A position-based framework for the prediction of probe-induced lesion displacement in Ultrasound-guided breast biopsy

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INTRODUCTION

The non-invasiveness and real-time capabilities of ultrasound (US) imaging make this technique appealing for guiding breast biopsy procedures. However, the fact that certain malignant lesions are often challenging to be distinguished on US has raised interest in finding some ways to combine knowledge about lesions position obtained from pre-operative modalities with real-time information provided by intra-operative US. To this purpose, several commercial and research platforms have implemented image fusion techniques able to co-register pre-operative data and US images [1]. However, none of these systems is able to account for the large deformations the breast undergoes due to the compression forces applied with the US probe by the physician to guarantee proper probe-tissue coupling and obtain acceptable image quality.

Biomechanical models represent a valuable tool to support the localization of suspicious areas identified on pre-operative imaging during US scanning, since they are able to account for anatomical deformations resulting from US probe pressure. Although the finite element method (FEM) has been extensively used in breast biomechanics, it was never employed to compensate for US probe-induced deformations, due to its incompatibility with real-time computation [2]. A valuable alternative to FEM is represented by geometry-based approaches, like the position-based dynamics (PBD). The PBD approach models objects as an ensemble of particles whose positions are directly updated as a solution of a quasi-static problem subject to geometrical constraints, thus making the method stable, robust and able to achieve real-time performances [3]. These are among the main reasons for the increasing popularity of this method in the medical field, especially for the development of surgical training simulators. The PBD scheme is used by Camara et al. to create a patient-specific biomechanical model of the kidney for the real-time simulation of intra-operative US [4]. In their work, optimal PBD parameters are estimated as those describing the deformation of kidney phantom subject to different levels of probe-induced deformations.

In this work, we present a biomechanical model of the breast based on the PBD formulation available in NVIDIA FleX. To the best of our knowledge, this is the first model able to predict in real-time the displacement of internal lesions due to the interaction with US probe. Since PBD parameters cannot be directly related to the real material properties, they are initialized with a calibration procedure performed on a phantom whose mechanical properties approximate those of the tissue of interest. In order to obtain a patient-specific description of the deformation, such parameters are then fine-tuned on the final anatomy (in our case, a realistic breast phantom) by tracking the displacement of a US-visible landmark. In this way, we obtain a patient-specific model that can accurately predict in real-time the displacement of the other internal areas during US scanning.

MATERIALS AND METHODS

The experimental data are acquired from a Freehand Ultrasound System (FUS) based on a MicrUs US device (Telemed, Vilnius, Lithuania) equipped with a linear probe (model L12-5N40) and an optical tracking system MicronTracker Hx40 (Claron-Nav, Toronto, Canada) (Figure 1). The overall probe spatial calibration error achieved is below 1mm (±0.7147).

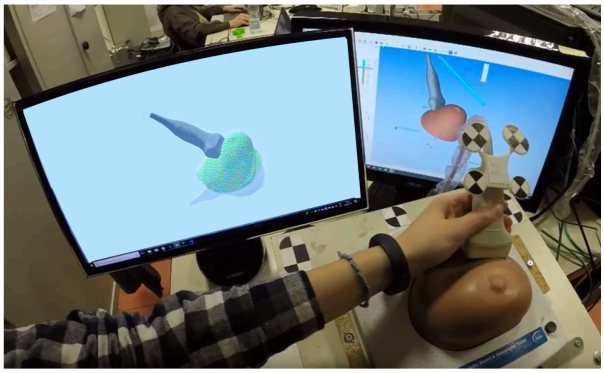

Figure. 1. The FUS system allows to map the real positions of the CIRS breast phantom and the US probe to the 3D Slicer scene (right monitor). Information about probe spatial transformation is communicated to the simulated environment in Unity (left monitor).

A box-shaped calibration phantom with three stiffer inclusions is manufactured with ballistic gel as described by Amini [5] and is used for the initial calibration of PBD parameters. In general, PBD simulations are controlled by a high number of parameters, but we focus on those closely controlling the deformable behavior of soft objects, which are related to the PBD constraint called "region-based shape matching". As a consequence, we optimize the value of *volume sampling, cluster spacing* and *cluster stiffness* parameters and we set other parameters in accordance to values reported in previous works [4]. Optimal model parameters are estimated with a greedy strategy as those minimizing the average localization error on the three internal inclusions, when applying four different input deformations with the probe

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(5, 10, 15, 20 mm). Localization error is computed as Euclidean distance between the model-predicted and the real displacement provided by the FUS of corresponding fiducial points.

