Partial Volume Compensated Reconstruction of Three-dimensional Mass Shapes in Mammographic Images

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Accurately reconstructing the three-dimensional mass shapes in mammographic images is important for classifying the abnormality into malignant or benign. In this paper, a partial volume compensated reconstruction technique for mass shapes is presented. The two-dimensional shapes of the masses are first automatically segmented using a region growing approach. The 3D mass shapes are then iteratively refined according to an algebraic reconstruction technique. Partial volume estimation is applied on the boundary to get a smoother 3D shape. Evaluation results show that the proposed algorithm improves the accuracy of the mass reconstruction.

KEY WORDS: 3D reconstruction, mass shape, mammography, partial volume effect, region growing

INTRODUCTION

Breast cancer is the most common form of cancer and a leading cause of death for women in the West, where about one in ten women will develop it during her life. It is obvious that the chance for cure is highest if the breast cancer is identified at an early stage before the tumor has spread. That's why most Western countries have adopted nationwide breast screening for postmenopausal women. X-ray mammography is currently the most effective imaging modality used in breast screening systems.

Often, two mammogram views are taken of each breast in a screening session. The two mammographic views are craniocaudal (CC), in which the X-ray projects from head to toe, and mediolateral Oblique (MLO), in which the X-ray direction is from one shoulder to the opposite hip. After the mammograms are taken, the radiologist attempts to detect the abnormalities in the mammographic views. If there is any suspicion of

malignancy, a biopsy is carried out to confirm the diagnosis.

Breast abnormalities in X-ray mammograms include microcalcifications, masses, architectural distortion, and asymmetry. These abnormalities may be associated with either benign or malignant conditions, depending on their shapes and structures. Microcalcification clusters have more chance of being malignant and are deemed as one of the most important mammographic signs of early breast cancer. A mass is another indication of a tumor. There are three categories of mammographic appearance of a mass: circumscribed, irregular-shaped, and spiculated. A circumscribed mass usually has a round, oval, or lobular shape. A well-defined mass may represent a fibroadenoma or a cyst. Most circumscribed masses are benign, although there are rare instances in which a well-defined mass is malignant. An irregular-shaped mass represents one with a poorly defined margin, which indicates possible infiltration of cancer into surrounding tissue. Irregular-shaped masses are considered suspicious. A spiculated mass is characterized by an irregular central mass surrounded with radiating spicules. Spiculated masses have a very high risk of being malignant.

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Online publication 16 February 2007

doi: 10.1007/s10278-007-9005-z

In computer-aided diagnosis (CAD), a manually or automatically detected mass has to be segmented before it can be classified as benign or malignant. After segmentation, the classification step is applied based on mass features, including shape, compactness, texture, etc. Shao and Brady¹ proposed an iterative method for reconstructing the 3D masses. However, the 2D mass shapes are segmented manually and the reconstructed 3D mass shapes are rather coarse in their algorithm. In the following sections, we will present an approach based on automated mass segmentation and partial volume compensated mass shape reconstruction from the two mammographic views. It is believed that an accurate 3D reconstruction contains more information for classification of masses into benign or malignant, or at least is valuable to the clinician by visualization.

The remaining of this paper is organized as follows. “Automated Mass Segmentation” section introduces the segmentation of the 2D mass shapes in the two mammographic views based on a region growing approach. “Mass Shape Reconstruction” section describes the 3D-reconstruction technique. Evaluation results are reported in the “Experimental Results” section. Finally, “Conclusion” section concludes this paper.

AUTOMATED MASS SEGMENTATION

The mass segmentation step is crucial because the 3D mass reconstruction is highly dependent on the accuracy of the segmented mass shapes. Mammograms have very low contrast, which makes it impossible to use a pure thresholding method to segment the mass regions in the CC and MLO views. We use a seeded region growing technique instead for segmentation of the mass regions. Region growing begins by locating a set of “seeds” and attempts to merge neighboring pixels into this growing region until no more pixels can be added to it.² This method first defines a homogeneity criterion. If the neighboring pixels satisfy the homogeneity criterion, they are merged into the target object region.

