

Alignment-by-Reconstruction for 3D Ultrasound Imaging

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Abstract

This paper addresses 3D reconstruction of human organs from a set of ultrasound images, assuming that the probe position and orientation is available. Unfortunately, pose measurement errors produce significant misalignments which degrade the performance of the reconstruction algorithms. This paper proposes a method for correcting these distortions by estimating the true position and orientation of the ultrasound probe. This is achieved by a joint computation of the 3D data and probe parameters using a MAP criterion. An evaluation of the proposed algorithm by Monte Carlo method is included in the paper.

1. Introduction

Three-dimensional reconstruction of Human organs and tissues is a wide spread operation in CT (Computed tomography) [5], MRI (Magnetic Resonance Imaging), PET (Positron Emission Tomography) [6] and SPECT (Single Photon Emission Computed Tomography) [12]. However it is much less common in ultrasound imaging [10] essentially due to four reasons: 1) non parallel inspection planes due to free hand probe manipulation, 2) tissue deformations during the acquisition process, 3) position sensor errors [2] and 4) low signal to noise ratio of the ultrasound images.

In the free-hand ultrasound technique the probe is in full contact with the human body, and it is moved and maintained under pressure by the medical doctor. This procedure compresses, distorts and modifies the organs shapes and positions during the acquisition process. Consequently, significant geometric distortions can be observed in the ultrasound images. Furthermore, the locator system coupled to the ultrasound probe also introduces significant errors in the position and orientation measurements. Some actions can be taken to alleviate these effects. e.g., improving of the accuracy

of the position sensor or by reducing the sensor pressure during the acquisition process (unfortunately some pressure is needed to achieve good energy coupling between the tissues and the probe).

This paper addresses the problem of image alignment. An algorithm is presented to correct the position and orientation measurements received from the spatial locator based on an joint analysis of the all ultrasound images acquired during the experiment. The position and orientation parameters are recursively adjusted to improve the spatial coherence of the images. The estimation is made on a Bayesian framework and the proposed algorithm is tested using synthetic and real data.

Other approaches were proposed for the alignment of ultrasound images. Some algorithms rely on the object surface [11, 4]. Object contours computed using snakes have also been used [9, 8, 3]. Both approaches rely on the extraction of edge points belonging to the object boundary. This is not always robust especially in the case of ultrasound images. The method proposed here is different since it uses all the reconstructed data as a model instead of searching for the transitions only. Furthermore, it is fully consistent with the multiplicative noise present in ultrasound images.

This paper is organized as follows: volume reconstruction assuming perfect position measurement is described in section 2. The joint estimation of the volume data and position correction is addressed in section 3. The proposed algorithm is evaluated in section 4. Section 5 concludes the paper.

2. Reconstruction Algorithm

The goal of volume reconstruction is the estimation of a scalar function $f(x)$, defined in a region of interest $\Omega \subset R^3$. This function describes the acoustic reflectivity which characterizes human organs and tissues. It is assumed that $f(x) = B(x)^T U$ where $B(x) = [b_1(x), b_1(x), \dots, b_N(x)]$ is a vector of known

basis functions and U a vector of coefficients to be estimated. The estimation of $f(x)$ can be performed in a Bayesian framework, using the MAP method.

The data used for estimating $f(x)$ is formed by a set of ultrasound images obtained with a free-hand ultrasound equipment similar to the one used in clinical diagnosis. A spatial locator was attached to the ultrasound probe, allowing the measurement of the probe position and orientation. Therefore, the data available for estimating $f(x)$ is a set of points, $\{(x_i^p, y_i^p)\}$ where x_i^p is a 3D vector describing the position of the image pixel in space and y_i^p the intensity of the i -th pixel at time instant p . The MAP reconstruction is achieved by:

$$\hat{U} = \arg \max_U \ln(p(Y|U)p(U)) \quad (1)$$

where $p(Y|U)$ is the sensor model and $p(U)$ is the prior density. This optimization problem is solved using numerical methods. This is not an easy task since the number of variable is large. In the sequel, it is assumed that the image pixels are realizations of a random variable with Rayleigh distribution [1] and a Gaussian prior is adopted, leading to

$$p(Y|U) = \prod_{p,i} \frac{y_i^p}{f(x_i^p)} e^{-\frac{(y_i^p)^2}{2f(x_i^p)}} \quad (2)$$

$$p(U) = \frac{1}{Z} e^{-\alpha \sum_{(n,m) \in \Gamma} (u_n - u_m)^2} \quad (3)$$

where Γ is the set of all neighboring nodes and Z is a normalization factor. The α parameter is used for controlling the prior influence (details of this algorithm can be found in [7]).

