# A Model-Free Unsupervised Method to Cluster Brain Tissue Directly From DWI Volumes

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**Introduction** We present a simple, novel approach to the voxelwise classification of brain tissue acquired with diffusion-weighted imaging (DWI). By working directly upon the individual DWI volume data, it makes no assumption of an underlying diffusion model. In addition, by summarising statistics across the diffusion gradient directions, we obtain features that are rotationally invariant. The method could have application during tractography pre-processing, and has potential as a complementary approach for analysis of DWI datasets.

**Data and Methods** Analysis was performed upon pre-processed DWI data (288 gradient volumes, of which 270 are with diffusion weighting) from a single subject from the Human Connectome Project (HCP) [1-3]. All code was written in Matlab, with the exception of the FA calculations which were performed using FSL [4].

For each voxel in turn, DWI data was pooled from all 27 voxels within a [3 x 3 x 3] neighbourhood. For each gradient direction, a histogram of the corresponding normalised diffusion signal was computed using 25 globally-determined bins, resulting in a collection of histograms indexed by the gradient directions. Next, for each of the 25 histogram bins, the entropy of the distribution of its values across all gradient directions was computed, generating a single rotationally-invariant measurement. This resulted in a 25-component entropy vector for each brain voxel. As entropy is a measure of the complexity of the distribution, isotropic diffusion signals are expected to show high entropy values, and anisotropic diffusion low entropy values. Figure 1 illustrates the method. This whole-brain entropy matrix was then clustered using a Gaussian Mixture Model, with the number of clusters arbitrarily fixed at 8 to accommodate a range of tissue classes. For comparison, the FA was calculated for the same data using FSL's 'dtifit' function and a weighted least squares fit and then thresholded at 0.5.

**Results** Figure 2 shows the labels for all 8 clusters. The red cluster in Figure 2 is also used in Figure 3 for comparison against the thresholded FA. The high overlap (Figure 3, brown region) would suggest that this cluster is comprised mainly of white-matter single-tract voxels (cortical-spinal tract). Several clusters in Figure 2 show good correspondence to other tissue classes, such as the cortical and sub-cortical grey matter (light blue, dark blue) and ventricles/CSF (pink), whilst others appear to capture boundary regions between them (green and yellow).

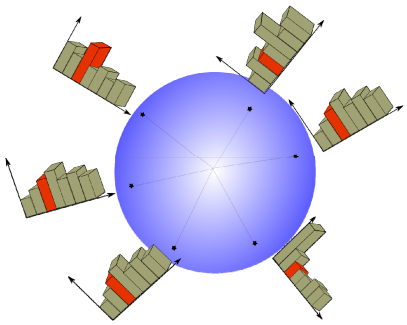

Figure 1: Illustration of how the histograms are calculated for each direction. An entropy is calculated for each bin index, across all the directions. For example, the third component is entropy of the red bins.

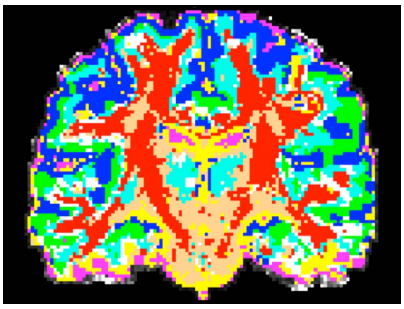

Figure 2: Labels of all 8 clusters. The red cluster is used in Figure 2.

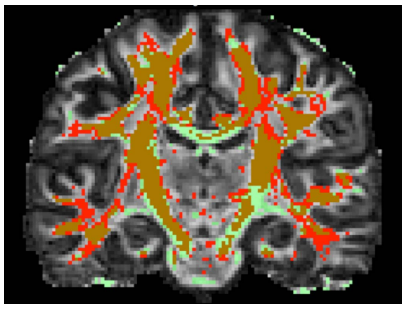

Figure 3: Agreement between a model-free cluster (red) and the thresholded FA (green). Overlap is shown in brown. Background is the FA image.

**Discussion & Conclusion** The proposed method is a simple, model-free approach to classifying DWI voxels based only upon their statistical properties. It clusters together voxels that have the same patterns of diffusion signal, doesn't require fitting of a diffusion model, and is rotationally invariant. As such, it doesn't necessitate the a priori choice of a particular representation of the diffusion signal (such as a simple, multiple or higher-order tensor). It could therefore be used as an unbiased estimation of a voxel's diffusion "fingerprint". Indeed, it motivates investigation into its potential as an estimator of diffusion biomarkers within development, ageing or disease. Developments are ongoing to optimise the number of clusters, improve the clustering performance, and investigate other metrics and statistics of the bin distributions.

**References**

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