features and vary known MF-related parameters (e.g. the spectral radius) in order to analyze model prediction dynamics.

Keywords: Connectome-constrained machine learning; Network neuroscience; Reservoir computing

Introduction

Connectome-constrained machine learning (CCML) is an emerging paradigm, combining insights from electron microscopy and network science for the purpose of advancing learning algorithms. Recent work has sought to characterize a taxonomy of mesoscale connectomes by their network features (Suárez et al., 2022). Building on this project, we present an investigation into the capacity of a taxonomy of mesoscale connectomes for informing multifunctionality in reservoir computers. We consider 18 connectome networks and their rewired counterparts on the Seeing Double problem (Flynn, Tsachouridis, & Amann, 2023), and observe a dramatic all-or-none difference in performance in a subset of the connectome-based networks. We furthermore identify network motifs which are aligned with said connectomes.

Methods

Continuous-time reservoir computers

The reservoir computer (RC) is a recurrent neural network best characterized by its single hidden (reservoir) layer. The

RC has two benefits in CCML: First, the reservoir layer is entirely customizable, and can thus accommodate connectome topologies; Second, training occurs only in the final (readout) layer, which preserves reservoir structure during training.

We consider the Continuous-time RC (CTRC) formulation from (Lu, Hunt, & Ott, 2018), which was shown to be multifunctional in Flynn et al. (2023):

$$\dot{r}(t) = \gamma[-r(t) + \tanh(\mathbf{M}r(t) + \sigma\mathbf{W}_{in}u(t))], \quad (1)$$

where $r(t) \in \mathbb{R}^N$ is the RC’s state at time t , N is the network size, γ is the reservoir decay-rate, $\mathbf{M} \in \mathbb{R}^{N \times N}$ is the reservoir adjacency matrix¹, $u(t) \in \mathbb{R}^D$ is the D -dimensional input time series, $\mathbf{W}_{in} \in \mathbb{R}^{N \times D}$ is the input weight matrix, and σ scales the input to the reservoir. Eq. (1) is solved using 4th order Runge-Kutta with time step $\tau = 0.01$. We defer to Morra, Flynn, Amann, and Daley (2023) for further training details.

Multifunctionality and seeing double

Multifunctionality (MF) is defined as the capacity of a biological or artificial neural network (BNN, ANN) to perform two or more mutually exclusive tasks without retuning its network connections (Briggman & Kristan Jr, 2008). MF was conceptualized from BNNs, and includes examples such as the land snail subesophageal ganglion complex and human pre-Bötzing complex (Flynn et al., 2023). It was later applied to ANNs (Flynn et al., 2023), and is at present useful for reconstructing overlapping attractors – e.g. modelling seizures (Lytton, 2008) or dynamics of unmanned aerial vehicle flight (Bi, Qi, Hu, Faradja, & Chen, 2020).

We consider the *Seeing Double* problem as proposed in Flynn et al. (2023) and as implemented in Morra et al. (2023), whereby an RC is trained on a blended input sequence of overlapping circular trajectories, C_A and C_B , rotating in opposite directions. As in Morra et al. (2023), we consider the most difficult case where the circles are entirely overlapping. For some model class instance, we define a train-validate trial as multifunctional (‘successful’) if the trained RC reconstructs a coexistence of C_A and C_B in its prediction space \mathbb{P} without retraining. We adopt criteria for what constitutes an acceptable trajectory from (Flynn et al., 2023), without any alterations.

Connectomes and rewired variants

We select 18 mesoscale connectomes from the publicly available dataset by Suárez et al. (2022), which has been constructed using the MaMI dataset – consisting of diffusion-, T1-, and T2-weighted MRI scans of 124 unique species. Connectomes are size $N = 300$. We rewire each connectome as in

¹ \mathbf{M} is typically a random graph (e.g. Erdős-Renyi). In this project we implant connectome topologies and their rewired counterparts.

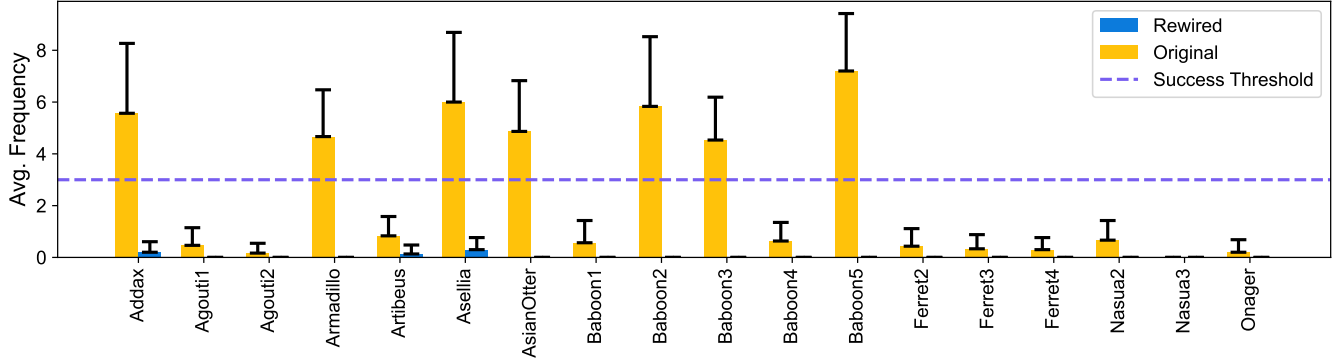


Figure 1: Average frequency of success in multifunctionality trials (out of 30) for 18 connectome-based reservoir computers and their rewired variants. A success threshold illustrates our margin for ‘successful’ networks, used in our graph comparisons.

