Mass Segmentation in Mammograms by Using Bidimensional Emperical Mode Decomposition BEMD

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Abstract— **Breast mass segmentation in mammography plays a crucial role in Computer-Aided Diagnosis (CAD) systems. In this paper a Bidimensional Emperical Mode Decomposition (BEMD) method is introduced for the mass segmentation in mammography images. This method is used to decompose images into a set of functions named Bidimensional Intrinsic Mode Functions (BIMF) and a residue. Our approach consists of three steps: 1) the regions of interest (ROIs) were identified by using iterative thresholding; 2) the contour of the regions of interest (ROI) was extracted from the first BIMF by using the (BEMD) method; 3) the region of interest was finally refined by the extracted contour. The proposed approach is tested on (MIAS) database and the obtained results demonstrate the efficacy of the proposed approach.**

I. INTRODUCTION

Breast cancer is one of the most common cancers among women. It is also one of the leading causes of cancer death. The statistics show that breast cancer affects one of every eight women in the United States and one of every ten women in Europe [1]. Women can have the highest chance of survival if physicians are able to detect the cancer at its early stages. Thus, early diagnosis plays a critical role in increasing the chance of survival. Therefore, segmentation of breast mass in the mammography computer aided diagnosis (CAD) plays an important role in the quantitative and qualitative analysis of medical images. It has a direct impact on the analysis and treatment of early breast cancer.

Generally, the procedure used by the (CAD) system for the detection of masses is divided into three steps: 1) detect the regions of interest's (ROIs), 2) segment the (ROIs) , 3) classification. The regions of interest's (ROIs) extraction is a capital step in the mammography segmentation. For that, several works have been presented, such as: multi-threshold method [2, 3], edge detection techniques [4, 5] and region based techniques (region growing [6] and region clustering [7]). For segmentation of the (ROIs), there are three common approaches [8, 9]: clustering methods, contour-based methods and region-based methods. However, the segmentation of masses in digital mammograms is not a trivial task, since the latter are: 1) different in size, shape and density; 2)

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background tissues surrounding the mass are non-uniform and have characteristics similar to the mass.

In this work, a novel segmentation approach by contour extraction was developed, based on two main phases: detection of (ROI) and region segmentation. In the literature, many methods have been developed for the automatic segmentation of masses in mammograms. X. Weidong et al [10] developed a method based on a DWT-based approach to locate the masses and active contour model to segment the masses. Y. Zhang et al [11] used texture analysis to identify suspicious masses in mammograms based on the energy descriptor (Haralick descriptors) computed from the co-occurrence matrix of the pixel. L. ke et al [12] introduced the wavelet transformation modulus maximum to identify in an automatic way the masses in mammograms and refine the detected masses through the extraction of their contour. Our approach consists of first finding regions of interests that can be suspicious masses in mammograms by using the iterative thresholding algorithm. Then the contours of the regions of interests are extracted from the first mode obtained by applying the (BEMD) Bidimensional Empirical Mode Decomposition method. Finally, the masses are refined by the contours extracted.

The setup of the paper is as follows: Section II-a describes the database we used for evaluation. Section II-b describes the (BEMD) method. In section III-a, we present the method of (ROI) extraction by using iterative thresholding. The Edge detection based on (FABEMD) is described in section III-b. In section III-c we present Edge linking process and results are given in section IV, we end with a discussion and conclusion in section V.

II. MATERIALS AND METHODS

A. Database

The Mammography Image Analysis Society (MIAS), which is an organization of UK research groups interested in the understanding of mammograms, has produced a digital mammography database. Films taken from the UK National Breast Screening Program have been digitized to 50 micron pixel. The database contains 161 patient files. Each patient file includes left and right breast images (322 images in total), which belong to three types such as Normal, benign and malignant. For each image, experienced radiologists give the type, location, scale, and coordinates as well as size of these lesions and other useful information. An example of image series is given in figure 1.
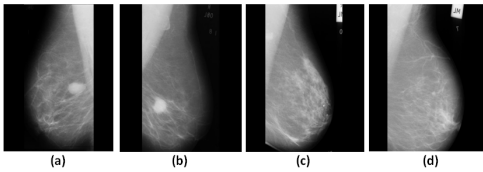
Fig. 1. series from a mammography study

B. BEMD

The (EMD) method is an adaptive decomposition which allows to break up any signal into a redundant set of signals denoted IMF and a residue [13]. These IMFs are obtained by means of an algorithm called sifting process. Given a signal s(t), the sifting process of (EMD) can be summarized as follows.

