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PRINCIPAL INVESTIGATOR: Dragana Brzakovic, Ph.D.

CONTRACTING ORGANIZATION: Lehigh University
Bethlehem, Pennsylvania 18015-3046

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Dragana Brzakovic, Ph.D..

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Bethlehem, Pennsyvalia 18015-3046

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13. ABSTRACT *(Maximum 200 words)*

This report describes part of a study aimed at developing a computer-based aid for mammogram screening that makes a detailed comparison between mammograms of the same patient acquired at different screenings and detects changes indicative of cancer. The focus of the work in the past three years has been on putting two mammograms acquired at different time into correspondence. The essence of the approach is identification of control points in two mammograms; these points are used to put regions in two mammograms into correspondence. The emphasis of the work in the past year has been on improving the procedure for determining control points, i.e., points that are the same in two images. For this purpose we have developed a model based approach to identify regions of interest in two mammograms. The model encompasses breast tissue characteristics, modeling of compression effects and formation of X-ray images. The model is utilized to develop appropriate segmentation operators and the report discusses utilization of the model to detect lobules and ducts. The model can also be utilized for generating synthetic mammograms. Presently, we are evaluating the improvements this approach offers, relative to our original approach, in terms of determining more reliably control points, namely branching points of ducts.

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1. INTRODUCTION

The long-range goal of this work is to couple computer technology and human expertise with the objective to improve accuracy and consistency of mammogram readings while reducing the cost. Specifically, this work is concerned with the problem of detecting early cancerous changes by comparing temporal sequences of mammograms of a same patient. An advantage of considering mammogram sequences relative to analyzing a single mammogram is that it involves comparison, using the older mammogram as a reference, and thus, is likely to reduce the high rate of false positives associated with many computer-based methods. More importantly, following subtle changes may provide for very early cancer detection. However, automating mammogram sequence analysis is a very complex task, and it requires solving a number of subproblems, including standardizing screening procedures, registering mammograms, and characterizing minor changes in texture patterns. The present work focuses on the initial step of mammogram registration. The specific goals of the on-going study are to develop and test digital image processing methods that register mammograms (acquired in regular screenings) and provide for regional mammogram comparison with the objective of detecting early cancerous changes. These methods are envisioned as an integral part of a computer-based aid for mammogram screening which draws the attention of medical experts to suspicious regions in mammograms.

The view taken in this work is that the precise mammogram registration is intractable. This is due to the fact that these images correspond to compressed, elastic 3-D objects and the images differ primarily due to the fact that there are variations in positioning and compression. These variations are in essence changes in viewpoint, and 2-D transformations can not countereffect 3-D changes in viewpoint. This work concentrates on developing an alternative to precise registration by defining corresponding regions in two images, as is done by medical experts. These regions can then be analyzed for changes indicative of cancer. The first step in defining regions is establishing landmarks in a mammogram pair and establishing their correspondence. An important advantage of this approach is that it avoids interpolation inherent in detailed registration and thus provides for meaningful comparison between temporally spaced screenings.

The focus of the work in the past has been on the problem of extracting the landmark points, also referred to as the potential control points, and establishing their correspondence. Our most recent work concentrates on improving performance of our earlier developed algorithms. During the past year we have investigated a model-based approach to identify regions of interest/control points in digital mammograms. The approach is based on mammogram simulation that gives an insight into properties of ducts that are used in identifying the control points, i.e., intersections of elongated structures. Figure 1 describes the relationship between the mammogram simulation and mammogram segmentation. Identification of regions of interest in a mammogram is achieved by the image processing suite that contains various operators, including wavelets, fractals, and operators that capture textural, shape and structural properties. Appropriate operators are selected based on the task objectives and the input provided by the modeling suite. The modeling suite contains relevant information about 3-D arrangement of tissues, and their anatomic, histologic and radiographic characteristics. This information, combined with general knowledge about mammogram acquisition and information about mammogram digitization, is used to derive expected properties of regions seen in a mammogram and select appropriate operators for task at hand. The report details mammogram modeling and simulation in Section 2 which is followed by its utilization for identifying more precisely the elongated structures.

2. MAMMOGRAM MODELING AND SIMULATION

The objective of this part of our work is to increase the understanding of relationship between the breast anatomic structures and their appearance in digital mammograms. Our

