Joint Segmentation and Deconvolution of Ultrasound Images Using a Hierarchical Bayesian Model based on Generalized Gaussian Priors

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Abstract

This paper addresses the problem of ultrasound (US) image deconvolution within a Bayesian framework. US images exhibit characteristic speckle patterns previously shown to be strictly correlated with the tissue structures. As a result, the statistical properties of the speckle have been extensively studied as source of information for applications such as image segmentation, deconvolution and tissue characterization. We investigate herein the generalized Gaussian distribution which has been recently shown to be one of the most relevant distributions for ultrasound radio-frequency signals. The main contribution of this paper is to propose a new hierarchical Bayesian model for a joint US image deconvolution and segmentation. Precisely, by introducing the labels for the image pixels, we propose a new Bayesian model allowing the US images to be jointly segmented into several statistically homogeneous regions and to be deconvolved resulting into tissue reflectivity maps. The Bayesian estimators associated with the proposed model are difficult to be expressed in closed form. Thus, we investigate a Markov chain Monte Carlo method to generate samples distributed according to the posterior of interest. These generated samples are finally used to compute the Bayesian estimators of the unknown parameters. The performance of the proposed Bayesian model is compared with existing approaches via several experiments conducted on realistic synthetic data and in vivo ultrasound images.

Index Terms

Generalized Gaussian distribution, Ultrasound imaging, Bayesian inference, Gibbs sampler, Potts-Markov field.

I. INTRODUCTION

ULTRASOUND (US) imaging is a well-established medical imaging modality widely used for clinical diagnosis, visualization of anatomical structures, tissue characterization or blood flow measurements. The popularity of US imaging compared to other imaging modalities such as computed tomography (CT) or magnetic resonance imaging (MRI) is mainly due to its efficiency, low cost and safety [1]. Despite these advantages and the recent advances in instrumentation [2] and beamforming [3], it also has some limitations, mainly related to its poor signal-to-noise ratio, limited contrast and spatial resolution. Furthermore, US images are characterized by speckle, which considerably reduces their quality and may lead to interpretation issues. For this reason, several despeckling methods can be found in the US literature [4], [5]. Despite its negative effect, speckle has also been extensively used as a source of information in applications such as image segmentation and tissue characterization [6], [7]. Specifically, it has been shown that the statistical properties of the speckle are strictly correlated with the tissue structures [7]. Thus, methods for US image restoration using the statistical properties of the speckle noise are also an interesting research track in US imaging [8], [9].

Under the first order Born approximation and the assumption of weak scattering classically assumed for soft tissues [10], the radio-frequency (RF) US images can be modeled as the convolution between a...
blurring operator/point spread function (PSF) and a tissue reflectivity function. The resulting linear model recalled hereafter has been extensively used in literature (see, e.g., [8]–[12])

\[ y(i, j) = h(i, j) \otimes x(i, j) + n(i, j) = \sum_{k=1}^{m} \sum_{l=1}^{n} h(i - k, j - l)x(k, l) + n(i, j) \]  

(1)

where \( (i, j) \in \{1, \ldots, m\} \times \{1, \ldots, n\} \) (where \( N = m \times n \) is the image size), \( \otimes \) is the two dimensional (2D) convolution operator, \( h \) is the system PSF, \( y(i, j) \), \( x(i, j) \) and \( n(i, j) \) are the samples of the RF image, the tissue reflectivity function and the additive white Gaussian noise (AWGN) (that herein mainly represents the measurement incertitude). We emphasize that the noise in (1) does not represent the multiplicative speckle noise considered in US despeckling techniques [5]. Indeed, the multiplicative speckle noise is not adapted to RF data but to envelope images obtained after amplitude demodulation of the raw signals. The linear model in (1) can be classically rewritten using a matrix-vector formulation as follows

\[ y = Hx + n \]  

(2)

where \( x \), \( y \), and \( n \) belong to \( \mathbb{R}^{N \times 1} \) (these vectors are obtained after lexicographical ordering the corresponding images) and \( H \in \mathbb{R}^{N \times N} \) is a block circulant with circulant block matrix associated with the PSF. Furthermore, the PSF in US imaging is shift-variant mainly along the axial direction due to physical effects caused by the wave propagation and imaging medium such as diffraction or attenuation. Generally, US images are divided into several local regions along the axial direction. In each region, the local PSF is assumed shift-invariant. The global blurring matrix is built in this case by combining these local shift-invariant PSFs. Mathematically, it can be formulated as \( H = \sum_{k} D_k H_k \), where \( H_k \) is the local shift-invariant PSF of the \( k \)-th region and \( D_k \) is the corresponding diagonal weighting matrix [8], [9], [13], [14] which satisfies \( \sum_{k} D_k = I_{N \times N} \) (\( I_{N \times N} \) is the \( N \times N \) identity matrix). The choice of the weighting matrix defines the type of interpolation between the \( k \)-th regions. Following the results in [8], [9], piecewise constant and piecewise linear interpolations were shown to be good choices for US images. Moreover, due to some physical corrections related to image formation (e.g., time gain compensation, dynamic beamforming), in most of soft tissues, \( H \) can be assumed shift invariant. In what follows, without loss of generality, we focus on the deconvolution of a stationary image segment and consider therefore that the PSF is shift-invariant [12]. Note that the PSF is unknown in practical applications and its estimation has been extensively explored in US imaging. A typical approach in US imaging, also adopted in this paper, is to estimate the PSF in a pre-processing step before applying the deconvolution algorithm (see, e.g., [9], [10]).

US image deconvolution, aiming to estimate the tissue reflectivity map \( x \) from the RF data \( y \) is a typical ill-posed problem. Imposing a regularization constraint is one traditional way to cope with this problem. The regularization constraint reflects the prior knowledge about \( x \). In US imaging, Gaussian and Laplacian distributions have been widely explored as prior distributions for the image \( x \), leading to \( \ell_2 \)-norm [15] and \( \ell_1 \)-norm [12], [16] constrained optimization problems. More recently, it has been shown that the statistical properties of the RF image [17] and of the tissue reflectivity map [9] can be accurately described by a generalized Gaussian distribution (GGD). Alessandri et al. proposed a GGD-based deconvolution algorithm dedicated to US imaging using an expectation maximization (EM) algorithm in [18]. Despite its accuracy when compared to several state-of-the-art US imaging deconvolution methods, the framework in [18] has two major drawbacks that we propose to tackle with in this paper. Firstly, it is well-known that the EM approach can easily converge to a local minima of the cost function and is sensible to the initial values of the parameters to be tuned, which may yield inaccurate estimates. Secondly, the EM can only be applied to cases where the mask (or labels) of the homogeneous regions are known.

We introduce in this paper a new hierarchical Bayesian model with GGD priors dedicated to US image restoration. Motivated by the fact that image segmentation and deconvolution are mutually supported, i.e., the solution of either problem would become fairly straightforward given the other one [19], [20], the proposed method combines the US image deconvolution and segmentation. Specifically, we consider a
mixture of GGDs with different parameters as prior distribution for the US tissue reflectivity image. The motivation of the GGD mixture model is two-fold. Firstly, it serves as prior information to regularize the ill-posed deconvolution problem. Secondly, it is common in the literature related to US image segmentation to consider that different anatomical structures result in regions of pixels having different features, i.e., the same statistics but with different parameters. Based on the dependencies between the adjacent elements and the label map, a Potts Markov random field (MRF) model is implemented as prior information to regularizing the ill-posed segmentation problem. To our knowledge, our method represents a first attempt to joint segmentation-deconvolution in US imaging.

