A New Fast Fractal Modeling Approach for the Detection of Microcalcifications in Mammograms

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In this paper, a novel fast method for modeling mammograms by deterministic fractal coding approach to detect the presence of microcalcifications, which are early signs of breast cancer, is presented. The modeled mammogram obtained using fractal encoding method is visually similar to the original image containing microcalcifications, and therefore, when it is taken out from the original mammogram, the presence of microcalcifications can be enhanced. The limitation of fractal image modeling is the tremendous time required for encoding. In the present work, instead of searching for a matching domain in the entire domain pool of the image, three methods based on mean and variance, dynamic range of the image blocks, and mass center features are used. This reduced the encoding time by a factor of 3, 89, and 13, respectively, in the three methods with respect to the conventional fractal image coding method with quad tree partitioning. The mammograms obtained from The Mammographic Image Analysis Society database (ground truth available) gave a total detection score of 87.6%, 87.6%, 90.5%, and 87.6%, for the conventional and the proposed three methods, respectively.

KEY WORDS: Breast cancer, mammograms, deterministic fractals, fractal image modeling, microcalcifications

INTRODUCTION

In the USA, one in eight women is affected by breast cancer, which kills more women than any cancer except lung cancer.[1] According to a study by the International Agency for Research on Cancer, there will be approximately 250,000 new cases of breast cancer in India by 2015. At present, India reports around 100,000 new cases of breast cancer annually.[2] Early detection of cancer helps in reducing the mortality rate by 30%. X-ray mammography is considered to be an effective and reliable method to detect breast cancer even before the tumors can be detected clinically by palpation. The presence of microcalcifications, which usually appear as bright spots in the breast tissue in X-ray mammograms, is an early indication of breast cancer. But all microcalcifications need not be malignant. These microcalcifications are very difficult to detect because of their small size (typically in the range of 0.05–1 mm). Moreover, they are embedded in the non-homogenous mammographic background consisting of overlapping projections of anatomical structures, thus making them difficult to detect even for an experienced radiologist. Several computer-aided techniques have been developed for processing the mammogram image and to detect the possible presence of microcalcifications. These methods can help the radiologists to have a "second opinion" when a large number of mammograms are to be analyzed.

Mini and Thomas[3] used a wavelet-based method to eliminate the structures in mammograms produced by normal glandular tissue of varying density, based on local average subtraction, and used probabilistic neural network for classification. Contrast enhancement by histogram transformation, attenuation coefficients, and by film characteristics curves were developed to detect microcalcification clusters in dense breast images.[4] Kim and Park[5] presented

a comparative study of conventional texture analysis methods and their proposed surrounding region dependence method along with a three-layer back-propagation neural network for detecting and classifying clustered microcalcifications. A two-stage relevance vector machine based on Bayesian estimation theory was proposed in[6] to locate the presence of microcalcifications in mammograms. Strickland and Hahn[7] developed a method to detect the presence of microcalcifications in mammograms using wavelet transform. The mammogram which is pre-processed with sub-band decomposition filter bank is divided into overlapping square regions in which higher order statistics like skewness and kurtosis are estimated for detecting the regions with microcalcifications in.[8] It is noted that most of the enhancement techniques used in the past research works not only enhanced microcalcifications but also enhanced background structure and noise. Microcalcifications are visible as small bright spots which appear to be added to the mammographic background. These microcalcifications have less structure when compared to the breast background structure. On the other hand, the mammographic parenchymal and ductal patterns in mammograms possess structures with high local self-similarity which is the basic property of fractals. These tissue patterns can be constructed by fractal models and can be taken out from the original image, and the microcalcification information can be enhanced. Li et al.[9] presented a fractal model of breast background tissues to enhance the presence of microcalcification.

In this paper, the conventional fractal coding technique presented in[9] is modified to reduce the encoding time required in the fractal modeling of the mammogram.

MATERIALS AND METHODS

Deterministic fractals have extremely high visual complexity with very low information content. They have high degree of redundancy such that they can be recursively made of transformed copies of either themselves or parts of themselves. Fractal image coding was first proposed by Barnsley.[10] Since then, fractals have been used in a lot of image processing applications, compression, segmentation, analysis, restoration, etc.[11–17] Jacquin[18] proposed a novel method for image compression by fractal block coding of images.