1) Initialise: $r_0 = z$ (the residual) and $j = 1$ (index number of IMF),
2) Extract the $jth - IMF$:
   a) Initialise $h_0 = r_{j-1}; i = 1$;
   b) Extract local minima/maxima of h_{i-1};
   c) Compute upper envelope and lower envelope funtions x_{i-1} and y_{i-1} by interpolating, respectively, local minima and local maxima of h_{i-1};
   d) Compute $m_{i-1} = (x_{i-1} + y_{i-1})/2$ (mean envelope),
   e) Update $h_i = h_{i-1} - m_{i-1}$ and $i = i + 1$;
   f) Calculate stopping criterion (standard deviation $SD_{ij}.Eq(1)$)
   g) Repeat steps (b) to (f) until $SD_{ij} \leq SD_{MAX}$ and put then $s_j = h_i(jthIMF)$
3) Update residual $r_j = r_{j-1} - s_j$;
4) Repeat steps $2 - 4$ with $j = j + 1$ until the number of extrema in r_j is less than

$$SD_{ij}^2 = \sum_{k=1}^{K} \left[\frac{\left|(h_{j(i-1)}(k) - h_{ji}(k))\right|^2}{h_{j(i-1)}(k)} \right] \quad (1)$$

SD_{MAX} is chosen to ensure nearly zero envelope mean of the IMF [13]. After IMFs are extracted through the sifting process, the original signal $s(t)$ can be represented like this:

$$s(t) = \sum_{j=1}^{n} IMF_j(t) + r(t) \quad (2)$$

Following Nunes and al. [14], the bidimensional (BEMD) sifting process is defined as follows:

- Identify the extrema (maxima and minima) of the image I.
- Generate the 2D envelope by connecting maxima points (respectively, minima points) with 2D interploation methods.
- Averaging the two envelopes to compute the local mean m_1.
- Since (BIMF) should have zero local mean, subtract out the mean from the image: $h_1 = I - m_1$.
- repeat until h_1 is (BIMF).

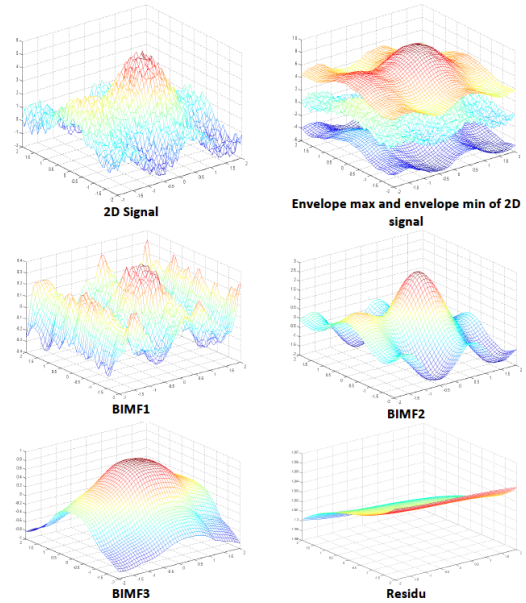In figure 2, we give an example of a 2D signal (BEMD) decomposition.

Fig. 2. BEMD Decomposition of 2D signal

In this paper we use the Fast and Adaptive Bidimensional Emperical Mode Decomposition (FABEMD) presented in [15].

