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DISTORTION-OPTIMAL SELF-CALIBRATING PARALLEL MRI BY BLIND INTERPOLATION IN SUBSAMPLED FILTER BANKS

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Abstract

Self-calibrating k-space-based image reconstruction in parallel MRI interpolates the subsampled multi-channel data to a fully sampled Nyquist grid in k-space. Adopting a filter bank interpolation framework, we provide a new formulation of the associated inverse problem and develop the theory for blind identification of the interpolant filters. The developed method is applied to imaging scenarios where high effective acceleration is desired and is shown to be capable of reconstructing artifact-free images with minimal amount of calibration data — hence, achieving high effective accelerations. Simulation and in-vivo results indicate that improved image quality, and thus greater scan time reductions compared to the state-of-the-art method of GRAPPA can be achieved.

Index Terms

Parallel MRI; Self-calibrating; Multi-channel Interpolation; Image Reconstruction; MIMO; Blind Identification

1. INTRODUCTION

The goal in self-calibrating parallel MRI (pMRI) [1, 2], which has several practical advantages over pre-calibrated pMRI [2, 3] is to reconstruct the underlying MR image (spin distributions) without the knowledge of the receiver channel (coil) characteristics. Most self-calibrating pMRI methods, especially the popular GRAPPA method [1, 2], perform image reconstruction by solving for missing k-space (spatial frequency domain) samples [4]. Such methods, also known as k-space-based pMRI [2, 4], utilize the redundancy in the multi-channel MR measurements [3] to compensate for the D -fold subsampling, referred to as the “acceleration factor,” relative to the Nyquist rate. In such methods, the goal is to solve for the missing k-space samples for *each* channel —i.e., to achieve perfect interpolation (PI) rather than perfect reconstruction (PR), which is unlike classical signal processing [5]. In essence, these methods solve the *inverse problem* of interpolating the acquired data to the Nyquist grid in the (k_x, k_y) space, where k_y is the phase-encode (PE) dimension.

A key feature of the k-space-based self-calibrating pMRI methods such as GRAPPA is the ability to perform the interpolation without the knowledge of the receiver channels. Therefore, such methods aim to solve a *blind* multi-channel interpolation problem by identifying an interpolation kernel. As in any interpolation problem, constraints are typically introduced to ensure certain “consistency” conditions. As depicted in Fig. 1(a), the consistency condition in GRAPPA is the matching of the reconstruction to the acquisition over a fully sampled region (typically at the center of k-space) called the auto-calibration scan (ACS) region [1, 2]. The calibration scheme, indicated by dashed lines in Fig. 1(a),

estimates the interpolation kernel to optimize the interpolated data and its consistency with the measured data. The final outcome of the interpolation process is the fully interpolated multi-channel k-space data set, which is then combined after inverse DFT, e.g., using sum of squared (SOS) magnitudes of individual images, to form the final reconstruction [2, 4].

The pMRI measurements consist of: (i) D -fold uniformly subsampled data from the C channel outputs; (ii) calibration data produced by the data truncation operator — denoted by Π_{ACS} in Fig. 1(a) — that removes all but the PE lines in the ACS region. Note that sampling more calibration data generally results in lower *effective acceleration* D_{eff} , defined as the ratio of the total number of PE lines to the number those measured. With the goal of maximizing D_{eff} , this work focuses on non-iterative Cartesian k-space-based auto-calibrated pMRI with minimal amount of calibration data.

Parallel MRI reconstruction can be addressed within the framework of multi-channel filter banks (FBs) [6, 7]. Building on our previous work in this area [8–10], we present a new method that achieves artifact-free image reconstruction for high acceleration factors with few ACS lines ($\approx 5\%$ of PE lines). A high-level overview of the method is depicted in Fig. 1(b), which emphasizes that the proposed method uses not only the data consistency (over the entire measured k-space) but also integrates a “predicted measure” of the aliasing distortion into the calibration process—hence employing a *total distortion* measure. The interpolation method uses a multi-input multi-output (MIMO) FB as its kernel and is dubbed ACSIOM (Auto-Calibrated Sensitivity-encoded Imaging using an Interpolation-Optimal MIMO bank).

A major advantage of the proposed ACSIOM method compared to GRAPPA is that it allows for rigorous performance analysis. After discussing the underlying theory, we demonstrate the effectiveness of the method and show the advantage of the developed signal processing theory for:

- i. Enabling accurate performance analysis, which is significant for understanding the limitations of self-calibrating pMRI in clinical applications;
- ii. Optimizing the reconstruction parameters (specifically, the size of the interpolation kernel) without the need for acquisition of additional data.

