Super-resolution reconstruction of diffusion parameters from multi-oriented diffusion weighted images

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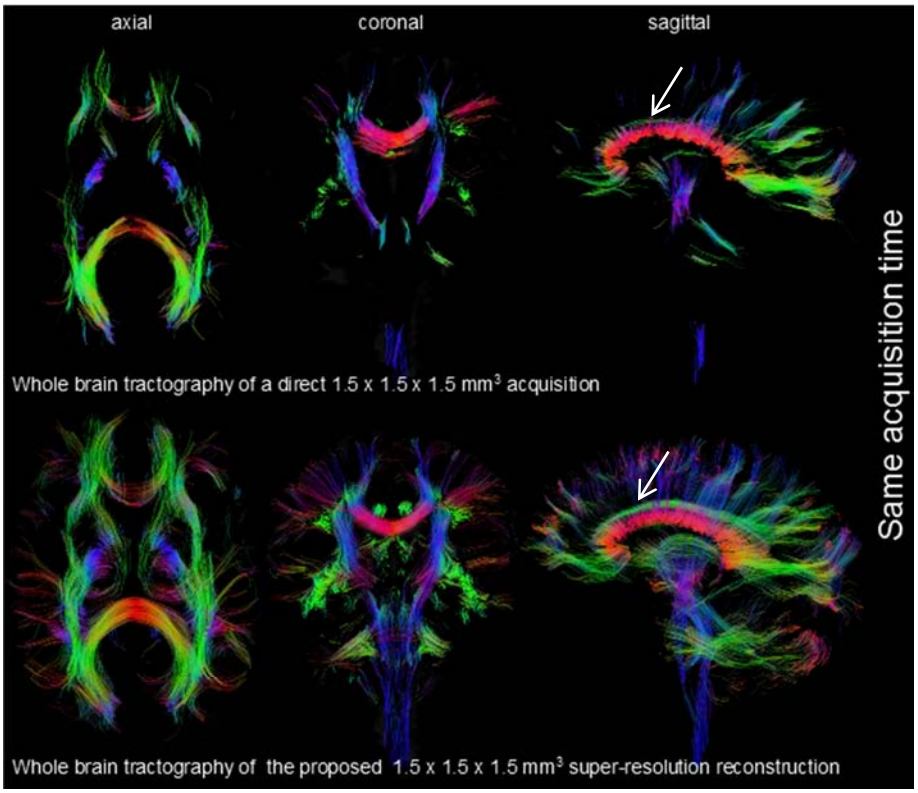
PURPOSE: Diffusion MRI (dMRI) is a noninvasive, in vivo imaging modality that allows investigation and characterization of tissue microstructure. The diffusion of water molecules will attenuate the signal in the diffusion weighted (DW) images. As a result, the signal-to-noise ratio (SNR) of DW images is relatively low. Increasing the SNR by acquiring more diffusion gradient directions, increases the scan time. To obtain DW images with a reasonable SNR within a clinically feasible scan time, it is most common to acquire the DW images with a resolution ranging from $2 \times 2 \times 2\text{mm}^3$ to $3 \times 3 \times 3\text{mm}^3$. Given that a large fraction of white matter fiber bundles are smaller than this spatial resolution, large partial volume effects occur. Recently a method [1] has been proposed that improves the trade-off between spatial resolution, SNR and acquisition time. This method acquires multiple low resolution (LR) anisotropic DW images with different slice orientations, and recovers the underlying high resolution (HR) diffusion tensor (DTI) parameters via super-resolution reconstruction (SRR) with an integrated DTI model. In this abstract we present an extended version of this SRR-DTI method, where for each slice orientation a different group of diffusion gradient directions is used. Furthermore, with the aid of full brain tractography we show that the SRR-DTI method gives diffusion tensor estimates that are improved over that obtainable from a direct HR acquisition with equal acquisition time.

