A Robust Algorithm Framework for Small DTI Samples

Ivan Maximov[1], Farida Grinberg[1], and N. Jon Shah[1,2]

[1]*Institute of Neuroscience and Medicine 4, Forschungszentrum Juelich GmbH, Juelich, Germany,* [2]*RWTH Aachen University, Department of Neurology, Faculty of Medicine, JARA, Aachen, Germany*

Introduction

Diffusion tensor imaging (DTI) is a very powerful technique with a great clinical and research potential. DTI allows one to perform a non-invasive, *in vivo* tissue characterisation of human brain pathologies in relatively short acquisition times. The rotational invariants of DTI such as an apparent diffusion coefficient, fractional anisotropy, etc., have established themselves as valuable biomarkers in various brain disorders. The estimation methods play a key role in tensor assessment and, in turn, in the consistency of potential diagnostic outcome. In clinical measurements, DTI data sets are typically acquired with only a very few repetitions and might be strongly corrupted by artefacts. The robust statistics allow us to localize and erase the outliers caused by physiological noise [1,2]. However, the robust estimators in small samples present a rather complicated problem [3-5]. In this work, we compare the efficiency of different algorithms for small DTI samples that are especially sensitive to various artefacts such as cardiac pulsation, bulk head motion, etc.

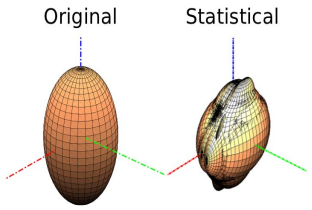

Figure 1. Diffusion tensors in ellipsoidal form where the eigenvalues are equal to the length of the main axes and the eigenvectors are the directions.

Theory and Methods

We applied three methods of diffusion tensor estimation: weighted least squares (WLS) [6], RESTORE based on the M-estimator [1], and the algorithm developed by us and based on the least trimmed squares (LTS) [2] and median absolute deviation (MAD) estimators. The LTS algorithm exploits the trimmed squares of the arranged residuals: $\min \sum_{i=1}^{h} (r_i^2)_{1:N}$ where r_i are the arranged residuals $r_1<r_2<...r_N$, N is the number of applied gradient directions, and h is a truncation factor [2]. In order to improve the estimation in the case of small samples, we used an objective function based on the MAD estimator $f_{MAD} = \mathrm{MAD}(r_i^2) = \mathrm{median}[r_i^2 - \mathrm{median}(r_j^2)]$. We used simulations of the diffusion tensor with eigenvalues [1.5; 1.5; 3.0]x10^{-3} mm^{2}s^{-1} for 6, 12 and 30 diffusion encoding gradients. In each case we artificially corrupted the signal attenuation by the Rician noise (SNR = 10) and a series of outliers.

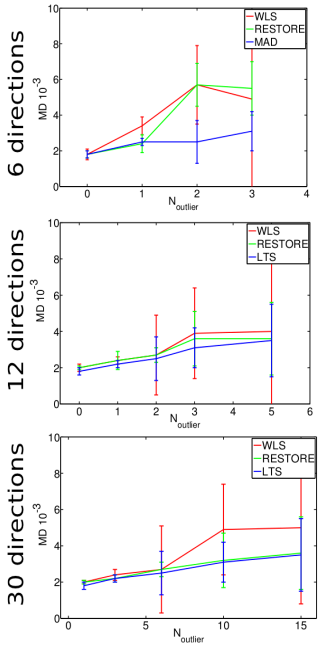

Figure 3. The deviation of the estimated MD from the original value equal to 2x10^{-3} mm^{2}s^{-1} as a function of the number of outliers.

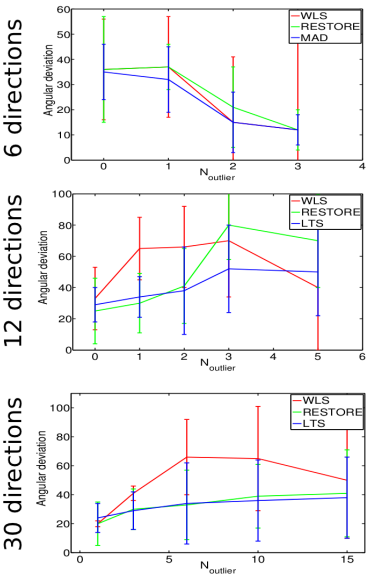

Figure 2. Angular deviation of the estimated main eigenvector from the original direction as a function of the number of outliers.

Results and Discussion

In order to provide a statistical comparison, we simulated 100 diffusion tensors for each data set (see, for example, Figure 1). Using the above three algorithms we evaluated angular deviations of the estimated main eigenvector from the original direction (see Figure 2) and of the estimated mean diffusivity (MD) from the original value, 2x10^{-3} mm^{2}s^{-1} (see Figure 3). We can see that in the case of a small sample (6 directions) the MAD estimator provides a significantly better assessment than WLS and RESTORE. For 12 and 30 gradient directions with a small number of outliers (less than 3 or 5), both the RESTORE and LTS estimators enable a very good evaluation of the eigenstates. In contrast, WLS provides very poor estimations in all cases.

Conclusion

The robust LTS and MAD estimators provide a better estimation in the case of small samples than WLS or RESTORE. In general, an application of robust estimators can be recommended in order to improve the evaluation of diffusion tensors, especially in the case of large physiological noise.

References: **[1]** Chang et al., MRM 53 (2005) 1088. **[2]** Maximov et al., JMR 213 (2011) 136. **[3]** Rocke, Biometrika 73 (1986) 175. **[4]** Rousseeuw and Verboven, Comp. Stat.&Data Anal. 40 (2002) 741. **[5]** Chang et al., Proc. Intl. Mag. Reson. Med. 19 (2011) 3898. **[6]** Koay et al., JMR 182 (2006) 115.