Consistency Checks for Partial Volume Correction of ASL perfusion maps

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Target Audience Scientists with interest in brain perfusion, working with arterial spin labeling (ASL) and familiar with partial volume correction (PVC).

Purpose PVC [1,2] has been used to estimate the perfusion of grey and white matter. Because the verification of PVC methods is difficult to achieve on real ASL data, due the lack of a gold standard, the methods are usually checked with simulated datasets. However these checks might not reflect all properties of real ASL data, such as a non-ideal point-spread function (PSF) or spatial mismatch of functional and structural data. To check the consistency of partial volume correction (PVC) on real ASL data, we propose two simple tests: the grey and white matter perfusion should not alter upon downsampling or upon spatial filtering of both partial volume estimates and ASL data. It is hypothesized that violation of these tests may indicate a spatial mismatch and/or a mismatch in PSF between functional and structural data. In this study, the CBF maps of six healthy volunteers were tested in conjunction with a linear regression PVC [1].

Methods ASL CBF maps were acquired for six healthy volunteers on a 3T MRI scanner (Discovery MR750, GEHC, Milwaukee, WI), using a 3D FSE stack-of-spiral readout combined with a pseudo-continuous labelling scheme. Written informed consent was obtained. The following settings were used: label time 1.5s, PLD 1.5s, TR 4.3s, TE 10.2ms, readout 8 arms x 512 samples, RBW 62.5kHz, effective resolution 3.2x3.2mm, reconstructed pixel size 1.7x1.7mm, 36 axial slices of 5.0 mm thickness, NEX 2, scan time ~4 min. In addition, a 3D T1-weighted scan was obtained (IR-FSPGR, TI 450 ms, TR 7.8ms, TE 3ms, voxel size 0.97x0.97x1 mm). 3D distortion correction was applied to correct gradient non-linearity.

Next, the CBF map was registered with 6 degrees of freedom (rigid body) to the T1W scan using FLIRT (FSL 4.1, FMRIB, Oxford). The T1W scan was processed with SIENAX (FSL 4.1) to obtain a whole brain mask and partial volume estimates (PVE). The PVE maps were transformed to the ASL data space, and linear regression (custom-written script, Matlab, MathWorks, Natick, MA) was used to correct for partial volume effects [1], using a 3D Gaussian weighted kernel (FWHM 9.5mm, or 19mm if indicated) instead of commonly used kernels such as 5x5x1 or 11x11x1. Tissue content with PVE <5% was excluded from the regression analysis. The average whole brain tissue-specific CBFs (i.e. CBF_{GM}, CBF_{WM}) were then calculated by weighted averaging of the PVC CBF maps, using the PVE as a weighting factor.

A simulated CBF map was created from the PVE data, with perfusion arbitrarily set to CBF_{GM}=85, CBF_{WM}=50, and CBF_{CSF}=0 without added noise, and PVC was also applied to the simulated CBF map. The proposed consistency checks were applied to both simulated and real data.

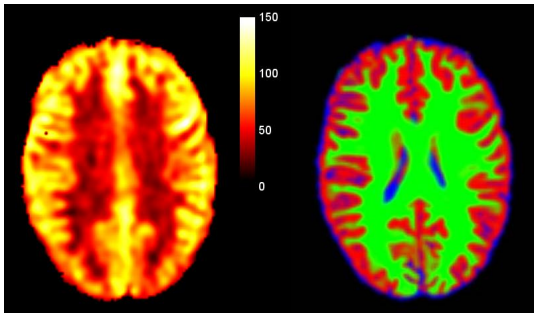

Figure 1: Example ASL CBF map (left), and PVE (right). Data were masked with the whole brain mask produced by SIENAX. Scale in [ml/100ml/min].