3. Alignment-by-Reconstruction Algorithm

The previous section assumes that the position and orientation measurements used to compute x_i^p are accurately known. This is not true in practice. Registration is needed for correcting the position and orientation parameters of the inspection planes, to minimize the effect of position errors which blur the reconstruction results.

In this paper we present an algorithm for the estimation and correction of the position errors. Instead of using a two step method (alignment followed by reconstruction) a joint estimation of the displacement and reconstruction variables is adopted.

Consider a pixel y_i^p corresponding to a 3D location x_i^p . It will be assumed that the measurement error, introduced by the spatial locator, corresponds to a shift

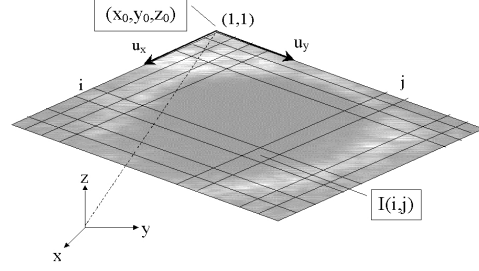


Figure 1: Inspection plane: displacement vectors of the inspection plane (see Fig. 1). Therefore, the geometric measurement available for reconstruction is:

$$\tilde{x}_i^p = x_i^p - K_1^p \cdot \vec{u}_1^p - K_2^p \cdot \vec{u}_2^p \quad (4)$$

where x_i^p is the true position, K_1^p and K_2^p are the position errors and u_1^p and u_2^p are two orthogonal vectors belonging to the p -th inspection plane (see Fig. 1). It is also assumed that the position errors, K_τ^p , are random variables with Gaussian distribution $N(0, R)$, $R = \text{diag}\{\sigma_1^2, \sigma_2^2\}$.

The goal of the alignment algorithm is the estimation of the displacement vectors, $\hat{K} = \{\hat{K}_1^p, \hat{K}_2^p\}$ such that

$$\hat{x}_i^p = \tilde{x}_i^p + \hat{K}_1^p \cdot \vec{u}_1^p + \hat{K}_2^p \cdot \vec{u}_2^p \quad (5)$$

is closed to x_i^p . The estimation method used for estimating the 3D data and probe displacements is an extension of the one adopted in section 2. It is based on the maximization of the joint density function $p(Y, U, K|R) = p(Y|U, K, R) \cdot p(U|K, R) \cdot p(K|R)$. Assuming that U and K are independent random variables,

$$\hat{K} = \arg \max_K \ln(p(Y|U, K, R)p(K|R)) \quad (6)$$

where $p(K|R)$ is the displacement prior:

$$p(K) = \prod_p \frac{1}{2\pi\sigma_1\sigma_2} e^{-\frac{(K_1^p)^2}{2\sigma_1^2}} e^{-\frac{(K_2^p)^2}{2\sigma_2^2}} \quad (7)$$

A stationary point of (6) with respect to K_τ^p will be computed. The Newton-Rapson method is used to minimize (6) leading to:

$${}^{n+1}\hat{K}_\tau^p = {}^n\hat{K}_\tau^p + \lambda \frac{\frac{1}{2} \sum_i \frac{(y_i^p)^2 - 2f(x_i^p)}{f^2(x_i^p)} \frac{df(x_i^p)}{dK_\tau^p} - \frac{n K_\tau^p}{\sigma_\tau^2}}{\sum_i \frac{(y_i^p)^2 - f(x_i^p)}{f^3(x_i^p)} \left(\frac{df(x_i^p)}{dK_\tau^p}\right)^2 + \frac{1}{\sigma_\tau^2}} \quad (8)$$

where sums are performed for all the pixels belonging to the p -th image and the derivatives are:

$$\frac{df(x_i^p)}{dK_\tau^p} = \vec{\nabla} f(x_i^p) \cdot \vec{u}_\tau^p \quad (9)$$

