Effect of analytical model assumptions on quantifying cerebrovascular network parameters evaluated using deterministic diffusion simulations

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Introduction

Transverse relaxation has seen renewed use in elucidating underlying tissue properties in recent years. In particular, the ability to quantify cerebrovascular network parameters such as blood volume and deoxyhemoglobin concentration from the NMR signal dephasing has seen intense focus as the ability to quantify BOLD signal changes and even the absolute deoxyhemoglobin concentration would be an invaluable aid in studying brain function. Yablonskiy and Haacke[1] developed a model for the static dephasing regime that has seen widespread application. This model is based on statistical averaging of randomly oriented cylinders. It is predicted that the error in estimated model parameters will have an inverse dependence on the square root of the number of vessels, N. Although the functional form of the error is expected, a systematic analysis of the magnitude of error introduced by violations of the statistical assumptions has not been undertaken.

Methods

To investigate the errors, a three dimensional simulation of MRI signal during a TE = 90 ms spin echo at 4 T was performed using a deterministic diffusion model based on a method first proposed by Bandettini and Wong[2]. The MRI simulation uses the iterative multiplication and convolution of three-dimensional arrays according to $\mathbf{M}_k = (\mathbf{M}_{k-1} \times \mathbf{R}) * \mathbf{G}$ where $\mathbf{M}_k$ is the magnetization array at the kth time point, $\mathbf{R}$ is a relaxation and precession array accounting for T_2 decay and differences in precession frequency, and $\mathbf{G}$ is a Gaussian diffusion kernel derived from the Einstein equation and the Gaussian distribution in three dimensions assuming isotropic Gaussian diffusion. The T_2 was 66 ms in tissue and 12.7 ms in blood and the main magnetic field was 4 T. The simulated MR signal was fit over the entire free induction decay and spin echo to obtain estimates of tissue hemoglobin concentration and blood volume fraction using the model equations proposed by Yablonskiy[3].

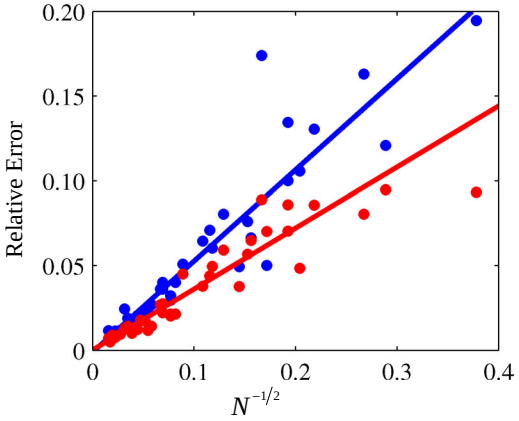

Figure 1 Error in hemoglobin (blue) and blood volume (red) has inverse linear dependence on square root of number of vessels.

Results

Using these simulations, the relative error in estimated blood volume fraction and deoxyhemoglobin concentration in the static dephasing regime is found to be inversely related to the square root of number of blood vessels with proportionality constants of 0.35 and 0.5 respectively (Figure 1). When the static dephasing model is used to predict deoxyhemoglobin concentration and blood volume form simulated signal intensity curves that included diffusion, the relative error of the predicted values drops sharply for vessel networks with radii below 10 microns (Figure 2). Including intravascular signal resulted in a significant underestimation of CBV by 25% if the initial FID was used in fitting. The superposition of two vessel networks with 2 micron and 15 micron radii shows that the large vessel network dominates predicted values.

Discussion

The error dependence on number of vessels means that to achieve less than 2% error, at least 625 blood vessels are required. For vessels on the order of 10 μm radius and blood volume fraction of 3 to 5% in brain parenchyma, this would require 3 mm isotropic voxels. The underlying tissue being investigated and not the imaging hardware therefore sets the lowest resolution limit. The effect of the intravascular signal is due to the increased intravascular transverse relaxation rate resulting in rapid decay of intravascular signal. In vivo measurements should be less sensitive to this error, due to the bulk movement of the intravascular water. Additional flow suppression can also be employed[4]. The overestimation of CBV results due to the sensitivity of estimates to the spin echo signal. Because diffusion reduces the spin echo signal even for large vessels, the CBV is overestimated. Diffusion effectively sensitizes the predicted values to larger vessels. This may even prove beneficial, as oxygen consumption requires a venous measurement of deoxyhemoglobin concentration.

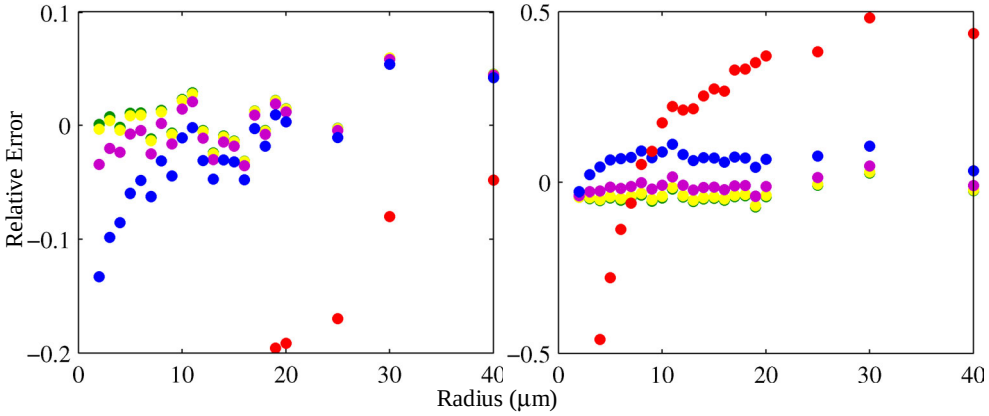

Figure 2 Error in hemoglobin (left) and blood volume (right) at diffusion rates of 0 (green), 0.8 (yellow), 1.0 (magenta), 1.2 (blue), and 2.5 (red) $\mu m^2/ms$

References

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