

Subject-specific AIF optimizes reproducibility of perfusion parameters in longitudinal DSC-MRI in comparison to session and population level AIF

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Introduction DSC-MRI is being used intensively in imaging studies tracking the effect of emerging treatment paradigms such as anti-VEGF therapy in brain tumor patients [1]. It is crucial to the success of longitudinal studies to obtain the best possible intra-patient reproducibility of perfusion indices, such as CBF, CBV and MTT, in order to detect subtle treatment effects. Intersubject differences in systemic circulation necessitate measurement of an arterial input function. However, partial volume and noise in EPI images challenges estimation of the true AIF, and therefore re-estimation of the AIF for each scan may compromise reproducibility. We hypothesize that intrapatient reproducibility is maximized by using a single, patient-specific AIF, in comparison to traditional re-estimation at each scan. Moreover, we hypothesize, that applying a patient specific AIF yields superior reproducibility in comparison to using a population-based reference AIF [2].

Materials and methods

DSC-MRI was performed with a 3T TimTrio Siemens with gradient-echo EPI (TR/TE=1330/34msec) with 128x128 matrix, 1.7mm in-plane- and 5-mm through-plane resolution, as part of a dual echo acquisition. A Gd-DTPA dose of 0.2 mmol/kg was injected at 5cc/s after 85 sec of imaging, with a total imaging time of 2:45 min. Thirty-one adult patients with recurrent glioblastoma received two baseline scans, at approximately day -5 and -1 before receiving anti-VEGF therapy [1]. Due to the short scan intervals and absence of intervening treatment, no change in systemic circulation is anticipated. An AIF was automatically determined for each scan [3,4] and CBF and MTT were calculated in three ways: (a) with the AIF determined at each scan (scanAIF), (b) with the AIF determined at the first scan, representing an AIF particular to the patient (patAIF) and (c) with an AIF obtained as the average over all patients and scans, representing a population based AIF (popAIF). Prior to analysis, the DSC images were motion corrected, partial volume corrected [4] and corrected for contrast agent leakage effects in the tumor [5]. Absolute values of CBF, MTT and CBV were calculated using singular value decomposition with Tikhonov regularization [4,6] and values between visits 1 and 2 were compared for all three methods using Pearson correlation. Imaging analysis was performed using nordicICE (NordicImagingLab AS, Bergen, Norway).

Results

Correlations between perfusion parameters estimated at visit 1 and visit 2 are shown in Table 1. The patAIF method yielded the highest interscan correlations for all perfusion parameters. In contrast, scanAIF showed the lowest correlation values in all parameters, while popAIF showed a better interscan correlation than scanAIF for CBF and CBV. Figure 1 illustrates the reduction in CBF variability obtained using patAIF in tumor (circled) and normal tissue. Moreover, for all perfusion parameters, the lowest bias was observed using patient-specific AIF, as seen in Table 2.

Conclusion In this study we demonstrate substantial improvements in reproducibility by revising the AIF search strategy. By using a single, patient-specific AIF, scan-rescan correlation values as high as of $r=0.89$ was achieved, considerably outperforming a scan-specific AIF ($r=0.29$). Also, a weaker reproducibility was observed using the population based AIF. **References** [1] Batchelor, Cancer Cell 2007. [2] Parker MRM 2006. [3] Mouridsen, MRM 2006. [4] Bjørnerud JCBFM 2010. [5] Boxerman AJNR 2006. [6] Hansen SIAM J Sci Comput 1993

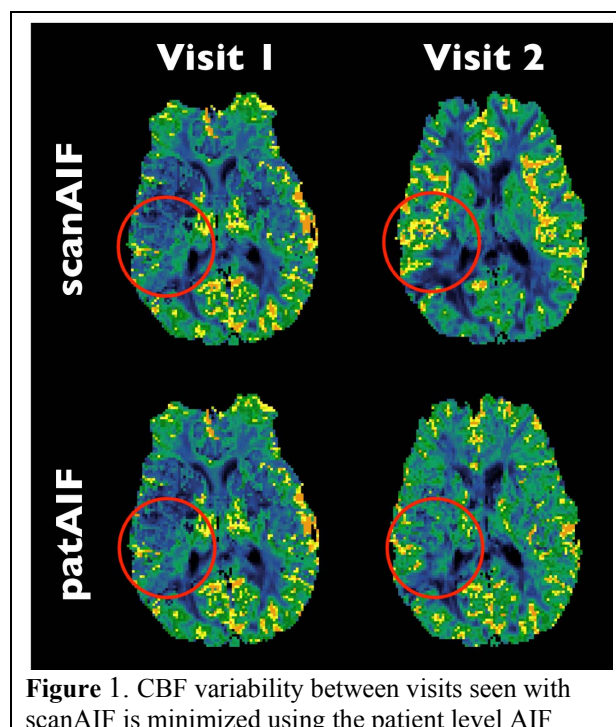


Figure 1. CBF variability between visits seen with scanAIF is minimized using the patient level AIF

	Scan	Patient	Population
CBF	0.29	0.89	0.72
MTT	0.36	0.71	0.26
CBV	0.42	0.74	0.71

Table 1. Correlations between visit 1 and visit 2

	Scan	Patient	Population
CBF	7.02 ± 29.01	-1.75 ± 15.19	-3.08 ± 10.21
MTT	-0.78 ± 1.91	-0.19 ± 1.35	0.42 ± 2.31
CBV	0.15 ± 1.71	-0.08 ± 1.18	-0.18 ± 0.99

Table 2. Mean difference ± standard deviation between visit 1 and visit 2