

Evaluating the accuracy of white-matter connectomes

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Target audience. Investigators using diffusion-weighted MRI (DWI) data and fiber-tractography algorithms.

Purpose. Diffusion weighted MRI (DWI) coupled with fiber tractography is a unique method for noninvasive measurement of the properties of white-matter fascicles in the living human brain. Investigators can choose from a large set of DWI measurements and tractography algorithms to estimate a full set of white-matter fascicles, the connectome. Each algorithm creates connectomes based on its own theoretical principles. It is current best practice in the field to choose one algorithm, generate a connectome and then interpret the results. But different algorithms can produce substantially different connectomes (e.g., Fig 1). We propose a method for evaluating the quality of connectomes by assessing how well the estimated connectomes predict an independent set of diffusion measurements.

Methods. We acquired DWI data with 150 diffusion-weighting directions ($b = 2000$) at 3T. We used the data to generate whole-brain human connectomes with three different tractography algorithms – two based on a tensor model (TEND¹, FACT²) and one based on fiber orientation distribution functions derived from constrained spherical deconvolution³. By assuming that fascicles represent bundles of axons⁴ we use connectomes to generate predictions of the diffusion measurements in a voxel as a weighted sum of the contributions from all fascicles in the voxel. We evaluate the predictions of different connectomes by cross-validation: we compare the prediction with the diffusion measurements obtained in an independent data set from the same subject. Prediction accuracy is quantified as the relative root mean squared error (rRMSE). This is the ratio of the RMSE of the prediction of the connectome in a second measurement and that of one data set over the other: $\sqrt{(model - data_1)^2} / \sqrt{(data_2 - data_1)^2}$. Values of rRMSE below 1 indicate that the connectome predicts the second diffusion measurements better than data-to-data reliability.

Results. The connectomes generated by TEND and FACT predict the diffusion data worse than data reliability (rRMSE > 1). For some parameter values CSD connectomes predict the diffusion data with higher reliability than the data (rRMSE < 1; Fig 2). CSD connectomes model accuracy increases with increasing order of the spherical harmonics basis functions used, up to intermediate model complexity ($4 < L_{max} < 16$; Fig 2).

Discussion. We present a method for evaluating the quality of connectomes of white-matter fascicles derived from diffusion-weighted data and tractography algorithms by predicting the diffusion data measured at each voxel. We tested predictions of three algorithms (TEND, FACT and CSD). CSD can predict diffusion data more reliably than the data themselves, which is to be expected of a good algorithm.

Conclusion. Evaluating the predictions made by different tractography algorithms allows for identifying connectomes that best represent the measured white-matter properties. Current algorithms predict new data sets about as well as the data predict new measurements.

References. 1. Lazar M. Weinstein DM, Tsuruda JS, Hasan KM, Arfanakis K, Meyerand ME, Badie B, Rowley HA, Haughton V, Field A, Alexander AL. White matter tractography using diffusion tensor deflection. *HBM* 2003; 306-321 2. Basser PJ, Pajevic S, Pierpaoli C, Duda J, Aldroubi A. In vivo fiber tractography using DT-MRI data. *MRM* 2000; 44(4):625-632. 3. Tournier JD, J-Tournier JD, Calamante F, Connelly A. Robust determination of the fibre orientation distribution in diffusion MRI: Non-negativity constrained super-resolved spherical deconvolution. *Neuroimage* 35 (2007) 1459-1472 4. Assaf & Basser Composite hindered and restricted model of diffusion (CHARMED) MR imaging of the human brain. *Neuroimage* 2005; 27(1):48-58.

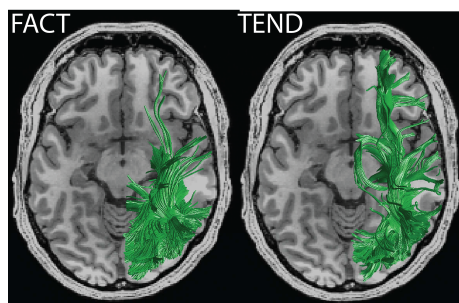


Figure 1. Estimates of connectomes from human visual area hV4 produced by two algorithms; FACT, TEND.

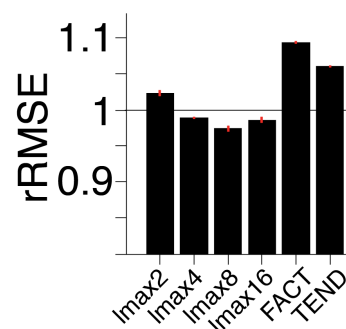


Figure 2. rRMSE (mean±1sem) for different connectomes. Left to right CSD with different L_{max} , FACT and TEND.