Complex and magnitude-only preprocessing of 2D and 3D BOLD fMRI data at 7 Tesla

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Introduction

Functional magnetic resonance imaging (fMRI) at ultra high fields facilitates new discoveries about brain function due to increased image signal-to-noise ratio and sensitivity to blood oxygenation level dependent (BOLD) signal changes [1]. However, a challenge with high field fMRI is the predominance of noise associated with physiological processes unrelated to the task of interest (e.g., respiration, cardiac motion/pulsatility, swallowing) [2]. This degradation in data quality may be reversed to some degree by using one or more post-acquisition algorithms designed to estimate and remove the effects of these noise sources. Suppression of aperiodic fluctuations from speaking, swallowing, or abrupt movements may be achieved using the Stockwell transform filter [3,4]. If respiration and cardiac pulsatility are monitored using external equipment, then retrospective image correction (RETROICOR) may be used to suppress these quasi-periodic fluctuations [5]. Finally, if complex data are preserved, then phase regression may also be used for dual purposes of suppressing BOLD signals from large vessels [6] and other sources of noise exhibiting correlated changes in magnitude and phase [7]. Although these algorithms are pseudo-complementary, they have been validated in isolation using only 2D EPI data. Thus, the goals of this work are to implement data-driven metrics to (1) validate the efficacy of Stockwell transform filtering (ST), complex phase regression (PR), and RETROICOR (RI) for use on 3D data and (2) investigate possible synergistic interactions between the sequential application of these algorithms at 7 Tesla.

Methods

Experiments were performed on a Philips 7T scanner with a quadrature transmit coil and 16-channel receive-only head coil. Twelve volunteers (eight females) were studied under a protocol approved by the institutional review board. The visual paradigm was a block design with four segments of 24 sec baseline (central fixation) and 24 sec activation (stationary 8 Hz flashing checkerboard wedge (22.5°) in the left visual field). Slices (2 mm thick) were planned parallel to the calcarine sulcus. Four runs were acquired using two sequences (in alternating order): <u>2D EPI</u>: TR = volume acquisition time (VAT) = 2000 ms, θ = 87°, 96 vols; <u>3D PRESTO</u> [9-11]: TR = 22.22 ms, θ = 12°, VAT = 1 s, 192 vols; <u>common parameters</u>: k-space matrix = 96 x 96, voxel size = 2.19 x 2.19 x 2 mm^3, TE = 28 ms, 12 slices, SENSE factor = 3.2.

ST was implemented in Matlab as described in [4] with the modification that filtering was applied to both magnitude and phase data, PR was implemented in Matlab as described in [6], and RI was implemented using AFNI (`afni_proc.py`) [8]. These three steps were either applied or not applied, resulting in 2^3 = 8 combinations. Data from each combination were then spatially smoothed (SS) with one of three levels appropriate for group analyses (low (L) = 8 mm full-width-at-half-maximum (FWHM); medium (M) = 12 mm FWHM; high (H) = 16 mm FWHM), resulting in a total of 24 pipelines (12 magnitude-only and 12 using phase information). Finally, data were transformed into MNI space (ICBM-152) with 2 x 2 x 2 mm^3 voxels for group analyses.

The quality of fMRI data was evaluated via metrics of *prediction* and *reproducibility* using NPAIRS[†] (<u>N</u>on-parametric <u>P</u>rediction, <u>A</u>ctivation, <u>I</u>nfluence and <u>R</u>eproducibility re-<u>S</u>ampling) [12,13]. Reproducibility ($r \in [0,1]$) measures the similarity (Pearson correlation coefficient) of activation maps generated from two independent data sets, and prediction ($p \in [0,1]$) evaluates the degree to which a trained model can assign correct class labels to an independent test set. NPAIRS currently uses principal component (PC) analysis to reduce the dimensionality of the data followed by split-half resampling and canonical variate analysis. Reported values for prediction and reproducibility are the median values across split-half samples for the range of PCs selected to jointly maximize prediction and reproducibility for each acquisition-processing pipeline.

