

Assessment of cortico-cortical connectivity in the presence of image artifact

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Introduction: MR diffusion tractography is becoming a popular tool in the investigation of the integrity of white matter tracts *in vivo*. A frequently used MR diffusion tractography derived metric to describe tract integrity is the number of streamlines connecting two different cortical regions. In the presence of pathology, the diffusion properties of the white matter are influenced locally, which in turn can cause streamlines to terminate prematurely. Therefore, pathology is expected to result in a reduced number of connecting streamlines in patients compared to healthy control participants.

However, it is a well known fact that patients are more likely to move during the diffusion data acquisition than healthy controls, resulting in a higher number of slices in the dataset that are affected by motion artifact. In this study, we investigated the effect of an increased number of corrupted image slices on cortico-cortical streamline number.

Methods: Ten healthy control participants were included in this study. HARDI data (64 diffusion encoding directions, $b = 3000 \text{ s mm}^{-2}$, 2.5 mm isotropic resolution) and high-resolution structural data (MPRAGE, 1 mm isotropic resolution) were acquired using a 3T Siemens Tim Trio scanner (Erlangen Germany). Using the structural images, the cerebral cortex of all participants was parcellated into 33 regions per hemisphere based on gyral and sulcal structure using freesurfer [1,2] (<http://surfer.nmr.mgh.harvard.edu/fswiki>; see Figure 1 (left)). Structural and diffusion data were aligned using rigid-body registration.

To study the influence of motion artifact (which is often characterized by signal loss within isolated slices due to bulk motion), we generated for every participant a "corrupted" and a "corrected" dataset from the original HARDI dataset. The corrupted data was generated by randomly selecting 10 slices (of 64 x 60 slices) from the HARDI dataset, and replaced those slices with Rician noise generated from the imaging data. Corrected datasets were generated by excluding those slices from further analysis.

The fibre orientation distributions were calculated for the original, the corrupted and the corrected data using constrained spherical deconvolution [3] with default parameters. Probabilistic tractography was performed using MRtrix (<http://www.nitrc.org/projects/mrtrix>). Every brain voxel was seeded with 50 probabilistic streamlines (see Figure 1 (right)). Streamlines were prevented from crossing cortical folds using a termination mask defined automatically on the structural images. The terminal end points of every streamline were tested with every cortical region, and for every possible connection the number of connecting streamlines was recorded. Thus, for every participant we obtained 3 connectomes: the original connectome, which is not affected by motion artifact; the corrupted connectome, which includes 10 corrupted slices; and the corrected connectome, which has 10 slices removed from the original data.

The set of corrupted connectomes was compared to the set of original connectomes using a paired t-test. The same test was repeated to compare the set of corrected connectomes to the set of original connectomes.

Results: Figure 2 shows the results of the paired t-test between the original and the corrupted datasets. Several cortico-cortical connections show significant differences in connectivity in the absence pathological causes. Importantly, no significant differences were found when comparing the original and the corrected datasets.

Interestingly, the introduction of 10 corrupted slices per dataset did not lead to an increased variation in streamline number compared to the original dataset. Instead, connectivity for any particular connection was either increased or decreased for all participants. Figure 3 shows the bias of the streamline number. No biasing was observed when comparing the original datasets with the corrected datasets.

Discussion and Conclusions: This study shows that cortico-cortical streamline number is significantly influenced by the presence of only a small number of corrupted image slices (10 out of 3840). In patient-control studies, patient data are in general more likely to be influenced by motion artifact. Therefore care has to be taken when interpreting cortico-cortical streamline number. If a large number of diffusion directions have been acquired ("oversampling"), the bias in streamline number can be easily corrected by excluding image slices affected by motion artifact, thereby removing the biasing effect.

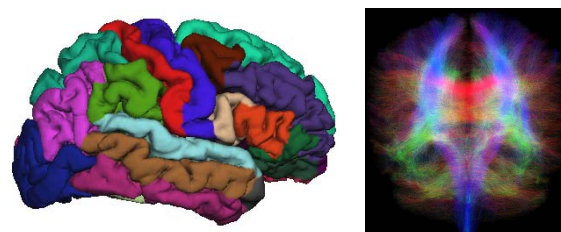


Figure 1: Freesurfer cortical parcellation (left) and probabilistic wholebrain tractogram (right)

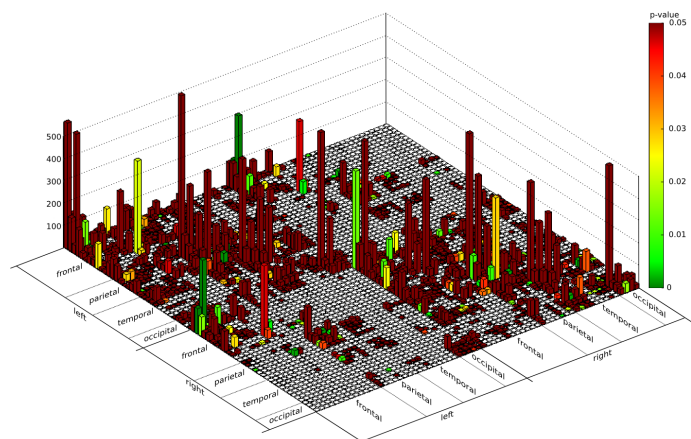


Figure 2: Results of the paired t-test between original data and corrupted data. The height of the bars indicates the number of connecting streamlines for every cortico-cortical connection. The colour of bars indicates the p-value obtained for this connection.

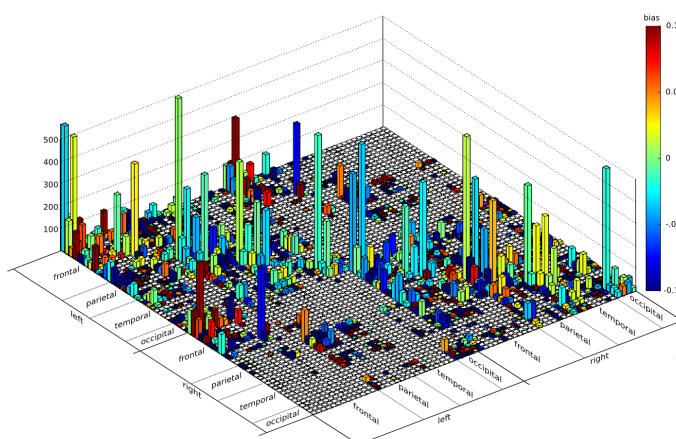


Figure 3: Bias of streamline number for the corrupted compared to the original data. The colour of bars indicates the bias.

References: [1] Fischl et al. 2004, Cereb Cortex 14(1): 11-22; [2] Desikan et al. 2006, Neuroimage 31(3): 968-80; [3] Tournier et al 2007, Neuroimage 35(4): 1459-72