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Assessment of Approximated Analytical B1+ Correction Method for prostate DCE-MRI with Multiple Noise Levels and in 3.0 T Systems

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Synopsis

B_1^+ correction is essential for quantitative prostate DCE-MRI. A simplified approximated analytical B_1^+ correction method was proposed previously, and we assess this method on a digital reference object (DRO) with various SNR levels and on 110 in-vivo cases from two 3.0 T systems. We find that the approximated analytical B_1^+ correction method achieves comparable performance to conventional correction method with substantially reduced computation. The approximated analytical correction method is simple and practical for application in the clinic.

INTRODUCTION

Dynamic contrast-enhanced MRI reveals tissue vasculature properties and is useful for the diagnosis and monitoring of prostate cancer[1]. Quantitative analysis is mainly comprised of MRI signal modeling to generate the contrast agent concentration vs. time curve and pharmacokinetic (PK) modeling to generate K^{trans} and v_e maps. Accurate quantification is challenging due to many factors, including B_1^+ inhomogeneity. B_1^+ inhomogeneity leads to flip angle variation and is known to introduce significant error into the quantification results[2]. Even when B_1^+ estimates are available, B_1^+ correction can be computationally burdensome. Recently we proposed an approximated analytical B_1^+ correction method[3], and have validated it in simulation and with a digital reference object (DRO)[4]. Here, we further evaluate this B_1^+ correction method on DRO with various SNR levels and on 110 in-vivo cases and compare it with conventional numerical correction method[5].

METHODS

As described previously[3], we proposed an approximated analytical B_1^+ correction method which only takes the B_1^+ map and uncorrected PK maps as the input. It is easy to implement and can reduce the computation time. The comparison between proposed approximated correction and conventional numerical correction is shown in Fig. 1.

To evaluate our proposed method, we created a prostate-specific digital reference object (DRO) based on the RSNA Quantitative Imaging Biomarkers Alliance (QIBA) project with our clinical protocol[4]. The DRO comprised of a series of realistic ground truth K^{trans} (ranged from 0.01 to 0.35 min^{-1}) and v_e (ranged from 0.01 to 0.5). Noise was added to each DRO images using the equation $\sqrt{(R+r_1)^2+r_2^2}$, which is similar to QIBA DRO v9[6]. R is the original signal, and r_1 and r_2 are noise with mean zero and standard deviation ranging from 5 to 150. The resulting baseline SNR of the DCE signal is from 7.8 to 234.5. With noise added in all DRO images, B_1^+ corrected PK maps using two correction methods were calculated for each noise level, and both correction methods were evaluated using mean percentage error compared to the ground truth PK parameters.

With IRB approval, 110 prostate patients acquired from two 3.0T systems (MAGNETOM Skyra and MAGNETOM Trio, Siemens Medical Systems) were retrospectively selected to evaluate the approximated analytical correction by comparing with the conventional numerical correction. For each case, relative flip angle maps were generated based on RR-VFA method[7,8], and three K^{trans} and v_e maps were calculated (uncorrected, approximated analytically corrected, and numerically corrected). Due to data availability, volumetric regions of interest (ROI) of the prostate region were defined for 82 cases, and the lesions on another 28 cases from the same RF system were contoured based on radiology report, as shown in Fig. 2. The approximated analytical correction method was evaluated using percentage error compared to the numerical corrected PK maps. All post-processing was implemented using an in-house script written in Matlab (Mathworks, Inc., Natick, MA, USA). Estimation parameters (K^{trans} or v_e) larger than 1 were excluded as outliers[9].

RESULTS and DISCUSSION

In the DRO experiment, the correction error with different levels of baseline SNR is shown in Fig. 3. Both correction errors decrease with increased baseline SNR level, and the difference between two correction methods is minimal compared to noise-induced correction error. Also, the numerical correction error has a minimum of 2.1%±4.3% with the maximum SNR of 234.5 in the simulation, which gives the correction uncertainty from noise.

Fig. 4 shows an example in-vivo case with PK maps and error maps. The error induced by the approximation is negligible compared to error induced by B_1^+ variation. Among the 82 cases, the percentage error of the approximated analytical correction is 0.11±0.27% for K^{trans}, and 0.11±0.38% for v_e. Fig. 5 shows the B_1^+ distribution and the approximated analytical correction error for both prostate ROI and lesion ROI. The B_1^+ patterns between two scanners (Fig. 5a) are significantly different ($p < 0.05$), indicating the necessity of B_1^+ correction for comparison between scanners. Similarly, within lesion ROIs, the average B_1^+ varies from 81.8% to 116.8%, showing the necessity for B_1^+ correction for lesion characterization. For all the evaluations, the K^{trans} and v_e errors are less than 0.4%, which is much smaller than the noise-induced uncertainty. Additionally, our proposed correction method computationally took 0.01s for a typical 3D volume cases, while the conventional correction methods took more than 3 hours with our implementation. Our proposed correction method can be a good alternative under some condition regarding computation efficiency.

