A Connectome-based Comparison of Diffusion MR Acquisition Schemes

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Introduction

Since the advent of Diffusion Tensor Imaging (DTI) [1], several acquisition schemes have been developed in order to study the connectivity of the human brain. Whereas DTI typically fails to correctly map diffusion in voxels where two or more fiber populations interfere, high angular resolution reconstruction schemes, such as Q-Ball Imaging (QBI) or Diffusion Spectrum Imaging (DSI), provide means for the mapping of complex diffusion structures in areas of "crossing" and "kissing" fibers [2]. However, it still remains unclear to which level QBI and DSI schemes provide a gain for *in vivo* whole-brain tractography. In this work, we aim at a better understanding of the relationship between the acquisition and the resulting tractography for DTI, QBI and DSI.

Material and Methods

Five healthy volunteers (age 26 ± 4 years) were scanned at 3T (Magnetom Trio a Tim System, Siemens, Germany) using a 32-channel receive head matrix coil. Five diffusion acquisitions were performed on two separate days as follows: two DSI scans [3] with 258 directions (DSIq5 day 1 and day 2), a DSI scan with 129 directions and 2 averages (DSIq4), a QBI experiment with 257 directions and a DTI scan (65 directions, 4 averages). To match SNR between the scans the acquisition time was kept constant (26 min.) by adequately choosing the number of averages. For all acquisitions, a diffusion weighted single shot spin echo EPI sequence [4] and identical imaging parameters were used (FoV=212 mm, matrix=96, T_{acq}=26 min, see Table 1). For anatomical reference, a T1-weighted MPRAGE scan was performed (TR/TI/TE=2300/900/7ms, matrix=256x256x160, isotropic 1mm resolution).

	DSIq5	DSIq4	QBI	DTI
TR [ms]	6000			
TE [ms]	138		110	89
Max b-value [s/mm^2]	8000	6400	3000	1000
Encoding gradients	258	129	257	65
Acquisition block (voxels)	96x96x34			
Spatial resolution [mm]	2.21x2.21x3			
Number of averages	1	2	1	4

Table 1. Diffusion acquisition parameters

For each diffusion acquisition a structural connection matrix was built using the following procedure. First, the high-resolution T1 volume was registered on the diffusion images using an affine registration method (http://www.fmrib.ox.ac.uk/fsl/). Then, the gray matter (GM) was identified with Freesurfer (http://surfer.nmr.mgh.harvard.edu) and partitioned into 998 small regions of interest (ROIs) [5]. Next, the DSI and QBI data were reduced into the Orientation Density Function (ODF) using the Trackvis software (http://www.trackvis.org). For each voxel a set of vectors corresponding to the local maxima of the ODF was built. For DTI data, the tensor field was computed (Trackvis) and the first eigenvector was extracted. White matter (WM) tractography was performed with a streamline algorithm [5] using the set of vectors obtained from each data set. In every WM voxel 32 fibers were generated along each vector of the set. The fibers stopped expanding when the end-points left WM mask. Finally, we built a connection matrix by computing the fiber density connecting every pair (left and right hemisphere) of ROIs [5].

Results

Fig. 1 maps the normalized connectivity for all scans. All data are presented as the normalized number of connections based on the findings from the DSIq5 scan of day 1. The normalized connectivity of the DSIq4, QBI and DTI scans are significantly decreased by 16%, 23% and 25% respectively. Fig. 2 shows how the differences in normalized connectivity are distributed over the connection distance (shortest path through WM between the corresponding pair of ROIs). The DSIq5 data dominate at medium and long connection distances. The difference is most evident in the connection distance range of 60-90mm, where DSIq4, QBI and DTI show only 66%, 50% and 43% of connections found with DSIq5. For illustration, two association bundles mapping from DTI and DSIq5 are shown in Fig. 3: the arcuate fasciculus (left) and the superior longitudinal fasciculus (right).

Discussion

The results indicate that, although all diffusion scans produce a biologically meaningful mapping of the human connectome, a careful choice of the acquisition scheme may provide higher sensitivity to more comprehensively map WM fiber connections at specific distance ranges. As shown exemplarily in Fig. 3, mapping of the arcuate fasciculus and the superior longitudinal fasciculus exhibit more complete and biologically meaningful results with the DSIq5 data (top) than with the DTI scan (bottom). The entire processing pipeline as applied should not bias a particular acquisition scheme. Due to the SNR match of all data the observations are considered to be dominated by the underlying differences among acquisition schemes. Before generalizing results, however, it should be noted that the acquisition times were 26 min. Such long scans are not acceptable for clinical routine scans. Clinical DTI scans are typically performed within ~5 minutes, which renders these scans less prone to subject motion than QBI and DSI. We conclude that a DTI scan may be an adequate solution when investigating large anatomical pathways, when scan time is a crucial factor and when dealing with uncooperative patients. However, some precautions have to be taken when considering fiber tracts running through large fiber crossing areas, such as the arcuate fasciculus or the superior longitudinal fasciculus. In that case, already a DSIq4 scan (acquisition time of ~12 minutes) should provide enough contrast to better identify the major bundles of the brain. Also, other reconstruction schemes could be investigated such as the CSD technique [6], which may be an interesting alternative to QBI. Particular caution has to be used when investigating neighboring association fibers (in the 60-90mm range). In that case, our observations show that the use of a DSI scan with 258 or more encoding gradients is preferable.

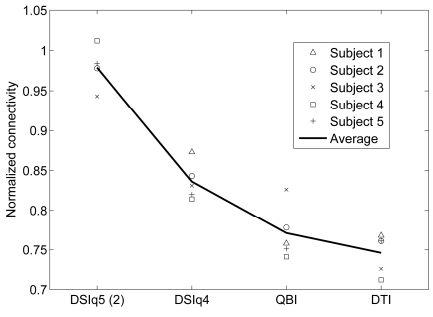

Fig 1. Normalized connectivity

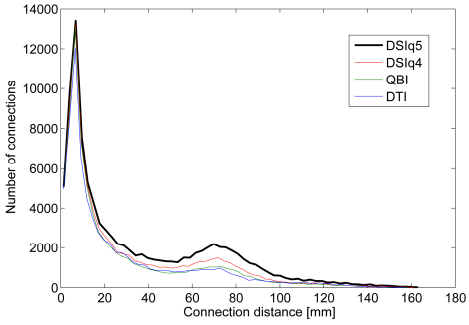

Fig 2. Connection distance distribution

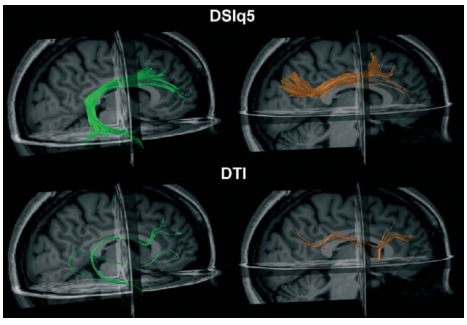

Fig 3. Associative fiber tracts

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