Blind Multichannel Deconvolution for Estimation of a Parametric AIF in DCE-MRI of Mice

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<u>Target audience:</u> Scientists developing new models and algorithms for DCE-MRI

<u>Purpose:</u>

The main challenge in dynamic contrast-enhanced (DCE) MRI, especially when applied to mice and rats, is to use a correct arterial input function (AIF). Measuring the AIF from an artery within the slice of interest leads to partial-volume, flow and dispersion artifacts. Measuring the AIF in a slice intersecting heart which is acquired in addition to the slice of interest minimizes the partial volume effect but at the cost of the time resolution in the acquired image sequence. An alternative avoiding these problems is to use blind multichannel deconvolution where the AIF is estimated directly from the measured contrast-agent concentration curves in several tissues. Compared to clinical DCE-MRI [1], application of this approach to small animal imaging is limited only to a nonparametric (model-free) AIF [2].
To improve the noise-robustness, a model-based AIF approach is introduced to multichannel blind deconvolution in small-animal DCE-MRI.

<u>Methods:</u>

The tissue contrast-agent concentration time development is a convolution of the AIF and the tissue residue function (TRF), multiplied by blood flow. Assuming a sufficiently short sampling period (around 1 image per second) and a sufficient signal-to-noise ratio (SNR), a complex TRF model, adiabatic tissue homogeneity (ATH) model (describing also the vascular phase of the contrast-agent distribution), is used instead of the commonly used Tofts model [1]. The new AIF model is a sum of three gamma variate functions. The deconvolution process is formulated as a minimization problem. The criterion function is the sum of the least-squares differences between the contrast-agent concentration time curve and its convolutional model for all channels. The channels represent the tissue regions from which the mean contrast-agent concentration time curves are extracted. Hence, the blind-deconvolution algorithm results in estimates of the TRF parameters (perfusion parameters) of each channel and of the AIF parameters (common for all channels). The estimated AIF is subsequently used in the pixel-by-pixel non-blind deconvolution [3] of the whole image sequence to calculate perfusion-parameter maps.

The proposed AIF estimation method is evaluated on simulated and real data. The simulated data are generated to closely mimic the real data used in the second step of the evaluation. The reference AIF was obtained by fitting of the AIF model to the AIF derived from the signal intensity in a pixel located in an artery of the recorded DCE-MRI image sequence. Three TRFs were generated based on literature perfusion-parameter values for human colon cancer [4] (region 1) and muscle [4] (region 2) and on the values expected in a necrotic tumor tissue (region 3). Gaussian noise was added to the convolution of the AIF and TRF. The noise variance was set according to the corresponding signals extracted from the real recording. The AIF estimation was performed 50 times (using 50 noise realizations for each channel).

The testing animal recording (approved by the National Animal Research Authority) was done on a BALB/c mouse with murine colon tumor cells CT26 subcutaneously implanted into the left flank. One axial slice through the tumor middle was imaged. The mouse was anesthetized with Isofluran, O2 and monitored continuously for respiratory rate and body temperature. As a contrast agent, Magnevist (Bayer Schering Pharma, Berlin-Wedding, Germany) was administered at a dose of 0.2 mmol/kg body weight, injected in the tail vein. The 9.4T BioSpin (Bruker Biospin MRI , Ettlingen, Germany) scanner was used, with the 2D FLASH sequence, TR/TE 14/2.5 ms, flip angle 25°, image matrix 128x96 pixels, slice thickness 1 mm, sampling interval 1.04 s, acquisition time 13 min. Before the bolus administration, 15 images were recorded with TR = 14, 30, 50, 100, 250, 500 ms to convert the dynamic image sequence to the contrast-agent concentration. Anatomical images were recorded using the RARE sequence (T2-weighted and T1-weighted pre- and post-contrast).

<u>Results:</u>

Fig. 1a) shows the reference AIF and the mean estimated AIF ± standard deviation. Fig. 1 b) shows the morphological T2-weighted image and Figs. 1 c,d) show examples of the perfusion-parameter maps: permeability-surface product of the vessel wall (PS) and blood flow (Fb).
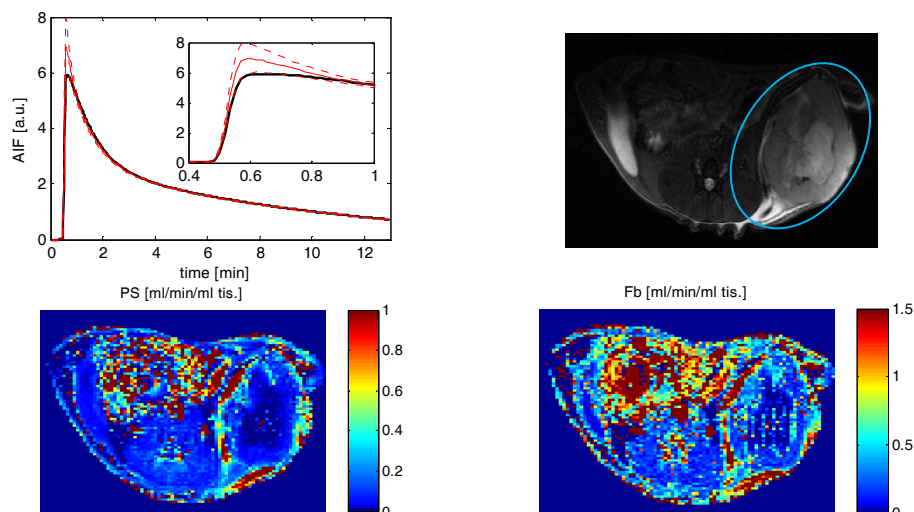

Figure 1: a) simulated data results, black – reference AIF, red – estimated mean (solid) ± standard dev.(dotted), inset is a magnified initial part; b) T2-weighted anatomy image (tumor denoted by ellipse); c), d) perfusion-parameter maps

<u>Discussion:</u>

The simulated data results show a fairly good fit of the estimated to the reference AIF, with a slight overestimation of the AIF peak.

For real mouse data, the resulting perfusion-parameter maps were spatially consistent and in the expected range[4]. They showed the expected characteristics according to the assumed histological composition. There was a clear distinction between the tumor rim and the fibro-necrotic center. On the PS map the permeability decreased towards the center. The Fb map was also with a good correlation with the expected malignant lesion features and other parametric images (not shown), the highest values on the outer lesion margin corresponded to the presence of the feeding and draining vessels.

<u>Conclusion:</u>

DCE-MRI of small animals is possible without measuring the AIF. This avoids the AIF measurement artifacts and enables faster image acquisition (when compared to the approach of an additional heart-intersecting slice for AIF detection) while keeping a reasonable spatial resolution. This allows application of more complex pharmacokinetic models, as the ATH model, and, consequently, enables reliable estimation of PS and Fb in addition to the standard parameters kep, Ktrans, ve and vb. Acknowledgement: 102/12/2380, CZ.1.05/2.1.00/03.0101, CZ.1.05/2.1.00/01.0017.

<u>References:</u>

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