

Joint Altered Calibration with Linear Interpolation for Cross-Sampling

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March 11, 2025

Joint altered calibration with linear interpolation for cross-sampling

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Abstract-Among the methods of sampling trajectories, cross-sampling can provide more autocalibration signal (ACS) data and enables better incoherent sampling with lower gradient control system requirements. However, there were still data registration regarding magnetic field inhomogeneities. So in this study, a self-calibrated off-resonance correction is proposed to coregistrate the inconsistency between the orthogonal readout data. This method employs a linear prediction operator to estimate the cross-sampled data and the corrected data undergo the same calibration, and reconstruction process as that used in conventional generalized autocalibrating partially parallel acquisitions (GRAPPA), in order to recover the missing k-space data and generate the final image. We will compare this calibration method with the traditional first-order k-space trajectory correction for crosssampling autocalibrating partially parallel acquisitions (CS-GRAPPA) and the experimental results on phantoms and human subjects demonstrate that the images reconstructed by this method exhibit fewer artifacts and higher signal-to-noise ratio (SNR).

Keywords—magnetic resonance imaging (MRI), crosssampling, autocalibration, linear interpolation

I. INTRODUCTION

Acceleration algorithms have been widely applied in magnetic resonance (MR) scanning, including parallel magnetic resonance imaging (pMRI) skipping some phaseencoding lines in k-space and Compressed Sensing exploiting 3rd Pei Yuan Medical Imaging Center, Department of Electronic Engineering andInformation Science University of Science and Technology of China Hefei, China py_crick@mail.ustc.edu.cn

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the intrinsic structural correlations of data to achieve fast MRI.[1-4] To enhance the performance and reconstruction accuracy of these algorithms, various non-Cartesian sampling methods, such as radial and spiral sampling, have been proposed. However, these acquisition methods can cause distortions, blurring, and intensity variations in MRI images due to off-resonance effects and trajectory errors caused by fast-switching readout gradients. To address these issues, high-precision gradient control systems are required, yet the development of such systems is challenging.

Cross-sampling[5-8] utilizes two orthogonal readout gradients to acquire two sets of Cartesian sampled data.[6, 9] This approach features a simple trajectory and low gradient switching rates. Moreover, by combining the cross-sampled data, it can emulate the effects of non-Cartesian sampling schemes for specific reconstruction algorithms. Although this method effectively mitigates the impact of gradient imperfections, there are still difficulties regarding magnetic field inhomogeneities.

To address the inconsistency, the traditional calibration in CS-GRAPPA uses a iterative co-registration approach to align the orthogonally acquired data. This method models the field inhomogeneity by using the first-order components, assuming that the two sets of k-space data may be misaligned in position and scaled by a complex constant. However, the inconsistency caused by the effects of practical conditions such as eddy currents, field inhomogeneity, and chemical shift, are not fully consistent with the first-order model .[5, 6, 10-12]

In this study, we initially investigate the efficacy of crosssampling in pMRI and Compressed Sensing under idealized

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conditions. Our results demonstrate that, with identical acquisition, the image quality achieved through crosssampling is markedly superior. We then propose a calibration method based on linear interpolation to predict the crosssampled points. By calibrating the k-space center data of the two orthogonal acquisitions and reconstructing the peripheral orthogonal acquisition data using a calibration kernel to align the reduced data. To control for confounding variables , the GRAPPA process is applied to the co-registered data and compared with traditional CS-GRAPPA. Simulation and experimental results show that this method can significantly reduce the aliasing artifacts in CS-GRAPPA and improve the SNR under the same number of ACS lines.

II. THEORY

A. Cross-sampling acquisition

In the cross-sampling approach, two one-dimensional(1-D) Cartesian datasets(denoted as S_x and S_y) can be obtained by using two orthogonal readout gradients, as explained in Fig1 (b) and (d). Ideally, we can express both datasets as

$$S_{x}(k_{x},k_{y}) = S_{y}(k_{x},k_{y}) = \iint \rho(x,y)e^{-i(k_{x}x + k_{y}y)}dxdy (1)$$

where $\rho(x, y)$ represents the spin density in a 2-D cross section in Cartesian coordinates (x, y), and k_x and k_y are the k-space coordinates. In the case, the combined k-space dataset $S(k_x, k_y)$ can be represented as

$$S(k_x, k_y) = \xi(k_x, k_y) [S_x(k_x, k_y) + S_y(k_x, k_y)]$$
(2)

$$\xi(k_x, k_y) = \begin{cases} 0.5(k_x, k_y) \in R\\ 1(k_x, k_y) \notin R \end{cases}$$
(3)

 ξ in (2) is a weighting function, defined in (3) to maintain data consistency in the overlapped dataset R.

