The effect of T1-relaxation on tensor-derived ADC-maps

F. Lennartsson[1,2], B. Nordell[1], and O. Flodmark[2]

[1]Karolinska University Hospital, Dept of Medical Physics, Stockholm, Sweden, [2]Karolinska University Hospital, Dept of Neuroradiology, Stockholm, Sweden

Introduction

The T1-relaxation process is a well-known issue in diffusion-weighted magnetic resonance imaging (DWI). The simplest model for describing the diffusion process is the mono-exponential tensor model (DTI): $S(\mathbf{r}) = S0 \exp(-\mathbf{b}^T(\mathbf{r})\,\mathbf{D}\,\mathbf{b}(\mathbf{r}))$. [1] A typical DTI scheme collects first the S0:s followed by gradient directions: $S0_1$,..., $S0_m$ $S(\mathbf{r}_1)$,..., $S(\mathbf{r}_n)$. The T1-weighting among the initial S0:s is not homogenous, giving an erroneously high baseline (mean of S0:s), which results in an overestimation of the tensor elements. In DTI the repetition time (TR) is often long in DTI (4-10 s), so a T1-equilibrium is reached quickly and if the initial S0/SO:s are discarded («dummies») the T1-relaxation effect can be avoided. Collecting multiple S0:s will ameliorate the effect. However, in a clinical setting time does not allow for discarding images or collect excessive S0:s. Furthermore, certain scanner manufactures do not provide acquisition with multiple S0:s or S0-dummies as out-of-the box features for DTI. This study aims to investigate the effect of T1-relaxation among the S0:s on the tensor-derived ADC-map (= trace(**D**)/3) in clinical DTI.

Method

At our hospital we have scanners from GE, Philips and Siemens, but only our GE scanners allow for multiple S0 acquisition. One healthy volunteer (m, 25 yrs) was scanned on a 1.5 T GE Signa Excite (General Electric, Milwaukee, WI) equipped with 4 G/cm gradients using a 8-channel head coil. DTI with a 8S0+6S(**r**) scheme (b=1000 s/mm^2, gradient directions [1 0 0, 0.446 0.895 0, 0.447 0.275 0.851, 0.448 -0.723 -0.525, 0.447 -0.724 0.526, -0.449 -0.277 0.85]) was performed using a standard clinical protocol (matrix 128x128, FOV=25.6 cm, TE=82.6 ms, TR=5 s). Twice-refocused, interleaved SS-EPI was used to collect the maximum number of slices (thk 2.5 mm) allowed. The DTI experiment were repeated 4 times with an inter-scan time interval of 30 s, mimicking a clinical situation and allowing for full T1-recovery. FSL (www.fmrib.ox.ac.uk/fsl, ver 4.0) was used for distortion-corrected and realignment and creation of binary brain masks. The S0:s were used individually with the set of S(**r**):s to create 8 seperate 1S0+6S(r) datasets $\mathbf{S}_i$. Matlab (MathWorks, Natik, MA) was used for repetition bootstrapping on each $\mathbf{S}_i$ and voxelwise tensors $\mathbf{D}_i$ were estimated for each bootstrap (using www.mathworks.com/matlabcentral/fileexchange/21130-dti-and-fiber-tracking). $\mathbf{ADC}_i$ = trace($\mathbf{D}_i$)/3 were then calculated for every tensor $\mathbf{D}_i$ in every dataset $\mathbf{S}_i$.

TABLE 1	S1	S2	S3	S4	S5	S6	S7	S8
mean($\mathbf{ADC}_i$) [10^-4 mm/s]	9.43	8.75	8.75	8.75	8.74	8.76	8.74	8.74
std($\mathbf{ADC}_i$) [10^-5 mm/s]	6.54	5.40	5.60	5.44	5.88	5.93	5.70	5.87

Results

The 11 central most slices in the binary brain mask were used to define voxels for the analysis. It has previously been shown [2] that the probability density function of **D** in the majority of voxels is a multivariate normal distribution, and thus $\mathbf{ADC}_i$ = trace($\mathbf{D}_i$)/3 has the same distribution. Therefore the mean and standard deviation for $\mathbf{ADC}_i$ was calculated for each dataset $\mathbf{S}_i$, and the results is shown in Figure 1 and Table1. It is clearly seen that the distribution of $\mathbf{ADC}_i$ is wider and slightly displaced towards higher values in $\mathbf{S}_1$ compared to other datasets. Likewise, the mean($\mathbf{ADC}_i$) in the mask is higher in $\mathbf{S}_1$, indicating a presence of a higher baseline in $\mathbf{S}_1$. To calculate which voxels in $\mathbf{S}_1$ that have a higher ADC, a difference map were generated between the lower and upper boundary of confidence intervals (two-sided 95 %, $\mu \pm 1.96\,\sigma$) of $\mathbf{ADC}_i$ for $\mathbf{S}_1$ and $\mathbf{S}_2$ respectively. Figure 2 shows the map in two adjacent slices indicating that the voxels are primarily found in CSF and that cross-talk between interleaved slices causes spin-saturation which speeds-up T1-relaxation.

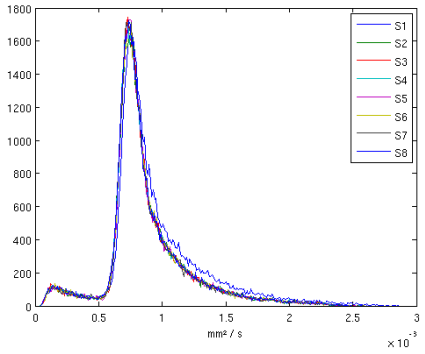

Figure 1: Histogram of ADCi for all datasets Si

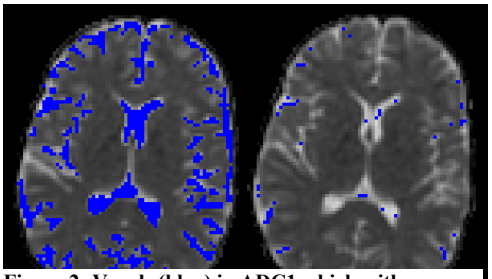

Figure 2: Voxels (blue) in ADC1 which with a certainty of 95 % have higher ADC-estimations than in ADC2. The binary map is overlayed on ADC1

Conclusion

T1-relaxation effects in the initial volumes of a DTI experiment have an impact on the estimation of a tensor-derived ADC-map, and the same effect is expected for non-tensor models. The effect is especially prominent in tissues with long T1 like CSF, where a overestimation of ADC is expected. This can also create an errenous estimation of ADC in the pathologic tissue, which often has an increased water content. At least one b0 should be discarded before the tensor reconstruction. Caution is also encouraged in situations with a varying effective TR, such as in cardiac gating, but this has not been investigated. Cross-talk between adjacent slices in interleaved slice-sampling schemes partially saturates spins speeding up T1-relaxation, but rendering an image stack with different ADC-estimation errors.

References

[1] Basser PJ, Mattiello J, LeBihan D. MR di□usion tensor spectroscopy and imaging, Biophys. J. 66 (1) (1994)

[2] Pajevica S & Basser PJ. Parametric and non-parametric statistical analysis of DT-MRI data. JMR 161 (2003)