

Removal of Residual Motion Artifacts in fMRI using Constrained Independent Component Analysis

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Introduction: Image registration of fMRI data only corrects for bulk movements while leaving secondary artifacts such as, - spin history effects, motion induced dynamic field inhomogeneity changes, and interpolation errors - untouched. Secondary artifacts increase variability in time-series and reduce sensitivity of activation detection. Methods such as the use estimated motion parameters as “Nuisance Explanatory Variables” (NEV) in a General Linear Model (GLM), [GLM+NEV] [1], or use of Independent Component Analysis (ICA) [2,3] to isolate and remove motion related components are commonly used to remove residual motion artifacts after image registration. Use of ICA, while very effective, is a two stage process involving, first, isolation and subsequent identification of motion components before removing them. The identification step can be tedious and time consuming as one has to manually inspect or use a similarity measure to identify/isolate components that are due to motion. However, ICA does have an advantage over use of motion parameters as NEVs in GLM. ICA is able to better isolate sources or components that are related to motion in a possibly non-linear and unpredictable fashion namely, interactions of susceptibility induced field inhomogeneity with motion, interpolation artifacts and other structured noises [2,3,4]. Thus, it is potentially a more complete method of correcting for residual motion artifacts compared to use of GLM+NEV. In this study, we used temporally constrained ICA (cICA) [5,6] to combine isolation and identification of residual motion artifact components into a single step using estimated motion parameters as references for the cICA algorithm. We also explored whether use of cICA with motion parameters as references improved quality and completeness of removal of residual motion artifacts in BOLD fMRI.

Methods: Separate scans, each 200 seconds long, were acquired while four volunteers performed a visual motor task inside the scanner. Each scan consisted of five 40-second cycles of alternating task and control periods. Each volunteer was instructed to intentionally move their head during the scans. These motion corrupted images in the time series were then realigned using MCFLIRT utility of FSL [7]. Statistical parametric analysis was carried out on the realigned images in four different ways.

- i) **GLM:** Activation parameters were estimated using a GLM as implemented in FEAT utility of FSL.
- ii) **cICA:** Six estimated motion parameters were used as references for cICA algorithm to isolate components most correlated to motion. These components were then removed and the rest combined to obtain a time series of images with reduced residual motion artifacts.
- iii) **GLM+NEV:** Similar to “GLM” method however estimated motion parameters were included as NEVs in the GLM design matrix.
- iv) **cICA+NEV:** Same as in **cICA** but, motion parameters were included as NEV in the GLM matrix for estimation of statistical parameters.

A **z-threshold of ≥ 3.5** was used to identify active pixels. Active pixels in the brain were aggregated into a histogram with ten bins over a range of z-scores, 3.5 up to max z-score value. Number of active pixels at each bin was added cumulatively to generate a graph that showed the incremental number of active pixels at each bin (z-score value) and the total number of active pixels detected thus far – the final data point represents the sum of all active pixels. These cumulative graphs were compared across the four analysis methods (see figure 1).

Results:

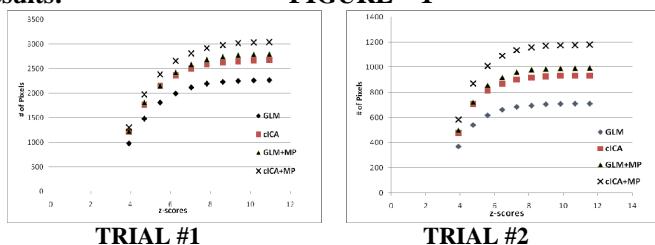


FIGURE – 1

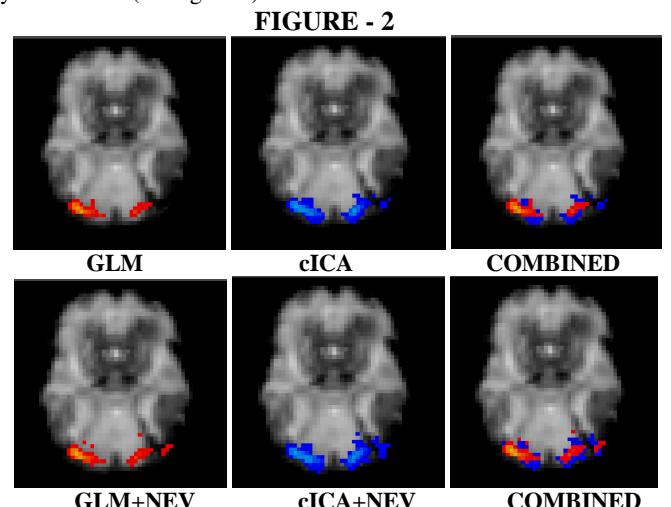


Figure 1: shows the cumulative graphs for two representative independent trials from two subjects for various analysis methods. In both, the total number of active pixels and the z-score of individual pixels show prominent improvements with **cICA** compared to **GLM** method. Further, **cICA+NEV** method showed a prominent increase in number of active pixels and z-scores of individual pixels compared to the **GLM+NEV**

Figure 2: (Top row) shows the active pixels detected with the **GLM** (red) vs. **cICA** (blue) [$z \geq 3.5$] for a slice in the visual cortex near in the lower region of the brain for subject in trial #1. The combined image clearly shows the additional pixels that are detected when cICA method is used to remove residual motion artifacts. (Bottom Row) compares the **GLM+NEV** (red) vs. **cICA+NEV** (blue) methods. Like the top row, the combined image shows the effectiveness of the **cICA+NEV** methods over the **GLM+NEV** as evident by the additional pixels detected.

Discussion: Our studies indicated that in use of cICA to remove residual motion components followed by a GLM+NEV analysis on the resulting time-series is more efficient and effective in isolating residual motion artifacts compared to using just GLM or GLM+NEV method. Use of cICA and cICA+NEV methods is better able to isolate linear and non-linear secondary image artifacts. This is evident from increased active pixels detected in the lower brain slices (figure 2). If left uncorrected, residual motion artifacts from motion induced field inhomogeneity changes are more likely to contribute to larger variances in time series in these lower slices and reduce sensitivity of detection. Further, cICA does not require an additional step of manual identification of the error components as with use of ICA only. In conclusion, cICA method significantly improves the sensitivity of detection of active pixels compared to GLM or GLM+NEV methods and, it does so more efficiently than traditional ICA methods.

References & Acknowledgements: [1] HBM 27(10), 2006, p.779-88. [2] HBM 6(3), 1998, p. 160-88. [3] NeuroImage 17(3), 2002, p. 1521-37. [4] IEEE-TNN, 16(1), 2005, p. 203-12. [5] IEEE. Sig. Proc. Lett. 12(11), 2005, p.792-95. [6] NeuroImage 25(2), 2005, p. 527-38. [7] <http://www.fmrib.ox.ac.uk/fsl/> Funding source: NIH Grant R01EB2683