In this paper, fractal block coding of the mammograms have been done using the method proposed by Jacquin. In fractal image coding, a contractive transformation is found such that after a number of iterations, the reconstructed image will be visually similar to the original image. These contractive transformations are determined by finding the most similar domain block for a corresponding range block. The presence of microcalcifications can be enhanced by taking out original mammograms from this modeled image. But this process takes a long time as the entire image has to be searched for the matching domain. Here, the image blocks are classified based on their mean and variance, dynamic range, and using mass center features. Only those domains whose parameters are similar to that of the range are included in the domain search pool. This tremendously reduces the encoding time.

Conventional Fractal Image Modeling

The conventional fractal coding of images for the enhancement of microcalcifications is presented by Li et al. in.[9] Let μ be the original image which is to be modeled. The image μ is divided into non overlapping range blocks R_i and overlapping domain blocks D_i, which are twice the size of range blocks. The objective is to find a region D_i in the mammogram which have similar structures as that of R_i. While searching for a matching domain, the condition $R_i \cap D_i = \varphi$ is imposed to avoid area of the range from the suitable domain region. Thus, when the difference between the original and the modeled mammogram is taken, the presence of microcalcifications is enhanced.

Each of the blocks in the domain pool is scaled to the size of range block to encode a range. It is then compared with R using intensity offset and contrast parameters as well as isometry transformations. The transformation w_i for the range blocks is defined by:

$$w_i(R) = s_i \times \overline{D} + o_i \qquad (1)$$

where s_i the contrast scaling factor and o_i the luminance shifting or offset factor are given by the following equations:

$$s_i = \frac{N\sum_k \sum_l R(k,l)\overline{D}(k,l) - \left(\sum_k \sum_l R(k,l)\right)\left(\sum_k \sum_l \overline{D}(k,l)\right)}{N\sum_k \sum_l R^2(k,l) - \left(\sum_k \sum_l R(k,l)\right)^2} \tag{2}$$

and

$$o_i = \frac{\sum_k \sum_l \overline{D}(k,l) - s_i\sum_k \sum_l R(k,l)}{N} \tag{3}$$

where $\overline{D}$ is the contracted domain block under one of the following isometry transformations: (1) identity, (2) rotation through $+90°$, (3) rotation through $+180°$, (4) rotation through $-90°$, (5) reflection about mid-vertical axis, (6) reflection about mid-horizontal axis, (7) reflection about first diagonal, and (8) reflection about second diagonal. N is the total number of pixels in the range block. The domain block which minimizes the distortion, $d(\mu|_{R_i}, w_i(\mu|_{R_i}))$, where $\mu|_{R_i}$ denotes the restriction on the set R_i, is chosen. The distortion measure is written as:

$$e_i = \sum_k \sum_l \left(R(k,l) - \left(s_i\overline{D}(k,l) + o_i\right)\right)^2 \tag{4}$$

The fractal code for R_i are s_i, o_i, and the location of D_i. The process is repeated for all the range blocks. The fractal code used to represent the entire image is the union of the parameters of all range blocks.

$$w = \bigcup_{i=1}^{n} w_i \tag{5}$$

If no matching domain is found for a particular range block, then that range is subdivided into four equal parts and is called quad tree partitioning. The domain search is performed for each of the four range blocks. Even if there is no matching domain, each of the four range blocks have been further subdivided into four smaller blocks and matching domain is searched for each of the blocks. If there is no matching domain after two divisions, a domain with minimum error in Eq. 4 is selected. Ranges of size 32×32, 16×16, and 8×8 were used while validating the algorithm.

If a range contains microcalcifications, there is a chance that its most similar domain will not have presence of microcalcifications since the area containing the range is not included in the domain search space. Therefore, when the modeled mammogram is taken out from the original mammogram, the presence of microcalcifications will be enhanced. In the conventional fractal encoding method, while searching for the matching domain, if a domain is not similar to the range, the next domain to be searched is chosen after a gap of R pixels or $R/2$ pixels, where $R\times R$ is the size of the range. It is found in[19] that the microcalcification detection rate will be only 46% if the domain search is carried out as in the conventional fractal encoding method. Therefore, in this paper, the conventional method is modified by choosing the domain from the adjacent pixel onwards. Furthermore, the modified fractal encoding method will be taken as the conventional fractal coding method in this paper. This search for a matching domain is a time-consuming process. In our paper, we propose three methods to reduce image encoding time. In all these methods, domain search is started from the adjacent pixel. This will help in detecting microcalcifications, which are too small in size.

