PERFUSION ANALYSIS IN T1-WEIGHTED DYNAMIC CONTRAST-ENHANCED MRI

Michal Bartoš
Doctoral Degree Programme(1), FEEC BUT
E-mail: michalbartos@phd.feec.vutbr.cz

Supervised by: Radovan Jiřík
E-mail: jirik@feec.vutbr.cz

ABSTRACT

Dynamic contrast-enhanced magnetic resonance imaging (DCE MRI) with following perfusion analysis is a powerful technique for measuring perfusion parameters. One of the possible techniques based on minimization of sum of squared differences between the measured dilution curve and the estimation according to the tracer kinetics with aaJW model (adiabatic approximation to the Johnson and Wilson model) is presented. The method is applied on time series of DCE MRI images of the heart to obtain perfusion maps of the myocardium.

1. INTRODUCTION

The aim of perfusion imaging is to determine perfusion parameters of a tissue, which are useful for tissue functionality assessments, often in diagnosis of tumors, ischemia etc. The principle of perfusion imaging is based on the analysis of DCE data obtained by some imaging modality, e.g. MRI. DCE data are time series of images with different contrast related to the concentration of the contrast agent. The contrast agent is applied into vein and is distributed trough the blood stream to the whole body. This dynamic process is recorded. Observing some region of interest (ROI) in tomografical plane, dilution curves can be obtained as a series of concentration values in time for each image pixel in ROI from the dataset. It is necessary that each image is registered to same reference image in the set, e.g. first time slice. After the concentration time curves are obtained, i.e. dilution curves, it is possible to extract information about perfusion of the tissue from them. This information (values of perfusion parameters) can create a perfusion map. For the comfortable generation of perfusion parameters a simply graphical interface was created.

2. THEORY AND APPLICATION

According to the theory of tracer kinetics, it is possible to model the dilution of the contrast agent as a linear system described by the equation [1]:

$$C_T(t) = F \cdot C_A(t) * R(t) \qquad (1)$$

where $C_T(t)$ means tissue residue function (TRF), i.e. contrast-time curve measured in the observed ROI, F is plasma flow trough the capillary, $C_A(t)$ is contrast-time curve entering

the observed region, also called arterial input function (AIF) and $R(t)$ is the impulse residue function (IRF). * symbolizes convolution operator.

If extracellular extravascular tracer (leaves capillary but does not diffuse into cells) such as Gd-DTPA is used and temporal resolution is sufficient [2], IRF can be modeled by aaJW model (adiabatic approximation to the Johnson and Wilson model) as [1, 3]:

$$\begin{aligned} R(t) &= 1 && 0 \le t < T_c \\ R(t) &= E \cdot e^{-EF/v_e(t-T_c)} && t \ge T_c \end{aligned} \qquad (2)$$

where E is extraction fraction, T_c is the transit time trough the capillary and v_e is fractional volume of the extravascular extracellular space.

These parameters along with plasma flow F describe perfusion. The goal of the perfusion analysis is to extract them from the dilution curve. This is done by fitting of the model (1) to the measured TRF curves. Another interpretation of the process is a parametric deconvolution. Here it is realized as a minimization of the penalty function based on the sum of squared differences (SSD):

$$\min\{f(F,E,T_c,v_e) = \sum_n (C_T(n) - \widetilde{C}_T(n))^2\} \qquad (3)$$

where $C_T(t)$ is discretized measured TRF, $\widetilde{C}_T(t)$ is TRF estimate based on the model (1) and its current parameters (F, E, T_c, v_e), n denotes discrete time samples.

For the minimization (3) it is necessary to measure $C_T(n)$, which is a concentration-time curve measured in the observed voxel or small region of interest (i.e. average curve in the ROI) and the arterial input function. The AIF is usually measured in the artery feeding the observed ROI. In the case of myocardium investigation, it is possible to take it from the left ventricle (Figure 1).

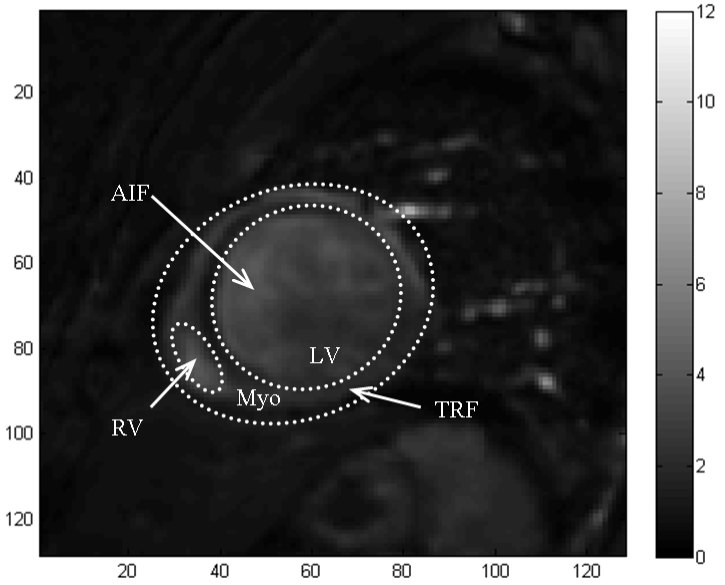

Figure 1: Image of the contrast agent concentration in the heart. LV – left ventricle, RV – right ventricle, Myo – myocardium. AIF, TRF – places of AIF/TRF curves in Figure 2

