EN.580.694: Statistical Connectomics
Final Project Report

akim1 · May 14, 2015

Effects of Spatial Resolution on Accurate Determination of Graph Connectivitiy

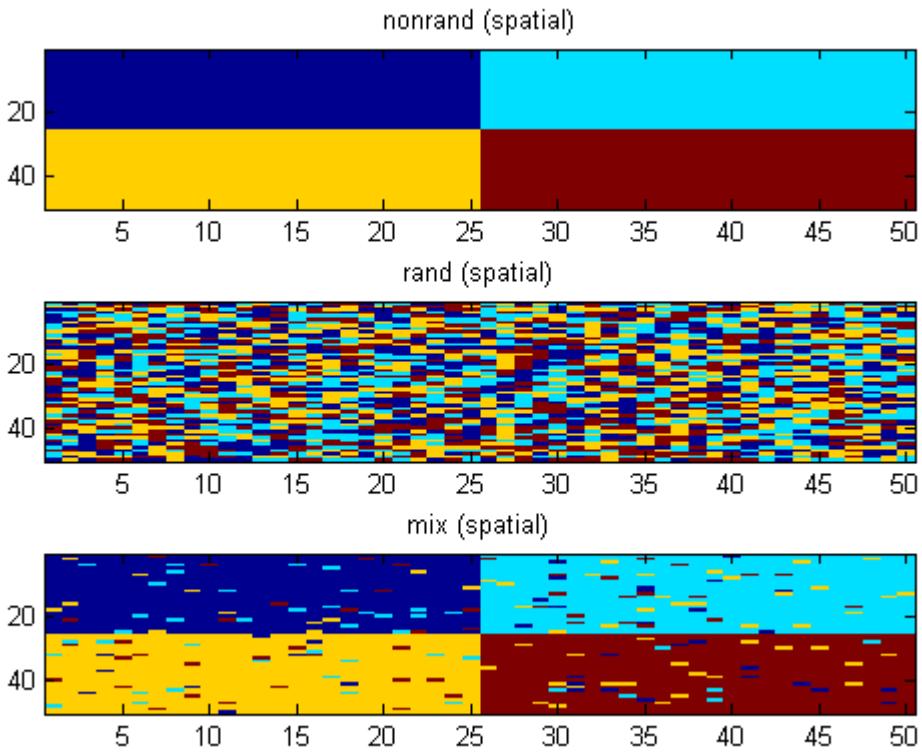

Figure 1: 2-dimensional grid with block identity of the pixels for the three different cases: non-random, random, and mixture of two.

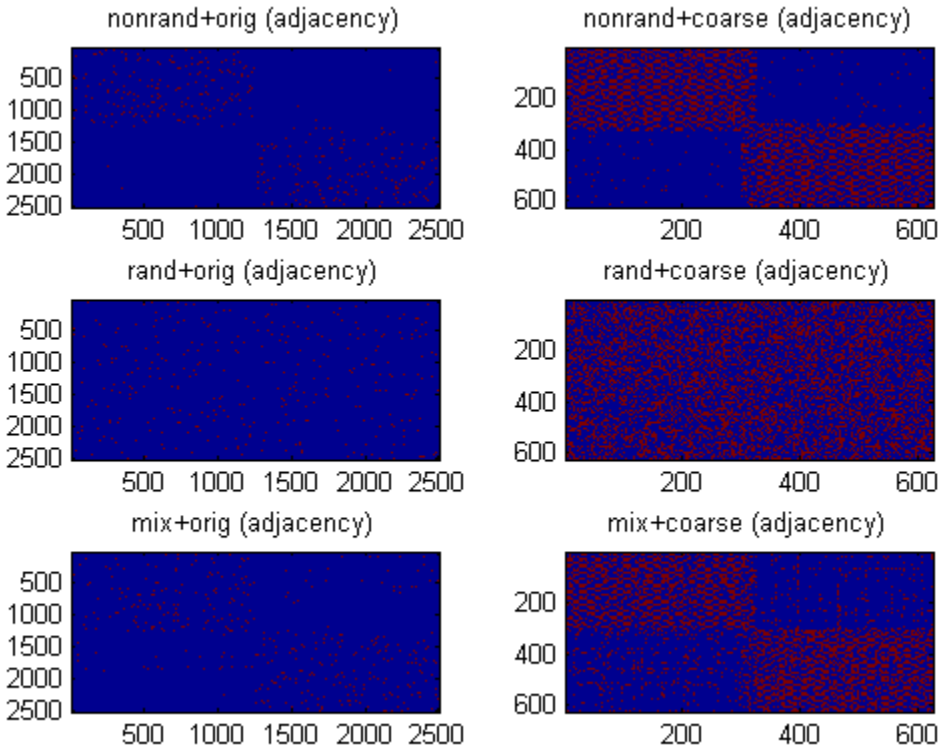

Figure 2: Representation of the adjacency matrix for non-coarsened and coarsened data for the three different cases.

