Use of cardiac output to improve measurement of tracer input function in dynamic contrast-enhanced MRI

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Introduction

Dynamic contrast-enhanced MRI (DCE-MRI) measures the transit of a tracer to estimate physiologic parameters. Applications include estimates of tumor angiogenesis and organ function such as kidney glomerular filtration rate (GFR). Accurate quantitative analysis of DCE-MRI data requires reliably measured arterial input function (AIF). Tracer concentration C(t) can be estimated by measuring the change in longitudinal relaxation time T1 due to T1-shortening effect of the tracer. This approach (termed direct conversion) is applicable to solid tissues, but is significantly less accurate in the aorta or other major arteries, because MR signal from these arteries can be distorted by several artifacts, such as inflow effect, dephasing, B1 inhomogeneity, partial volume effect. These signal errors are amplified in direct conversion. To minimize the adverse effect of the distortions, Parker et al. [1] proposed to average AIFs obtained from a group of controls, and to apply this averaged AIF for data analysis. However, this method may not be able to correct for systematic artifacts such as inflow and partial volume effect, and by disregarding differences between patients, additional sources of errors can be introduced.

This study presents a new method to compute AIF using a constrained conversion that takes into account the subject’s cardiac output (Q). We compared the proposed method with conventional methods in simulation studies for measurements of (a) tumor perfusion and (b) renal function, and in MR renography for volunteers.

Methods and Materials

The new approach utilizes the indicator dilution principle [2] to constrain the area under AIF. The principle states that D = Q×AUC, where AUC is the area under the “first pass” component of AIF, D is the mass of the injected tracer, and Q is the cardiac output. Q can be measured using velocity-encoded phase contrast MRI with RPF and v were estimated by a 3-compartment model [5]. Image registration and segmentation was done to obtain signal versus time curves for aorta, renal cortex and medulla [6]. The simulation signal curve was also shifted vertically with a shift randomly chosen within ±30% range of S(0), reflecting the various MR artifacts. Three methods were used to convert the simulated signal curve to AIF: direct conversion, the proposed method, and the averaged input function (constructed using Bae’s model separately). In direct conversion, FA was randomly chosen within ±1º range of true value, and 5% random noise was added to T1(0). In the proposed method, 10% random noise was added to Q to reflect its measurement error. For tumor simulation, a model by Tofts et al [4] with Ktrans and v were employed to convolve with the ideal AIF to obtain tissue data. For kidney simulation, a three-compartment renal model [5] with GFR and RPF was used. Deconvolution of the tissue data and the converted AIF resulted in the parameter estimates. Random simulations were repeated 2000 times, to obtain 2000 estimates for each parameter. Two-sampled F-test was used to compare standard deviation (SD) of the estimates from different methods.

In patient study, coronal 3D MR renography was repeated on three separate days for each of the 4 healthy volunteers: TR 2.3 ms, TE 0.8 ms, flip angle 9º, field of view 309 mm x 450 mm, slice thickness 3.0 mm, 32 slices, acquisition time 3 s. After a bolus injection of 4 ml Gd-DTPA, the acquisitions were repeated over 10 min. Image registration and segmentation was done to obtain signal versus time curves for aorta, renal cortex and medulla [6]. The signal curves for the renal tissues were converted to concentrations by direct conversion. The aortic signal intensity curves were converted to concentration using the same three methods as in simulation. GFR and RPF were estimated by a 3-compartment model [5].

Results and discussion

In simulation, the proposed method improved the precisions for all the parameters by at least a factor of three compared with the direct method (Figure 1). For example, in the high-perfusion tumor simulation (nominal value Ktrans = 0.5 min-1), the SD of Ktrans was 0.08 min-1 using the constrained AIF versus 0.31 min-1 using the conventional direct conversion method. The averaged AIF was associated with a systematic deviation of computed parameters. For example, the systematic bias for high-perfusion Ktrans was -4% and for v was 8%, whereas, the differences by the proposed method showed minimal deviation from their true values: -4.6% for Ktrans, -0.8% for v. In patient study, SD of GFR by the proposed method, 6.4±4.4 ml/min, was significantly lower than that by direct conversion, 20.5±12.7 ml/min, and also significantly lower than that by the averaged input approach, 7.8±4.4 ml/min (Figure 2 (a)). The SD of RPF estimates by the proposed method, 27.4±17.8 ml/min, was lower than that by direction conversion, 97.8±32.1 ml/min, or by averaged input approach, 92.7±64.5 ml/min (Figure 2(b)).

Several features of the proposed method make it advantageous over the previous methods. First, AIF is calibrated using the area under the first-pass curve, which is calculated for each individual patient. Second, more than one source of artifacts can be corrected. Because of its ability to improve reproducibility, the proposed method should be of value in applications where repeated measurements are compared, for example in the monitoring of tumor response to therapy, or pharmacologic challenge such as angiotensin-converting enzyme inhibitor-enhanced renography. We note that in these applications, the measurement of cardiac output is not absolutely necessary, provided that cardiac output change across serial DCE-MRI exams can be neglected.