Estimation of Cerebral Perfusion Parameters Using Bayesian Probability Theory

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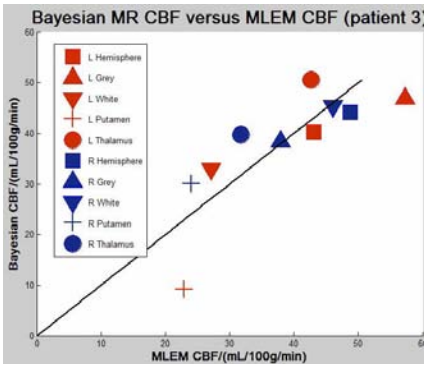
INTRODUCTION: The method of dynamic susceptibility contrast (DSC) MR relies on performing a deconvolution between the tissue concentration curves in each pixel and the arterial input function (AIF) [1]. Current methods have several drawbacks that include instability of the deconvolution operation when performed on noisy data and selection of a single AIF. Using a single AIF cannot account for the different delay and dispersion that occur before the contrast bolus arrives at different capillary beds, especially in patients with hemodynamic impairment. An additional problem with the AIF measurement arises from the high concentration of contrast within the arteries during the peak of the bolus. This often causes saturation of the signal making it difficult to accurately estimate the contrast agent concentration during this period [2].

We propose a tissue perfusion model that estimates a separate AIF for each pixel in the image. The model provides estimation of additional parameters that may be of clinical importance. The parameters appearing in this model are estimated using Bayesian probability theory and Markov chain Monte Carlo simulations to sample the joint posterior probability. Preliminary results using this model compare favorably to PET results and to traditional MR methods.

METHODS: As part of the St. Louis Carotid Occlusion Study perfusion measurements were performed in 19 patients using both PET and DSC MR within the same day. Written informed consent was obtained on all subjects in accordance with guidelines of the local institutional review board. Tracer kinetic perfusion models [1] derive the following relationship between the tissue concentration (C_T), cerebral blood flow (CBF), pixel impulse residue curve (R(t)), and the AIF (C_A): $C_T(t) = CBF \cdot R(t) \otimes C_A(t)$. The residue curve was approximated as an exponential with a mean transit time (MTT) decay constant: $R(t) = \exp\left[-(t - t_0)/MTT\right]$. The AIF was modeled as having three distinct components: $C_A(t) = aGV(t,t_0) + bGV(t,t_1) + c$. The main contrast bolus was modeled as a gamma variate function (GV) arriving at t_0. The re-circulation peak was also modeled using a GV arriving at a later time t_1. The steady state component was modeled as a constant. These expressions were substituted into the first equation and the convolution was performed analytically. The posterior probabilities for the model parameters were computed for each pixel given the time series data using Bayesian probability theory [3] and Metropolis-Hastings Markov chain Monte Carlo simulation with simulated annealing [4]. Regions of interest (ROI) were selected in different anatomic structures of the brain in all subjects to evaluate the perfusion parameters.

RESULTS: Parameter estimates in a patient with left hemodynamic impairment are presented in the left figure. This patient had asymmetry in the MTT and CBV maps, but not in CBF. Figure left is a map of the rise time exponent of the GV function. Figure middle and right show asymmetry between left and right in the primary and secondary bolus arrival time, which is longer on the left (neurology convention). The right figures present a comparison in the same patient between the CBF calculated using the proposed method vs. Maximum Likelihood DSC MR CBF (top) and PET CBF (bottom).



CONCLUSION: Parameter estimation based on the proposed model using Bayesian inference produces parameter values comparable to traditional methods and overcomes many of the disadvantages of current techniques. Many of the model parameters are unique and could provide important physiological information not available using current techniques.

REFERENCES:

[1] Ostergaard L et al., MRM 36:715-725, 1996.
[2] Akbudak E et al., MRM 36:809-815, 1996.
[3] Jaynes ET, Probability Theory: the logic of science, Cambridge Univ. Press, 2003.
[4] Metropolis N et al. J Chem Phys 21:1087-1091 (1953).