

Title of submission to PLOS journals

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Abstract

Text

Author summary

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Introduction

Connectivity in brain networks is not uniformly distributed. Network elements with high node degree – i.e., a large number of connections to other areas – are called 'hubs'. When hubs are more densely interconnected than expected by chance they form a 'rich-club', the idea being that the richest members of the network (in terms of connections) are tightly connected to each other, thus forming a club. These densely interconnected hubs are thought to promote efficient integration between anatomically distinct areas and play an important role in brain functioning. It has been shown that hubs exhibit distinct transcriptional signatures in both humans [?] and mice [?]. According to Fulcher Fornito [2], connections involving rich club hubs carry a distinctive genetic signature, which is driven by genes regulating the synthesis and breakdown of adenosine triphosphate (ATP) – the primary energetic substrate of neuronal signaling [2]. These findings highlight a close relationship between metabolic expenditure and the high signaling load of hub regions in the brain, as has been previously proposed [3]. We therefore have some preliminary indications that the transcriptional signature of hubs may be a consistent feature of mammalian brain networks, but it is not known how distinctive this expression signature is; and in particular, whether it holds true for networks resolved at the scale of individual neurons and synapses. To test this possibility, we aimed to replicate findings presented in [2] using microscale connectivity data in C. elegans and gene expression data from WormBase. We sought to determine whether hubs in the C. elegans connectome exhibit

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Materials and methods

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Results

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1. react

- 2. diffuse free particles
- 3. increment time by dt and go to 1

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Discussion

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Conclusion

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Supporting information

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References

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