Results The simulated data proved correct implementation of the PVC method. Moreover the simulated data also passed our consistency test with resulting average perfusion of CBF_{GM}=82.6 and CBF_{WM}=49.5. Downsampling of simulated data by a factor 2 in all directions (i.e. factor 8 increase of voxel volume) yielded CBF_{GM}=83.2 and CBF_{WM}=49.3. For the volunteer data, Figure 1 shows an example CBF map and corresponding PVE. Figure 2 shows the resulting CBF for a variety of downsampling and filtering options. Note that the ratio of GM/WM perfusion, which is often regarded as an indicator of data quality, varied between 1.6 and 5.1. Downsampling of data resulted in an increase in GM perfusion compared to the original data space. The perfusion obtained with low-pass spatial filtering (FWHM of 3.2x3.2x10mm) was similar to factor 2 downsampled data, as would be expected for an equivalent effective resolution. PVC CBF as a function of PVE showed an overestimation of CBF for low PVE, i.e. corrected curves were not as flat, with increased downsampling or smoothing (Figure 3). Additionally the regression kernel size slightly modified results (while making certain that the set of equations was always overdetermined).

Discussion The in-vivo ASL data did not pass the proposed consistency checks. Additionally the results indicate that CBF_{GM}, CBF_{WM} and their ratio were dependent on resampling and spatial filtering, which is highly undesirable. After downsampling with a factor 2 or 4, it was expected that the resolution would be rather independent from the ASL acquisition resolution, and registration issues would not be relevant. However no convergence was observed with increased downsampling or smoothing. Additional simulations of non-ideal PSF and registration errors (data not shown) did show the expected behaviour, therefore, the stated hypothesis tends to be rejected and the errors are contributed to other sources such as noise amplification by extrapolation in the regression algorithm, artefacts or non-ideal pointspread function in the ASL image, incorrect assumptions about homogeneity of the perfusion or errors in the PVE. Further investigation is needed to identify which factors are of interest.

Conclusion While the simulated data suggest a properly working PVC method, the real ASL data fail the proposed consistency tests. This may indicate that the PVC data does not provide a reliable estimate of GM and WM perfusion. Uncorrected data should always be published aside the PVC data.

References [1] Asllani, MRM 2008; 60:1362-1371. [2] Chappell, MRM 2011; 65: 1173-1183.

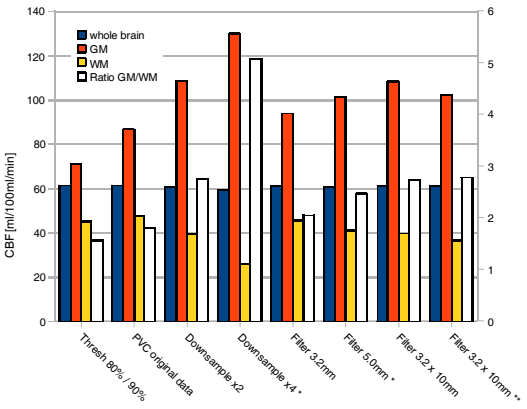

Figure 2: Average perfusion and GM/WM perfusion ratio for variants of thresholding, downsampling and spatial filtering. Ratio scale is on seconday axis. Regression kernel size was 9.5mm, 19mm or whole brain**.*

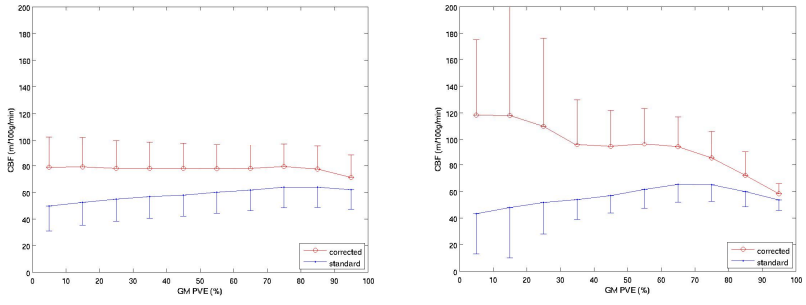

Figure 3: Single subject example of GM perfusion as function of PVE, showing both original data (blue) and the corrected data (red), for original resolution (left) and smoothed FWHM 3.2x3.2x10mm resolution (right).