An Automatic Computation Tool for the Estimation of B1-Corrected Pharmacokinetic Parameters

Robert Merwa[1], and Gernot Reishofer[2]

[1]*Medical Engineering, Upper Austria University of Applied Sciences, Linz, Austria,* [2]*Department of Radiology, Medical University of Graz, Graz, Austria*

Introduction: Dynamic contrast-enhanced (DCE) T1-weighted MRI provides a technique for the determination of human tissue parameters [1, 2, 3]. The principle of this method is the analysis of the time-variant signal intensities of the DCE data and the quantification of these parameters relies on the deconvolution with the arterial input function (AIF), which can be determined from the signal changes in a major artery. For field strength above 1.5 T RF-field inhomogeneities (B1-inhomogeneities) occur which produce considerable intensity variations and the estimation of these tissue parameters fails. In order to tackle this challenge a huge amount of images and complex mathematical calculations are used hence the manual handling is pretty difficult and not fail-save. The aim of this work was to develop an graphical user interface (GUI) guided software package for the automatic calculation of the (a) temporal T_1-relaxation time [4], (b) concentration of the contrast agent which is used for the estimation of tissue parameters, (c) AIF in a major artery and (d) pharmacokinetic parameters K^{trans} and V_e for user defined regions. Furthermore the software package provides an algorithm for the automatic correction of all obtained parameters with respect to B1-inhomogeneities if an additional defined scan [5] is applied.

Methods: The software-package was developed in MATLAB (The MathWorks, Inc.). Due to the implementation of various GUIs the operation is very easy to handle. The software is able to read data from the database of the MR-System or from the PACS-System of the hospital. If a patient is selected, all image acquisitions are listed in the main GUI, which can be seen in figure 1.

If the Perfusion-Mode is selected in the menu, the corresponding images for the calculation of the temporal T_1-relaxation time and for the concentration of the contrast agent in tissue can be chosen by mouse from the listed image acquisitions. General settings can be selected and set such as (a) image noise removal, (b) adjustment of different image planes (e.g. for the B1-correction [5]) by means of different interpolation methods, (c) different filter-kernels for smoothing the selected images (d) value of the T1-relaxivity of the contrast agent and (e) different kinds of image calculations such as differential images, temporal T1-relaxation images and concentration images with or without B1-inhomogeneity correction.

With these settings it is possible to calculate automatically the images for the time-dependent T1-relaxation time and the time-dependent tracer concentration in the tissue. Based on the concentration images the pharmacokinetic parameters can be calculated for a defined perfusion model.

The software-package calculates the T_1-relaxation time by means of equation 1. $SI_{DCE}(t)$, α_{DCE} and T_{RDCE} are the signal intensity at the time point t the flip angle and the repetition time of the DCE scan respectively and the index $_{REF}$ characterises the parameters of the reference scan. For the calculation of the tracer concentrations in (mmol / l) equation 2 is implemented, whereby $T_1(t)$ is the temporal longitudinal relaxation time, T_{10} is the relaxation time without contrast agent and r_1 is the relaxivity of contrast media. The Tofts-model (3) was used for the estimation of the kinetic parameters K^{trans} and V_e. $C_T(t)$ is the tracer concentration in the tissue at time t and $C_A(\tau)$ represents the AIF which is the tracer concentration in the arterial whole blood at time τ. Hct represents the hematocrit, V_e is the volume of extravascular extracellular space per unit volume of tissue and K^{trans} is the volume transfer constant between blood plasma and V_e.

In the result images different kind of regions (points, lines and polygons) can be selected by mouse in order to obtain statistical information such as mean value, standard deviation, variance and coefficient of variation for the corresponding region. Figure 3 shows the AIFs, which are automatically calculated, stored and displayed if the corresponding region is selected by mouse. Figure 4 and figure 5 show the mean values for K^{trans} and V_e which are automatically estimated in the regions 1-4. Furthermore it is possible to correct all results with respect to B1-inhomogeneities (figure 3 - 5).