2. PROBLEM SETUP AND NOTATIONS

Note that in 2D Cartesian pMRI, subsampling is applied only along k_y . By taking an inverse DFT along k_x , we address the resulting 1D sampling/interpolation problem in the hybrid (x, k_y) domain by considering each x location independently; hence, dependence on x is not included in the analysis.

In this work we tackle the problem of multi-channel blind interpolation wherein the channel characteristics are un-known. To enable distortion-free interpolation, a nonuniform sampling scheme is employed, which is especially suited to the pMRI application. The 1D sampling scheme partitions the support of the channel outputs $\{w_i\}$ into two sections: (i) the calibration region, which is fully sampled (no subsampling); and (ii) subsampled region, wherein one out of every D samples is acquired. Figure 2 shows the definition of the two sampling operators corresponding to calibration and sub-sampled data denoted by $\Pi \downarrow 1$ and $\Pi \downarrow D$, respectively. Let $\mathcal{S}_s$ denote the corresponding nonuniform subsampling operator (for all acquired samples, i.e., filled circles in Fig. 2).

The goal of perfect interpolation (PI), allowing for n_0 delay, is equivalent to $\hat{W}_\ell(z) = z^{-n_0} W_\ell(z)$, for $\ell = 1, \dots, C$. For carrying out the multi-channel PI task, we propose a MIMO signal processing structure shown in Fig. 4, which consists of C^2 finite-impulse response

(FIR) interpolant filters. The MIMO interpolant FB is characterized by a $C \times C$ polynomial matrix $\mathbf{V}(z) = [V_{i,\ell}(z)]$, where $\{V_{i,\ell}(z)\}_{i=1}^C$ is the set of transfer functions for the interpolant filters corresponding to the ℓ -th channel, i.e., those generating the output $\hat{W}_\ell(z)$. Length of a signal s is denoted by m_s . For notational simplicity, we assume that the analysis and interpolation FBs have equal filter lengths m_h and m_v , respectively.

With $\mathcal{C}_{m_s}\{f\}$ denoting the length- m_s convolution operator (matrix) for filter f , we define a C -stack of convolution matrices corresponding to filters $\{f_i\}_{i=1}^C$ as follows:

$$\overline{\mathcal{C}}[\{f_i\}_{i=1}^C]_{m_s} = [\mathcal{C}_{m_s}\{f_1\} \ \mathcal{C}_{m_s}\{f_2\} \ \dots \ \mathcal{C}_{m_s}\{f_C\}]. \quad (1)$$

3. THEORY OF BLIND MULTI-CHANNEL INTERPOLATION

3.1. Conditions for Blind Perfect Interpolation

Consider the MIMO interpolation FB structure (Fig. 4), whereby interpolation of the ℓ -th channel's data, namely $\hat{W}_\ell(z)$, is performed by the interpolant filters $\{V_{i,\ell}(z)\}_{i=1}^C$. The following proposition states *necessary and sufficient* conditions on the MIMO interpolant FB for the blind PI problem.

Proposition 1—Given a C -channel D -fold subsampled analysis FB, a FIR MIMO interpolation bank $\mathbf{V}(z) = [V_{i,\ell}(z)]$ achieves PI for all input signals if and only if the following holds for some nonzero input signal $x \in \ell_2(\mathbb{Z})$:

$$\mathcal{W}_m(z) \begin{bmatrix} V_{1,\ell}(z), V_{2,\ell}(z), \dots, V_{C,\ell}(z) \end{bmatrix}^T = D \begin{bmatrix} W_\ell(z), 0, \dots, 0 \end{bmatrix}^T, \quad (2)$$

where

$$\mathcal{W}_m(z) \triangleq \begin{bmatrix} W_1(z) & W_2(z) & \dots & W_C(z) \\ W_1(z\gamma_D) & W_2(z\gamma_D) & \dots & W_C(z\gamma_D) \\ \vdots & \vdots & \vdots & \vdots \\ W_1(z\gamma_D^{D-1}) & W_2(z\gamma_D^{D-1}) & \dots & W_C(z\gamma_D^{D-1}) \end{bmatrix}.$$

Examining (2), it can be shown that the zeros on the right-hand side enforce *zero-aliasing conditions* — similarly to modulation-domain PR conditions in FBs [5]. Furthermore, it is clear that the analysis filters are not involved —indeed, the condition only involves the outputs of the analysis filters (prior to downsampling) and the interpolant filters. Hence, the conditions in (2) have the desired feature of being *blind* with respect to the channels, i.e., having no explicit dependence on the analysis channels.

