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A Method to Compute Respiration Parameters for Patient-based Simulators

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Abstract. We propose a method to automatically tune a patient-based virtual environment training simulator for abdominal needle insertion. The key attributes to be customized in our framework are the elasticity of soft-tissues and the respiratory model parameters. The estimation is based on two 3D Computed Tomography (CT) scans of the same patient at two different time steps. Results are presented on four patients and show that our new method leads to better results than our previous studies with manually tuned parameters.

Keywords. Deformable model, optimization method

1. Introduction

During the last decade, the use of simulators in medical training has grown significantly. They are either based on mannequins or computer based. They allow the teaching of medical reasoning processes and emergency situations with relatively low investment costs. A key challenge in developing such simulators is to provide the trainees with a large number of cases that fully covers parts or aspects of the teaching curriculum. A high level of fidelity can be achieved only if the data closely replicates real patient's anatomy (i.e. organ geometry) and physiology (i.e. organ functionalities and tissue elasticity).

Within the CR@IVE consortium [1], we aim to build such patient-based simulators, for example, an ultrasound guided needle puncture simulator for liver biopsy [2, 3]. This paper introduces patient-based physiology in the form of a respiratory motion model. The hardware is built around an immersive workbench that includes a virtual 3D patient and two haptic devices: one to replicate the biopsy needle, and a second one to mimic the ultrasound probe used to generate the ultrasound-like images in real-time. Real-time concerns due to the dual haptic rendering have dictated the choice of algorithms deployed.

We previously studied a simulation method to reproduce the respiration process with haptic feedback based on real patient anatomies [4]. All the parameters of the

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mathematical models were manually tuned. We propose here a new method to automatically estimate the soft-tissue and respiratory motion parameters based on image data.

2. Methods & Materials

The model simulates a tidal respiration as occurred during an actual liver biopsy. In such a case, the intrinsic motion of organs is mainly due to the action of the diaphragm. The diaphragm is acting like a pump by pushing and pulling the lower part of the lungs causing inhale and exhale. The diaphragm's model is anatomically similar to reality. It is attached to the 12th rib and to the spine, it contains muscular fibers that contract/relax moving its upper part made of tendinous fibers. The other structures involved, such as the ribcage, are static.

The respiration model is solving displacements and deformations using inverse kinematics: the tendon part of the diaphragm translates and the muscular fibers follow this translational motion with parts attached to the spine and the 12th rib. The elastic behavior of the muscle, and all the surrounding soft organs (e.g. the liver), is simulated using the Generalized Chainmail algorithm [5]. Moreover the liver is attached under the diaphragm.

Appropriate parameters that can be tuned for each patient need to be identified. Various techniques exist to measure the organ elasticity, such as elastography [6] and *in-vitro* measurements [7]. Similarly, the respiratory model can be parameterized using image-based deformable registration [8] or uniform pressure with sliding contact [9]. In our approach, all the features of our model have been extracted to estimate them (see Fig. 1).

The tissue elasticity parameters are directly dependent on the Chainmail definition. Only the muscles and organs of interest for liver biopsy are taken into account here. The parameters for the diaphragm and the liver are: the compression modulus C_D and C_L , the stretching modulus St_D and St_L and the shear modulus Sh_D and Sh_L respectively.

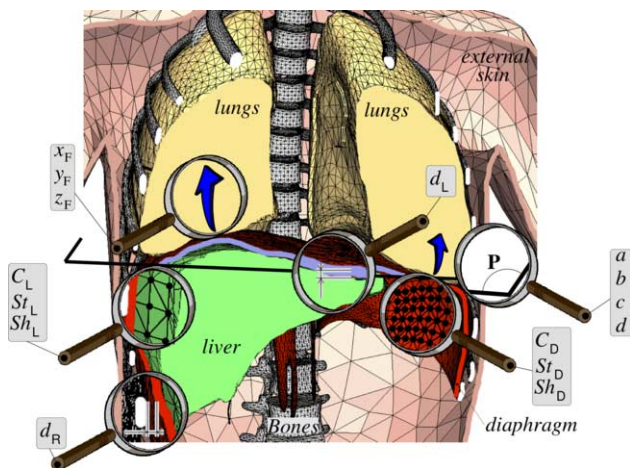


Figure 1. Respiratory model parameterization: 15 parameters to be tuned

For the respiration parameters we have the diaphragm course represented by its amplitude and direction. It is a 3D force vector characterized by its three components x_F , y_F and z_F . There is also the anatomical boundary between the different parts of the diaphragm (the stiff tendon part and the elastic muscle part). It is a 3D plane defined by four coefficients: a , b , c and d . Mechanical constrains are optionally set to attach the liver to the diaphragm and the ribs, respectively, to influence their motion. There are two threshold distances d_r and d_L . In total, 15 parameters need to be accurately set for each patient: 6 for the Chainmail parameters (three for both diaphragm and liver), 3 for the tendon force vector, 4 for the plane separating the tendon fibers to the muscle fibers, 1 for the attachment distance from the ribs to the diaphragm, and 1 for the attachment distance from the diaphragm to the liver.

