Comparison of Bayesian and Linear Regression-based Partial Volume Correction in Single Time Point ASL

Ruth Oliver[1], Michael Chappell[2,3], David Thomas[1], and Xavier Golay[1]

[1]*Institute of Neurology, University College London, London, United Kingdom,* [2]*Institute of Biomedical Engineering, University of Oxford, Oxford, United Kingdom,* [3]*FMRIB Centre, University of Oxford, Oxford, United Kingdom*

Target Audience: Clinicians interested in measuring perfusion and quantifying changes in grey matter CBF.

Introduction: ASL is usually acquired at low resolution, resulting in cerebral blood flow (CBF) measurements that are significantly affected by partial volume (PV) effects. This can be particularly problematic in quantifying perfusion in patients where structural atrophy is occurring and can lead to an apparent decrease in perfusion without appropriate PV correction. Recent PV correction efforts have focused on a local linear regression (LR) within a kernel to separate voxel signal into GM and WM contributions for single-TI data [1][2]. However, this strategy introduces a spatial smoothing dependent on kernel size, leading to a trade-off between minimizing smoothing while maintaining sufficient information to satisfy the LR equations. More recently a Bayesian approach has been proposed that exploits the difference in white matter (WM) and grey matter (GM) kinetics and employs an adaptive spatial smoothing by combining kinetic information with PV constraints [3]. However, this latter method has not been applied to the more common single-TI data where kinetic information is not present. This work investigates whether the Bayesian approach offers an advantage over the LR method on single-TI including the extension of the LR method to a 3D kernel.

Methods: Assuming no contribution from CSF in an ASL difference image, the signal can be modelled as:

$$\Delta \boldsymbol{M} = \Delta \boldsymbol{M}_{GM} \boldsymbol{PV}_{GM} + \Delta \boldsymbol{M}_{WM} \boldsymbol{PV}_{WM}$$

where PV_{GM} and PV_{WM} are the partial volume estimates (PVE) for GM and WM obtained from a structural segmentation from a high resolution T1-weighted scan. The separate tissue contributions can be estimated using LR by making the assumption that they remain constant over the kernel area. This introduces an inherent spatial smoothing based on the kernel size but that also varies with PVE. Previous studies using LR methods have focused on 2D regression kernels, which impose a minimum kernel size due to the need to obtain sufficient equations to solve the LR. Recently it has been shown that a 3D kernel of size 3x3x3 is viable and produces less smoothing than its 2D equivalent [4]. On the other hand, the more recently proposed Bayesian method starts from the same equation but exploits the differing kinetics from the contributions of GM and WM to the difference image, as well as employing a spatial prior to exploit spatial homogeneity in the signal. In single TI data kinetic information is not available; however, spatial priors can still be employed. These would operate like the spatial kernel in the LR method, except the effective amount of spatial smoothing with this method is determined automatically from the data and can adaptively vary across the brain. Data were analysed according to the standard model that does not account for PV effects [6], using the LR method (with kernel sizes in 2D and 3D) and using the spatial prior method using the FSL toolbox (www.fmrib.ox.ac.uk/fsl) implementation [7][8].

Experimental data: Resting state ASL data of 6 healthy controls was acquired using a pulsed Q2TIPS labelling scheme with background suppression [5]. A 3D-GRASE read out was employed with total inflow time = 2s, bolus length = 0.8s, matrix size = 64 x 64 x 20, image resolution = 3.75 x 3.75 x 3.8 mm^3. The 3D-GRASE data was acquired in 8 segments to mitigate the effect of T2 decay. High resolution MPRAGE images were acquired in the same session, matrix size = 208 x 256 x 256, resolution = 1.0 x 1.0 x 1.0 mm^3. All images were acquired on 3T Siemens Trio using a 32-channel head coil. The T1-weighted images were segmented using SPM8 into PV fractions for GM, WM and CSF. These were transformed to ASL space via linear registration and resampling to ASL resolution using FSL FLIRT and applywarp as in [3]. To estimate the amount of smoothing each of the methods introduced, the spatial gradient was calculated at each voxel for the PV corrected GM CBF images in all 3 spatial dimensions, the magnitude of this vector was taken as a measure of detail. Regions of interest (ROI) were defined according to the PV fraction in a similar manner to [3], allowing quantitative comparisons to be made of the mean GM CBF and spatial gradient across the PV range for the two methods. The ranges were 10-20, 20-30…90-100%, with the expectation that PV corrected GM CBF would not correlate with PV fraction, but that the mean spatial gradient would reduce for LR methods whilst increasing for spatial prior method as PV estimate increases due to the adaptive nature of the method. Simulated data were generated from a subject PV fraction obtained from a structural image transformed to a 3.75 x 3.75 x 3.8 mm^3 resolution. The simulated data was composed of a homogenous region of 60 ml/100g/min, with a hypo and hyper intense region of 20 and 100 ml/100g/min respectively. WM CBF was set to 20ml/100g/min. Bolus duration of 0.8s and TI of 2s were chosen to match the actual acquisition parameters.

