Three Dimensional Reconstructive Elastographic Imaging

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Abstract

Recently, a variety of methods for generating elastic contrast images of biological tissue have been put forward [1,2,3]. To date the large majority of these methods have been developed under assumptions of two dimensional mechanical behavior for the tissue in question. While this may well be valid in certain idealized conditions, it is by no means accurate for the general case, especially for non-symmetric tissue geometries or property distributions. In these situations, a three dimensional property reconstruction scheme will be necessary. Here, our efforts to develop a three dimensional elastic property reconstruction scheme are discussed and simulation results are presented.

Introduction

MR based elastic property imaging is a rapidly evolving field which seeks to determine the mechanical property distribution within a tissue region using displacement or strain information obtained for that region. This approach is necessary as a tissue's characteristic elastic makeup is not directly visible by means of magnetic resonance or ultrasound imaging. For the most part, the schemes developed for reconstructive imaging have been presented using two dimensional assumptions. While such assumptions are valid in certain cases, namely perfect symmetry in both property distribution and geometry, they will not be valid in a general heterogeneous tissue, such as the human breast. In these instances motion or strain in the third dimension is not insignificant and must be accounted for.

Methods

Previously, a finite element implementation of a subzone based elasticity reconstruction scheme has been presented [2]. This method uses the full field displacement data available from the MR to drive a non-linear reconstruction process based on squared error minimization. This approach, documented using a two dimensional plane strain approximation, is fully amenable to a complete, three dimensional treatment. Using a linear elastic model as the basic assumption for tissue motion, the governing equation for the harmonic tissue response is

$$\nabla \cdot G\nabla \mathbf{u} + \nabla(\lambda + G)\nabla \cdot \mathbf{u} = \rho\omega^2\mathbf{u}. \qquad (1)$$

The inversion process based upon the three dimensional equations of linear elasticity is executed in a similar fashion to the two dimensional scheme, with one notable exception. The automated zoning process for the two dimensional inversion problem is driven by a hierarchical ordering of element based error, requiring a global solution using the current property distribution estimate for every global iteration. For high resolution three dimensional problems global solutions are too costly to perform at each global inversion iteration. Thus, for the three dimensional inversion algorithm the zone location is selected in a random manner from the list of elements not yet operated on during the current iteration step.

Results & Discussion

Initial simulation experiments have been performed, fig. 1,

using displacements generated through a finite element solution with 15% random noise added to the data. To minimize the effects of such added noise on the inversion solution, a small degree of spatial filtering was used during the inversion process. This is achieved by incorporating the current property estimate of nodes in direct contact with a given node, i, such that $E_i^{new} = (1-\theta)E_i^{old} + \frac{\theta}{N_i}\sum_{j=1}^{N_i} E_j^{old}$, where N_i is the number of neighbor nodes connected to node i. For this experiment a value of 0.05 was used for θ.
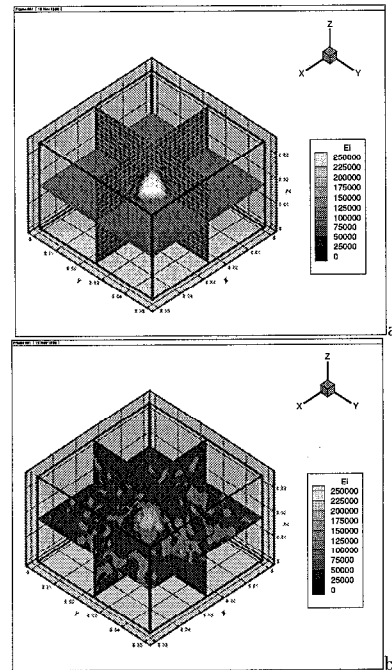

Figure 1: Three dimensional phantom simulation reconstruction for a 5cm x 5cm x 3.5cm geometry with a 25 kPa background Young's modulus and a 1 cm diameter 250 kPa spherical inclusion. (a) Inversion solution for 0% noise case. (b) Inversion solution for 15% noise solution.

The inversion process consisted of roughly 20 global iterations, each consisting of 300 zone based parameter updates on average, with the average zone size being roughly 330 nodes. The total solution consists of 24094 nodal stiffness values. This work was supported in part by NIH grant P01 #CA80139-01.

References
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