Sensitivity to point-spread function parameters in medical ultrasound image deconvolution

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ABSTRACT

Clinical ultrasound images are often perceived as difficult to interpret due to image blurring and speckle inherent in the ultrasound imaging. But the image quality can be improved by deconvolution using an estimate of the point-spread function. However, it is difficult to obtain a sufficiently accurate estimate of the point-spread function *in vivo* because of the unknown properties of the soft tissue in clinical applications. Local variations in the speed of sound and attenuation change the pulse and beam shape. These in turn affect the point-spread function. The purpose and novelty of this paper is therefore to explore the sensitivity of a state-of-the-art deconvolution algorithm to uncertainty in the point-spread function. The point-spread function in our restoration algorithm is made shift invariant in the lateral dimension but shift dependent in the axial direction, and is modelled to match a 128-element 1D linear array often found in clinical use. We present simulated and *in vitro* sensitivity analyses of *two-dimensional* deconvolution while varying six parameters on which the point-spread function depends. Uncertainty in the ultrasound machine is analysed by varying the axial depths of lateral and elevational foci alongside height and width of transducer elements. Sensitivity to tissue influence is investigated by varying the speed of sound and frequency-dependent attenuation of the electro-mechanical impulse response. The results are analysed both quantitatively and in terms of the perceived image quality. First, the assessment of deconvolution using the logarithmic image amplitude is found to be a better indicator of the perceived improvement in the restoration. Secondly, the two most critical parameters for *two-dimensional* deconvolution are discovered to be the lateral focus and the speed of sound, because the success of deconvolution is perceived primarily in terms of deblurring. We also observed similar patterns for the simulation and *in vitro* experiment. Finally, we show that it is possible to restore *in vivo* ultrasound images using an assumed point-spread function and hence conclude that an exact point-spread function is not necessary for enhancing ultrasound image quality by deconvolution.

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1. Introduction

Ultrasound scanners are widely used in medical imaging applications [1–3]. Compared to most other modalities, they are portable, cost-effective and capable of real-time operation. Ultrasound scanners do, however, produce images which are often hard to interpret due to the nature of the image formation process. Noticeable effects are blurring in areas of the image which are not well focused, and the presence of a characteristic pattern called speckle, which results from the constructive and destructive interference of scatterers within the range of the point-spread function (PSF) of the ultrasonic imaging system.

Deblurring has been a keenly pursued topic in the realm of general image signal processing. It is one of main objectives of image restoration. The physical phenomenon of blurring is mathematically modelled as convolution, hence deblurring can be described as deconvolution. For the process of deconvolution, two distinct approaches have been developed depending on the availability of prior knowledge of the point-spread function: blind and non-blind deconvolution. Non-blind algorithms are generally more successful than blind techniques as they make use of more prior information. In [4–6], we proposed a novel, non-blind deconvolution algorithm which is capable of taking into account the structure of ultrasound speckle. However, the algorithm requires prior knowledge of the PSF. While this can be measured *in vitro* or calculated from knowledge of the transducer design, there is always uncertainty *in vivo* because of variability in the overlying tissue through which any scan must be performed. The main motive and novelty of this paper is therefore to establish the sensitivity of the deconvolution algorithm to variation in the assumed PSF, and consequently to establish the feasibility of deconvolution *in vivo*, where the exact PSF is unknown.

In so doing, first we have identified key parameters of a PSF in ultrasound imaging: they are axial depths of lateral and elevational foci, the height and width of transducer elements in the ultrasound imaging system, and the speed of sound and frequency-dependent attenuation of the impulse response in soft tissue. Our experiments involve systematic variation of these parameters. The findings relating to sensitivity are presented qualitatively in terms of human perception and also in quantitative terms when applicable. We show that the quantification of deconvolution using logarithmic image amplitudes performs better for the perceived enhancement in the restoration. It will be also demonstrated that, for *two-dimensional* deconvolution, the lateral focus and the speed of sound are the parameters which mainly determine the deblurring and subsequent speckle-reduction capabilities in our deconvolution algorithm. They are hence the two most essential parameters which influence the human perception of ultrasound image enhancement. We also show that the errors associated in these parameters of ultrasound imaging are tolerable as far as human perception is concerned and that restored images are perceived better than the original B-mode ultrasound images. We therefore point out that the *exact* point-spread function may not be required to improve the quality of a clinical ultrasound image.

We briefly introduce our deconvolution method in Section 2. Section 3 outlines the structure of the simulation, followed by a description of the metrics quantifying the restoration in Section 4. Our findings relating to the deconvolution sensitivity on PSF parameters are presented in Section 5 (simulation) and Section 6 (*in vitro* experiment). Next, we demonstrate the restoration of *in vivo* ultrasound image by our algorithm in Section 7. Finally, conclusions are drawn.

2. Non-blind ultrasound deconvolution

In this section, we begin by briefly reiterating the essential parts of our deconvolution method. It is worth noting that our algorithm deals with linear ultrasonic propagation and hence lacks any non-linear capability. Although such non-linearity is present in *in vivo* scans of clinical applications, our approach is still applicable to ultrasound images when dominated by linearity. Many ultrasound imaging systems still operate within a range in which linear acoustics provides an adequate description (see p. 477 in [1]). Recently, tissue harmonic imaging has gained recognition and its clinical value is now considered indisputable. But it imposes extra requirements on an imaging system. Under some circumstances, however, fundamental imaging performs better (see p. 411 in [3]) with less requirement on the system. Such fundamental frequency component of diagnostic ultrasound can be enhanced further by our deconvolution algorithm. The core structure of the methodology is illustrated in Fig. 1. However, its complete details can be found in previous publications [4,5].

