MODELLING IN PERFUSION MR IMAGING

Hana Válková
Master Degree Programme (2), FEEC BUT
E-mail: xvalko05@stud.feec.vutbr.cz

Supervised by: Jiří Kratochvíla
E-mail: xkrato30@stud.feec.vutbr.cz

Abstract: This paper deals with quantitative perfusion analysis of dynamic contrast enhanced magnetic resonance data. The perfusion parameter estimation method is based on approximation of tissue concentration time sequences with convolution models. The method is evaluated on synthetic data and illustrated on clinical data of the renal cell carcinoma patient. The main contribution of the article is the inclusion of dispersion model to capture the signal changes on the way from artery to remote tissues.

Keywords: Perfusion imaging, DCE-MRI, arterial input function, tissue residual function, dispersion of arterial input function, curve modelling

1 INTRODUCTION

Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is used for estimation of maps of tissue perfusion parameters. The main application field of DCE-MRI is in oncology. Diagnostic benefit is the short time response (changes in perfusion parameters) to selected treatment compared to morphological approaches. The tissue concentration time sequences of measured DCE-MRI data and concentration time curve from supplying artery (AIF) are necessary to estimate perfusion parameters of tissues.

The major disadvantage of the DCE-MRI method is unreliability of the AIF measurement. The AIF is unable to measure correctly in tissue region of interest (ROI). The obtained AIF is from a large artery far away from the ROI. The dispersion of the AIF to the ROI is neglected and it brings inaccuracies in perfusion parameter estimates. This article provides a solution in using of AIF dispersion models. In addition to dispersion effects the measured AIF has low signal dynamics. It is caused by signal saturation with high concentration of contrast agent in many acquisition techniques. This contribution brings the parametric models of the AIF and solves the signal saturation effect. The estimation of perfusion parameters is done from tissue concentration time sequences by the deconvolution algorithm. The algorithm is tested on synthetic data and illustrated on clinical data – patient with renal cell carcinoma (RCC).

2 METHODS

In DCE-MRI the measured tissue concentration time sequence can be expressed by the convolution of models according to the equation:

$$C_t(n) = (VTF(n) \otimes AIF(n)) \otimes TRF(n), \tag{1}$$

where C_t is the measured tissue concentration time sequence, AIF is the arterial input function (concentration time curve from artery), VTF is the vascular transport function (VTF models the dispersion of the AIF), TRF is the tissue residual function (tissue impulse response function), n is the time index and $\otimes$ represents the discrete convolution. [1, 2]

Perfusion parameter estimations are determined by the estimated parameters of the TRF model. In this contribution deconvolution is used for TRF and VTF estimation. It is the optimization problem, where the tissue concentration time sequences are approximated with convolved models in eq. 1. The optimization algorithm is performed in Matlab, using the `fmincon` function, which finds the minimum of constrained multivariable function. Searched parameters are therefore physiologically constrained. In frame of this contribution 11 AIF, 5 TRF and 3 VTF literature based models are implemented. Figure 1 shows some of the models. [1, 2]

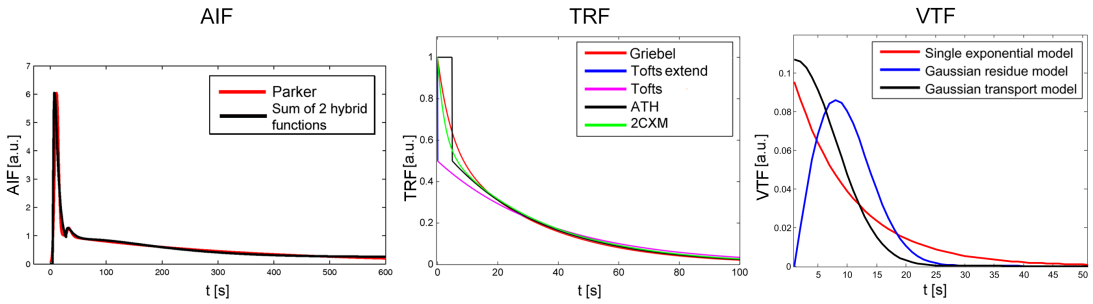

Figure 1: Illustration of created models.

3 SYNTHETIC DATA - EVALUATION AND RESULTS

The generation of tissue concentration time sequences was done as the convolution of the AIF, TRF and VTF models. Datasets of three synthetic tissue types (RCC tumor, psoas muscle and vertebrae) were generated using parameter value ranges obtained from clinical data. The sampling period was 1.2 seconds. Figure 2 shows synthetic (blue) tissue concentration time sequence for RCC tumor and the estimation (red), using deconvolution, where the AIF was known and parameters of TRF and AIF dispersion (VTF) were estimated. Models used for generation and estimation (Figure 1) were Tofts extended [2] for TRF, population based Parker's AIF [3] and exponential model for VTF. All of the synthetic and estimated parameter values in Figure 2 show good correspondence. Initial estimates for all parameters were set to the value 0.1 in units of parameter. The parameter K_{trans} means volume transfer constant between blood flow and extravascular extracellular space, v_e is volume of extravascular extracellular space per unit tissue volume, v_b is volume of vascular space per unit tissue volume and MTT_{vtf} is parameter of the AIF dispersion related to mean transit time.

