Effect of Arterial Blood Signal Measurements on the Repeatability and Accuracy of Whole Brain CBF Values with 3D-PULSAR Imaging

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Introduction: Modification of the PULSAR technique [1] by use of a non-selective background suppression inversion pulse along with 3D-Turbo Field EPI (TFEPI) acquisition, labeled BSIR-3D-PULSAR, provides whole brain perfusion imaging in about five minutes. Furthermore, use of flip angle modulation reduces blurring when using centric-ordered slice encoding (along k_z) followed by a single-shot gradient-echo EPI acquisition [2]. Quantification of CBF is then done using a general kinetic model (GKM) developed by Buxton [3]. The derived CBF values follow an inverse relationship with arterial blood signal (M_{0A}). Measurement for M_{0A} is typically done in a voxel completely filled with blood in the sagittal sinus. Correction is then applied for differences in relaxation between venous and arterial blood as well as inversion efficiency [4]. Measurement of M_{0A} is considered to be the single most important source of error in CBF determination using GKM with a bolus cutoff pulse (QUIPSS II). Here we investigate the reproducibility and repeatability of CBF values across volunteers with and without this source of error. It is shown that as long as partial volume and saturation effects are avoided, M_{0A} measurement does not significantly alter results when compared with other sources of error.

Materials and Methods

Quantification of CBF was done using $f(\mathrm{TD})=\Delta M / [2\eta M_{0A}\tau\, exp(-\mathrm{TD}/T_{1A})]$ (Eq. (2) in [3]), 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. 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.

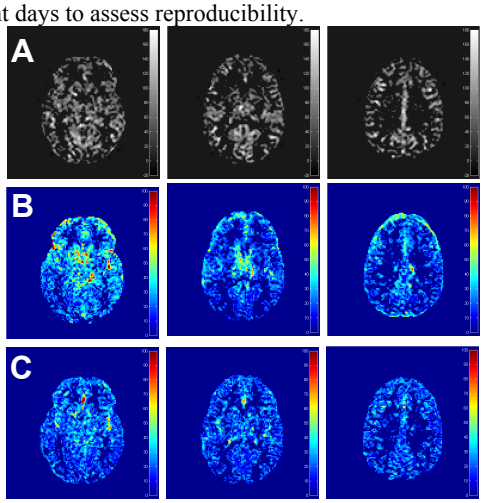
Six healthy volunteers were scanned under an IRB approved protocol on a Philips 3T Achieva scanner (Release 2.5.3). Bolus definition was through the use of a QUIPSSII saturation pulse, with same spatial width as the tagging pulse, τ ms after tagging. Four repeat scans were performed on each volunteer without use of a background suppression inversion recovery pulse. M_{0A} was measured in the sagittal sinus in the voxel showing the highest signal corresponding to unsaturated blood and relatively free of partial volume effect for each scan. Correction was applied for venous versus arterial signal while η was assumed to be 0.91 [4]. CBF values were also calculated for the four scans using average value for M_{0A} to reflect other (pulse imperfections, differences in transit delay etc) errors. Four repeat scans were also performed with a non-selective BSIR pulse. Since introduction of a BSIR pulse alters signal in the sagittal sinus**,** the average value of M_{0A} (denoted $\langle M_{0A}\rangle$) from four scans without BSIR was also used for CBF calculation with 3D-BSIR-PULSAR. Scan parameters for 3D-PULSAR were: TR/TD/τ =2460/1800/900 ms; 60 pairs of control/label images; data acquisition: 3D-Turbo Field EPI with variable flip angle scheme and α_{max}=30°, 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. For BSIR-3D-PULSAR, a non-selective inversion pulse was introduced with TI=925ms. While CBF values obtained from 3D-PULSAR scans reflect variation mainly due to M_{0A}, values obtained using $\langle M_{0A}\rangle$ reflect other errors. The calculated CBF maps (in ml/100gm/min.) were compared for perfusion values globally. Automated segmentation based on Otsu's algorithm available in Matlab® was applied to all CBF maps to separate regions of higher perfusion (approximating gray matter-GM) from lower perfusion (white matter-WM). Average value of gray matter was determined globally over 24 slices for each of the scans. The mean and standard deviation (σ) across four repeated scans was calculated for 3D-PULSAR and BSIR-3D-PULSAR. In addition, the various scans were repeated on two volunteers on two different days to assess reproducibility.

Results

Table 1 shows mean and standard deviation (σ) values across repeated scans for the globally averaged GM segmented images for the two cases: (a) 3D-PULSAR and (b) 3D-BSIR-PULSAR.

Vol.	3D-PULSAR	3D-BSIR-PULSAR
1	57±3.4	59±3.9
2	53±5.6	54±0.9
3	64±2.4	62±1.3
4	58±3.0	61±2.2
5	59±4.9	56±2.6
6	71±4.3	73±4.2

WM CBF values were not compared as the values were very low with both acquisition schemes since the transit delays for WM are much longer (~1.6s) ([5, 6]). Figure 1 shows three select segmented GM CBF image slices from the 3D stack (row A) obtained with 3D-BSIR-PULSAR; standard deviation images across four repeated scans for 3D-PULSAR (B) and (C) standard deviation images for 3D-BSIR-PULSAR. (Window/level for images in (B) and (C) is the same but different from images in (A).) Images obtained with $\langle M_{0A}\rangle$ for 3D-PULSAR show a similar qualitative appearance as images in Figure 1(B). Average σ across six volunteers is 3.93 for 3D-PULSAR when using individually measured M_{0A}s but is 3.15 with use of $\langle M_{0A}\rangle$ while it is just 2.51 for 3D-BSIR-PULSAR. Average GM CBF values were within 3% for two volunteers across two different scanning sessions.



Conclusions

Standard deviation maps for 3D-PULSAR reflect errors due to measurement of M_{0A} as well as errors due to relatively poorer background suppression. M_{0A} measurement errors result in a σ that is higher than when M_{0A} variation is absent (as when $\langle M_{0A}\rangle$ is used with 3D-PULSAR). The average COV (σ/μ) is higher by about 19.8%. The fact that the σ map for 3D-PULSAR is more heterogeneous when compared with the BSIR-PULSAR maps, particularly adjacent to CSF spaces, reflects the superior background suppression of BSIR-PULSAR; COV is further reduced by about 21% with 3D-BSIR-PULSAR over 3D-PULSAR using $\langle M_{0A}\rangle$. However, performing the Student t-test reveals no significant difference between values obtained using individual M_{0A} or $\langle M_{0A}\rangle$ (t-value=1.14<2.23 for a p-value of 0.05) for 3D-PULSAR indicating that M_{0A} measurements do not change results significantly.

References: [1] X. Golay et al., MRM, 2005; 53: 15-21. [2] N. Gai et al., *ISMRM*, 2009: 3648 [3] R. Buxton, *JMRI*, 2005; 22: 723-726. [4] E. Peterson et al., *MRM*, 2006: 55: 219-232. [5] J. Butman et al., *ISMRM*, 2002: 1706 [6] P. van Gelderen et al., *ISMRM*, 2007: 1416.