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Motion estimation-based image enhancement in ultrasound imaging

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ABSTRACT

High resolution medical ultrasound (US) imaging is an ongoing challenge in many diagnosis applications and can be achieved either by instrumentation or by post-processing. Though many works have considered the issue of resolution enhancement in optical imaging, very few works have investigated this issue in US imaging. In optics, several algorithms have been proposed to achieve super-resolution (SR) image reconstruction, which consists of merging several low resolution images to create a higher resolution image. However, the straightforward implementation of such techniques for US imaging is unsuccessful, due to the interaction of ultrasound with tissue and speckle. We show how to overcome the limit of SR in this framework by refining the registration part of common multiframe techniques. For this purpose, we investigate motion estimation methods adapted to US imaging. Performance of the proposed technique is evaluated on both realistic simulated US images (providing an estimated best-case performance) and real US sequences of phantom and *in-vivo* thyroid images. Compared to classical SR methods, our technique brings both quantitative and qualitative improvements. Resolution gain was found to be 1.41 for the phantom sequence and 1.12 for the thyroid sequence and a quantitative study using the phantom further confirmed the spatial resolution enhancement. Furthermore, the contrast-to-noise ratio was increased by 27% and 13% for simulated and experimental US images, respectively.

1. Introduction

Among all the diagnostic imaging modalities, medical ultrasound (US) imaging is currently considered to be on the cutting edge of noninvasive technologies. Its cost-effectiveness, safety and portability are the main grounds of its common usage in the detection of various cancers, in the assessment of blood velocity or for the investigation of common biological soft tissues. Compared to other modalities such as magnetic resonance imaging or X-ray computed tomography, the various advantages of US imaging are however counterbalanced by its comparatively poor image quality. The main drawback of US images is their overall low contrast and their limited ability to distinguish between two small adjacent objects. Depending on the working frequency, which is related to the design of US transducers as well as the desired penetration depth, low spatial resolution can even further decrease the image quality [1,2]. Furthermore, due to underlying instrumentation constraints and random location of scatterers, US images are contaminated by an intrinsic noise called "speckle" which greatly reduces the general image quality and can hence lead to interpretation concerns. Nevertheless, in some cases, the speckle can be taken into account by a trained observer and may lead to complementary diagnostic information. The statistical properties of the speckle can, moreover, be exploited within several signal processing-based applications such as tissue characterisation and image segmentation [3].

As a result, over the past few decades, extensive efforts have been put into improving US image quality. In US, image quality can be improved in either pre- or post-processing. The former is usually achieved through the modernization of the US scanners, for instance by using high frequency transducers (at the cost of limited penetration depth [4]), backprojection image recovery methods [5] or by designing a proper adaptive beamforming (ABF) algorithm such as Diffuse Time-domain Optimized Near-field Estimator (dTONE) [6] to replace the conventional delay and sum beamforming (at the cost of high computational load). Unfortunately, such techniques lead to tremendous instrumentation constraints that hinder the experimental reproducibility. An alternative consists of investigating post-processing resolution enhancement techniques similar to the works proposed in optical image or video fields [7,8].

The so-called "super-resolution (SR) approach" was originally based on a sequence of low resolution (LR) optical images of the

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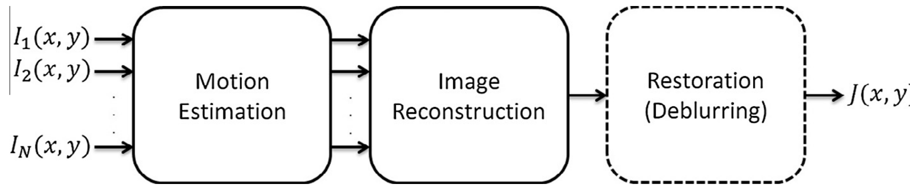

Fig. 1. The classical three-step scheme for super-resolution image reconstruction. $I_1(x,y), I_2(x,y), \ldots, I_N(x,y)$ are N low resolution input images and $J(x,y)$ is the desired high resolution output image. The final restoration stage is optional and will not be addressed in this paper.

same scene using a frequency domain method [9]. The desired high resolution (HR) was obtained by using the relative sub-pixel motion between LR images and has been greatly improved [10] during the past decades. The straightforward implementation of such algorithms for US imaging was unsuccessful, due to the intrinsic nature of tissue elastic motions, speckle and the point spread function (PSF) [11]. Note that unlike strain compounding [12–14], which consists in averaging several ultrasound images acquired under different strain conditions in order to reduce the speckle, our goal is to improve the resolution of US images without altering their intrinsic characteristics.

In this paper, we show how to overcome the intrinsic limit of SR in the US imaging framework and how to preserve the native aspect of US images by refining the registration stage of common multiple frame SR before reconstructing the HR image. A realistic US simulation addressing the experimental limit of such a method is also provided.

