Phase-based contrast agent quantification using statistical modelling

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Introduction

In dynamic contrast-enhanced (DCE) magnetic resonance imaging (MRI), quantifying contrast agent (CA) concentration is fundamental. Intensity changes in blood or tissue due to changes in T1 is used to estimate the CA concentration, however issues like flip angle inhomogeneity, partial volume effects, inflow effects, insufficient spoiling, unknown proton exchange rates and uncertainties in relaxivity can affect the accuracy. Phase changes linearly with susceptibility and thus CA concentration[1]. However, the inversion of the magnetic field shifts is an ill-posed problem since the convolution between the susceptibility and a magnetic dipole is a non-invertible operation[2]. We propose a method for CA quantification where the systems of equations from phase data can be regularized by incorporating the magnitude data, i.e. optimally combine phase and magnitude data using a statistical approach.

Materials and methods

The CA estimation is based on the model described by Eq. (1), using a maximum likelihood estimator. In Eq. (1) $\circ$ represents element-by-element multiplication, $\mathbf{c_m}$ is the estimated CA concentration from magnitude signal only, $\mathbf{\Delta\varphi}$ is the phase shift, $\mathbf{\Psi}$ is the convolution matrix corresponding to a magnetic dipole, $\mathbf{c}$ is the true CA concentration, ξ is a multiplicative noise term, and ε_m, ε_φ are additive noise terms. The resulting large system of linear equations was solved using the conjugate gradient method. We simulated DCE-MRI exams using a digital phantom[3], and a region with "tumor tissue" was added to the phantom. AIFs were calculated using the parker model[4] and the modified Kety model was used to calculate time- and tissue-specific CA concentrations. We simulated a gradient echo sequence with TR/TE = 5.6/3.0 ms, FA = 20° using a matrix size of 64 × 64 × 64 and a FOV of 18.1 × 21.7 × 18.1 cm^3 on a 3 T scanner with 11 SNR values ranging from the equivalent of a body coil to an 8 channel head coil. The time resolution was 2 s for the first 30 s to capture details in the peak and circulation peak, 5 s between 30 and 60 s. Each data point was simulated 50 times to examine the precision of the model for a total of 12 100 simulated points. Calculations were performed on the HPC2N computing cluster at Umeå University using approx. 5000 CPU hours.

$$\mathbf{c_m} = \xi \circ \mathbf{c} + \varepsilon_m \qquad \Delta\varphi = \mathbf{\Psi c} + \varepsilon_\varphi \qquad (1)$$

Results

Figure 1 shows a typical AIF estimate with phase and magnitude data and magnitude data only for an SNR corresponding to an 8 channel head coil. The RMS error for the estimated CA concentration over time for different SNRs using the proposed method and the conventional magnitude based approach are shown in Fig. 2. The phase based method performed very well for CA concentration estimates in vessels compared to the conventional method. The performance was also better in tumor tissue, where the blood-brain-barrier leakage generates high CA concentrations and therefore large phase shifts. For white matter no performance increase was observed.

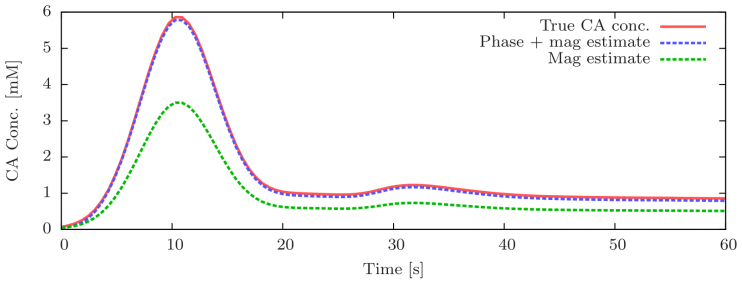

Figure 1*. Estimated AIFs with phase and magnitude data and magnitude data only with noise characteristics of an 8 channel head coil.*

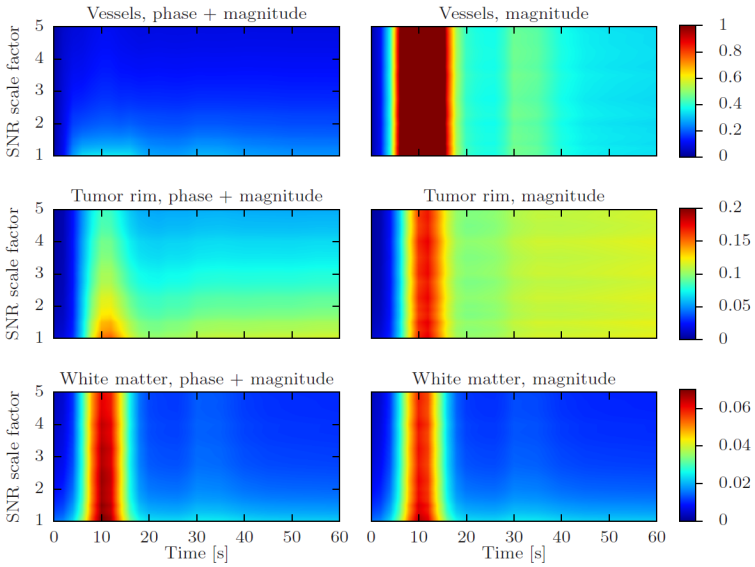

Figure 2. *The RMS error in CA concentration [mM] over time for different SNRs in vessels, enhancing tumor and white matter during 60 s of a DCE experiment. SNR is scaled relative to that of a body coil in a 3 T scanner and the highest SNR-factor (=5) corresponds to an 8 channel head coil. The left and right columns correspond to the proposed method and a magnitude only based approach, respectively.*

Conclusion and discussion

For tissues with high CA concentrations the proposed method performed better than using magnitude information only. Combining phase and magnitude information seems to be a viable option to get improved accuracy, and better SNR improves the situation. The next step is to test the method on in-vivo data where many challenges still remain, such as phase-drift.

References

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