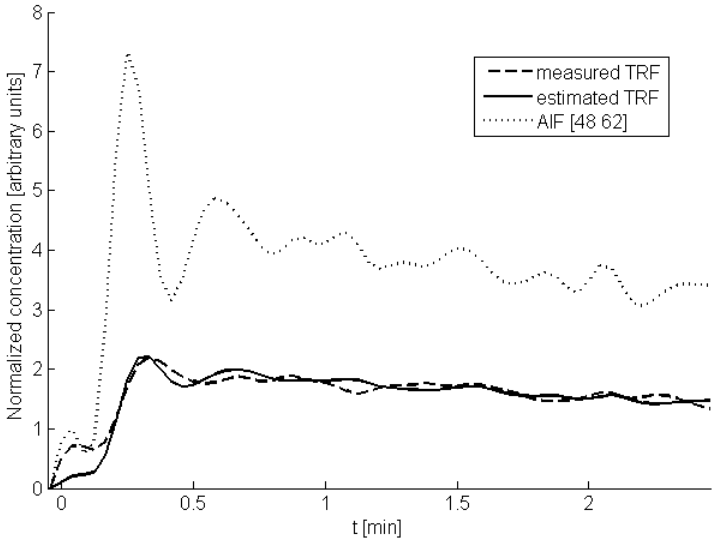

Figure 2: Concentration time curves

Characteristic curves of the concentration in part of the left ventricle and in one of the voxels in myocardium, i.e. AIF and TRF, are shown in Figure 2.

The perfusion maps (Figure 4) were created by minimizing of the penalty function (3) for myocardium tissue. An example of the TRF estimate is shown in Figure 2. The values of the penalty function, which symbolizes the quality of TRF estimation, or similarity of measured TRF with the estimated TRF, can be seen on Figure 3. White represents areas, where the minimization algorithm did not converge to satisfactory solution. It can be seen in the area of right ventricle, because it was not excluded from investigated region due to its size in the image. This can be expected because the right ventricle is not a parenchymal tissue and the model (1) does not apply to it The values in neighboring white area (left in the image) are incorrectly estimated too, probably because of uncertainty in image registration.

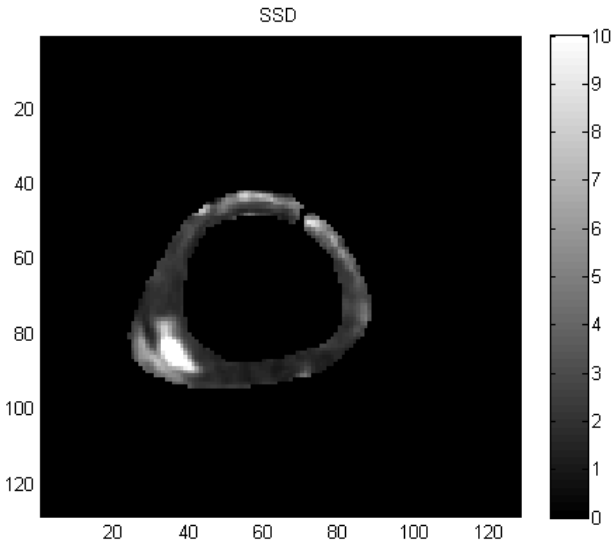

Figure 3: Values of penalty function.