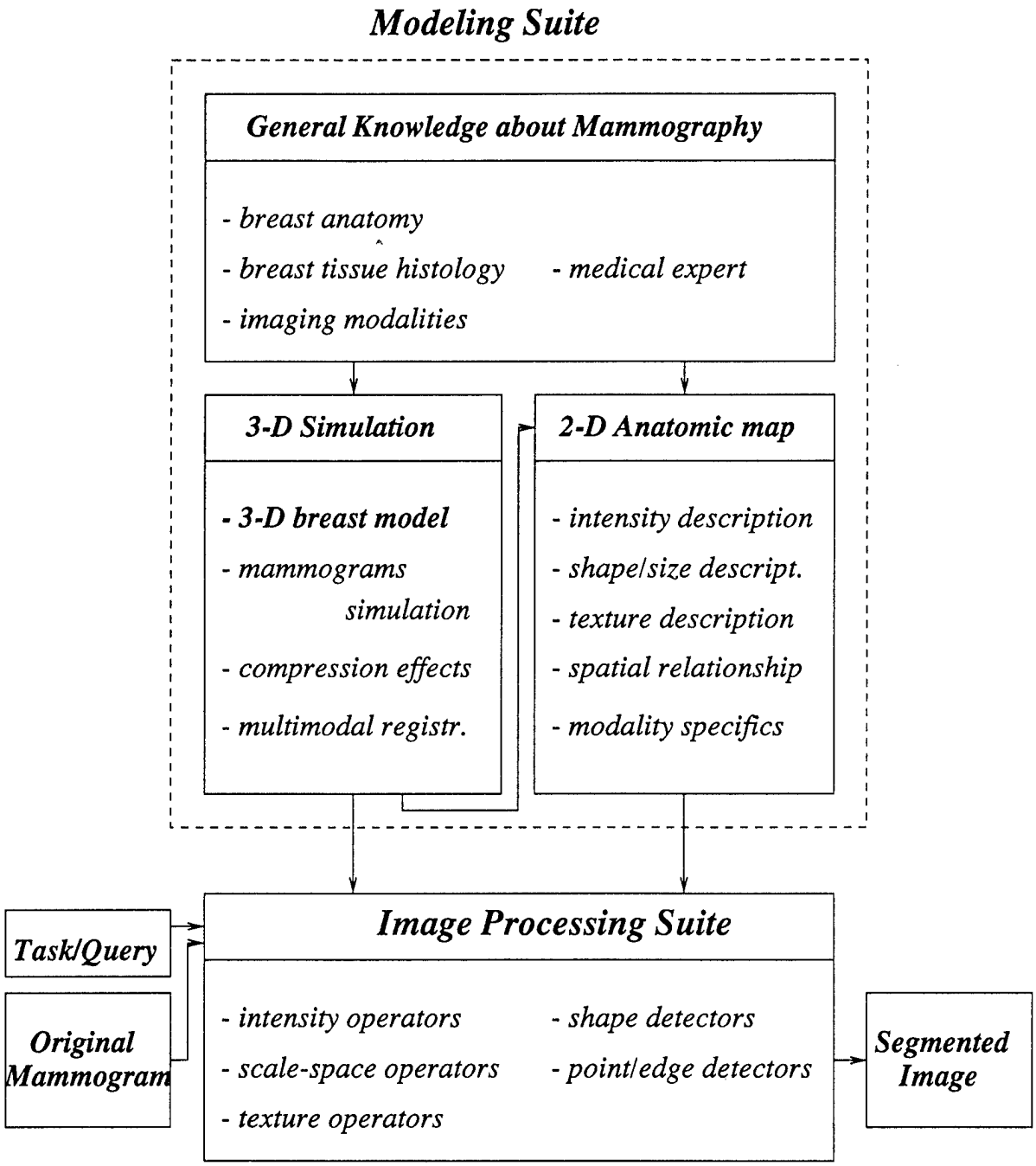


Figure 1. Conceptual relationship between mammogram modeling and identification of regions of interest in mammograms.

accomplishments up-to-date incorporate rudimental modeling of digital mammograms [1],[2]; the approach comprises of three major steps:

- modeling breast anatomic structures,
- modeling breast tissue compression, and
- modeling X-ray image acquisition.

The breast structures are modeled based on their anatomic properties obtained from description in literature and histologic slice images. Breast compression deformation is estimated using tissue elastic properties and the proposed deformation model. The resulting synthetic mammograms can be used in analysis of positioning and compression effects, and for testing computer algorithms for detection of abnormalities. The following three subsections discuss each of the steps.

2.1 Modeling Breast Anatomic Structures

2.1.1 Anatomic Background

Major tissue types comprising breast anatomy are fibro-glandular tissue, FGT, adipose (fatty) tissue (AT) and pectoral muscles (PM). While the muscular tissue is grouped together and located near the chest wall, the adipose and fibro-glandular tissue are interwoven and distributed throughout the breast volume. Their relative percentage and distribution determine the parenchymal patterns on mammograms and decide whether the breast is classified as ``dense", ``fatty", or ``mixed" type [3].

Adipose tissue consists of very large cells grouped into small compartments visible with the naked eye [4]. Compartments are separated by the connective tissue. Within the breast volume, adipose tissue is located (i) frontally, in subcutaneous layer between the skin and FGT, (ii) posteriori, in a layer of retromammary fat between the FGT and PM, and (iii) within the FGT, in the fatty cavities between the lobes and surrounding the ducts [3],[5],[6].

Fibro-glandular tissue is located between subcutaneous and retromammary fatty layer. It consists of the ductal network -- parenchymal, i.e., functional part -- and the fibrous connective tissue -- stromal, or supportive part. These two types of tissue are very closely interwoven within the FGT region. Moreover, they have practically the same X-ray attenuation and are difficult to separate on a mammogram. The FGT can extend far in the upper-lateral breast portion toward axilla (armpit) and behind the PM, forming Tail of Spence [7]. This part of the FGT is important because it is sometimes missed in a mammogram due to incorrect breast positioning which presents a risk to miss abnormalities. Fibrous stroma is described in the literature as a 3D fibro-fatty matrix [6], the connective tissue sponge-like structure with cavities filled by adipose tissue. At the periphery of the matrix, the connective tissue extends into Cooper's ligaments, providing breast with the attachment to the subcutaneous layer of skin. Ducts, as well as the nerves, blood and limphatic vessels pass through the FGT matrix. This fibro-fatty concept can be related to the FGT distribution seen at the subgross histologic slices of the breast [8]. Ductal network is associated with high incidence of breast cancer. About 90% of cancers originate in the ductal epithelium, and remainder in the lobular epithelium, with a very small percentage arising from fibrous stromal tissue [3]. Ductal network consists of ducts and lobules, made of glandular epithelial tissue, and surrounded by connective tissue. Ducts extend from the nipple toward the chest wall, branching into a network of smaller and smaller ducts, separated into lobes by the fibrous connective tissue (Cooper's ligaments). The clusters of lobules occupy the chambers, similar to the fatty cavities. There are 15-20 lobes each drained by its own major duct [5]. Several major ducts join in the ampulla, a wider channel beneath the nipple. Therefore, there are fewer, 6-8, independent openings in the nipple. Major ducts and the nipple openings are 2-4.5 mm and 0.4-0.7 mm in diameter, respectively [5]. There are very few attempts to reconstruct breast ductal network. Ohtake et al [9] and Moffat and Going [10] used photographs of a series of subgross histologic slices, and a computer algorithms to trace the points of duct entrance to and exit from the successive slices. Moffat and Going reconstructed ``duct catchiments", i.e., portions of breast

