A Unifying Approach to Inverse Problems of Ultrasound Beamforming and Deconvolution

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Abstract—Beamforming is an essential step in the ultrasound image formation pipeline and has recently attracted growing interest. An important goal of beamforming is to increase the image spatial resolution, or in other words to narrow down the system Point Spread Function (PSF). In parallel to beamforming approaches, deconvolution methods have also been explored in ultrasound imaging to mitigate the adverse effects of PSF. Unfortunately, these two steps have only been considered separately in a sequential approach. Herein, a novel framework for unifying beamforming and deconvolution in ultrasound image reconstruction is introduced. More specifically, the proposed formulation is a regularized inverse problem including two linear models for beamforming and deconvolution plus additional sparsity constraint. We take advantage of the alternating direction method of multipliers algorithm to find the solution of the joint optimization problem. The performance evaluation is presented on a set of publicly available simulations, real phantoms, and in vivo data. As compared to Delay-And-Sum (DAS) beamforming, simulation results indicate improvements of 45% and 44% in terms of axial and lateral resolution, respectively. Moreover, the proposed method improves the contrast of simulation data by 6.7% in comparison to DAS. The superiority of the proposed approach in comparison to the sequential approach as well as the state-of-the-art beamforming and deconvolution approaches is also shown.

Index Terms—Beamforming, deconvolution, plane-wave imaging, inverse problem, ADMM.

I. INTRODUCTION

MEDICAL ultrasound imaging has the advantages of being cost-effective, non-invasive, portable, and real-time as compared to other prevalent medical imaging modalities. Ultrasound images, however, suffer from several artifacts such as clutter and poor resolution, which emanate from the wide Point Spread Function (PSF) of the imaging system. There are several approaches to tackle this problem, among which beamforming [1] and deconvolution [2] are the foci of the current work.

Beamforming is an essential step in the medical ultrasound image formation pipeline. In the transmission step, beamforming specifies the firing time, as well as the shape of the excitation pulse, applied to each element of the transducer in order to create the desired acoustic wave [3]. In the receive step, beamforming is applied to trace back the backscattered echoes from each voxel of the medium [3]. Receive beamforming can be accomplished in time [4] and frequency [5], [6], [7] domains. Delay-and-sum (DAS) beamforming is the most common time-domain approach due to its simplicity and efficacy. DAS involves aligning the recorded pre-beamformed channel data by applying the propagation delays and combining them using a set of predefined apodization weights. DAS is restricted by the classical trade-off between the width of the main lobe and the level of side lobes in apodization windows in the frequency domain. Adaptive methods have been extended to optimize the apodization weights based on the received channel data. They have shown the capability of providing significant improvements in lateral resolution and contrast of B-mode images [8], [9], [10].

Ultrasound beamforming has also been formulated as an inverse problem in recent years [11], [12], [13]. In this formulation, the desired ultrasound image is directly estimated from the observation signals without calculating apodization weights. This framework allows the consideration of any additional constraint, such as Gaussian and Laplacian statistics, in the recovery of desired data.

Although a better beamformer improves the system PSF, ultrasound imaging still has a non-ideal PSF due to many factors such as the limited bandwidth of piezoelectric crystal elements, the physical phenomena of acoustic wave propagation in the tissue, etc. [3]. Under the assumption of weak scattering for soft tissues and using the first-order Born approximation, the ultrasound Radio-Frequency (RF) data can be linearly modeled as the result of convolution between the ground-truth Tissue Reflectivity Function (TRF) and the PSF of the ultrasound imaging system [2], [14]. Therefore, another line of research has been devoted to mitigating the adverse effect of non-ideal PSF using the deconvolution approach [2], [15], [16]. To our knowledge, deconvolution has only been applied as a post-processing approach after reconstructing the ultrasound image based on existing beamforming procedures, essentially DAS.

As shown in Fig. 1, the current study is motivated by the novel idea of unifying the beamforming and deconvolution steps together to simultaneously take advantage of both methods.
in image reconstruction. The proposed framework is a joint inverse problem including two linear models of beamforming and deconvolution plus an additional sparsity constraint. In other words, our method is designed to estimate the desired image directly and concurrently minimize the adverse effect of the PSF. The resulting optimization problem is solved using split-variable Alternating Direction Method of Multipliers (ADMM) algorithm [17], [18] as it allows the minimization of each term of the objective function separately. The performance evaluation is completed on a set of publicly available simulations, real phantoms, and in vivo data from the Plane-wave Imaging Challenge in Medical UltraSound (PICMUS) [19]. Furthermore, the superiority of the proposed approach in a comprehensive comparison with the sequential approach and each of the beamforming and deconvolution approaches alone is also shown.

II. RELATED WORK

In the rich body of literature on the topic of ultrasound beamforming and deconvolution, the most recent and relevant studies are reviewed in this section.

Beamforming approaches can be categorized into four main groups. The first set is time-domain methods, among which DAS is the most popular non-adaptive method. Filtered-delay multiply and sum (F-DMAS) is based on a pairwise multiplication of delayed RF signals before summation [10]. Another extension to DAS is based on null subtraction imaging [20], wherein envelope images reconstructed by different apodization windows are linearly combined in order to overcome the classical trade-off and have both a low side lobe level and a narrow main lobe.

Among the adaptive algorithms, Minimum Variance beamforming (MVB) [21] is the most potent approach that mainly improves the lateral resolution [22]. The MVB requires the estimation of the covariance matrix from the data, which makes it computationally expensive [8]. The MVB has also been extended using singular value decomposition (SVD) of the covariance matrix to improve the contrast [23]. But there is no clear criterion for removing small eigenvalues, and a part of the speckle texture might be omitted in this method. A fast version of MVB has been developed based on principal component analysis (PCA) [24] as well as Legendre polynomials [25]. In [26], the apodization weights are estimated using independent component analysis (ICA).

