Comparison of the Signal Difference Methodology with the Conventional Technique for DCE-MRI Perfusion Parameter Accuracy in the Presence of Flip Angle Deviations

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Introduction: DCE-MRI has become a useful tool for assessing tumor perfusion. Typically, tumor perfusion parameters (K^{trans}, v_e, v_p) are estimated by converting the detected signal to contrast agent (CA) concentration, which also requires the knowledge of the intrinsic tissue T_1. Alternatively, recent reports have demonstrated that these parameters can be derived more directly from the signal difference between the DCE-MRI time series and its pre-contrast baseline signal [1, 2]. Compared to the conventional method, the latter technique is simpler: baseline T_1 is not required; conversion from signal intensity to CA concentration is not necessary; and no CA relaxivity has to be assumed. It has also been shown that the excitation flip angle can vary substantially throughout the body, leading to errors in tumor perfusion calculations with conventional techniques [3]. The goal of this study is to systematically compare the performance of conventional and signal difference methods for determining perfusion parameters in the presence of these flip angle errors.

Methods: Using a range of flip angles observed in the body with the actual flip angle imaging (AFI [4]) technique, numerical simulations were performed for the comparison. The following parameters were used: CA (Multihance) relaxivity=7.8s^{-1}/mM, blood T_1=1200ms, tumor T_1=800ms, nominal flip angle = 25°, TR=3.2ms, K^{trans}=0.4min^{-1}, v_e=0.4, and v_p=0.02. Parker's model of the AIF [5], slightly modified to match the curves we typically observe, was utilized. For T_1 measurements, the VFA technique [6] was used with nominal flip angles (4°, 10°, 15°). For the flip angle deviations, a range of -40% ~ +40% error in the nominal flip angle was assumed as observed *in vivo* [3]. The nominal flip angle (25°) for the DCE-MRI sequence was also adjusted to account for the error. After the MR signals for VFA and DCE-MRI data were generated using the actual (erroneous) flip angles, the perfusion parameters were subsequently computed for the conventional method using the nominal flip angles. To compute the perfusion measures for the signal difference method, only the signal changes of the dynamic image series were needed.

Results and Discussion: Figure 1 shows a flip angle error map observed in a DCE-MRI protocol, demonstrating that errors on the order of ±40% can occur throughout the body. Figure 2 compares the errors in the perfusion parameters for the conventional and signal difference methodologies for various flip angle deviations at the locations of the AIF and tumor.

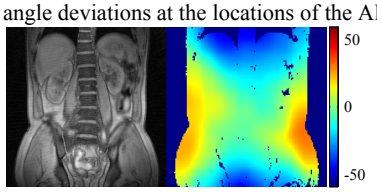


Figure 1. Anatomic image and its flip angle error map on a 3.0T MRI system. The unit for the color bar is percentage (%).

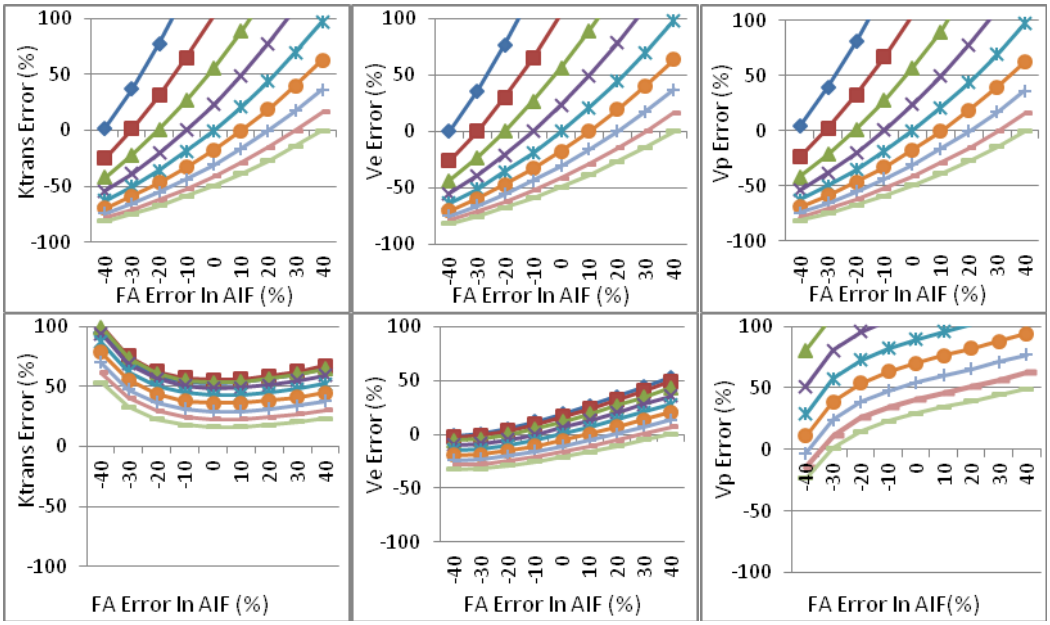
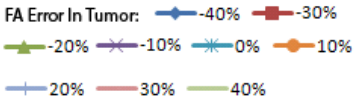


Figure 2. Perfusion parameter measurement errors: conventional method (top row) and signal difference method (bottom row). The horizontal axis represents the relative flip angle (FA) error at the location of the AIF, and each curve corresponds to different flip angle error at the tumor location. All flip angle errors (%) are relative to the nominal flip angle 25°.



Overall trends in the error curves for all three perfusion parameters are quite similar for the conventional method. Interestingly, when flip angle errors are identical at the locations of the tumor and AIF, the errors are close to zero, as indicated by the points that lie horizontally along the 0% error line. The absolute error steadily rises as the flip angles at the two locations increasingly differ. For the signal difference method, the range of errors is substantially smaller for K^{trans} and v_e, although there is an overall positive bias for K^{trans}. The smaller error range indicates that this method is less sensitive to flip angle deviations and may be more suitable to detect changes in these perfusion parameters in follow-up examinations, e.g. following treatments. The bias in K^{trans} is related to the fact that the signal difference method assumes a linear relationship between signal difference and CA concentration, which is not strictly true, particularly at lower flip angles. Additional simulations using a 50° nominal flip angle showed that, while the error range slightly increases, the bias (the center of the curve cluster) is reduced from 43% to 12%. As this bias is expected to be constant between scans utilizing identical flip angles, it should not substantially influence the measurement of relative changes in the perfusion parameter.

This work focuses on the effect of flip angle inhomogeneity in the measurement of perfusion parameters. It should be noted that unlike the conventional technique, the signal difference method can be susceptible to receiver coil sensitivity. Thus, in order to realize the potentially improved measurement precision of the signal difference methodology, a coil sensitivity map should be included in the protocol. When using the conventional technique, our results suggest that a flip angle map, e.g. using AFI, may be required to more accurately measure the perfusion parameters.

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References: **[1]** Ashton *et al*. ISMRM 2007; 2813. **[2]** Walker-Samuel *et al*. Phys Med Biol 2007; 52: 589. **[3]** Yu *et al*. ISMRM 2011; 1076. **[4]** Yarnykh *et al*. Magn Reson Med 2007; 57:192. **[5]** Parker *et al*. Magn Reson Med 2006; 56: 993. **[6]** Cheng *et al*. Magn Reson Med 2006; 55: 566.