Partial Volume Correction of 3D GRASE ASL images using T1 maps acquired with the same readout scheme

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Target Audience: Clinicians and physicists 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. PV effects are caused by tissue signal mixing at a structure boundary. This is particularly problematic in the cortex, where most voxels represent a mixture of GM and WM (or GM and CSF). As GM CBF is three times higher than WM CBF, whilst CSF CBF is null, significant underestimation of GM CBF can occur. Recent approaches to PV correction make use of an additional high-resolution structural image, which is segmented into tissue types, registered and downsampled to provide a probabilistic estimate of partial volumes. These estimates can then be used as the basis of a linear regression to separate the ASL signal into GM and WM contributions [1][2]. However, this approach is non-ideal for two reasons: segmentation of structural data can be poor when applied to atrophied brains. Additionally, registration of anatomical data to ASL data is non-trivial, particularly when background suppression is applied to improve the ASL SNR. A recent study [3] proposed creating probabilistic tissue maps from a Look-Locker EPI acquisition using the FRASIER [4] method for deriving PV fractions. The method offers the advantage of creating the PV maps directly in ASL space and removes the needs for registration and resampling. Here, we aim, using the method of [3] to create PV fractions from a 3D GRASE-based saturation recovery sequence.

Methods: The measured signal after a 90° saturation can be modelled as a linear combination of three mono-exponential functions:

$$S(t) = \sum_i S_i \left(1 - e^{-\left(\frac{t}{T1i}\right)}\right)$$

where Si is the fractional signal of tissue i (GM,WM,CSF), with relaxation T_{1i}. Considering a saturation recovery acquisition of n time-points with voxelwise signals $Sobs = [S_1 \ldots S_n]^T$, we can write $Sobs = X\,Fs$, where $X = (1 - exp(-t/T_{1i}))$ and $Fs = [F_{S,GM}\ F_{S,WM}\ F_{S,CSF}]^T$. Fs contains the fractional signal for each tissue type, which can be calculated from $(X^TX)^{-1}X^T\,Sobs$ using a least squares estimation, assuming that the different tissue T1 values are known. The T1 value of WM was obtained from a histogram of the whole brain T1 map as in [4]. CSF T1 was assumed to be 4.3s [3]. As there are no pure GM voxels at this resolution, the T1 of GM was found by iterative minimisation of the residual norm between the observed signal and modelled signal. Tissue fractional signals were converted to PV fractions (PV_{satrec}) by correcting for the variable water density. PV fractions were also created from anatomical MPRAGE data, by the usual method of segmentation and transformation to ASL space (PV_{MPRAGE}). The data was analysed using the general kinetic model modified for QUIPSS II [5] which does not account for PV effects, and by using the linear regression method of [1] with a 3x3x3 kernel [6] together with the two PV maps obtained from the saturation recovery sequence and anatomical data. Both PV maps were used to create regions of interest in a similar manner to [7]. The ranges were GM fraction 10-20, 20-30,…90-100%, representing a pseudo-random sample across the brain, allowing a quantitative comparison of mean GM CBF at each PV fraction. Validation of the PV-corrected results from the two different PV maps was performed by recombining the separated tissue flows with associated PV map and comparing with the uncorrected CBF. The method of PV correction does introduce an inherent spatial smoothing of tissue signal, but it is assumed the effect will be similar for PV_{satrec} and PV_{MPRAGE}, and that any difference can be attributed to errors in the PV maps.

Experimental data: ASL data of 4 healthy controls was acquired using a pulsed QUIPSS II labelling scheme with background suppression. A 3D-GRASE readout 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 blurring effect of T2 decay during the echo train. Additionally, high resolution MPRAGE images matrix size = 208 x 256 x 256, resolution = 1.0 x 1.0 x 1.0 mm^3 and saturation recovery 3D GRASE images (TI = 200,500,750,1000,1500,2000,3000,4000 ms) were acquired and used to calculate PV maps in [3]. All images were acquired on a 3T Siemens TIM Trio using a 32-channel head array coil. The anatomical 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].

