Optimal Singular-Value Shrinkage for fMRI Denoising

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Synopsis

Singular-value truncation techniques have shown promise for reducing thermal noise in fMRI, where singular-values below a certain threshold are assumed to be noise and are discarded. However, this approach could lead to suboptimal signal recovery, since the remaining singular-values could still have variance contributed by noise. Here instead we propose to use a theoretically MSE-optimal function to shrink the remaining singular-values. The proposed method is evaluated using simulations and high-resolution in-vivo human brain data, and is shown to improve signal-to-noise ratio and functional statistics while leaving the spatial precision intact.

Introduction

Thermal noise —that under linear image reconstruction is assumed to be zero-mean complex Gaussian distributed— can dominate the fMRI signal at high imaging resolutions (e.g., in laminar fMRI)¹. This motivates the development of denoising methods to extract the relevant signals from noisy, complete measurements. A recently proposed promising method, NORDIC², works by singular-value hard-thresholding (SVHT) of spatiotemporal matrices formed by image patches. Presuming that small singular-values should only be contributed to by noise, NORDIC truncates singular-values below an empirical threshold found using a Monte-Carlo simulation.

However, any choice of a hard threshold would lead to suboptimal denoising because the remaining components could still be biased by noise. Effectively, SVHT would result in the best low-rank estimate of the noisy matrix, while leaving the problem of estimating the true underlying data matrix unanswered. This issue is even more pronounced in an ultra low-SNR regime where thermal noise could also inflate a considerable number of retained singular-values.

Instead we propose to apply a function to shrink the remaining singular-values. In the context of random matrix theory, recently a shrinkage function has been proposed that can guarantee optimality in the MSE sense⁴. Here, we used preprocessing steps similar to NORDIC to make the thermal noise identically distributed, but then unlike NORDIC, we used this shrinkage function to deflate the singular-values in each spatiotemporal patch. The proposed method is evaluated using simulations and high-resolution 7T human fMRI data where it shows improved performance compared to NORDIC, without introducing extra spatial smoothing penalties.

Methods

We consider the reconstructed complex-valued volumetric fMRI image series $m \in \mathbb{C}^{N_xN_yN_zN_t}$ where N_x, N_y, N_z are spatial dimensions, and N_t is the number of time frames. For each voxel a $p_x p_y p_z$ image patch at each time frame $\tau = 1...N_t$ is vectorised to y_τ . These vectors are then used to generate a noisy data matrix $\mathbf{Y} \in \mathbb{C}^{MN_t}$, where $M = p_x p_y p_z$.

Normalising the data by the g-factor maps estimated separately makes the thermal noise independent identically distributed (iid) across the field of view³. Then, assuming the noise matrix \mathbf{Z} to have entries with zero mean and unit variance, the denoising problem is to recover the underlying data matrix \mathbf{X} by minimising the mean-squared error $||\mathbf{X} - \hat{\mathbf{X}}||_F^2$, where $\hat{\mathbf{X}}$ is the estimated data, under the model $\mathbf{Y} = \mathbf{X} + \mathbf{Z}$.

Take $\mathbf{Y} = \sum_{i=1}^m y_i v_i u_i$ for the Singular-Value Decomposition of \mathbf{Y} , where v_i and u_i are the right and left singular vectors corresponding to the singular-value y_i . We wish to use a shrinkage function $\eta(y)$ such that the estimate $\mathbf{\hat{X}} = \sum_{i=1}^m \eta(y_i) v_i u_i$ is MSE-optimal. It has been shown that such a function is well defined and can be expressed as $\mathbf{\hat{X}} = \mathbf{\hat{X}} = \mathbf{\hat{X}}$

$$\eta(y) = \begin{cases} \frac{1}{y} \sqrt{(y^2 - \beta - 1)^2 - 4\beta} & y \ge 1 + \sqrt{\beta} \\ 0 & y < 1 + \sqrt{\beta} \end{cases}$$

where $\beta = M/N_t$ (Fig. 1). For the general case of noise level σ , calibrated shrinker $\eta_{\sigma}(y) = \sigma \eta(y/\sigma)$ should be used⁴.

In a simulation experiment, 120 frames of a 217x181x10 dimensional noise-free simulated phantom data were corrupted by iid Gaussian noise with zero mean and standard deviation $\sigma \in \{0.08...0.16\}$ relative to signal strength. A patch size of 5x5x5 was used. MSE was compared between NORDIC and the proposed approach.

Furthermore, in-vivo fMRI data from a block-design (30secs on/off) experiment with flickering checkerboard visual stimuli were acquired on a 7T scanner with parameters: 3D GE-EPI, 32channel head coil, 0.67mm isotropic voxels, 28 slices, 128 volumes, R=4 iPAT, TR/TE=2400/30, FA=20°, 288x214 matrix size. Data in each channel were denoised individually and then combined, and the GLM models were fit. We evaluated the proposed method against NORDIC by comparing temporal signal-to-noise ratio (tSNR), model goodness of fit, z-statistics, and smoothness of the residual field.

Results

Figure 2 shows the simulation results. The proposed method performs better than NORDIC denoising in reducing the MSE, at all tested noise levels.

Figure 3 shows the tSNR improvement in the in-vivo dataset. This tSNR gain is reflected in reduced model fit residuals, as shown in Figure 4, demonstrating more accurate GLM fits compared to NORDIC.

Figure 5 shows the thresholded z-score activation maps, and their distribution. The proposed method yields significant gain in the voxelwise z-scores (bootstrap test, $p < 10^{-4}$), leading to more voxels with significant activation.

