Dynamic Perfusion Evaluation Based on a Tissue Model

P. Gall[1], K. Mouridsen[2], and V. G. Kiselev[1]

[1]Diagnostic Radiology, Medical Physics, University Hospital Freiburg, Freiburg, Germany, [2]CFIN, Neuroradiology, Aarhus University Hospital, Aarhus, Denmark

Introduction

Dynamic susceptibility contrast MRI is a widely used technique for quantification of cerebral perfusion parameters such as cerebral blood flow (CBF) and cerebral blood volume (CBV). Accurate estimation of CBF and CBV depends on correct estimation of the tissue concentration of intravascular contrast agent during bolus passage. Typically, the tissue concentration is (simplistically) assumed to be proportional to the change in transverse relaxation. However, by considering the relaxation effects in a theoretical tissue model, it has been shown [1,2], that the observed relaxation depends critically on the local, microvascular architecture. Consequently, CBF estimates are biased when microvascular morphology is neglected. Here we present a model based estimation scheme yielding unbiased estimates of intravascular concentration as well as an index of average vessel size (VSI). A multi echo EPI (mEPI) sequence with a GE block followed by a SE block for each excitation is used to ensure that the model inversion problem is well-determined. We also demonstrate that this method correctly estimates CBF over a broad range of microvascular compositions.

Methods

Tissue model

We use the tissue model presented in [1,2]. The radii of arterioles and venules were fixed at R_a=100 µm and R_v=120 µm with relative volumes ξ_a=0.5% and ξ_v=1%. We used a diffusion constant of D=0.8 µm^2 /s and the field strength was assumed to be 1.5 T. Using this model, the change in relaxation rate measured using GE and SE can be calculated for a known concentration for given values of the capillary radius R_c, which we leave as a free parameter. Arterial signals were generated by setting ξ_c=ξ_v=0, R_a=100 µm.

Estimation of intravascular concentration of contrast agent

As shown in [1], the VSI is proportional to the slope of the (regression) line in a plot of $dR2_{GE}$ against $dR2_{SE}^{\wedge}(^3/_2)$. The capillary radius, R_c, can be computed by weighted averaging from VSI, R_a, R_v and rCBV = ξ_a + ξ_v + ξ_c. The estimation of the concentration curve proceeds in two steps: (i) Using the tissue model the $dR2_{GE}$ over $dR2_{SE}^{\wedge}(^3/_2)$ curve is generated by linearly increasing the concentration to a maximum that exceeds the expected value of around 20 $^{mmol}/_{ml}$ [1] (red line in Fig. 1) at R_c determined by the VSI. (ii) For each measured point, the concentration associated with the nearest point in normal direction on the simulated curve (dashed lines in Fig. 1) is taken as an estimate of the underlying true concentration.

Validation

Concentration curves were generated as in [3] convolving a gamma-variate AIF with an exponential residue function. Simulated signals (changes in relaxation rate) for GE and SE measurements at TE_{GE}/TE_{SE}/TR 25/85/1800 ms were generated from the concentration curves using the tissue model with R_c between 7 µm and 30 µm. Concentration curves were then estimated based on the signal using (i) the standard linear relation for SE and GE and (ii) the tissue model fit approach but with R_c 50% higher than used in the simulation (predicted overestimation of VSI [1]). CBF was estimated by circular deconvolution as presented in [3].

Results

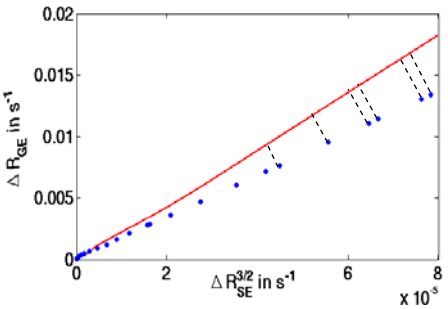

Fig. 1: *Simulated relaxation rates (blue dots) for tissue. ΔR curve (red line) generated from a linearly increasing concentration and* R_c *overestimated by 50%.*

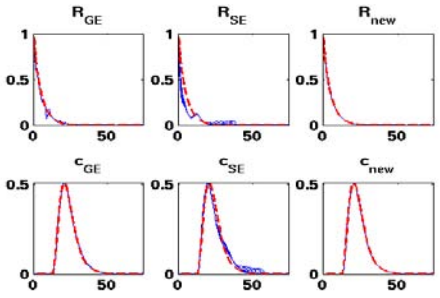

Fig. 2: *The upper row shows the input residue function (red) overlaid with the computed residue functions (blue lines). The lower line shows the same for the normalized concentrations.*

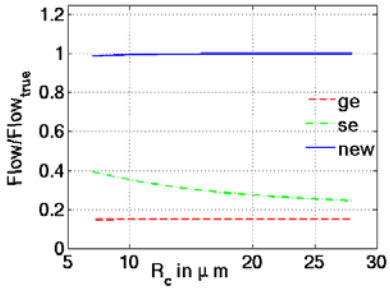

Fig. 3: *Comparison of the flow estimates obtained by* ΔR_{GE}, ΔR_{SE}, *and the new concentration estimate.*

As shown in Fig. 2 the proposed technique and GE relaxation time courses recover the input residue function and concentration (normalized in Fig. 2) better than SE relaxation time courses. Fig. 3 shows that the tissue model technique estimates CBF at high accuracy over the whole range of encountered capillary radii. The flow determination from the GE relaxation time courses shows as previously reported a constantly underestimated flow for the whole radii range. The SE evaluation shows its expected instability over the encountered R_c interval.

Discussion

We have demonstrated that detailed modeling of tissue properties is crucial for quantitative perfusion. Simulated relaxation time courses generated with such a model leads to a promising estimate of the true concentration. However, additional measurements are necessary in order to estimate relevant tissue parameters. The simulations show that the use of SE/GE mEPI measurements allows a more accurate assessment of perfusion parameters. Using such sequences one has to compromise either resolution (to 64x64 pixels per slice, as two echoes have to be sampled), or SNR (true parallel imaging techniques that allow 128x128 pixels per slice). These sequences do not require an increase of the time window available in protocols that contain perfusion measurements. For the application to patient data an accurate experimental determination of assumed model parameters has to be carried out for physiologically determined tissue types that can be automatically segmented in anatomical images.

References

[1] Kiselev et al, MRM 53: 553-563 (2005) **[2]** Kiselev et al, MRM 41: 499-509 (1999) **[3]** Wu et al: MRM50: 164-174 (2003)