volume drained by the same duct subsystem (corresponding to individual lobes). Ohtake et al gave more precise visualization of ductal network 3D structure by processing samples of breast conservation surgery (quadrantectomy). Another approach is reconstruction of 3D ultrasound scan data, by Moskalik et al [11]. Semiautomatic computer algorithm starts by locating ampulla and a major duct which is further traced in a single plane. Other major ducts (corresponding to other lobes) are found by rotating the search plane approximately 20 degrees axially (assuming that breast contains 15-20 lobes).

2.1.2 Radiographic Appearance

Radiographically, there are two differing components visible in a mammogram: (i) opaque connective fibrous tissue and ducts and (ii) lucent -- fatty compartments. In addition, one can distinguish microcalcifications and pectoral muscles, which have characteristic intensity, shape, and location. Ducts are often too small to be resolved by mammography or are obscured by the surrounding connective tissue structures. They can be more visible when dilated or accompanied by microcalcifications of characteristic elongated shape. Specialized technique for X-ray imaging of duct abnormalities, ductography, uses agents with high X-ray attenuation, which are injected into a single opening in the nipple, therefore visualizing few lobes only. Visibility of the FGT is affected by the water content and the glandular development related to age. However, the most profound impact on the appearance of the FGT region in a mammogram has the 2D nature of mammographic imaging. Breast 3D structures (ducts and the fibrous elements) are projected onto the 2D film plate in an overlapping manner. Superposition of X-ray attenuation of the overlapped structures produces variety of grey-levels seen in mammograms and also creates characteristic large-scale mammogram texture, called parenchymal patterns. Parenchymal patterns are important since they present the background intensity variations that can corrupt the algorithms for detection of breast abnormalities. In addition, there is no precise definition of the normal breast parenchymal pattern.

2.1.3 Mammogram modeling

Modeling Borders of the AT and FGT Regions

As a first step, our goal is to model 3D breast composition for the purpose of simulating the mammographic medio-lateral (MLO) view. During the MLO view the compression and film plates are positioned tilted for 40-60 degrees from the vertical breast plane toward the axilla. The angle used depends on the orientation of the pectoral muscles, since the compression applied parallelly to the PM allows the best visualization of the breast [7}.

The vertical symmetry plane of the proposed 3D breast model corresponds to the MLO view plane. Breast volume is approximated by the quarters of two ellipsoids, attached horizontally at the nipple level, representing the upper and lower breast halves. Dimensions of the ellipsoids are selected from the published data on the average size of the breast subgross histologic slices [5]. Dimensions, (height x width x depth), of the relaxed breast model are (Figure 2):

- 12cm x 10cm x 5cm, upper half -- above the nipple level;
- 5cm x 10cm x 5cm , lower half -- below the nipple level.

It should be noted that our model proportions (vertical to horizontal dimension ratio) agree with the ``standard breast'' [12] – defined by averaging dimensions of 27 compressed breasts used in analysis of deformation during mammographic compression. Our model can be obtained by scaling down the ``standard breast'' for 15%.

The extent of the FGT in our model is bordered by two ellipsoidal surfaces, anterior (front) and posterior (rear), which differ above and below the nipple level. The region between the FGT and the border of the breast volume models the extent of the AT. Dimensions of the FGT region are estimated from the drawings of breast anatomy with inclusion of the axillar FGT extension, Tail of Spence. Dimensions of the relaxed breast FGT region are shown in Figure 2.