Results: Fig 1b,c show GM PV maps for a middle slice from subject 1. The same trend was seen for all subjects in that the GM PV_{MPRAGE} maps were generally showed greater GM fractions the deep GM regions. Fig 1d,e show the recovered CBF maps when the calculated PV fractions are applied to generate GM and WM pure tissue flows and then recombined. Departures from the uncorrected CBF map in fig. 1a reflect errors in the PV maps. Ideally, a one to one correspondence for the voxel intensity in the standard and recovered maps would be observed. Figures 2 and 3 show correlation plots of the uncorrected CBF map and the recovered maps obtained using PV_{MPRAGE} (r^2=0.51) and $PV_{sat\ rec}$ (r^2=0.68) respectively. Figure 4 shows mean GM results as a function of PV fraction as in [6][7]. PV correction should remove any dependency on PV fraction. The dashed lines represent the uncorrected CBF map values, and the solid lines represent PV corrected GM CBF flows. The PV_{satrec}-corrected GM CBF values demonstrate very good consistency for all PV fractions, whereas the PV_{MPRAGE} maps produce greater estimates of GM CBF at low GM PV fractions and follows a downward trend to produce a lower estimate than PV_{satrec} at greater PV fractions. This may be caused by poor registration at the brain boundaries.

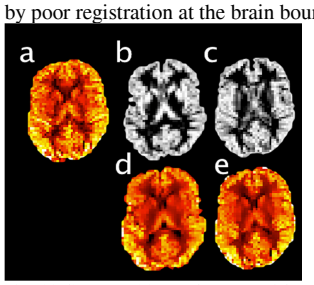

Fig1 (a) CBF map (b) PVF from MPRAGE image (c) PVF from saturation recovery data (d) Recovered CBF using (b) (e) Recovered CBF using (c)

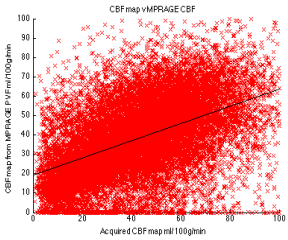

Figure 2 Correlation for MPRAGE CBF data and uncorrected data

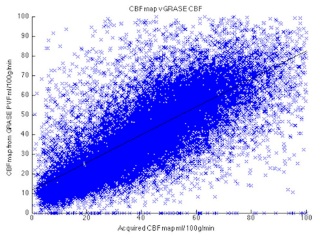

Figure 3 Correlation for Saturation Recovery CBF data and uncorrected data

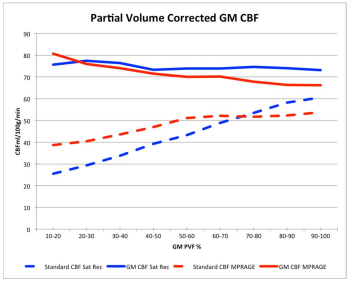

Figure 4 Uncorrected CBF and GM CBF using PVsatrec and PVmprage maps for ROI based on ranges of GM content.

Discussion: The FRASIER method for generating PV maps assumes the T1 values of GM, WM, and CSF are constant across the brain, yet is highly sensitive to these values. However, it removes the need to acquire a separate anatomical image and the problematic steps of registering structural data to lower resolution ASL data. The importance of a good registration for reliable PV correction cannot be overstated, and is difficult to achieve, particularly when applying the technique to many patients through a clinical trial. The FRASIER segmentation method can be improved further by varying the T1 of tissue on a regional basis. We have shown the FRASIER technique can be used to generate PV estimates for 3D GRASE data and produces superior PVC results compared to using anatomical data.

References:1.Asllani, I., et al., MRM, 2008. 60:1362-1371. **2**. Liang, X, et al., MRM, 2012. **3**. Petr, J., et al., MRM 2012 **4.** Shin, W, et al., Neuroimage 52(2010)1347-1354 **5**. Wong, EC, et al., MRM 41 :1 246-1254(1999) **6**.Oliver, RA., et al Proc ESMRMB 2012 **7**.Chappell M.A.., et al., MRM, 2011. 65:1173-1183. **Acknowledgements:** Grant sponsor: EU COST AID Action BM1103