Slice-by-slice prospective hardware motion correction in EPI and simultaneous multislice sequences

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Target Audience Researchers using EPI based sequences (BOLD/diffusion), particularly those studying populations that exhibit head motion.

Purpose

A considerable amount of recent research has shown that head motion can cause spurious group differences in functional[1-3] as well as structural[4] connectivity analyses. These differences persist even in the presence of compensatory retrospective techniques (such as volume-based retrospective motion correction and regression of motion estimates). Both analysis techniques rely on MRI data acquired with an echo planar imaging (EPI) readout. This abstract examines slice-by-slice prospective hardware motion correction in EPI based sequences in order to mitigate such spurious group differences.

Methods

A system designed for interventional-MRI tool tracking (Endoscout; Robin Medical, Baltimore MD) has been repurposed to track head motion. A sensor, which consists of 3 orthogonal pairs of parallel coils, is attached to the subject's head. The sensor's position can be inferred by using the scanner's gradients to create a time-varying magnetic field across the sensors which induce an electric potential in each coil. The sensor is programmed to detect three triangular gradient waves – one on each gradient axis – played with a slew rate of 60mT/m/ms and a total duration of 1.5ms. This sub-block can be inserted into a sequence and the resulting sensor position can be queried from the tracker's server ~5ms later. We have inserted these tracking blips into a BOLD sequence immediately after the EPI readout and query the server for the updated position before the slice selective excitation pulse (see Figure 1). In the present implementation, we require a 12ms gap between the tracking blip and position update. This is mostly due to inter-process synchronization issues in our communications routines, and we expect this delay to be substantially reduced with further optimization. In order to compensate for this time penalty, we have also modified a simultaneous multislice (SMS) BOLD sequence[5] in a similar fashion. We have tested both sequences using a phantom (pineapple) on a 1.5 T Avanto (Siemens Healthcare, Erlangen, Germany) using the product 32-channel head matrix. A sensor was attached to a pineapple, which was in turn attached to a device that allows them to be rotated by 8°. One hundred volumes were acquired with each sequence (BOLD, SMSx3-BOLD) while performing a rapid 8° rotation every 30s. The BOLD sequence had a 4000ms TR and a 90° flip angle. The SMS-BOLD sequence had a 2000ms TR, 90° flip angle and slice acceleration factor of 3. Both sequences shared the following parameters: 30ms TE, 51 slices, 2442 Hz/px bandwidth and an in-plane imaging matrix of 64x64. We compared the temporal signal to noise ratio (tSNR) of the resulting timeseries without any motion (nomove) to timeseries with motion compensated using our motion tracking method (scout), Siemens' prospective and retrospective volume-based motion tracking (pace-pro, pace-retro) as well as no motion correction at all (nomoco). After our initial experiment, we observed that the penalty to tSNR incurred by susceptibility due to motion was larger than the penalty due to the motion itself. We therefore designed another condition to measure the tSNR loss due to susceptibility alone (without motion). First, the pineapple was shimmed and imaged in position 1 (s1p1). Then the pineapple was rotated 8° and re-imaged with the same shim in the new position (s1p2) before reshimming and imaging once more in the same position (s2p2). The s2p2 series was rigidly registered[6] to the s1p1 series and the resulting transform was used to align and concatenate the s1p2 and s1p1 series. The tSNR of the resulting series was measured (suscept) which allows us to measure the effect of susceptibility, free from the confounds of motion.

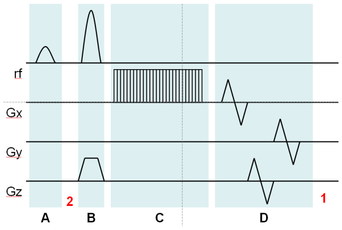

Figure 1: Pulse sequence timing diagram (not to scale). A) fat saturation pulse B) rf excitation pulse C) EPI readout D) Endoscout tracking blips. In the present implementation, we require a 12ms gap between the tracking blips (1) and the position update (2) in the next TR

Results

Table 1 presents the mean tSNR results for our six conditions and 2 acquisition methods. In the standard BOLD condition, when compared to 'suscept', no motion correction incurs a 38.5% penalty to tSNR whereas our 'scout' method only incurs a 7.8% penalty. It is interesting to note that under these conditions PACE performs worse that no motion correction. This is likely due to the difficulty in registering volumes with a considerable amount of non-rigid distortion. In the SMSx3-BOLD condition, when compared to 'suscept', retrospective pace incurs a 23.8% penalty whereas our method incurs a 15.9% penalty. Figure 2 illustrates sample log(tSNR) maps through a single slice.

	BOLD	SMSx3 BOLD
nomove	16.2745	12.6099
suscept	11.5426	9.1842
nomoco	8.3330	6.5534
pace-pro	8.2132	6.6096
pace-retro	7.8504	6.9938
scout	10.6464	7.7252

Table 1: Mean tSNR results for both BOLD and 3x simultaneous multislice BOLD across various experimental conditions.

Discussion

It is interesting to observe that, in these sequences, the reduction of tSNR from motion-induced susceptibility variations is on a similar scale to the loss of tSNR due to the motion-induced misalignment of slices. It is unclear if this is a specific to our choice of phantom; we plan to repeat this experiment with humans as the next experiment. If this finding holds, it may further explain the spurious group differences in structural and functional connectivity analyses that persist despite correcting for and regressing out motion effects.

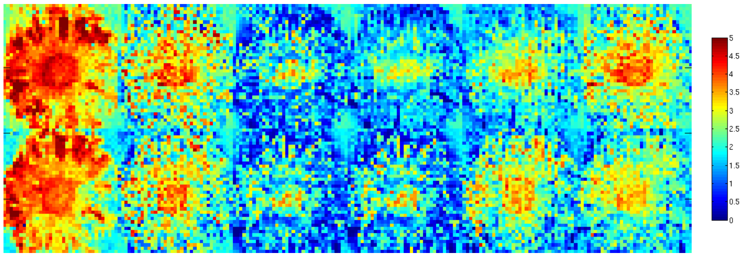

Figure 2: log(tSNR) maps from a representative slice through the pineapple for BOLD sequences (top) and SMSx3-BOLD sequences (bottom). Left to right, the conditions are 1) nomove 2) suscpet 3) nomoco 4) pace-pro 5) pace-retro and 6) scout

References

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