3.2. Minimum Feasible Interpolant Filter Length

For efficient computation of the MIMO interpolant FB, we need to state the blind PI conditions in (2) in the sampling (time) domain, i.e., in form of constraints on the filter coefficients. Let us assume that the analysis FB (Fig. 4) is FIR (or FIR to a good approximation) with known filter length m_h . In Section 6, we study the applicability of this assumption in pMRI. The relevant feasibility question is to determine the range of interpolant filter lengths m_v that allow for PI, i.e., for which (2) is feasible. In a recent work (Ch. 9 in [10]), we have addressed the feasibility of short FIR synthesis banks for PR and/or

PI where the analysis FB is “generic” [11] and oversampled (i.e., $C/D > 1$). It is easy to verify that the channels in pMRI are both generic and oversampled. Further, for $C/D \geq 2$ — a condition that is easily satisfied for all practical pMRI applications — choosing $m_v \geq m_v^S(C, D, m_h)$ guarantees feasibility of PI, where m_v^S is defined as follows.

Definition—Define the *sufficient length* m_v^S as:

$$m_v^S(C, D, m_h) = \min \left\{ m_v \in \mathbb{N} \mid \frac{C}{D} \geq 1 + \frac{1}{D} \sum_{p=0}^{D-1} \left\lceil \frac{m_h p - 1}{\lfloor m_v/D \rfloor} \right\rceil \right\}$$

The integer functional m_v^S is easy to compute and has an approximate inverse relation to the oversampling factor C/D .

Proposition 2—For a D -fold subsampled C -channel length- m_h FIR analysis FB with $\frac{C}{D} \geq 2$, a length- m_v MIMO interpolant achieving PI exists generically if $m_v \geq m_v^S(C, D, m_h)$.

Here, assuming that these conditions are satisfied, we can write the sampling-domain counterpart of (2) as

$$\underbrace{\begin{bmatrix} \overline{C}[\{w_i\}_{i=1}^C]_{m_v} \\ \overline{C}[\{w_i \odot e(\gamma_D^D)\}_{i=1}^C]_{m_v} \\ \overline{C}[\{w_i \odot e(\gamma_D^{D-1})\}_{i=1}^C]_{m_v} \end{bmatrix}}_{\overline{v}_{\bullet, \ell}} \underbrace{\begin{bmatrix} v_{1, \ell} \\ v_{2, \ell} \\ \vdots \\ v_{C, \ell} \end{bmatrix}}_{\overline{v}_{\bullet, \ell}} = D \underbrace{\begin{bmatrix} w_\ell \\ 0 \\ \vdots \\ 0 \end{bmatrix}}_{\overline{\omega}_\ell}, \quad (3)$$

where $\odot$ denotes the Hadamard product, $\overline{C}$ was defined in (1), and $e_m(\gamma_D) = [1, \gamma_D, \gamma_D^2, \dots, \gamma_D^{m-1}]^T$ with $\gamma_D = e^{-j2\pi/D}$.

4. ACSIOM: CALIBRATION-ASSISTED BLIND IDENTIFICATION OF THE INTERPOLANT FB

As explained in Sections 1 and 2, in self-calibrating pMRI only a subset of the channel outputs $\{w_i\}_{i=1}^C$ are known. Given the nonuniform calibration-added sampling scheme described above — and owing to the “modulated” structure of $\mathbf{W}$ — it is easy to see that, with enough calibration samples, several rows of $\mathbf{W}$ will be fully known. Let us denote those known subset of rows by $\mathcal{S}_p \mathbf{W}$, where $\mathcal{S}_p$ is the row-pruning operator. The blind identification scheme therefore reduces to

$$\mathcal{S}_p \mathbf{W} \overline{v}_{\bullet, \ell} = D \mathcal{S}_p \overline{\omega}_\ell, \quad \ell = 1, \dots, C, \quad (4)$$

where we used the notation introduced in (3). It can be shown that the vector $\mathcal{S}_p \overline{\omega}_\ell$ on the right-hand side is also fully known. We refer to this system of equations as the *ACSIOM equation*.

The ACSIOM equation suggests the following algorithm for solving the blind PI problem with partial calibration: for each $\ell = 1, \dots, C$, solve the linear system of equations in (4).

Here, we choose to solve (4) using the Moore-Penrose pseudo-inverse. In the Section 5, we provide an assessment of the optimality of this solution in terms of the signal-to-noise ratio (SNR). After identification of the MIMO interpolant bank by solving the ACSIOM equation, the interpolation result is computed by MIMO filtering of the upsampled multi-channel data (Fig. 4).