The complicated form of the resulting posterior distribution makes it too difficult to compute closed form expressions of the corresponding Bayesian estimators. Therefore, a Markov Chain Monte Carlo (MCMC) method based on a Gibbs sampler is investigated in this paper to sample the posterior distribution of interest. The principle of the Gibbs sampler is to generate samples distributed according to conditional distributions of the joint posterior of the unknown variables. Estimations of the unknown variables can then be computed using these generated samples.

This paper is organized as follows. The statistical hierarchical Bayesian model proposed for image segmentation and deconvolution is introduced in Section II. Section III studies a hybrid Gibbs sampler, which generates samples distributed according to the conditional distributions of the proposed model. Simulation results obtained on synthetic data, realistic simulated and \textit{in vivo} US data are presented in Section V. Conclusions are finally reported in Section VI.

II. PROBLEM FORMULATION

Bayesian inference assumes that the vector containing the unknown model parameters (denoted as $\theta$) is a realization of a random vector with an appropriate prior distribution. Combining this prior distribution with the likelihood of the observation allows the posterior distribution of $\theta$ to be computed. The unknown parameter vector $\theta$ can then be estimated by computing the mean or the maximum of the posterior distribution. The resulting Bayesian estimators are referred to as minimum mean-squared error (MMSE) or maximum a posteriori (MAP) estimators. This section defines the likelihood of model (2) and the priors assigned to the unknown parameters of the proposed hierarchical model.

A. Likelihood function

Assuming the additive noise is white Gaussian noise (AWGN) with variance $\sigma_n^2$, the likelihood function associated with the linear model (2) is

$$p(y|x, \sigma_n^2) = \frac{1}{(2\pi \sigma_n^2)^{N/2}} \exp \left( -\frac{1}{2\sigma_n^2} \|y - Hx\|^2_2 \right)$$

where $\|\cdot\|_2$ is the Euclidean $\ell_2$-norm.

B. Prior Distributions

1) Reflectivity image $x$: Following the works conducted in [9], [17], [21], the samples of the US RF image in different homogeneous regions (representing different anatomical structures) can be assigned GGD priors with different shape and scale parameters. Assuming the image is made up by $K$ homogeneous regions, we introduce a label vector $z \in \mathbb{R}^N$ mapping the image into the $K$ regions, i.e., $\{R_1, ..., R_K\}$. More precisely, $z_i = k$ if and only if the corresponding pixel $x_i$ belongs to the region $R_k$. The conditional distribution of pixel $x_i$ is then defined as

$$x_i|z_i = k \sim GGD(\xi_k, \gamma_k)$$
where $\xi_k$ and $\gamma_k$ are the shape and scale parameters of the GGD associated with the region $R_k$. Assuming that the pixels are independent conditionally to the knowledge of their classes, we obtain the following prior for the target image

$$p(x|z) = \prod_{k=1}^{K} \prod_{i=1}^{N_k} \frac{1}{2 \gamma_k^{1/\xi_k} \Gamma(1 + 1/\xi_k)} \exp\left(-\frac{|x_i|^{\xi_k}}{\gamma_k}\right)$$

$$= \prod_{k=1}^{K} \frac{1}{2 \gamma_k^{1/\xi_k} \Gamma(1 + 1/\xi_k)}^{N_k} \exp\left(-\frac{\sum_{i=1}^{N_k} |x_i|^{\xi_k}}{\gamma_k}\right)$$

$$= \prod_{k=1}^{K} \frac{1}{2 \gamma_k^{1/\xi_k} \Gamma(1 + 1/\xi_k)}^{N_k} \exp\left(-\frac{\|x_k\|^{\xi_k}}{\gamma_k}\right)$$

(4)

where $\xi_k$ and $\gamma_k = (\sqrt{\sigma_k^2 \Gamma(1/\xi_k)}/\Gamma(3/\xi_k))^{\xi_k}$ are the shape and scale parameters of the $k$th region ($\sigma_k^2$ is the variance of class $k$), $N_k$ is the number of pixels in region $R_k$, $x_k$ contains all the pixels assigned to $R_k$, $\Gamma(\cdot)$ is the gamma function and $\|x_k\|_\xi = (\sum_{i=1}^{N_k} |x_i|^{\xi_k})^{1/\xi}$ denotes the $\ell_\xi$-norm.

2) Noise variance $\sigma_n^2$: In the presence of an AWGN, it is very classical to assign a conjugate inverse gamma (IG) prior to the noise variance, i.e.,

$$p(\sigma_n^2) \sim IG(\alpha, \nu)$$

$$= \frac{\nu^\alpha}{\Gamma(\alpha)} (\sigma_n^2)^{\alpha-1} \exp\left(-\frac{\nu}{\sigma_n^2}\right).$$

(5)

This prior has two adjustable parameters $\alpha, \nu$ which make it very flexible and thus appropriate to the variance of most statistical models. The values of $\alpha$ and $\nu$ have been fixed by cross validation in our experiments leading to $(\alpha, \nu) = (0.1, 0.1)$.

3) Labels $z$: A Potts model (generalization of the Ising model) is considered as prior for the image label field. The Potts MRF has been shown to be particularly suited for image segmentation [22], [23]. This idea is motivated by the need to establish dependencies between pixels that are nearby in an image [7], [23]. More specifically, adjacent labels of the image are dependent and tend to be in the same class. The conditional distribution of $z_n$ (associated with pixel $x_n$) for the Potts MRF is defined as

$$p(z_n|z_{-n}) = p(z_n|z_{\mathcal{V}(n)})$$

(6)

where $z_{-n} = (z_1, ..., z_{n-1}, z_{n+1}, ..., z_N)$ and $\mathcal{V}(n)$ contains the neighbors of label $z_n$, which are strongly correlated. In this paper, the first order neighborhood structure (i.e., 4 nearest pixels) is considered. The whole set of random variables $z$ forms a random field.

Using the Hammersley-Clifford theorem [24], the prior of $z$ can be expressed as a Gibbs distribution, i.e.,

$$p(z) = \frac{1}{C(\beta)} \exp[\Phi_\beta(z)]$$

(7)

with

$$\Phi_\beta(z) = \sum_{n=1}^{N} \sum_{n'\in\mathcal{V}(n)} \beta \delta(z_n - z_{n'})$$

(8)

where $\beta$ is the granularity coefficient or smooth parameter, $\delta(\cdot)$ is the Kronecker function and $C(\beta)$ is the normalizing constant (often referred to as partition function). The value of $\beta$ has been fixed by cross validation in this paper ($\beta = 1$ for all experiments presented in Section IV). However, it is interesting to mention the works conducted in [7], [23] aiming at estimating the value of $\beta$ from the image samples. Note that small values of $\beta$ are adapted to large numbers of classes and vice versa.
4) Shape and scale parameters: The GGD prior for the US tissue reflectivity defined in (4) depends on the shape parameters $\xi = (\xi_1, ..., \xi_K)$ and the scale parameters $\gamma = (\gamma_1, ..., \gamma_K)$ of the GGDs, which are usually referred to as hyperparameters. Following the works in [25], we have chosen the following priors for the hyperparameters

$$p(\xi) = \prod_{k=1}^{K} p(\xi_k) = \prod_{k=1}^{K} \frac{1}{3} I_{[0,3]}(\xi_k)$$  
(9)

$$p(\gamma) = \prod_{k=1}^{K} p(\gamma_k) = \prod_{k=1}^{K} \frac{1}{\gamma_k} I_{R^+}(\gamma_k)$$  
(10)

where $k \in \{1, ..., K\}$ and $I_A$ is the indicator function on the set $A$. Note that the range $[0, 3]$ covers all the possible values of $\xi_k$ and that $p(\gamma_k)$ is the uninformative Jeffreys prior for $\gamma_k$. Note also that this particular choice for the hyperparameter priors was also made in [25] and provided interesting results for frame-based image restoration.

