Tractography in the fetal brain with correction of fetal and maternal motion using model-based slice to volume registration

A. Bertelsen[1], S. Counsell[1], J. Allsop[1], A. McGuinness[1], S. Jiang[1], R. Nunes[1], P. Aljabar[2], D. Rueckert[2], M. R. Rutherford[1], and J. V. Hajnal[1]

[1]Robert Steiner MRI Unit, Imaging Sciences Department, MRC Clinical Sciences Centre, Hammersmith Hospital, Imperial College London, London, United Kingdom,
[2]Department of computing, Imperial College London, London, United Kingdom

Introduction Diffusion tensor imaging (DTI) of the fetal brain is attracting increasing interest [1-3] with recent papers starting to present tractography results [4]. To overcome maternal motion, many studies have been performed using breath-hold methods, although this severely reduces the amount of available data. However, even in breath-held acquisitions, the fetus can move substantially, so that individual diffusion weighted (DW) images acquired at the same geometrical slice position can be anatomically inconsistent. This problem was addressed by Jiang et al. [5], who extended the Snapshot to Volume Reconstruction (SVR) technique [6, 7] for application to DTI. The SVR approach works on single shot image slices with image registration to determine their correct location in an anatomical space, and then uses scattered data interpolation to reconstruct self consistent high resolution volume images. For snap-shot images of consistent contrast the registration process can employ cost functions like cross correlation (CC) and this has been shown to position slices in anatomical space with sub-voxel accuracy. In the case of DW images, the contrast changes with sensitization direction, so a more general cost function has to be used. Using this approach, high quality apparent diffusion maps of the fetal brain were made, but fractional anisotrophy (FA) maps proved less robust, and tractography was not demonstrated. In this work, we improved the DTI-SVR algorithm using more robust model-driven registrations, which improved the final reconstructed images and allowed white matter tracts to be obtained using a standard tracking approach.

Snapshot to Volume Reconstruction In SVR the fetal brain is first oversampled by repeatedly imaging it with multiple stacks (or *loops*) of single shot slices (typically 4-8 loops). The loop that is least corrupted by motion is chosen as a target and all the remaining ones are registered to it [6]. Then, loops are divided in *packages* containing a reduced number of slices, and each one of these is registered to a custom target image that is constructed onto a regular grid using scattered data interpolation from all rest of available data, using the alignments determined from the previous stage. Once all these registrations are complete, the data is divided into smaller packages and the process is repeated, until each package only contains a single slice. As the positions of the slices in anatomical space are refined, increasing anatomical detail is depicted in the reconstructed volumes. The extension to DTI involved first performing SVR on the b_0 images to create a target volume which all the DW images were then registered to using normalized mutual information (NMI) as the cost function. This makes no assumptions about contrast but is less powerful than the previously used CC. Finally the six independent elements of the diffusion tensor (D) were calculated for a grid of regularly spaced locations in anatomical space from the registered DW images taking into account their changed orientations which modify the directions of diffusion sensitization of each slice.

New Snapshot to Volume Reconstruction for DTI. We improved the SVR method by replacing its final stages by a model driven algorithm. Related work has been published on similar techniques for whole volume registration in [8]. Using the current estimates of the slice locations, D was calculated throughout anatomical space. This was then used together with the already reconstructed b_0 volume to calculate DW target images S_m by solving the standard diffusion equation $S_m = S_0 \exp(-b_m (R_m g_m)^T D (R_m g_m))$, in which b_m, R_m and g_m are the b-value, rotation and diffusion sensitization vector corresponding to package P_m and S_0 is the previously estimated b_0 image (Note that R_m correspond to the rotation part of transformation T_m, which also includes translations). At each stage of the algorithm, D is calculated from all available data: each package $-P_m$- is mapped into a high-resolution coordinate space with its transformation T_m, generating a transformed package P'_m. Afterwards, we loop through each voxel in the target coordinate space and collect all valid data in the corresponding location in all P'_m images, building a linear system of equations to calculate the six diffusion parameters for that particular voxel. As P_m and S_m have similar contrast, they are registered using the more robust CC similarity metric, updating the transformation T_m. At the end of each stage, the data becomes more coherent, as transformations T_m place their corresponding packages closer to their correct positions and so does the quality of a new estimation of D. All reconstructions of D were produced using nearest neighbor interpolation onto the high resolution grid, in which each source voxel was subdivided into 8 sub-voxels. After initial registration using the previous method down to packages of 8 slices, three stages of model based approach were run, with four, two and one slice per package respectively. Implementation used Matlab (http://www.mathworks.com/), FSL (http://www.fmrib.ox.ac.uk/fsl/) and IRTK (http://www.doc.ic.ac.uk/~dr/software/index.html).