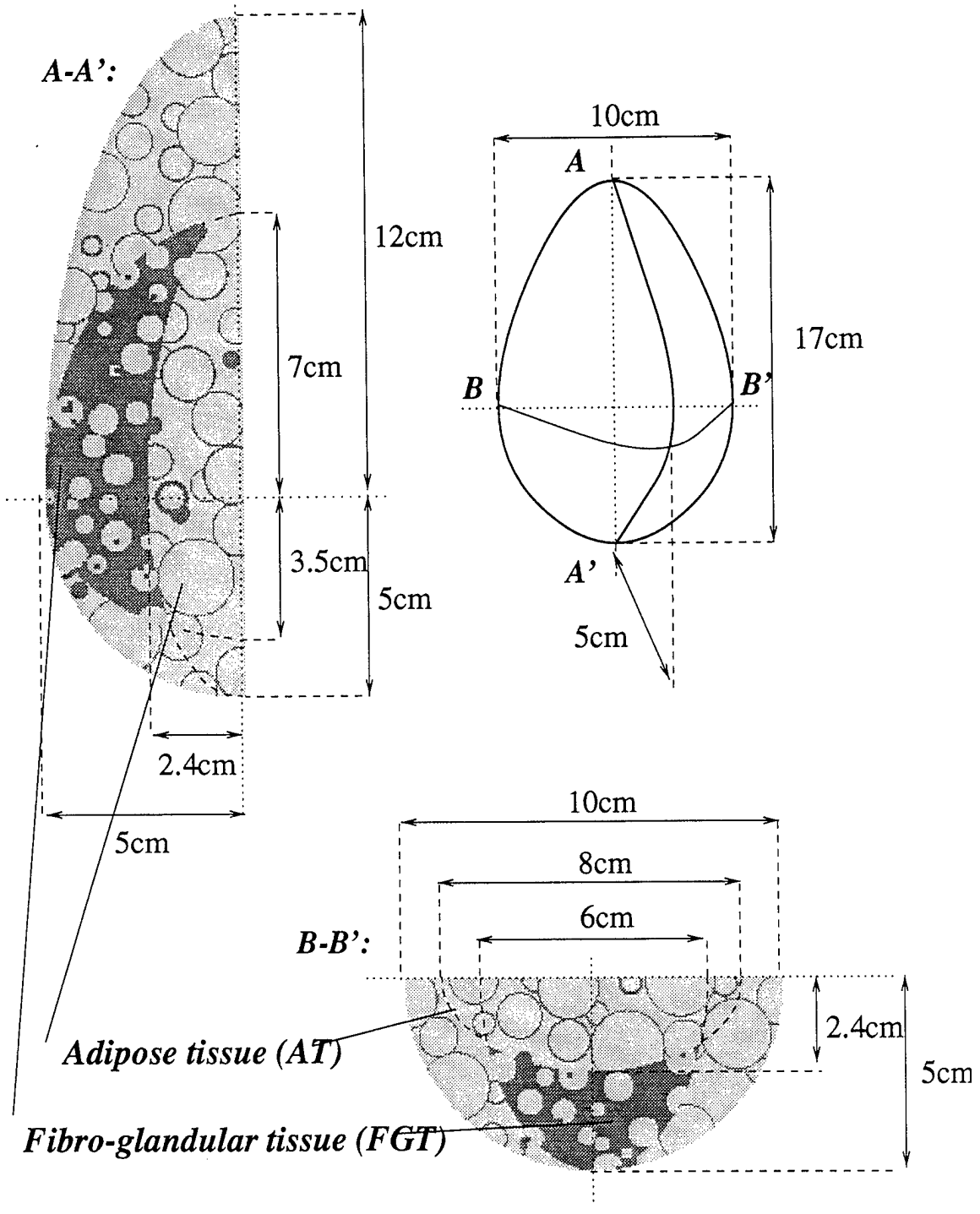


Figure 2. Illustration of elements incorporated in the model and dimensions of the major parts.

Modeling internal structure of the AT and FGT Regions

In our model, internal structure of adipose tissue is represented by the random distribution of the fatty compartments throughout the AT region. Compartments are bounded by thin spherical shells, which are associated with the X-ray and elastic properties of the connective tissue. Compartments themselves -- interiors of the shells -- are associated to the properties of fat. During the random placement of the shells they keep the constant radius until no new compartment can be added without intersecting other spheres. The radius is then decreased and the placement of compartments continues. The thin shells also model the Cooper's ligaments -- attachment of the breast to the subcutaneous skin layer. In the regions near the breast outer border the spheres are allowed to fit only partially within the breast region, so that the intersections of the shells with the breast border model the points where Cooper's ligaments are attached to the skin.

Modeling the FGT Region

The internal structure of the FGT region is modeled using description of the fibro fatty matrix [6]. The modeling starts by defining a region associated with the X-ray attenuation and elastic properties of the connective tissue, bordered by the anterior and posterior FGT ellipsoids. Fatty cavities are then perforated within the FGT by random placement of the spheres and their interior is associated with the properties of the adipose tissue. Radii of the cavities are selected in a similar manner as when modeling the AT fatty compartments. More analysis is needed to determine the optimal range of values for radii of the fatty cavities and compartments and to replace the idealized spherical compartment shape with the more realistic one.

Modeling Ductal Network

It is important to include ducts into a breast model for mammography simulation, due to their high cancer incidence and because they are important factor in formation of parenchymal patterns -- mammographic texture consisting of overlapped projections of breast fibrous structures and ductal network. Large variation in parenchymal patterns affects computer methods for detection of abnormalities by masking lesions and introducing false abnormalities.

In our early work on mammogram simulation [1], [2] we have approximated ducts by short linear segments placed randomly inside the FGT region and oriented toward the nipple. This approach was justified by description of mammogram constituent elements [13], used for classification of parenchymal patterns. This approximation offers a relatively good simulation of parenchymal patterns, but neglects connectivity of the ductal network. An alternative approach to duct modeling based on fractal set theory was reported in the literature [14]. Branching pattern of such obtained ductal network corresponds to an ideal binary tree, and therefore the generated mammogram texture has too regular appearance.

More realistic model of ductal network may be achieved by various tree modeling algorithms [15]-[17]. Typically, they approach modeling at two levels: (i) topological, where a topological tree, underlying the real one, is constructed, and (ii) geometrical, where the individual tree elements, branches and leaves, are designed in order to capture the shape of the real tree as close as possible. Focus of most algorithms is on capturing rules of tree development, used in recursive modeling of tree shape [15],[16]. An approach based on the ramification matrices [17], on the other hand, focuses more on description and control of the final shape, while still on the topological level. Ramification matrices describe branching pattern of a tree and allow classification between different groups of tree structures (e.g., the basic ones: perfect tree, random binary tree, self similar fern, etc.) which can be further refined to capture the real features of a tree (dense, bushy,etc.).