Adams and Bischof³ proposed a seeded region growing algorithm, which takes an intensity image and a set of seeds as input. This algorithm is efficient, robust, and parameter-free. Unfortunately, this method is dependent on the order of

the pixels being processed, which means the region growing result is different if the pixels are processed in different orders. Muller et al.⁴ proposed an automated 3D region-growing algorithm, which is based on an assessment function. The principle of this algorithm is to build a region-growing sequence by increasing the maximal homogeneity threshold from a very small value to a large one. On each segmented region, a 3D parameter that has been validated on a test image assesses the segmentation quality. This set of values called assessment function is used to determine the optimal homogeneity criterion. The main advantages of this algorithm are its capability of eliminating isolated points due to the noise and preserving connectivity of the target object structure. Revol and Jourlin² developed a region-growing technique, which reconsiders the assignment of pixels at each step by a process minimizing variance through special dilations. Therefore, the region created by an initial seed can be non-connected and possibly does not contain this seed. The homogeneity criterion of this method is based on an adequate tuning between spatial neighborhood and histogram neighborhood.

The drawback of the above methods is that they are rather time-consuming computationally and not effective for our mass segmentation problem. We propose a simple but efficient seeded region growing approach here. The seed is estimated from the manually segmented mass regions as used in the work of Shao and Brady.¹ Assume that R is the manually segmented mass region, the seed is computed as:

$$x_s = \frac{1}{k} \sum_{x_i \in R} x_i \quad y_s = \frac{1}{k} \sum_{y_i \in R} y_i \quad (1)$$

where (x_i, y_i) represents the location of a pixel belonging to R and k is the number of pixels in R . A dilation operation of neighborhood N is applied to the seed (x_s, y_s) . N is obtained as follows:

$$N = \min(x_{\max} - x_s, x_s - x_{\min}, y_{\max} - y_s, y_s - y_{\min}) \quad (2)$$

where $x_{\max}$, $x_{\min}$ are the maximal and minimal values of x_i , and $y_{\max}$, $y_{\min}$ are the maximal and minimal values of y_i , respectively. The foreground

measure I_F is estimated from the intensity values within the dilated seed region S_D as follows:

$$I_F = \frac{1}{m} \sum_{(x_i, y_i) \in S_D} I(x_i, y_i) \quad (3)$$

where m is the number of pixels belonging to the dilated seed region S_D .

The background measure I_B is estimated from the dilation of the manually segmented mass region R . A dilation operation of neighborhood L is applied to R , which results in a region R_D . Typically, we set L to be 5 in our experiments. The background measure is computed as follows:

$$I_B = \frac{1}{n} \sum_{(x_i, y_i) \in R_D - R} I(x_i, y_i) \quad (4)$$

where $I(x_i, y_i)$ is the intensity value of the region $R_D - R$, n is the number of pixels in the region $R_D - R$.

The local signal dependent threshold can be defined as:

$$T = I_B + \alpha(I_F - I_B) = \alpha I_F + (1 - \alpha)I_B \quad (5)$$

where α is a constant with values between zero and one. We set α as 0.5, i.e., $T = 0.5(I_F + I_B)$, in our experiments.

Now, we have obtained the global limit of region growing. We also need the homogeneity condition for region growing. For each seed point S_i belonging to S_D and its neighboring pixels, the standard deviation of gray levels σ_{S_i} is calculated. Let σ_{mean} be the mean value of σ_{S_i} :

$$\sigma_{mean} = \frac{1}{N_S} \sum_{S_i \in S_D} \sigma_{S_i} \quad (6)$$

where N_S is the number of pixels within the region of S_D .

The region growing process is applied recursively. At each step, a homogeneity region $R_n (R_0 = S_D)$ is dilated by a neighborhood 1, yielding a region D_{n+1} . For each pixel $(x_i, y_i) \in D_{n+1} - R_n$, if the standard deviation (σ_i) of gray levels of (x_i, y_i) and its neighbors is less than $\beta \sigma_{mean}$, and the gray levels of I_i exceeds T , it is marked as belonging to R_{n+1} . That is, if $\sigma_i < \beta \sigma_{mean}$ and $I(x_i, y_i) > T$, $(x_i, y_i) \in R_{n+1}$; otherwise, $(x_i, y_i) \notin R_{n+1}$. The region growing procedure is iterated until the region R_n can no longer be increased. We set β as 1.2 in our experiments.