B. Data inconsistency analysis

As previously mentioned, cross-sampling is employed to obtain two sets of orthogonally acquired data using



Fig 1 All trajectories have a reduction factor R = 3.5 (a) 1-D Cartesian trajectory for pMRI (b) cross-sampling trajectory for pMRI (c) 1-D Cartesian trajectory for compress sensing (d) cross-sampling trajectory for compress sensing

orthogonal readout gradients(G_x and G_y), which implies the introduction of distinct phase error. Such error may not be significant in single 1-D Cartesian as it's constant within the same data set.[13, 14] The error is dependent on the characteristic of gradient coils, the shape and material of the pole piece, etc. In addition to the phase error caused by pulse sequence or hardware imperfections, the NMR signal is modified by an inhomogeneous magnetic field, which causes intensity variation and image distortion. So Eq. (1) can be rewritten as:

$$S_{x}(k_{x},k_{y}) = \iint e^{-i\Delta\varphi_{x}}\rho(x,y)e^{-i(k_{x}x+k_{y}y+\Delta B_{0}(x,y)t_{x})}dxdy (4)$$

$$S_{y}(k_{x},k_{y}) = \iint e^{-i\Delta\varphi_{y}}\rho(x,y)e^{-i(k_{x}x+k_{y}y+\Delta B_{0}(x,y)t_{y})}dxdy (5)$$
where $\Delta \phi_{0}$ and $\Delta \phi_{0}$ indicate the phase errors caused by G

where $\Delta \varphi_x$ and $\Delta \varphi_y$ indicate the phase errors caused by G_x and G_y , $\Delta B_0(x, y)$ represents the magnetic field inhomogeneity.[15-18]

In the context of MRI, these inhomogeneities and phase across the image must be accounted for during the reconstruction process to ensure accurate image representation. However, the weighting function in Eq.(3) does not address this issues. Cross-sampling correction, therefore, is required to resolve these effects and improving the overall image quality.



Fig 2 Schematics of joint altered Calibration for A) Two datasets of cross-sampling. B) Calibration of each dataset on the grid requires the full neighborhood data from both datasets



Fig 3 Effects of the different trajectories for different reduction factor R. GRAPPA((a), (b) and (c)) and Compressed Sensing((d), (e) and (f)) were used to show the enhancement of reconstruction with ideal cross-sampling trajectory. Structure Similarity Index Measure, Root Mean Square Error and Peak Signal-to-Noise Ratio were compared.

C. Data co-registration

In magnetic resonance imaging (MRI), 1-D Cartesian sampling has been widely adopted due to its robustness against magnetic field inhomogeneities, susceptibility effects, and gradient imperfections. This robustness stems from its simple trajectory design and high tolerance for sampling errors. So this study proposes a calibration method based on linear interpolation. The core idea is to complete a cross-sampling trajectory while preserving the consistency of 1-D Cartesian sampling in one direction. This is achieved by replacing the calibrated data $S(k_x, k_y)$ in Eq. (2) with data from a specific direction (e.g., S_x) and estimating the missing sampling points through linear interpolation in that direction. We define the completed data along the G_x direction as \tilde{S}_x , then we have

$$\tilde{S}_{x}(\vec{k}) = \begin{cases} S_{x}(\vec{k}) & \vec{k} \in \Omega_{x} \\ P_{\Gamma}(S_{x}, S_{y}) & \vec{k} \in \overline{\Omega}_{x} \end{cases}$$
(6)

where \vec{k} is the k-space coordinate, Ω_x is the set of points using the G_x readout gradients, respectively, and $\overline{\Omega}_x$ represents missing points. P_{Γ} denotes the interpolation function.

Multiplexed sensitivity encoding (MUSE)[19] has been reported to enable the reconstruction of phase information through a two-step sensitivity encoding reconstruction, effectively correcting shot-to-shot phase variations. Additionally, AseDiWA[20] (autocalibrating segmented diffusion- weighted acquisition) has been demonstrated that a joint reconstruction of segments can be applied to k-space-based algorithms to address the phase differences between segments. Therefore, AseDiWA is used to construct the interpolation function. To fully exploit the prior information, for $\vec{k} \in \overline{\Omega}_x$, all the acquired points of S_x and S_y within the region of interest are employed.

$$\tilde{S}_{xi}(\vec{k}) = \sum_{t} \sum_{j} g_{ijt} (\% R_t S_{tj})$$
(7)

where the nonacquired k-space data at a position k acquired from the *i*-th coil and the dataset $\tilde{S}_{xi}(k)$ is calculated from the acquired data of all coils (1...j) of datasets $(t = x \text{ or } y \text{ for } G_x$ or G_y readout data) selected by an operator $\Re R_t$. The weight g_{rijt} is calculated according to calibration data:

$$\min_{g} \sum_{\tilde{S}_{xi}(k)\in Calib} \left\| \tilde{S}_{xi}(\vec{k}) - \sum_{t} \sum_{j} g_{ijt}(\% R_{t} S_{tj}) \right\|^{2}$$
(8)