Fractal Modeling with Mean and Variance

Variance can be used to classify the simplicity or complexity of the block. The variance of a block B is defined as:

$$\mathrm{Var}(B) = \sqrt{\frac{1}{N}\left(\sum_k \sum_l \mu^2(k,l)\right) - \left(\frac{1}{N}\sum_k \sum_l \mu(k,l)\right)^2} \tag{6}$$

The domain block is divided into four sub-blocks, top left, top right, bottom left, and bottom right, and then the mean value for each sub block is calculated as m_1, m_2, m_3, and m_4, respectively. The isometry transformation algorithm sets four classes as:

Class1: If $m_1 = m_2 = m_3 = m_4$, it makes only first isometry transformation listed in "Conventional Fractal Image Modeling."

Class2: If $m_1 = m_4$ and $m_2 = m_3$, it makes the first two transformations.

Class3: (i) If $m_1=m_2=m_3$ or $m_1=m_2=m_4$ or $m_2=m_3=m_4$ or $m_1=m_3=m_4$, or
(ii) If $m_1=m_2$ and $m_3=m_4$, or
(iii) If $m_1=m_3$ and $m_2=m_4$, or
(iv) If $m_1=m_4$ and $m_2 \neq m_3$, or
(v) If $m_2=m_3$ and $m_1 \neq m_4$, it makes the first three isometry transformation

Class4: If it does not belong to class1, class2 or class3, it must make four isometry transformations.

The variance of the range and domain blocks is computed using Eq. 6. For each range block, search only those domain blocks that satisfies $|\mathrm{Var}(R) - \mathrm{Var}(D)| \leq$ threshold, which is varied from 0.01 to 1. Then those selected domains are classified by the individual mean value and included in the domain search pool. The proposed method searches only the domain blocks whose mean value classes are the same or adjacent to the class of range block to reduce the searching time. The domain block with minimum mean square error is selected from the above reduced domain pool.

Fractal Modeling by Classification into Shade and Non-shade Blocks

In this method, the range blocks are classified into shade and non-shade blocks based on their variations in the texture. Shade blocks are those blocks that have no large gradient values or texture and the grayscale of pixels change slowly with respect to the perception of the human eye, while the non-shade block has sudden changes in pixel intensities like texture or distinct edges.

Jacquin[18] had classified the image into shade, midrange, and edge blocks. In this paper, midrange blocks are not used, as mammograms are images with low-intensity variations and the classification of the blocks into three different classes is not necessary for the detection of microcalcifications. If the range block is a shade block, no searching is required and only the mean of the pixels is required for decoding. Also, if the domain is a shade block, it is not included in the domain search pool. If the dynamic range of the block is ≤ 0.05, it is classified into shade block. Non-shade blocks are encoded using the fractal coding method

discussed in "Conventional Fractal Image Modeling." The offset factor is given by:

$$o_i = \mathrm{mean}\,(R_i) - \mathrm{mean}\,(\overline{D_i}) \qquad (7)$$

while the scaling factor s_i is given by:

$$s_i = \min\left(\frac{\mathrm{dr}(\mathrm{range})}{\mathrm{dr}(\mathrm{domain})}, s_{\max}\right), \ [0, \ 1] \qquad (8)$$

where dr, the dynamic range of the respective blocks, is defined as dynamic range=max pixel value/min pixel value.

Fractal Coding Based on Mass Center Features

Polvere et al.[20] presented a feature vector coding scheme based on mass center of the block. The best matching domain for a range block is the one that has a shape similar to that of the range up to the isometric transformation. The shape of a block is determined by the distribution of pixel mass, i.e., sum of the gray levels within the block, so that similar distributions correspond to similar shapes.[20] Thus, the blocks which are not similar can be discriminated by features which characterize the mass distribution of the block. Such a feature is the position of the mass center (MC) in the block, since similar mass distributions have the MC close to each other. Therefore, if two blocks are not similar, their MCs are distant from each other. For a block B of size $N \times N$, the coordinates of the MC expressed with respect to the center of the block are given by:

$$x = \frac{1}{M} \sum_{i=1}^{N} \sum_{j=1}^{N} iB(i,j) - \frac{N}{2} \qquad (9)$$

$$y = \frac{1}{M} \sum_{i=1}^{N} \sum_{j=1}^{N} jB(i,j) - \frac{N}{2} \qquad (10)$$

$$\theta = \tan\left(\frac{y}{x}\right) \qquad (11)$$

where M is the mass of the block. To further characterize the mass distribution of a block B, it is transformed into a new block B_2 according to the following equation:

$$B_2(i,j) = (B(i,j) - \eta)^2 \qquad (12)$$

where η is the average mass of the block B_2. As above, a new feature is developed for the second block. Thus, the feature vector of a block is defined as (θ_1, θ_2), where θ_2 is the phase angle of the new block B_2. During fractal modeling, the feature vector $V_r = (\theta_1, \theta_2)$ of the range is calculated. Only those domain blocks whose feature vectors $V_d = (\phi_1, \phi_2)$, are adjacent to V_r in the feature space are included in the search space. For a fixed threshold $\varepsilon \leq 0.05$, the domains which satisfy the following inequality only are considered:

$$d(V_r, V_d) \leq \varepsilon, \tag{13}$$

where d is a distance function in the feature space between the two vectors. The suitable distance function is:

$$
\begin{aligned}
&d((\theta_1, \theta_2), (\phi_1, \phi_2)) \\
&= \max\{m(\theta_1, \phi_1), m(\theta_2, \phi_2)\}, \text{ where } m(a, b) \\
&= \min\{|a - b|, 2\pi - |a - b|\}.
\end{aligned}
\tag{14}
$$

Database Used

The proposed methods were validated using the mammograms obtained from the freely available database provided by The Mammographic Image Analysis Society (MIAS) digital mammogram database.[21] The images in the database are digitized at a resolution of 50 μm per pixel, with $1,024 \times 1,024$ pixel size and at 256 gray levels. The accompanied "ground truth" contains details regarding the character of the background tissue, class, and severity of the abnormality and x, y coordinate of its center and radii. The size of microcalcification generally varies from 50 to 1,000 μm. The smallest microcalcification is equivalent to 1 pixel of the image. The subtlety rating of these mammograms are found to be 1, 2, and 3 as per[22], which indicates that the lesions are detectable only by an expert mammographer, likely to be detected by an expert, and likely to be detected by observer with good mammographic training, respectively.

Enhancing the Presence of Microcalcifications

While decoding, the modeled image is obtained by applying w_i to the domain locations of any starting arbitrary initial image of the same size as the original mammogram iteratively. Convergence is obtained after 10–12 iterations. The difference between the original image and the modeled image is found out to enhance the presence of microcalcifications. The difference image is converted to binary to identify the presence of microcalcification so that it will appear as white spots in black background. The threshold, T, for binary conversion is obtained from the image itself in a two-level thresholding process.[9]

1. Initial threshold T_0 is taken as 3.5 times the standard deviation of the image.
2. Standard deviation is found once again from those pixels of the difference image whose gray level values are below T_0. The new threshold, T_1, is arbitrarily selected as 3.5 times this standard deviation.

The final threshold T is determined in such a way that no subtle cases are missed using human judgment. In our study, 0.7 times the standard deviation of the original image was a suitable choice for T. The image is made binary by equating the pixels whose gray level is less than T to 0 and others to 255. The locations of the microcalcifications alone can be identified from the difference image.

RESULTS AND DISCUSSIONS

The available 28 mammograms containing microcalcifications and 110 normal ones obtained from the MIAS database[21] were used in the study. The different regions of interest (ROIs) from the mammogram used in the study were 64×64, 128×128, and 256×256. The sizes of the range varied from 32×32, 16×16, 8×8, and 4×4 to 2×2. Only the first four of the isometry transformations, discussed in "Conventional Fractal Image Modeling," of the averaged domain were chosen in all the methods, as these was sufficient enough to detect the presence of microcalcifications. The size of 1 pixel in the database is 50 μm. Hence, while searching, if the domain is not chosen leaving a

gap of 1 pixel, microcalcifications which are very small will be missed during detection.

We observed that to find the most similar domain block for a particular range block, the average number of domains searched, for an ROI of 64×64, in the conventional method is 1,767, with an average time for each domain search of 1.5 s. In the mean and variance method, only one third of the total range blocks have the variance less than the chosen threshold, and only these blocks need to be coded by fractal encoding method. In shade and non-shade classification, about 99% of the blocks are shade blocks when the range size is 2×2. This tremendously reduces the encoding time. In the mass center feature method, the number of domains searched per range block is on an average 122/range. Because of the reduction in the domain pool, the encoding times of the proposed methods are reduced by a factor of 3, 89, and 13 respectively, when compared to the conventional method.

