

The B1 field and variability in left-right brain perfusion with 3D IR-PULSAR and its implications on symmetry studies

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Introduction: Brain perfusion asymmetry is thought to be associated with Alzheimer's, schizophrenia and other cerebrovascular diseases [1,2]. To a radiologist interpreting brain images, particularly those images that are either purely qualitative or only semi-quantitative (eg, CBF maps), left-right asymmetry serves a critically important function as a visual cue to the presence of pathology. The ability to assess inter-hemispheric symmetry in the human brain with precision is therefore of importance. Arterial spin labeling has now found routine clinical relevance. A non-segmented 3D EPI acquisition method [3] based on the PULSAR technique [4] provides whole brain CBF values in ~5min. Here we study the effect of B1 field inhomogeneity on the spin labeling method and show that correcting for transmit and receive field B1 inhomogeneity is essential before any inferences can be made based on CBF values particularly related to perfusion asymmetry.

Materials and Methods: Quantification of CBF was done using $f(TD) = \Delta M / [2\eta M_{0A} \tau \exp(-TD/T_{1A})]$ (Eq. (2) in [5]), where ΔM is the perfusion signal, τ is the duration of the bolus, η is the inversion efficiency, TD is the delay between tagging and acquisition and T_{1A} is assumed to be the T_1 of arterial blood. Bolus definition was through the use of a QUIPSSII saturation pulse, with same spatial width as the tagging pulse, τ ms after tagging. For the 3D case, TD is defined by the time between the tagging inversion pulse and the $k_z = 0$ slice encoding which for our centric-ordered case corresponds to approximately the beginning of data acquisition. Where B1 map correction is applied, two B1 maps using the Actual Flip Angle (AFI) method [6] were obtained in the single (SM) and dual (DM) transmission mode. CBF images were then corrected for residual B1 inhomogeneity based on the acquired maps by using the corresponding B1 map (SM/ DM for SM/DM acquired perfusion data). A linear relationship between flip angles and the B1 map is assumed. The calculated CBF maps (in ml/100gm/min) were used for analysis. Erosion and dilation (to remove skull) followed by automated segmentation based on Otsu's algorithm [7] available in Matlab® was also applied to all CBF maps to separate regions of high perfusion (approximating gray matter-GM) from lower perfusion (approximating white matter-WM). GM CBF values were found for the left and right hemisphere by dividing each slice along the longitudinal fissure groove. The asymmetric index (as a %) was then defined as $200 \times (GM_{CBF_R} - GM_{CBF_L}) / (GM_{CBF_R} + GM_{CBF_L})$ where GM_{CBF_R} and GM_{CBF_L} refers to total GM CBF of the right and left hemispheres, respectively. A second measure of asymmetry was the total count of voxels classified as GM in the two hemispheres.

MRI experiments: Six healthy volunteers were scanned under an IRB approved protocol on a Philips 3T Achieva scanner (Release 3.2.1) using an eight channel head coil. Patients were positioned carefully and mobility restricted using pads and headphones. Using the mid-plane scan feature, the imaging slab was prescribed such that the transverse imaging slab was perpendicular to the inter-hemispheric fissure. Imaging was performed in single source RF mode and with dual-source parallel RF transmission. Scan parameters for 3D-IR-PULSAR were: TR/TD/τ = 2460/1800/900 ms; non-selective inversion pulse (for background suppression) with TI=925ms; 60 pairs of control/label images; data acquisition: 3D-Turbo Field EPI with variable flip angle scheme and $\alpha_{max}=30^\circ$, 24 slices, 4mm slice thick., 80×80 matrix, SENSE factor=2.5, centric-encoding; tagging region width=200mm, applied 20mm inferior to imaging slab; DAQ window=670ms; scan time=5 min. Scan parameters for the B1 mapping sequence were: TR1/TR2=25/125ms, TE=2.5ms, $\alpha_{max}=60^\circ$, 24 slices, 4mm slice thick, 80×80 matrix, scan time = 4mins 42s.