An interesting question to address is whether solving the ACSIOM equation (under ideal no-noise conditions) would result in PI for practical (limited calibration) cases, say if the calibration samples are less than 10% of m_w . The following proposition addresses this question by providing a sufficient condition for achieving blind PI. In what follows, $\mathcal{N}(A)$ denotes the null space of a matrix A , and, for a subspace $\mathcal{L}$, $\dim\{\mathcal{L}\}$ denote its dimension.

Proposition 3

A FIR MIMO interpolation bank $\{v_{i,\ell}\}_{i,\ell \in C}$ that solves the ACSIOM equation (4) achieves PI if

$$\dim\{\mathcal{N}(\mathcal{S}_p \mathbb{W})\} = \dim\{\mathcal{N}(\mathbb{W})\}.$$

Next, we describe a numerical simulation to demonstrate this result. The plots in Fig. 5 correspond to interpolation of the first channel data in an 8-channel generic FB [11] using the proposed blind PI scheme. The analysis and interpolant FB parameters are described in the figure caption. The following are plotted as a function of the number of calibration (extra) samples: (i) interpolation error (normalized) for $\hat{w}_1$; (ii) difference in the dimensionality of the null space of $\mathbb{W}$ and $\mathcal{S}_p \mathbb{W}$. As is seen from the plot, blind PI is achieved only when the null space dimensions match. Further, the plot shows a sharp transition for this phenomenon at 19 calibration samples. With this number of calibration samples, the number of rows in $\mathcal{S}_p \mathbb{W}$ is only 8% of the total number of rows in $\mathbb{W}$. This verifies the feasibility of blind PI with only a few calibration samples collected according to the nonuniform sampling scheme described in Figs. 2 and 3.

5. NOISE AND DISTORTION PERFORMANCE ANALYSIS

A major advantage of the proposed ACSIOM method compared to heuristic methods such as GRAPPA is that it allows for rigorous performance analysis. In this section, we discuss the noise and distortion properties of the ACSIOM algorithm.

The input (intrinsic) noise in the MR signal is well approximated by additive white Gaussian noise (in k-space) with a “cross-channel noise covariance” matrix [3]. Here we consider a

diagonal approximation of this matrix, denoted by $\sum_n = [\sigma_1^2, \sigma_2^2, \dots, \sigma_C^2]$, where σ_ℓ^2 is the noise variance in channel ℓ . Before entering the MIMO interpolant bank $\mathbf{V}$, the noise signal for the ℓ -th channel passes through downsampling and upsampling operations (Fig. 4).

Assuming an infinite-length input noise sequence, it can be shown that the random sequence at the input of $\mathbf{V}$ is cyclo-stationary and its power spectral density (PSD) is a constant:

$S_\ell^{\text{in}}(\Omega) = \sigma_\ell^2 / D$, $\Omega \in [-\pi, \pi]$. Hence, at the output of $\mathbf{V}$, i.e., after interpolation, the PSD for channel ℓ is given by

$$S_\ell^{\text{out}}(\Omega) = \frac{\sigma_\ell^2}{D} \sum_{i=1}^C |V_{i,\ell}(\Omega)|^2 \quad \Omega \in [-\pi, \pi]. \quad (5)$$

Given that the spectral variable Ω here corresponds to the spatial location in image domain, this expression provides an estimate of the noise amplification map for ACSIOM reconstruction in channel ℓ — akin to the geometric factor (g-factor) in SENSE reconstruction [3]. Furthermore, it shows that the pseudo-inverse solution to the ACSIOM equation in Section 4 is SNR-optimal if σ_i^2 are considered to be equal.

Besides noise, the other source of error in pMRI reconstruction is aliasing distortion, which typically manifests as structured artifacts in the reconstructed images. Let us assume that the ACSIOM algorithm has been applied and the resulting MIMO interpolant FB is $\{\widehat{\mathbf{v}}_{\bullet,\ell}\}_{i=1}^C$, identified by solving (4). Denote the corresponding $\mathbf{W}$ and ω_ℓ by $\widehat{\mathbf{W}}$ and $\widehat{\omega}_\ell$, respectively. Using the theory described in Section 3 and based on (3), we propose the following *distortion measure* for AC-SIOM reconstruction:

$$\mathcal{D}(\mathbf{V}) = \sum_{\ell=1}^C \|\widehat{\mathbf{W}}\widehat{\mathbf{v}}_{\bullet,\ell} - D\widehat{\omega}_\ell\|_2^2. \quad (6)$$

A key feature of this measure is that it can be computed purely based on the available data (Fig. 3). In the following section we demonstrate its utility for optimizing the choice of m_v .

