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EARLY DETECTION OF BREAST CANCER THROUGH AN INVERSE PROBLEM APPROACH TO STIFFNESS MAPPING: SIMULATIONS AND EXPERIMENTAL VALIDATION WITH FORCE DATA

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INTRODUCTION

Early detection of breast cancer will continue to be crucial in improving patient survival rates. Manual breast exams and mammograms are the most widely used early detection techniques. Manual breast exams are limited in their ability to detect tumors since they only produce qualitative information. Mammograms, while effective, expose the patient to radiation and do not quantify tissue stiffness, an identifying characteristic of breast tumors.

Our ultimate goal is to develop a system that exploits this stiffness difference to automate, quantify, and enhance the resolution of the manual breast exam. An electro-mechanical device will gently indent the tissue surface in various locations, recording the indentation force and the tissue surface displacements. This force and displacement data will be used with inverse techniques involving finite element methods (FEM) and genetic algorithms (GA) to provide 3D maps of the elastic modulus of the interior of the breast tissue to identify suspicious sites.

Using only displacement data [1], we have developed appropriate computational algorithms and experimentally validated the technique with 180 g gelatin tissue phantoms. The algorithm correctly identified the presence or absence of 2 g tumors (approximately 1.3 cm cubes) in 12 tumor-free phantoms and 14 tumor-containing phantoms. To put this in context, breast cancer tumors less than 2 cm where the cancer has not spread to other sites are collected into the lowest risk group for invasive cancers with a relative 5-year survival rate of 99% [2].

Our results with displacement-only data are promising, but the natural next step would be to incorporate force measurements into the algorithm. Force data could be used in conjunction with displacement data or it might be possible to use only force data instead of the (somewhat difficult to acquire) displacement data.

In what follows, we show results from numerical simulations of force-only data and preliminary results from experimental validation.

METHODS

We adjusted the computational algorithms to use force data and have studied the performance of the algorithm with simulated data. A fine FEM mesh was used to generate the "true" force measurements. Noise was added to the "true" measurements to create "measured" forces with asignal-to-noise ratio of 13 dB. This noisy data and a coarser FEM mesh were used as input to the GA.

The genetic algorithm identifies the FEM material properties in the coarse mesh which minimize the cost function:

$$Cost = (Force\ Error) + w*(Tumor\ Radius)$$

Here *Force Error* is the difference between the forces from the coarse FEM and the "measured" force, and *Tumor Radius* is the mean size of the tumor in the coarse FEM (which acts as a regularizer). w is a weighting factor which adjusts the balance between the two terms to stabilize the solution. We seek a single w that works for all cases.

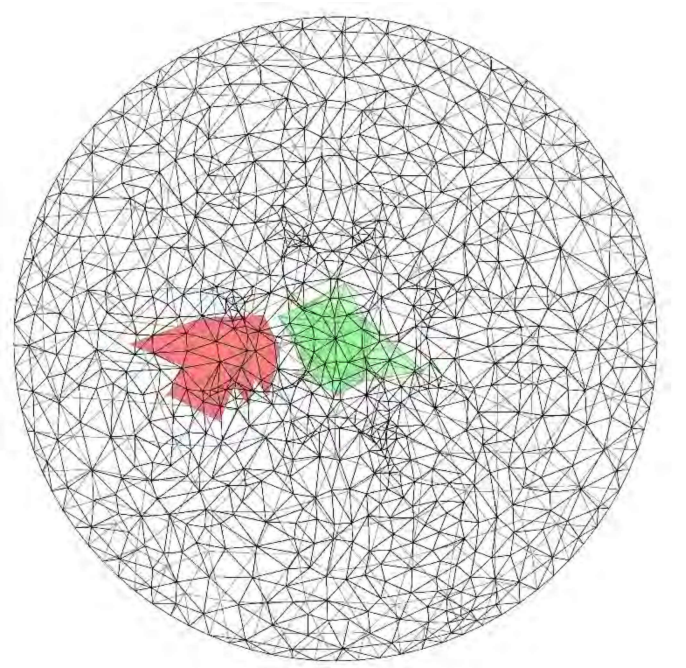
We tested a tumor-free case and eight cases with tumors, running 20 noise trials for each. Two tumor case locations ("First Tumor" and "Center Tumor") were selected manually and the remaining six tumor case locations ("Tumor A", "Tumor B", etc.) were selected randomly. The size of the domain was roughly 180 cc and the tumors were roughly 2 cc.