There is another type of adaptive method, in the time domain, based on the coherence factor (CF), which is defined as the ratio of coherent to incoherent energy across the aperture [27]. CF was used as an adaptive weight on top of DAS to improve the image quality [9]. Generalized CF (GCF) was derived from the spatial spectrum and defined as the ratio between the energy of a predefined low-frequency range (the coherent portion of RF data) to the total spectral energy [28]. Subsequently, phased CF (PCF) was proposed based on the phase, rather than amplitude information of aperture [29].

The second group of beamforming methods is implemented using the Fourier transform. The pioneer studies were based on synthetic aperture focusing [6], [30]. Later on, the Fourier beamforming was extended for plane-wave Imaging [5] and implemented through different strategies [31], [32], [33], [34]. Wagner et al. proposed compressed beamforming that works on the sub-Nyquist RF data [35]. Consequently, this idea has been extended as a general beamformer in Fourier domain [7], [36], [37].

Szasz et al. proposed the third group of beamforming methods [11], which assume a linear model between the observed data (i.e., the RF channel data) and the desired image to be recovered. Beamforming is then performed by solving a regularized inverse problem for each image depth separately. The results have been presented for focused [11] as well as plane-wave imaging [13]. Subsequently, this idea was further extended by considering more regularizations in the objective function and reconstructing all image depths jointly [12]. Two matrix-free formulations have been proposed in [38] that are both faster and more memory efficient than other inverse problem formulations. Recently, denoising-based regularization terms have been adapted in the inverse problem of ultrasound beamforming [39], which noticeably improves the contrast and preserves the speckle statistics. The inverse problem formulation has also been used in inverse scattering problems (e.g., [40]) and ultrasound tomography (e.g., [41], [42], [43]).

The last group of ultrasound beamforming methods is based on deep learning [44], [45], [46], [47]. While deep models have a great potential for estimating non-linear mapping functions between high dimensional input-output pairs and solving ill-posed problems, deep beamformers usually require a massive amount of training data which is commonly unavailable. Since the training ground truth is not known especially for in vivo data, it is common to train deep models using simulation datasets. However, there might be a performance reduction on test data due to domain shift between simulation and real data. The challenge on ultrasound beamforming with deep learning (CUBDL) was organized in conjunction with the 2020 IEEE International Ultrasonics Symposium (IUS) [46]. In [48], a general ultrasound beamformer was designed, based on deep learning, to mimic MVB. In terms of image quality, it was ranked first. Overall, considering the network size as well, it was jointly ranked first with another submission [49].
Finally, in ultrasound image deconvolution, Taxt et al. proposed a 2-D blind homomorphic approach wherein the PSF was estimated in the complex cepstrum domain followed by Wiener filtering for the deconvolution [50]. An approach based on parametric inverse filtering was proposed in [15]. Subsequently, Yu et al. introduced a single-input multiple-output (SIMO) channel model for the deconvolution of ultrasound images [51]. Two frameworks of Compressive Sensing (CS) and deconvolution were combined in [16], and the resulting method was called compressive deconvolution. An analytical model for the spatially-varying PSF in ultrasound imaging was proposed in [52]. A physical model for the nonstationary blur in the plane- and diverging-wave imaging was proposed in [53].

Recently, the nonlinearity of ultrasound wave propagation in the tissue was considered in the deconvolution problem, and the enhanced image was reconstructed by the minimization of a joint cost function including the deconvolution models for both fundamental and harmonic RF images [54]. Most of the deconvolution studies reviewed here are categorized as blind methods as they are based on the estimation of PSF of the imaging system, while non-blind methods [55] assume that the PSF is known (e.g., through experimental measurement). In the current study, the nonlinearity of ultrasound wave propagation in the tissue is not considered, and the proposed framework is based on blind deconvolution with the assumption of spatially-invariant PSF.

III. BACKGROUND

A. Inverse Problem of Ultrasound Beamforming

This section provides a brief summary of our recent work [39] to make this paper self-contained. The purpose of ultrasound beamforming is to reconstruct a high-quality spatial map of the medium echogenicity. Without loss of generality, let us consider a N-element ultrasound linear probe with a transducer pitch of \( p \), as shown in Fig. 2, from which \( L \) piezoelectric elements transmit an acoustic wave into a medium with the constant sound speed of \( c \). We also assume that backscattered signals are recorded with all elements of the same probe with a specific sampling frequency \( (f_s) \). To form a single image, this process may be repeated several times depending on the probe type (e.g., linear, phased array, or curvilinear) and the imaging technique (e.g., plane-wave, line-per-line, or synthetic aperture imaging). The beamforming grid is partitioned with a pixel size of \( d_z = \frac{c}{f_s} \) in the axial (i.e., the wave propagation direction) and \( d_x = p \) in the lateral directions.

If there is no time offset after wave transmission (i.e., the elements immediately start to collect the backscattered waves), the \( m^{th} \) sample of the elements’ outputs corresponds to the actual time of \( t = (m - 1)/f_s \), where \( m = \{1, 2, \ldots, M\} \). In order to trace back the echoes corresponding to each pixel, the associated time delay \( (\tau) \) equal to the sum of two-way propagation times of transmitted wave reaching that pixel \( (\tau_i) \) and getting back to the transducer elements \( (\tau_e) \) needs to be applied to each signal recorded by piezoelectric elements of the probe. Considering digitization error, the following condition determines all pixels contributing to a sample of element’s output:

\[
| t - \tau | \leq \frac{1}{f_s},
\]  

(1)

where \( \tau = \tau_e + \tau_i \) depends on pixel location, assumed speed of sound, the type of transmitted ultrasound wave (e.g., plane-wave, focused, or spherical wave), and the probe geometry. (1) leads to an elliptical region with different weights as illustrated in Fig. 2. Therefore, a linear forward model between each sample of the RF channel data and the pixels’ values in the desired image can be written as follows:

\[
y_{ch} = \Phi x + \nu,
\]  

(2)

where \( x, y_{ch} \in \mathbb{R}^{MN} \) are the vectorized versions of the desired image and the collected pre-beamformed channel data, respectively. \( \Phi \in \mathbb{R}^{MN \times MN} \) is the weighting matrix, and \( \nu \) represents the additive white Gaussian noise (AWGN).