III. MASS SEGMENTATION

A. ROI extraction by using iterative thresholding

The first step in segmentation of masses is the identification of regions of interest (ROIs). To achieve this, we used the iterative thresholding method [10]. We present below the principle of the iterative thresholding method :

1) t_0 is the initial threshold defined as the mean intensity in the image ;
2) $t_i = \frac{m_a + m_b}{2}$, where, m_a is the mean intensity beyond t_{i-1} and m_b is the mean intensity below t_{i-1}
3) we repeat step 2 until the threshold t_i converges [10].

In this step we will select the regions of interest on which our next treatment will be performed. As an illustration, we give below in figure 3 an example of a region of interest's extraction by using the iterative thresholding algorithm.
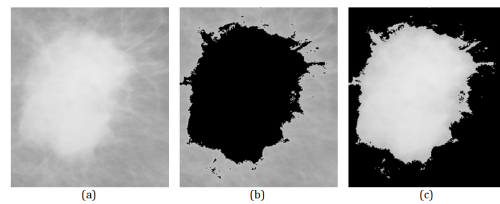

Fig. 3. (a) original image; (b) image without (ROI); (c) detected (ROI)

B. Edge detection based on (FABEMD)

The (FABEMD) is employed to decompose the image into several (BIMFs) that provide access to frequency information of the image content. The first (BIMF) represents the local variation of the image at different spatial scales, it contains the higher frequency components. Since the edges are basically discontinuities in the image intensity due to changes in the image structure, they correspond to higher local spatial frequencies [17]. Therefore, the edges are generally extracted into the first (BIMF) of an image [17]

The given image $I(x,y)$ is decomposed into the (BIMFs), $F_i(x,y)$, and the residue $R(x,y)$, where $i = 1, 2, .., k$, and k is the total number of (BIMFs). The $F_i(x,y)$ is binarized to $B_i(x,y)$ with a suitable threshold T_i, where T_i is given by :

$$T_i = max\{F_i\} \times r_i. \qquad (3)$$

In Eq. (3), $max\{F_i\}$ represents the maximum value of the elements (pixels) in the (BIMF), $F_i(x,y)$; and $0 \le r_i \le 1$, where the value of r_i is chosen as per the desired need. The binarization operation may be expressed as:

$$\begin{cases} B(x,y) = 1, & if \quad F_i(x,y) > T_i \\ B(x,y) = 0, & otherwise. \end{cases} \qquad (4)$$

where (x,y) represents the coordinate of the corresponding (BIMF) or the binary image. The non-zero pixels in the binary image are the candidate edge pixels (fig 4). Once the binary image is extracted, morphological thinning/skeletonization operation is applied to get the single segment. As we can see on the figure 4, the thinning/skeletonization operation [18] removes pixels on the boundaries of masses. It allows the isolation of the segment that should be linked to build the contour of the masses [19].
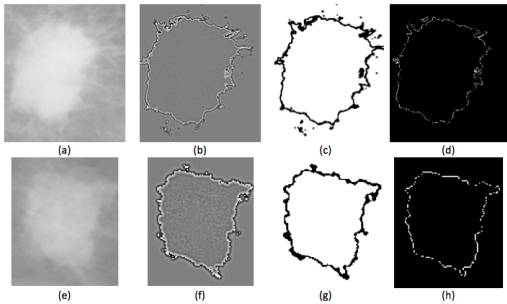

Fig. 4.   (a) and (e) original images; (b) and (f) first (BIMFs); (c) and (g) binary images; (d) and (h) skeleton images.

C. Edge linking

Edge detection is usually followed by edge linking algorithms designed to assemble edge pixels into meaningful edges. We can link adjacent edge pixels by examining each pixel-neighbor pair and verifying if they have similar properties. In this section, we describe the used edge linking algorithm.

- Analyze each pixel of edge in a 3x3 neighbourhood.

