# Removing CSF Contamination in Brain DT-MRIs by Using a Two-Compartment Tensor Model

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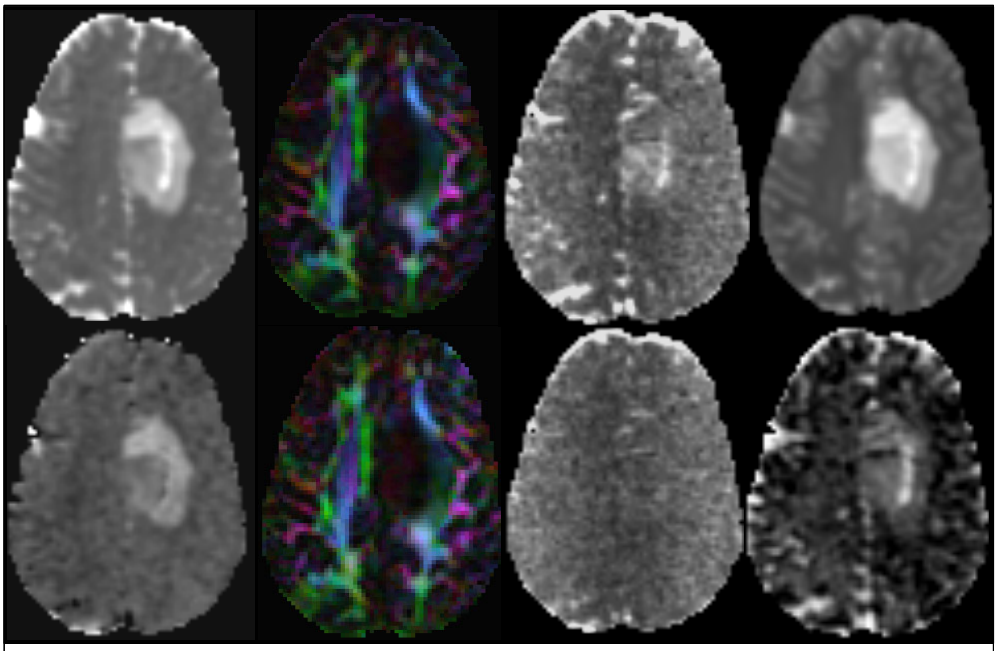
**Introduction:** Diffusion measurements in brain tissue adjacent to CSF-filled cavities suffer from CSF partial volume contamination. As the diffusivity of water in CSF is 3 times larger than in normal brain parenchyma, even a small amount of CSF can severely bias diffusion measurements in the cortex and periventricular areas. As the cortical thickness is ~2mm, it is virtually impossible to obtain diffusion data in the cortex that are unaffected by CSF contamination at the image resolution of clinical DT-MRI. This is particularly problematic when investigating conditions in which small changes in the diffusion properties of the parenchyma are accompanied by volumetric changes of the CSF spaces. These include brain development, aging, degenerative disorders, and several psychiatric disorders. A common approach to suppressing CSF contamination is to acquire FLAIR diffusion weighted images (DWIs)[1]. Although effective in solving the problem of CSF contamination, FLAIR DWI has some disadvantages such as lower SNR than conventional DWIs, longer acquisition time, and the preclusion of using cardiac gating. Here we explore the possibility of extracting diffusion tensor quantities free from CSF contamination by fitting conventional DWIs to a two-compartment tensor model. We analyze data acquired in healthy volunteers and in a patient with a low-grade glioma to assess the robustness of our approach in presence of edema.