Results: Figure 1 shows the middle slice of a subject for each of the analyses. The increased smoothing by LR is readily apparent, although both LR and the Bayesian PV methods perform well for correcting PV, increasing CBF by a factor of 1.6-1.7 as previously found for multi-TI data [3]. (see Table 1). Figure 2 shows the variation in mean CBF with increasing PVE for the same subject. Across all six subjects, there was a distinct trend for each method; LR estimates were usually higher than the Bayesian methods at large PVE, whilst the converse was true for smaller PVE. It is not clear whether LR overestimates at high PVE, or if Bayesian methods underestimate at low PVE. In figure 3 we see a comparison of the mean spatial gradient at each PVE for the Bayesian method, as well as the LR method for a 3D 3x3x3 and a 2D 5x5 kernel. Both LR kernels contain a similar number of voxels and therefore information, yet we see increased retained detail by the 3D kernel as it is drawn from a smaller region of the image. However, both LR kernels are substantially out performed by the Bayesian method, which produced a mean spatial gradient which was a factor of 1.3 and 1.4 greater than the 3D and 2D kernels respectively.

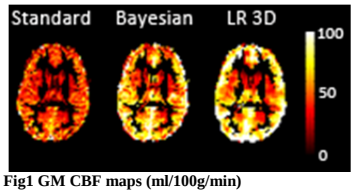

Fig1 GM CBF maps (ml/100g/min)

Discussion: Adaptive spatial methods appear to be better at retaining detail and reducing smoothing across the whole spectrum of PVE. These advantages must be weighed against the increased complexity of the method. LR is currently faster to compute and provides a comparable average GM CBF to spatial methods, although requires a user selected kernel. The Bayesian PV method adaptively chooses the degree of smoothing, as was evident in the results. This work indicates that both methods are readily applicable to both single and multi-TI data, although currently the LR method when applied using a 3D kernel is best suited to isotropic resolution to avoid greater smoothing in the slice direction.

Subject	Standard	Bayesian	LR
1	39.32	61.6	63.6
2	38.8	66.82	71.64
3	33.02	56.75	55.9
4	34.81	55.52	63.49
5	34.25	57.86	63.38
6	30.61	54.00	53.54

Table 1 Mean CBF ml/100g/min for all subjects for each method of CBF calculation. 3D 3x3x3 kernel used for LR.

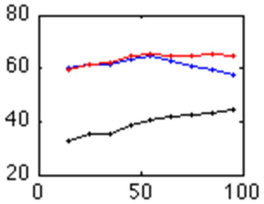

Fig2 Subject 1: CBF ml/100g/min v GM PVE%. LR=red, Bayesian=blue, Std=black

Subject	Bayesian	LR 3x3x3	LR 5x5
1	21.47	18.84	16.93
2	20.23	16.47	15.99
3	18.93	14.01	13.71
4	16.05	13.86	13.20
5	21.64	17.24	16.49
6	27.9	15.09	13.94

Table 2 Mean spatial gradient for all subjects for Bayesian and 2 LR kernel size analyses.

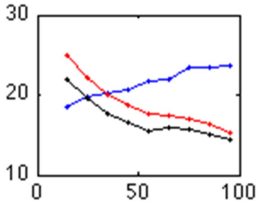

Fig3 Subject 1: Spatial gradient v GM PVE%. Bayesian=blue, LR 3D=red, LR 2D=black.

References:1.Asllani, I., et al., MRM, 2008. 60:1362-1371. **2**. Liang, X, et al., MRM, 2012. **3**.Chappell M.A.., et al., MRM, 2011. 65:1173-1183 **4**.Oliver, RA., et al Proc ESMRMB 2012. **5**.Gunther M., et al., MRM, 2005. 54:491-498 **6**.Buxton, R.B., et al., MRM, 1998. 40:383-396 **7**.Chappell M.A., et al, IEEE Trans. Sig. Proc. 2009 57(1):223-236 **8**.Groves, A.R., et al., NeuroImage, 2009 45(3) 795-809

Acknowledgements: Grant sponsor: EU COST AID Action BM1103