Robust DSC-MR Perfusion Using a Patient Motion Correction Scheme

R. K. Kosior[1,2], J. C. Kosior[1,2], and R. Frayne[2,3]

[1]Electrical and Computer Engineering, University of Calgary, Calgary, Alberta, Canada, [2]Seaman Family MR Centre, Foothills Medical Centre, Calgary Health Region, Calgary, Alberta, Canada, [3]Radiology and Clinical Neurosciences, Hotchkiss Brain Institute, University of Calgary, Calgary, Alberta, Canada

Introduction

Dynamic susceptibility contrast (DSC) MR perfusion imaging reveals blood flow in brain tissue by tracking a contrast agent bolus with a 4D image series (3D volume with time).[1] Patient-motion during a DSC-MR exam causes mixing of temporal signals and adjacent tissue locations in the brain, which compromises the accuracy of quantitative cerebral blood flow (CBF). For example, the arterial input function (AIF) used to derive CBF via deconvolution is chosen from an artery (small region) and can become distorted by patient-motion from partial volume effects (PVE) with surrounding tissue, leading to errors across derived CBF maps.[2] Using data from stroke patients and a digital brain phantom, we investigated the effect of motion on CBF maps and evaluated the efficacy of a realignment scheme to salvage motion-corrupted DSC-MR data.

Methods

DSC-MR data from nineteen ischemic stroke patients exhibiting motion were selected for analysis. The data was acquired using gradient-echo echo planar imaging (GE-EPI) 2D sequences with TR/TE/flip angle = 1750 ms to 2000 ms/30 ms to 45 ms/45º, 160 × 96 or 144 × 144 acquisition matrix, 32 cm × 19.2 cm or 24 cm × 24 cm FOV, 5 mm slices with a 0 mm to 2 mm gap. We used a digital anthropomorphic phantom to estimate accuracy with "true" motion-free data.[3] Each voxel had a known DSC-MR signal based on tissue PVE derived from a normal subject. The phantom incorporated noise (signal-to-noise ratio of SNR = 40 in white matter, WM) and an ischemic region (co-registered from a stroke patient). Three motion profiles were investigated: (a) A simulated motion profile, generated by misaligning the original phantom data series in the para-axial plane to a maximum x-translation of 7.5 mm and z-rotation of 5° in order to keep the posterior part of the brain relatively stationary and to coincide with the passage of the contrast bolus, as observed in many patient data sets. (b) A patient motion profile, generated by applying the realignment parameters from one of the patients to the phantom data. (c) Motion free data (for control). To correct motion, registration was performed using SPM2 (FIL Methods Group, UK, 2004) with 6-parameter affine rigid-body registration, a least-squares metric and 4th-degree B-spline interpolation. The third image volume in the DSC-MR series served as the reference image. CBF maps were generated for both motion-corrupted and corrected data from patient and phantom DSC-MR data sets using PerfTool[4] by selecting an AIF from the middle cerebral artery and then cross-calibrating so that WM was 22 ml/min/100 g.[5] The 6 registration parameters were recorded for each patient registration as a function of time and the standard deviation (SD) for each parameter was calculated. Mean CBF was recorded in regions drawn in normal grey matter (GM) for all DSC-MR data and in the core of the ischemic lesion (IL) for patients exhibiting a visible ischemic region on the CBF map (WM not considered due to cross-calibration).

Results

Eleven patients exhibited ischemic lesions and 9 patients exhibited motion during the initial bolus passage. All patients exhibited visibly reduced inter-volume misalignment after motion correction. Patient results were grouped into two categories: severe motion (9 patients, 6 visible IL) and minor motion (10 patients, 5 visible IL) based on the average translational and rotational SD of realignment. In most patients, improved flow delineation between WM and GM and a more clearly defined IL were achieved in the motion-corrected CBF maps (Fig a, b). The motion-corrected data exhibited more realistic AIF signals likely due to a reduction in temporal PVE. Quantitatively, the greatest difference occurred in GM, followed by IL with average absolute differences of 6.1 ml/min/100 g and 3.4 ml/min/100 g for severe motion and 4.2 ml/min/100 g and 1.2 ml/min/100 g for minor motion, for GM and IL respectively. Degraded depiction of WM/GM boundaries, and reduced IL conspicuity were seen in the phantom motion CBF maps, as with the patient data (Fig c). In the simulated motion profile data, a large difference in the GM was observed (-10 ml/min/100 g) while all other values were within 2.5 ml/min/100 g of truth. However, as illustrated by the line profiles, a large deviation from truth is observed at tissue/flow boundaries (Fig c, d). Registration error was minimal for the phantom datasets (<0.57 mm translation, <0.35° of rotation).

Conclusions

Motion-corrupted data caused mixing of tissue signals, reducing the presence of meaningful AIF signals and reducing flow differentiation in quantitative CBF maps between adjacent tissues. The proposed motion correction scheme improves both the quantitative accuracy and image quality across the entire CBF map and can be used to salvage DSC-MR data corrupted by patient-motion for improved diagnosis.

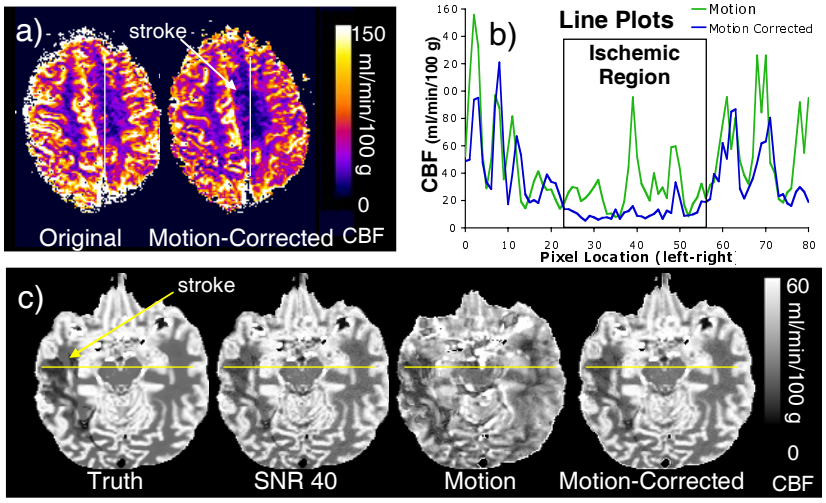
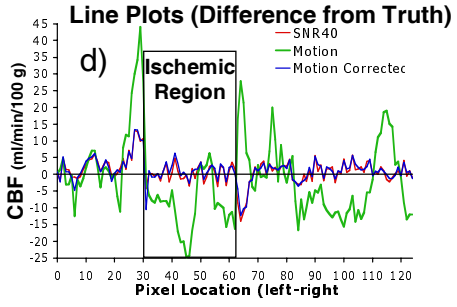


Fig. As seen in the patient example (a,b), the motion-corrected CBF map has a larger, more severe ischemic region with more clearly defined tissue boundaries compared to the motion-corrupted CBF map. Phantom CBF maps of truth, SNR 40, simulated motion and motion-corrected data (c). Line profiles are shown graphically as the difference from truth (d). Motion correction mostly eliminated mixing of flow regions and errors at tissue boundaries.



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