A COMPREHENSIVE QUALITY ASSURANCE ROUTINE FOR DIFFUSION MRI

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Introduction

In the last 20 years, MRI techniques based on the diffusion of water (DTI, tractography, Q-ball imaging, CHARMED) have gained a widespread popularity across the research and clinical community [1]. These techniques allow the estimation of different quantitative parameters, which have been shown to reflect specific tissue properties. To compare serial data acquired over time, it is vital to maximise not only the precision of the measurements, which can be achieved through careful optimization of the sampling scheme [2], but also the accuracy of the measurements avoiding systematic errors. The hardware components that are most likely to influence accuracy comprise the gradient system: it has been shown that errors in gradient amplitude, direction and linearity can contribute up to 10% inaccuracy in diffusion measurements [3]. Despite several phantoms having been proposed and characterised to analyse gradient performance [4], there is no consensus on a quality assurance (QA) routine specific for diffusion acquisitions. An informal study has shown that across the diffusion MRI community rarely – if not ever – a comprehensive QA check is performed. In this work, we propose a simple and easily-implemented routine to perform QA, and will make the analysis software freely available, in the hope that provision of such tools will mean that QA of diffusion MRI becomes more widespread. The routine comprises diffusion-weighted (DW) acquisitions on a phantom along different gradient directions at different b-values; each repetition lasts less than 5 minutes.

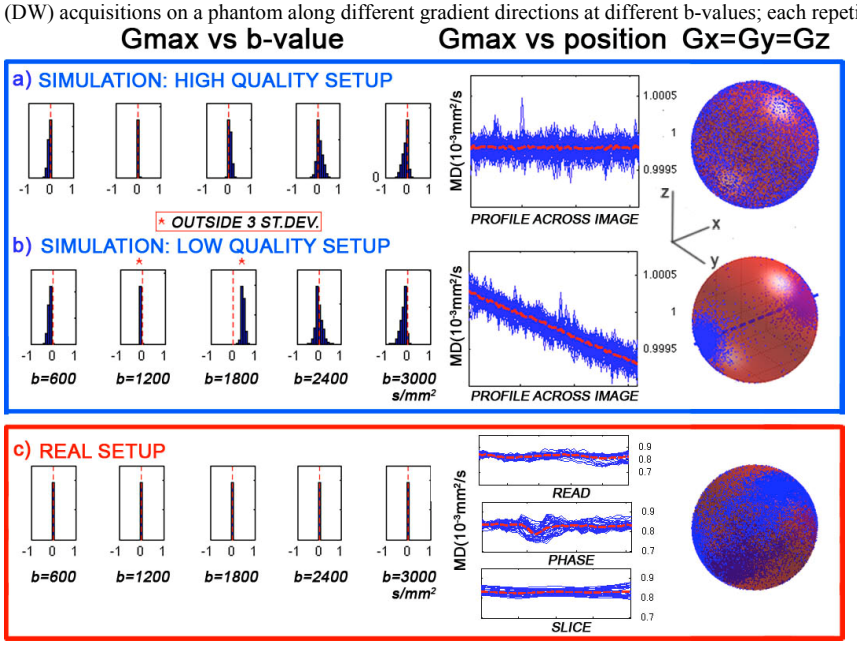

Fig1a. Left: histogram of the residuals of linear fit log(S) vs. b. Asterisk indicates that the zero (dashed red line) is more than 3 SD further than the distribution mean. Centre: MD profile (continuous blue line) and mean value (dashed red line). Right: PE orientations shown as blue dots on the unit sphere. Dashed line indicates significant attractor (if present). Results shown for simulated data on the ideal setup. **Fig1b.** Same results shown for the low quality setup. **Fig1c**. Same results shown for real data.

Methods

Dodecane was used as a test liquid due to the similarity of its diffusivity to that of white matter and relatively long T2 [4]. The first time it is run, the QA protocol comprised 100 scans performed at b=0s/mm^2. The QA script automatically calculates the signal-to-noise ratio (SNR) and return the maximum b-value to be used for all the following QA checks, based on the need to maintain a SNR>5 (safe threshold to avoid the influence of the Rician nature of the signal [5]) on all the DW images. For our scanner (GE HDx Signa 3T), SNR=122 and b_{max}=3000s/mm^2. b_{max} and the provided gradient list are used to acquire DW images along 12 gradient directions for 5 different b-values (in the range 600-3000 s/mm^2), repeated 5 times in a loop. Other parameters are: TE/TR=90/4000ms, matrix=128x128, 6 slices, voxels size 2.4mm isotropic. The proposed QA script performs the following checks: 1) *Linearity of b*: the linearity of the log of the signal vs. the b-value is tested performing a linear fit for each voxel and generating residual maps and histograms of the residuals (expected to have zero mean if linearity holds). The latter are tested to check if the mean is statistically different from zero; 2) G_{max}: the uniformity of G_{max} across the field-of-view (FOV) is tested calculating the mean diffusivity (MD) for each voxel. The MD profile is shown across read, phase and slice direction to check whether a uniform G is applied across the FOV; 3) *Gx=Gy=Gz:* the mutual agreement of gradient power across the three logical axes is tested calculating the dispersion of the principal eigenvector (PE) of DTI across voxels. The PE dispersion is modelled as a Watson distribution and compared with the dispersion of a uniform distribution, according to [6]. The test is repeated for all the b-values; and 4) *Temporal stability*: the performances are compared across time. The routine has been tested on synthetic DW data, using D=10^{-3}mm^2/s, SNR=122 and b_{max}=3000s/mm^2. Each of the four steps is tested using both the accurate gradient scheme and a gradient scheme in which the accuracy has been artificially altered. The QA routine is then used on real data.

Results and Discussion

The QA routine shows the ability to discriminate between an optimal (Fig.1a) and a poor gradient setup (Fig.1b). Specifically, in the latter the log of the signal is not linear vs. the applied b-value, showing systematically negative residuals for b=1200s/mm^2 and positive residuals for b=1800s/mm^2. In the second setup, G_{max} is not uniform across the read direction but has a linear dependence with position. In addition, PEs are not uniformly distributed in space, indicating a miscalibration of the x gradient. The QA run on the real scanner is a good indicator of its performance (Fig.1c). The results indicate the log of the signal to be linear vs. the applied b-value. G_{max} is uniform across read and slice directions, but not so along phase. The PEs distribution shows that the PEs are preferentially aligned along x and z directions. The temporal stability analysis shows no difference in the measured performance across different repetitions. From this analysis, the y gradient seems to be not perfectly calibrated. A biased gradient calibration is an issue that can have important consequences in DTI and tractography studies, altering the measured anisotropy, trace and estimates of fibre orientation. For this reason, we propose this QA routine as a fundamental tool to monitor periodically the gradient performance.

Conclusion

We propose a comprehensive QA routine specific for diffusion MRI, to be run periodically for checking the diffusion gradient performance. The routine is easy to implement and takes only few minutes. Nonetheless, fundamental insight into the scanner performance can be gained, allowing long-lasting studies to be run consistently, possibly increasing the statistical power of the analysis.

References: [1] Basser PJ NMR Biomed 8:333 (1995) Tuch et al. MRM 48:577 (2002) Assaf and Basser MRM 52:965 (2004) [2] Jones DK MRM 51:807 (2004) [3] Conturo et al. NMR Biomed. 8:307 1995 [4] Tofts MRM 43:368 (2000); Pierpaoli proc. ISMRM (2009) [5] Jones and Leemans Methods Mol Biol 711:127 (2011) [6] Schwartzman et al. MRM 53:1423 (2005)