Model Based Blind Estimation of Kinetic Parameters

J. Fluckiger[1], M. Schabel[2], and E. DiBella[2]

[1]Bioengineering, University of Utah, Salt Lake City, Utah, United States, [2]Radiology, University of Utah, Salt Lake City, Utah, United States

Introduction: Dynamic Contrast-Enhanced (DCE) MRI is widely used for assessing changes in diseased tissue, both in cancer imaging as well as a range of other conditions. Quantitative measurements of kinetic parameters typically require a specified arterial input function (AIF). In such cases the concentration of contrast agent in the tissue is often represented by a simple two compartment model, giving: $TC = AIF \otimes k_{trans} \cdot e^{-k_{ep} \cdot t}$ (1), where k_{trans} and k_{ep} are constants that describe the wash-in and wash-out respectively of contrast agent into the tissue. However, in many imaging cases either no suitable artery exists in the imaging field of view, or the AIF is inaccurate. Several blind estimation methods have been applied to DCE-MRI to determine quantitative parameters without a priori knowledge of the AIF [1]. This work uses the iterative method for blind estimation as proposed by [2]. The method in [2] is improved upon by implementing a novel theoretical form for the AIF in the iterative process.

Method: Tissue concentration curves were extracted pixel-wise from a standard clinical DCE-MRI scan. The MRI studies were performed on a 1.5T system (Siemens Medical Systems) using a proton density-weighted spoiled gradient echo sequence. The tissue curves (TCs) could also have been obtained from any particular region of interest. For uniqueness, the IQML method requires only multiple TCs with different expected kinetic parameters. Each tissue curve can be represented in generalized matrix form as: $[TC] = [H]\vec{b}$ (2), where TC is a matrix of vertically concatenated tissue curve, $\vec{b}$ is the AIF vector and H is a matrix of vertically concatenated nonsymmetric Toeplitz matrices representing the convolution in equation 1. The function to be minimized by the IQML process is then $R = \left\| TC - H\vec{b} \right\|$ (3), which can be done by alternately varying $\{k_{trans}, k_{ep}\}$ and $\vec{b}$. Additionally, in each iteration, the estimated blood curve was then fit to a particular functional form for the AIF consisting of two gamma variate curves with a time-delayed sigmoid function. This functional form was found to closely match in physically observed sharp rise in concentration upon the contrast bolus first reaching the target artery, as well as the second pass of this bolus and subsequent washout of concentration. Figure 1 shows a typical blood concentration curve along with the associated estimated AIF. This particular form for the AIF requires 11 parameters to be fully described. Fitting the AIF to this form reduced the noise amplification inherent in the blind estimation process.

Results: Figure 2 shows typical results from the IQML-model method. In this particular situation, four tissue curves, or channels, were used to estimate the kinetic parameters for two types of tissue (i.e. two curves from each type of tissue). Using four tissue curves with at least two distinctly different sets of parameters in IQML provides more precise measurements of the parameters. Kinetic parameters from typical patient data are k_{trans}: .4426, k_{ep}: .9533, both well within published ranges. These parameters were also estimated using conventional AIF deconvolution, yielding values of k_{trans}: .4431, k_{ep}: .9012 Figure 3 compares kinetic values obtained from IQML with those obtained from the conventional method.

Discussion: Model-based blind estimation of kinetic parameters yields estimates comparable to conventionally obtained values. In situations with particularly noisy AIFs, or when no easily measured AIF is available, blind estimation provides an accurate method for quantification of DCE-MRI.

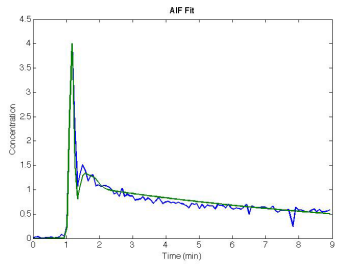

Figure 1 – A representative curve fit to an arterial input function measured in the brachial artery.

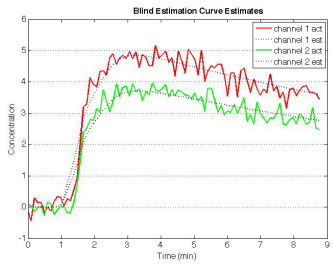

Figure 2 - Tissue curves from a single region of interest with curves fitted via IQML blind estimation.

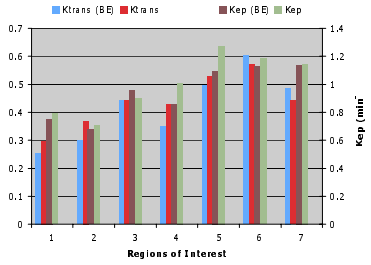

Figure 3 - Comparison of kinetic parameters obtained through blind estimation and deconvolution with a known AIF.

[1] Wong, K.P. et al, 2001. *Simultaneous Estimation of Physiological Parameters and the Input Function.* IEEE Trans. Inform. Technol. Biomed.
[2] Riabkov, D.Y. et al, 2002. *Estimation of Kinetic Parameters Without Input Functions.* IEEE Trans. Biomed. Eng.