As mentioned before, the way matrix \( \Phi \) is designed has been described in our previous work [39]. In this method, the linear propagation in the medium is assumed and PSF of the probe is not incorporated. As Fig. 2 and (2) depict, rows of matrix \( \Phi \) contain the contributions of image pixels into samples of RF channel data. For every single sample of pre-beamformed data, the pixels’ contributions are determined using the following equation:

\[
\Phi(i, j) = \begin{cases} 
1 - \frac{|t_i - \tau_j|}{t_{\text{max}}} & |t_i - \tau_j| \leq \frac{1}{f_s} \\
0 & |t_i - \tau_j| > \frac{1}{f_s} 
\end{cases},
\]  

(3)

where \( t_i \) is the actual time corresponding to a sample of element’s output, and \( \tau_j \) is the propagation delays of pixels which contribute to that sample (i.e., only the ones respecting the condition of (1)). \( t_{\text{max}} \) is the maximum absolute difference between \( t_i \) and \( \tau_j \). Since only a small portion of pixels satisfy (1), matrix \( \Phi \) becomes highly sparse. Furthermore, data independent matrix \( \Phi \) can be precalculated based on the known imaging settings. A reception apodization matrix, commonly used in DAS beamforming, is also multiplied with matrix \( \Phi \) in order to take into account the directionality of transducer elements and fix the f-number for the entire image depths. It
has to be mentioned that matrix $\Phi$ is not necessarily a square matrix because it can be determined for any grid partitioning not equal to pre-beamformed data. Further explanations regarding the construction of matrix $\Phi$ can be found in supplementary material (Section I).

The most straightforward inverse problem formulation of ultrasound beamforming is to estimate $x$ by solving the following least-squares optimization problem:

$$\hat{x} = \arg\min_{x} \| y_{ch} - \Phi x \|_2^2 .$$  \hspace{1cm} (4)

In contrast to common beamforming approaches (such as DAS, MVB, and CF), there is no need to estimate the apodization weights, and the beamformed image is directly reconstructed. It has been shown in [11], [12] that (4) does not solely provide the best results, and additional constrains should be considered. Furthermore, (4) can be sequentially solved for each depth of the image (as performed in [11]) or solved at once for the whole image depths (as performed in [12]). Herein, we follow the second approach because of two main reasons. First, independently solving the inverse problem for each depth increases the computational cost because the iterative algorithm needs to be run many times, especially for high-depth images. Second, the noise level of the ultrasound images increases with depth due to a multitude of reasons including attenuation [56]. Therefore, when different depths are reconstructed separately, the iterative algorithm may converge to a different solution for each depth leading to border artifacts.

### B. Deconvolution of Ultrasound Images

Under the assumption of weak scattering for soft tissues and using the first-order Born approximation, the linear model, given in (2), can also be used to express beamformed RF image as the result of convolution between the TRF and the PSF of the ultrasound imaging system as following [2], [14], [16]:

$$y_{DAS} = H x + \nu,$$  \hspace{1cm} (5)

where $y_{DAS}$ is the RF image resulting from DAS beamforming. $H$ is a block circulant with circulant block (BCCB) matrix formed based on the PSF and accounting for circular convolution. Although the assumption of the convolution model may not be valid in practice (especially for biological tissues), it has long been shown that the linear model is a good approximation and helps to reduce the adverse effect of PSF through deconvolution. Same as before (i.e., (4)), we consider the inverse problem formulation of deconvolution for finding the desired TRF.

The PSF is usually spatially variant in the ultrasound images mainly due to wave divergence, attenuation, and a limited number of crystal elements in the lateral direction. There are a few settings such as time gain compensation (TGC) and transmitting several focused beams (in line-per-line imaging) that help to have less variation in PSF across the image [47]. Therefore, a part of deconvolution studies solves the problem with the assumption of having a spatially-invariant PSF [15], [16], [54]. Herein, the experiments are based on plane-wave imaging and we have also considered a fixed PSF in our formulation.

### C. Basics of ADMM

As we use ADMM for solving the proposed optimization problem, a short overview of the method is provided in this section. More details of the ADMM algorithm can be found in [17].

Let us assume that our goal is to solve the following constrained optimization problem:

$$\begin{align*}
(\hat{u}, \hat{v}) &= \arg\min_{(u, v)} \{ f(u) + g(v) \} \text{ s.t. } Au + Bv &= c,
\end{align*}$$  \hspace{1cm} (6)

where $u, v \in \mathbb{R}^n$, and $f : \mathbb{R}^n \rightarrow \mathbb{R}$ and $g : \mathbb{R}^n \rightarrow \mathbb{R}$ are closed convex functions. $A$ and $B$ are known matrices, and $c$ is a given constant vector. To solve the corresponding unconstrained problem, the augmented Lagrangian function can be written as:

$$\mathcal{L}(u, v, \lambda) = f(u) + g(v) - \lambda^T (Au + Bv - c) + \frac{\beta}{2} \| Au + Bv - c \|_2^2 .$$  \hspace{1cm} (7)

The penalty term with parameter $\beta > 0$ is added to enforce the constraint, and $\lambda \in \mathbb{R}^n$ is the Lagrange multiplier.

(7) can be written in an equivalent but more compact form as follows [57]:

$$\mathcal{L}(u, v, \lambda) = f(u) + g(v) + \frac{\beta}{2} \| Au + Bv - c + \frac{\lambda}{\beta} \|_2^2 .$$  \hspace{1cm} (8)

The standard split-variable ADMM algorithm finds the solution of (8) through an iterative process as following [17]:

$$\begin{align*}
\begin{cases}
    u^{i+1} &= \arg\min_u \mathcal{L}(u, v^i, \lambda^i) \\
    v^{i+1} &= \arg\min_v \mathcal{L}(u^{i+1}, v, \lambda^i) \\
    \lambda^{i+1} &= \lambda^i + \beta (Au^{i+1} + Bv^{i+1} - c)
\end{cases} .
\end{align*}$$  \hspace{1cm} (9)

As used in the next section, split-variable ADMM minimizes each term of the cost function separately. This property is beneficial in practice when a single optimization approach is not appropriate for both $f$ and $g$ functions. While the alternating minimization of $f$ and $g$ is much easier, it has been proven that ADMM iterations converge in convex optimization problems [17].

