

Using DCE-MRI Data to Constrain and Simplify PET Kinetic Modeling

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INTRODUCTION Quantitative modeling of kinetic PET data can report the distribution and retention of various radiotracers (1). However, such modeling may be limited by an inability to separate the tissue time activity curve (TAC) into separate blood, extravascular extracellular space (EES), and extravascular intracellular space (EIS) components, as well as the large number of physiologic parameters that must be fit. Using data available from dynamic contrast enhanced magnetic resonance imaging (DCE-MRI), it may be possible to separate the whole tissue TAC into blood, EES, and EIS curves, and reduce the number of unknown parameters that must be fit. The approach is based on a partial volume correction algorithm provided by Allani *et al* (2).

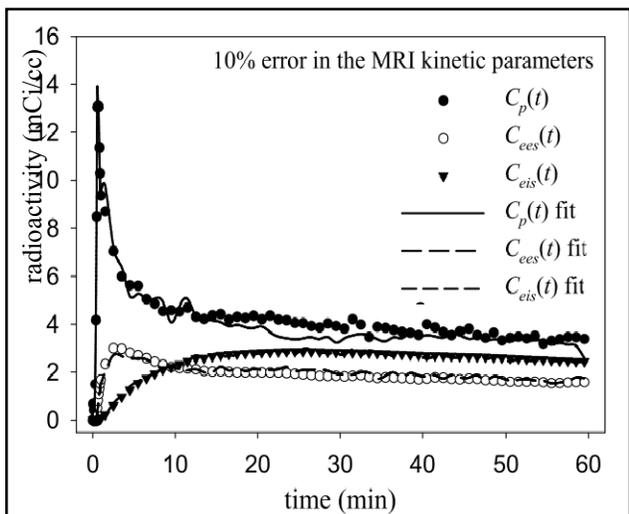


Figure 1 - Simulation results of the time courses of tracer in each compartment with model fits.

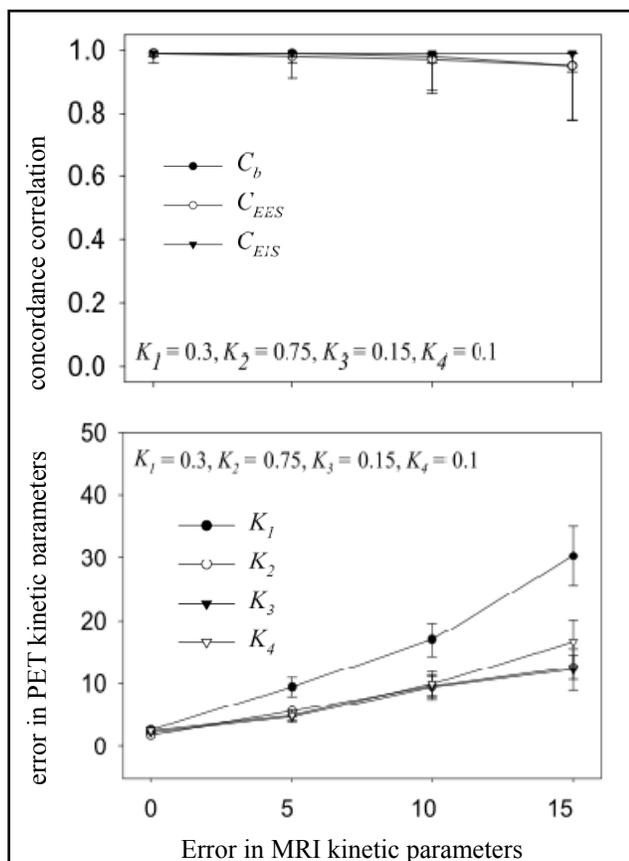


Figure 2 - Mean CCC of the time courses of the compartment tracer activity (top). Model error in the PET kinetic parameters (bottom). Results are from a single combination of simulated PET parameters.

The goal of this method is to determine C_B , C_{EES} , and C_{EIS} for PET time courses at the native PET spatial resolution (which is substantially lower than that for DCE-MRI data). We begin by registering the PET data to the DCE-MRI data resulting in a PET data set with voxel sizes equivalent to the DCE-MRI data. At this point, we have the tissue compartment volumes from the DCE-MRI data (3) and tissue curves from the PET data at the (smaller) DCE voxel size. The average (unknown) PET C_B , C_{EES} , and C_{EIS} time courses (at native resolution) can then be taken to be the weighted product of the distribution of compartment volumes and PET time courses from the smaller voxel sizes: in vector form, $C_{tissue} = \mathbf{A}C_i$, [1] where C_{tissue} is the measured PET tracer, \mathbf{A} is an $N \times 3$ matrix containing the fractional volumes measured from the DCE-MRI studies, N is the number of DCE-MRI voxels that compose a single PET voxel at native resolution, and C_i is a column vector consisting of the concentrations of tracer in the blood, EES, and EIS compartments.

By inverting the system described by Eq. [1] we obtain C_B , C_{EES} , and C_{EIS} PET time courses at the native PET resolution and these time courses are compared to the actual data via the concordance correlation coefficient (CCC). The estimated C_B , C_{EES} , and C_{EIS} time courses are then used to determine the PET kinetic parameters which are then compared to the actual values. This method was tested in simulation.

Using an arterial input function (AIF) measured from the left ventricle of a mouse after an injection of FLT, whole tissue TACs were generated over a range of kinetic parameter values. We show that the method can be used to separate the three components under various noise levels. The accuracy of the method is assessed by computing the concordance correlation coefficient (CCC) between the known and extracted TACs. Then the accuracy of the extracted PET kinetic parameters is assessed by comparison with their true values.

The simulations show that, over a wide range of combinations of PET kinetic parameters, the method returns accurate blood, EES, and EIS TACs. Figure 1 shows example data from one realization of the noise. The CCC for all parameter combinations and noise levels tested here was > 0.9 (see Figure 2). Additionally, provided the estimated DCE-MRI parameters are within 10% of their true value, the error in the PET kinetic parameters is within approximately 20% of their true values. When the error in the DCE-MRI parameters approaches and exceeds 15% of their true values, the error in the PET kinetic parameters can exceed 30% (Figure 2).

RESULTS The simulations show that, over a wide range of combinations of PET kinetic parameters, the method returns accurate blood, EES, and EIS TACs. Figure 1 shows example data from one realization of the noise. The CCC for all parameter combinations and noise levels tested here was > 0.9 (see Figure 2). Additionally, provided the estimated DCE-MRI parameters are within 10% of their true value, the error in the PET kinetic parameters is within approximately 20% of their true values. When the error in the DCE-MRI parameters approaches and exceeds 15% of their true values, the error in the PET kinetic parameters can exceed 30% (Figure 2).

CONCLUSIONS Given sufficient accuracy in the calculation of DCE-MRI parameters, it is possible to separate the PET time activity curve measured in whole tissue into blood, EES, and EIS components thereby enabling PET kinetic modeling with fewer free parameters.

REFERENCES

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