Correction of partial volume effects in PASL perfusion measurements

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Introduction:
Arterial spin labeling (ASL) methods potentially allow the non-invasive, quantitative measurement of perfusion, or regional cerebral blood flow (CBF). However, typical ASL acquisitions suffer from severe partial volume effects (PVE's) due to the coarse spatial resolution of the images. Although several methods have been developed to correct for the effects of signal cross-contamination by including local tissue fractions, only one report has addressed this issue in ASL [1]. In our study, we aimed to develop a simple model to correct for partial volume effects in ASL imaging and to study its performance in the estimation of grey matter (GM) and white matter (WM) perfusion, as well as in the application of ASL to brain activation measurements in functional magnetic resonance imaging (fMRI).

Methods:
Fifteen healthy volunteers were studied on a Siemens Verio 3.0 T system using a 32-channel head coil. The imaging sessions included the acquisition of a high-resolution anatomical image using a 3D MP-RAGE sequence, with TR/TE/TI/flip = 2250 ms / 2.26 ms / 900 ms / 90°, 160 sagittal slices 1.0 mm thick, 256 x 240 mm^2 FOV and 256 x 240 matrix size, yielding an isotropic spatial resolution of 1 mm^3. A pulsed ASL Q2TIPS-PICORE sequence with a GE-EPI readout was used for the ASL acquisition, with TR/TE/TI_1/TI_{1s}/TI_2 = 2500 ms / 11 ms / 700 ms / 1600 ms / 1800 ms, 9 contiguous axial slices 6 mm thick, positioned parallel to the AC-PC line, 224 x 224 mm^2 FOV and 64 x 64 matrix size, yielding a resolution of 3.5 x 3.5 x 6.0 mm^3. A FOCI 180° inversion pulse was applied to a 10 cm thick labelling region, positioned 18.8 mm below the proximal imaging slice. Between TI_1 and TI_{1S}, saturation pulses were applied over a 20 mm thick saturation slab. For the fMRI experiment, the subjects performed a sequential thumb-digit apposition task. The fMRI paradigm employed a block design consisting of 5 cycles of rest and task periods of 25 sec duration each. A total of 101 volumes alternating between tag and control were acquired, resulting in a total scan of 4 min 12.5 sec. Pre-processing was performed using FSL (www.fmrib.ox.uk/fsl) and included: motion correction, spatial smoothing with a 5 mm Gaussian kernel and high-pass temporal filtering with a 100 ms frequency cutoff. The control-tag pairwise differences were computed to yield the mean ΔM maps. FAST from FSL was used to segment the MP-RAGE images of each subject into GM, WM and cerebrospinal fluid (CSF), producing GM, WM and CSF masks, as well as partial volume (PV) maps, which were registered to the space of the ASL images. The ΔM maps were averaged and normalized by the mean M_0 in each mask, for each slice, and CBF was computed using a standard kinetic model [2]. The average perfusion, f, over the GM and WM masks was modeled as a function of the true GM and WM perfusion values (f_{GM}) and (f_{WM}), as well as the GM and WM volume fractions in the mask ($\langle pve_{GM}\rangle_{GMmask}$) and ($\langle pve_{WM}\rangle_{GMmask}$), according to the equations on the right. These were then solved in order to determine f_{GM} and f_{WM} for each subject and each slice. The group average ratio of GM to WM CBF was computed for each slice with and without PVE correction. The fMRI data were analyzed with a standard General Linear Model (GLM) approach using FEAT from FSL and the perfusion-based activation has been considered.

$$\begin{cases} \langle f\rangle_{GMmask} = \langle pve_{GM}\rangle_{GMmask} f_{GM} + \langle pve_{WM}\rangle_{GMmask} f_{WM} \\ \langle f\rangle_{WMmask} = \langle pve_{GM}\rangle_{WMmask} f_{GM} + \langle pve_{WM}\rangle_{WMmask} f_{WM} \end{cases}$$

Results:

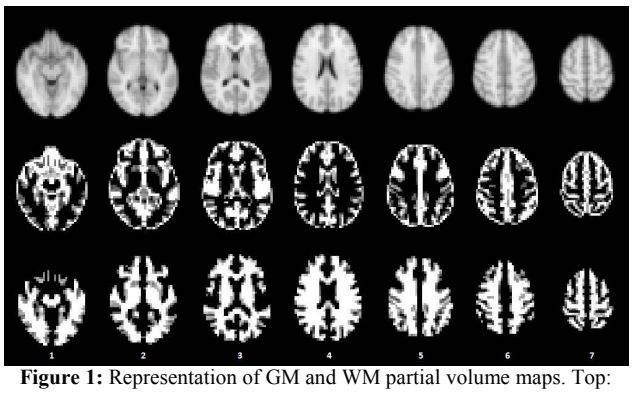

Figure 1: Representation of GM and WM partial volume maps. Top: MP-RAGE images. Middle: GM PV maps. Bottom: WM PV maps.