### IV. PROPOSED JOINT BEAMFORMING-DECONVOLUTION ALGORITHM

The main idea of the current work is to find the desired TRF by solving a joint inverse problem of beamforming and deconvolution. Using the same variables introduced in Section III, the proposed optimization problem is as follows:

$$\begin{align*}
\hat{x} &= \arg\min_{x} \gamma_D \| y_{DAS} - Hx \|_2^2 \\
&\quad + \gamma_B \| y_{ch} - \Phi x \|_2^2 + \mu \| x \|_1 .
\end{align*}$$  \hspace{1cm} (10)

In addition to least-square terms for beamforming and deconvolution, the $\ell_1$-norm regularization term is also considered to enforce the sparsity of the solution, which is a common choice in ultrasound imaging [11], [12], [13], but other regularization terms such as wavelet frames [38], $\ell_2$-norm [11], $\ell_p$-norms [58] can also be used with the proposed framework. $\gamma_D$, $\gamma_B$, and $\mu$
Algorithm 1: ADMM Algorithm for solving (10).

1: Input: \( H, \Phi, y \)
2: Set: \( \gamma_D > 0, \gamma_B > 0, \mu > 0, \beta > 0, u^0, v^0, \lambda^0, \epsilon \)
3: While stopping criterion \( > \epsilon \) do
   4: \( u^{i+1} = \text{argmin}_{u} \frac{\gamma_D}{2} \| y_{DAS} - H u \|_2^2 + \frac{\mu}{2} \| Au + Bv + \lambda_i \|_2^2 \)
   5: \( z^{i+1} = \text{argmin}_{z} \frac{\gamma_B}{2} \| y_{ch} - \Phi z \|_2^2 + \frac{\beta}{2} \| z \|_2^2 \)
   6: \( w^{i+1} = \text{argmin}_{w} \mu \| w \|_1 + \frac{\beta}{2} \| u^{i+1} - w + \lambda_i \|_2^2 \)
   7: \( \lambda^{i+1} = \lambda_i + \beta \left( A u^{i+1} + B v^{i+1} \right) \)
8: End

are constant hyperparameters controlling the contribution of the deconvolution, beamforming, and sparse regularization terms, respectively. It is obvious that the objective function in (10) is convex. The \( \ell_1 \) term, however, makes it nondifferentiable without a closed-form solution. Therefore, we split the independent variable \( x \) into three equivalent variables \( u, z, \) and \( w \) and consider the equality constraints. Hence, the new, but equivalent, form of (10) is as following:

\[
(u, w, \hat{z}) = \text{argmin}_{(u, w, z)} \left\{ \frac{\gamma_D}{2} \| y_{DAS} - H u \|_2^2 + \frac{\gamma_B}{2} \| y_{ch} - \Phi z \|_2^2 + \mu \| w \|_1 \right\} \text{ s.t. } \begin{cases} u = z, \\ u = w. \end{cases} \tag{11}
\]

By looking closely at (11), it can be considered as a specific form of the general formulation presented in (6) with the following correspondences:

\[
\begin{align*}
    f(u) &= \frac{\gamma_D}{2} \| y_{DAS} - H u \|_2^2 \\
g(v) &= \frac{\gamma_B}{2} \| y_{ch} - \Phi z \|_2^2 + \mu \| w \|_1 \\
v &= \begin{bmatrix} w \\ z \end{bmatrix}, \quad \lambda = \begin{bmatrix} \lambda_1 \\ \lambda_2 \end{bmatrix}, \\
A &= \begin{bmatrix} I \\ I \end{bmatrix}, \quad B = \begin{bmatrix} -I \\ 0 \end{bmatrix}, \quad c = 0
\end{align*}
\tag{12}
\]

where \( I \) refers to an identity square matrix of size \( n \), therefore, the augmented Lagrangian function of (11) is exactly the same as what was presented previously in (8), and its solution can be found using the split-variable ADMM approach.

Algorithm 1 describes the proposed solution of our cost function in the ADMM framework. Different terms of the (10) are minimized separately in each iteration. The algorithm is initialized by setting the hyperparameters \( \gamma_D, \gamma_B, \mu, \) and \( \beta \). A small constant value \( \epsilon \) is chosen as the threshold for the stopping criterion. The iterative optimization procedure is started with arbitrary initial values for the Lagrange multiplier \( (\lambda) \) and the new variables (i.e., \( u, w, \) and \( z \)). The proposed ADMM solution can be summarized in three steps as follows.

A. Deconvolution Update

In this step, the solution of the deconvolution term \( (u) \) is found by minimizing the corresponding subproblem written in line 4 of Algorithm 1. Since this cost function is convex and differentiable, the solution can be easily found by taking the gradient and setting it to zero. By doing so, the following closed-form solution is derived:

\[
u^{i+1} = \left( \gamma_D H^T H + 2\beta J \right)^{-1} \times \left( \gamma_B H^T y_{DAS} + \beta w^i + \beta z^i - \lambda_1^i - \lambda_2^i \right), \tag{13}
\]

where \( J \) is a matrix of ones with the same size as \( H^T H \). (13) can also be solved in the Fourier domain. This implementation has been successfully used in [16, 54] to reduce the computational complexity of the solution in each iteration.

