Model Regularization with Blind Deconvolution

J. U. Fluckiger[1], M. C. Schabel[1], and E. V. DiBella[1]
[1]University of Utah, Salt Lake City, UT, United States

Introduction: Dynamic contrast-enhanced MRI (DCE-MRI) is physiological imaging tool used clinically to aid the diagnosis and treatment monitoring of a variety of diseases. Pharmacokinetic parameters can be estimated by fitting DCE-MRI data to one of many mathematical models. The two-compartment model used here describes the concentration of contrast agent (CA) in tissue with respect to three parameters as well as the CA concentration in the plasma through the relationship: $C_t(t) = K^{trans} C_p(t) \otimes e^{-k_{ep}t} + V_p C_p(t)$ (1) where K^{trans} and k_{ep} are the transfer constant and rate constant respectively, $\otimes$ is the convolution operator, v_p is the blood plasma volume fraction, and $C_p(t)$ is the concentration of CA in the blood plasma [1]. We have developed an alternating minimization with model (AMM) algorithm for estimating the AIF directly from measured tissue activity curves.

Method: The performance of the AMM algorithm was determined by comparing traditional deconvolution with a known AIF to an estimated AIF with and without and with an analytical form for the AIF. The model chosen here consists of two normalized gamma-variate curves representing the first and second passes of the CA bolus, and a normalized sigmoid function representing the decaying washout of CA from the ROI. Four sets of kinetic parameters were randomly generated within bounds set to match those from previously measured data and "true" tissue curves were generated with a population averaged, noise-free AIF. Zero-mean Gaussian noise with standard deviations of 0.02, 0.04, 0.08, and 0.16 mM was added to the tissue curves and the AMM algorithm was applied.

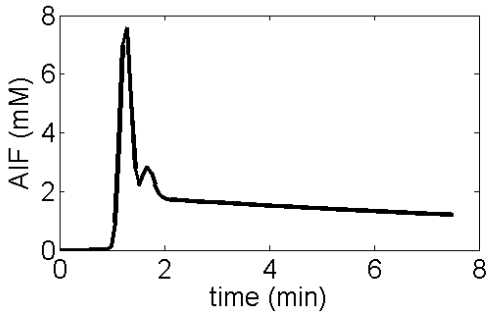

Figure 1 – Noise free population averaged AIF used in simulations.

For conventional estimation of the kinetic parameters from the simulated data, noise corresponding to the level added to the tissue curves was added to the simulated AIF, scaled by the square root of 19, a typical number of pixels from which to measure an AIF. The AIF was shifted by a random fraction of the time step to simulate temporal jitter. This AIF was then used to calculate the kinetic parameters. The kinetic parameters were then estimated using the AMM algorithm. In addition, the estimation algorithm was implemented at each noise level without including any analytic form for the input function. 50 realizations were used at each noise level. The estimation was then repeated with three different sets of 'true' kinetic parameters for a total of 200 realizations at each noise level. The resultant kinetic parameters from the simulated measured AIF, the AMM method and the alternating minimization without model were then compared with truth, and the absolute error was computed.

Results and Discussion: As seen in Fig. 2, at low noise levels the AMM method performs equally well whether or not the model regularization is included. However, as the noise levels increase, the model smoothes the AIF at each iteration of the AMM algorithm, preventing noise from being amplified. vp measurements were more sensitive to both noise and small changes in the AIF, however studies showed that this was more due to the poor temporal resolution in the noise simulations.

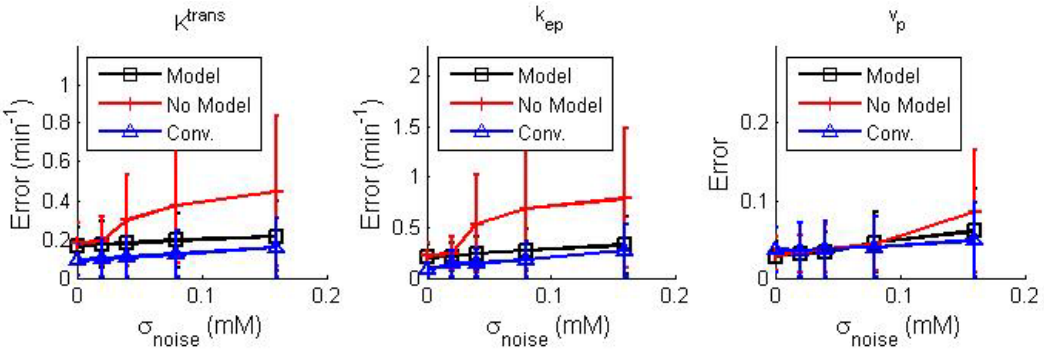

Figure 2 - Mean and standard deviation of the absolute error in kinetic parameter measurements from conventional deconvolution (blue), AMM with model regularization (black) and AMM with no regularization (red).

References:

1. Tofts PS, et al. Estimating kinetic parameters from dynamic contrast-enhanced T(1)-weighted MRI of a diffusable tracer: standardized quantities and symbols. J Magn Reson Imaging 1999;10(3):223-232.