**Methods:** Neglecting the effect of noise, the signal intensity in presence of diffusion sensitization in a voxel with two compartments having different diffusion properties and no exchange follows a bi-exponential decay according to:

$$S = S_0\left(f\, e^{-\mathbf{bD_a}} + (1-f)e^{-\mathbf{bD_b}}\right), \qquad [1]$$

where **b** is the *b*-matrix; $\mathbf{D}_a$, $\mathbf{D}_b$ are the diffusion tensors of compartments a and b; $S_0$ is the signal at **b**=0; and *f*, (1-*f*) are the relative volume fractions of the two compartments. (We note that this expression has been used previously by others[2] to examine partial volume effects in DT-MRI, but not with the intention of suppressing CSF contamination). We used equation [1] to fit our data given that it is reasonable to assume no exchange between CSF water and parenchymal water. We tested four models with increasing complexity: 1) one tensor only; 2) one tensor + one isotropic compartment with fixed diffusivity (the diffusivity of free water at 37 C: $3 \times 10^{-3}$ mm$^2$/s). 3) one tensor + one isotropic compartment. 4) two tensors. In models with more than one compartment, the diffusivity of the first compartment was constrained to be $< 3 \times 10^{-3}$ mm$^2$/s and the diffusivity of the second compartment was constrained to be $\geq 3 \times 10^{-3}$ mm$^2$/s. Images were acquired with a DW-EPI sequence with 2×2×2 mm$^3$ resolution and 8 different *b*-values. For each *b*-value, different directions were sampled following the "repulsion" scheme proposed by Jones *et al*.[3] for a total of 107 *b*-matrices. The *b*-value (s/mm$^2$)/number of directions scheme was: *b*=3/dir=3, 10/6, 65/10, 113/12, 350/16, 570/18, 850/20, 1200/22. The goodness of fit of the various models was compared using the chi-squared distribution and Schwarz criterion of parsimony[4].

**Results:** The goodness of fit was generally good for all models with the exception of Model 1 (single tensor) in voxels at the interface of CSF and tissue and in portions of the tumor. All two compartment models achieved a significant suppression of the CSF contribution to Trace(**D**) in regions with partial volume contamination. The Schwarz measure indicated that the simplest two-compartment model, Model 2, was superior to the more complex models in regions where the single tensor model failed. Surprisingly, Model 2 provided a better fit to the data than Model 1, also in several regions apparently free from CSF contamination. In normal brain parenchyma and in edematous regions, Trace(**D**) of the parenchymal compartment was about 20% lower than Trace(**D**) estimated with Model 1, anisotropy was variably higher, and the principal direction of diffusion appeared unaffected. In the glioma subject, the CSF volume fraction was most elevated in the cystic center of the lesion, followed by the tumor area and, interestingly, only slightly elevated in edematous white matter.



Top row: Images from a single compartment fitting. From left to right: Trace(**D**); Fiber color map; Chi-square; Amplitude. Bottom row: Images from Model 2 (i.e. fitting 1 tensor + 1 isotropic compartment with a fixed diffusivity of $3 \times 10^{-3}$ mm²/s). From left to right: Trace(**D**); Fiber color map; Chi-square; Volume fraction of the CSF compartment.

**Discussion:** We have shown that bi-exponential fitting of diffusion measurements is a promising alternative to FLAIR DWI in suppressing CSF partial volume contamination in DT-MRI. For clinical studies it is interesting that a two-compartment model with only one additional parameter over the conventional single tensor fitting appears adequate. This approach seems to work also in edematous regions. Unlike CSF, water in interstitial edema should be in relatively fast exchange with tissue water and it is reassuring that the CSF compartment does not result in dis-proportionally elevated in edematous regions. Interestingly, the tumor and the peritumoral edematous area, which have similar diffusion characteristics when a single compartment model is used, show different features when data are analyzed with a two-compartment model. Whether this initial observation would be of clinical relevance requires further investigation.

**References: 1.** Liu G *et al*., *MRM* 35: 671-677, 1996; **2.** Alexander A. *et al*., *MRM* 45: 770-780 (2001); **3.** Jones DK *et al*., *MRM* 42: 515-525, 1999; **4.** Schwarz G. *Ann Stat* 6: 461-464, 1978.