The algorithm was found to converge after 10–12 iterations in all the three methods. As the range size is increased, blocking artifacts were present in the modeled image. Here, the intension is not to get the perfect reconstruction of the original image but to detect microcalcifications which are very small in size. Therefore, microcalcifications can be detected up to a range size of 16×16.

Figure 1 shows the original mammogram of ROI 64×64 used for modeling. The modeled image by the conventional fractal coding method and the microcalcifications which are detected by the conventional method are given in Figure 2.
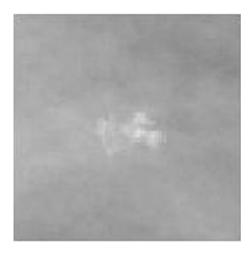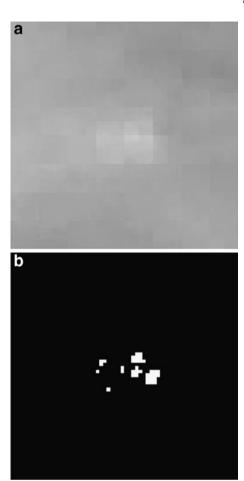

Fig 1. Original mammogram.

Fig 2. a, b Modeled mammogram and detected microcalcifications respectively by the conventional method.

Figure 3 shows the modeled image and the detected microcalcifications in the proposed three methods. From the above figures, it can be seen that even if all the domains are not included in the domain search pool while encoding, all the microcalcifications which were detected in the conventional fractal coding method are detected by the proposed three methods.

The four parameters used to indicate the detection accuracies are true positive (TP), true negative (TN), false positive (FP), and false negative (FN).[23] The first letter indicates whether the test result is correct (true) or not (false), and the second letter indicates whether the disease is present (positive) or not (negative); that is, if a normal mammogram is correctly classified as normal, it is called TN, and if incorrectly classified as abnormal, then a FP is counted. Similarly, when a mammogram with microcalcifi-
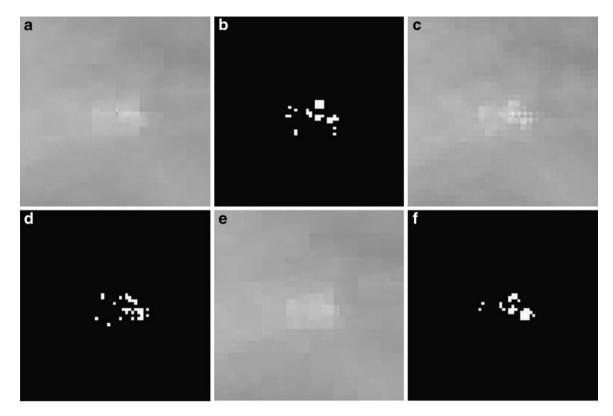
Fig 3. a, b Modeled mammogram and detected microcalcifications, respectively, using mean and variance method. c, d Modeled mammogram and detected microcalcifications, respectively, using shade and non-shade blocks. e, f Modeled mammogram and detected microcalcifications, respectively, using mass centre features.

cation is correctly classified, then it is a TP; otherwise, if it is incorrectly classified as a normal one, it is a FN. To determine the detection accuracies of the different methods, three percentage detection scores are defined: abnormal detection score, $S_A = TP/N_A \times 100$, normal detection score, $S_N = TN/N_N \times 100\%$, and total detection score, $S_T = (TP+TN)/T_M$, where N_A and N_N are the number of mammograms with microcalcifications and without microcalcifications and T_M is the total number of mammograms (with and without microcalcifications). The total detection score (S_T) of any method is the percentage by which the mammograms are correctly classified into normal or abnormal.

Table 1 shows the detection results obtained for the conventional and proposed new methods. Microcalcification detection score, S_A, of 85.7% was obtained for shade and non-shade classification and with mass center features, while mean variance method gave an accuracy of 82.14%. The total detection score of the shade and non-shade block classification is obtained as 90.5%.

It is reported in[3] that only a recognition efficiency of 72% was obtained using wavelets and probabilistic neural networks based on statistical features with the same MIAS database used in this paper.