Our 3D breast model includes duct network model developed using ramification matrices. This approach is selected because it provides a realistic appearance of duct branching pattern; however, it does not capture underlying breast development process. Example of using ramification matrix and the corresponding ductal network model is shown in Figure 3.

Ductal network model for our mammography simulation uses ramification matrix corresponding to a random binary tree. This matrix was selected after analysis of small number of available ductograms. The analysis traced the network of larger ducts from ductograms. The elements of the ramification matrix were inferred using described procedure. The problem in this approach is in similar appearance of the points where ducts branch or overlap. We applied reasoning that the points of duct overlap should look brighter in mammograms, due to doubling X-ray attenuation of two ducts on the top of each other, compared to the points of duct branching. Identification of the branching pattern was done manually by first marking the points of branching and overlap and further tracing the large ducts by connecting the branches. The procedure was repeated several times in order to increase the confidence of the finally traced duct network. The ramification matrix inferred this way had a trend of elements similar to the matrix obtained for a random binary tree. Due to the small number of analyzed ductograms we decided to use the ramification matrix corresponding to the random binary tree rather then the inferred one. Intuitively, random binary tree seems to be the most natural choice out of the structures analyzed in the literature [17] -- ideal binary tree, random binary tree, self-similar fern.

Our 3D model of the breast ductal network consists of several ramified trees, each representing a duct lobe. Duct curvature is modeled by modifying a vertical tree, generated using a ramified matrix, to follow an anticipated lobe direction -- a curved path between lobe starting point in the ampulla beneath the nipple and the final point on the posterior edge of the FGT region. The lobe final points were selected assuming that the lobes are placed under approximately equal angles between each other.

2.2 Modeling Mammographic Compression

The model of breast compression described here includes deformation of the large-scale anatomic structures (i.e., the AT and FGT region borders) with independent analysis of 2D slices of the breast model. Deformations of the internal structures of the AT and FGT are modeled by transforming spherical shape of the fatty compartments and cavities into the ellipsoidal ones.

Deformations of the AT and FGT regions are estimated for each slice positioned normally to the compression plates, using a 2-D composite beam model. The estimation incorporates the following steps:

- *Rectangular Approximation of Breast Model Slice* We model breast deformation during the MLO compression. Modeling starts with slicing the 3D breast model normally to the compression plates. Thickness of the slices corresponds to the vertical resolution of the model that can be selected at the beginning of mammography simulation. A slice of the breast model is replaced by its rectangular approximation. The whole slice region and its FGT part are approximated by the rectangles having the same area and the center of gravity, as the corresponding regions of the slice. In order to compute rectangle sides, we need an additional constraint. Thus, we assume that the rectangle side, parallel to the line nipple -- chest wall is equal to dimension of the corresponding slice region in that direction.
- *Slice Deformation Estimation Using 2D Composite Beam Model* Approximation rectangles keep the same elastic parameters as the corresponding slice regions. There is very little reported in literature about the elastic properties of the breast tissue. It is, however, usually assumed that the human soft tissue is incompressible [18] -- its volume does not change with deformation. We also assumed that the elastic properties of the AT and FGT could be approximated by linear Young's elastic moduli. More accurate analysis of deformations should use hyperelastic or viscoelastic models, due to the large relative deformations