Results

Figure 1 plots prediction vs. reproducibility for NPAIRS analyses of (A) 2D EPI data and (B) 3D PRESTO data, where noiseless fMRI data with a perfect model would be mapped to the point (1,1). Each 'x' represents a magnitude-only pipeline, and the 'o' of the same color and size represents that pipeline with PR. The inclusion of PR decreased the Euclidean distance d from (p,r) to the ideal point at (1,1) in 11/12 pipelines for EPI and 6/12 pipelines for PRESTO. Of the 6 pipelines where PR increased d, 4 were with SS=L, 1 with no processing and SS=M, and 1 with no processing and SS=H. For EPI data, the optimal preprocessing pipeline (i.e., minimum d) was PR+RI with SS=H ($d \approx 0.22$), and for PRESTO data the optimal pipeline was ST+PR+RI with SS=H ($d \approx 0.31$).

Discussion

The results for EPI data (Fig. 1A, $r \approx 0.9$) confirm a report [7] observing increased t-statistics when PR is included in the preprocessing pipeline. The ST, RI, and ST+RI pipelines decreased d for all SS, showing that these algorithms are, as expected, effective in suppressing physiological noise in EPI data. For PRESTO data (Fig. 1B), the RI and ST+RI pipelines decreased d for all SS; however, an interaction is observed as ST alone slightly increased d for SS=L and M, but decreased d for SS=L.

This report explores the dependence of physiological noise suppression on *a priori* decisions that pertain to data acquisition. If MR data are magnitude-only and physiological monitoring equipment is not used (or not available), then only 2 of these 8 pipelines (none, ST) may be used; if MR data are magnitude-only but physiological processes are monitored, then 4 pipelines are possible (none, ST, RI, ST+RI); if complex data are retained but physiological processes are not monitored, then 4 pipelines are also possible (none, PR, ST, ST+PR); and only if both complex data are retained and physiological processes are monitored are all 8 pipelines possible. The minimization of d with both PR and RI demonstrates the synergy between algorithms and the importance of retaining complex data and using physiological monitoring equipment to improve fMRI data quality. Future work will investigate the SS interactions for PRESTO as well as explore possible explanations for differences (as per Fig. 1) in how these algorithms affect prediction and reproducibility in 2D and 3D data at 7T.
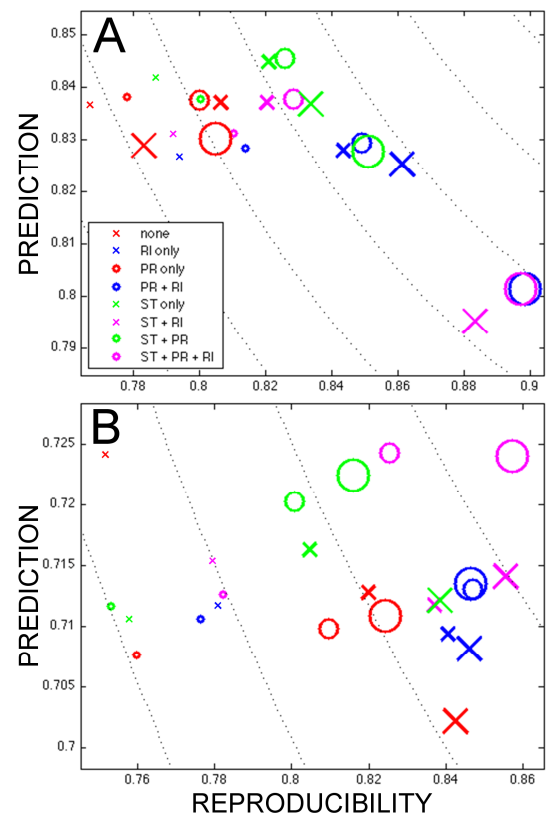

Fig. 1: Plots of prediction vs. reproducibility for data acquired with (A) 2D EPI and (B) 3D PRESTO. The processing pipeline represented by each symbol is defined in the legend. The SS kernel used is represented by the size of the symbol (small=L, medium=M, large=H). Each concentric dotted curve is equidistant to perfect reproducibility and prediction at (1,1).

References

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