Using Dimensionality Reduction to Explore Virtual Reality Lobectomies

Allen Q. Ye[1], Olusola Ajilore[2], Alessandro Febretti[3], Andrew Johnson[3], Johnson GadElkarim[2], Shaolin Yang[2], Richard Magin[1], Anand Kumar[2], and Alex D. Leow[2]
[1]Dept. of Bioengineering, University of Illinois at Chicago, Chicago, IL, United States, [2]Dept. of Psychiatry, University of Illinois at Chicago, Chicago, IL, United States, [3]Dept. of Computer Science, University of Illinois at Chicago, Chicago, IL, United States

Target audience – Members of the MR community who are interested in novel methods and technologies for interpreting and visualizing connectome data based on diffusion tensor MRI and tractography.

Purpose – Complex interactions between different regions of the brain have necessitated the development and growth of the field of connectomics. The brain connectome is typically mathematically represented using connectivity matrices, which describe either structural or functional interaction among different brain regions.[1] Most current connectome study designs - based on brain connectivity matrices - involve the computation of summarizing statistics on a global or nodal level. However, current methods visually represent this data using somewhat arbitrary or heuristic methods.[2] In previous studies[3], attempts were made to fundamentally address this issue by proposing a framework that realizes the intrinsic complexity and geometry of a brain network. We propose to further this work by selectively removing nodes from the dimensionality reduced embedding and examining how removing hub areas can affect brain anatomy in the new depiction visualized using Omegalib, a scalable framework for virtual reality environments.[4]

Methods – Forty-six healthy control subjects (HC, 20 male/26 female; age: 59.7 +/- 14.6) were scanned on a Philips 3.0T Achieva scanner (Philips Medical Systems, Best, The Netherlands) using an 8-channel SENSE head coil under an approved IRB protocol. DTI images were acquired with a single shot EPI sequence (FOV = 240 mm; voxel size = 0.83 x 0.83 x 2.2 mm^3; TR/TE = 6,994/71ms; Flip angle = 90°). Sixty seven contiguous axial slices aligned to the anterior commissure–posterior commissure (AC-PC) line were collected in 32 gradient directions with b=700s/mm^2 and one acquisition without diffusion (B0 image). We then generated structural brain networks using several steps: correcting for eddy currents followed by the computation of diffusion tensors and deterministic tractography using the fiber assignment by continuous tracking algorithm.[5] T1-weighted images were used to generate label maps using the Freesurfer software (http://surfer.nmr.mgh.harvard.edu). These 82 Freesurfer ROI labels were then further subdivided using an algorithm that continuously bisected each region across all subjects at an identical angle until the average region size reached a certain threshold in order to better distribute brain regions for visualization. For this project, bisections were made until each brain region was about 1 cm^3. All networks were examined to ensure that all regions were directly connected to at least one other region, preventing the formation of any isolated "islands". To compensate for inter-subject variations, we averaged all 46 brain networks to obtain a group average network. Next, using the Dijkstra algorithm, we created the graph distance matrix of the average network[5]. This network either had the "Rich Club" nodes removed (as defined by Van den Heuvel[6]) or an equal but random removal of nodes (n=20,000 permutations). Using this graph distance matrix we explored brain's intrinsic geometry by feeding these distances into the Isomap dimensionality reduction algorithm in Omegalib. Average distance was measured after three dimensional embedding from each node to the isocenter of the visualization.

Results and Discussion – Rich club nodes were 20.09% of all nodes within our network. Average distance from nodes to isocenter was calculated for all 20,000 trials of random lobectomies. The results can be summarized in **Figure 1** which has an error bar representing the 99% confidence interval. This suggests the importance of the since removing these hub regions disperses our embedding suggesting a more disconnected brain. **Figure 2** shows the side view for the entire brain in standard anatomical format and the front view for various embeddings both pre- and post-removal in the Omegalib Isomap visualization program. Of importance, we note that the middle-right image looks very qualitatively similar to the original embedding (middle-left), while the rich club removed embedding (far-right) looks starkly different.

