Bayesian Estimation of Perfusion Parameters Using a Physiological Model of the Microvasculature

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Introduction

Perfusion weighted MRI has proven very useful for deriving haemodynamic parameters such as CBF, CBV and MTT. These quantities are important diagnostic tools, e.g. in acute stroke, where they are used to identify ischemic regions. In this study we estimate perfusion parameters based on a vascular model specifically representing heterogeneous capillary flow. We use a fully Bayesian approach in order to obtain posterior probability distributions for all parameters. This allows us to perform inference on perfusion parameters at the voxel level, either within or between subjects.

Theory

We use a vascular dynamic model similar to [1] and [2] (see Fig. 1). At each voxel, blood is delivered from an artery to a capillary network represented by *N* tubes in parallel. The transit time for a particle in the *i*'th tube is T_i and the fraction of particles passing through this tube is h_i. Hence the h_i's give an estimate of the transit time density function h(T). The mean transit time (MTT) can be estimated as $\sum_{i=1}^{N} T_i h_i$. CBV is estimated by $\sum_{i=1}^{n} C(t_i) \Big/ \sum_{i=1}^{n} C_a(t_i)$, where *C(t)* is the concentration time curve and $C_a(t)$ is the (known) arterial input function. Finally, CBF can be calculated using the central volume theorem, i.e. CBF = CBV/MTT. The effect of the artery is modeled using a delay parameter *d*.

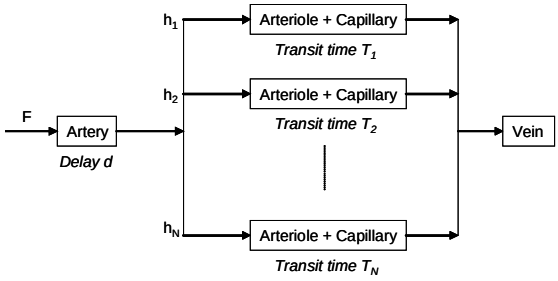

Figure 1 The vascular model

Materials and methods

To solve for the parameters $\theta = (h_1, ..., h_N, d)$ we use a Bayesian system identification approach described in [3]. The input presented to the system is $C_a(t)$ and the states of the system are the tracer concentrations in each tube. The output is the total concentration of intravascular tracer *C(t)* in the system, observed at each scan. We assume Gaussian observation error with zero mean and unknown variance σ^2 , i.e. white noise. To create a physiologically informed model we assume a Gaussian prior, i.e. $\theta \sim N(\mu, \Sigma_\theta)$. Data was acquired using GRE-EPI on a 1.5T scanner with TR=1.5s.

Results

Fig. 2 shows a typical CBF image obtained using our vascular model. Inspection of fits of concentration time curves shows mostly good agreement between an SVD-based approach [4] and our approach. However, when a delay effect (1.7 s) is present our method seems to better capture the response (Fig. 3).

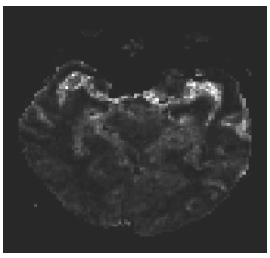

Figure 2 CBF obtained using vascular model

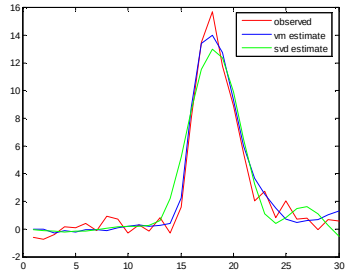

Figure 3 Fitted concentration time curves

Discussion

The major advantage of our model, compared to the SVD-based approach, is its parameterization in terms of physiological states. This allows us to use existing physiological prior knowledge. Using prior knowledge can increase sensitivity when classifying ischemic tissue. Priors can be either derived from the same subject, e.g. by using global tissue-specific priors, or from an age-matched control group. The Bayesian techniques employed here can also be used to visualize voxel-specific point estimates and their posterior standard deviations.

References: [1] Kroll et.al., AM. J. Physiol 1996. [2] Østergaard et.al., JCBFM 1999. [3] Friston et.al, NeuroImage 2003. [4] Østergaard et.al, MRM 1996.