A realistic multi-modality breast phantom (Model 073; CIRS, Norfolk, VA, USA) is used to evaluate the capability of the PBD model to provide correct estimates of biopsy targets. Although we expect that simulation parameters obtained for the calibration phantom provide a good approximation of the breast behavior under the same kind of input deformations, it is unlikely that the same exact parameters will be optimal to describe the deformations of a structure with some major differences, mainly in shape and material properties. In order to account for the specificity of the final scenario, some experiments are conducted to refine the values of selected simulation parameters before applying the model to predict lesions displacement. This process, which we refer to as fine tuning, consists of tracking the position of a US-visible landmark (in our case, one of the internal lesions) subject to four probe-induced deformations (15, 20, 25, 30 mm) in a similar fashion to what has been done for the calibration phantom. It's worth mentioning that this fine-tuning could (and should) be performed with any internal structure which is detectable on US. The PBD model with updated optimal parameters is then used to infer the displacement of the other 9 segmented lesions under four deformations as done previously.

RESULTS

Optimal values for the volume sampling, cluster spacing and cluster stiffness parameters for the calibration phantom are 5, 10 and 0.7 respectively. The fine-tuning process for volume sampling and cluster spacing converges to values of 7 and 8. Instead, cluster stiffness is not further optimized and kept to 0.7, since changes in its value did not impact significantly the calibration results already obtained. An improvement of 16% in the overall mean target error is observed thanks to the fine-tuning process.

Figures 2 and 3 compare the performances of the proposed deformation model with a rigid one. Localization errors relative to the rigid case are computed as difference between the lesion position at rest (which always corresponds to the predicted position) and the real current lesion position, both identified on US images. Whereas, error associated to the use of the PBD model is computed as difference between the predicted position and the real position, at each deformation level. The green and orange lines in Figure 2 show the trend of the localization error at increasing deformation levels for the PBD and rigid model. It is evident that, while the errors relative to the rigid case significantly increase with the induced deformation, PBD errors never exceed the threshold of 10 mm, even when the input deformation becomes large (in the order of 30 mm). On average, the PBD biomechanical model performs better than the rigid scenario for every lesion, as emerges from Figure 3.

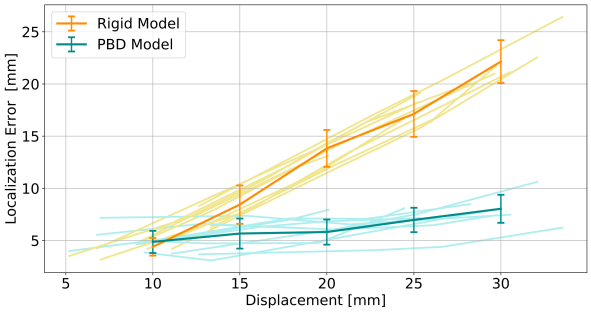

Figure. 2. Target error in mm at different levels of applied deformations for rigid (orange) and PBD (green) models. Solid lines represent the average errors on all the tumors, whereas shaded lines represent errors on each individual tumor.

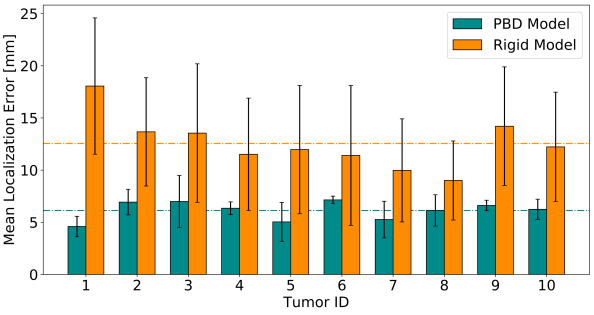

Figure. 3. Average localization error obtained for each tumor with (green) and without (orange) the PBD deformation model. Horizontal dashed lines represent the corresponding average error.

CONCLUSION AND DISCUSSION

Exploiting position-based dynamics formulation for modelling breast deformations has proved successful in predicting in real-time probe-induced displacement of internal lesions during US scanning. The proposed approach outperforms rigid models usually employed for lesion tracking in biopsy procedures. To strengthen our results, we will compare the PBD model with a FEM formulation, both in terms of accuracy and computation time. As future work, we plan to employ a more systematic multi-dimensional optimization procedure for parameters estimation and to improve the setup by replacing freehand scanning with a robotic acquisition. Finally, we will provide a more complete tool for guiding US-based percutaneous procedures by including needle insertion simulation.

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