C. Joint posterior distribution

The Bayes rule is classically defined as

$$p(\mathbf{x}|\mathbf{y}) \propto p(\mathbf{y}|\mathbf{x})p(\mathbf{x})$$  
(11)

where $\propto$ means “proportional to”. From (11), the joint posterior distribution of the unknown parameters $\mathbf{x}, \sigma^2, \xi, \gamma, \mathbf{z}$ is

$$p(\mathbf{x}, \sigma^2, \xi, \gamma, \mathbf{z}|\mathbf{y}) \propto p(\mathbf{y}|\mathbf{x}, \sigma^2, \xi, \gamma, \mathbf{z})p(\mathbf{x}, \sigma^2, \xi, \gamma, \mathbf{z})$$

$$\propto p(\mathbf{y}|\mathbf{x}, \sigma^2, \xi, \gamma, \mathbf{z})p(\mathbf{x}|\xi, \gamma, \mathbf{z})p(\sigma^2) \propto p(\mathbf{z})p(\mathbf{y})p(\mathbf{x})$$

$$\propto \frac{1}{(2\pi\sigma^2)^{N/2}} \exp\left(-\frac{1}{2\sigma^2} \sum_{n=1}^{N} (y_n - Hx_n)^2\right) \times \frac{1}{(\sigma^2)^{a+1}} \exp\left(-\frac{\nu}{\sigma^2}\right)$$

$$\times \prod_{k=1}^{K} \left\{ a_k^{N_k} \exp\left(-\frac{1}{a_k^{N_k}} \sum_{n=1}^{N_k} (z_n - z_n')\right) \times \frac{1}{3} I_{[0,3]}(\xi_k) I_{R^+}^{[0,\infty]}(\gamma_k) \right\}$$  
(12)

where $a_k = \frac{1}{2\gamma_k^{N_k} \Gamma(1+1/\xi_k)}$ and the hyperparameters are supposed to be a priori independent.

Computing the closed-form expressions of the MMSE or MAP estimators for the unknown parameters $\mathbf{x}, \sigma^2, \xi, \gamma, \mathbf{z}$ from (12) is clearly complicated. In this case, a possible solution is to consider MCMC methods in order to generate samples distributed asymptotically according to the distribution of interest (here (12)) and to use the generated samples to build estimators of the unknown parameters. It is precisely the objective of the next section. Fig. summarizes the proposed hierarchical Bayesian model as a directed acyclic graph (DAG), in which the relationships between the parameters and hyperparameters are indicated.

III. HYBRID GIBBS SAMPLER

The principle of MCMC methods is to construct a Markov chain whose equilibrium distribution is the target posterior distribution. One of the most popular MCMC methods is the Gibbs sampler, which generates samples according to the conditional distributions of the target distribution, or to the conditional distributions of parameter subvectors (block Gibbs sampler). The generated samples are then used to build Bayesian estimators such as the the minimum mean square error (MMSE) or the maximum a posteriori (MAP) estimators.

When a conditional distribution of the unknown parameter vector cannot be sampled easily, we can generate this variable or subvector of interest according to an appropriate proposal and accept or reject this generated sample using the Metropolis acceptance ratio. When Metropolis moves are used inside a Gibbs
sampler, the resulting MCMC method is referred to as Metropolis-within-Gibbs or hybrid Gibbs sampler. The reader is invited to consult [26] for more details. The proposed hybrid Gibbs sampler investigated in this paper is a 5-step algorithm summarized in Algo. 1. The algorithm is explained in detail in what follows.

Algorithm 1: Hybrid Gibbs Sampler

```plaintext
/* Sampling the noise variance \(\sigma_n^2\) */ 1
/* Sampling the noise variance \(\sigma_n^2\) according to the conditional distribution (14). */
/* Sampling the shape parameters \(\xi\) */ 2
/* Sampling the shape parameter \(\xi_k\) according to the conditional distribution (16) by using a Metropolis Hastings move with a Gaussian proposal. */
/* Sampling the scale parameters \(\gamma\) */ 3
/* Sampling the scale parameter \(\gamma_k\) using (20). */
/* Sampling the labels \(z\) */ 4
/* Sampling the labels \(z\) according to the normalized conditional distribution (24). */
/* Sampling the reflectivity image \(x\) */ 5
/* Sampling the reflectivity image \(x\) using an HMC method. */
```

A. Sampling the noise variance

The conditional distribution of \(\sigma_n^2|y, x, \xi, \gamma, z\) can be expressed as follows

\[
p(\sigma_n^2|y, x, \xi, \gamma, z) \propto p(y|x, \sigma_n^2, \xi, \gamma, z)p(\sigma_n^2)
\]

\[
\propto \frac{1}{(2\pi\sigma_n^2)^{N/2}} \exp \left( -\frac{1}{2\sigma_n^2} \|y - Hx\|_2^2 \right) \times \frac{\nu^\alpha}{\Gamma(\alpha)(\sigma_n^2)^{\alpha+1}} \exp \left( -\frac{\nu}{\sigma_n^2} \right)
\]

\[
\propto (\sigma_n^2)^{-\alpha-N/2-1} \times \exp \left[ -\frac{1}{\sigma_n^2} \left( \nu + \frac{1}{2} \|y - Hx\|_2^2 \right) \right]. \tag{13}
\]

It is the inverse Gamma distribution

\[
IG \left( \alpha + N/2, \theta + \frac{1}{2} \|y - Hx\|_2^2 \right) \tag{14}
\]

Therefore, the generation of samples from the conditional distribution of \(\sigma_n^2\) is straightforward.
B. Sampling the shape parameter vector $\xi$

The conditional distribution of the shape parameter vector of the proposed GGD satisfies the following relation

$$p(\xi|y, x, \sigma^2_n, \gamma, z) \propto p(y|x, \sigma^2_n, \xi, \gamma, z)p(x|\xi, \gamma, z)p(\xi)$$

Assuming that the shape parameters are a priori independent, we have

$$p(\xi_k|x, \gamma, z, \xi_{-k}) \propto p(x_k|\xi_k, \gamma_k, z_k)p(\xi_k)$$

$$\propto d_k^{N_k} \exp \left( -\frac{\|x_k\|_{\xi_k}}{\gamma_k} \right) I_{[0,3]}(\xi_k)$$

(16)

where $\xi_{-k} = (\xi_1, ..., \xi_{k-1}, \xi_{k+1}, ..., \xi_K)$ for $k \in \{1, ..., K\}$, $x_k$ contains the pixels belonging to class $k$ and $z_k$ is built from the corresponding labels. Unfortunately, the conditional distribution (16) is not easy to sample directly. Thus, we propose to consider a random walk Metropolis Hastings (RWMH) move [27]. Specifically, the proposal used in this move is a truncated Gaussian distribution whose variance (or stepsize) can be adjusted to obtain a suitable average acceptance ratio, i.e., a candidate $\xi_k^*$ is generated as follows

$$\xi_k^* \sim \mathcal{N}(\xi_k^{(t)}, \delta)I_{[0,3]}(\xi_k^*)$$

(17)

This candidate is then accepted or rejected according to the following ratio

$$\rho = \min \left\{ \frac{p(\xi_k^*|x, \gamma, z, \xi_{-k})}{p(\xi_k^{(t)}|x, \gamma, z, \xi_{-k})}, 1 \right\}$$

(18)

We propose to adjust the stepsize $\delta$ every 100 iterations to achieve a reasonable acceptance rate (30% – 90%) [28]. Specifically, if the acceptance ratio during 100 iterations is larger than 90% (respectively smaller than 30%), then the stepsize $\delta$ is decreased (respectively increased) of 20% compared to its previous value. Note that to ensure the homogeneity of the Markov chain after the burn-in period, this tuning procedure is only executed during the burn-in period. The stepsize is then fixed during the following iterations.

