A Biophysical Model for Retrospective Motion Correction in fMRI and a Comparison of Current Methodologies

Target Audience: This presentation will be of most interest to those involved in patient or paediatric research using fMRI where motion control is particularly problematic.

PURPOSE: Currently motion correction approaches applied to the 2D gradient echo EPI typically used to obtain fMRI data do not account for rapid changes in head position that occur at a timescale less than the volume repetition rate (TR). Usually volume to volume spatial realignment is used and the transformation parameters are employed as a model of head motion[1]. In ascending slice-ordered sequences this type of movement can result in slice specific signal drop-out > 30%. This is due to parts of a slice being excited twice in rapid succession with associated spin history effects. While methods exist to correct for these problems, many rely on modelling derivatives of the transformation parameters. However as the resulting regressors are sampled at 1/TR they cannot account for movement effects between volumes. A different approach is to use robust least squares to de-weight entire volumes if their residual variance is high[2]. However in the case of slice specific dropouts the assumption of no spatial structure to the noise is violated and the method is also limited. Therefore we propose to develop a biophysical model that identifies spurious signal variations at every voxel. The model then corrects the time series in order to address the limitations of these other methods

METHODS:

Method Theory: To identify spurious variation a threshold needs to be set in terms of percentage signal intensity change. To estimate the percentage signal intensity change relative to baseline we assume that the Blood Oxygen Level Dependent signal can be modelled according to the following equation: $S = S_{max} * e^{-TE/T2^*}$, where S = BOLD Signal Intensity, S_{max} =100, TE= echo time and T2* = 1/R2 +1/R2', R2 = spin- spin relaxation rate and R2' = relaxation due to magnetic field inhomogeneities. Empirical and theoretical models allow for the estimation of R2 and R2' [3,4]. To make a robust threshold we can estimate $S_{max} * e^{-TE/T2} - S_{max} * e^{-TE/T2^*}$, where T2 =1/R2. The resulting threshold now represents the percentage deviation from baseline that would be observed in the BOLD signal should a voxel be completely depleted of Deoxyhaemoglobin. It is therefore plausible that signals outside this range represent non-physiological signals and artefacts. Once these non-physiological signals are identified they can be spline interpolated to correct them.

The primary limitation of this model is that it will break down in areas where the noise is exceptionally high such as at the edge of the brain and in the veins and arteries. However we can segment these areas from the BOLD images by using the Expectation Maximisation (EM) algorithm on the median/(median absolute deviation (MAD)) image. Once these noisy areas are segmented the first six principal components are extracted. These regressors contain information on pulsatile motion (from the arteries) and of subject head movement (figure 1). They can be included as effects of no interest in one's regression analysis in order to improve one's model of motion.

Retrospective Correction Techniques Comparison: A number of other retrospective motion correction methods were also examined for the purpose of comparison. The other methods included were: Robust Weighted Least Squares (RWLS)[2], Motion Fingerprint (MF)[5], Realignment Parameter Expansion(RPE)[1,6] and simply including the realignment parameters as effects of no interest in the GLM.

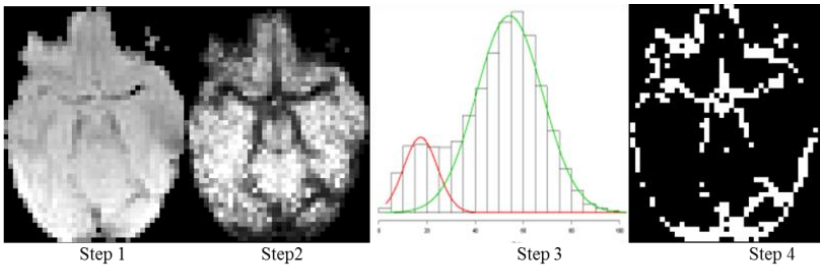

Figure 1. Step 1: The median image is calculated. Step 2: Divide by the MAD image. Step 3 segement using EM. Step 4: Extract principal components from the resulting mask. A lower axial slice is shown to demonstrate the ability to observe both the Circle of Willis and the Transverse sinus

