Optimization of Diffusion Sequences Using Bootstrap Algorithms

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Introduction

The experimental determination of measurement precision of diffusion parameters is infeasible due to the requirement of a large number of scan repetitions. Thus, to date, only theoretical simulations have been performed to optimize diffusion sequences [1-3]. Recently, bootstrap techniques have been introduced which allow quantifying the imprecision of diffusion measurements on the basis of only a few [4, 5] or a single measurement [6, 7]. This approach opens up the possibility of optimizing diffusion sequences experimentally with respect to prospective clinical studies. Up to now, the performances of these algorithms have only been evaluated on the basis of Monte Carlo simulations.

The present work compares the predicted measurement precision of two model-based bootstrap algorithms, the regular bootstrap [4, 5] and the bootknife [7], and two non-model-based approaches, the wild [6] and the residual bootstrap [7], using experimental measurements. Therefore, a variety of sequence parameters influencing the precision of diffusion measurements are investigated.

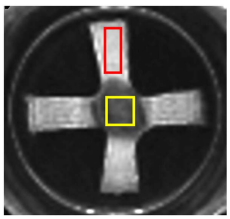

Fig 1: FA map of the anisotropic diffusion phantom: The red region contains a single, the yellow two crossing, fiber populations.

Methods

Diffusion-weighted single-shot spin-echo EPI scans were performed in a diffusion phantom [9] in order to evaluate the influence of several sequence parameters on the precision of the apparent diffusion coefficient (ADC) and the fractional anisotropy (FA) value. The investigated sequence parameters were: *(a) the field strength, (b) the number of signal averages (NSA), (c) the impact of eddy current compensation, (d) the influence of the diffusion encoding scheme, and (e) the benefit of acquiring more diffusion directions rather than NSA.* In (d) the default schemes of the scanner were compared with diffusion encoding schemes with the same number of diffusion directions but a spatial distribution that was derived using an electrostatic repulsion algorithm [1]. The main scan parameters were: FOV = 180 x 180 mm^2, matrix = 96 x 96, slice thickness = 1.9 mm, partial Fourier = 60%, SENSE factor = 2.1, TE = 50ms, TR = 4000 ms, b = 1000 s/mm^2. Eddy current-induced image warping was corrected and all data sets were coregistered prior to data analysis. To perform the non-model based bootstraps each scan was repeated 10 times. The relatively large number of repetitions thereby ensured robust results [8]. The first scan of each series was used for calculations with the model-based techniques. 1000 bootstrap iterations were performed in each case to minimize inherent bias [8]. Subsequently, the standard deviations of the mean ADCs and the mean FA values [7] were determined in two regions of interest (ROIs) in a diffusion phantom (Fig. 1).

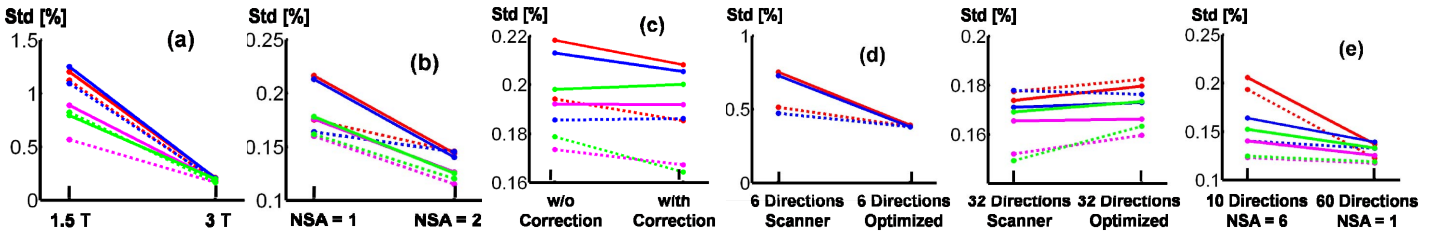

Fig. 2: Standard deviations for the ADCs in the two phantom ROIs for the investigated parameters (see Methods section).

