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Reducing false positive connection in tractograms using joint structure-function filtering

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INTRODUCTION

Due to its ill-posed nature, tractography generates a significant number of false positive connections between brain regions [3]. To reduce the number of false positives, Daducci et al. [1] proposed the COMMIT framework, which has the goal of re-establishing the link between tractography and tissue microstructure. In this framework, the diffusion MRI signal is modeled as a linear combination of local models associated with streamlines where the weights are identified by solving a convex optimization problem. Streamlines with a weight of zero do not contribute to the diffusion MRI data and are assumed to be false positives. Removing these false positives yields a subset of streamlines supporting the anatomical data. However, COMMIT does not make use of the link between structure and function and thus weights all bundles equally. In this work, we propose a new strategy that enhances the COMMIT framework by injecting the functional information provided by functional MRI. The result is an enhanced tractogram filtering strategy that considers both functional and structural data.

METHODS

We randomly selected 3 subjects from the HCP500 dataset, each processed with the HCP minimum pipeline [4]. For each subject, we performed probabilistic tractography using the vertices of the cortical mesh as seed locations. We then parcellated the cortex into 74 regions based on their extrinsic anatomical connectivity using the algorithm proposed by Gallardo et al. [2] Using the resting state functional MRI of each subject, we computed the functional connectivity between the cortical regions. To do so, we first high pass filtered the time series and computed the average functional MRI signal inside of each region. Finally, we divided the signals into windows of 100 seconds and computed the maximum sliding window correlation between every pair of regions. These correlation coefficients were used to define a regularization coefficient for each bundle of the tractogram. The regularization coefficients were designed to favor streamlines associated with a high correlation while penalizing but not excluding those with a low correlation. The rationale is that streamlines connecting regions that are functionally correlated should be favored to explain the diffusion MRI data. As in the non functional COMMIT, we solved the optimization problem and removed streamlines with a weight of zero. For comparison, we also filtered the tractograms using equal weights for all bundles, i.e. without functional priors.

RESULTS

To measure the performance of the proposed algorithm we evaluated the quantity of candidate false positive streamlines that we were able to detect and the diffusion MRI signal fitting error. A filtering strategy is considered superior if it is able to remove more streamlines while still explaining the diffusion MRI signal. Figure 1 illustrates that including functional information allows us to increase the number of candidate false positives detected without affecting the data fitting error, therefore indicating enhanced filtering. Interestingly, the addition of functional information modified the spatial location of the removed bundles in a non-uniform manner. The streamlines removed by both filtering strategies and those removed by one or the other are illustrated in Figure 2.

CONCLUSION

We proposed a new method to enhance tractogram filtering using functional information. Our preliminary results indicate that injecting functional data increases the number of streamlines removed while maintaining data fit and modified the spatial location of removed streamlines across the brain.

REFERENCES

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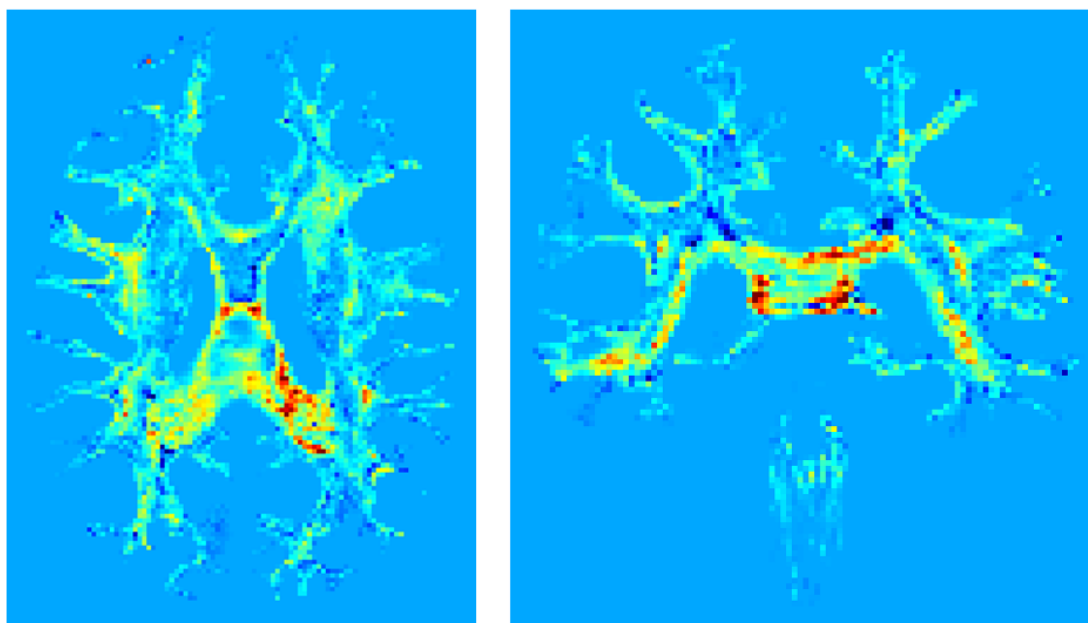
[4] Van Essen, D.C., et al. (2012) "The Human Connectome Project: a data acquisition perspective." *Neuroimage* 62.4: 2222-2231.