Results We tested the algorithm on four fetuses, with gestational ages (GA) between 25 and 34 weeks, all were referred for clinical scans. On conventional images one fetus showed normal brain appearances at 25 weeks. The remaining three showed ventricular dilation, two had associated cerebellar abnormalities and one showed agenesis of the corpus callosum (CC). Although the detected fetal head motion involved excursions of 11 mm and up to 8 degrees of rotation, the diffusion tensor for the whole brain was successfully reconstructed in all cases. Maps of the Mean Diffusivity (MD) and FA were also estimated (see example in Figure 1). In all cases the new algorithm produced clearly more coherent reconstructions than the previous approach. The quality of reconstructions was good enough to do tractography using FSL. Both corticospinal tracts could be extracted in all subjects, as well as the optic radiations. In two subjects the splenium and genu of the CC were also extracted.

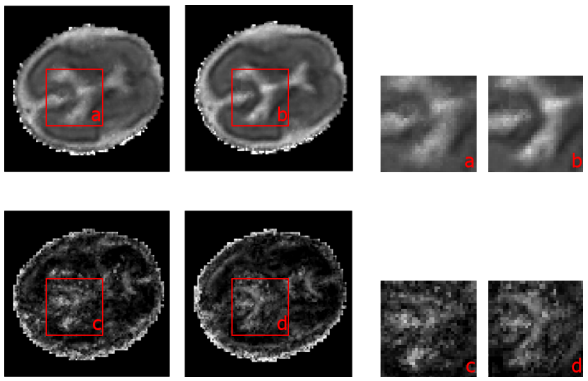

Figure 1 MD (top row) and FA (bottom row) maps of a subject before (left) and after (right) correction. Anatomical detail increases in the reconstructed images as the slices position are corrected.

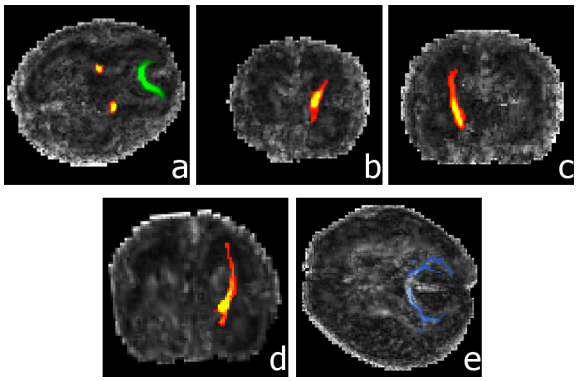

Figure 2 FA maps with white matter tracts overlayed (a,b,c) Genu of the corpus callosum and corticospinal tracts, GA 25w (d) Corticospinal tract, GA 26w (e) Splenium of the corpus callosum GA 34w

Conclusions We have presented a method to reconstruct diffusion tensor estimates of the full fetal brain in utero, with improved performance and have demonstrated tract extraction. Future work will focus in replacing the interpolation method used in the generation of the P'_m packages and on including outlier rejection to deal with slice data that is corrupted by extreme motion. We will also increase the study population so that the method can be more systematically tested and applied.

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