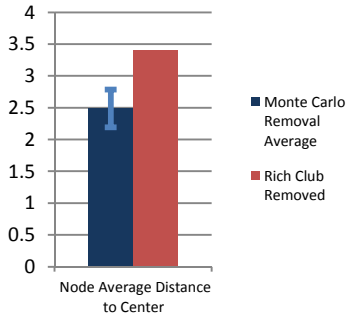

Figure 1: Difference between the node average distances for Monte Carlo removal (with 99% CI) versus targeted rich club

Conclusion – We propose a novel framework for exploring the intrinsic geometry of brain networks using both a targeted and random removal approach that can be visualized on a desktop computer. We posit that researchers in the future will be able to deduce neurodegeneration in the brain by observing an alteration in this intrinsic geometry with these visualization technologies. The present work consists primarily of methodological development, and although applied to a dataset of human subjects remains relatively qualitative in nature. Future work will include the further development of necessary mathematical and statistical theories for group and/or longitudinal studies.

Acknowledgments: We would like to acknowledge the help of Galen Ramos-Thomas, Lance Long, Arthur Nishimoto, and Victor Mataveetsi. Research reported in this publication was supported by Grants TL1TR000049, R01 MH-073989, and K23 MH-081175.

References 1. Sporns, O., Tononi, G. & Kötter, R. The Human Connectome: A Structural Description of the Human Brain. *PLoS Comput. Biol.* **1,** e42 (2005). 2. Margulies, D. S., Böttger, J., Watanabe, A. & Gorgolewski, K. J. Visualizing the human connectome. *NeuroImage* (2013). 3. Ye, A. *et al.* Visualizing Connectomes Elucidated from Dimensionality Reduction in an Immersive Virtual Reality Environment (CAVE2™). in *Proceedings of the 22nd ISMRM* 4.Febretti, A. *et al.* Omegalib: A multi-view application framework for hybrid reality display environments. in *Virtual Reality (VR), 2014 iEEE* 9–14 (IEEE, 2014). 5. Mori, S., Crain, B. J., Chacko, V. P. & Van Zijl, P. C. M. Three-dimensional tracking of axonal projections in the brain by magnetic resonance imaging. *Ann. Neurol.* **45,** 265–269 (1999). 6.Van den Heuvel, M. P. & Sporns, O. Rich-Club Organization of the Human Connectome. *J. Neurosci.* **31,** 15775–15786 (2011).

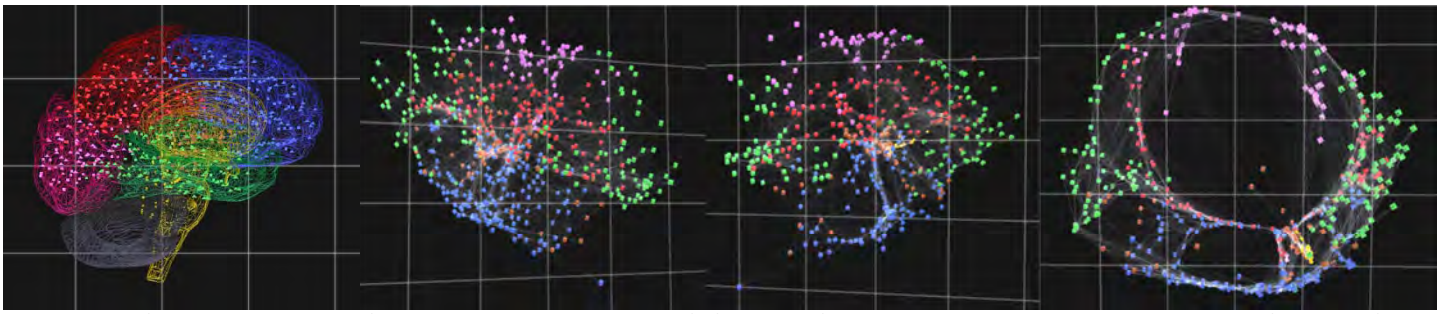

Figure 2: Far left, anatomical side view of our group average brains; middle left; front view of a 3-dimensional Isomap embedding; middle right, front view of the 3D Isomap embedding after 20.09% of nodes were removed; far right, 3D Isomap embedding of the same data set with a selected 20.09% of nodes removed (rich club, targeted removal). For Isomap embeddings, 95% of all fibers are shown with thickness of the streamlines describing the number of fibers between node regions.