B. Beamforming Update

The second step corresponds to the minimization of beamforming term written in line 5 of Algorithm 1. Same as step 1, if we set the gradient of the cost function to zero, we arrive at the following analytical solution:

\[
z^{i+1} = \left( \gamma_B \Phi^T \Phi + \beta J \right)^{-1} \left( \gamma_B \Phi^T y_{ch} + \beta u^{i+1} + \lambda_2^i \right), \tag{14}
\]

where \( \Phi^T \Phi \) is usually a square matrix of size several hundreds of thousands, and not even diagonal, nor one that can be diagonalized through Fourier transform. Therefore, (14) is intractable in practice as involves large matrix inversion. Fortunately, the modular property of ADMM provides the possibility of adopting iterative numerical methods to tackle this problem and find the solution of this step. Among different numerical algorithms, only the ones which do not involve the calculation of the Hessian matrix are applicable because the large size of matrix \( \Phi \) makes the calculation of Hessian intractable. Within this group of methods, the limited-memory Broyden–Fletcher–Goldfarb–Shanno (BFGS) solver\(^1\), as well as Least-Squares with QR factorization (LSQR) algorithm\(^2\) are tested herein. Limited-memory BFGS is a quasi-Newton approach that is highly efficient for unconstrained optimization of differentiable real-valued high-dimensional functions [59]. However, Limited-memory BFGS is still very time-consuming in our beamforming sub-problem since it uses its previous iterations to form a low-rank approximation of the Hessian matrix.

LSQR is an adaptation of the conjugate gradient algorithm for least-squares problems based on QR factorization at each iteration [60]. LSQR can only be used to find a solution to linear or damped least-squares problems. Therefore, to solve step 5 of Algorithm 1 using LSQR, it must be written in the form of a damped least-squares problem as follows:

\[
\hat{p} = \text{argmin}_{p} \left\| \frac{\Psi p - q}{\sqrt{\rho I}} \right\|_2^2. \tag{15}
\]

The above equation can be represented as follows:

\[
\hat{p} = \text{argmin}_{p} \frac{1}{2} \| \Psi p - q \|_2^2 + \frac{\rho}{2} \| p \|_2^2. \tag{16}
\]

\(^1\)MATLAB implementation is publicly available in this link: http://www.cs.ubc.ca/~schmidtm/Software/minFunc.html

\(^2\)MATLAB implementation is publicly available in this link: https://web.stanford.edu/group/SOL/software/bfgs
By looking closely at line 5 of Algorithm 1, it can be considered as a specific form of the general formulation presented in (16) with the following variable changes:

\[
\begin{align*}
    p &= z - u^{i+1} - \frac{\lambda_1}{\beta}, \\
    \Psi &= \Phi, \\
    q &= y_{ch} - \Phi u^{i+1} - \frac{\Phi \lambda_2}{\beta}, \\
    \rho &= \frac{1}{\beta}.
\end{align*}
\]

(17)

In practice, we have observed that both Limited-memory BFGS and LSQR methods converge to the same solution for beamforming step. As will be shown in Section VI-D, LSQR method helps to improve the speed of image reconstruction and make the ADMM iterations faster.

C. Sparsity and Lagrange Multiplier Updates

The final step of our method entails the optimization of sparsity constraints and updating the Lagrange multiplier. The minimization problem presented in line 6 of Algorithm 1 is commonly called as the proximal mapping of the \( L_1 \) norm as follows [57]:

\[
\text{prox}_{\mu\|\cdot\|_1/\beta} (u^{i+1} + \frac{\lambda_1}{\beta}) = \arg\min_w \mu \| w \|_1 + \frac{\beta}{2} \| u^{i+1} - w + \frac{\lambda_1}{\beta} \|_2^2.
\]

(18)

(18) is the minimization of a strictly convex function, and its unique minimizer can be presented in terms of shrinkage function [57], which acts as a soft-thresholding operator:

\[
w^{i+1} = \text{soft}_{\mu/\beta} (u^{i+1} + \frac{\lambda_1}{\beta}) = \max \left\{ \left| u^{i+1} + \frac{\lambda_1}{\beta} - \frac{\mu}{\beta} \right|, 0 \right\} \text{sign} \left( u^{i+1} + \frac{\lambda_1}{\beta} \right).
\]

(19)

Finally, the Lagrangian multiplier needs to be updated using the equation in line 7 of Algorithm 1.

In each iteration of Algorithm 1, the original objective function (i.e., (10)) is calculated, and its relative error for two consecutive iterations is used as the stopping criterion. The theoretical convergence of the split variable ADMM algorithm to a global minimum in any convex optimization problem has been shown [61].

V. EXPERIMENTS

A. Dataset

The performance of the proposed method is evaluated on a set of simulations, real phantoms, and in vivo publicly available PICMUS benchmark datasets [19]. PICMUS is the first beamforming competition that was held in conjunction with the 2016 IEEE International Ultrasonics Symposium (IUS) and designed to create a benchmark plane-wave dataset and facilitate the comparison of different approaches [19]. Details regarding PICMUS datasets can be found in [19] and are not repeated here to keep the paper concise. In short, simulation and experimental phantom images containing point targets are considered to assess the proposed methods in terms of spatial resolution (denoted by Simulation Resolution (SR) and Experimental Resolution (ER)). Also, simulation and experimental phantom images containing anechoic cysts are considered to assess the proposed methods in terms of contrast (denoted by Simulation Contrast (SC) and Experimental Contrast (EC)). In vivo images have been collected from the carotid artery of a volunteer subject, including cross-sectional (denoted by Carotid Cross (CC)) and longitudinal views (denoted by Carotid Longitudinal (CL)).

B. Evaluation Metrics

The images reconstructed using the proposed method are evaluated in terms of two main specialized ultrasound assessment indexes, including resolution and contrast. Furthermore, full-reference image quality measures containing Mean Square Error (MSE) as well as Structural Similarity index Measure (SSIM) are also reported to provide a better understanding of the performance of different methods. To do so, the result of Coherent Plane-Wave Compounding (CPWC), on 75 insufflation angles, is considered as the reference quality, and the indexes are calculated on the envelope data.

As for the resolution index, the Full Width at Half Maximum (FWHM) is calculated in the axial and lateral directions. The contrast index is reported in terms of the Contrast-to-Noise Ratio (CNR) as well as generalized CNR (gCNR). The CNR is calculated as follows:

\[
\text{CNR} = 20 \log_{10} \left( \frac{\mu_{ROI} - \mu_B}{\sqrt{\sigma_{ROI}^2 + \sigma_B^2}/2} \right),
\]

where \( \sigma_{ROI} \) and \( \sigma_B \) are the standard deviation of the image over the region of interest (ROI) and background, respectively. \( \mu_{ROI} \) and \( \mu_B \) are the means of image over the ROI and background, respectively.