It is found that if the domain search is done after leaving a gap of two pixels, microcalcifications which are smaller than two pixels, i.e., 100 μm will be missed. To detect the microcalcifications which are 50 μm or 1 pixel, the domain search is done from the adjacent pixel onwards. Thus, the conventional method took an average of 26.241 min for modeling. In mean variance and mass center feature methods, this encoding time is reduced to 7.898 and 1.5848 min, respectively. In shade and non-shade block classification, shade blocks are not coded by fractal method; only the mean of the block is required for decoding as explained in "Fractal Modeling by Classification into Shade and Non-shade Blocks". Only the remaining blocks need to be coded by fractal method. Therefore, the number of blocks searched for these remaining range blocks is the same as the conventional method, but the number of
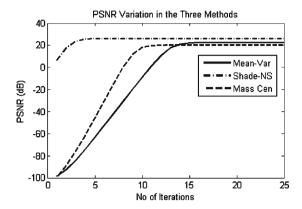
Fig 4. Variation of PSNR between the original image and modeled image in the proposed three methods.

such range blocks is limited to 14 when range size is 8×8 and ROI is 64×64. therefore, shade and non-shade blocks take only an average of 0.2937 min for the whole mammogram modeling.

The signal to noise ratio (SNR), correlation, and the mean square error (MSE) between the original image and the modeled image was found to be in the same range as in the conventional fractal coding, with least MSE and highest correlation for shade and non-shade classification. The peak signal-to-noise ratio (PSNR) which is used in the analysis is given as:

$$PSNR(dB) = 20 \log_{10}$$

$$\times \left(\frac{\text{Variance of the Original Image}}{\text{Variance of the (Original − Modeled) Image}} \right) \quad (15)$$

The variation of PSNR in decibels in the three methods is shown in Figure 4.

We were able to detect microcalcifications of size 50 μm in our experiment. In the mean and variance method, when the difference in variance between the blocks is less than 0.8 and the range size is below 16×16, microcalcifications in the mammograms are detected. In the second method of classification into shade and non-shade blocks until a range size of 16×16, all microcalcifications were detected. The mass center feature difference should be between 0.001 and 1 for a range size less than 16×16 for detecting microcalcifications.

When the range size is increased, more breast parenchymal structures are included in it. Since the size of the domain is larger than the range, i.e., twice the size of the range, even the matching domain for a range may have large error value in Eq. 4 compared to a range of small size. Therefore, if the range size is increased beyond 16×16, microcalcifications which are small objects are not detected.

CONCLUSIONS

Three methods for modeling the breast background tissues in mammograms using deterministic fractals with reduced encoding time are presented in this paper. The main drawback in any fractal coding method is the enormous time encountered to search for a matching domain for all the range blocks. If all the domain blocks are

Table 1. Comparison of the Detection Sensitivities of the Conventional Fractal Coding Method with the Proposed Three Methods for ROI of 64×64 and Range Size 8×8

Method	Detection score			Encoding time (range/avg) (min)	No. of domains searched/range (range/avg)	No. of ranges encoded by fractal method (range/avg)	Avg. PSNR (dB)	Avg. MSE	Avg. correlation
	Abnormal S_A	Normal S_N	Total S_T						
Conventional	82.14	89.09	87.6	24.22−28.57 26.241	1,453−2,228 1,767	64−89 72	25.94	5.211	0.9684
Mean and variance	82.14	89.09	87.6	3.69−11.74 7.898	1,462−2,118 1,706	64−89 71	25.71	5.264	0.9642
Shade and non-shade	85.7	91.81	90.5	0.11−0.63 0.2937	1,435−1,754 1,745	1−38 14	24.31	3.593	0.982
Mass center	85.7	88.18	87.6	0.8−1.83 1.5848	113−226 124	64−89 66	24.68	5.446	0.949

Twenty-eight mammograms with microcalcifications; 110 normal mammograms

not included in the domain pool search, it reduces the encoding time. Here, the domain pool is reduced based on mean and variance, dynamic range, and mass center features of the block. The breast background regions are effectively modeled by fractal method. A normal mammogram detection score of 89.09%, 89.09%, 91.81%, and 88.18% is obtained for conventional, mean variance, shade and non-shade block, and mass center feature methods, respectively. Shade and non-shade block method gave a total detection score of 90.5%, while the other methods gave total detection scores of 87.6%. The same MIAS database gave a recognition efficiency of 72% in[3] using wavelets and probabilistic neural networks based on statistical features.

The domain search is performed in all the methods from the adjacent pixel of the current domain. This increases the searching time. But this searching scheme ensures that the microcalcifications which are small objects, 50 μm, are not missed in the detection process.

Accuracy of the study can be increased substantially if noise preprocessing is also included. When the number of screening mammograms is very high, the radiologists must interpret large number of mammograms, causing additional burden for them. The proposed study has the ability to change the breast cancer detection procedure by offering a more accurate and less time-consuming method for radiologists all over the world.

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