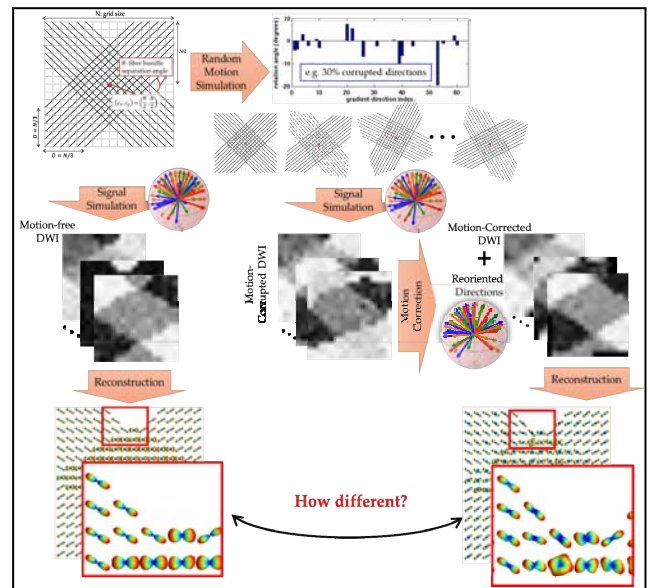# SUBJECT-MOTION CORRECTION IN HARDI ACQUISITIONS: CHOICES AND CONSEQUENCES

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Purpose: Unlike anatomical MRI where subject motion can most often be assessed by quick visual quality control, the detection, characterization and evaluation of the impact of motion in diffusion imaging are challenging issues due to the sensitivity of diffusion weighted imaging (DWI) to motion originating from vibration, cardiac pulsation, breathing and head movement. Post-acquisition motion correction is widely performed, e.g. using the open-source DTIprep software [1,2] or TORTOISE [3], but in particular in high angular resolution diffusion imaging (HARDI), users often do not fully understand the consequences of different types of correction schemes on the final analysis, and whether those choices may introduce confounding factors when comparing populations. Although there is excellent theoretical work on the number of directional DWI and its effect on the quality and crossing fiber resolution of orientation distribution functions (ODF), standard users lack clear guidelines and recommendations in practical settings. This research investigates motion correction using transformation and interpolation of affected DWI directions versus the exclusion of subsets of DWI's, and its effects on diffusion measurements on the reconstructed fiber orientation diffusion functions and on the estimated fiber orientations. The various effects are systematically studied via a newly developed synthetic phantom and also on real HARDI data.

Methods and Experiments: Effects of motion correction were studied on synthetic data and on real HARDI acquisitions. A synthetic, analytical phantom (see Figure) was constructed including two crossing fiber bundles, a choice of spatial rotation, a user-selected separation angle and generation of diffusion signals following the multi-tensor model [4] with 64 gradient directions and b-value of $3000s/mm^2$. Random subject motion was simulated for (30, 50 and 70%) affected gradient directions with random rotations (Normal distribution $N(0,5°)$). We computed fiber orientation distribution functions (fODFs) based on [5] and calculated fiber orientations following [6]. The real data consisted of two HARDI acquisitions (Siemens Tim Trio, 64DWI, b-value $2000s/mm^2$, twice-refocused SE) and subject rotation of about 10° between scans. Considering the first scan as un-corrupted, we replace 30%, 50% and 70% DWIs from the second scan to simulate three scans with different degrees of motion corruption. The impact of motion correction on the estimated fODFs was evaluated a) via Jensen-Shannon divergence (JSD) of the differences between fODF's, and b) by mean angular deviations of original fiber orientations. Tested scenarios include four image interpolation schemes (nearest neighbor, trilinear, sinc, spline) and removal of bad directions, under 30%, 50% and 70% affected gradient directions.

Results: Results and findings from the synthetic phantom simulations and from real HARDI experiments were consistent. On 70% and 50% motion corrupted scans, correction by rotation/interpolation of affected DWIs was far better than removing those directions. This was evident in the fODF difference and the angular deviations of the first and second detected fiber orientations. In particular, for the 70% corrupted scans, the average fiber deviation angle was ~39° in case of directions removal in contrast to ~23° for motion-corrected ones. With 30% motion corruption, removing those directions was slightly better than rotation/interpolation correction (on average 21° versus 23°). This can be explained by the fact that the remaining number of directions was sufficient for robust estimation of the ODFs and of fiber separation. In regard to the type of interpolation, trilinear and sinc turned out to be very similar in all scenarios, but better than spline and nearest neighbor.

Discussion and conclusions: The consistent findings on real and phantom data confirmed that the simulations reflect well real world scenarios and can therefore be used as a flexible concept to test other combinations of settings adapted to specific clinical studies and available HARDI sequences, and considering motion patterns different from random corruptions. As expected, our analysis did not provide a simple yes/no answer, but did reveal different "best choices" depending on the degree of corruption and other factors. Such evaluations will be critical to optimally adjust settings as available in correction tools such as DTIprep [2] or TORTOISE [3] and thus avoids the current situation where we use pure heuristics, vague assumptions and intuition.

References:
[1] Z. Liu et al., "Quality control of diffusion weighted images," Proc. SPIE, vol. 7628, no. 1, p. 76280J, Mar. 2010
[2] DTIPrep: http://www.nitrc.org/projects/dtiprep/
[3] TORTOISE: https://science.nichd.nih.gov/confluence/display/nihpd/TORTOISE
[4] David S Tuch, "Q-ball imaging," Magnetic Resonance in Medicine, vol. 52, no. 6, pp. 1358–1372, 2004.
[5] Y.T. Weldeselassie et al., "Symmetric positive semi-definite Cartesian tensor fiber orientation distributions (ct-fod)," Med. Image Anal. 16(6):1121-9, 2012.
[6] Jiao F. et al., "Detection of crossing white matter fibers with high-order tensors and rank-k decompositions," in IPMI, 2011, pp. 538–549.