Recently, it has been shown that quantitative indexes such as CNR and FWHM are not reliable when the dynamic range of the final image has been transformed [62], [63]. For example, FWHM improves by taking the square of an image while there is no new information content [63]. Therefore, it is recommended to use histogram matching (HM) prior to the visualization and making the quantitative measurements, which lead to fairer comparisons between different methods and would be an acceptable alternative [62], [63]. In the current study, HM is applied to all the presented results in the next section except for the SR experiment for which HM brings additional artifacts due to its binary content. Since a homogeneous speckle region of interest (ROI) has a well-behaved log-Rayleigh distribution for B-mode images, ROI-based HM (details can be found in [62]) is applied to the result of each method, and DAS output is considered as the reference image.

We have also reported generalized CNR (gCNR) criterion introduced in [64], which has been shown to be robust against
dynamic range alterations. \( g_{\text{CNR}} \) formula is as follows:

\[
g_{\text{CNR}} = 1 - \int_{-\infty}^{\infty} \min \{ p_{\text{ROI}}(x), p_B(x) \} \, dx,
\]

where \( p_B(x) \) and \( p_{\text{ROI}}(x) \) are the histograms of pixels measured in the background and ROI, respectively. \( g_{\text{CNR}} \) specifies the overlap intensity distributions of two regions regardless of grayscale intensity transformations. Higher distributions overlap leads to lower \( g_{\text{CNR}} \) values. When the two distributions are independent, \( g_{\text{CNR}} \) is equal to its maximum value of 1 [64].

It has to be mentioned that the resolution and contrast indexes are not reported for the in vivo datasets because there is no point or cyst target with a known position for which the index can be calculated. But full-reference image quality measures are calculated for all datasets since the reference image quality is always available. In order to remove the subjectivity in our quantitative evaluation, the resolution and contrast indexes are calculated by the codes provided by the PICMUS organizers. For each dataset, the regions of interest from which the index is calculated are shown on top of the CPWC results in the supplementary material (Section II).

VI. RESULTS

In this section, the results of the proposed joint formulation are compared with the sequential approach that entails beamforming followed by deconvolution. To better understand the effect of each term in the proposed joint cost function, the images reconstructed by only solving the inverse problem of beamforming (i.e., \( \gamma_D = 0 \) and \( \gamma_B = 1 \) in (10)) or deconvolution (i.e., \( \gamma_D = 1 \) and \( \gamma_B = 0 \) in (10)) are also presented in Section VI-A. Furthermore, to demonstrate the superiority of the proposed approach in comparison with the previous beamforming methods, the results of Eigenspace-based MV (EMV) [23], PCF [29], Fourier domain technique based on Stolt’s migration [34], and ultrasound Fourier slice beamforming (UFSB) [36] are included in Section VI-B. In order to have a fair comparison with the previous deconvolution methods, we need to keep the same regularization term. In other words, our results should be compared to a \( \ell_1 \) norm regularized deconvolution. As for the spatially-invariant PSF, it basically comes to canceling the beamforming data fidelity term in our algorithm, which is mentioned above. We have also compared our results with the previous method (called PMNB) [53] in which the spatial variance of the PSF is taken into account. The sensitivity analysis of the proposed method to initial points and parameter selection is presented in Section VI-C. Finally, in Section VI-D, the convergence graphs of the ADMM algorithm in different problems are presented. The convergence graphs of the ADMM and the Fast Iterative Shrinkage-Thresholding Algorithm (FISTA) are compared. Furthermore, the reconstruction times of all methods are reported and discussed for a single experiment.

Hereafter, we consider the Hanning apodization window with \( f_\# = 0.5 \) for DAS and other methods on top of DAS (except for in vivo datasets for which the Tukey (tapered cosine) window with constant parameter of 0.25 and \( f \)-number equals to 1.75 is considered). \( \epsilon = 10^{-3} \) is selected as the threshold for stopping criterion. The iterative algorithms are started with initial values equal to zero. Since the proposed joint formulation and also deconvolution approach require PSF, the method proposed in [65] has been adopted to estimate the unknown PSF from the RF data. The quantitative indexes are calculated independently for different point targets or cyst regions, and the average values are reported. The hyperparameters of each method are set independently to achieve the best results. Therefore, detailed information on the selected hyperparameters of each method is provided in the Appendix Section.

A. The Proposed Joint Formulation

1) Simulation and Experimental Data: The images reconstructed from the single 0\(^\circ\) plane-wave are presented in Fig. 3. The results of CPWC on 75 insuffications are illustrated in the second column of Fig. 3. The proposed joint formulation can successfully reconstruct high-quality images in terms of both resolution and contrast. Fig. 3 shows that the sequential approach has a poor performance because a part of image content get lost in the two consecutive soft-thresholding steps. As for the result of beamforming and deconvolution alone, the artificial improvement in contrast has been revoked by HM. And Fig. 3 depicts that only the results of CPWC and the proposed method are robust to HM.

As quantitative results of Table I confirm, the proposed method gives high axial and lateral resolutions for both simulation and experimental data similar to or even better than CPWC. The highest contrast corresponds to CPWC results since it averages over 75 angles and perfectly suppresses the side-lobe artifacts. For a single 0\(^\circ\) insuffocation, the proposed approach improves the contrast as compared to other methods. This point can also be seen in the quantitative comparison reported in Table I.

2) In Vivo Data: The proposed method is also evaluated on real data collected from the carotid artery. The visual comparison of different approaches is illustrated in Fig. 4. As can be seen in Fig. 4, the proposed method is able to suppress the clutter artifacts caused by diffuse reverberation from shallow layers.
and create a dark image of the artery in both cross-sectional and longitudinal views (pointed out by red arrows). The results of previous beamforming and deconvolution approached on the in vivo datasets are provided in the supplementary material (Section III).