The algorithm used to sample $\xi_k$ is finally divided into three procedures that are summarized in Algo. 2.

**Algorithm 2: Adjusted RWMH Algorithm**

```plaintext
/* Initialization Procedure */
1 Choose an initial value $\xi_0$;
/* Candidate Generation Procedure */
2 for $t = 1 : N_{MC}$ do
   3 $\xi_k \sim \mathcal{N}(\xi_k^{(t)}, \delta)I_{[0,3]}(\xi_k^*)$;
      /* Accept/Reject Procedure */
      if rand $\leq \rho$ then
         5 $\xi_k^{(t+1)} = \xi_k^*$;
      else
         7 $\xi_k^{(t+1)} = \xi_k^{(t)}$;
      end
   9 Adjust $\delta$ in order to obtain a suitable acceptance rate.
end
```
C. Sampling the scale parameter vector $\gamma$

The conditional distribution of the scale parameter vector of the proposed GGDs satisfies the following relation

$$
p(\gamma | y, x, \sigma_n^2, \xi, z) \propto p(y | x, \sigma_n^2, \xi, \gamma, z)p(x | \xi, \gamma, z)p(\gamma)
\quad \propto p(x | \xi, \gamma, z)p(\gamma). \tag{19}
$$

Assuming that the scale parameters are independent, we have

$$
p(\gamma_k | x, \xi, \gamma_{-k}) \propto p(x_k | \xi_k, \gamma_k, z_k)p(\gamma_k)
\quad \propto a_k^N \exp \left( -\frac{\|x_k\|_{\xi_k}^{\xi_k}}{\gamma_k} \right) \gamma_k^{N_k / \xi_k - 1}
\quad \propto \mathcal{IG} \left( \frac{N_k}{\xi_k}, \frac{\|x_k\|_{\xi_k}^{\xi_k}}{\gamma_k} \right) \tag{20}
$$

where $\gamma_{-k} = (\gamma_1, ..., \gamma_{k-1}, \gamma_{k+1}, ..., \gamma_K)$ for $k \in \{1, ..., K\}$. Drawing samples from the inverse gamma distribution (20) is straightforward.

D. Sampling the labels $z$

The conditional distribution of the labels $z$ can be computed using Bayes rule

$$
p(z | y, x, \sigma_n^2, \xi, \gamma) \propto p(y | x, \sigma_n^2, \xi, \gamma, z)p(x | \xi, \gamma, z)p(z)
\quad \propto p(x | \xi, \gamma, z)p(z). \tag{21}
$$

Considering the dependency between a label and its neighbors, the conditional distribution of the label $z_n$ (corresponding to image pixel $x_n$) is given as follows

$$
p(z_n = k | z_{-n}, x, \xi, \gamma) \propto p(x_n | z_n = k, \xi, \gamma)p(z_n = k | z_{V(n)}) \tag{22}
$$

where $z_{-n}$ is the vector $z$ whose $n$th element has been removed and $z_{V(n)}$ represents the neighbors of label $z_n$. Note that a four-pixel neighborhood structure has been adopted in this paper.

Denoting the left hand side of (22) as $\pi_{n,k}$, we have

$$
\pi_{n,k} \propto a_k \exp \left( -\frac{|x_n|_{\xi_k}}{\gamma_k} \right) \exp \left( \sum_{n' \in V(n)} \beta \delta(k - z_{n'}) \right). \tag{23}
$$

The normalized conditional probability of the label $z_n$ is defined as

$$
\tilde{\pi}_{n,k} = \frac{\pi_{n,k}}{\sum_{k=1}^K \pi_{n,k}}. \tag{24}
$$

Finally, the label $z_n$ can be drawn from the set $\{1, ..., K\}$ with the respective probabilities $\{\tilde{\pi}_{n,1}, ..., \tilde{\pi}_{n,K}\}$. 
E. Sampling the reflectivity function

The conditional distribution of the target image we want to estimate is defined as follows

\[ p(x|y, \sigma_n^2, \xi, \gamma, z) \propto \exp \left( -\frac{1}{2\sigma_n^2} \|y - H x\|^2 - \sum_{k=1}^{K} \frac{\|x_k \|_{\xi_k}^2}{\gamma_k} \right). \]  

(25)

Sampling according to (25) is the critical point of the proposed algorithm. Due to the high dimensionality of x, classical Gibbs or MH moves are inefficient. Thus we propose to implement an efficient sampling strategy referred to as Hamiltonian Monte Carlo (HMC) method. The principles of this method have been presented in [29] with an application to neural networks. It is widely reported that HMC generally outperforms other standard Metropolis-Hastings algorithms, particularly in high-dimensional scenarios [30]. This empirical observation is in agreement with recent theoretical studies showing that HMC has better scaling properties than the Metropolis adjusted Langevin algorithm (MALA) and RWMH [31]. This section recalls the main steps of the HMC method and explains how its parameters can be adjusted.

1) HMC Algorithm: The main idea of HMC is to introduce a vector of momentum variables \( p \in \mathbb{R}^N \) that is independent of \( x \) and to sample the pair \((x, p)\) instead of just sampling \( x \). The conditional distribution of \((x, p)\) can be written

\[ p(x, p|y, \sigma_n^2, \xi, \gamma, z) = p(x|y, \sigma_n^2, \xi, \gamma, z)p(p). \]

The Hamiltonian of the system is defined as

\[ H(x, p) \triangleq -\log p(x, p|y, \sigma_n^2, \xi, \gamma, z) = U(x) + V(p) \]

where \( V(p) \) and \( U(x) \) are the kinetic and potential energies of the Hamiltonian system. They are defined as

\[ V(p) = \frac{1}{2}p^T p \quad \text{and} \quad U(x) = -\log[p(x|y, \sigma_n^2, \xi, \gamma, z)]. \]

At the iteration \( \#t \), the HMC consists of two steps:

1) generate a candidate pair \((p^{(*)}, x^{(*)})\) from the current state \((p^{(t)}, x^{(t)})\) using a discretizing method, such as the leapfrog and Euler methods;
2) accept or reject the candidate with the probability \( \rho \)

\[ \rho = \min\{\exp[H(p^{(t)}, x^{(t)}) - H(p^{(*)}, x^{(*)})], 1\}. \]

(26)

