Reproducibility of Quantitative Cerebral Blood Flow Measurement Using Contrast Agent

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Introduction: Measurement of cerebral blood flow (CBF) based on dynamic susceptibility contrast (DSC) is rapidly becoming a mainstay of diagnostic algorithms for cerebrovascular diseases, such as stroke and cancer. While there have been many attempts to quantify CBF, limited attention has been directed toward establishing the reproducibility of techniques used for CBF quantification. The reproducibility, however, is a critical criterion for diagnostic tests that are to be used clinically. We have developed a novel MRI imaging protocol that can be used to quantify CBF. Our approach does not depend on population averaged quantitative CBF (qCBF) values, which have been shown to perform poorly in patients with compromised flow. qCBF can be determined in individual patients based on: (1) measuring parenchymal T1-changes, (2) correcting the parenchymal T1-changes for intra-cellular-to-extracellular water exchange and (3) eliminating user error in post-processing with a fully automated reconstruction chain. In this investigation, the reproducibility of this technique was evaluated by obtaining serial qCBF measurements in individual volunteers.

Methods: Eight volunteers were scanned twice within a one week interval using a clinical 3.0T scanner (Trio, Siemens). To minimize diurnal variation, all subjects were scanned between 7:00 and 8:00 a.m. (Subjects were also asked to abstain from caffeine consumption for 12 hours prior to scan). To quantify blood flow, the bookend technique was used [1]. T1 measurements were performed with segmented inversion recovery Look Locker echo planar imaging (IR-LL-EPI); (TR/TE= 21/9.9ms, 120 time points). Perfusion weighted images were acquired with a gradient echo–EPI (GE-EPI) sequence between T1 measurements with single dose of contrast injection (0.01mmol/kg); (TR/TE = 1500/40 ms, partial Fourier 7/8, 13 slices, 50 measurement). Total scan time was under 4:00 minutes.

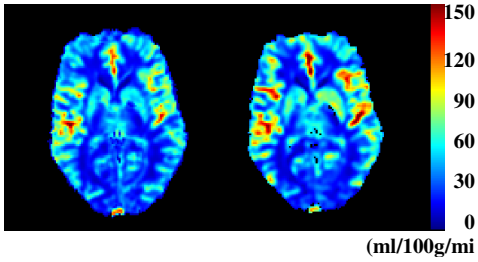

Figure 1. qCBF images from the same subject were coregistrated and resliced by SPM.

Quantitative analysis : From T1 measurements before and after contrast injection, parenchymal T1 changes CBV was quantified (in ml/100g). The T1 change in the blood pool was chosen automatically based on the extreme (~ 1000 ms) T1 changes and found to correlate anatomically with the sagittal sinus. A correction to the absolute CBV was applied to account for the effects of water exchange [2]. The arterial input function (AIF) was chosen based on adaptive thresholding for auto-analysis [3], and chosen by a trained operator for manual analysis. For the deconvolution, the singular value decomposition method was used. CBV maps from DSC analysis were calibrated by the ratio of absolute CBV from T1 changes value to CBV value from DSC analysis in white matter (WM). WM regions of interest (ROI) were chosen automatically based on the T1 distribution.

Data analysis: Two measured qCBF images on each subject were coregistered and resliced based on a pair of 13 slices of EPI images in pre-contrast using SPM2 (Wellcome Department of Cognitive Neurology, London, England) (see Figure 1). To determine the test-retest reliability of this method, intraclass correlation coefficients (ICC) were determined for white matter (WM) and gray matter (GM), as well as for global brain (both WM and GM). The segmentation of WM and ROIs were obtained from SPM2 using 75% probability threshold and weighted averaging was used to calculate average qCBF values, respectively

	Auto	Manual
WM	0.836	0.576
GM	0.957	0.882
Global Brain	0.951	0.825

Table 1. Intraclass correlation (ICC) for CBF measurements in White matter (WM), Gray Matter (GM), and global brain.

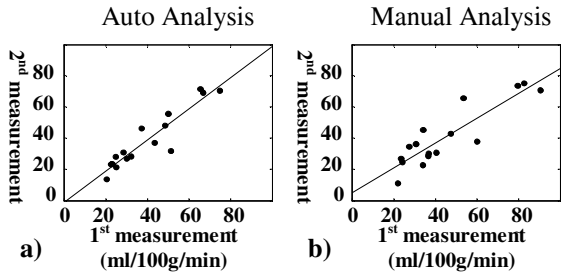

Figure 2. Scatterplots of the serial global brain. qCBF values for each subject were compared between test-retest with automated analysis (a), and manual anlaysis(b).

Result and Conclusions:

The intraclass correlation coefficients (shown in Table 1) indicate that both manual and automated methods of calculating the qCBF showed very good to excellent reproducibility for WM, GM and global brain, with generally higher reproducibility for the automated analysis (shown in Figure 2). These results indicate that quantification of CBF using this protocol is highly reproducible within individual subjects and has considerable potential diagnostic utility for clinical settings.

References: 1. Sakaie et al., JMRI, 2003. 2. Shin et al., MRM, 2006. 3. Carroll et al., Radiology, 2003.