Fully Automatic Postprocessing and Evaluation of DTI Data: Unsupervised Pipeline for Batch Jobs

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Introduction:
Diffusion Tensor Imaging (DTI) data has become an important tool to analyze the structure and integrity of neural tissue, especially of white matter structures. However, the data to process is usually quite complex and needs tedious post processing. We built a pipeline, which filters noise and artifacts of DTI data automatically. We included the registration to a standard atlas, which we created from high resolution EPI data instead of spin echo images, avoiding mis-registration due to EPI-induced distortions in the images. We created so far seventeen gray and white matter structures from this atlas data. These binary parcellations facilitate a fully automatic analyses of regional DTI metrics.

Materials and Methods:
MRI scans were performed on a 7 Tesla horizontal bore scanner. Up to sixty, 0.5 mm thick contiguous axial images were acquired from Sprague-Dawley rats with spin echo prepared EPI-DWI (128 X 128 matrix, four-shots). DWI were acquired using a rotationally-invariant icosahedral encoding scheme with 21 directions with alternating polarity (**1**). Eddy Current induced artifacts were corrected by intra subject registration (**2**). Hahn et al. (**3**) suggested to assume Rician statistics for the noise of low SNR DWI. We therefore used a nonlinear filter provided by Hahn to suppress biased mean, variance, and skewness of the data (**3**). Extrameningeal tissue was stripped by an in house developed algorithm that detected the negative gradient from brain to bone, starting from the center of the image. A digital atlas was created from a high resolution DTI data set. Seventeen 3D-parcellations were defined manually from RGB-FA maps of this atlas. Seven data sets were registered (**4**) and parcellated.
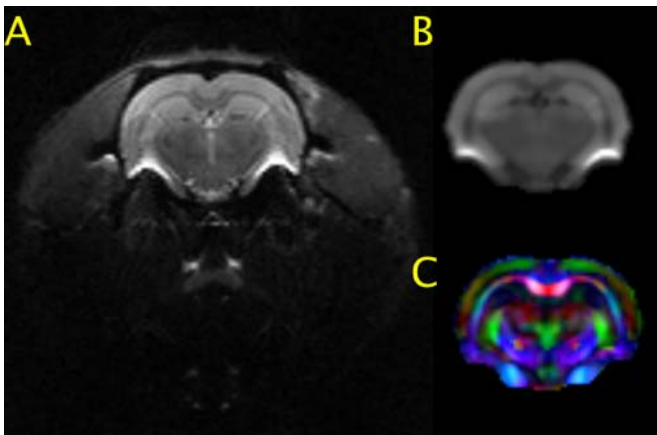
Figure 1: A; Unstripped axial raw DTI of a rats splenium (nine b_0 images, averaged). B; Corresponding slice of the atlas. C; RGB-FA map after registration of A to B.

Results:
Figure 1A displays averaged raw data of axial unweighted DWI images. This data was stripped and registered to the reference atlas (Figure 1,B), which was created from a high resolution DTI data set (spatial resolution 0.27 by 0.27 by 0.5 mm, 60 slices). We defined in this atlas -so far- seventeen structures with the help of RGB-FA maps and the Paxinos and Watson rat brain atlas (**5**): anterior commisure, brainstem, corpus callosum, cerebellum, cingulate, colliculus, cortex, caudate putamen, external and internal capsule, fimbria, hippocampus, olfactory bulb, periaqueductal gray, pineal gland, and the thalamus. Further masks will be added. Figure 1C displays the corresponding RGB-FA map to Figures 1 A and C.

Discussion:
The proposed procedure significantly reduces the workload inherent in post-processing of DTI data and allows batch processing of large DTI datasets. The batch job runs fully automatically in a non-supervised mode and therefore eliminates human errors. It can be integrated into scanner software and automatically be started once the data acquistion has finished. Batch jobs can be initiated outside the scanner environment by individuals who are not familiar with DTI, MRI, or the anatomy of the structure under investigation. The only input needed is a text file, which contains the paths to the raw data files to be processed. The automatic evaluation of DTI metrics has been added by the introduction of binary parcellations.

References:
1: Madi et al, Magn Reson Med 53: 118-125 (2005), **2**: Smith et al, Neuroimage 23: S208-19 (2004)
3: Hahn et al, Int J Biomat Biostat in press (2009), **4**: Woods et al, J Comput Assist Tomogr 22: 139-152 (1998)
5: Paxinos et al, Elsevier, Amsterdam (2005).