Data Collection: Data was collected from 42 children aged 6-18 while performing a listening comprehension task. This task was chosen as there was a strong a priori hypothesis about what constituted the ground truth (Bilateral superior temporal gyrus, left inferior frontal, bilateral cerebellum, left temporal pole, bilateral supplementary motor area) and the data was severely corrupted by motion artefacts. The data was obtained using a 1.5T Siemens Avanto scanner, TR = 2.16s, TE=30 ms, FOV=210mm, flip angle=75 degrees, number of slices=30, slice thickness= 3mm, slice gap=1mm. There were 212 volumes acquired using continuous image acquisition, covering the brain with resolution 3.3 x 3.3 x 4mm.

RESULTS: Figure 2 displays a comparison of the 5 different methods examined. It was found that both RPE and MF had a negative impact on the group map as far fewer voxels were identified in the a priori specified regions of interest compared to the standard GLM, most notably below in the bilateral superior temporal gyri and the lack of activation in the left inferior frontal gyrus. RWLS recovers some activation in the inferior frontal gyrus but the extension of the superior temporal gyrus to the temporal pole is lost. Furthermore the activations do not follow the shape of the cortex and present with a number of false positives in the white matter. The method which uses the biophysical model performs qualitatively best as it recovers a substantial amount of the inferior frontal gyrus which none of the other methods do. This method also strengthens the activations identified using the standard GLM. All clusters in the Biophysical approach display larger local maxima than all the other methods in the a priori specified regions of interest.

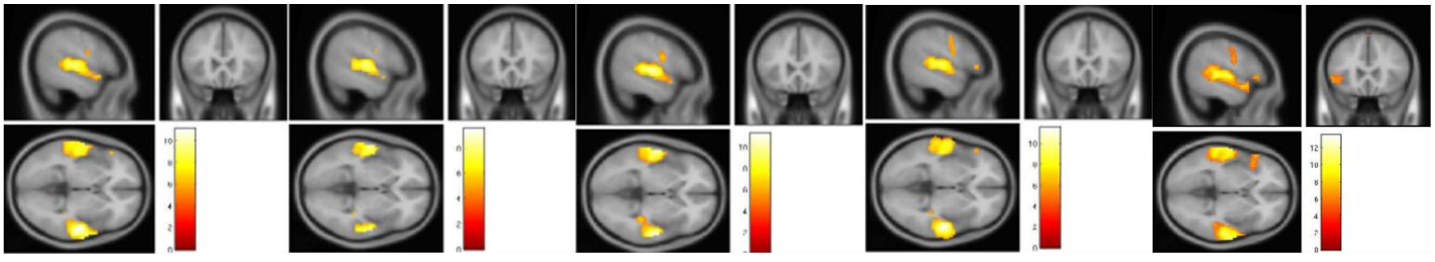

Figure 2. Comparison of retrospective motion correction techniques. The t-maps are overlaid on a normalised T1 and are thresholded at FWE(p<.05)

To assess the impact of the model quantitatively we calculated mutual information between each individual t-map and the group map. The resulting method would therefore represent how the method changes the inter-subject variability in activations. Mutual Information (MI) was calculated between the group t-maps of the corrected and uncorrected datasets and their respective first level t-maps. The effect size, r, was calculated [7]. The mean of the difference was .118 (95% CI = .095, .141), t (41)= 10.311, p < .05, r = .845.

DISCUSSION: The method proposed results in a substantial qualitative (recovery of inferior frontal gyrus) and quantitative improvement (increased local maxima and lower individual variability). However it must be noted that while a comparison of methodologies is presented this method is not directly competitive with these other methods. It can be used in addition to the others reviewed. The primary limitation of this method is the direct imputation of values due to interpolation. For future work it may be worthwhile to consider multiple imputation as opposed to spline interpolation.

CONCLUSIONS: The proposed method can improve severely corrupted datasets. This has direct clinical relevance in the presurgical evaluation of patients who need to undergo either language or motor mapping such as those with focal epilepsy.

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