Comparison of Quantitative Perfusion 3D IR-PULSAR with Multi-Slice 2D and Single Slice Imaging

N. D. Gai[1], S. L. Talagala[2], and J. A. Butman[1]

[1]Diagnostic Radiology Department, National Institutes of Health, Bethesda, MD, United States, [2]NINDS, National Institutes of Health, Bethesda, MD, United States

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]. The duration of the 3D data acquisition window (DAQ~590ms) as well as transit times in this case raises some concerns on the validity of quantitative values obtained with such a technique. Here we compare CBF values obtained with a 3D acquisition to the 2D multi-slice case as well as to corresponding single slice imaging.

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 2D multi-slice case, TD is assumed to be the delay between the tagging IR pulse and the acquisition time for a particular slice while 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. Three corresponding slices were also acquired in a single-slice acquisition mode for comparison.

Five healthy volunteers were scanned under an IRB approved protocol on a Philips 3T Achieva scanner (Release 2.1.3). Earlier described 2D and IR-3D PULSAR were modified to introduce a QUIPSSII saturation pulse of the same width as the tagging pulse for bolus cutoff τ ms after tagging. Scan parameters for IR-3D-PULSAR were: TR/TD/τ=2380/1800/900 ms; non-selective inversion pulse TI=925ms; 62 pairs of control/label images; data acquisition: 3D-Turbo Field EPI with α=30°, 24 slices, 4mm slice thick., 80×80 matrix, SENSE factor=2.5, centric-encoding; tagging region width=150mm applied 20mm inferior to imaging slab; DAQ window≈590ms; scan time≈5 min. 2D multi-slice acquisition (24 slices) was in ascending order with similar acquisition parameters except α=90° was used. Single slice perfusion images at three different matching locations (slice 10, 15 and 20) were acquired using similar scan parameters. M_{0A} was measured in the sagittal sinus and corrected while η was assumed to be 0.91 [4]. 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 also applied to all CBF maps to separate regions of higher perfusion (approximating gray matter-GM) from lower perfusion (white matter-WM). Average values of the maps were also determined and compared. For comparison with single-slice GM CBF values, the segmentation threshold for the 3D GM CBF maps was adjusted so that the mask thereby generated approximated the single slice case. This was done to reduce blurring related WM contamination in 3D images. Finally single slice images were subtracted from corresponding 3D-IR-Pulsar acquisition slices and the difference images are presented.

Results

Table 1 shows mean values for the GM segmented images for the two cases: (a) Global (Glo) GM average across all 24 slices for the 3D and 2D multi-slice (MS) case (b) Average GM CBF values for the three slices in the 3D case and corresponding single slices (SS10, SS15 and SS20). WM CBF values were not compared as the values were very low with all acquisition schemes since the transit delays for WM are much longer (~1.6s) ([5, 6]). Figure 1 shows select CBF image slices from the 3D stack, corresponding images from single-slice acquisition and subtracted images.

Volunteer	3D CBF(Glo)	MS CBF(Glo)	SS10/3D	SS15/3D	SS20/3D
1	66.1	64.9	67.9/67.0	77.9/71.0	86.7/84.2
2	50.6	52.9	61.2/58.2	57.0/56.3	62.2/58.2
3	65.3	64.9	73.8/71.5	79.5/74.5	78/77.3
4	55.1	56.1	73.7/66.9	70.1/65.3	64.5/64.0
5	54.8	51.8	71.9/68.3	79.0/71.5	55.6/56.2

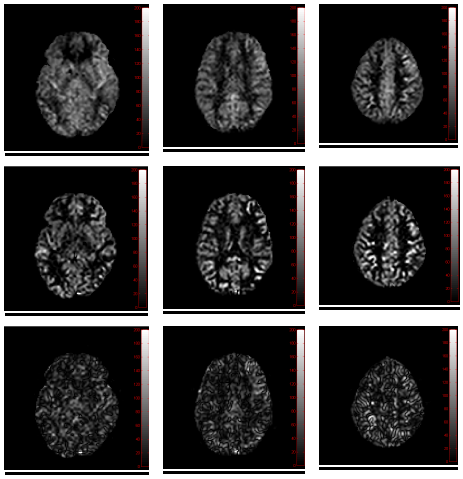

Figure 1: Top row shows CBF maps for slices 10, 15 and 20 obtained using 3D acquisition. Second row shows the same slices acquired as a single-slice acquisition while the bottom row shows the corresponding difference images. Scale is shown on the right and is the same for each image.

Conclusions

Global CBF values in GM show good agreement between 3D and 2D multi-slice or corresponding single slice acquisition. In general, GM CBF values for the 3D acquisition are somewhat lower (4.6% on average over all volunteers and slices) than corresponding single-slice values due to blurring. White matter CBF comparison is unreliable using ASL [6]. Some regional differences in GM can also be seen as a result of heterogeneity in transit delays (~850-1.2s). CBF quantification with extended 3D image acquisition IR-PULSAR is reliable as long as the above limitations are kept in mind.

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] 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.