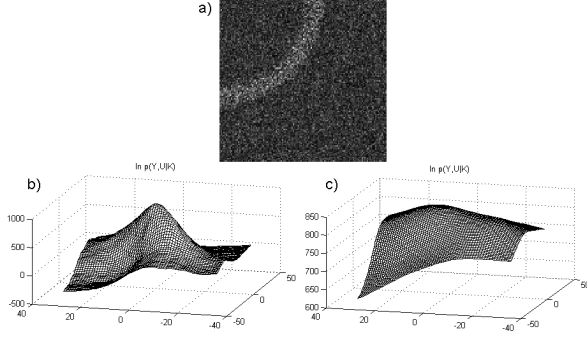


Figure 2: a) Synthetic cross-section of a tube. $p(Y, U|K)$ surface for several displacements of the shown image using b) the original set of coefficients c) a estimated set of coefficients.

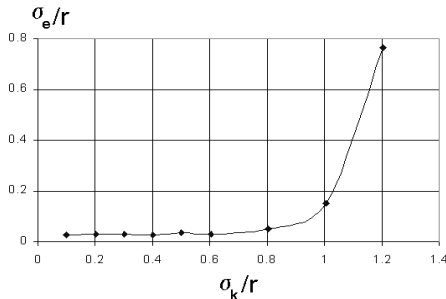


Figure 3: Results obtained from Monte Carlo method for 9 different values of position noise with 20 experiments per each.

($\frac{dx_i^p}{dK_1^p} = \vec{u}_1$ and $\frac{dx_i^p}{dK_2^p} = \vec{u}_2$), where $\vec{\nabla} f(x_i^p)$ is the gradient of $f(x_i^p)$ computed in x_i^p and $\vec{\nabla} f(x_i^p) \cdot \vec{u}_\tau^p$ is the derivative of $f(x_i^p)$ along the \vec{u}_τ^p direction. The σ_τ parameters can also be recursively estimated in each iteration through:

$$\sigma_\tau^2 = \frac{\sum_i (K_\tau^i)^2}{N_i - 1} \quad (10)$$

where N_i is the number of images. To initialize the algorithm a first estimate is computed without position correction as described in the section 2. This estimate is used for initializing the algorithm described in this section. In the next iterations all the coefficients are updated using the best position estimates. Volume reconstruction and matching alternate until $P(Y, U, K|R)$ is maximized.

4. Experimental Results

This section evaluates the performance of the proposed algorithm by Monte Carlo techniques. The reconstruction of human organs obtained from ultrasound images is also presented.

First, it is important to characterize the advantages of the joint volume/alignment estimation. Consider a cross section of a tube corrupted by multiplicative noise (Fig. 2a). Fig. 2b,c display the likelihood $p(Y, U|K)$ as a function of the displacement K . The true coefficients, U are used in Fig. 2b which allows an accurate estimation of K . Unfortunately, U is not available in practical situations. Fig. 2c displays $p(Y, U|K)$ using the MAP estimates, \hat{U} , obtained without pose correction (first iteration of the alignment-by-reconstruction algorithm). The estimation of K is much more difficult in this case since the function is smooth (the reconstructed volume is blurred). The iterative algorithm is an attempt to improve the $p(Y, U|K)$ in such a way that we may approach Fig. 2b starting from Fig. 2c.

Monte Carlo tests were carried out to assess the performance of the alignment-by-reconstruction algorithm. The alignment results are characterized by the standard deviation of the alignment error $e^p = K^p - \hat{K}^p$. The standard deviation is computed from 20 reconstruction experiments, each of them using 50 ultrasound images. The probe position is corrupted by Gaussian noise with standard deviation σ_K . The 20 experiments were repeated for several values of σ_K . Results are shown in Fig. 3. (These results concern the reconstruction of a tube with radius r . The dimension of each image is $r \times r$). Very good error correction is achieved for $\sigma_K < .8r$. The algorithm has a break point at $\sigma_K = .8r$. After this level, the probe errors are so high that prevent the convergence of the volume and pose estimates towards acceptable values (without reasonable volume estimates no matching is possible).

