Comparison of Perfusion Values Obtained by Single Subtraction and Multiple Subtraction Strategies in ASL

O. Ozyurt[1], A. Dincer[2], and C. Ozturk[1]

[1]Bogazici University, Biomedical Engineering Institute, Istanbul, Bebek, Turkey, [2]Radiology Department, Acibadem University, School of Medicine, Istanbul, Turkey

Introduction: A pulsed Arterial Spin Labeling (ASL) technique named QUIPSS II was offered for quantification of cerebral blood flow (CBF) in a single parameter control-tag experiment [1]. This single subtraction (SS) strategy is based on the assumption that imaging time is longer than the time for the passage of all the labeled blood through the imaging slice. However, under the conditions where this assumption is violated, it is necessary to sample the ASL kinetic curve in multiple time points. This is because the multiple subtraction strategy [2] had been used in the occlusive diseases [3]. Even in normal subject, it is shown that the arrival of labeled blood (i.e. transit time, δt) to the imaging slice may be prolonged due to vascular anatomy [4,5]. In this study, voxel-wise comparison of CBF maps obtained from normal volunteers by single subtraction (typically, TI2 = 1400) and multiple subtraction (MS) experiments were presented. Voxels that gave significant differences between two methods are identified.

Methods: Normal volunteers (4 males, mean age 27) were imaged using a Siemens 3T Trio scanner equipped with on 8-channel head coil. All the volunteers were subject to the same imaging protocol which includes the acquisition of the data sets from 5 axial slices (with 1 mm interslice gap) for segmentation and for ASL calculations (QUIPSS II with PICORE tagging scheme). For voxel-wise comparison all the images were taken with same spatial resolution (4x4x10 mm) and bandwidth = 1100 Hz/pixel with TE=23 ms.

(IR-GE) EPI sequence with three varying TI's (250, 3500, 15000 ms) was used to create T1 maps which are used for the segmentation of GM and WM. Delay time (TR –TI) was kept constant (15 sec) during these scans. Obtained M_0 maps were used to determine M_{0B} (equilibrium magnetization of blood), used in perfusion quantification [1] and T_1 maps were used for segmentation [6]. Pulsed ASL sequence was applied using TR=2500 ms, TI_1=600 ms and 10 uniformly distributed TI's ($TI \equiv TI_2 - TI_1$) between 400 and 2200 ms. For studies with TI shorter than TI_1, the saturation pulse was switched off. 20 control-tag pairs were acquired for TI = 800, and 10 pairs for other TI's. PASL gap = 10 mm and GRAPPA (x2) used with maximum number of reference lines. Total scan time ≈ 12 min.

Standard model describes the magnetization difference time course in three phases [2]. Expression describing the third phase is used with TI= 800 measurements for quantification in SS (i.e. CBF_{ss}). For MS, the measured magnetization differences were fitted to the ASL kinetic curve, yielding CBF_{ms}, δt, and R^2 (determination of coefficient) maps. T_1 of blood is assumed to be equal to 1.5 s, q is the correction term [1] and taken 0.9 in this study. The first and the last slices were discarded and one of the remaining mid-slices was selected depending on perfusion contrast for further analysis.

Results and Discussion: The results of linear regression between the both method's CBF measurements in all voxels in the selected slices were recorded (Table 1). It shows a good correlation. However, for high perfusion values the variability increases (Figure 2). To identify these regions, low-correlated voxels ($R^2 < 0.36$) and WM voxels were checked and discarded. Among the remaining voxels, the two groups were formed with δt<150 ms and δt>800 ms. Because of the higher velocity of blood in the arteries, the first group consists of mostly arterial voxels. In these sites, ASL signal starts to increase very early, and until TI_2=1400 ms most of the carried magnetization is decayed (bipolar flow-crushing gradients can be used to suppress the signal from large arteries; however this will affect the quantification process). Second group violates the assumption of QUIPSS, so misquantification of SS strategy is expected in these voxels. It is recorded that, for subjects 1, 3 and 4, the mean differences between two techniques for these groups are larger than the mean differences in measured CBF from all voxels (Table 1). Because of that it is expected for MS strategy to give better estimates of perfusion in case of good correlation between measured signal and ASL kinetic curve, the positive value of CBF_{ms} - CBF_{ss} possibly means the underestimation of CBF by SS strategy (Table 1). If we assume that the average CBF in GM of a healthy brain is around 70 ml/100g.min, differences observed between two methods are around 21% for δt<150 ms and 13% for δt>800 ms of basal perfusion. Also, these groups of voxels successively identify the outliers out of confidence interval (Figure 2).

Conclusion: It is previously stated that in the occlusive diseases, the usage of MS ASL is necessary [3]. In this study, it is shown that even for a healthy brain; SS method may result in underestimation in CBF in some voxels. Additionally, these voxels were identified as arterial sites and the regions with prolonged transit times, and the amount of differences in CBF estimates are calculated.

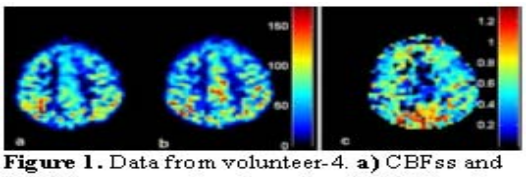

Figure 1. Data from volunteer-4. **a)** CBFss and **b)** CBFms maps given in units of ml/100g.min. **c)** Transittime map is given in units of seconds. All the images belong to the same slice.

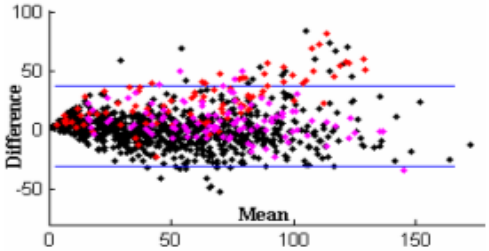

Figure 2. Bland-Altman plot shows (CBFms- CBFss) in y-axis and (CBFms+CBFss)/2 in horizontal. All the pixels in the slice (shown in Figure 1) were included in the graph. Red ones shows δt<150ms, purple ones shows δt>800ms. Blue lines indicate 95% confidence intervals.

Table 1. The first column gives the result of linear regression where $CBF_{ms} = a*CBF_{ss} + b$ and r is correlation coefficient. Other columns state the mean of the differences given the conditions below where Diff = CBF_{ms} - CBF_{ss}.

Subject #	a& b | r	Mean(Diff) All	Mean(Diff) δt < 150ms	Mean(Diff) δt > 800 ms
1	1.06 & 5.9 | 0.82	8.2	17.1	13.2
2	1 & 4.8 | 0.8	5.1	13.9	3.4
3	0.94 & 8.5 | 0.85	5.7	13.5	11.1
4	0.91 & 8.2 | 0.87	3.4	18.1	8.6

References: [1] Wong et. al. MRM 1998 39:702-8, [2] Buxton et al., MRM 1998 40:383-396,[3] Hendrikse et al. Radiology 2004; 233:899–904, [4] Wong et. al. NMR Biomed. 1997 10 237-49, [5] D. Gallichan ISMRM, 2006: 3432, [6] Luh et al., MRM 2000 44:137–143