Improved 3-Dimensional Reconstruction of Diffusion Data using Overlapping Slices

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Introduction: To study fiber structure in the brain using Diffusion-Weighted imaging (DWI), a set of images corresponding to different diffusion directions need to be collected. As DW images are inherently very sensitive to motion, full brain coverage is achieved by imaging multiple 2D single shot slices. However, as most fiber tracts in the brain have a 3-dimensional structure, ensuring that the anatomy is fully sampled along all three dimensions is likely to be important to obtain a good representation. Conventionally, the same slice prescription is used for all diffusion sensitization directions. The goal of our study was to test whether by acquiring slices with an offset along the slice direction, a more coherent fiber structure could be reconstructed. This approach has been shown to be successful in the context of super-resolution applied to T_1-weighted imaging [1]. To further improve data robustness, we propose combining slices acquired also along orthogonal directions, taking care to ensure geometrical distortions are matched.

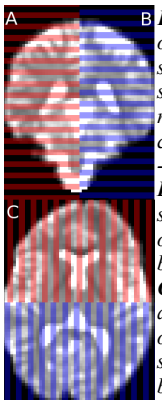

Fig. 1: *Geometry of the three data sets – odd slices shown:* ***A)*** *in red, transverse contiguous slices - 4 repeats;* ***B)*** *transverse slices with overlap, red and blue – 2 repeats;* ***C)*** *transverse and sagittal overlapping slices, red and blue – 1 repeat.*

Methods: To test this hypothesis, three different DW single-shot Echo Planar Imaging (EPI) data sets were acquired on one subject – Fig. 1. For data set A, transverse images with contiguous slices were acquired. Data set B consisted of overlapping transverse slices, with the overlap set to half of the slice thickness and keeping the in-plane FOV the same as in A. In the case of data set C, transverse and sagittal images with overlapping slices were acquired. The phase encode direction was set to Anterior-Posterior in all cases, so that the EPI geometrical distortions would be the same. The diffusion directions were also kept fixed in relation to the magnet frame. To ensure the data sets would be signal-to-noise ratio (SNR)-matched so that the produced Fractional Anisotropy (FA) maps could be compared [2], set A consisted of four repeats, B of two, whilst single instances of sagittal and transverse acquisitions were collected for C. The data were acquired on a 1.5T Philips Achieva using the following parameters: in-plane resolution 2.5 mm, slice thickness 5mm, TE/TR 90/8000 ms, one non-DW image and 15 diffusion directions per repeat, b-value of 1000 s/mm^2. For data sets A and B, the FOV was set to 240×240×180 mm^3 (RL×AP×FH). Sagittal slices in C were acquired with a FOV of 180×240×240 mm^3 (RL×AP×FH). The data was analyzed using FSL [3]. Prior to further processing, the images in data set A were interpolated onto an isotropic 2.5 mm grid using nearest-neighbor interpolation with FLIRT [4]. To correct for eddy current distortions, affine registration was performed for each repeat using the corresponding non-DWI (b0) image as target. All b0 images were registered to a reference b0 image and this transformation was applied to the registered DW images. For each DW volume, the corresponding gradient direction was corrected accounting for rotations [5,6]. Tensor fitting and probabilistic fiber tracking, seeding from multiple seed voxels [7], were performed. Given the low number of directions, only one fiber population was modeled. The FA maps obtained for the different data sets were compared using Bland-Altman plots [8].

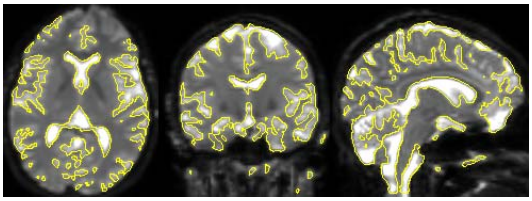

Fig. 2: *Non-DW images from data set C: contour of transverse image overlaid on the sagittal image.*