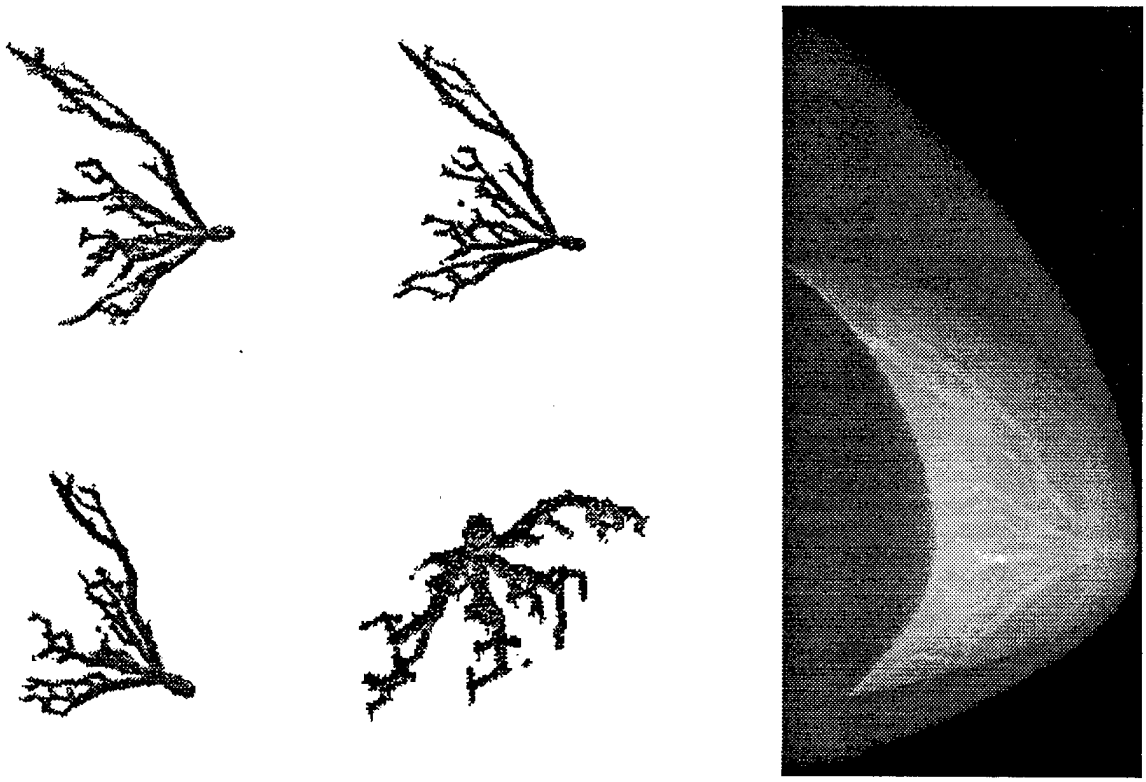


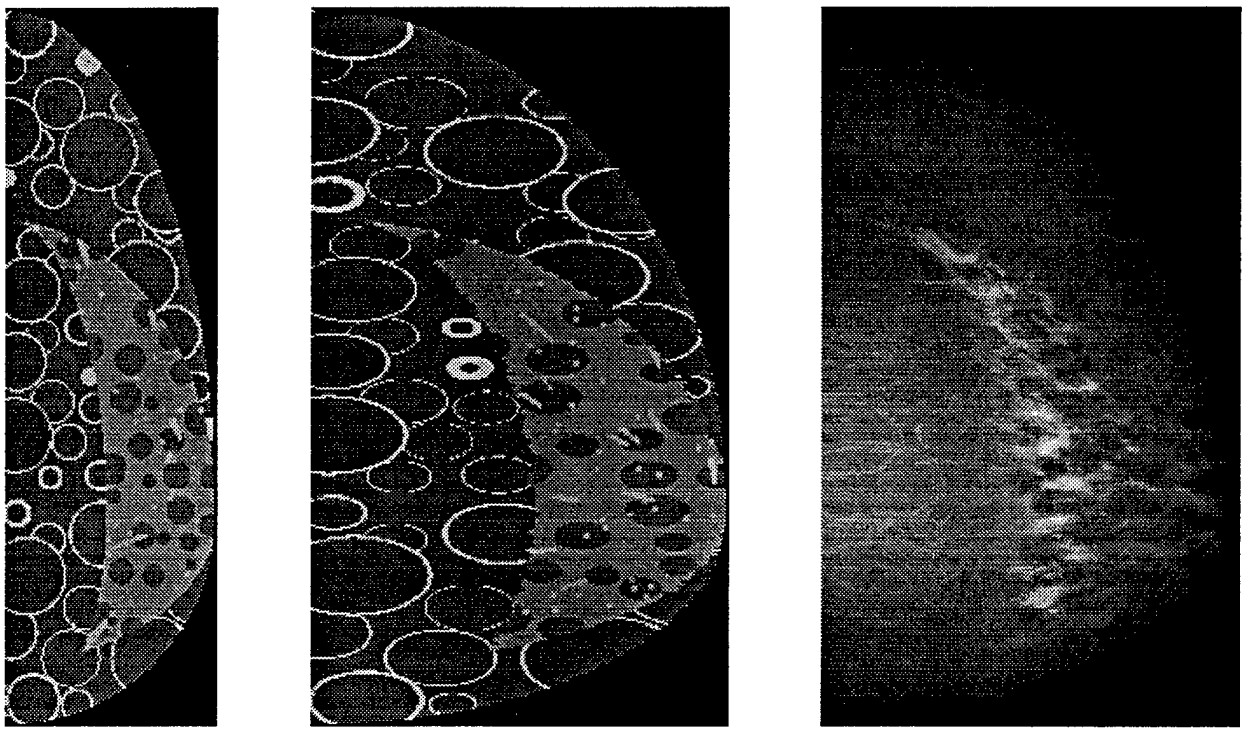
Figure 3. Duct modeling using ramification matrix; examples of duct trees and superposition of ducts onto a mammogram.

encountered in mammography. Our compression model uses the relative ratio of the AT and FGT elastic moduli, which was determined using published values of the ultrasound velocity in different tissue types [19] and relation between the velocity and the elastic modulus [18]. Rectangular slice approximation practically has a shape of a composite 2D elastic beam, positioned between two bars corresponding to the compression plates. Breast deformation is estimated by applying the force to the compression plates which in turn deforms the composite beam. There is very little reported in the literature about the analysis of the mammographic compression force. As a first approximation our compression model assumes the uniform distribution of the mammographic compression force across the slice. The intensity of the compression force is included indirectly, by assuming the thickness of the compressed breast. Application of the Hooke's law to the rectangular approximation yields the deformed 2D composite beam.

