Diffusion weighting bias correction for quantitative IVIM metrics in kidney

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Introduction

Quantitative diffusion weighted imaging (DWI) studies that employ the apparent diffusion coefficient (ADC) as a clinical marker are confounded by significant spatial bias observed for off-center anatomy¹. This platform-dependent bias is primarily caused by nonuniform diffusion weighting due to gradient nonlinearity (GNL)^{2,3}. Previously, a framework was proposed³ to correct for the bulk of the ADC bias error for mono-exponential medium of arbitrary anisotropy using three orthogonal DWI measurements. In present work, the proposed DW bias correction was tested for IntraVoxel Incoherent Motion (IVIM) diffusion in renal tissue^{4,5} on a clinical scanner. Different implementation scenarios correcting bias in DWI intensities or b-values for the slow molecular diffusion component ADC were compared.

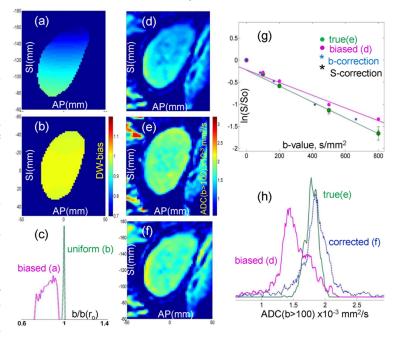
Methods

Sagittal DWI scans of an IVIM renal tissue (volunteer) were performed on a 3T Philips Ingenia MRI scanner near isocenter and offset superiorly by 120mm, using five b-values (b=0,100,200,500,800), with "lab" and "overplus" DWI directions. Eight free-breathing single-shot EPI dynamics were acquired and co-registered before averaging for each direction and b-value. System nonlinearity tensor, L(r), was constructed using gradient design (spherical harmonics) coefficients provided by the vendor. The Frobenius norm of biased $b'_k = Lb_kL^T$ -matrix normalized to nominal b-value at the isocenter, $b_n = ||b(r_0)||$, was used to generate bias corrector maps for each gradient direction, $C^k = ||Lb_kL^T||/b_n$, on a Cartesian grid sampled every 5mm within a 360mm FOV. For experimental data, each static corrector was interpolated for direction-average map according to DICOM header information on imaged volume and resolution. The corrector was then applied pixel-by-pixel to yield corrected DWI intensities or b-maps to derive unbiased ADC³. "Slow" ADC component in the presence of IVIM was obtained from mono-exponential fit for b≥200 values 4.5. The original spatial bias for off-center locations was obtained as deviation from diffusion value measured for the same anatomy close to the isocenter.

Results

Consistent with the GNL-model, the observed bias (~20%) was independent of b-value and mainly affected the "slow" ADC slope. The steep DW nonuniformity bias across kidney ROI, Fig.1a,d, resulted in additional (non-biological) broadening of the corresponding ADC histograms, Fig.1c,h. Application of the corrector map, Fig.1f, effectively reduced the nonuniformity and the mean bias to <3% for slow diffusion in presence of IVIM, Fig.1h. ADC derivation using either corrected trace-DWI intensities or corrected b-values produced similar results (within measurement and fit uncertainty, Fig.1g). No significant change (<2%) due to bias was observed for IVIM perfusion fraction (intercept ~ 0.23).

Figure 1: DW-bias across a sagittal slice through kidney predicted from system gradient design for "lab" gradients and SI offset of (a) z=120mm and (b) z=0mm (with the corresponding $b/b(r_0)$ -histograms shown in (c)) causes nonuniformity error in "slow" ADC map off-center (d), compared to the same anatomy close to the isocenter (e), which is corrected in (f). In (g), the slope error of linear fit for ROI-mean log-intensity dependence on b-value (magenta) is effectively corrected either for b-values (blue



asterisks) or intensities (black asterisks). (h) shows ADC histograms for all ROI pixels of a renal tissue slice (d-f) in the vicinity of isocenter (green) and at superior offset (magenta). The original mean ADC bias of 20% (magenta) was reduced to 2.3% after correction (blue).

Conclusion

The DW nonuniformity bias at off-center locations results both in shift and broadening of the ADC histograms for renal tissue. For this well-perfused, nearly isotropic media, ADC bias for off-center measurements is effectively removed by applying direction-average DW-bias correctors, based on the known gradient design. Comparable performance is achieved using corrected DWIs or b-values. No significant bias impact is observed for IVIM perfusion fraction.

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References: ¹ T. Chenevert, et. al. ISMRM #3550 (2011): JMRI 37:1238 (2013); ² R. Bammer, et.al. MRM 50:560 (2003); ³ D. Malyarenko, et. al. MRM 71:1312 (2014); ⁴ S. Ichikawa, et.al. MRI 31:414 (2013); ⁵ N. Jerome, et.al. JMRI 39:235 (2104)