Suárez, Richards, Lajoie, and Misić (2021) by randomly swapping edge pairs while retaining the size, sparsity, and degree sequence of the network. We also preserve the set of connectome adjacency matrix weights during the rewiring process.

Results

Seeing double trials

We compare the multifunctional (MF) performance for a selection of 18 connectomes and their rewired analogues on the Seeing Double task. Each connectome-based RC is trained and validated on 30 sets of 30 trials. At the end of each set, we track the frequency of ‘successful’ trials (out of 30). We use the standard deviation of the trial performance across sessions to create error bars. See Fig. 1. We observe that nearly all connectomes significantly outperform their rewired variants, with the exception of the Nasua3 network. Significance is determined via a Wilcoxon signed-rank test ($p < 0.05$). We describe seven of these connectomes as ‘successful’ networks by way of a chosen MF threshold average frequency of 3 versus ‘unsuccessful’ networks. Interestingly, inter-species MF success is mostly preserved, with the exception of the Baboon1 and Baboon4 networks.

Discussion

Graph comparisons

For the sake of comparing more MF versus less MF networks, we showcase averaged network statistics for ‘successful’ versus ‘unsuccessful’ original connectomes in Table 1. We consider the mean shortest path length (MSPL), average clustering coefficient (C), betweenness centrality (\bar{B}_G), rich club coefficient ($\phi(k)_G$) and degree centrality (\bar{D}_G) for each graph G . From these comparisons we report that degree centrality for successful connectomes is significantly lower (by Mann Whitney U test, $p < 0.05$) than that of unsuccessful variants, pointing towards the importance of more localized roles, as noted in (Suárez et al., 2022). We furthermore show in Fig. 2 that unsuccessful networks appear to take on a small-worldness criterion as opposed to successful networks. Although the dif-

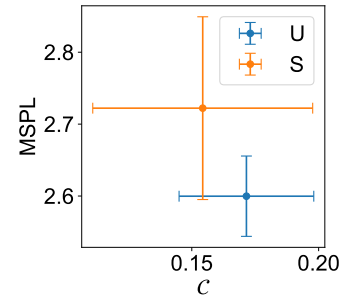


Figure 2: MSPL vs. C for successful vs. unsuccessful graphs.

ferences observed may indicate a factor to consider in further work, they are not significant for this connectome selection.

Table 1: Successful (S) vs. unsuccessful (U) graph statistics.

| Statistic | μ_S | σ_S | μ_U | σ_U | p -value |
|-------------|---------|------------|---------|------------|--------------|
| MSPL | 2.722 | 0.127 | 2.600 | 0.056 | 0.073 |
| C | 0.154 | 0.043 | 0.172 | 0.027 | 0.479 |
| \bar{B}_G | 0.00565 | 0.00044 | 0.00533 | 0.00017 | 0.085 |
| $\phi(k)_G$ | 0.221 | 0.068 | 0.227 | 0.071 | 0.860 |
| \bar{D}_G | 0.044 | 0.005 | 0.049 | 0.002 | 0.044 |

Future Work

The continuation of this project will address localized graph differences and their impact on multifunctionality. We will furthermore create feature-removed models by ablating relevant factors, and determine each model’s performance on Seeing Double, as in Morra and Daley (2023). We will also seek to characterize model prediction dynamics in \mathbb{P} for all connectome-based RCs versus their rewired analogues.

Acknowledgments

We wish to give special thanks to Drs. Andrew Flynn and Laura Suárez for use of their code bases, featured in Flynn et al. (2023) and Suárez et al. (2022), respectively.

References

- Bi, H., Qi, G., Hu, J., Faradja, P., & Chen, G. (2020, September). Hidden and transient chaotic attractors in the attitude system of quadrotor unmanned aerial vehicle. *Chaos Solitons Fractals*, *138*, 109815.
- Briggman, K. L., & Kristan Jr, W. (2008). Multifunctional pattern-generating circuits. *Annu. Rev. Neurosci.*, *31*, 271–294.
- Flynn, A., Tsachouridis, V. A., & Amann, A. (2023, November). Seeing double with a multifunctional reservoir computer. *Chaos*, *33*(11).
- Lu, Z., Hunt, B. R., & Ott, E. (2018). Attractor reconstruction by machine learning. *Chaos*, *28*(6), 061104.
- Lytton, W. W. (2008, August). Computer modelling of epilepsy. *Nat. Rev. Neurosci.*, *9*(8), 626–637.
- Morra, J., & Daley, M. (2023, June). Using connectome features to constrain echo state networks. In *2023 international joint conference on neural networks (IJCNN)* (pp. 1–8).
- Morra, J., Flynn, A., Amann, A., & Daley, M. (2023, October). Multifunctionality in a Connectome-Based reservoir computer. In *2023 IEEE international conference on systems, man, and cybernetics (SMC)* (pp. 4961–4966). IEEE.
- Suárez, L. E., Richards, B. A., Lajoie, G., & Misić, B. (2021, August). Learning function from structure in neuromorphic networks. *Nature Machine Intelligence*, *3*(9), 771–786.
- Suárez, L. E., Yovel, Y., van den Heuvel, M. P., Sporns, O., Assaf, Y., Lajoie, G., & Misić, B. (2022, November). A connectomics-based taxonomy of mammals. *Elife*, *11*.