In our experiments, we have considered the leapfrog discretizing method due to its better performance compared to the Euler method, also noticed in [29]. The three steps of the leapfrog method are defined as:

\[
\begin{align*}
p_{i}(t + \epsilon/2) &= p_{i}(t) - \frac{\epsilon}{2} \frac{\partial U}{\partial x_{i}}[x(t)] \\
x_{i}(t + \epsilon) &= x_{i}(t) + \epsilon p_{i}(t + \epsilon/2) \\
p_{i}(t + \epsilon) &= p_{i}(t + \epsilon/2) - \frac{\epsilon}{2} \frac{\partial U}{\partial x_{i}}[x(t + \epsilon)]
\end{align*}
\]

where \( \epsilon \) is a so-called stepsize and \( L \) is the number of leapfrog iterations. We should note that \( U(x) \) is not differential when \( \xi_k \leq 1 \). To deal with this problem, a smoothing approximation has been considered, i.e., \( | \cdot | \approx \sqrt{\cdot^2 + \epsilon} \), with \( \epsilon \ll 1 \). The algorithm based on the leapfrog discretization and this approximation is summarized in Algo. 3. Compared to other MCMC algorithms, the HMC method has the noticeable advantage to generate efficiently a candidate \( x \) even in the case of a high dimensional and complicated distribution.
Algorithm 3: Adjusted HMC Algorithm

```latex
/* Initialization Procedure */
1 \( x^{(0)} = y \)

2 for \( t = 1 : N_{MC} \) do

3 /* Candidate generation Procedure */
4 \( p^{(t,0)} \sim \mathcal{N}(0, I^{N \times N}) \)

5 /* Leapfrog Method */
6 for \( i = 1 : L \) do
7 \( p^{(t,i)} = p^{(t,i)} - \frac{\epsilon}{2} \delta U / \delta x^{(t,i)} \)
8 \( x^{(t,i)} = x^{(t,i)} + \epsilon p^{(t,i)} \)
9 \( p^{(t,i)} = p^{(t,i)} - \frac{\epsilon}{2} \delta U / \delta x^{(t,i)} \)
10 end
11 \( p^{(*)} = p^{(t,L)} ; \)
12 \( x^{(*)} = x^{(t,L)} ; \)

13 /* Accept/Reject Procedure */
14 Compute \( \rho \) with (26)
15 if \( rand \leq \rho \) then
16 \( x^{(t+1)} = x^{(*)} \)
17 else
18 \( x^{(t+1)} = x^{(t)} \)
19 end
20 Adjust \( \epsilon \) in order to obtain a suitable acceptance rate.
21 end
```

2) Tuning the parameters \( \epsilon \) and \( L \): The performance of the HMC algorithm mainly depends on the values of parameters \( \epsilon \) (stepsize) and \( L \) (number of leapfrog steps). Fortunately, these two parameters can be tuned independently in most applications \([29]\). It is recommended to select a random number of leapfrog steps \( L \) to avoid possible periodic trajectories \([29]\). In our algorithm, \( L \) is sampled uniformly in the interval \([50, 70] \). The leapfrog stepsize \( \epsilon \) has been adjusted by in order to ensure a reasonable average acceptance rate over every 100 iterations. Specifically, when the acceptance rate is too large, \( \epsilon \) should be decreased and vice versa. The range of the acceptance rate has been set to \( 30\% - 90\% \) in the burn-in period. Note that the tuning of \( \epsilon \) is just carried out during the burn-in period to ensure the Markov chain is homogeneous after the burn-in period. The acceptance rate can achieve \( 60\% - 80\% \) when the Markov chain has converged, while the acceptance rate is around \( 25\% \) in standard MH moves for high dimensional target distributions \([32]\).

F. Parameter estimation

Bayesian estimators of the unknown parameters of interest can be computed using the samples generated by the proposed hybrid Gibbs sampler. Since the labels are discrete variables, marginal MAP estimators were chosen for the labels. The other variables (the tissue reflectivity \( x \), noise variance \( \sigma_n^2 \) and GGD hyperparameters \( \xi, \gamma \)) are estimated by averaging the generated samples (after the burn in period) following the principle of MMSE estimators. For example, the MMSE estimator of the reflectivity image \( x \) is computed as follows

\[
\hat{x}_{\text{MMSE}}|\hat{z}_{\text{MAP}} \triangleq E\{x|z = \hat{z}_{\text{MAP}}\} = \int p(x|z = \hat{z}_{\text{MAP}})dx.
\] (27)
For each pixel, we have

\[
\hat{x}_{n,\text{MMSE}} | \hat{z}_{n,\text{MAP}} = \frac{1}{M} \sum_{i=1}^{M} \hat{x}^{(i)}_{n} | z^{(i)}_{n} = \hat{z}_{n,\text{MAP}}
\]  

(28)

where \( M \) is the number of iterations after the burn-in that satisfy \( z^{(i)}_{n} = \hat{z}_{n,\text{MAP}} \), the superscript \( i \) represents the \( i \)th generated sample and the subscript \( n \) represents the \( n \)th pixel. Note that \( \hat{z}_{n,\text{MAP}} \) is the marginal MAP estimator of the label map and that \( \hat{x}_{n,\text{MMSE}} \) is the MMSE estimator of the reflectivity. Note also that, a similar estimator was implemented in [33] for image blind deconvolution.

IV. SIMULATION RESULTS

This section presents experimental studies carried out on simulated and real data to evaluate the performance of the proposed algorithm. Note that, due to the introduction of labels, the algorithm is able to jointly segment the images into statistically homogeneous regions and estimate the tissue reflectivities of these homogeneous regions via deconvolution. All the algorithms have been implemented using MATLAB R2013a on a computer with Intel(R) Core(TM) i7-4770 CPU @3.40GHz and 8 GB RAM in this paper.

A. Synthetic data

In order to validate the proposed method, some toy experiments have been first conducted on simulated synthetic data with controlled ground truth conditions. More precisely, the proposed algorithm has been applied to three groups of 2D random images with the same image size \( N = 50 \times 50 \). The first experiments consider independent and identically distributed (i.i.d.) image pixels distributed according to GGDs with different shape and scale parameters, as reported in Table I. Each image has been corrupted by a \( 5 \times 5 \) Gaussian blurring kernel with standard deviation \( \sigma_b = 3 \) and an additive white Gaussian noise (AWGN). The level of noise is characterized by the blurred signal-to-noise ratio (BSNR) expressed in decibels as follows (see, e.g. [34], for a definition of BSNR)

\[
\text{BSNR} = 10 \log_{10} \left( \frac{\|Hx - E(Hx)\|_2^2}{N\sigma_n^2} \right)
\]  

(29)

where \( E(\cdot) \) is a mean operator and \( N \) is the total number of image pixels. Note that BSNR was set to 40 dB in the first three experiments. Regarding the MCMC algorithm, 50 chains of 6000 iterations (including a burn-in period of 2000 iterations) were run for each simulation scenario. In each Monte Carlo chain, the stepsize was initially set to \( \epsilon = 10^{-5} \) and the number of leapfrog steps was uniformly sampled in the interval \([50, 70]\).

Fig. 2 shows the histograms of the generated samples from one single Markov chain for the GGD parameters of three representative images. These histograms are clearly in good agreement with the true values of the parameters indicated by the vertical lines. The typical deconvolution performance for one column of each of the three observed images is depicted in Fig. 3. These results show a good performance of the proposed image deconvolution algorithm. More quantitative results are reported in Table I including the MMSE estimates of the parameters and the corresponding standard deviations.