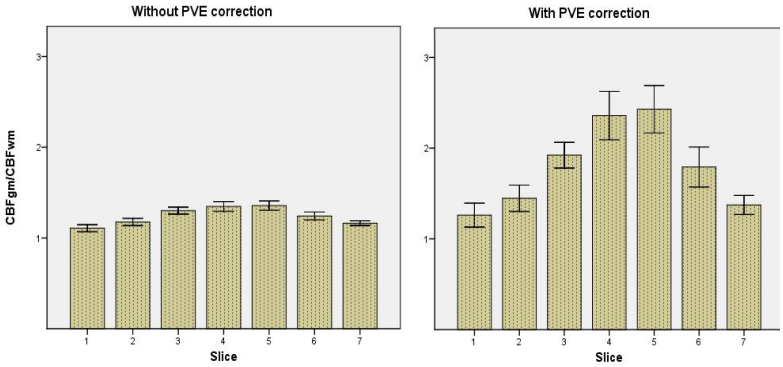

Figure 2. Mean ratios of grey to white matter perfusion in each of 7 slices calculated with (right) and without (left) PVE correction.

The results show a significant increase in the ratio of GM to WM CBF after PVE correction, as expected. However, the effect of PVE correction varied across slices. An accurate segmentation (in the middle slices) allows for PVE's to be well corrected, yielding an expected GM to WM CBF ratio ~2-3. However, where GM structures are mis-classified as WM (bottom slices), WM CBF is overestimated and therefore the GM to WM CBF ratio is underestimated.

Figure 4 shows the GM and WM CBF changes due to activation obtained before and after correction for PVE's. The group mean change in GM CBF has been found to be significantly larger ($p < 0.05$) after PVE's correction, which is in agreement with previous findings [1]. Most interestingly, WM CBF change was significantly reduced and became negligible, as would be expected.

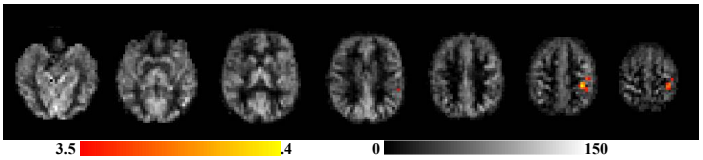

Figure 3: Activation Z maps (hot colour scale) superimposed on CBF map (grey scale in ml / 100g / min) from one representative subject.

Conclusion:
Our results reveal the importance of performing an accurate segmentation in order to achieve correction of PVE's, which can influence GM to WM perfusion ratio and also the CBF changes due to activation.

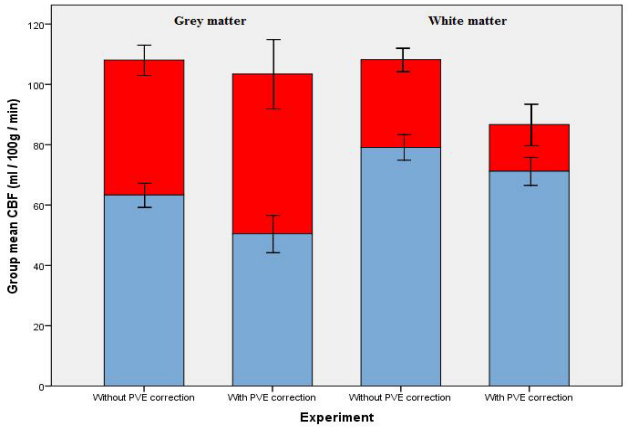

Figure 4: Comparison of activation data averaged across subjects with and without PVE correction. Baseline CBF is shown in blue and the amount of CBF change due to activation is shown in red.

References:
[1] Asllani, MRM 2008. 60:1362-71. [2] Buxton, MRM 1998, 40(3) 383-96.

Acknowledgements: Hospital da Luz. Project PTDC/SAU-BEB/65977/2006.