MicroQIT - A Computational Framework for Population Microstructure Imaging

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Synopsis

Microstructure imaging provides a quantitative tool for characterizing neural tissue with diffusion MRI and expanding our understanding of how the brain changes in health and disease. However, robust computational tools are needed for population imaging studies, so we developed a computational framework (MicroQIT) using the Quantitative Imaging Toolkit to meet this need by providing regional summaries and spatially normalized microstructure parameter maps. It supports a variety of ways to extract microstructure information from multi-shell diffusion MRI, leverages grid computing environments, and is available for use by the research community for future studies.

Introduction

Microstructure imaging constitutes a wide variety of techniques for estimating quantitative parameters that describe brain tissue using diffusion MRI[1]. These techniques can expand our understanding of how the brain changes in health and disease; however, robust computational tools are needed for conducting microstructure imaging studies and evaluating the efficacy of microstructure models[2]. While a variety of software packages exist for estimating microstructure parameters from individual scans[3,4] there remains a need for integrated workflows for processing large datasets from population imaging studies. To address this challenge, we developed a computational framework (MicroQIT) using the Quantitative Imaging Toolkit[5] and provide it for use by the research community. We describe the design of the framework, present results from evaluative studies of its reliability and sensitivity to age associations in neurodevelopment, and discuss its capabilities and prospects.

Design

The primary design goal of MicroQIT is to automate the microstructure imaging studies that involve large populations. It can be used from the command line or from the LONI Pipeline[6] to take diffusion-weighted MRIs as input and produce spatially normalized microstructure parameter maps and statistical summaries from region-based analysis. A variety of parameters are included, such as diffusion tensor imaging with and without free water elimination (DTI, fwDTI)[7], neurite orientation dispersion and density imaging (NODDI)[8], white matter tract integrity (WMTI)[9], and multi-compartment microscopic diffusion imaging (MCSMT)[10].

MicroQIT uses a template-based approach to spatially normalize data and statistically aggregate parameters through ROI analysis[11]. To provide accurate alignment within white matter[12], it uses the tensor-based registration algorithm provided by DTI-TK[13]. We created population averaged diffusion tensor image based on the IIT template[14,15] for coregistration and added ROIs from the Johns Hopkins University (JHU) and Desikan-Killiany (DK) white matter atlases. The JHU ROIs were aligned using FSL fnirt[16], and the DK ROIs were found by averaging Freesurfer segmentations[17] in the HCP subjects.

MicroQIT is implemented using GNU Make. Make provides a declarative interface for choosing which type of analysis to conduct, and it facilitates parallel computing and data reuse. Unlike previous neuroimaging applications using Make[18], we extend it to include data provenance regarding the workflow, commands, and compute environment in each run. We also include extensions to support grid computing, which enables parallel processing of subjects when a cluster is available and parallel model fitting when a particularly expensive optimization is needed.

Evaluation

We evaluated our framework with two experiments with the following typically used microstructure parameters: DTI fractional anisotropy (FA), DTI mean diffusivity (MD), fwDTI FA, fwDTI MD, NODDI neurite density index (NDI), NODDI orientation dispersion index (ODI), MCSMT neurite density, and WMTI axonal water fraction (AWF). First we conducted a scan-rescan analysis to assess reproducibility. We used 44 pairs of test-retest in vivo human scans with 1.25 mm isotropic voxels and b=0,1000,2000,3000 s/mm^2 from the Human Connectome Project (HCP)[19]. We measured the coefficient of variation (CV) and intra-class correlation (ICC) of each ROI in several commonly used microstructure parameters. Figure 1 shows excellent reliability with mean CV < 2.5% and ICC > 0.85 cross all metrics. Second, we investigated the relative sensitivity of these parameters to age-associated changes in white matter

neurodevelopment. We used 133 in vivo scans with 2.0 mm isotropic voxels and b=0,1000,3000 s/mm^2 from the CMIND dataset. We fit cubic polynomials to the ROI averaged parameters and compare the results from the region with the highest R^2. Figure 2 shows the relative sensitivity of the parameters, where the highest performing methods achieved an $R^2 > 0.8$.