Moreover, to ensure that the proposed denoising method does not lead to oversmoothing, the full-width at half maximum (FWHM) of the residual field were compared as a proxy indicating the image smoothness. FWHM across read-out, phase-encoding, and slice direction is [1.38,1.29,1.22]mm in the proposed method, and is [1.36,1.27,1.22]mm using NORDIC, demonstrating that the proposed method does not achieve improved denoising performance at the cost of overly spatial smoothing.

Conclusion

Singular-value hard thresholding for patch-based fMRI denoising is suboptimal. We propose a denoising method based on optimal shrinkage of individual singular-values that minimises the MSE. The proposed approach is evaluated using simulations and high-resolution in-vivo fMRI experiments, and is shown to enhance functional data quality more than what is achievable with similar SVHT-based methods. However, a limitation of this method is that similar to other SVHT-based denoising methods, shrinking any number of singular-values to zero could reduce temporal degrees of freedom, potentially skewing the statistical analyses downstream. In conclusion, the proposed approach provides a simple analytical function to modify the singular-values, eliminating the need for ad-hoc thresholds. It can make fMRI more efficient, enabling faster acquisitions without the need to radically change the current denoising pipelines.

Acknowledgements

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References

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Figures

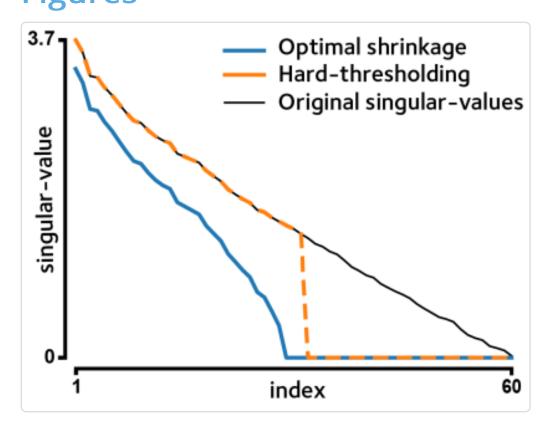


Figure 1. A single slice of the simulated brain phantom data were corrupted by iid standard Gaussian noise.

Singular-values of the noisy data is shown. Hard-thresholding discards all singular values below a certain threshold, but the surviving singular-values could also be inflated by noise. Optimal shrinkage reduces the contribution of noise in the remaining singular-values, yielding a MSE-optimal estimate of the ground-truth data.

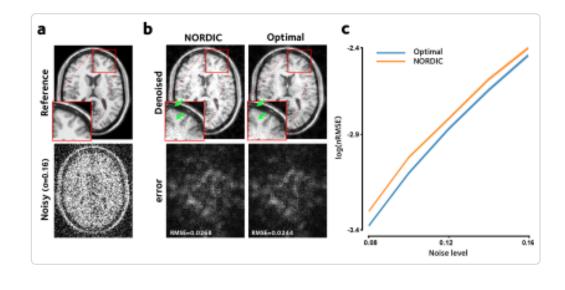


Figure 2. Denoising of the simulated brain phantom. **(a)** The reference data were corrupted by standard Gaussian noise, and **(b)** were denoised using NORDIC and using the proposed method. Optimal shrinkage of singular-values leads to reduced MSE, **(c)** consistently across all tested noise levels (mean±std across slices and time).

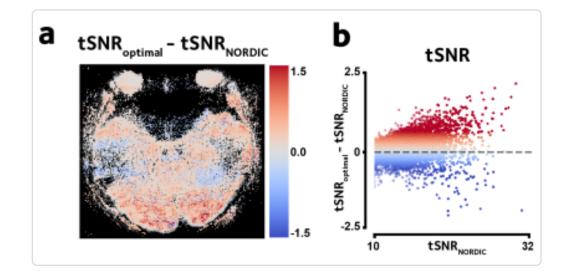


Figure 3. Improvement in voxelwise tSNR in a representative slice from the in-vivo dataset is shown. **(a)** The proposed method yields higher tSNR compared to the SVHT-based method NORDIC. **(b)** tSNR enhancement is more pronounced in voxels where signal contribution is higher.

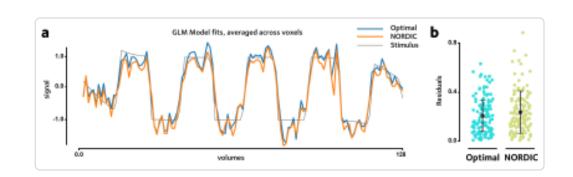


Figure 4. (a) tSNR enhancement leads to more accurate GLM fits, **(b)** reflected in reduced GLM model fitting residuals.

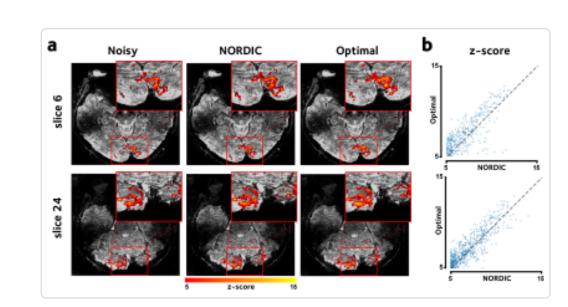


Figure 5. Voxelwise z-scores of the fit GLM models are shown in two representative slices. (a) The proposed method leads to a higher number of voxels with activations above the threshold. (b) Moreover, the z-scores in the shown voxels are higher using the proposed method compared to NORDIC.