6. RECONSTRUCTION RESULTS

All reconstruction experiments used MR data for a resolution phantom acquired with 12 receiver channels (head coil array) on a 3T whole-body MRI scanner (Siemens Medical Solutions, Erlangen, Germany). The image matrix size was 256×256 (fast spoiled gradient echo, TR/TE: 300/10 ms, FOV: 200×200 mm). Fig. 6(a) shows the fully-encoded root SOS image. All reconstructions that used the proposed AC-SIOM algorithm were performed in the hybrid (x, k_y) space by first taking an inverse DFT along k_x .

The analysis filters corresponding to the receiver channels in pMRI have smooth spectrums and therefore have fast decay in the sampling domain. In Section 3.2, we assumed that the analysis filters are well approximated by FIR channels. To investigate this hypothesis, we conducted ACSIOM reconstructions with varying interpolant filter lengths m_v , assuming the ideal full-calibration scenario, i.e., where the ACS region is the entire k-space (without replacement of ACS data after reconstruction). This assumption ensures that the observed reconstruction error is dominated by the m_v choice. The results are summarized in Fig. 6(b). As is seen from the mean squared error (MSE) plots, excellent MSE is achieved with very short interpolant filter lengths.

Next, we turn to the practical case of limited calibration (few ACS lines) with $D = 3$ subsampling and 13 ACS lines. Fig. 7 plots, as a function of m_v , both the MSE and the distortion measure $\mathcal{D}$ in (6) (with arbitrary scaling). Note that unlike the MSE, computation of $\mathcal{D}$ only requires the subsampled data. As is seen from Fig. 7, the distortion measure identifies the nearly-optimal choice of $m_v = 5$ (the MSE for $m_v = 7$ is better than $m_v = 5$ by 0.01%).

Finally, for the same scenario as in Fig. 7, Fig. 8 shows the result corresponding to (i) state-of-the-art implementation of GRAPPA [2, 4] (with recommended 2D kernel size of 4×5); (ii) ACSIOM with $m_v = 13$; and (ii) ACSIOM with $m_v = 5$ (optimal choice based on $\mathcal{D}$). The error images in Fig. 8 suggest that the m_v -optimized ACSIOM reconstruction only exhibits low-level noise-like error without any detectable distortion. In contrast, the GRAPPA and the non-optimized AC-SIOM reconstructions show significant aliasing distortion.

In conclusion, the reconstruction results demonstrate the effectiveness of the ACISOM method and show its advantage in that it allows for rigorous analysis — compared to heuristic schemes such as GRAPPA — specifically, for optimizing the interpolation kernel size. The developed framework also has important implications for understanding the limitations of self-calibrating pMRI, e.g., allowing for *automatic* image quality analysis immediately after an accelerated scan.

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Fig. 1.

(a) State-of-the-art (GRAPPA) identification scheme. Dashed lines represent the kernel estimation performed by the calibration scheme. (b) Proposed blind identification scheme (ACSIOM) using a distortion-optimal MIMO interpolation FB.

Fig. 2.

Example (with $D=3$) of the two sampling operators corresponding to subsampled and calibration data, respectively; acquired samples are shown as filled circles and skipped ones as hollow circles.

Fig. 3.

The proposed blind PI scheme, which uses additionally acquired calibration data to identify the PI MIMO interpolant FB.

Fig. 4.

The proposed structure for carrying out the multi-channel interpolation task. The $C \times C$ MIMO interpolant FB is identified based on the PI goal, which is to achieve $\hat{W}_\ell(z) = z^{-n_0} W_\ell(z)$

Fig. 5.

Interpolation of the 1st channel in a generic FB using the proposed blind PI scheme. FB parameters are: $C = 8$, $D = 3$, $m_x = 256$, $m_h = 15$, $m_v = m_v^S = 9$. The following are plotted as a function of the number of calibration samples: (i) normalized interpolation error for $\hat{w}_1$; (ii) difference in null-space dimensions of $\mathbb{W}$ and $s_p \mathbb{W}$.

Fig. 6. (a) MR phantom (root SOS) image; (b) MSE as a function of m_v for three different subsampling factors.

Fig. 7. The ACSIOM distortion measure and MSE as a function of m_v . The vertical axis scaling (logarithmic) only applies to MSE.

Fig. 8. Reconstructions ($D=3$, root SOS) and error images (same grayscale) for GRAPPA (2D), non-optimized ACSIOM ($m_v=13$), optimized ACSIOM ($m_v=5$). Arrows point to aliasing artifacts.