Summary and Discussion: A special software-package was developed which makes possible to read image data and special parameters of a MR-examination. Different functions are implemented for the calculation of the temporal T_1-relaxation time, the concentration gradient of the contrast media and for the estimation of pharmacokinetic parameters. Furthermore the obtained results can be improved by means of a special B1-inhomogeneity correction algorithm. In collaboration with two hospitals we intend to implement post-processing tools for stroke imaging and additional algorithms for functional MRI.

References: [1] S.M. Galbraith, NMR Biomed., 15, 132-142 (2002), [2] P.S. Tofts, J. Magn. Reson. Imaging, 10, 223-232 (1999), [3] A.R. Padhani, NMR Biomed., 15, 143-153 (2002), [4] K. Hittmair, Magn. Reson. Med. 31, 567-571 (1994), [5] W.H. Perman, Magn. Reson. Med. 9, 16-24 (1989)

Fig. 1: Image-series of a selected patient

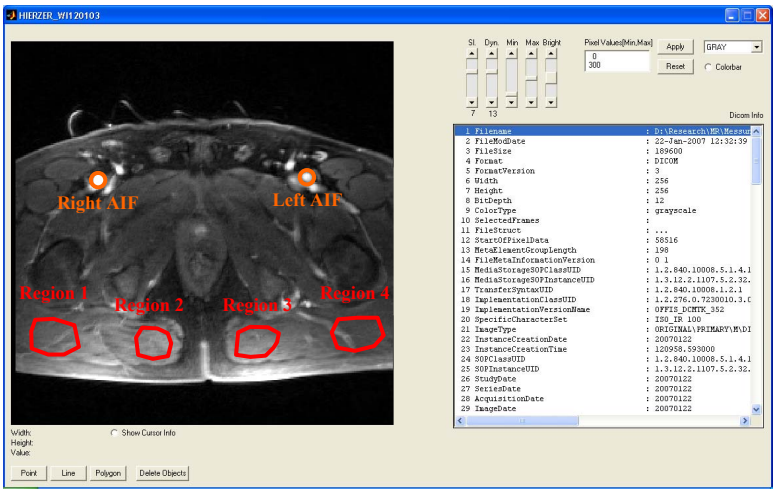

Fig. 2: Selected Image and defined regions

$$T_1(t) = -\frac{T_R}{\ln\left(\frac{SI_R \cdot \sin(\alpha_D) - SI_D(t) \cdot \sin(\alpha_R)}{SI_R \cdot \sin(\alpha_D) - SI_D(t) \cdot \sin(\alpha_R) \cdot \cos(\alpha_D)}\right)} \quad (1)$$

$$C(t) = \left(\frac{1}{T_1(t)} - \frac{1}{T_{10}}\right) \cdot \frac{1}{r_1} \quad (2)$$

$$C_T(t) = K^{trans} \cdot \int_0^{t_M} \frac{C_A(\tau)}{(1 - Hct)} \cdot e^{-\frac{K^{trans}}{V_e}(t-\tau)} d\tau \quad (3)$$

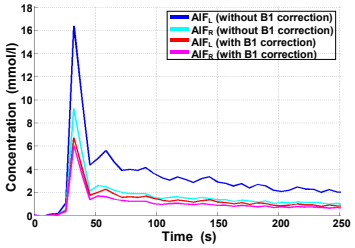

Fig. 3:Left and right AIF

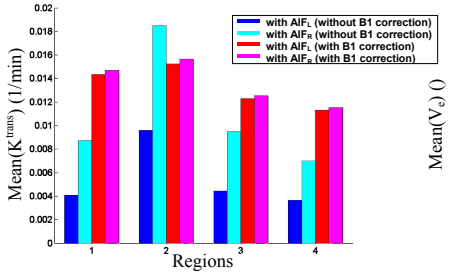

Fig. 4:Mean values of K^{trans} in the regions 1-4

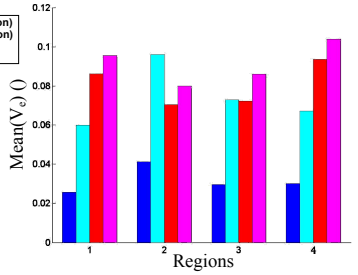

Fig. 5:Mean values of V_e in the regions 1-4