Radiotherapy CT scans are used to build up a database of patient based cases, as they contain at least two 3D volumes for the dosimetry computation. Our strategy is to extract the patient initial geometry and initial organ position on the first CT scan and to extract the final organ positions from the second CT scan. We have currently built a database composed of four patients. The original medical volumes consist of three 3D CT scans at breath hold during full inhale and full exhale, and one 4D CT scans from which we only keep the two extremes in the breathing cycle.

For each patient, the liver and the diaphragm are manually segmented. The skin, the lungs and the bones are also automatically segmented using a single threshold. An iso-surface made of a triangular mesh is extracted for each segmented anatomical structure. Iso-surfaces are then processed using quadratic-based edge collapse and Laplacian smoothing until each mesh is decimated to around 2000 elements. This provides a good compromise between computation time, accuracy and visual quality obtained.

Let the initial state of real organs (S_i) be the geometries extracted from the 3D CT scan at inhale, and the final state of real organs (S_f) be the geometries extracted from the 3D CT scan at exhale. Let S'_i and S'_f be the respective states of the simulated organ. During the simulation, the respiratory model characterized by a set of parameters is applied on the initial state S_i to obtain the simulated final state S'_f . To quantify the accuracy of the simulation, a distance metric is used as a measure of the difference between S_f and S'_f [10]. It requires computing the root mean square error of the Euclidean distances between a point p and the surface S'_f . This quantity is called $d_{\text{rmse}}(S_f, S'_f)$:

$$d_{\text{rmse}}(S, S') = \sqrt{\frac{1}{|S|} \iint_{p \in S} d(p, S')^2 dS} \tag{1}$$

This value indicates how close is the simulation to the real position of the organs. For each iteration of the simulation, two metrics are available: one for the diaphragm ($d_{\text{rmse}}(\text{Diaph})$), and one for the liver ($d_{\text{rmse}}(\text{Liver})$). As a result, the overall quality measure of a simulation is:

$$\text{Quality} = \alpha \cdot d_{\text{rmse}}(\text{Diaph}) + \beta \cdot d_{\text{rmse}}(\text{Liver}) \tag{2}$$

with α and β coefficients to modulate the influence of the diaphragm and the liver, respectively.

The 15 parameters used to control the whole model correspond to real numbers. Boundary conditions have first to be estimated for each parameter. A random strategy is employed to explore this 15-Dimensional search space, and n iterations of the simulation are computed with sets of non-correlated parameters. For each parameter, a random value is chosen using a uniform distribution within its boundaries. The set of parameters that provides the lowest Quality value over n iterations is selected as it gives the closest estimation to the real data.

3. Results

Fig. 2 shows the root mean square errors for the diaphragm and the liver of four patients. Results for both the manual parameterization (see manual-diaph/manual-liver) and the automatic parameterization (see random-diaph/random-liver) are presented.

Given the number of parameters, 15 in total, we chose $n = 15^3 + \text{margin} = 5000$ for the experiments. α is set to 25% and β is equal to 75%. More influence is given to the liver over the diaphragm as in our application the needle biopsy is performed within the liver. A random search is performed 15 times for each patient. This allows us to check the stability of the results. They are shown using box plots in **Fig. 2**. The error given by the random search for diaphragms is generally smaller than or equal to the one given by the manual parameterization, although we note that the range of errors can be as high as 1 mm. The impact on the liver is, however, negligible. Indeed, the range of errors is relatively small, less than 0.5 mm, except for P2 (~1 mm) and the results provided by the random search are always significantly smaller than those given by the manual parameterization (up to 2.7 mm error reduction for P2). Some cases may be more difficult than others, i.e. the range of errors is relatively wide. However the median error for the liver remains ~3 mm lower than with manual parameterization.

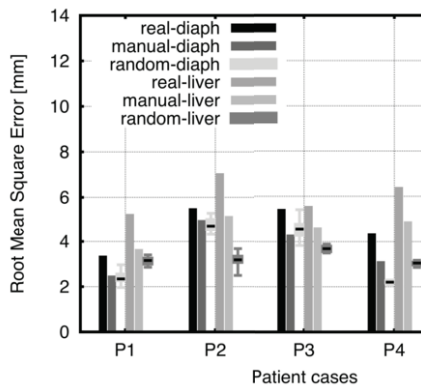


Figure 2. Respiratory model errors for the manual and automatic parameterizations

4. Conclusions & Discussion

We have presented a new method to automatically tune a complex analytical model used in an abdominal haptic-based needle insertion simulator. Fifteen parameters are

involved in the respiration process and in the soft tissue deformation. They are estimated from the position of organs and their respective topology at the two extreme stages of the respiration cycle (inhalation and exhalation).

Previously, parameters were set manually. However, this is difficult and time consuming to explore the search space as it involves 15 dimensions, in which it is not particularly clear how parameters are correlated. The advantages of the method presented here are: it is faster for the user - having just to set the attribute boundaries; and the results are significantly more accurate for the liver (only if n is high enough).

Future work will include the replacement of the random search method by an optimization technique to further refine the accuracy of the results. We also plan to incorporate more organs in the quantification process such as the lungs. Finally, we plan to obtain medical data with a more significant influence of the rib motion to validate our ribcage model.

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