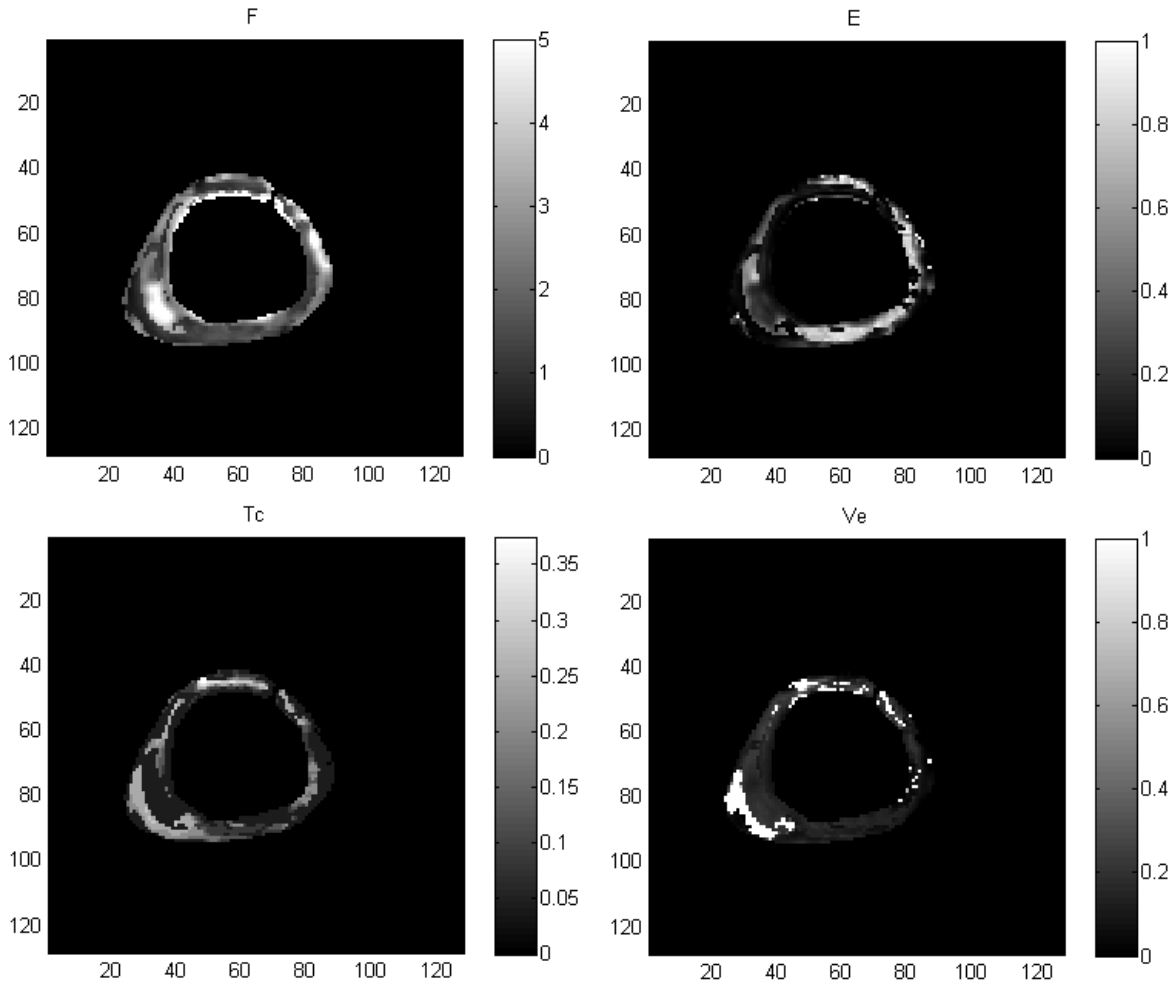

Figure 4: Perfusion maps of myocardium for basic perfusion parameters. Brightness represents values of perfusion parameters, F [ml/g min], E [-], T_c [min], v_e [-].

3. CONCLUSION

The paper presents perfusion analysis based on the aaJW model and the estimation of its parameters calculated as minimization of a SSD penalty function. For the comfortable estimation of perfusion parameters and generation of perfusion maps a simple graphical user interface was created. It allows listing in time slices of contrast agent concentration, selecting of AIF and regions for calculating of perfusion parameters on the level of voxels. The perfusion map was created for myocardium. Estimated parameter values are inside the interval of usual physiological values for myocardium [4, 5]. Future work will be based on the analysis of more hearts and other tissues in comparison with the known tissue states assessed by medical doctor.

ACKNOWLEDGEMENT

The project has been supported by the research frame of Grant agency of The Czech Republic (grant No.: 102/09/1690). We are grateful to Mr. Torfin Taxt and Mr. Terje Larson for participating in this project.

REFERENCES

[1] Henderson E, Sykes J, Drost D, Weinmann HJ, Rutt BK, Lee TY. Simultaneous MRI measurement of blood flow, blood volume, and capillary permeability in mammary tumors using two different contrast agents. Journal of Magnetic Resonance Imaging. 2000 Dec; 12(6):991-1003.

[2] Henderson E, Rutt BK, Lee T-Y. Temporal sampling requirements for the tracer kinetics modeling of breast disease.Magnetic Resonance Imaging 1998;16:1057–1073.

[3] St Lawrence KS, Lee TY. Adiabatic Approximation to the Tissue Homogeneity Model for Water Exchange in the Brain: I. Theoretical Derivation. Journal of Cerebral Blood Flow and Metabolism 1998; 18:1365 - 1377.

[4] Nielsen G, Fritz-Hansen T, Dirks CG, Jensen GB, Larsson HB. Evaluation of heart perfusion in patients with acute myocardial infarction using dynamic contrast-enhanced magnetic resonance imaging. Journal of Magnetic Resonance Imaging. 2004 Sep; 20(3):403-10.

[5] Jerosch-Herold M, Seethamraju RT, Swingen CM, Wilke NM, Stillman AE. Analysis of myocardial perfusion MRI. Journal of Magnetic Resonance Imaging 2004; Vol. 19, No. 6. pp. 758-770.