2. Motion estimation-based image enhancement in ultrasound imaging

The main goal of this work is to address the SR reconstruction of US images when the motions can be estimated within sub-pixel accuracy. Here, the motion to be estimated for the HR image estimation is induced by the US transducer held by the practitioner and the associated compression of the local medium in the context of static elastography. This non-rigid tissue deformation has been used in many applications such as thyroid nodular disease characterisation [15]. More details regarding the magnitude of this motion can be found in Sections 4.1 and 4.2 for a sequence of phantom and thyroid images, respectively.

Note that any US image sequence exhibiting a non-integer displacement (in terms of number of samples) between consecutive frames can, in theory, be processed via the proposed method. This displacement may be natural (e.g. cardiac motion) or manually induced by the practitioner as in our case.

One should note that the overall displacement in the US sequences considered here is relatively small (especially in the thyroid case, where only a slight compression with the ultrasound probe has been applied) compared to the natural motion of the body (e.g., cardiac motion). In the case of image sequences with larger motions, the original low resolution images would be further decorrelated and would theoretically enhance the quality of the non-uniform interpolation process. This greater decorrelation would however be a drawback with respect to the registration step, whose accuracy is crucial in the proposed approach.

2.1. Image sequence model

Let $\mathbf{I}(x,y) = \{I_1(x,y), I_2(x,y), \ldots, I_N(x,y)\}$ be a given set of N LR images. In order to create the desired HR image $J(x,y)$, the employed multiframe SR algorithm relies on a three-step scheme depicted in Fig. 1.

The first task deals with accurately estimating the motion between the N input images. The relation between two consecutive frames is given by

$$I_{n+1}(x,y) = I_n(x + u_n(x,y), y + v_n(x,y)) \tag{1}$$

for $1 \leqslant n \leqslant N-1$, where $u_n(x,y)$ and $v_n(x,y)$ are the spatially varying displacement fields along the two directions between images n and $n+1$. Various algorithms have been used to perform this motion estimation step, e.g., [7,16] depending on the motion characteristics, but very few works have investigated applying it to SR in US [17].

Once both the estimated relative motions $\hat{\mathbf{u}}(x,y) = \{\hat{u}_1(x,y), \hat{u}_2(x,y), \ldots, \hat{u}_{N-1}(x,y)\}$ and $\hat{\mathbf{v}}(x,y) = \{\hat{v}_1(x,y), \hat{v}_2(x,y), \ldots, \hat{v}_{N-1}(x,y)\}$ are computed, the N images can be aligned according to a reference frame onto an HR grid, taking into account the motion estimation sub-pixel accuracy. The set of registered images is denoted by $\hat{\mathbf{I}}(x,y) = \left\{\hat{I}_1(x,y), \hat{I}_2(x,y), \ldots, \hat{I}_N(x,y)\right\}$. By convention, the first frame is considered as the reference frame, i.e., $\hat{I}_1(x,y) = I_1(x,y)$. Non-uniform interpolation is then performed onto this HR grid in order to fuse the N images contained in $\hat{\mathbf{I}}(x,y)$. Unlike uniform interpolation, which would be employed on the set of images without pre-alignment, non-uniform interpolation processes the images registered using the motion estimated in the first step. In

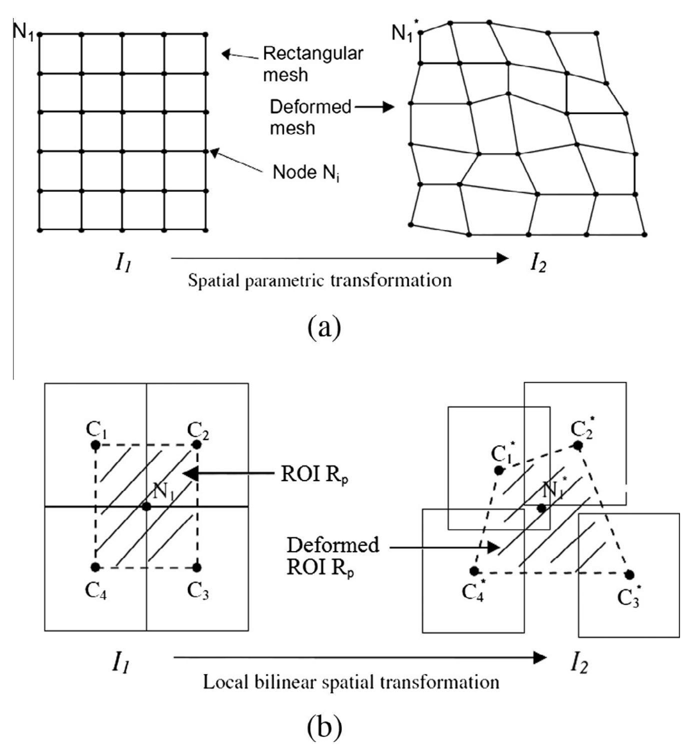

Fig. 2. Overview of BDBM, adapted from [15]. (a) Rectangular mesh on image I_1 and deformed mesh on image I_2. (b) Parametric estimation for a given region of interest (ROI) (hatched region) around one node.