To eliminate the possible holes in the segmented regions, a linkage process is applied. Any pixel with at least six of its eight neighboring pixels belonging to the segmented region is included to be part of the segmented region.

MASS SHAPE RECONSTRUCTION

The initial 3D mass shape, which is represented by a binary volume image, is reconstructed based on an algebraic reconstruction technique^{5,6}, similar to that of Shao and Brady.¹

Let $v(i, j, k)$ be the 3-D reconstructed object image, $i = 1, \dots, n, j = 1, \dots, n, k = 1, \dots, n$, which is a discrete three-dimensional image that represents a binary object. In this study, we assume that the mass lesion to be reconstructed is incompressible and that the attenuation coefficient within a mass is constant. For this reason, we represent the reconstructed object as a binary three-dimensional image.

Let $P_{CC}(r, c)$, $P_{MLO}(r, c)/P_{LM}(r, c)$ represent the mass regions in the CC and MLO/LM views and the background, $r = 1, \dots, n, c = 1, \dots, n$. $P_{CC}(r, c)$, $P_{MLO}(r, c)/P_{LM}(r, c)$ is equal to h_m (h_m is the background compensated intensity of a mass region), if (r, c) belongs to the mass region; and is equal to 0, if (r, c) belongs to the background.

Then, we convert $v(i, j, k)$ into $v_j, j = 1, 2, \dots, n^3$. We also convert $P_{CC}(r, c)$ into $P1_i, i = 1, \dots, n^2$, $P_{MLO}(r, c)$ into $P2_i, i = 1, \dots, n^2$, respectively. We can write the linear equations as follows:

$$w_{11}v_1 + w_{12}v_2 + w_{13}v_3 + \dots + w_{1N}v_N = P1_1$$

$$w_{21}v_1 + w_{22}v_2 + w_{23}v_3 + \dots + w_{2N}v_N = P1_2$$

$$w_{n^2 1}v_1 + w_{n^2 2}v_2 + w_{n^2 3}v_3 + \dots + w_{n^2 N}v_N = P1_{n^2}$$

$$w_{(n^2+1)1}v_1 + w_{(n^2+1)2}v_2 + w_{(n^2+1)3}v_3 + \dots + w_{(n^2+1)N}v_N = P2_1$$

$$w_{(2n^2)1}v_1 + w_{(2n^2)2}v_2 + w_{(2n^2)3}v_3 + \dots + w_{(2n^2)N}v_N = P2_{n^2}$$

w_{ij} represents the influence of a voxel v_j on a ray r_i passing through pixel p_i and it is determined by the length of ray r_i in voxel v_j .

Fig 1. (a) CC and MLO views; (b) results of automated mass segmentation; (c) results of reconstruction viewed at two different angles.

We start by guessing the initial value of the voxel vector, $\mathbf{V} = \mathbf{V}^{(0)}$. Currently, we do that using the shape from silhouette method. At each iteration, we use a correction procedure to update the volume vector $\mathbf{V}$. At iteration step k , the value of $p_i^{(k)}$ is measured as projected from the present state of the volume vector $\mathbf{V}^{(k)}$. The difference between p_i and $p_i^{(k)}$ is then back-projected to the 3-D volume object which generates $\mathbf{V}^{(k+1)}$ to make sure that if $p_i^{(k+1)}$ were computed from $\mathbf{V}^{(k+1)}$, it would be closer to p_i than $p_i^{(k)}$. The correction procedure is only applied to the boundary voxels because our initially reconstructed object is a binary volume image and solid. Let $b(V)$, $b(\bar{V})$ be

the boundary voxels. When $v_j = 1$, and its neighboring voxels have both 0s and 1s, $v_j \in b(V)$. On the other hand, when $v_j = 0$, and its neighboring voxels have both 0s and 1s, $v_j \in b(\bar{V})$. The correction procedure can be expressed as follows:

- If $v_j \in b(V)$, and $\frac{\sum_{i=1}^{v_j^2} (p_i - \sum_{n=1}^N w_n v_n) (w_j > 0.71 \cdot 0)}{\sum_{i=1}^{v_j^2} w_j} < -\text{Threshold}$, change v_j from 1 to 0;

Table 1. Average Mean Deviation Rates of Reconstructions of 28 Pairs of CC and MLO Views

Algorithm	Reference [1]	Proposed
Mean deviation rate	9.47%	5.82%

- If $v_j \in b(\bar{V})$, and $\frac{\sum_{i=1}^{2d^2} (P_i - \sum_{j=1}^N w_{ij} v_{ij}) (w_{ij} > 0.71.0)}{\sum_{i=1}^{2d^2} w_{ij}} > \text{Threshold}$, change v_j from 0 to 1.

We set *Threshold* as 0.5 in the current reconstruction procedure. The above procedure is applied recursively, until the reconstruction converges to a particular shape.

The above reconstructed binary 3D mass shape is rather coarse and is affected by the partial volume effect (PVE). PVE arises if more than one tissue type occupies a single voxel element. The intensity value of the partial volume pixel (or voxel) is a combination of the intensity values of each tissue type present. The accuracy of assigning these partial volume pixels (or voxels) to one single tissue type is inherently limited, especially when the image resolution is low.

To obtain a more accurate 3D mass shape, partial volume estimation is applied on the initial binary boundary as follows:

- If $v_j \in b(V)$, and $\frac{\sum_{i=1}^{2d^2} (P_i - \sum_{j=1}^N w_{ij} v_{ij}) (w_{ij} > 0.71.0)}{\sum_{i=1}^{2d^2} w_{ij}} < 0$,

$$v_j = 1 + \frac{\sum_{i=1}^{2d^2} (P_i - \sum_{j=1}^N w_{ij} v_{ij}) (w_{ij} > 0.71.0)}{\sum_{i=1}^{2d^2} w_{ij}};$$
- If $v_j \in b(\bar{V})$, and $\frac{\sum_{i=1}^{2d^2} (P_i - \sum_{j=1}^N w_{ij} v_{ij}) (w_{ij} > 0.71.0)}{\sum_{i=1}^{2d^2} w_{ij}} > 0$,

$$v_j = \frac{\sum_{i=1}^{2d^2} (P_i - \sum_{j=1}^N w_{ij} v_{ij}) (w_{ij} > 0.71.0)}{\sum_{i=1}^{2d^2} w_{ij}}.$$

The initial three-dimensional binary boundary is replaced by partial volume voxels accordingly. The above procedure is applied recursively until the difference between the current reconstruction and the previous one is smaller than a threshold. Therefore, we have obtained a three-dimensional reconstruction with the inner voxels as 1 and the boundary voxels having the values between 0 and 1.

EXPERIMENTAL RESULTS

We apply our reconstruction algorithm on real mammographic images. Figure 1 shows the results of mass segmentation and reconstruction of a pair of CC and MLO views.

To evaluate the accuracy of the reconstructed algorithm, we project the reconstructed objects to two planes, which are parallel to the CC and MLO views. The mean deviation rate of the projections of the reconstructed masses from the original 2D mass regions is used as the error measure of the

algorithm. The mean deviation rates of our proposed algorithm in comparison to the method in¹ are shown in Table 1. The results are the average of reconstructions of 28 pairs of CC and MLO views. We can see that the proposed algorithm significantly reduces the reconstruction error.

CONCLUSION

In this paper, we developed a reconstruction algorithm for mass regions in mammograms. The 2D mass shapes are first segmented using an efficient region growing technique in CC and MLO views. The 3D mass shapes are then iteratively refined by an algebraic reconstruction technique. Partial volume estimation is applied on the boundary voxels to get a more accurate 3D representation of the mass. More accurately reconstructed mass shapes are useful for breast cancer diagnosis and treatment purposes. Radiologists can use the reconstructed three-dimensional mass coupled with the two-dimensional masses in the CC and MLO views to classify the lesion into malignant or benign. The reconstructed mass shapes can be also used as a visualization tool for medical education.

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