Connectivity based segmentation of the Corpus Callosum using a novel data mining approach

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Introduction: Connectivity based parcellation/segmentation of brain regions was suggested by Brodmann[1] about 100 years ago. Recently, there has been increased interest [2-6] in discovering finer segmentation of anatomical regions using DTI based connectivity. Such finer segmentations have also been shown to be useful in differential diagnosis for mental disorders.[7] Most of these methods do not make use of two types of underlying structure in the data.[2-6] First, connectivity from two adjacent seed voxels to remaining voxels is expected to be more similar than that of seed voxels that are farther apart. Second, we noticed, in our data, that two adjacent seed voxels are not necessarily connected to exactly the same voxels in the brain, but to largely adjacent voxels. In this work we studied the problem of segmenting Corpus Callosum (CC) using a Shared Nearest Neighbor (SNN) based algorithm that has been found to be promising in climate and biological networks.[8-9] This approach inherently makes use of the first type of structure, but ignores the second type. We improved this approach to make use of the second type of structure and we refer to it as Spatial-SNN. Using our Spatial-SNN approach, we can obtain consistent segmentation results with known anatomy using 3T and 7T DTI data acquired at different spatial resolutions.

Methods: Two datasets from the same subject of the HCP[10] database were analyzed. HCP 3T data was acquired with a 1.25mm^3 voxel size, at 3 *b*-values (1000, 2000 and 3000 s/mm^2) with 90 directions per *b*-value.[11] HCP 7T data was acquired with a 1.05mm^3 voxel size, at 2 *b*-values (1000 and 2000 s/mm^2) with 65 directions per *b*-value.[12] Diffusion MRI data was analyzed by probabilistic tractography using FSL[13] to generate connectivity maps for each individual voxel with masks of the corpus callosum that were manually defined.

SNN approach works by first computing similarity in tractography between every pair of adjacent seed voxels. A typical approach to compute this similarity between two adjacent voxels is to assess the number of target voxels to which both the adjacent seed voxels are connected to. However, we found that in reality two adjacent seeds are often not typically connected to identical target voxels, but to adjacent target voxels. This is illustrated in Figure 1, where the blue and red regions show the voxels that are connected from two adjacent seed voxels in CC. We incorporate this into our measure for computing the similarity in connectivity between two adjacent seed voxels by accounting for connections to adjacent target voxels. Our Spatial-SNN approach first computes this adjusted similarity between all pairs of adjacent seed voxels and this information is represented in the form of a graph where a seed voxels is a node and similarity between adjacent seed voxels is treated as edge strength. Then a normalized graph cut approach [10] is used to split this graph into desired number of segments.

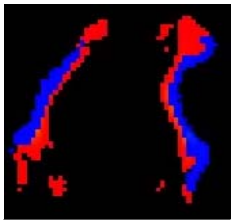

Figure 1: Connectivity from two adjacent seed voxels.

Results: We found that Spatial-SNN resulted in more consistent segmentations of CC for 3T and 7T data, with different spatial resolutions. The segments found using Spatial-SNN were also coherent in space than some of the segments found using SNN (shown using green circles in Figure 2). Moreover, SNN segmented the posterior part (splenium) of the CC into two parts in the 3T data while it was segmented into 3 parts in the 7T data (shown in red circles in Figure 2). In this situation, we hypothesize that the greater spatial resolution of the 7T data might "help" SNN identify two clusters (green and light blue) in the more dorsal part of the splenium. On the other hand, Spatial-SNN segmented the splenium into 3 parts in both 3T and 7T.

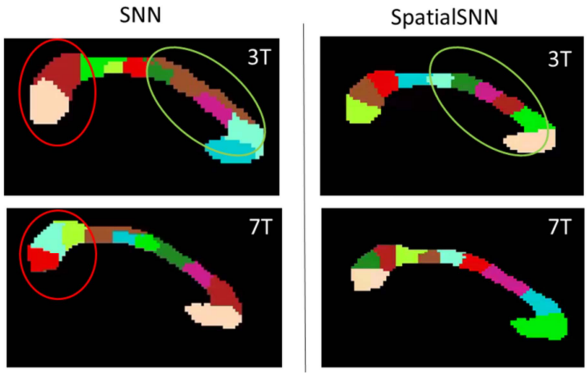

Figure 2: Comparison between SNN and Spatial-SNN at 3T and 7T.

Discussion: The observed differences between SNN and Spatial-SNN are due the ability of Spatial-SNN in handling the spatial information in the target locations that is typically ignored by the alternative approaches. Hierarchical Dirichlet process mixture models that have been used earlier for segmentation using DTI data take into account the similarity in adjacent seed voxels using a spatial prior.[5] However, they ignore the spatial similarity in the target voxels. Additionally, our approach is computationally efficient because only the similarity between adjacent seed voxels is computed and not between all pairs of seed voxels.

References: [1] Brodmann, Localisation in the Cerebral Cortex 1909. [2] Jakab *et al. Brain topo.* 25.3 (2012): 264-271. [3] Nanetti *et al. Neuroimage* 47.4 (2009): 1666-1677. [4] Jbabdi *et al. NeuroImage* 44.2 (2009): 373-384. [5] Gorbach *et al. Fron. Neuroinfo.* 5 (2011). [6] Cloutman *et al. Fron. Neuroanat.* 6 (2012). [7] Menke *et al. Neuroimage* 52.4 (2010): 1175-1180. [8] Kawale *et al. Proc. SDM.* (2011). [9] Pandey *et al. PloS one* 9, no. 10 (2014): e109130. [10] Van Essen *et al. Neuroimage* 2012;62(4):2222-31 [11] Sotiropoulos *et al. NeuroImage* 80:125-43, 2013 [12] Vu et al *Proc. ISMRM* #1000, 2014 [13] Jenkinson *et al. Neuroimage*, 2012; , 62(2), 782-790. [14] Shi *et al. IEEE PAMI* 22.8 (2000): 888-905.

Acknowledgement: Data were provided by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University. This work was partially supported by NIH grants P41 EB015894 and P30 NS076408, NSF grant 1355072, and MnDRIVE postdoctoral fellowship.