A patient-specific global residue function improves reproducibility in longitudinal monitoring of perfusion changes in low-grade gliomas

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Introduction: In longitudinal monitoring of tumor growth and progression by MRI, reproducibility between consecutive patient scans is crucial. In DSC-MRI, although automatic methods have improved the reproducibility of the arterial input function (AIF) selection [1,2], re-estimation of the AIF at each scan may induce unwanted variations in the hemodynamic response making detection of often subtle differences in tumor status difficult. In our study, we hypothesize that a global patient-specific residue function can be estimated which define the mean patient-specific hemodynamic properties in unaffected white- and grey-matter tissue. Once these parameters are known and the arterial input function (AIF) is measured at one time-point, the corresponding AIF in later scans can be estimated from the difference in global tissue response compared to the reference scan.

Materials and methods: The global residue function is related to the global tissue response and measured AIF according to: $C_g^{ref}(t) = F_g R_g(t) \otimes C_a^{ref}(t)$, where ⊗ is the convolution operator, $C^{ref}_g(t)$ is the global tissue response in unaffected tissue in the reference scan, $C^{ref}_a(t)$ is the corresponding AIF, F_g is global mean perfusion and $R_g(t)$ is the global tissue response function. F_g and $R_g(t)$ can then be estimated using standard deconvolution methods and the AIF in subsequent scans can be estimated from: $C_g^i(t) = F_g R_g(t) \otimes C_a^i(t)$,where $C_g^i(t)$ is the global tissue response. $C_a^i(t)$ is the (unknown) AIF for any subsequent scan, which can then be estimated from deconvolution. The session specific AIF can then be used to estimate tumor perfusion values and residue functions at each specific session. In 6 adult glioma patients with a minimum of 4 longitudinal scans, unaffected tissue used as basis for the global residue function was identified automatically in the first visit of each patient using cluster analysis and deconvolution was performed using singular value decomposition (SVD) with Tikhonov regularization[2]. Using the global residue method and a traditional scan-specific AIF method, values of CBV and CBF were derived at each visit.

Results: Figure 1 show comparisons between CBV values normalized to the first visit for a traditional scan-specific AIF selection and the global residue method, respectively. Across the 6 patients, the coefficient of variation (CV) for CBV ranged from .01 to 0.03 using the global residue method and from .25 to .47 for the scan-specific AIF. Similarly, for CBF, the CV ranged from .03 to 0.15 for the global residue method and from .05 to .42 for the scan-specific AIF.

Discussion: The proposed patient-specific global residue method may have advantages compared to using a scan-specific or population-based AIF in that any potential scan-specific variations in the AIF (due to changes in systemic circulation or injection rate) is corrected for and does not affect the resulting perfusion estimations. It should be noted that mean perfusion values in unaffected tissue was assumed to be relatively constant over time compared to changes in the tumor. In a clinical setting, this may be a plausible assumption in the follow-up of untreated patients with low-grade gliomas.

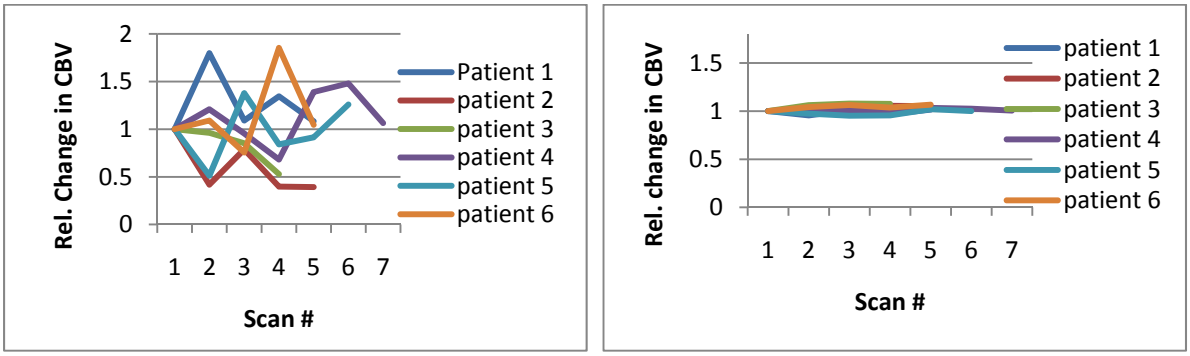

Figure 1: Left: CBV values normalized to the first visit using a traditional scan-specific AIF selection. Right: Corresponding CBV values when using the global residue method. For both CBV and CBF, the range of the coefficient of variation was considerably reduced when using the global residue method.

[1] Mouridsen et al, MRM 2006;55(3):524-31, [2] Bjornerud et al, JCBFM 2010;30(5):1066-78