Bayesian inference of multi-modal perfusion FMRI data

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INTRODUCTION: The development of multi-modal FMRI pulse sequences means several types of complementary hemodynamic information (e.g. blood flow, volume and BOLD changes) can be acquired simultaneously. Most analysis is currently performed using separate linear methods that attempt to obtain pure information on each type of signal. In actuality, the images acquired are not pure and there is cross-contamination between the different hemodynamic changes. Furthermore, these effects are inherently nonlinear and interrelated, making accurate quantification difficult.

Recent research has demonstrated that a nonlinear perfusion model in a Bayesian framework can analyze dual-echo ASL data more efficiently than traditional General Linear Model (GLM) approaches [1]. However, the Markov-Chain Monte Carlo (MCMC) method used for this inference was very computationally intensive, limiting the data set size and model complexity. This work takes the same nonlinear model but performs inference using a fast approximate method called Variational Bayes (VB) [2]. VB makes the assumption that the posterior distribution is "factored" into subsets of parameters. In addition, we also need to linearize the nonlinear perfusion model about the estimated mean parameters. This reduces the marginalization integrals to a set of linear equations which are solved iteratively, similarly to expectation maximization.

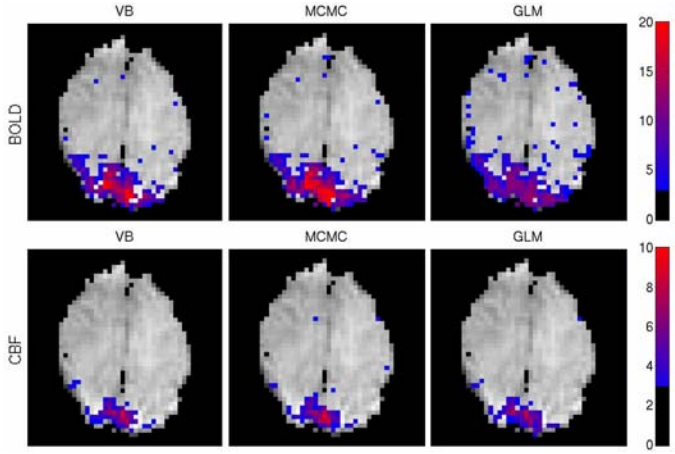

Figure 1: Z-statistics (Z>3) for the BOLD and CBF effects. VB and MCMC show higher BOLD confidence and less spurious activation than GLM.

METHODS: Data from a dual-echo ASL sequence [1] was analyzed using a nonlinear perfusion model, using both MCMC and VB inference methods. In the model, each voxel's magnetization consists of static magnetization **M** (defined as anything that remains in the voxel between the time of tag and acquisition) and blood inflow **Q** (ASL), both of which vary in time with the stimulus. This is weighted by the T_2* decay rate **R**, which is also time-varying (the BOLD effect). Two echo times are acquired for each inversion, and tag and control images are alternated.

As in [1], a first-order autoregressive noise model helps to de-emphasize the low-frequency noise. This introduces an autoregression parameter $\boldsymbol{\alpha}$ and noise variance Λ^{-1} for each echo time, which are tuned probabilistically based on the data. Non-informative priors are used on parameters of interest **M**, **Q**, and **R**, and on the noise estimates $\boldsymbol{\alpha}$ and Λ^{-1}. A Gaussian prior of 0.5±0.25 s was applied on the ASL delay Δ**t**.

The results shown are from a single representative subject. For comparison, the same data was analyzed using a state-of-the-art GLM approach [3], and the Bayesian estimates were transformed back into percent-change and Z-statistic estimates of BOLD and CBF.

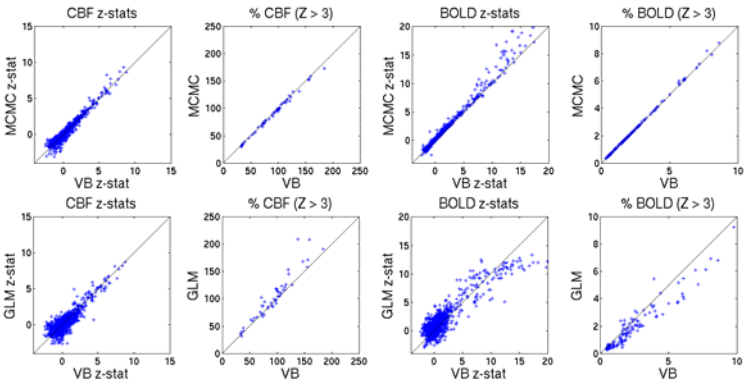

Figure 2: (Top) The VB and MCMC methods give very similar results, with VB having lower BOLD confidence. (Bottom) VB makes lower CBF and higher BOLD estimates than the GLM, with higher BOLD confidence.

RESULTS AND DISCUSSION: The spatial plots (figure 1) reveal that the two Bayesian methods provide cleaner and more confident BOLD measurements, while CBF is largely unaffected. A point-by-point comparison (figure 2) shows that VB and MCMC are in close agreement about values, but VB loses some statistical power in BOLD. However, compared to the GLM it still extracts additional information and shows improved statistical power.

Using MCMC or VB with the nonlinear perfusion model allows the static magnetization changes to also be inferred (figure 3). Note that it is not possible to model these static magnetization changes with the GLM approach, and that this deficiency causes the GLM to underestimate BOLD changes by approximately 15% (figure 2). The static magnetization changes are thought to be due to a combination of blood flow and volume changes [1].

In this application VB offers at least an order of magnitude speed increase over MCMC while maintaining most of the advantages, and may make it computationally feasible to explore more detailed models of functional MRI.

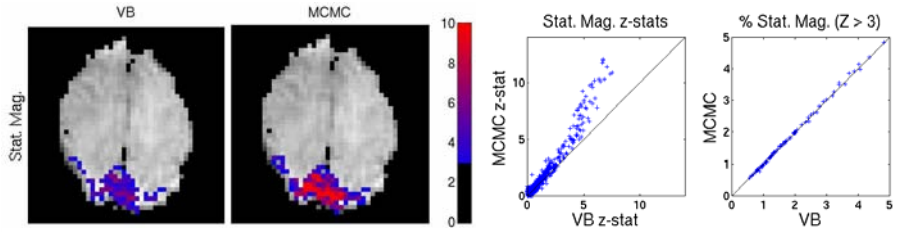

Figure 3: VB and MCMC strongly agree in their estimates of changes in static magnetization, but VB underestimates the confidence of this estimate relative to MCMC.

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