B. Comparison With Other Methods

In this section, the results of previous beamforming and deconvolution methods are shown. We have included an example from each group of classical beamforming methods reviewed in
Fig. 5. Simulation and experimental images reconstructed through previous beamforming and deconvolution approaches. Rows indicate datasets while columns correspond to different approaches. (a) EMV [23]. (b) PCF [29]. (c) UFSB [36]. (d) Stolt’s migration [34]. (e) PMNB [53]. (f) The proposed joint formulation. All the results are from a single 0° insonification. The sharp point targets and dark cyst regions are desired.

Section II plus a deconvolution method based on nonstationary PSF [53]. The results of DAS and inverse problem formulation are presented along with the proposed approach in Section VI-A. The visual comparison of results, presented in Fig. 5, indicates that EMV only gives a better lateral resolution for SR dataset as compared to the proposed method. This point can also be understood from the quantitative comparison reported in Table I. PCF works better than DAS in terms of axial resolution, while its results are still worse than the proposed method. In terms of lateral resolution, however, the results are discussible. While EMV substantially improves the lateral resolution of simulation data, the same improvement was not achieved in the real phantom experiment. The reason behind this difference is the number of eigenvectors of the covariance matrix used for creating the signal subspace. More specifically, EMV only needs the principal eigenvectors of the SR data to successfully reconstruct the image because it only includes some point targets. However, if we only consider some of the eigenvectors in the ER case, a part of the speckle texture would be lost. This variation in improvement is also seen in terms of contrast. That is because of the additional noise of experimental data, which reduces the quality of covariance matrix estimation.

In short, the comparison with previous approaches reveals that the proposed method gives the most consistent improvement in image quality for all datasets. Although other methods may provide better qualities in specific cases, their performance drops in other experiments. This point can also be seen for Stolt’s migration [34] as well as PMNB [53] approaches, which give a high resolution in ER experiment but has a low performance for other datasets.

In Table II, the results of all methods are compared with the CPWC’s outputs. The MSE, as well as SSIM indexes, depict that the proposed method’s output is of high similarity to the reference image. Although the general metrics are less informative as compared to the specialized ultrasound assessment indexes, the superior performance of the proposed method can still be observed in comparison to other approaches.

C. Sensitivity Analysis

As mentioned in Algorithm 1, the proposed method is initialized with the arbitrary values for the Lagrange multiplier (λ) and new variables (i.e., u, w, and z). Furthermore, hyperparameters γD, γB, μ, and β, which respectively specify the weights of deconvolution, beamforming, sparsity, and penalty terms, need to be set.

Generally, the initial values of λ and new variables do not make any difference to the final solution because the proposed
TABLE II

| dataset   | SR     | ER     | SC     | BC     | CC     | CL     |
|-----------|--------|--------|--------|--------|--------|--------|
| index     | MSE    | SSIM   | MSE    | SSIM   | MSE    | SSIM   |
| DAS       | 6.15x10^-5 | 0.9    | 4.17x10^-4 | 0.85 | 0.0016 | 0.75   | 4.62x10^-4 | 0.82 | 2.05x10^-4 | 0.88 | 6.33x10^-4 | 0.82 |
| Beamforming | 2.32x10^-5 | 0.98   | 3.91x10^-4 | 0.85 | 0.0018 | 0.67   | 4.69x10^-4 | 0.8   | 2.08x10^-4 | 0.88 | 6.41x10^-4 | 0.82 |
| Deconvolution | 1.28x10^-4 | 0.98   | 4.27x10^-4 | 0.85 | 0.0018 | 0.73   | 4.45x10^-4 | 0.81 | 3.01x10^-4 | 0.87 | 6.77x10^-4 | 0.81 |
| Sequential | 2.48x10^-6 | 0.98   | 1.46x10^-4 | 0.84 | 0.0018 | 0.67   | 5.14x10^-4 | 0.76 | 2.62x10^-4 | 0.88 | 6.43x10^-4 | 0.82 |
| Joint     | 2.1x10^-6 | 0.99   | 3.65x10^-4 | 0.86 | 0.0017 | 0.77   | 4.44x10^-4 | 0.82 | 2.14x10^-4 | 0.88 | 6.16x10^-4 | 0.82 |

EMV [23] 1.47x10^-4 0.97 0.012 0.55 0.04 0.61 0.0039 0.66 8.39x10^-4 0.78 0.0028 0.69
PCF [29] 6.41x10^-5 0.96 0.013 0.83 0.006 0.48 0.0031 0.54 0.014 0.74 0.0024 0.57
Solt [34] 2.32x10^-5 0.85 0.73 0.43 0.04 0.2 0.0035 0.59 5.54x10^-4 0.83 0.0011 0.75
UPSB [36] 2.29x10^-5 0.9 0.44 0.52 0.02 0.31 9.74x10^-4 0.69 7.3x10^-4 0.77 0.0021 0.65
PMNB [53] 5.29x10^-5 0.94 0.001 0.79 0.003 0.55 0.0019 0.6 0.0021 0.76 0.0015 0.69

Herein, the result of cpws, on 75insonation angles, is considered as the reference quality. Bold numbers refer to the best performances among different methods.

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objective function is convex, and there is no local minimum. Notwithstanding, the starting points can affect the processing time and the number of iterations for convergence. For all the results presented here, zero is used as the initial value, and the proposed algorithm always converges in less than 40 iterations. The code is implemented in Windows 10 using the MATLAB R2021a programming platform.

The parameter $\beta$ determines the weight of penalty term in the augmented Lagrangian function. It is necessary to set a large value to $\beta$ because the split-variable ADMM algorithm must perfectly accomplish the equality constraints of new variables (11). Otherwise, a small $\beta$ allows the algorithm to converge toward different values for $u$, $w$, and $z$ which is not justifiable.