B. Simulated ultrasound images

The previous simulation was performed on synthetic data with homogeneous statistical properties. The second set of experiments considers a more realistic scenario (see [8] for more details) with three groups of results. The PSF was simulated within a realistic state-of-the-art ultrasound simulator Field II [35] corresponding to a 3.5 MHz linear probe as shown in Fig. 4(a). All images were simulated with the same realistic PSF.
Fig. 2. Ground truth values (vertical lines), estimated marginal posterior distributions (histograms) of $\sigma^2_n$ (a)-(c) and hyperparameters $\xi$ (d)-(f) and $\gamma$ (g)-(j).

Fig. 3. Restoration results for one column of the synthetic image (the red curves are the observed lines of the image, the blue curves are the ground truth and the green curves are the estimated signals obtained with the proposed method).
### TABLE I

<table>
<thead>
<tr>
<th>Group</th>
<th>Parameters</th>
<th>True values</th>
<th>MMSE</th>
<th>Std. †</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group 1</td>
<td>$\sigma_n^2 \times 10^{-5}$</td>
<td>3.72</td>
<td>3.65</td>
<td>0.35</td>
</tr>
<tr>
<td></td>
<td>$\xi$</td>
<td>2</td>
<td>1.98</td>
<td>0.04</td>
</tr>
<tr>
<td></td>
<td>$\gamma$</td>
<td>2</td>
<td>2.00</td>
<td>0.05</td>
</tr>
<tr>
<td>Group 2</td>
<td>$\sigma_n^2 \times 10^{-5}$</td>
<td>3.22</td>
<td>3.63</td>
<td>0.61</td>
</tr>
<tr>
<td></td>
<td>$\xi$</td>
<td>1.50</td>
<td>1.41</td>
<td>0.09</td>
</tr>
<tr>
<td></td>
<td>$\gamma$</td>
<td>1.26</td>
<td>1.16</td>
<td>0.09</td>
</tr>
<tr>
<td>Group 3</td>
<td>$\sigma_n^2 \times 10^{-5}$</td>
<td>3.13</td>
<td>4.15</td>
<td>0.60</td>
</tr>
<tr>
<td></td>
<td>$\xi$</td>
<td>0.60</td>
<td>0.59</td>
<td>0.03</td>
</tr>
<tr>
<td></td>
<td>$\gamma$</td>
<td>0.37</td>
<td>0.37</td>
<td>0.02</td>
</tr>
</tbody>
</table>

†Represents standard deviation.

1) **Group 1:** The tissue reflectivity image $x$ mimicking a hyperechoic (bright) round inclusion into an homogeneous medium was blurred by the simulated PSF (using a 2D convolution) and contaminated by an AWGN $n$. The size of the US reflectivity image is $128 \times 128$ and BSNR = 30 dB. The pixels located inside and outside the inclusion, indicated by the label map in Fig. 4(c), are distributed according to GGDs with parameter vectors $(\xi, \gamma) = (0.6,1)$ (inside) and $(\xi, \gamma) = (1.8,2)$ (outside) as highlighted in Fig. 4(b). The simulated RF image and its corresponding B-mode image (the log-compressed envelop image which is commonly used for visualization purpose in US imaging) are shown in Figs. 4(d) and 4(e). For this experiment, the number of Monte Carlo iterations was set to 6000 (including 2000 burn-in period iterations).

2) **Group 2:** The tissue reflectivity image $x$ is an homogeneous medium with two hypoechoic (dark) round inclusions (see Fig. 7(a)) that was blurred by the same simulated PSF and contaminated by an AWGN $n$. The size of the US reflectivity image is $100 \times 100$ and BSNR = 30 dB. The pixels located inside and outside the inclusions are distributed according to GGDs with parameter vectors $(\xi, \gamma) = (0.8,10)$ (inside) and $(\xi, \gamma) = (1.5,1)$ (outside) as highlighted in Fig. 7(a). The simulated RF image and its corresponding B-mode image are shown in Figs. 7(b) and 7(c) whereas the ground truth of the label map is given in Fig. 7(d). The number of Monte Carlo iterations was set to 8000 (including 4000 burn-in period iterations).

3) **Group 3:** The third simulated image was obtained by using a clean tissue reflectivity function $x$ of size $275 \times 75$ (see Fig. 8(a)) blurred by the same simulated PSF and by adding a Gaussian noise corresponding to BSNR = 30 dB. A more realistic geometry of the simulated tissues was however considered, inspired by one of the in vivo results provided in the next section (see Fig. 9(i)). Three different structures have been generated mimicking respectively the skin, the tumor and the surrounding tissue (green, red and blue regions in Fig. 8(d)). The pixels in the different regions are distributed according to GGDs with different parameters: $(\xi, \gamma) = (0.5,1)$ for the blue region, $(\xi, \gamma) = (1,30)$ for the green region and $(\xi, \gamma) = (1.8,2)$ for the red region. For this experiment, the number of Monte Carlo iterations is 10000 (including 5000 burn-in period iterations).

The proposed joint deconvolution-segmentation algorithm (denoted as “JointMCMC”) was compared to the technique proposed in [18] that performs US deconvolution with GGD priors using an EM framework (denoted here by “DeconvEM”). Since “DeconvEM” was proposed for statistical homogeneous regions, we assumed that the labels associated with the statistically homogeneous regions were known for “DeconvEM”. In order to test the robustness of our method to label estimation errors, we also implemented the proposed algorithm using the true labels (denoted as “DeconvMCMC”). In this case, similar to “DeconvEM”, only the deconvolution process was performed, without label estimation.

The performance of the reflectivity image estimation is assessed in terms of improvement in SNR (ISNR), normalized root mean square error (NRMSE), peak signal-to-noise ratio (PSNR) and image...
structural similarity (MSSIM). The definitions of these four metrics are given below

\[
\text{ISNR} = 10 \log_{10} \frac{\|x - y\|^2}{\|x - \hat{x}\|^2} \tag{30}
\]

\[
\text{NRMSE} = \sqrt{\frac{\|x - \hat{x}\|^2}{\|x\|^2}} \tag{31}
\]

\[
\text{PSNR} = 10 \log_{10} \frac{\max(x, \hat{x})^2}{\text{MSE}} \tag{32}
\]

\[
\text{MSSIM}(x, \hat{x}) = \frac{1}{W} \sum_{j=1}^{W} \text{SSIM}(x_j, \hat{x}_j) \tag{33}
\]

where the vectors \(x, y, \hat{x}\) are the reflectivity image, the RF image and the restored reflectivity image respectively. Note that \(W\) is the number of local windows, \(x_j\) and \(\hat{x}_j\) represent the local reflectivities of \(x\) and \(\hat{x}\) located in one of these windows and SSIM is the structural similarity measure of each window (defined in [36]). The performance of the label estimation is assessed using the overall accuracy (OA), defined as the ratio between the number of correctly estimated labels over the total number of labels.

The quantitative results are reported in Table II for Group 1 and in Table III for Groups 2 and 3. Visually, we remark that all the three methods provide images with better object boundary definition (better spatial resolution) than the observed blurred images. The quantitative results confirm that given the same conditions (knowledge of the true label map), our approach “DeconvMCMC” is more accurate than the existing “DeconvEM”. Moreover, we remark that the proposed joint segmentation-deconvolution technique “JointMCMC” is able to robustly estimate the label map with a precision of more than 98% and with a small quality loss for the estimated tissue reflectivities.