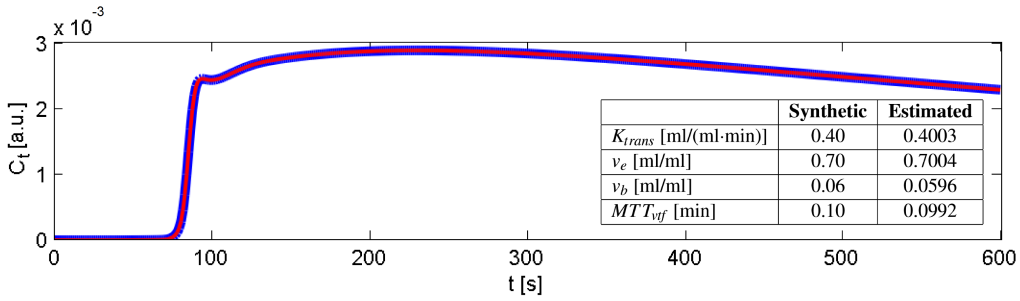

Figure 2: Synthetic data - generated (blue) estimated (red) tissue concentration time sequence.

Then white Gaussian noise was added to each generated tissue tracer time sequence. SNR values were 10, 20, 30, 40 and 50 dB. 50 different noise realizations were generated for each SNR. SNR in this paper is defined as the mean value of the signal without the noise divided by the standard deviation of the noise. Deconvolution was then applied to the synthetic data for different noise realizations. Table 1 shows the estimated parameters. The initial estimates were the same as for noise-less analyses. Results show good estimation accuracy even for low SNR.

	Real	Estimated	50 dB	40 dB	30 dB	20 dB	10 dB
K_{trans}	**0.40**	Mean±Std	0.4002±0.0006	0.4002±0.0018	0.3990±0.0074	0.3987±0.0187	0.3984±0.0377
v_e	**0.70**	Mean±Std	0.7003±0.0008	0.7004±0.0025	0.6986±0.0088	0.6984±0.0207	0.6945±0.0356
v_b	**0.06**	Mean±Std	0.0597±0.0008	0.0596±0.0024	0.0615±0.0094	0.0625±0.0219	0.0662±0.0370
MTT_{vtf}	**0.10**	Mean±Std	0.0994±0.0017	0.0992±0.0048	0.1027±0.0182	0.1033±0.0446	0.1160±0.0809

Table 1: Estimations of parameters versus different SNR, 50 noise realizations

4 CLINICAL DATA – ILLUSTRATION OF RESULTS

Clinical data were acquired at Masaryk Memorial Cancer Institute on a patient with RCC. Own acquisition was done using the Siemens Avanto 1.5T MRI scanner, T1-weighted 2D saturation recovery prepared Turbo FLASH sequence, sampling period 1.2 seconds, 10 minutes of acquisition. For estimation of perfusion parameters on clinical data it was required to take into account the bolus arrival time difference between the used tissue regions. This was modelled as the convolution of estimated tissue concentration time sequence with a narrow Gaussian function. Figure 3 illustrates estimated pixel by pixel perfusion maps of parameters K_{trans} and v_b, left map of each parameter is estimation without VTF, right is with dispersion of the AIF. Maps of K_{trans} have similar values, same result gives parameter v_e. Maps of v_b show the inclusion of VTF (v_b is underestimated without the dispersion).

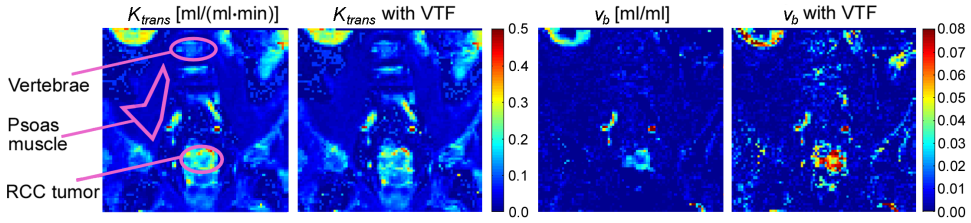

Figure 3: Comparison of clinical data perfusion map estimates without and with dispersion.

5 CONCLUSION AND CHALLENGES

The method of estimation of perfusion parameters including dispersion effects of the AIF is presented and tested on synthetic and clinical data. In the current setup the non-blind (known AIF) deconvolution algorithm is used for estimation of perfusion parameters. The synthetic data results show nearly consistent estimates through various SNR. The clinical data illustration shows the difference of perfusion map estimates with and without the dispersion of the AIF. In future work the estimates should be expanded by other models from Figure 1 and detailed evaluation should be done on synthetic and clinical data, on different estimation algorithms and the main challenge – on the blind deconvolution [4], where all curves – AIF, TRF and VTF are unknown.

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