Motion Correction in Diffusion Magnetic Resonance Imaging

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Introduction This abstract reveals an artifact in diffusion images introduced by standard motion and distortion correction methods for high-angular resolution acquisition and introduces a new correction scheme that avoids the artifact. The artifact is the misalignment of the tissues boundaries between T2 and FA maps.

Methods The standard correction scheme uses the T2-weighted (b=0) image as the reference for registration, since it has the highest SNR [1], and registers each diffusion-weighted image to the reference by a 3D rigid or affine transformation computed by maximizing a similarity measure such as cross-correlation or mutual information. The problem with that scheme is that measurements with different gradient directions have the different contrasts. The differences between diffusion-weighted images and the non-diffusion weighted reference image cause mismatching to occur during registration. One consequence of this mismatching is shown in Figure 2 (a) which shows misalignment of edges, particularly around the corpus callosum, between the T2-weighted and FA maps.

We propose two methods to improve the motion correction and remove the errors that the standard correction scheme introduces. Both methods use the diffusion tensor to synthesize the diffusion-weighted image for each measurement in the acquisition. The motion-corrupted images are then registered to the corresponding synthetic image. The first method is called Fit Tensor from All the Measurement (FTAM) and contains four steps: 1) fit the diffusion tensor to the measurements; 2) make a synthetic reference image for each diffusion-weighted measurement from the fitted tensor; 3) register each measurement volume to the corresponding synthetic reference; 4) repeat step 1-3 to convergence. Figure 1 illustrates the FTAM procedure.

Step 1 reconstructs diffusion tensors from the *whole* set of measurements; Step 2 generates target image volumes for each measurement by synthesizing the measurement $A(\mathbf{q})=\exp(-t\mathbf{q}^T D\mathbf{q})$, where D is the diffusion tensor, $\mathbf{q}$ is the sample wave number and t is the diffusion time.; In step 3, we register every measurement volume to the synthetic target image with the same $\mathbf{q}$, using FLIRT [2] with 3D affine transformations and the normalized cross-correlation similarity measure. The final step 4 is repeating steps 1-3 until convergence, which occurs when the difference between the present output and the output from previous cycle is acceptably small.

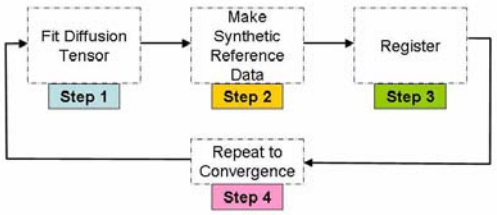

Fig 1: Flowchart for FTAM

The second method is Fit Tensor from the Selected Measurements, (FTSM), which is identical to FTAM except for step 1. Instead of using all the measurements for tensor fitting, FTSM uses only *selected minimally corrupt* measurements to fit the tensor. To decide whether an individual measurement will contribute to tensor fitting, we compute the overlap of the brain region found by the thresholding each image and compare it to the brain region derived from thresholding the *b=0* image. If the overlap is below a fixed percentage, we assume the measurement is corrupt and exclude it during tensor fitting. After each iteration, individual measurements whose motion correction is deemed sufficient are included for tensor fitting in the subsequent iterations. This method has an advantage over FTAM when motion is large or many measurements are corrupt which can cause FTAM to fail to converge.

Experiments and Results We illustrate the artifact on a single human-brain image in experiment 1. The diffusion imaging sequence uses 60 diffusion-weighted measurements in each voxel. The first 54 measurements are at a fixed | q | giving b = 1050 s mm^{-2}, with the gradient directions spread evenly on the hemisphere. Six of the 54 diffusion-weighted measurements are repeated with b = 260 s mm^{-2}, and six measurements are made with b = 0. The misalignment using the standard method is most pronounced when using the normalized correlation similarity measure, as in Fig 2. In experiment 2 we test the FTSM method on a synthetic data set. Using the diffusion tensor image from experiment 1: we synthesize the first 27 measurements at b = 1050 smm^{-2}. We then rotate the tensor image by 5 degrees about the x, y, and z axes, and synthesize the rest of the measurements. The FTSM algorithm correctly rejects the measurements from the rotated tensor volume, and fits the tensor using the first 27 diffusion-weighted measurements only. Fig. 3 shows the results of the correction after one iteration of FTSM. The standard method (using mutual information as the similarity measure) also improves the alignment, but still has some mismatch, and the structure of white matter is better preserved with FTSM.

Discussion The standard method of registering all diffusion-weighted images to the b=0 image can correct some motion distortions, but it can also add errors, which can be seen in the comparison between the T2-weighted and FA (fractional anisotropy) images in Figures 2 and 3. As our new methods choose different reference images for different diffusion gradients, they avoid the mismatching caused by the intensity differences between component images.

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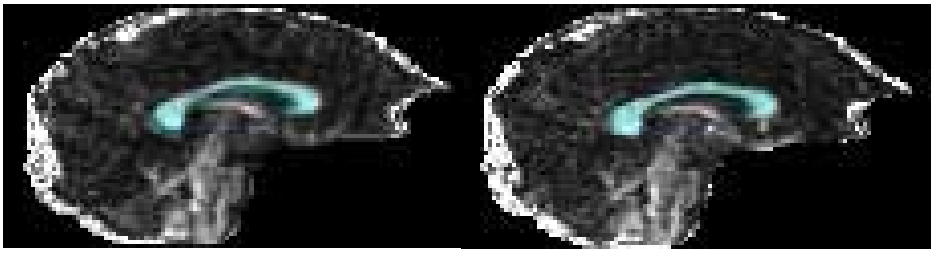
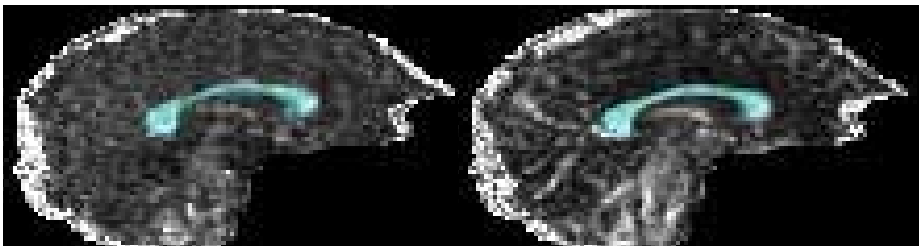


(a) Fig 2 (b)

FA maps overlaid with the corpus callosum as segmented from the b=0 image, after (a) standard motion correction and (b) FTSM correction (experiment 1).



(a) Fig 3 (b)

FA maps from synthetic data (experiment 2) overlaid with the corpus callosum as segmented from the b=0 image, after (a) standard motion correction and (b) FTSM.

References

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