Discussion and Conclusions

MicroQIT provides a robust computational framework for analyzing microstructure parameters across a large population. The results of our evaluation demonstrates high reliability provided in a variety of parameters and high sensitivity to typical changes in white matter through neurodevelopment. The design of MicroQIT can be easily extended to use new microstructure models that can be useful for population studies, and the present implementation may help to understand the changes in the brain in future studies. MicroQIT is available for download online[20,21].

Acknowledgements

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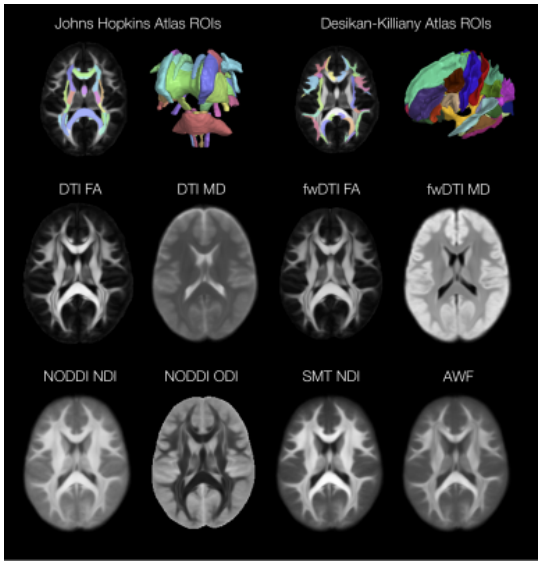
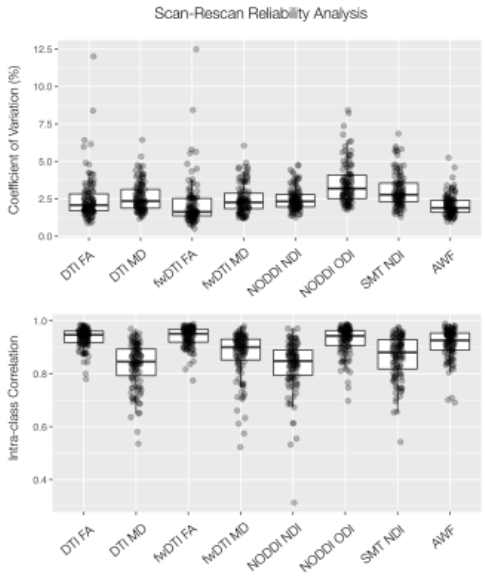
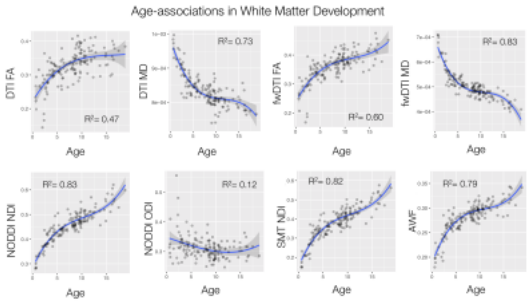
Figures



A visualization of features supported by MicroQIT. The top row shows regions-of-interest from the Johns Hopkins and Desikan-Killiany white matter atlases, which can be used in MicroQIT to summarize microstructure parameters. The middle and bottom rows show a sampling of microstructure parameters that are provided. 88 scans from the Human Connectome Project were averaged to produce the parameter maps.



Results from evaluating the scan-rescan reliability of MicroQIT. The top panel shows the coefficient of variation (smaller is better) and the bottom panel shows the intra-class correlation (bigger is better). Each point represents the average reliability of a given region-of-interest. The results show high reliability across all parameters.



Results from evaluating an application to age-associated changes in typical white matter neurodevelopment. The plots show metrics in left superior temporal white matter, and each point represents an individual subject. The results demonstrate high sensitivity ($R^2 > 0.8$) of cubic polynomial modeling with age.