

Inter-slice artifact reduction for slice-GRAPPA reconstruction of simultaneous multi-slice (SMS) acquisitions

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Introduction: For full-brain coverage simultaneously acquiring multiple slices can significantly improve acquisition time (1-5). In this work we focus on the single-shot two-dimensional (2D) EPI acquisition methods important for improving temporal resolution in fMRI and acquisition efficiency in diffusion imaging. The EPI compatible approach of (6) examined ‘blipped-CAIPI’ to achieve slice dependent spatial shifts in the PE direction. The slice-GRAPPA reconstruction fits a linear model to determine the kernel and unaliases the shifted slices with a convolution. Controlling this unaliasing process is extremely important given the presence of noise and artifacts in fMRI and diffusion. In this work we test a constrained optimization technique which constrains the aliasing artifact and show that this method can reduce the amount of slice artifact arising in the unaliasing process.

Theory: A linear model can be used to relate the simultaneously acquired slices across all channels to a given slice/channel of interest. In slice-GRAPPA reconstruction, channel j data from slice z (the product of coil sensitivities C and a true magnetization ρ) can be unaliased using all of the collapsed images: $C_{j,z}(x, y)\rho_z(x, y) = \sum_{l=1}^L \left(\sum_{s=1}^S C_{l,s}(x, y)\rho_s(x, y) \right) K_{l,j,z}(x, y)$. The fitting kernel K is spatially smooth and can be solved for efficiently in the frequency domain. The slice-GRAPPA method involves a least squares solution with a collapsed calibration matrix, which is a sum of contributions from the simultaneously excited slices. The overall fitting depends on the range of this calibration matrix, where ideally only data from the slice of interest will propagate: $0 = \sum_{l=1}^L C_{l,s}(x, y)\rho_s(x, y)K_{l,j,z}(x, y)$, $s \neq z$. However, there are often dependencies between the slice contrasts (linear dependency of slice calibration matrices), as illustrated in Figure 1. In addition, non-common contrast can result in data overfitting that manifests as inter-slice artifacts. The reduction of these artifacts is the focus of our work. By looking at the singular value decomposition (SVD) of each slice calibration matrix one can easily determine a basis for the contrast of the slices (U_1 for slice z_1 is shown in Figure 1). The non-common contrasts can then be determined through orthogonal projection, i.e. the notation $z_1 \setminus z_2$ represents the projection of the calibration matrix from z_1 onto the space orthogonal to the basis from z_2 . Excluding undesirable contrast from $z_1 \setminus z_2$ would require a calibration matrix ($\perp U_2$) ($\perp U_2$) $^* U_1 D_1 V_1^*$. Thus, an alternative optimization problem can be formulated to

$$\min \left\| C_{j,z}(x, y)\rho_z(x, y) - \sum_{l=1}^L \left(\sum_{s=1}^S C_{l,s}(x, y)\rho_s(x, y) \right) K_{l,j,z}(x, y) \right\|_2^2$$

separate the slices while constraining the relative amount of artifact ε . In our model the norm of the induced artifact from each $s \setminus z$ calibration matrix is restricted

relative to the norm of the original image z . This convex optimization problem can be solved using log-barrier or interior-point methods (7) that ensure a globally optimal solution.

Methods and Results:

All experiments were performed on a Siemens TIM Trio scanner with a 32-channel head array coil. Single shot EPI was acquired with TE/TR = 64 ms / 5.6s, with a 205×205 mm² FOV, 2.5mm isotropic resolution, 6/8 partial Fourier, 82 matrix, and 51 total slices. Using averaging across 10 repetitions we constructed a reduced noise ‘gold standard’ data set. We compared the slice-GRAPPA method to the constrained approach for various constraint tolerances $\varepsilon = 1e^{-1}, \dots, 1e^{-3}$ and SMS acceleration factors $R = 3, 5$. Figure 2 illustrates the prevalence of slice artifacts using slice-GRAPPA for 3× SMS acceleration and FOV/2 CAIPIRINHA slice shift. Each row shows the 5×5 kernel K_i for a given slice i applied across the reduced noise slices. Therefore, the sum across each row corresponds to a final unaliased image. As you can see by looking across each column non-relevant slices are being used to overfit the data. Note that we have increased the contrast of the artifact images (off-diagonal) to 4% of the original image peak intensity. Figure 2 shows that the artifacts have been significantly reduced **and the overall intensity is substantially decreased** with the constrained optimization. Assuming an $\varepsilon = 1e^{-2}$ for the non-common contrast, we see a decrease from 4.1% to 0.15% average relative error per-slice, for the 3× SMS acceleration. For the case of 5× SMS (FOV/2 slice shift) we see a decrease from 4.4% to 0.14% average relative error per-slice.

Conclusion: The inter-slice artifact constrained SMS optimization model can be used to decrease slice artifacts by more than 10 fold. The improved kernels can be used in both fMRI and diffusion weighting studies for increased accuracy. The convex model ensures optimal solutions given the constraints and is implemented easily using readily available optimization packages.

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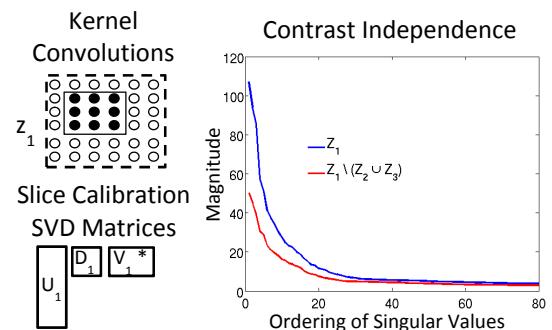


Figure 1: Convolution across calibration data from each slice Z_i is combined for 3× SMS kernel fitting. SVD of slice calibration matrix is illustrated. The dependence of contrast is shown with decrease of largest singular values.

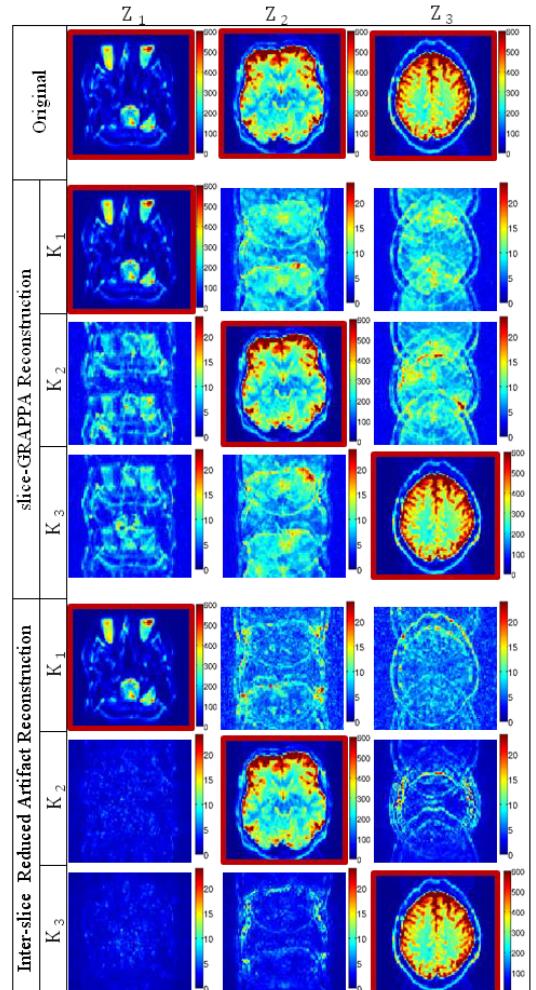


Figure 2: Comparison of slice-GRAPPA and constrained kernel fitting. Each row represents a 5×5 slice kernel K_i applied across the reduced noise slices.