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FIGURE 1

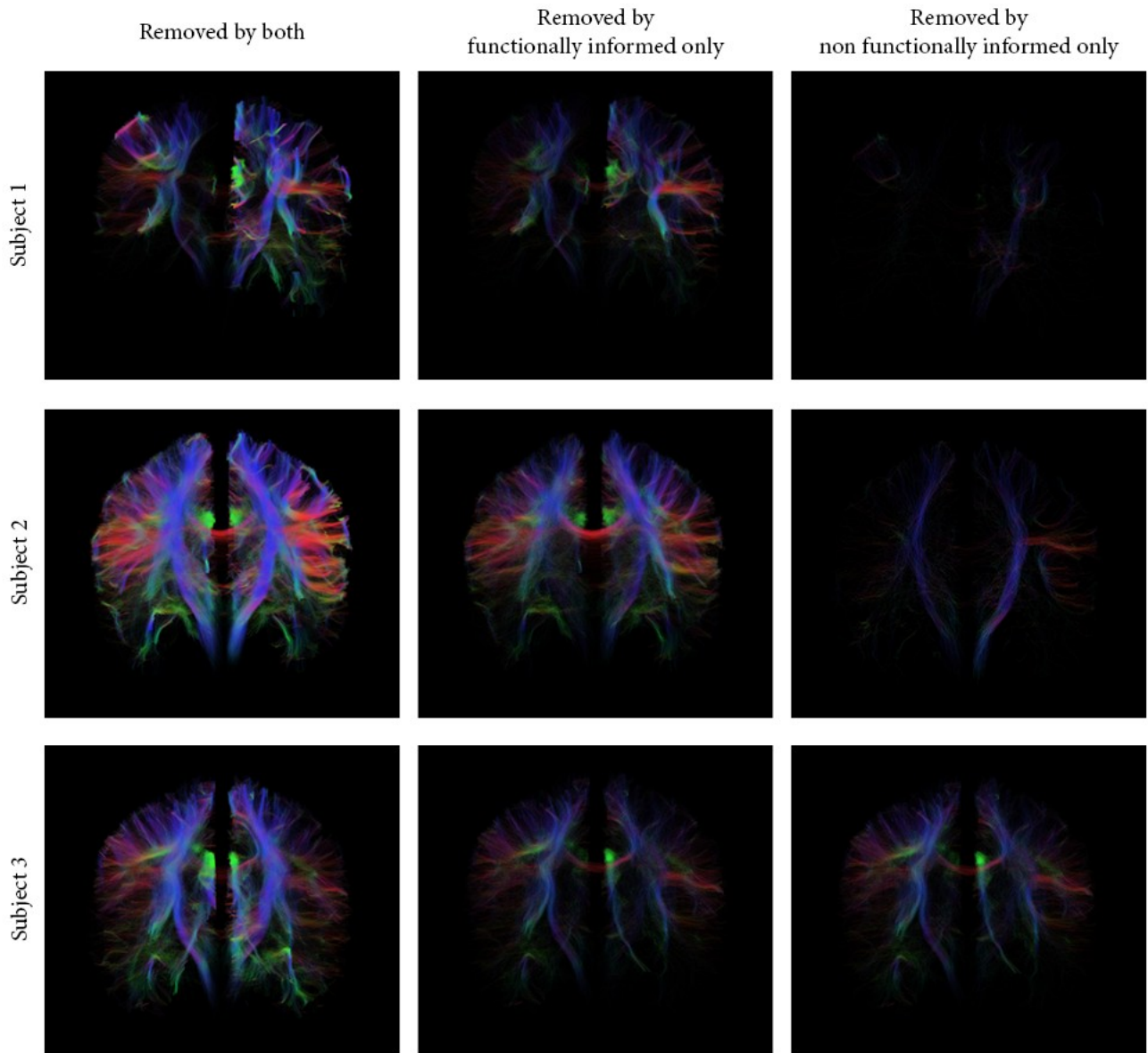
	without functional		with functional	
	% removed	residual	% removed	residual
Subject 1	12.26	958.47	16.01	931.07
Subject 2	18.85	828.58	24.19	808.27
Subject 3	13.55	847.07	16.35	828.95



The table compares the performance of the functionally informed and non functionally informed algorithms. The functionally informed approach was able to remove more candidate false positives while simultaneously reducing the data fitting residual.

The figures represent the difference between the normalised root mean square error of the results of the two algorithms for one subject. Warm colors represent regions where the functionally informed algorithm performed better than the non functionally informed one. These images confirm that functional information leads to better fitting, as shown in the table.

FIGURE 2



The images above illustrate the streamlines that were removed by each algorithm. The first column contains streamlines removed by both the functionally informed and the non functionally informed algorithms. The second one shows streamlines removed by only the non functionally informed algorithm. Each line corresponds to one subject.