

# How Many Shells? - Investigating a Long Held Tradition in DT-MRI

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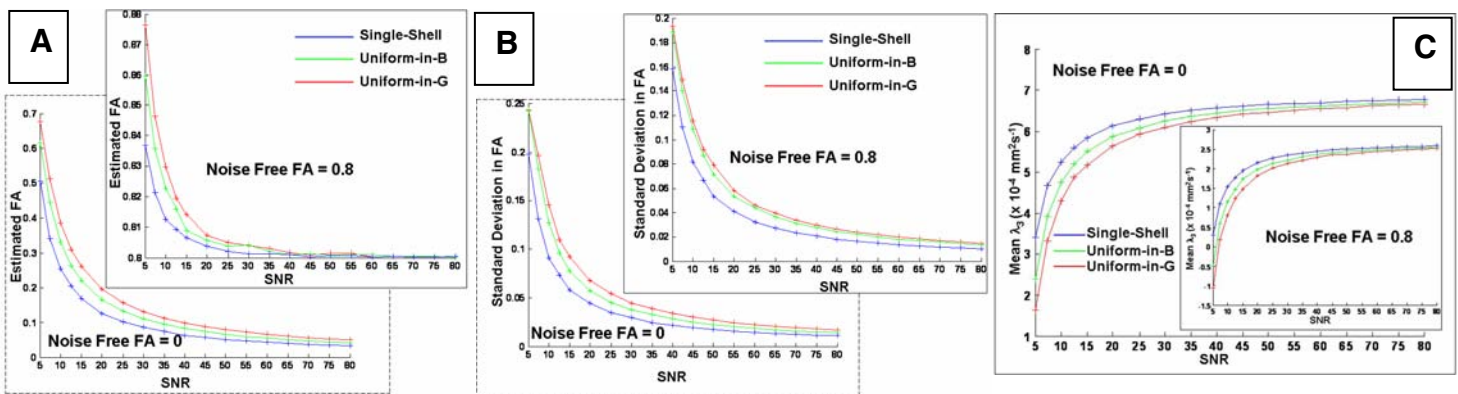
**INTRODUCTION:** In this abstract we answer a very simple, albeit extremely important, question concerning the acquisition of DT-MRI data. The literature is saturated with studies on optimal DT-MRI acquisition design, with focus on the choice of sampling orientations. Generally, however, only two  $b$ -values are used: a value that is close to zero ( $b_0$ ), and a single higher  $b$ -value, such that the end of the sampling vectors all lie on the surface of a sphere [e.g. 1]. We refer to this as a ‘single shell’ acquisition. While it has been shown that the use of just two  $b$ -values ( $b=0$  and  $b = b_{\max}$ ) is optimal for estimation of a single scalar ADC[2], surprisingly – and despite widespread usage – whether such a design is the most optimal when estimating an anisotropic diffusion tensor, has never been addressed. Alternative ‘multiple-shell’ schemes include (but are not limited to), uniform spacing in gradient strength, and uniform in  $b$ -value (proportional to the square of gradient amplitude). Here we use Monte Carlo simulation to compare the bias and precision of tensor-derived parameters obtained with three different  $b$ -value spacing strategies.

**METHODS: Sampling schemes:** For a fixed number of acquisitions / scan time, and fixed number of sampling orientations, three different sampling schemes were considered: Single-Shell: For a fixed set of  $N$ -directions,  $M$  repeat samples of the DW-signal along each direction are made, all with the same  $b$ -value; Uniform-In-G: For each of the  $N$ -directions, a single measurement is made at each of  $M$  different  $b$ -values, whose values are spaced uniformly in  $\sqrt{b}$ ; Uniform-In-B: Same as Uniform-In-G, but spaced uniformly in  $b$ .

**Monte Carlo Simulations:** Sets of diffusion tensors with different eigenvalues and eigenvectors were established and for the three different sampling schemes (for given  $M$  and  $N$ ), the noise-free diffusion-weighted intensities were generated. Rician noise was then added to generate a range of SNR values. The tensor was subsequently re-estimated and decomposed to yield estimates of eigenvalues, eigenvectors, as well as Trace and fractional anisotropy (FA) measures. Repeating this 5000 times for each condition yielded a mean and distribution for all parameters. The standard deviation was used for the scalar parameters, and the 95% cone of uncertainty (CU)[3] for eigenvector estimates.

**RESULTS:** We examined the mean and standard deviations in the following parameters:  $\lambda_1, \lambda_2, \lambda_3$ , Trace, FA, as well as the 95% CU for the principal eigenvector, for a range of SNR’s (ranging from 5 to 100) and FA values (ranging from zero to 0.95). Figure 1 shows example results obtained for the three different sampling schemes for two different anisotropies and range of SNRs. The general shape of these curves is in accordance with the first observations of the ‘sorting bias’ reported by Pierpaoli and Basser[4].

In \*all\* cases, (FA / SNR), **without fail**, the scalar measures were the least biased and most precise, when using the single-shell acquisition, whereas the Uniform-In-G scheme performed the worse in all cases. In Panels A and B, the blue line corresponding to single-shell acquisitions is always below the other two lines, i.e. closer to the true value. Likewise, in Panel C, the blue line is always above the other two lines – again indicating less negative bias in the eigenvalues. Similar results were seen for the Trace, FA and the 95% CU.



**Figure 1: Example results showing how parameters vary with SNR: A. Estimated FA for 2 different noise free FA’s (FA = 0, and FA = 0.8); B. Standard deviation in FA estimates for FA = 0 and FA = 0.8; and C. Mean estimated third eigenvalue for FA = 0 and FA = 0.8.**

**DISCUSSION:** The results indicate that, of the three schemes investigated here, the single-shell scheme always provides the least biased and most precise estimates of tensor-derived parameters of the three schemes. This has extremely important implications for ‘off-the-shelf’ DTI acquisitions provided by manufacturers where users are free to choose between increasing the ‘number of  $b$ -values’ and the NEX (Here, by increasing the NEX - we refer to the magnitude averaging that is provided by scanner manufacturers on diffusion sequences, as opposed to averaging of raw data). As an aside - many groups currently use a single-shell acquisition, graphs of sorting bias should be revisited – since the results presented in [4] were actually derived for a ‘Uniform-in-G’ sampling scheme and therefore over-estimate the degree of sorting bias present in single-shell acquisitions – as show in Figure 1.

**CONCLUSION:** For a fixed scan time, our results show that the most accurate and precise estimates of scalar indices derived from the diffusion tensor are obtained by opting not to increase the ‘number of  $b$ -values’ (be it uniformly spaced in  $b$  or in  $g$ ), but to increase the NEX.

**REFERENCES:** Jones et al. *Magn Reson Med* 1999; 42:515-; [2] Eis et al. *J Magn Reson B* 1995; 108:222-; [3] Jones *Magn Reson Med* 2003; 49: 7-; [4] Pierpaoli and Basser *Magn Reson Med* 1996; 36:893-;