Quantitative comparison of two biophysical models for the BOLD fMRI signal: a theoretical study

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INTRODUCTION: Among the metabolic and hemodynamic changes related to neuronal activation, cerebral metabolic rate of oxygen (CMRO2) is perhaps the most accurate index for the neuronal activities. Therefore, evaluating CMRO2 changes have been the interests of many fMRI studies. Unfortunately, techniques for direct measurement of CMRO2 are not well established (although it is emerging), and most CMRO2 studies use biophysical models to estimate its changes from BOLD, CBF and CBV data. Various models for BOLD quantification have been proposed and they all have similar general principles. One of the major differences among different models is the number of compartment considered in the voxel. Here we performed theoretical comparison between two of these models: a single-compartment model [1] in which the spins within a voxel are approximated as one compartment and the coefficient related to the approximation is obtained from a hypercapnia calibration scan, and a multi-compartment model [2] in which the signals from tissue, arterial blood and venous blood are separately written out analytically. The coupling relationship between CBF and CMRO2 was also investigated for these two models. The similarity and difference between these two models are given.

METHODS: Using these two models and assuming CBV and CBF have a relationship $CBV/CBV_0 = (CBF/CBF_0)^{\alpha}$, the iso-$CMRO_2$ curves are drawn (Fig. 1) in the BOLD-CBF plane. The model parameters were taken from respective literatures (at 1.5T). For the multi-compartment model, the curves have a lower slope than that of the single-compartment model within the practical range of ΔBOLD and ΔCBF. Therefore, for a certain ΔBOLD and ΔCBF measurement, the CMRO2/CBF ratio will be lower in multi-compartment model than that in single-compartment model (the $\Delta CMRO_2\%/\Delta CBF\%$ response ratio calculated using the multi-compartment model is 0.3 [2], as apposed to 0.5 in the single compartment model [1]).

The key differences between these two models lie in the dependence of BOLD signal on CBV change and Yv change (Eq.6 in [1], using $[dHb]_v/[dHb]_{v0}=(1-Yv)/(1-Yv_0)$, and Eq.3 in [2]). The surface plot among these three parameters is shown in Fig.2. To further quantify the differences, we used Taylor series to expand these two equations. Specifically, BOLD signal change can be written as: $\Delta BOLD\% = a_{10}\cdot \Delta CBV\% + a_{01}\cdot \Delta Y_v\% + a_{20}\cdot (\Delta CBV\%)^2 + a_{11}\cdot(\Delta CBV\%)(\Delta Y_v\%) + a_{02}\cdot (\Delta Yv\%)^2 + \cdots$, where $\Delta x\% = (x-x_0)/x_0$. Parameters a_{ij} are listed in Table 1. In the single-compartment model (assume β = 2,), each coefficient is decided by the parameter M, e.g. a_{10}=-M. For the multi-compartment model, the coefficients are determined by the assumptions on MR parameters (e.g. T1, T2 of tissue and blood). To investigate whether these two models can be reconciled by parameter selections, we tested to use M = 0.068 in the single-compartment model. The iso-CMRO2 curves and Taylor coefficients are plotted and listed in Fig.3 and Table 1, respectively, and the curves appear to be reasonably close to each other.

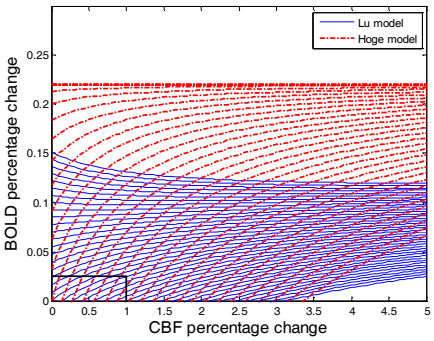

Fig.1 Iso-CMRO2 curves of the single-compartment and multi-compartment models. Within the practical range (which is shown as a rectangle area at the lower left corner, approximately), the curves have a lower slope in the multi-compartment model than that of the single-compartment model.

RESULTS AND DISCUSSION: From the model point of view, even though they use different approaches and approximation, the curvatures of the plots are comparable. When using parameter assumptions exactly as in the original literature [1,2], the amplitude and slope of the curves appear to be different (Fig. 1 and 2). Specifically, the single-compartment model shows a higher $CMRO_2$/CBF ratio than that of the multi-compartment model, which is closer to the results in PET literature [3] .The single-compartment model is greatly influenced by parameter M as shown in Table 1. On the other hand, the coefficients of the multi-compartment model are affected by various MR parameter assumptions. We evaluated the sensitivity of the coefficients on these assumptions, and found that with ±30% of variation in the assumed values, the coefficients using multi-compartment model only varied by 20-30%. For example, the a10 was never able to reach below -0.1. .However, it should be noted that these two models can be reconciled by using proper assumed parameters (Fig. 3), suggesting that there is no fundamental difference between these two model. The choice of the parameter selections should be the focus of future work. By inspecting the linear term coefficients (a10 and a01) in Table 1, we can see that CBV decreases the BOLD signal (a10 is negative), whereas venous oxygenation increases the BOLD signal (a01 is positive) and the BOLD signal is indeed more sensitive to blood oxygenation than to the CBV (the amplitude of a01 is about 3 times that of a10).

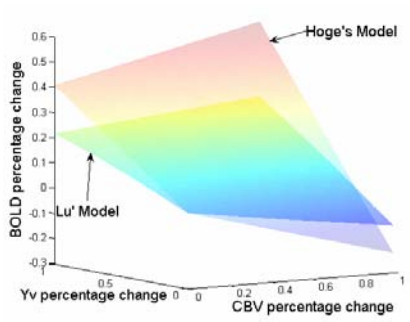

Fig.2 ΔBOLD as a function of ΔCBV and ΔYv using the two models. The parameters were the same as in the original literature.

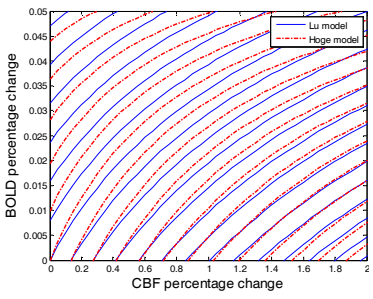

Fig.3 The multi-compartment model corresponds to the single-compartment model with M = 0.068, where the iso-CMRO2 curves of two models match well.

Table 1: Polynomial coefficients comparison between single-compartment and multi-compartment models. When M = 0.068, two models match well.

Model		a10	a01	a20	a11	a02
Hoge's	M = 0.22	-0.22	0.82	0	0.82	-0.76
	M = 0.068	-0.068	0.25	0	0.25	-0.24
Lu's		-0.068	0.18	0.0041	0.17	-0.004

REFERENCES

[1] R.D.Hoge, et al, MRM, 42:849 (1999); [2] H.Lu, et al. JCBFM, 24:764 (2004); [3] A. Lin, et al. OHBM meeting, 676M-PM (2006).