Post-Processing Correction for Extended Data Acquisition in Whole Brain 3D Quantitative 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 IR-3D-PULSAR, provides whole brain perfusion imaging in about five minutes [2]. Quantification of CBF using the Buxton model [3] requires specific value of delay time (TD) between the tagging pulse and the readout acquisition. For the 3D acquisition, this is typically set to be the time from the tagging pulse to the $k_z = 0$ slice encoding step. For the 2D multi-slice acquisition case, slices are obtained sequentially and therefore have different TDs associated with each slice. However, for the 3D TFEPI acquisition, the readout window is relatively long so that assuming a single TD may not be appropriate, as the signal loss in the tagged blood is on the order of 30% from the beginning of data acquisition to the end of an ~ 600 msec acquisition window. Here we attempt to partially correct for the signal decay during extended data acquisition by applying a correction in the hybrid (x, y, k_z) plane

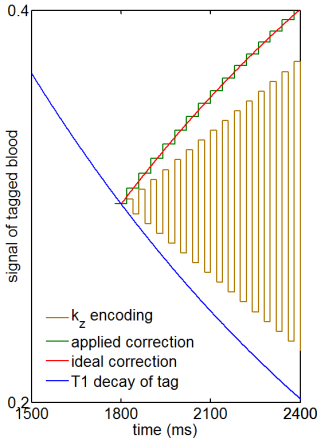
Materials and Methods

Quantification of CBF: CBF values are given by $f(t)=\Delta M(t) / [2\eta M_{0A}\tau\, exp(-t/T_{1A})]$, where $\Delta M(t)$ is perfusion signal at time t, M_{0A} is the equilibrium magnetization of arterial blood, τ is bolus duration, η is inversion efficiency and T_{1A} is T_1 of arterial blood.

Correction for decay: In the 3D case, the CBF values can be expressed as $f(TD)=\Delta M(TD) / [2\eta M_{0A}\tau\, exp(-TD/T_{1A})]$ as a zeroth order approximation, where TD is the delay between the tagging adiabatic inversion pulse and the beginning of data acquisition corresponding to k_z=0 centric-ordered slice encoding. An approximate first order correction can be applied to each slice in the hybrid (x, y, k_z) plane by multiplying a factor $exp(n\times TS/T_{1A})$ to the corresponding k_z acquisition, where n=1,…,nslices and TS is the sequence time of each single-shot EPI slice acquisition. The correction in operator notation is stated simply as:

$$[\mathfrak{F}^{(-1)}\{[\mathfrak{F}^{(1)} f](x, y, k_z) \bullet \exp(n \bullet \mathrm{TS} / T_{1A})\}](x, y, z)$$

where $[\mathfrak{F}^{(1)} f]$ refers to the 1-D forward Fourier transform of the CBF map along the z-direction while $\mathfrak{F}^{(-1)}$ is the inverse transform along the k_z direction. However, post-reconstruction, only magnitude images which provide the CBF maps are available. A Fourier transform along the z direction will then show Hermitian symmetry. This means that there is inherent ambiguity between data at positive k_z versus negative k_z. A simple approximation would then be to multiply both k_z (=±1 or = ±2 etc) lines by the average of n and (n+1)•TS. An inverse Fourier transform along k_z gives CBF values after correction for decay of blood inversion spins due to the extended duration of the acquisition window. Figure 1 schematically shows the k_z slice encoding order, the corresponding normalized decay of the blood signal during that time, the ideal correction and our approximate first order correction. The correction was tested against corresponding single-slice acquisitions for comparison.



MRI Scanning: Five healthy volunteers were scanned under an IRB approved protocol on a Philips 3T Achieva scanner running Release 2.1.3 software. Scan parameters for IR-3D-PULSAR were: TR/TD/τ=2380/1800/900 ms; background suppression inversion pulse TI=925ms, 62 pairs of control/label images; data acquisition: 3D-TFEPI with 24 slices (31 encoding steps with 3D oversampling), 4mm slice thick., 80×80 matrix, SENSE factor=2.5; DAC window≈590ms; scan time≈5 min. Single slice (SS2D) perfusion images at three different matching locations (slice 10, 15 and 20) were acquired using the same scan parameters. Otsu's algorithm (using Matlab®) was applied to CBF maps to segment regions of high perfusion (approximating gray matter-GM) from lower perfusion (approximating white matter). Average CBF values determined from these masks were applied to each method and compared.

Results

The mean values for GM CBF (ml/100g/min) for slices 10, 15 and 20 obtained with a 24 slice 3D acquisition (before and after correction) and as single-slice 2D acquisition are shown in the Table (*right*). WM matter CBF values were not compared as they were very low (< 10 ml/100g/min) and inconsistent due to the relatively long transit delay (~1.6s) [4], blurring and partial volume effects [5]. On average, the uncorrected values are 4.6% lower than single-slice values while the corrected values are only 2.8 % lower.

	Slice 10			Slice 15			Slice 20		
Vol	SS2D	3D	3D corr	SS2D	3D	3D corr	SS2D	3D	3D corr
1	67.9	67.0	67.8	77.9	71.0	71.8	86.7	84.2	85.8
2	61.2	58.2	59.0	57.0	56.3	57.2	62.2	58.2	59.7
3	73.8	71.5	72.6	79.5	74.5	75.4	78	77.3	79.2
4	73.7	66.9	68.1	70.1	65.3	66.6	64.5	64.0	65.8
5	71.9	68.3	70.0	79.0	71.5	73.0	55.6	56.2	57.8

Conclusion

CBF values obtained using 3D whole brain coverage can be corrected for the transit time differences due to the extended acquisition window. The correction reduces modulation effects due to differences in transit times which lead to dispersion of the perfusion signal. As a result, values in GM are higher after correction. This corresponds well with the single-slice acquisition values. Blurring introduced as a result of modulation in k-space due to constant flip angle non-steady state acquisition is not addressed here.

References

[1] X. Golay et al., MRM, 2005; 53: 15-21. [2] N. Gai et al., *ISMRM*, 2006: 3486 [3] R. Buxton, JMRI, 2005 ; 22: 723-726. [4] J. Butman et al., *ISMRM*, 2002: 1706 [5] P. van Gelderen et al., *ISMRM*, 2007: 1416.