Different hyperparameters’ values may completely change the final solution. To demonstrate the effect of each one in the proposed algorithm, the SC image is reconstructed multiple times with different sets of hyperparameters. First, (10) is solved by only considering the beamforming term (i.e., $\gamma_D = 0$ and $\mu = 0$ in (10)). As explained in Section III-A, each row of matrix $\Phi$ contains the contribution of all pixels that simultaneously arrive to a piezoelectric element. Therefore, as can be seen in the first column of Fig. 6, the result is even worse than DAS, mainly due to the off-axis echoes. The second column of Fig. 6 only depicts the effect of the deconvolution term (i.e., $\gamma_B = 0$ and $\mu = 0$ in (10)) in which the speckle texture is sharper due to the mitigation of PSF. However, the cyst regions still suffer from clutter artifacts. The beamforming and deconvolution terms are combined with the same weights in the third column of Fig. 6. The resulting image confirms that the beamforming term was dominant since the solution is similar to the first column. Therefore, the beamforming weight (i.e., $\gamma_B$) is reduced to ensure a better balance between both terms. As the fourth column of Fig. 6 shows, the resulting image is of better contrast, while the speckle texture is also sharp. In order to reduce clutter artifacts in the cyst regions, the sparsity regularization term is also considered in the fifth column of Fig. 6. However, a large $\mu$ wipes out the speckle texture and the resulting image becomes too dark. This artificial improvement in contrast index is always revoked by HM. Finally, once the regularization term is also reduced, the resulting image is of high quality and takes the benefits of all three terms simultaneously (the sixth column of Fig. 6).

D. Convergence Analysis

Generally, an important point regarding the optimization algorithms used for solving the inverse problem of imaging is the convergence. The theoretical analysis of the convergence for the ADMM algorithm and its computational cost is out of the scope of the current work. Therefore, a plot of stopping criterion versus iteration for different problems solved by ADMM is provided in Fig. 7(a). As mentioned in Section IV-C, in each iteration ($i$) of the proposed algorithm, the objective function (i.e., (10)) is
calculated and its relative error for two consecutive iterations is used as the stopping criterion. The proposed joint formulation clearly starts with a higher relative error since it consists of both beamforming as well as deconvolution terms while ADMM converges roughly in 40 iterations for all three problems. In addition to ADMM, (10) is also solved by the Fast Iterative Shrinkage-Thresholding Algorithm (FISTA) [66]. Fig. 7(b) illustrates the convergence of ADMM and FISTA for the reconstruction of the SC dataset. Although FISTA needs more iterations for convergence, its reconstruction time is better than ADMM if the ADMM iterations include the time-consuming BFGS solver. Otherwise, if we use LSQR instead of BFGS in the beamforming step, the reconstruction time of ADMM is better.

VII. DISCUSSIONS

The sequential approach and joint formulation comparison, presented in Figs. 3 and 4, confirm that solving the beamforming and deconvolution problems separately does not lead to the same quality. This might be due to a loss of information in the first step of the sequential approach. The same observation has been reported in [16].

Another important advantage of the proposed joint formulation is the substantial improvement in axial resolution, which is reported in Table I. As reported in Section VI-B,
other beamforming approaches either do not change or have a lower effect on the axial resolution as compared to our results. This point is crucial because the resolution in the axial direction is usually increased by transmitting pulses with a higher center frequency.

The achieved improvement in image quality can reduce the need to transmit several plane waves with different angles. Furthermore, the proposed framework provides the possibility of considering the result of any other beamforming approach (not only DAS) in the deconvolution term. More specifically, (5) can also be written for other beamformers, and consequently, \( y_{DAS} \) in the deconvolution term of (10) can be substituted by the result of other methods such as MVB.

Using ADMM makes the optimization step of the proposed method easy to implement. As the proposed algorithm is iterative and the variables are updated serially, parallel implementation is not straightforward. Therefore, although our method is faster than a computationally expensive algorithm such as MV, real-time image reconstruction using the proposed method might not be possible. This would be the subject of our future research.

Although the proposed idea can be applied to any imaging technique (i.e., focused, plane-wave, and synthetic aperture imaging) or probe type (i.e., linear, convex, and phased array), only the benchmark PICMUS dataset is used here because it is publicly available and the comparison with previous approaches is easier. It also helps the readers to reimplement the algorithm and verify the results easily. The proposed method can also be applied on top of the CPWC. However, the presented results are only limited to a single transmission angle in order to make
ensure that the achieved improvement is due to the advantages of the proposed approach, not due to increasing the number of transmissions.

It has been previously shown that solving the inverse problem of beamforming gives images with high resolution and contrast [11], [12], [13]. This improvement, however, comes at the expense of speckle information loss. Furthermore, the inverse problem of deconvolution cannot solely improve the image quality. Combining both terms in our proposed objective function helps to achieve a high resolution and contrast while the speckle texture is also preserved. This point can be seen in Fig. 3 for ER data. The proposed method’s ability to preserve the speckle texture is of crucial importance in image computing applications such as speckle tracking and tissue classification. In addition, experienced radiologists often rely on the speckle pattern for diagnosis.

The performance of the proposed method directly depends on the quality of the estimated PSF of the imaging system. Herein, we utilize a common approach used in previous literature [15], [16], [54]. However, any method for PSF estimation can also be used to improve the results. An interesting avenue for future work is to incorporate deconvolution models based on the non-stationary PSF [53] or harmonic components in the RF data [54].

### VIII. Conclusion

Beamforming and deconvolution have only been used separately in a sequential approach. Herein, we proposed a novel formulation for combining both methods. A regularized inverse problem including two linear models for beamforming and deconvolution plus additional sparsity constraint is solved using the ADMM algorithm. The proposed image reconstruction approach is a joint optimization problem that uses DAS results as an observation. The results show that the proposed iterative method gives ultrasound images with a high resolution and contrast.

### Appendix

Table III includes the value of hyperparameters selected for different approaches in each experiment. In the EMV method, the subarray size equals 64, the temporal averaging factor is set to 1.5, and the diagonal loading is 0.01. The signal subspace is created using all eigenvectors of the covariance matrix except for the SR experiment, for which only considering the largest 10% is enough.

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