Results: Figure 1 shows four contiguous GM CBF slices (out of 24) obtained in the single transmission mode without B1 map correction (SM no B1) and the same slices with dual source transmission and with B1 map correction (DM with B1). Differences between the two sets can be very subtle (as indicated by arrows). A better discriminator is the asymmetry index defined earlier. Figure 2 shows the absolute GM CBF asymmetry across the six volunteers. Asymmetry in the number of voxels classified as GM is also shown for the four methods. The overall asymmetry (not absolute) seen between the two hemispheres (with the right hemisphere showing higher perfusion than the left hemisphere) was 5.4%, 2.83%, 4.32% and 2.65% for the four methods. The mean GM CBF values were 58.8, 58.6, 60.1 and 60.7ml/100g/min, respectively.

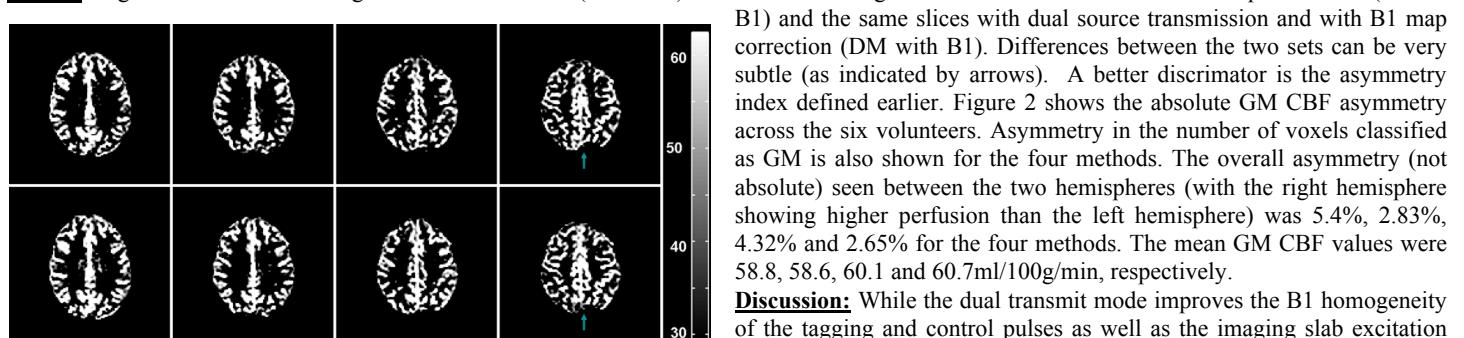


Fig 1: GM CBF maps of four contiguous slices (of 24) obtained with SM no B1 (top) and DM with B1 (bottom).

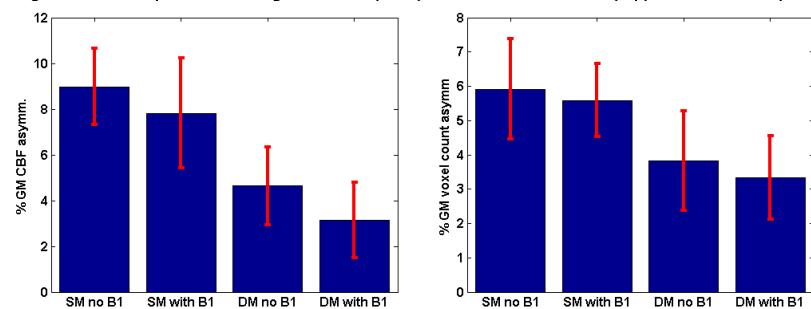


Fig 2: Percentage asymmetry in GM CBF value (left) and GM CBF voxels (right) for the four methods.

not compared as they were very low and inconsistent due to much longer transit delays (~1.6s) [8].

References: [1] Van Laere K et al. *Eur. J. Nucl. Med.* 2001;28:873-887. [2] Kovalev V et al. *MICCAI* 2006; 4191:421-428. [3] N. Gai et al. *JMRI* in print. [4] X. Golay et al., *MRM* 2005; 53: 15-21. [5] R. Buxton, *JMRI*, 2005; 22: 723-726. [6] Yarnykh V. *MRM* 2007; 57:192-200. [7] Otsu N. *IEEE Trans Syst, Man, Cyber* 1979;9:62-66. [8] P. van Gelderen et al., *ISMRM*, 2007: 1416.