Thus, a corrected k-space dataset shown in Fig.1 (b) and (d) can be obtained by using with interpolated data, as shown



Fig 4 The reconstructed results and their corresponding difference images with reference when different combinations of parallel- and cross-sampling are used. The reduction factor is 4, and the number of ACS lines is 32.

in Eq.(7) and (8). What's more, another corrected dataset \tilde{S}_y can be available by the same token.

III. EXPERIMENTS

The proposed method was evaluated using simulation, phantom experiment, and two in vivo experiments. All reconstruction schemes were implemented in MATLAB (MathWorks, Natick, MA) with 4.00 GHz and 16 GB RAM. All experimental data were conducted on a 1.5 T MRI scanner (CLIMBER 150, Anhui Fuqing Medical Equipment Co., Ltd) with a 16-channel coil. Here, CS expresses cross-sampled. Sampling mask depicted in Fig.1 corresponds to the reconstruction as follows: (a) GRAPPA, (b) CS-GRAPPA, (c)Compressed Sensing, (d) CS-Compressed Sensing.

The simulation experiments was performed using a water phantom to show the enhancement of reconstruction with ideal cross-sampling trajectory. Fully sampled 1-D Cartesian data was scanned using a T1GRE sequence (TE/TR = 10/370 ms, matrix size = 192×192 , FOV = 240 mm²) to generate the traditional trajectory and cross-sampling trajectory. Then, Compressed Sensing and Generalized Autocalibrating Partially Parallel Acquisitions were used for the undersampled data. The reconstruction results were compared with different trajectories at the Fig. 1. We compared Structure Similarity Index Measure(SSIM), Peak Signal-to-Noise Ratio(PSNR) and Root Mean Square Error(RMSE) at the reduction factors of 3, 4, 5 and 6, respectively.

Two in vivo human datasets were sampled by a T1SE sequence (TE/TR = 25/400 ms, matrix size = 256×256 , FOV = 240 mm²). Each dataset includes undersampled data(R = 4) and orthogonally acquired ACS lines. Real in vivo experiments using the coregistered data from two orthogonal directions were performed on both datasets. The images reconstructed directly according to Eq.(2) were provided. What's more, we compared conventional CS-GRAPPA and the GRAPPA with the interpolation function to the effectiveness of the proposed method.

IV. RESULT AND DISCUSSION

Fig.3 depicts the reconstruction of the water phantom data with trajectories of the 1-D Cartesian(in blue) and cross-sampling(in orange). Cross-sampling significantly enhances the performance of reconstruction algorithms. Regardless of whether it is GRAPPA or Compressed Sensing, there is a notable improvement in Structural Similarity Index(Fig.3 (a) and (d)) and Peak Signal-to-Noise Ratio(Fig.3 (c) and (f)), and a reduction in Root Mean Square Error(Fig.3 (b) and (e)) after

employing cross-sampling. Moreover, comparing Fig.3 the first row images with the second row, we can find that Compressed Sensing, which depends on sparsity of signal, shows a more pronounced enhancement as cross-sampling provides incoherence in one more direction than 1-D Cartesian. In 3D imaging, this can further extend the sparsity to three dimensions.

However, the simulation experiments for Fig.3 utilized fully sampled 1-D data and did not take into account the actual acquisition scenario. Fig.4 presents the test results using actual undersampled data and orthogonally acquired ACS lines. From the direct reconstruction results, it can be observed that the direct reconstruction of cross-sampled data introduces significant artifacts. This issue is somewhat ameliorated in the CS-GRAPPA using traditional calibration methods, but structured aliasing artifacts still persist. In contrast, the reconstruction employing the linear interpolation function proposed in this paper exhibits artifacts without distinct structure, resembling noise, and correspondingly, the RMSE is reduced by approximately 3 percentage points.

V. CONCLUSIONS

In this study, we proposed joint altered calibration to address the phase errors associated with cross-sampling. Our approach improves the performance of cross-sampling correction by integrating data registration and calibration into self-consistent calibration. Compared to CS-GRAPPA, images reconstructed using our method demonstrate superior quality. In water phantom experiments, we observed the potential of cross-sampling in algorithms that rely on the inherent structure of the sampled data.[21] Consequently, our future work will focus on data calibration for reconstructions such as CS and LORAKS, aiming to achieve higher acceleration rates.

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