Our experimental validation to date has used gelatin phantoms having used them in the displacement-only approach. Indentation forces were measured at 36 sites on the phantom surface.

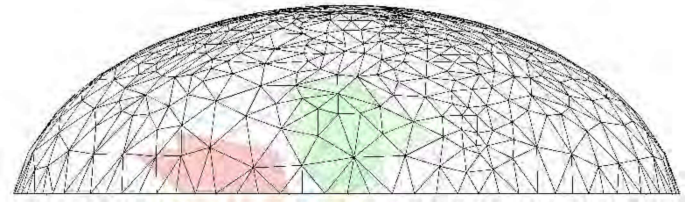
RESULTS

Figure 1 shows the results from one force-only simulation trial for the most challenging case: "Center Tumor" near the bottom center of the domain. The green elements indicate the true location of the tumor in the original fine mesh, and the red elements indicate the predicted

tumor location in the coarse mesh. Note that, since this is envisioned as a screening tool only, the presence or absence of a tumor is more important than the precise location of the tumor.



(a) Top View



(b) Side View

Figure 1: Typical result for "Center Tumor" with *w*=0.6. (Green = true tumor; Red = predicted tumor location)

Figure 2 summarizes the results for all twenty trials for all nine simulation test cases. The green region shows the *w* for which all trials for all cases are correctly identified. If *w* is too small the algorithm matches the data too closely and identifies small spurious tumors even in tumor-free cases. A blue '*' indicates the smallest w that gave a correct identification for a single trial of a tumor-free case. The blue horizontal line indicates the range of *w* for which all tumor-free trials were correctly identified. If *w* is too big then even realistic tumors are eliminated in tumor-containing cases. A red '*' indicates the largest w that gave a correct identification for a single trial for a particular test case. The red horizontal lines indicate the *w* range over which each tumor case was correctly identified.

The algorithm correctly identified all trials/cases for a range of weighting factors *w*. These results are all from simulations.

Our experimental validation for force-only mapping to date has used gelatin phantoms. We were able to correctly identify two tumor-free phantoms and two tumor-containing phantoms. However, we observed that the stiffness of the background gelatin changed by roughly 50% during the testing, making those phantoms unsuitable for force-only mapping validation. We are switching to silicone phantoms which should be more stable and will present results from those experiments.

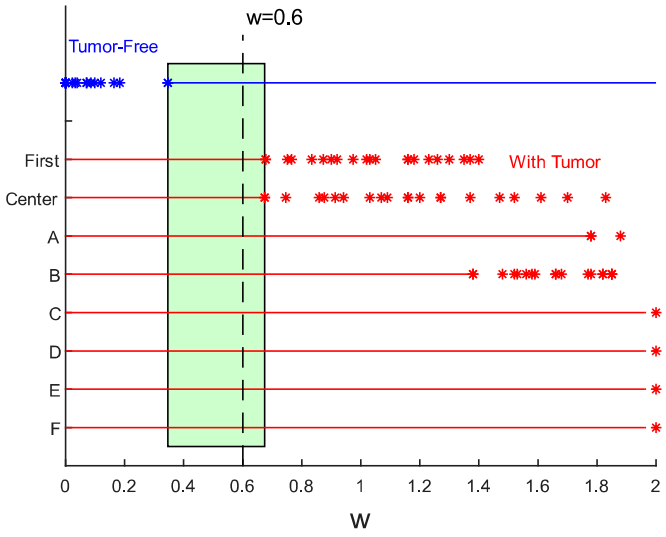


Figure 2: Ranges of *w* for successful identification for all twenty trials for nine simulation test cases. (Green rectangle = all tests/trials correctly identified; Vertical axis = test case name)

DISCUSSION

Displacement-only stiffness mapping has been validated experimentally with gelatin phantoms. Simulations of force-only stiffness mapping indicate that the method has promise as well. Our experimental validation of force-only mapping with gelatin phantoms, while encouraging, revealed that the gelatin phantoms' properties vary too rapidly to make them useful for force-only mapping validation.

It is important to realize that the benefit of displacement-only mapping is that the results do not depend on the absolute stiffness of the tissues. Thus, the gelatin phantom validation for the displacement-only mapping method also demonstrated its robustness with stiffness variations. However, the force-only mapping relies on a background tissue stiffness which is stable during testing since the forces are directly proportional to the stiffness.

We anticipate that the stiffness of silicone phantoms will be sufficiently stable to allow us to validate force-only mapping procedures and then move to a combination of displacement and force mapping.

ACKNOWLEDGEMENTS

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[2] www.cancer.org, 2020.