Model-Based Parameter Identification using Analytic Convolution

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Introduction:

There is a considerable interest in the quantitative determination of tissue parameters in dynamic contrast enhanced MR imaging (DCE-MRI). Tracer kinetic modeling is used to derive physiological parameters, such as plasma perfusion F_p, permeability-surface area product PS, plasma volume v_p and the interstitial volume v_e, from the measured tissue contrast agent concentration-time curve and the concentration-time curve of the arterial input function (AIF). With the usually applied generalized kinetic model [1, 5] the interesting parameters F_p and PS cannot be separated. Furthermore, this model neglects the first pass of the contrast agent. This is, however, possible by using more complex models like the adiabatic approximated solution of the Johnson and Wilson (aaJW) model, introduced by Lawrence and Lee [2]. Another approach was developed by Griebel [3] and is based on a specific solution of the generalized approach of the indicator dilution theory [4]. In current work, we have described the AIF by an analytic function and derived an analytic solution of the convolution. Simulations of tissue contrast agent concentration-time curves were performed to compare the physiological parameters provided by analytic and discrete data analysis.

Methods:

For analyzing the concentration-time data the following convolution (⊗) equation was used:

$$c_t(t) = F_p \, c_a(t) \otimes R(t) \qquad (1)$$

where $c_t(t)$ represents the concentration-time curve in the tumor tissue and $c_a(t)$ the AIF. F_p denotes the tissue plasma flow and $R(t)$ the impulse residue function of the model. The AIF is described by gamma-variate functions in combination with a biexponential decay of the arterial contrast agent concentration. An analytic convolution was preformed using the Laplace transform. $R(t)$ of the model described by Griebel is given by expression (2):

$$R(t) = e^{-k_{iv}t} - \frac{\left(e^{-k_{iv}t} - e^{-k_{in}t}\right)k_{iv}E}{k_{iv} - k_{in}} \quad \text{where} \quad k_{iv} = \frac{1}{T_c} \quad \text{and} \quad k_{in} = \frac{F_p E}{v_e} \qquad (2)$$

where T_c denotes the capillary mean transit time ($=v_p/F_p$). The extraction ratio E can be calculated by E=1-exp(-PS/F_p). A measured DCE-MRI data set was used for AIF modeling and a set of representative physiological parameters for the tissue residue function. Reference parameters were chosen from a breast tumor and were defined as 0.57 ml/g/min, 0.33 ml/g/min, 0.06 ml/g and 0.45 ml/g for F_p, PS, v_p and v_e, respectively [6]. For simulations the Griebel model and the acquired AIF parameter were used to create sets of 100 contrast agent concentration-time curves for the AIF and the tissue. The concentration-time response of the tissue was overlaid with normal distributed noise. The temporal resolution was 8 s, which was reduced by acceleration factors up to the theoretical value of 8. These data were then analyzed analytically and discretely for comparison. The difference caused by the different analyzing methods was given by boxplots for the various sampling intervals.

Results:

Figure 1 shows the measured AIF data and the fitted analytic AIF. In figure 2 the differences between the two analyzing methods are shown in boxplots of the plasma flow F_p and permeability-surface area product PS. The variation of fitted parameters is caused by the noisy concentration-time curves used for parameter estimation. The most significant difference between the two analyzing methods was evident for low sampling rates. The median of estimated parameters shows also less influence of the sampling interval for the analytic analysis. For higher sampling rates discrete and analytic analyzing resulted in similar parameters and comparable χ^2 goodness-of-fit values of the fitted tissue concentration-time curves. In addition, the analytic tissue parameter estimation needed less iteration for fitting than the discrete analysis.

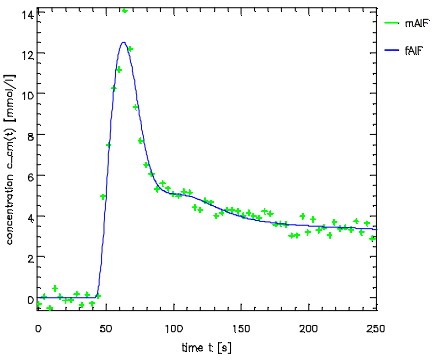

Fig. 1. Measured AIF data (mAIF) and fitted AIF (fAIF) used for simulation from an injected bolus.

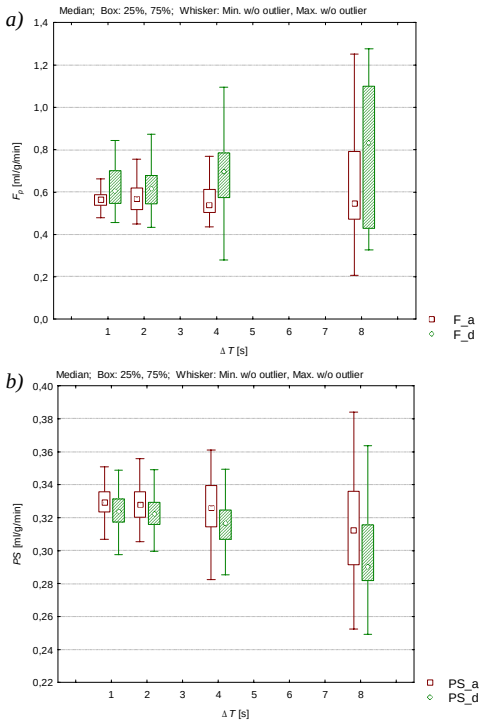

Fig. 2. Boxplots of the estimated tissue parameter values of a) F_p and b) PS. The analysis was performed discretely (F_d, PS_d) and analytically (F_a, PS_a) using model by Griebel depending on the sampling rate ΔT (1 s, 2 s, 4 s, and 8 s).

Discussion/Conclusion:

It should be considered, that fitting of complex model functions in noisy concentration-time curves calculated from DCE-MRI data makes physiological tissue parameter estimation very challenging. In this work we have derived a complex analytic description of tissue concentration-time curves. Also the first pass of the contrast agent can be considered by using a model for the AIF. One advantage of the analytic analysis is that noise-induced errors of the AIF can be eliminated in physiological parameter estimation. Additionally, the errors resulting from discrete convolution can also be avoided and the influence of the sampling interval can be reduced. Using analytic functions makes also the implementation of the aaJW model easier because of the box function in this parameter model. To improve reliability of this parameter estimation, it is necessary to minimize the influence of noise and the sampling interval. Using this analytic technique enables tissue parameter estimation with less influence of data noising of the AIF and no discrete convolution errors.

References:

[1] Tofts PS et al. J Magn Reson Imaging 1999;10(3):223-232
[2] St Lawrence KS, Lee TY. J Cereb Blood Flow Metab 1998;18:1365-1377
[3] Griebel J, et al. Proc ISMRM 9th Annual Meeting 2001:629
[4] Zierler KL. Circ Res 1963;XII:464-471
[5] Tofts PS, Kermode AG. Magn Reson Med 1991;17(2):357-367
[6] Buckley DL. Magn Reson Med 2002;47(3):601-606

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