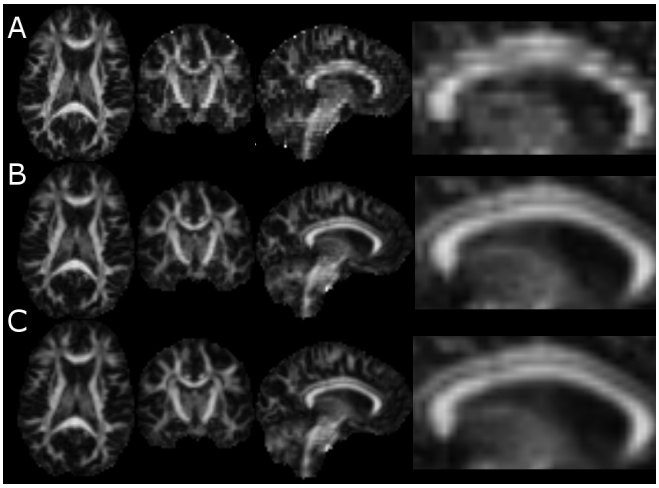

Fig. 3: FA maps reconstructed for each data set. On the right is a zoomed up version of the sagittal cut showing the corpus callosum.

Results: In Fig. 2 the sagittal and transverse non-DW images from data set C are compared, showing good agreement regarding EPI geometrical distortions. The FA maps obtained for all data sets are show in Fig. 3. The detail shows the corpus callosum area, showing improved reconstructions with geometries B and C. Fig. 4 shows a Bland-Altman plot comparing the FA values measured for data sets A and B. The outlier points in this plot (red circle) arise from locations where data set B recovered much higher FA values than A, which is consistent with increased coherence in the data. Similar results were obtained when comparing C and A (not shown). The principal eigenvector maps were also more coherent in those two cases. Tracts reconstructed for all three data sets largely overlapped, but were subtly different. However, given the absence of ground-truth it is not possible to be sure which set provided the most accurate tracts.

Discussion and Conclusions: The results suggest that by using overlapping slices (B and C), an improved 3-dimensional representation of the diffusion tensor field in the brain can be reconstructed. Although not performed here, as sub-pixel shifts were applied along the slice encode direction, sets B and C are suitable for super-resolution processing [1]. In the example shown, no significant improvements were obtained by using geometry C instead of B. However, as the data were acquired on a compliant subject, 3D registration was found to be sufficient to align the data. Using overlapping and/or orthogonal geometries should have a bigger impact in the presence of more severe subject motion, as it increases the chances of fully sampling all the anatomy. In this case a more complex reconstruction would be required capable of accounting for individual slice motion – slice-to-volume (SVR) reconstruction [5]. For the purposes of comparison, multiple measurements of the same diffusion sensitization directions were used here. If the approach is adopted, it would be appropriate to combine the dense spatial sampling with dense angular sampling, so that data contributing to each spatial location contains samples from the largest possible number of diffusion directions, which has been shown to lead to better diffusion estimates [9].

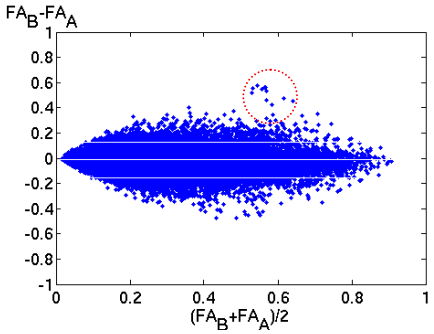

Fig 4*: Bland-Altman plot comparing FA values measured for A and B (outliers at the edge of the brain were excluded).The white lines show the mean difference +/- 2 STD. The points within the red circle arise from locations where set B recovered higher FA values compared to A.*

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References: [1] Greespan H et al, MRI, 2002; 20:437; [2] Pierpaoli C et al, MRM, 1996, 36:893; [3] Smith SM et al, NeuroImage, 2004; 23:208; [4] Jenkinson M et al, NeuroImage, 2002; 17:825; [5] Jiang S et al, MRM, 2009; 62:645; [6] Leemans A et al, MRM, 2009; 61:1336; [7] Behrens TEJ et al, MRM, 2003; 50:1077; [8] Bland JM and Altman DG, Lancet, 1986, 1:307; [9] Jones DK, MRI, 2004; 51:807.