Fig. 4 shows two cross-sections of the tube without and with alignment. The improvement achieved by the alignment algorithm in this example is clear. The edges become much sharper and the blurring introduced by the sensor position errors is removed. Fig. 4c shows the evolution of the likelihood function, $p(Y, U|K)$, in both tests. A significant increase of the likelihood function is observed when alignment is applied. This can be seen after the 8-th iteration because no alignment is used before. The first 8 iterations are used to initialize the volume estimate. A multi-scale algorithm is used during these iterations: a coarse volume representation is adopted in the first iteration which is recursively refined in following 7 iterations. This is a way to improve the convergence of the reconstruction process.

Fig. 5 shows reconstruction results obtained with real data. A set of 94 ultrasound images is used to reconstruct a volume containing an human organ. Fig. 5a shows the results obtained without alignment and Fig. 5b shows the results with the alignment correction. The pose correction introduced in Fig. 5b allowed

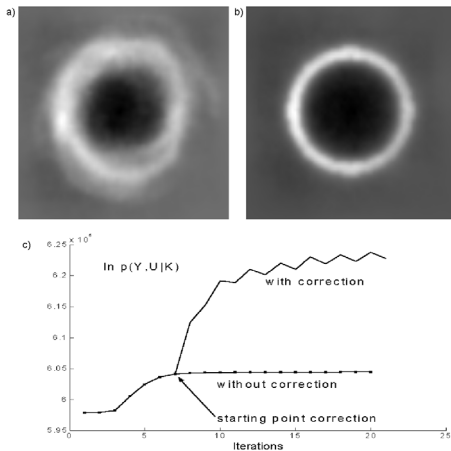


Figure 4: Reconstructed volume a) without alignment, b) with alignment, c) Evolution of $p(Y, U|K)$ during the estimation process

to eliminate the reconstruction artifacts observed in Fig. 5 a inside the dark cavity. These results were obtained after 15(8+7) iterations.

5. Conclusions

This paper describes an algorithm for the correction of the probe position errors in ultrasound imaging. A non-Gaussian model is used for describing the observed images. The position error is modeled as a random displacement of the inspection plane. A joint alignment and reconstruction algorithm is proposed based on the optimization of the posteriori distribution of the parameters. This provides a solid framework for the estimation of all unknown variables, therefore avoiding the use of ad hoc criterion for the estimation of each type of variable. Experimental results with real data and Monte Carlo tests showed that a significant improvement of the reconstruction results is achieved by the proposed algorithm.

The use of alignment-by-synthesis combined with multi-scale methods will be addressed in a forthcoming paper.

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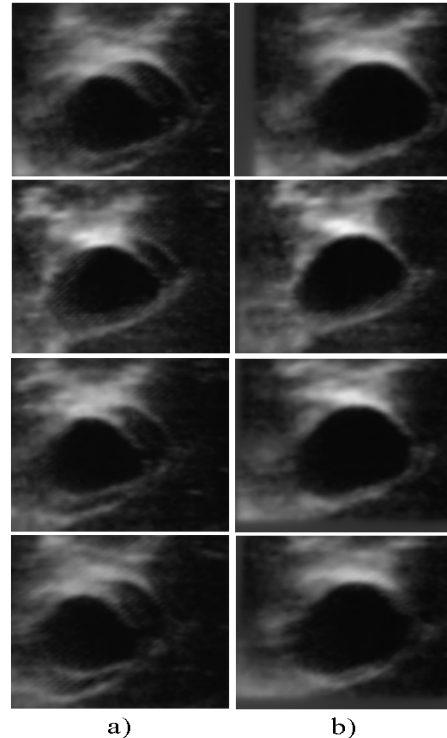


Figure 5: Reconstructed volume without(a) and with(b) alignment from real data.

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