METHOD: The SRR-DTI method [1] was extended so that instead of the diffusion tensor $\boldsymbol{D}$, the matrix logarithm of the diffusion tensor $\widetilde{\boldsymbol{D}}$ is estimated. This ensures that the estimated tensor is positive definite. $\widetilde{\boldsymbol{D}}$ and the non-DW signal $\boldsymbol{a}$ can be estimated from a group of LR anisotropic DW images $\boldsymbol{r}_m$ (u_mx1) by $\hat{\boldsymbol{a}}, \hat{\widetilde{\boldsymbol{D}}} = \arg\min_{\widetilde{\boldsymbol{D}},\boldsymbol{a}} \sum_{m=1}^{N} \sum_{l=1}^{u_m} \|\boldsymbol{s}_m(l) - \boldsymbol{r}_m(l)\|_2^2 + \lambda \boldsymbol{R}(\widetilde{\boldsymbol{D}}, \boldsymbol{a})$, $\boldsymbol{s}_m(l)$ the simulated LR DW signal in voxel $l \in \{1, \ldots u_m\}$ [1], $\boldsymbol{r}_m(l)$ the acquired LR DW signal in voxel l, N the number of LR DW images, $\boldsymbol{R}$ the regularization which computes the squared laplacian of $\widetilde{\boldsymbol{D}}$ and $\boldsymbol{a}$, and λ the corresponding weighting factor. This nonlinear least squares problem is solved using the trust-region Newton method. The problem is very 'large-scale' due to the large number of parameters and the coupling between the different parameters. To reduce memory consumption and the number of iterations required by the optimization, the region of interest, the brain, is split in several blocks, where the HR DTI parameters are reconstructed in each block separately. To avoid artifacts at the edge of the blocks due to regularization, the blocks had an overlap of a few voxels. For the evaluation two data sets were acquired with a 3T scanner with a 12-channel head coil. The acquisition parameters were chosen such that the acquisition time of both data sets was between 4.5 and 5.5 min. Both DW data sets were acquired with a multislice single shot EPI sequence without a slice gap, the acquisition matrix was 158x158 and no averaging took place. 1) A LR DW data set with voxel dimensions $1.5 \times 1.5 \times 3\text{mm}^3$, consisting of 4 subsets of LR DW images. Each subset was acquired with a different slice orientation, which was rotated around the phase encoding axis. This set-up ensures that the EPI distortions are in the same direction for each acquired DW image, making EPI distortion correction unnecessary for a good SRR. Each of the subsets included 1 non-DW image (b=0 s/mm) and 7 DW images (b=1000 s/mm). The diffusion gradient directions were sampled differently for each subset, leading to 28 unique diffusion gradient directions in total. The LR DW data set had a TR=9700ms, TE=97ms, 64 slices and a total scanning time of 5.17 min. 2) As a reference, a direct isotropic HR data set with voxel dimensions $1.5 \times 1.5 \times 1.5\text{mm}^3$ is acquired. This data set consisted of 1 non-DW image (b=0 s/mm) and 14 DW images (b=1000 s/mm). The HR DW data set had a TR=19426ms, TE=97.4ms, 128 slices and a total scanning time of 4.85 min. For each acquired data set, the SNR was computed in the non-DW images by calculating the ratio of the mean and standard deviation of the same uniform region in the corpus callosum. The LR DW data set was used to construct HR DTI parameters, with voxel dimensions $1.5 \times 1.5 \times 1.5\text{mm}^3$, with the SRR-DTI method. HR DTI parameters were directly estimated from the acquired HR data set using a weighted linear least squares estimation [2]. For each reconstruction, whole brain deterministic DTI tractography was performed using MRtrix [3]. For each data set 10000 streamlines were launched throughout the brain.



RESULTS: The SNR values of the non-DW images are SNR_{HR}=4.3 and SNR_{LR}=7.7. The figure on the left illustrates the whole brain tractography results. The HR data set (top figure) provides a poor tractography result due to the low SNR, with many known fiber bundles missing. The SRR-DTI method is able to recover these bundles and thus they are visible in the SRR-DTI data set (bottom figure). For example, the cerebellum is not tracked in the HR data set, while it is in the SRR-DTI data set. Another tract that is hardly visible in the HR data set but is clearly present in the SRR-DTI data set is the cingulum (green structure pointed out with a white arrow).

DISCUSSION AND CONCLUSION: A SRR-DTI method was evaluated on clinical data by means of a whole brain tractography. The higher SNR of the SRR-DTI data sets leads to a more accurate white matter fiber tracking. SRR-DTI makes it possible to acquire diffusion parameters with a high resolution and SNR within a clinically feasible scan time. The promising results encourage us to investigate the strengths and limitations of the technique. Higher spatial resolution would reduce partial volume effects and provide an improved representation of the orientation of the fiber tract and thereby improve the accuracy of the fiber tractography.

REFERENCES:

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