The histograms of the generated GGD parameters (\(\xi, \gamma\)) for Group 1 are shown in Fig. 6. The red and green vertical lines indicate the MMSE estimates and the true values of the parameters respectively. The hyperparameter estimates of Group 2 are also shown in Table IV. The reported results show that the errors associated with the hyperparameter estimates have only a limited influence on the accuracy of the tissue reflectivity restoration, that represents the main target of our work. Note that the shape parameters might be ordered as \(\xi_1 < \xi_2 < \cdots < \xi_K\) to avoid the label switching phenomenon during the label sampling phase. However, this is not necessary with our approach thanks to the MRF prior used for label estimation, which avoids the label switching phenomenon [37]. It is also worthy to note that the proposed segmentation is based on the statistical properties of the US images. If the statistical properties of different tissues are very close or similar, it will be obviously more difficult (or even impossible) to achieve high accuracy for label estimation. However, this is not a specific limitation of our method, but is shared by all the statistical segmentation techniques commonly used in US imaging.

<table>
<thead>
<tr>
<th>Method</th>
<th>ISNR</th>
<th>NRMSE</th>
<th>PSNR</th>
<th>MSSIM</th>
</tr>
</thead>
<tbody>
<tr>
<td>JointMCMC</td>
<td>16.37</td>
<td>0.31</td>
<td>34.07</td>
<td>0.69</td>
</tr>
<tr>
<td>DeconvMCMC</td>
<td>16.32</td>
<td>0.31</td>
<td>34.22</td>
<td>0.70</td>
</tr>
<tr>
<td>DeconvEM</td>
<td>13.04</td>
<td>0.46</td>
<td>30.74</td>
<td>0.58</td>
</tr>
</tbody>
</table>

C. In vivo study

In this section, we analyze the segmentation-deconvolution results obtained with the proposed method on \textit{in vivo} US images. Precisely, three groups of experiments have been conducted to evaluate the performance of the proposed method. The data were acquired with a 20 MHz single-element US probe. In contrast to the simulation cases studied previously, the PSF and the reflectivity images were not available for \textit{in vivo}
### TABLE III
**Deconvolution Quality Assessment of Simulated Data**

<table>
<thead>
<tr>
<th>Group</th>
<th>Method</th>
<th>ISNR</th>
<th>NRMSE</th>
<th>PSNR</th>
<th>MSSIM</th>
<th>OA</th>
<th>ISNR</th>
<th>NRMSE</th>
<th>PSNR</th>
<th>MSSIM</th>
<th>OA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group 2</td>
<td>Joint MCMC</td>
<td>14.89</td>
<td>0.42</td>
<td>24.72</td>
<td>0.56</td>
<td>0.99</td>
<td>11.20</td>
<td>0.60</td>
<td>22.11</td>
<td>0.41</td>
<td>0.98</td>
</tr>
<tr>
<td></td>
<td>Deconv MCMC</td>
<td>15.09</td>
<td>0.41</td>
<td>24.92</td>
<td>0.57</td>
<td>N/A</td>
<td>12.40</td>
<td>0.52</td>
<td>23.58</td>
<td>0.45</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>Deconv EM</td>
<td>14.82</td>
<td>0.42</td>
<td>24.65</td>
<td>0.55</td>
<td>N/A</td>
<td>11.67</td>
<td>0.57</td>
<td>22.59</td>
<td>0.43</td>
<td>N/A</td>
</tr>
</tbody>
</table>

### TABLE IV
**Hyper Parameter Estimation of Simulated Data (Group 2)**

<table>
<thead>
<tr>
<th>Method</th>
<th>ξ1</th>
<th>ξ2</th>
<th>γ1</th>
<th>γ2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ground truth</td>
<td>0.8</td>
<td>1.5</td>
<td>10</td>
<td>1</td>
</tr>
<tr>
<td>Joint MCMC</td>
<td>0.82</td>
<td>1.37</td>
<td>11.24</td>
<td>0.82</td>
</tr>
<tr>
<td>Deconv MCMC</td>
<td>0.80</td>
<td>2.15</td>
<td>10.05</td>
<td>1.50</td>
</tr>
<tr>
<td>Deconv EM</td>
<td>0.60</td>
<td>0.96</td>
<td>21.10</td>
<td>0.42</td>
</tr>
</tbody>
</table>

Fig. 4. Group 1: (a) the simulated PSF; (b) the simulated tissue reflectivity; (c) ground truth of label field; (d) the US RF image; (e) the B-mode image.

Fig. 5. Group 1: (a), (b) represent the estimated reflectivity in B-mode form and the estimated label field with the proposed method Joint MCMC; (c), (d) are the estimated reflectivities in B-mode form with the method Deconv MCMC and Deconv EM.

Fig. 6. Group 1: (a) Histograms of shape parameters ξ (left corresponding to the pixels inside the round inclusion, right corresponding to the pixels outside the inclusion); (b) Histogram of scale parameters γ for the pixels inside the inclusion; (c) Histogram of scale parameters γ for the pixels outside the inclusion. The red vertical lines and green vertical lines are the MMSE estimation and the true values of the variables ξ, γ respectively.
Fig. 7. Group 2: (a), (b), (c) are the simulated tissue reflectivity, RF image and its corresponding B-mode image; (d) ground truth of label field; (e), (f) are the estimated label map and tissue reflectivity in B-mode form with the method $\text{JointMCMC}$; (g), (h) are the estimated tissue reflectivities in B-mode form with the method $\text{DeconvMCMC}$ and $\text{DeconvEM}$.

Fig. 8. Group 3: (a), (b), (c) are the simulated tissue reflectivity, RF image and its corresponding B-mode image; (d) ground truth of label field; (e), (f) are the estimated label map and tissue reflectivity in B-mode form with the method $\text{JointMCMC}$; (g), (h) are the estimated tissue reflectivities in B-mode form with the method $\text{DeconvMCMC}$ and $\text{DeconvEM}$.

experiments. For this reason, the PSF was estimated from the RF data and thus the standard performance metrics used previously could not be computed. Note that the PSF estimation method of [13] was adopted in this work due to its accuracy. The quality of the deconvolution results is evaluated using two metrics commonly used in US imaging: the resolution gain (RG) [16] and the contrast-to-noise ratio (CNR) [38], [39]. The resolution gain (RG) is the ratio of the normalized auto-correlation (higher than 3 dB) of the original RF US image to the normalized auto-correlation (higher than 3 dB) of the deconvolved image or estimated reflectivity image. The definition of the CNR is expressed below

$$\text{CNR} = \frac{|\mu_1 - \mu_2|}{\sqrt{\sigma_1^2 + \sigma_2^2}}$$

where $\mu_1$, $\mu_2$, $\sigma_1$ and $\sigma_2$ are the mean and standard deviations of pixels located in two regions extracted from the image. These two regions were manually chosen so that they belong to two different tissue structures. Moreover, as in most of US studies, they have been considered at the same depth in order to avoid issues related to wave attenuation. The regions selected for the computation of CNR are shown in
the red rectangles in Figs. 9(a), 9(e) and 9(i). Note that the higher the values of RG and CNR, the better the deconvolution performance.