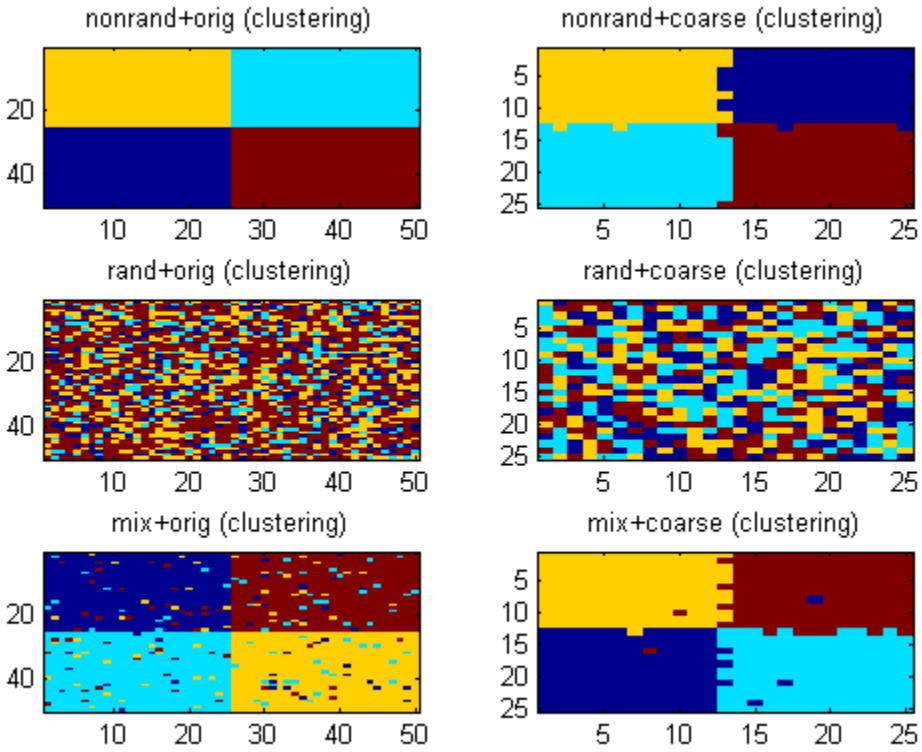

Figure 3: Result of k-means clustering for non-coarsened and coarsened data for the three different cases.

Opportunity The ability to measure individual connectomes holds great promise in advancing our knowledge of the brain and consciousness. Despite these promises, current technology and state of knowledge prevents the rescaling of this measurement process into a computational problem that can be solved within a reasonable time with finite resources. The complexity of the problem inevitably poses a challenge both in validation of data and establishment of a consensus dataset. This proposal posits that one factor that may contribute to these challenges is the spatial resolution at which the data is obtained.

Challenge Previous studies have explored the role of resolution in diffusion spectrum MRI [1]. Despite the fact that a voxel is the elementary unit of MRI imaging, voxels represent information from collections of neurons. Thus, there exists an inherent loss of information that results from the observation of aggregate behaviors. Changes in "hubs" of a connectome have previously been reported to be a characteristic of many diseases of the brain [2]. Information of these "hubs" can be lost without sufficient level of resolution, and their activities can be drowned out by the presence of their neighboring neurons. In this study, a purely computational approach was taken to study the implications of observing aggregate behavior and resulting potential information loss.

Action A neuron connectivity network was generated based on a stochastic block model. The block identity of each neuron was assigned based on their relative location in a 2-dimensional grid. In one limiting case, contiguous pixels were assigned to one block (nonrand case), while in another limiting case, all pixels were randomly assigned to a block (rand case). An intermediate case was also explored where a probability distribution was used to create a mixture of the two limiting cases (mix case). Once the connectivity network was generated, the network was coarsened by combining the spatial and connective properties of pixels in a two-by-two square into one new pixel. K-means clustering was performed on this new coarsened grid to qualitatively characterize any notable losses of information in respect to true information and non-coarsened data.

Resolution Representation of the adjacency matrices showed the geometric delineation of the pixels and their respective connections. Coarsening the 2-dimensional grid led to a decrease in sparsity as shown across all three different cases. Subsequently, k-means clustering was used to correctly recapitulate the true information in the non-random and mixture cases. Whether the true information was correctly determined in both random cases was difficult to ascertain from the generated figure. Coarsening the data led to the introduction of artifacts at the boundaries in the nonrandom and mixture case. This was accompanied by a significant decrease in the heterogeneity of the region, suggesting that potentially important neuronal activity is lost in aggregate information.

Future Work Much of the work presented in this report was limited by the availability of the necessary computational resources. Future work would include the expansion of the analysis into 3-dimensions with significantly greater number of pixels and inclusion of physiological regions. A rigorous framework would also be established to determine statistical confidence, and empirical data would be used to validate these findings.

References

[1] Leila Cammoun, Xavier Gigandet, Djalel Meskaldji, Jean Philippe Thiran, Olaf Sporns, Kim Q Do, Philippe Maeder, Reto Meuli, and Patric Hagmann. Mapping the human connectome at multiple scales with diffusion spectrum mri. *Journal of neuroscience methods*, 203(2):386–397, 2012.

[2] Nicolas A Crossley, Andrea Mechelli, Jessica Scott, Francesco Carletti, Peter T Fox, Philip McGuire, and Edward T Bullmore. The hubs of the human connectome are generally implicated in the anatomy of brain disorders. *Brain*, 137(8):2382–2395, 2014.