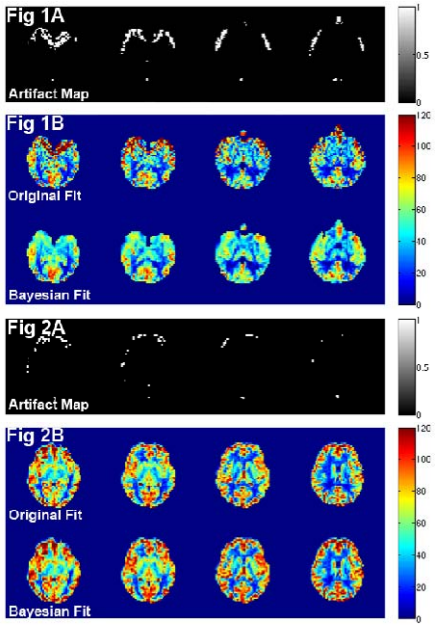
Robust and Fast Quantification of CBF measures for Multiphase PCASL using Bayesian Nonlinear Model Fitting

David D Shin[1], Michael A Chappell[2], and Thomas T Liu[1]

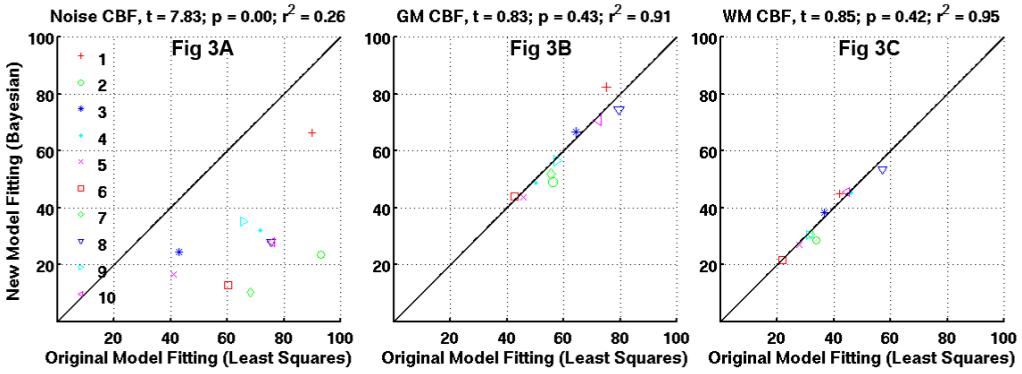
[1]*Center for Functional MRI, University of California, San Diego, La Jolla, CA, United States,* [2]*Institute of Biomedical Engineering & FMRIB Centre, University of Oxford, Oxford, United Kingdom*

Purpose: Despite its growing popularity, one main drawback of PCASL is its sensitivity to off-resonance effects and gradient imperfections at the labeling plane. Specifically, the inversion efficiency of labeled blood may be compromised due to the mismatched phase (referred to here as the phase tracking error) between the RF pulse of the PCASL train and the blood magnetization. Multiphase PCASL (MPPCASL) has been proposed as a way to overcome this drawback [1]. Unlike other phase tracking error correction methods [2, 3], MPPCASL requires no additional scan time as the correction is done retrospectively during post processing. Specifically, the RF phase modulated magnetization of arterial blood is fit to a model function using a nonlinear optimization routine. One drawback of this method is that the fitting algorithm greatly overestimates CBF in regions of high pulsatility and motion where the modulated blood signal deviates greatly from the model function. This can result in CBF maps with apparent hyperperfusion in these regions, making the map difficult to interpret. We present an alternate CBF quantification approach based on a Bayesian nonlinear model fitting routine that incorporates spatial information [4, 5] and greatly mitigates erroneous CBF estimates from these regions while preserving the fidelity of CBF estimates from other regions.



Methods: Ten healthy subjects (mean age: 48.3, 6 males) were randomly selected from the CBFBIRN Database [6]. Each subject was scanned on a 3T GE MR750 scanner using an 8-channel head coil. A MPPCASL scan was acquired using 8 RF phase offsets with the following scan parameters for a whole-brain baseline CBF protocol: tag duration=2000ms, post labeling delay=1600ms, TR=4200ms, single-shot spiral acquisition (TE=3.3ms), 220mm FOV, 20 slices (5mm thick, skip 1mm), 64 reps, and scan time = 4:30 min. Per-voxel CBF estimates were obtained by fitting a modified Fermi function to the acquired blood signal using both the original unconstrained nonlinear optimization method [1] and a Bayesian nonlinear method that incorporated a spatial prior on the CBF parameter [4, 5]. The quantified CBF maps generated from these two methods were compared within gray matter (GM), white matter (WM), and in the regions where the original optimization routine produced artificially high CBF estimates. This error prone region was defined by a subject-specific binary artifact mask (Fig. 1A, Fig. 2A), which was generated by identifying voxels in which the ASL signal fluctuations were greater than 10% of the baseline signal. The white matter and gray matter masks were derived from a high resolution anatomical scan and excluded the voxels identified as noise inside the artifact mask.

Results & Discussion: Figures 1 and 2 show CBF maps from two representative subjects. The defined artifact maps (Fig. 1A, and 2A) correspond well with the regions of hyperperfusion (e.g. near front of brain) related to the poor performance of the original model fitting algorithm. The new Bayesian model fitting greatly reduces the hyperperfusion within the artifact mask while preserving the accuracy of the CBF estimates from other regions. Figure 3 shows scatter plots of whole-brain mean CBF values (new fitting method vs. original) within (a) the artifact mask, (b) the gray matter, and (c) the white matter. The t-statistic and p-value associated with each paired t-test are shown in the title of each plot, as well as the r^2 value. The two fitting methods produced no statistical difference in the estimated CBF values within the GM and WM regions (Fig. 3B, C). The t-test showed a significant difference between the two fitting methods in the noisy regions (Fig. 3A), indicating that the Bayesian model successfully reduced overestimation of CBF in these regions.



References: [1] Jung, et al. MRM 64:799-810, 2010. [2] Jahanian et al. NMR Biomed. 24:1202-1209, 2011. [3] Shin et al. MRM 68:1135-1144, 2012. [4] Chappell et al. IEEE Trans. Sig. Proc., 57:223-236. 2009. [5] Groves, et al. NeuroImage 45:795-809, 2009. [6] Shin, et al. Front. Neuroinform. 7:21, 2013.