- *Computing Compressed Slice from Deformed Rectangular Approximation* The final step of deformation estimation is computation of the compressed breast slice from its deformed rectangular approximation. In our preliminary work, we have assumed that the breast slice keeps its elliptical shape after the compression. Parameters of the deformed ellipses were computed preserving the region area and dimension along the nipple -- chest wall line. Requirement that the whole FGT region is contained within the borders of the slice was used to define the two elliptical borders of the FGT. The elliptical shape of the compressed breast slice, used in our previous model, does not match the real breast shape. Published literature [7],[12] shows that the compressed breast has constant thickness -- equal to the distance between the compression plates -- everywhere except in a narrow region close to the front breast edge. Analysis of that region on a mammogram was used to estimate the breast thickness directly from mammograms [20]. Therefore, a breast sliced normally to the compression plates does not have elliptic but rather flattened shape. To compensate for the deficiency of our previous approach we have applied correction to the preliminary compression model. Correction assumes that the deformed breast slice consists of (i) a rectangle positioned at the chest wall side and (ii) a semiellipse attached to the rectangle, extending forward to the nipple. Sum of the rectangle and semiellipse area is equal to the whole uncompressed slice area. One side of the rectangle and one axis of the semiellipse are equal to the compressed breast thickness. In order to find the rest of parameters, an additional constraint is needed. We compute those parameters using the fact that the region where the breast thickness drops from its constant value, contains about 10% of the whole mammogram area [20]. Described correction for flattening of the compressed breast is used only to determine the border of the whole compressed slice. Deformation of the FGT region is still computed using the 2D composite beam approximation. The separate processing of individual model slices is followed by stacking them together to form the deformed 3D breast model. The slices whose thickness, in relaxed state, was smaller than the compressed breast thickness, are not processed at all; they are assumed to preserve their relaxed shape. The compression model is illustrated in Figure 4.

2.3 Modeling X-ray Image Acquisition

Detailed description of diagnostic X-ray imaging principles, [21] and basic principles of X-ray mammography [3], [5] are given in the literature. There are various effects of X-ray interaction with human tissue. Three of them occur in the energy range used for diagnostic X-ray imaging -- photoelectric effect, coherent, and Compton scattering, [21]. Photoelectric effect is related to X-ray attenuation of tissue and absorption of X-rays by tissue. Attenuation of X-rays is a desired effect since it enables imaging of minute differences in tissue density related to the normal or abnormal changes. However, absorption of X-rays is harmful for tissue, requiring protection measures to reduce radiation dosage received during mammography. Other two scattering effects degrade quality of obtained images by introducing undesired background noise. It can be noted that the first models of mammography were developed with a goal of computing radiation dosage received during mammography. Based on the description of X-ray imaging process, relations between the energy imparted during imaging, tissue X-ray attenuation, and the film



(a) (b) (c)

Figure 4. Modeling of compression effects: (a) relaxed breast, (b) compressed breast, (c) corresponding synthetic mammogram.

density (or alternatively, pixel intensity on a digitized image) were derived in the literature [22]. We use these relations in our mammography simulation in order to bridge proposed model of compressed breast anatomic structures and resulting synthetic mammogram.

Mammogram formation is based on the overlapping projection of the breast anatomic structures on a film plate. This overlapped projection of the breast fibro-glandular structures generates characteristic mammographic large-scale texture called parenchymal pattern. Parenchymal patterns are important because they can affect performance of computer methods for detection of abnormalities. These patterns can be considered as large-scale mammogram texture, since scattering effects and other degrading noise generate fine background variation of film density -- small-scale texture. By modeling breast anatomic structures and X-ray acquisition process, we have basically simulated large-scale mammogram texture. Small-scale texture can be simulated using the analysis of the scattering [22], [23], which is one of the possible improvements of the proposed model.

The final result of the mammography simulation is a synthetic mammogram. It combines the effects of all three major steps of simulation -- modeling anatomy, compression, and X-ray image acquisition. Examples of synthetic mammograms are shown in Figure 4 (c).

3. IDENTIFICATION OF REGIONS OF INTEREST USING MAMMOGRAM MODEL

The objective of our work is putting a mammogram pair into correspondence for the purpose of performing automated follow-up. Our approach of achieving correspondence is identification of similar regions in two images. During the last year we have focused on developing more precise segmentation methods that more reliably determine landmarks that can be used in identifying corresponding regions. The essence of our approach was using our simulation model to develop segmentation techniques. Based on our prior work, we have focused on identifying elongated structures in mammograms, specifically emphasizing identifying ductal network.

Modeling approach proposed in this work is used to develop an anatomic map -- description of expected properties of breast regions seen in mammograms, which provides relational information and spatial scales needed for mammogram processing and thus allows derivation and selection of appropriate image processing operators to detect regions of interest in a mammogram. In this study, focus is on identification of ductal network and lobules; ductal network is the basis of determining control points (described in earlier reports) and the two regions of interest are associated with high incidence of breast cancer origin. Detection of ducts and lobules is based on simulation of mammography. The breast model is used to derive the expected properties of the mammographic regions, which are in turn used in selection of proper image processing operators and their spatial scales for desired segmentation task and given acquisition and digitization parameters. Developed algorithms for identification of regions of interest are first tested on synthetic mammograms (obtained by mammography simulation) with known distribution of different tissue types, and then applied to real mammograms.

Lobules are detected using the following steps: (i) Morphological ``top-hat'' operator is applied to an enhanced contrast mammogram; (ii) Obtained result is combined with local variance image; and (iii) Regions with desired shape and size (1-2mm spheres) are selected. Detection of ducts is done with the following steps: (i) Linear structures detector is applied to the original mammogram, (ii) End points of major ducts in the nipple are detected, (iii) Duct following procedure is performed using directional map. Examples of detection of lobules and ducts are shown in Figure 5.