Results

The algorithms show a similar trend when comparing different diffusion sequence designs; however, the absolute values of the standard deviations differ strongly in some cases. It should be noted that the standard deviations are generally smaller for the two model-based bootstrap algorithms.

The results are shown in detail in the figures which compare the standard deviations calculated with the four bootstrap algorithms in the two phantom ROIs for the ADCs (Fig. 2) and the FA values (Fig. 3). Two points should be highlighted; firstly, precision of the optimized diffusion scheme with 6 diffusion directions exceeds the default scheme of the scanner; however, the two diffusion schemes with 32 directions perform equally well. Therefore, it is concluded that the influence of the spatial distribution of the diffusion directions on the precision diminishes with increasing number of acquired directions. Secondly, the algorithms show that the precision of diffusion measurements benefits more strongly from increasing the number of diffusion directions than increasing the NSA.

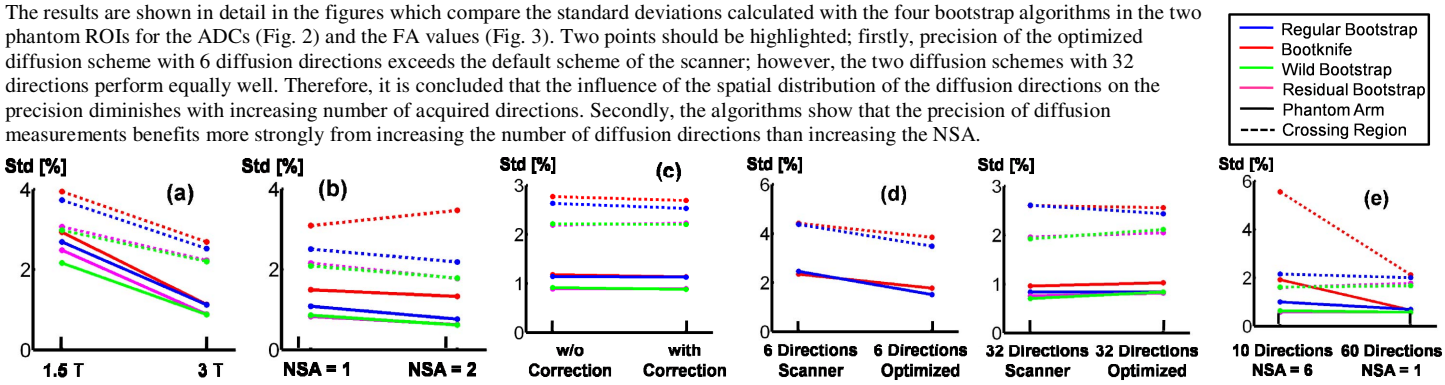

Fig. 3: Standard deviations of the FA values in the two phantom ROIs for the investigated parameters (see Methods section).

Discussion and Conclusion

Bootstrap algorithms enable a relative comparison of DTI acquisition schemes by providing an objective measure of sequence performance. A quantification of measurement precision, however, is challenging since the calculated standard deviations differ strongly at times. The application of the model-based bootstrap methods, requiring just one measurement, is feasible for in-vivo comparison. This provides a powerful tool for experimental optimization of diffusion sequences for studies and in clinical diagnostics.

References: [1] Jones, D. K. et al., [1999], MRM, 42: 515-525. [2] Skare, S. et al., [2000], JMR, 147: 340-352. [3] Jones, D. K., [2004], MRM, 51: 807-815. [4] Pajevic, S. et al., [2003], JMR, 161: 1-14. [5] Jones, D.K. et al., [2003], MRM, 49: 7-12. [6] Whitcher, B. et al., [2008] HBM, 29: 346-362. [7] Chung, S. W. et al., [2006], NeuroImage, 33: 531-541. [8] O'Gorman, R. L. et al., [2006], MRM, 56: 884-890. [9] Reischauer, C. et al, [2008], JMRI, accepted.