CONCLUSION

The approximated analytical correction method gives comparable results to conventional numerical correction. This is a practical alternative to conventional B_1^+ correction for prostate DCE-MRI.

Acknowledgements

This work was supported in part by the Integrated Diagnostics Program, Departments of Radiological Sciences at UCLA.

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Figures

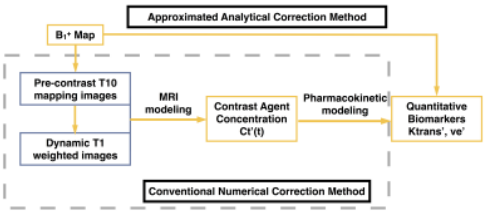

Figure 1. Comparison between the two B_1^+ correction approaches. Conventional correction method needs to repeat MRI modeling and PK modeling pixel by pixel with original T_{10} images and dynamic T_1 weighted images, while approximated analytical correction method only requires the uncorrected PK parameters to perform the correction and simplifies the computation.

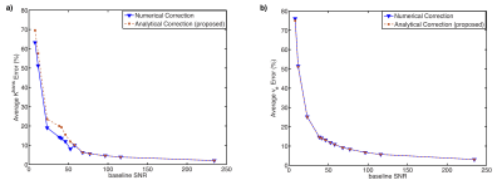

Figure 2. Comparison of correction residual errors between two correction methods for K^{trans} maps (a) and v_e maps (b) with various levels of noise added. There are 100 Monte-Carlo simulations for each PK parameter combination. For each SNR level, noise-induced errors for 3000 pixels (5 × 6 × 100) excluding outliers were averaged.

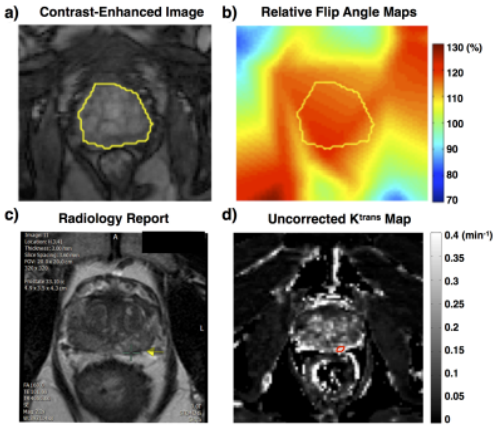

Figure 3. Example of ROI positioning for prostate (a-b) and lesion (d). The volumetric prostate ROI is defined by contrast-enhanced images, and the 2D lesion ROI is defined on uncorrected K^{trans} maps based on the radiology report (d).

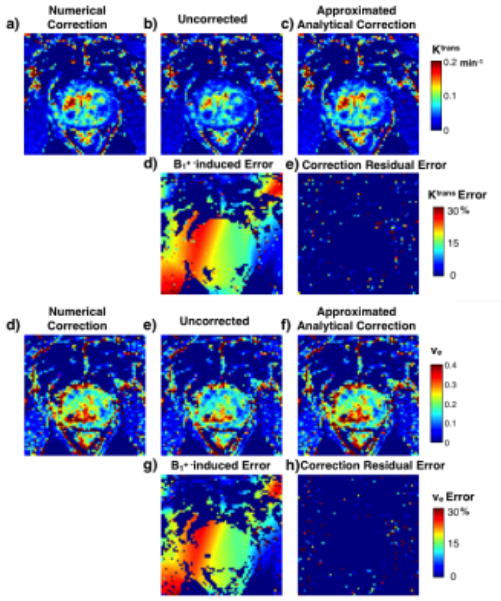

Figure 4. K^{trans} maps after numerical B_1^+ correction method (a), before B_1^+ correction (b) and after approximated analytical correction method (c), B_1^+ induced error for Ktrans (d), correction residual error of K^{trans} (e), v_e maps after numerical B_1^+ correction method (f), before B_1^+ correction (g) and after approximated analytical correction method (h), B_1^+ induced error for v_e (i), and correction residual error of v_e (j).

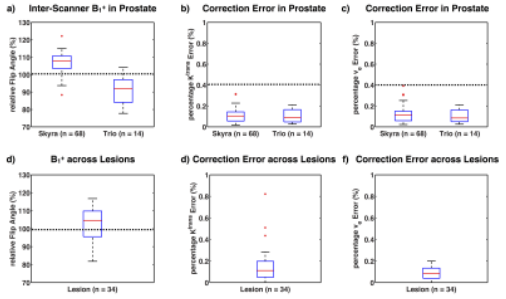

Figure 5: Boxplot of average relative flip angle (%) distribution between two 3.0 T systems (a) and corresponding correction residual error for K^{trans} (b) and v_e (c) within volumetric prostate ROIs for 82 patients. Boxplot of average relative flip angle (%) distribution across 34 lesions within 2D ROI from 28 in-vivo cases (d) and corresponding correction residual error for K^{trans} (e) and v_e (f). All correction errors are smaller than 1%.