The algorithms for identification of regions of interest are presently undergoing first phase evaluation on synthetic mammograms and on real images. The real mammogram tests involve visual evaluation by medical experts, on two sets of mammograms, MIAS mammogram database, [23], and temporal sequences of mammograms acquired at Lehigh University. The

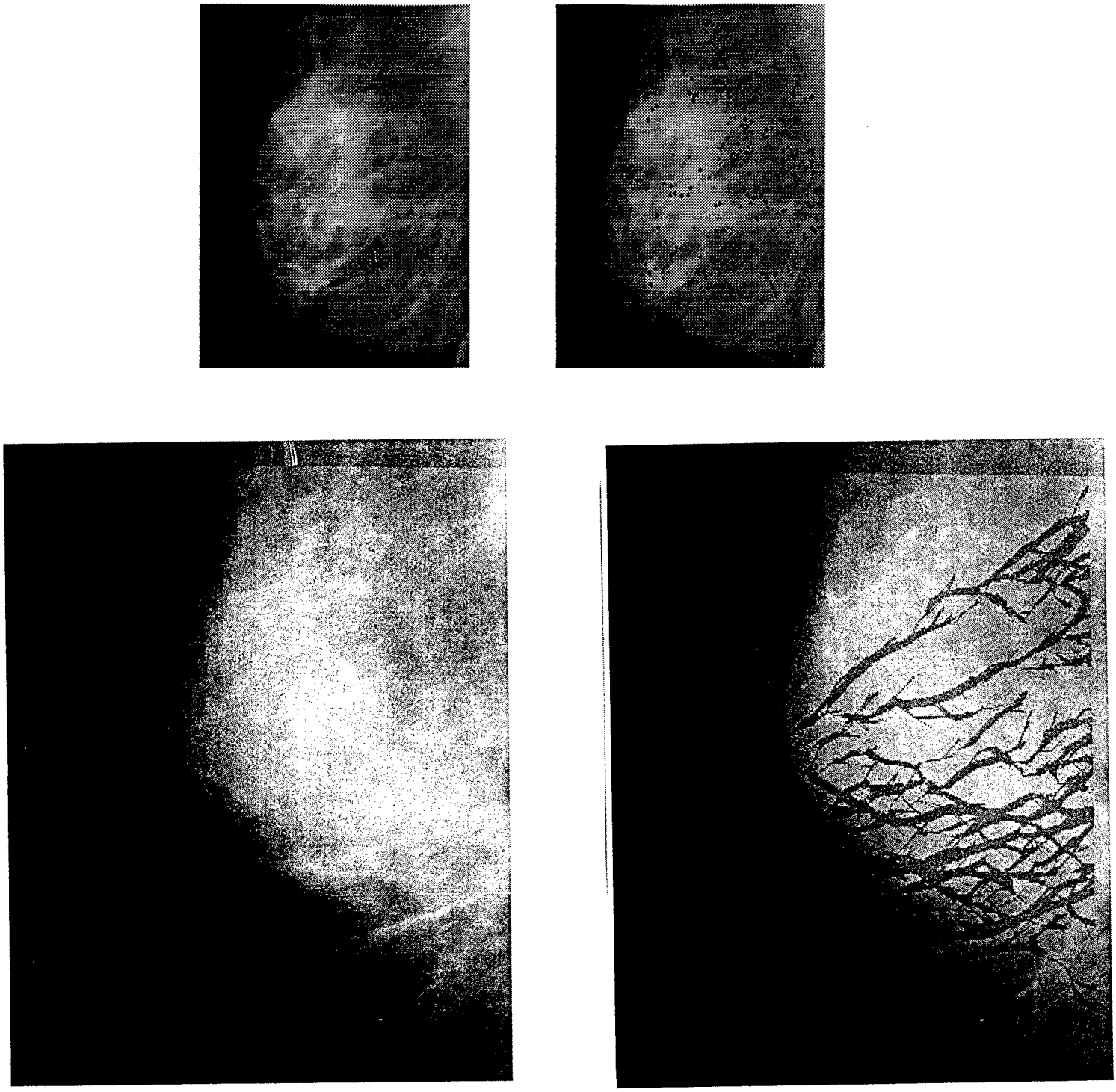


Figure 5. Identification of regions of interest: Top—identification of lobuli; bottom—identification of ducts.

preliminary results indicate that the proposed methods are capable of detecting ductal network successfully.

4. KEY RESEARCH ACCOMLISHMENTS

The primary concentration of the work in the past year was on improving already developed algorithms for establishing correspondence between two mammograms. Because there is very limited understanding of nature of mammogram images, we have focused on obtaining an insight into these images through mammogram simulation. The primary accomplishments in the past year are:

- Modeling of breast tissue characteristics
- Modeling of compression effects
- Modeling of X-ray image acquisition and formation of synthetic mammograms
- Utilizing these models to develop more reliable segmentation techniques, focusing on detection of ducts which were the key to determining control points (discussed in earlier reports)

It is pointed out that this part of our work goes beyond the original workstatement, and is in response to a need to develop more reliable algorithms for putting a mammogram sequence into correspondence.

5. REPORTABLE OUTCOMES

The results of our work was reported in following papers during 1998 and 1999

- P. Bakic and D. Brzakovic, ``Simulation of Digital Mammogram Acquisition,'' Proc. SPIE 3659 Medical Imaging, pp. 866-877, San Diego, CA, Feb. 1999.

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Also, this work is focus of a Ph.D. dissertation expected to be finished by December of 1999.

6. CONCLUSIONS

During the first two years of the project, we have developed algorithms for putting mammogram pairs into correspondence, as planned by our original workstatement. During the past year we have focused on improving reliability of detecting control points which were the essence of our approach to putting a mammogram sequence into correspondence. For that purpose, we have developed a model-based approach to segmenting mammograms, i.e., identifying regions of interest with focus on detecting ducts. The model-based approach was developed by first studying properties of mammogram images and developing simulation algorithms for modeling breast tissue, modeling compression effects and acquisition of X-ray images. The importance of

these models goes beyond this project, because they provide for better understanding of digital mammograms.

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