

Dual Compartmental Fitting of Dynamic Susceptibility Contrast MRI in Early Ischemic Stroke

M. Ethan MacDonald^{1,2}, Estee Lee^{1,2}, Ting Lee^{2,3}, Jordan Woehr⁴, Chris d'Esterre^{2,5}, Michael R Smith^{4,5}, and Richard Frayne^{2,5}

¹Biomedical Engineering, University of Calgary, Calgary, AB, Canada, ²Seaman Family Magnetic Resonance Research Centre, Hotchkiss Brain Institute, Foothills Medical Centre, Calgary, AB, Canada, ³Imaging Research Labs, Robarts Research Institute, London, ON, Canada, ⁴Electrical & Computer Engineering, University of Calgary, Calgary, AB, Canada, ⁵Radiology & Clinical Neurosciences, University of Calgary, Calgary, AB, Canada

Target Audience: Clinicians and scientists interested in cerebral contrast kinetics modeling and acute ischemic stroke.

Purpose: The purpose of this work was to investigate dual compartmental model fitting of T_2^* based dynamic susceptibility contrast (DSC)- magnetic resonance (MR) imaging. A five-parameter model consisting of a rectangle and exponential decay was used to fit to the residue function [1]. To assess the quality of the fitting process, goodness of fit parameter maps were produced.

Methods: Imaging of an ischemic stroke patient was performed with a 3-T MR scanner (Discovery 750, GE Healthcare, Waukesha, WI). As part of this protocol, DSC-MR images were collected. Echo planar images with a flip/TE/TR of 20°/30 ms/2000 ms, an acquisition matrix of 144 × 144 was used to cover a 22 cm × 22 cm field of view. 17 slices were collected each 5 mm thick. There were 50 image volumes of the brain collected with a 2 s period. 20 ml of contrast agent (Magnevist; Berlex Canada, Pointe-Claire, QC) was injected at a rate of 5 ml/s, followed by a saline flush at the same rate and volume. The contrast agent concentration functions were calculated from the MR signal, and a signal from a feeding artery was selected to perform deconvolution with the rest of the tissue concentration functions [2]. A two compartmental model consisting of a rectangular function and exponential decay [3] was fit to the impulse response function, residue function ($R(t)$). The model could be described mathematically as,

$$R(t) = \begin{cases} 0 & t \leq ATD \\ CBF & ATD < t \leq ATD + MTT \\ CBF F_E e^{-kTrans(t-ATD-MTT)} & ATD + MTT < t \end{cases}$$

where, CBF is the cerebral blood flow, F_E is the extravascular flow, ATD is the arterial transit delay time, MTT is the tissue mean transit time and $kTrans$ is the extravascular flow time constant. Initial guesses for each of the parameters were obtained based on the geometry of the residue function, then an iterative non-linear least squares conjugate-gradient solution was obtained [2]. The non-linear least squares fit of the model produced several 'goodness of fit' parameters, including: sum of square error (SSE), root mean square error (RMSE), R-square and adjusted R-square, and the degrees of freedom in the error (DFE).

Results: Figure 1 shows the parametric maps of the five model parameters (top row), and displays the goodness of fit maps (bottom row). The CBF map indicates a tissue region with low flow ($<10 \text{ ml } 100 \text{ g}^{-1} \text{ min}^{-1}$) indicated by the white arrows in the figure, and the MTT map indicates a larger region of potentially ischemic tissue making this subject a good test case for the model. The low flow region shows similar SSE and RMSE values to the contralateral side, while the R-square and adjusted R-square values suggest a compromised outcome in this region.

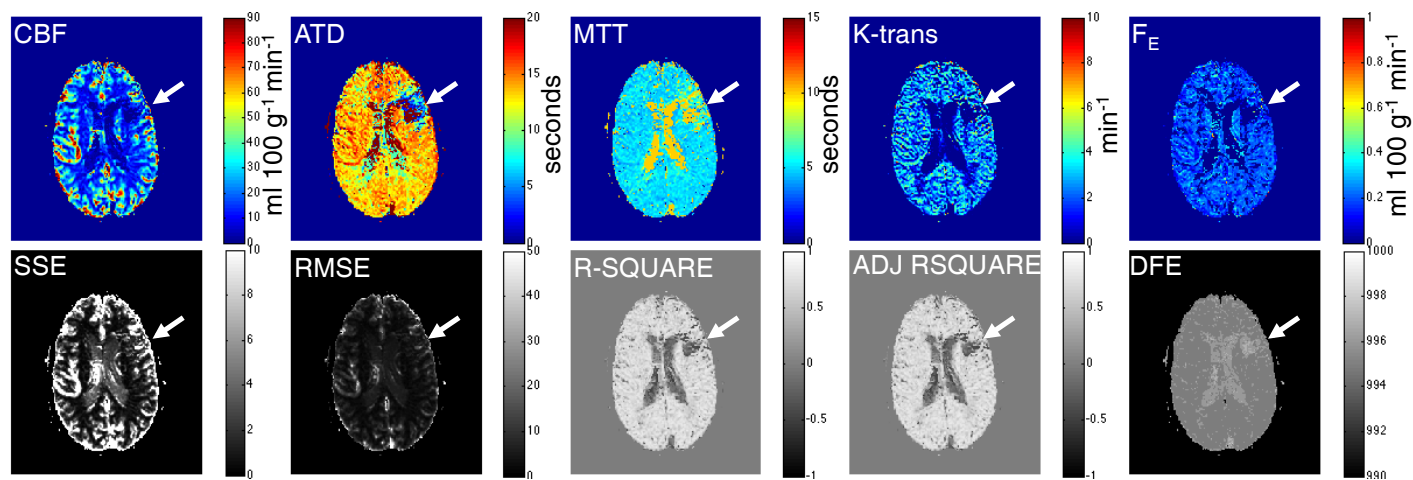


Figure 1: Model fitting outcome. The top row shows the parametric maps of the five model parameters. An ischemic region can be seen which consists of a region with low flow (arrows), and a larger region of increased MTT. The bottom row shows the goodness of fit parameters generated from the model fitting process. The SSE and RMSE show somewhat symmetric error, while the R-square parameters and DFE show increased error in the low flow region suggesting that the model does not fit as well at this location.

Discussion: There have been several two compartmental models proposed for fitting to the residue function in the brain [4,5]. Often the hemodynamic model parameters are derived from only their relation to the geometry of the residue function. In this work, the fitting was extended with an iterative least squares fitting. The iterative fitting is computationally expensive, which is one reason it is rarely used. However, use of the iterative method improves the quality of all of the goodness of fit. The outcome values are often shown, but in this analysis the calculated goodness of fit parameters are presented to validate how closely the model fits the biological derived residue function. F_E is likely overestimated with respect to computed tomography imaging due the smoothing of the rectangular function in the empirical data. In the ischemic region with low flow, it would appear that the values are unreliable (low R-square values), which suggests that the acquisition method/model fails in that region and that parameters other than CBF should not be trusted.

References: [1] Henderson E, *et al.*, JMRI, 2000;12:991-1003 [2] MacDonald, *et al.*, MRI, 2011;29(5):620-629 [3] Østergaard L, *et al.*, MRM, 1996;36:715-725 [4] Lee TY, Trends in Biotechnology, 2002;20(8):3-10 [5] Sourbron S, *et al.*, MRM, 2009;62(1):205-217