Correction algorithm for singular value decomposition artifact in quantitative cerebral perfusion images using SCALE-PWI

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INTRODUCTION

Quantitative cerebral perfusion has been achieved via the Bookend technique [1,2] using dynamic susceptibility contrast (DSC) MRI and T_1 changes in normal white matter (WM) in relation to the changes in the blood pool in a calibration slice, after contrast injection. Quantitative cerebral blood flow (qCBF), quantitative cerebral blood volume (qCBV) and mean transit time (MTT) measured by the Bookend technique have been proven reproducible, reliable and accurate [3]. An accelerated and simplified version of the Bookend protocol has been achieved through a Self-CALibrated Epi Perfusion Weighted Imaging (SCALE-PWI) MRI pulse sequence [4], which combines three Bookend scans into one. Improvements to SCALE-PWI imaging protocol and perfusion image reconstruction have just been reported [5]. A correction method for an additional artifact is presented in this work. This consists of a singular value decomposition (SVD) algorithmic artifact due to the interleaved (odd/even) order of slice acquisition of the dynamic susceptibility contrast (DSC) images, which introduces apparent changes, by fractions of TR, in the arrival time of the contrast bolus to each slice in the brain with respect to the arterial input function (AIF). It normally causes alternating signal intensity modulation in the reconstructed quantitative perfusion (qCBF, qCBV and MTT) maps of consecutive slices. This artifact could be unnoticeable when looking at relative perfusion maps, but it is more of a problem when dealing with quantitative perfusion parameters, and could be misleading in some cases whereby accurate patient diagnosis is needed.

MATERIALS AND METHODS

Imaging Protocol

A total of twenty-two human subjects were scanned with the SCALE-PWI sequence on a 1.5 T MR scanner (MAGNETOM Espree, Siemens AG Healthcare Sector, Erlangen, Germany). These subjects were randomly selected to be scanned with two different delay times between consecutive SCALE-PWI modules: 0 s and 20 s. The SCALE-PWI imaging parameters were: TE/TR = 34/1090 ms, flip angle = 20º, FOV = 220 mm x 220 mm, slice thickness = 5 mm, resolution = 128 x 128, GRAPPA with acceleration factor = 2, for 13 slices in the brain and a total of 50 measurements. Images were acquired with a single-dose injection of Gd-DTPA (0.1 mmol/kg b.w.) at a rate of 4 ml/s. In this setting, 35 time series of LL measurement for T_1 mapping were acquired after each IR pulse for a single "calibration" slice, with a time gap between acquisitions = 84 ms. The SCALE-PWI scan was preceded and followed by a segmented LL-EPI scan of the same "calibration" slice, according to the conventional Bookend protocol, in order to obtain a reference calibration for the relative DSC perfusion measurements.

Correction Algorithm and Image Postprocessing

The correction algorithm was implemented in MATLAB V7.2 as part of our fully automated perfusion reconstruction code [3], and was then ported into SCALE-PWI Siemens Image Calculation Environment (ICE) inline perfusion reconstruction algorithm. This algorithm selects voxels, belonging to one slice only, whom signal vs. time curves best represent an AIF signal, and averages these signals out to be used as the AIF signal. A gamma variate fit of the concentration-time curve of the average AIF signal is performed. Then, a time-shifted version of the fitted AIF model, by an appropriate fraction of TR, is created for each of the acquired brain slices, following the interleaved order of slice acquisition. The algorithm takes into account the different cases whereby the AIF is chosen from an odd- or even-numbered slice. Each AIF version is then used to deconvolve the concentration time curves of all the voxels belonging to its corresponding slice. The direct effect is the elimination of the signal intensity artifact in the resulting perfusion maps.

RESULTS

Figure 1 shows MTT maps, in a representative subject, that demonstrate the correction effect, ranging from -2.11 to 29.42% for this subject. The effect is greatest in slices that are acquired at later times from the AIF slice (slice 5 for this subject) acquisition time, and increases with the interleaved order of slice acquisition (odd then even numbered slices), as shown in Figure 2. The alternating signal intensity modulation is reduced by the correction. A Student's *t* test performed on one set of 11 subjects to compare mean MTT values in slices that are 3 samples away from the AIF slice in the order of slice acquisition resulted in $p=9.02\times10^{-8}<0.05$ and $r=0.996$, indicating statistically significant differences between values measured before and those measured after correction, at the 5% significance level. MTT values in the AIF slice did not vary at all in any subject due to correction, which is expected by the algorithm. Finally, correlational analyses between SCALE-PWI and the reference Bookend protocol measurements of qCBF and qCBV values, in white matter (WM) and gray matter (GM) ROIs, resulted in similar, excellent correlations before and after applying the correction algorithm. For the 0 s delay group of subjects, qCBF before correction: slope/r = 0.92/0.95, and after correction: slope/r = 0.89/0.95; qCBV before correction: slope/r= 0.89/0.92, and after correction: slope/r = 0.88/0.92. For the 20 s delay group, qCBF before correction: slope/r = 0.96/0.95, and after correction: slope/r = 0.99/0.94; qCBV before correction: slope/r = 0.95/0.92, and after correction: slope/r = 0.95/0.92.

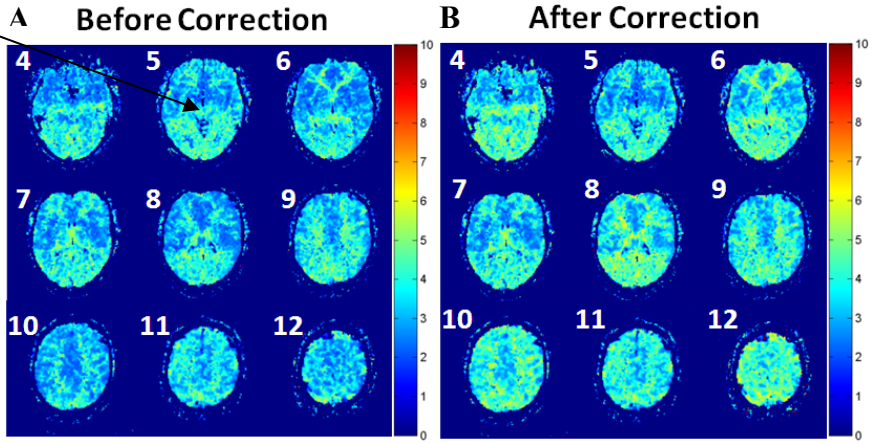

Figure 1. *MTT maps (in seconds) for slices # 4 through 12 before (A) and after (B) applying the correction algorithm in a representative subject, obtained from the DSC module of SCALE-PWI which was used to compute both SCALE-PWI and reference perfusion measurements.*

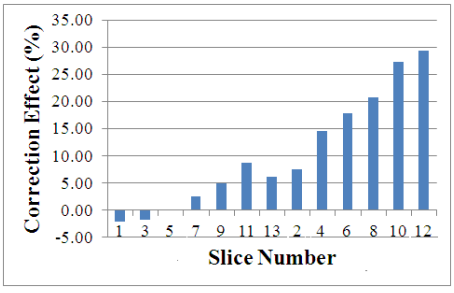

Figure 2. *Increasing correction effect, measured as a percent change in mean MTT value in each given slice due to the correction, when moving away from the slice where the AIF was selected (slice 5) based on the interleaved order of slice acquisition.*

CONCLUSION

We have demonstrated the significant efficiency of the intensity modulation correction algorithm which makes SCALE-PWI quantitative perfusion maps more accurate and less misleading for radiologists who are trying to get immediate and accurate diagnosis following a SCALE-PWI scan.

REFERENCES

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