As stated in the introduction, Gaussian and Laplacian priors have been extensively used in the US image deconvolution literature [12], [15], [16]. Therefore, it is reasonable and interesting to compare the proposed algorithm using GGD prior to the approaches using Gaussian and Laplacian priors. The Gaussian and Laplacian priors lead to $\ell_2$ norm and $\ell_1$ norm convex optimization problems. For the $\ell_2$ norm optimization problem, a numerical solution is given as below

$$\hat{x} = (H^T H + \lambda I)^{-1} H^T y$$ (35)

where $\lambda$ is the regularization parameter fixed manually to its optimum value for each experiment. Concerning the $\ell_1$ norm optimization problem, numerous dedicated algorithms, e.g., ISTA [40], [41], FISTA [40], TwIST [41] or GEM [42] are available in the literature. The ISTA algorithm was considered in this paper.

a) Group 1: The US blurred image is shown in Fig. 9(a), in its B-mode form. This image shows a mouse bladder. The US transducer was placed into a small water container to ensure an efficient transmission of the US waves into the tissues. As there is no US scatterer in the water, the region located in the upper part of the image in Fig. 9(a) appears dark (no signal). It is also the case for the region located inside the bladder that also contains a fluid with poor reflection for the US waves. The number of homogeneous regions was set to $K = 3$ in this experiment, which is sufficient to represent the anatomical structures of the image. The number of Monte Carlo iterations was fixed to 10 000 (including 5 000 burn-in iterations). The parameters of the HMC method were adjusted to the same values as in the previous experiments.

Figs. 9(b), 9(c) and 9(d) display the restored reflectivity images obtained with the proposed method and the $\ell_1$ and $\ell_2$ optimization algorithms. The proposed method allows good restoration results to be obtained. Fig. 10(a) shows the marginal MAP estimates of the labels which segment the estimated image into several statistically homogeneous parts. The different anatomical structures of the image can be clearly recovered. Note that the two regions corresponding to fluids are identified with the same estimated label.

b) Group 2: The second set of in vivo image represents a skin melanoma tumor acquired in the same conditions as previously. The location of the tumor is indicated by the blue arrow in Fig. 9(e). Water-based gel was placed between the US probe and the skin of the patient. It represents the dark regions in the upper part of the image in Fig. 9(e). The rest of the tissues corresponds to the skin layers. Unlike the previous in vivo image, the number of homogeneous regions was fixed to $K = 4$ in order to take into account the presence of the tumor. The number of Monte Carlo iterations was fixed to 20000 (including 10000 burn-in period) for this example and the HMC parameters were adjusted as in the previous experiments. Figs. 9(e), 9(f), 9(g) and 9(h) show the US blurred image, restored images with the proposed method, the $\ell_1$ and $\ell_2$ optimization algorithms. It is interesting to note in Fig. 9(f) the improved contrast between the tumor and the healthy skin tissue compared to the native image in Fig. 9(e). The marginal MAP estimates of the labels for this image are shown in Fig. 10(b). The four estimated labels correspond to the water-gel (yellow), the tumor (red) and the skin tissues (the two shades of blue).

c) Group 3: The last group of US data represents a healthy skin image shown in Fig. 9(i). The number of homogeneous regions was set to $K = 2$. The number of Monte Carlo iterations was 6000 including a burn-in period of 2000 iterations). The restored reflectivity images are displayed in Figs. 9(j)-9(l). The marginal MAP estimation of the label field is also shown in Fig. 10(c).

In addition to the visual inspection, the deconvolution results were evaluated using the RG and CNR criteria, as shown in Table V. The CPU times obtained are also reported in Table V. Despite its higher computational complexity, the visual impression and the numerical measurements confirm that a better contrast and more defined boundaries between the different tissues is achieved with our method. However, for two out of the three experiments, our method provides a better value of RG than the $\ell_1$ approach and outperforms the $\ell_2$ technique in all three cases. This result can be explained by the fact that the RG metric naturally benefits from sparse solutions. Finally, we remark that in addition to the restored image,
### TABLE V
DECONVOLUTION QUALITY ASSESSMENT

<table>
<thead>
<tr>
<th>Group</th>
<th>Group 1</th>
<th>Group 2</th>
<th>Group 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Metrics</td>
<td>RG</td>
<td>CNR</td>
<td>Time (s)</td>
</tr>
<tr>
<td>Proposed</td>
<td>1.23</td>
<td>1.43</td>
<td>5495.6</td>
</tr>
<tr>
<td>$\ell_2$</td>
<td>0.93</td>
<td>0.77</td>
<td>0.002</td>
</tr>
<tr>
<td>$\ell_1$</td>
<td>1.22</td>
<td>1.13</td>
<td>11.07</td>
</tr>
</tbody>
</table>

(a) Observation  | (b) Proposed  | (c) $\ell_1$  | (d) $\ell_2$  
(e) Observation  | (f) Proposed  | (g) $\ell_1$  | (h) $\ell_2$  
(i) Observation  | (j) Proposed  | (k) $\ell_1$  | (l) $\ell_2$  

Fig. 9. 1st row: Group 1; 2nd row: Group 2; 3rd row: Group 3. From left to right: Observed B-mode image; Restored B-mode images with the proposed method, $\ell_1$-norm and $\ell_2$-norm optimization methods.

Fig. 10. Marginal MAP estimates of labels. In (a), The estimated red labels correspond to liquid regions whereas the other labels represent tissue regions with different statistical properties. In (b), The yellow region shows the water-based gel ensuring an efficient contact between the US probe and the skin, the red pixels correspond to the tumor and the healthy skin tissues appear in blue. In (c) the skin tissue appears in blue.
our algorithm also provides a segmentation result. To our knowledge, there is no other existing method in US imaging able to achieve this joint segmentation and deconvolution performance.

V. CONCLUSIONS

This paper proposed a deconvolution method for ultrasound images using a Bayesian framework with generalized Gaussian distribution priors. Due to the introduction of labels, the method allowed an ultrasound image to be segmented into several statistically homogeneous regions. In addition to the deconvolution quality improvement, our model allows us to consider images including several anatomical structures, unlike existing tissue characterization methods such as those developed in [9]. The parameters of the generalized Gaussian distributions associated with these homogeneous regions were also estimated. According to the author’s knowledge, it is the first time a joint segmentation and deconvolution method is proposed for ultrasound images. Despite the high computation complexity of our MCMC algorithm that limits its real-time application (improvements may be obtained by exploring parallel techniques such as [43]), it is still interesting for numerous offline applications. For example, improving the readability of US images (e.g., spatial resolution, contrast, SNR) offline may allow the clinician to better appreciate the anatomical structures, especially when very accurate measurements are required (e.g., for cancer detection) or when very small structures must be identified (e.g., vessel walls). Computer-aided detection, often performed offline and based on a quantitative analysis of the images, could also take advantage from the deconvolved images provided by our approach.

Future studies include the application of the proposed deconvolution method to medical applications requiring tissue characterization. The ability of our technique to recover the clean tissue response and to segment the image in statistically homogeneous regions may improve the existing characterization approaches when working on the native data. Taking into account additional information such as shape or entropy information could also improve the segmentation or tissue characterization. Another research track that would deserve some attention is to include the estimation of the point spread function within the Bayesian algorithm, resulting into a blind deconvolution approach. The spatially varying nature of the PSF could also be considered with more sophisticated block-wise techniques ensuring its continuity and regularity of the restored tissue reflectivity images. Finally, combining our MCMC approach with deterministic optimization methods (such as the PMALA approach [28], [44]) could be an interesting alternative to accelerate our algorithm.

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