2.1. Ultrasound image formulation

The A-lines of an ultrasound imaging system can be mathematically modelled as a Fredholm integral of the first kind [4]. Here, the wave propagation is assumed linear. Without loss of generality, if we adopt a *discrete* space-time formulation, the integral can be further simplified using a vector–matrix notation with $\mathbf{x}$ as the field of scatterers and $\mathbf{y}$ as the ultrasound signals

$$\mathbf{y} = \mathbf{Hx} \tag{1}$$

$\mathbf{H}$ is a block diagonal matrix along the lateral and elevational dimensions. Each block matrix maps from the axial depth dimension to the time domain at a given lateral and elevational position. Here, multi-dimensional images are rearranged into 1D equivalents
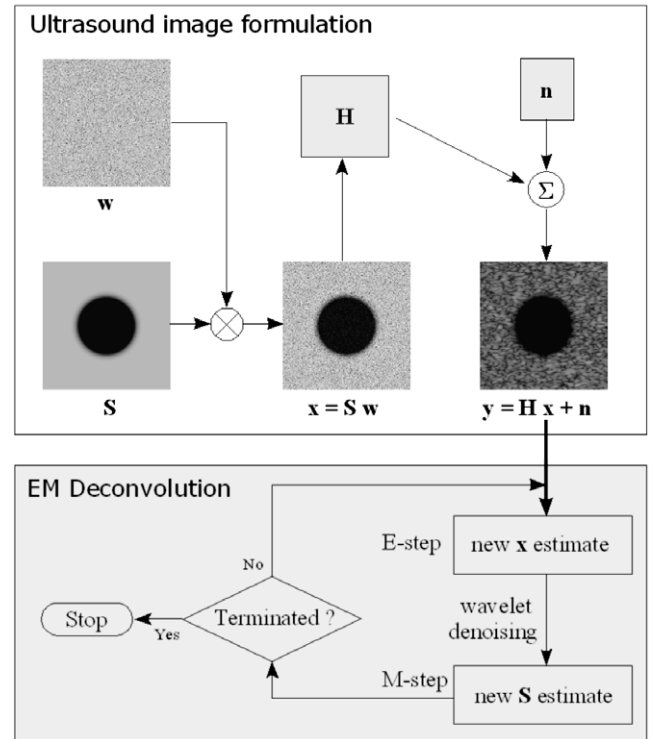

Fig. 1. Diagram showing the key aspects of our deconvolution algorithm. The upper half shows the ultrasound image model ($\mathbf{y} = \mathbf{Hx} + \mathbf{n}$) with our interpretation ($\mathbf{x} = \mathbf{Sw}$). The lower part is the algorithmic flow chart of the deconvolution itself. Notation: echogenicity ($\mathbf{S}$), random component ($\mathbf{w}$), reflectivity function ($\mathbf{x}$), linear blurring operator ($\mathbf{H}$), white Gaussian noise ($\mathbf{n}$), and ultrasound image ($\mathbf{y}$).

by lexicographic orders, and hence $\mathbf{x}$ is a $N_x N_y N_z \times 1$ vector, $\mathbf{H}$ is a $N_x N_y N_t \times N_x N_y N_z$ matrix, and $\mathbf{y}$ is a $N_x N_y N_t \times 1$ vector. Although N_t is usually assumed to be equal to N_z, we distinguish them at this stage to highlight the mapping from the spatial z to the temporal t dimension achieved by the operator $\mathbf{H}$.

It is worth noting that, in traditional deconvolution algorithms, a blurring function is usually assumed to be spatially shift invariant. This tends to be true along the lateral and elevational dimension of an ultrasound image, but the blurring function is significantly shift dependent in the axial direction (i.e. with depth). Our deconvolution algorithm is therefore designed to be capable of dealing with the blurring operator ($\mathbf{H}$) as spatially shift dependent along the axial direction and shift invariant along the lateral and elevational dimensions [4].

2.2. Deconvolution

Further to the discrete modelling of the Fredholm integral equation, we introduce additive noise ($\mathbf{n}$) to take into account potential measurement errors [5]

$$\mathbf{y} = \mathbf{Hx} + \mathbf{n} \tag{2}$$

Our goal is therefore to estimate $\mathbf{x}$ from a noisy and blurred image $\mathbf{y}$. For simplicity, we denote the sizes of the vectors and the matrix as $N \times 1$ for $\mathbf{x}$, $\mathbf{n}$, and $\mathbf{y}$, and $N \times N$ for $\mathbf{H}$.

Our deconvolution algorithm operates in a Bayesian context. The scatterer field ($\mathbf{x}$) is estimated from the observed blurred ultrasound image ($\mathbf{y}$) corrupted by Gaussian noise ($\mathbf{n}$). Because of the ill-posed blurring process ($\mathbf{H}$) caused by finite resolution cells, a direct inverse approach is likely to fail, hence regularisation is incorporated in a maximum *a posteriori* framework (see p. 314 of [7]) with a prior on the scatterer field. Possible priors could involve assum-