- Pixels that are similar are linked
- Principal properties used for establishing similarity:
  1) $|\nabla f(x,y)|$: Magnitude of gradient vector.
  2) $|\alpha(x,y)|$: Direction of gradient vector
- Edge pixel with coordinates (x_0, y_0) in a 3x3 neighbourhood of (x,y) is similar in magnitude to pixel at (x,y) if $|\nabla f(x,y) - \nabla f(x_0, y_0)| \le E$
  – where E is a positive magnitude threshold
- Edge pixel with coordinates (x_0, y_0) in a 3x3 neighbourhood of (x,y) has an angle similar to pixel at (x,y) if $|\alpha(x,y) - \alpha(x_0, y_0)| \le A$
  – where A is a positive angle threshold
- Edge pixel (x_0, y_0) is linked with (x,y) if both criteria are satisfied

Once the links are established, we take sets of linked pixels and use them to build the contour of the massive lesion. Finally, we segment the massive region in mammogram image by the contour extracted from the first (BIMF) (fig 5). Fig 6 shows algorithm block diagram of mass segmentation in mammography images based on (BEMD).
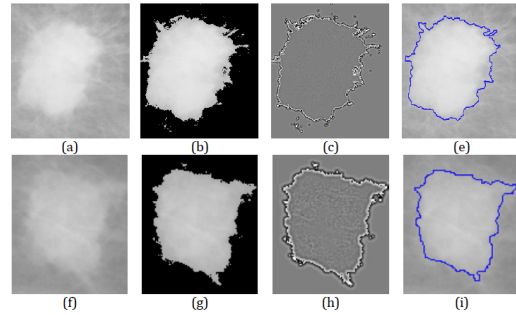

Fig. 5.   (a) and (f) original images; (b) and (g) (ROI) images; (c) and (h) firsts, (e) and (i) are the results of the masses segmentation algorithm
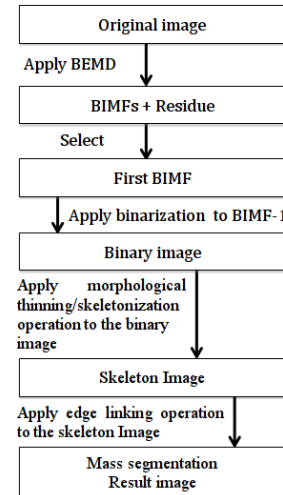

Fig. 6.   Process of mass segmentation in mammography images based on (BEMD)

IV. RESULTS AND DISCUSSION

This section presents the results of the experiments performed on the mammographic image analysis society (MIAS) database. The proposed approach has been applied to a (MIAS) database containing 111 cases of masses. For evaluating our approach we used some informations offerd by the (MIAS) database, such as:

- class of abnormality;
- image-coordinates of centre of abnormality;
- radius (in pixels) of a circle enclosing the abnormality.

The evaluation criterion is the overlapped area ratio, which is the ratio of the overlapped area between the auto-segmented region and the criterion region segmented by the radiologists manually. In the case of (MIAS) database, the criterion region is the circle formed by the coordinates of center and radius. We give below the principle of our evaluation method.

1) for each image containing a massive lesion, we apply our algorithm;
2) precision is computed, through the percentage of overlapping area between the auto-segmented region and the criterion region (fig 7).
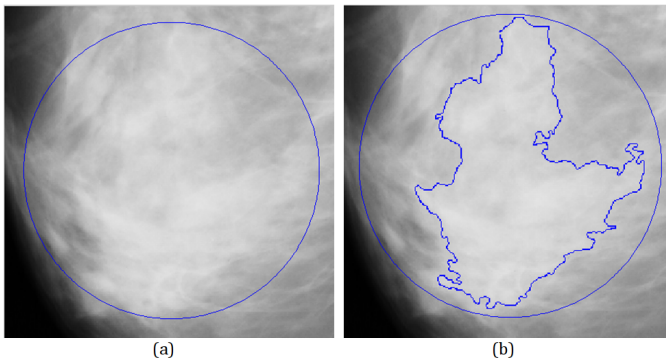3) Finally, we compute the mean precision on all cases.

(a)   (b)

Fig. 7. (a) the orginal image with the circle enclosing the abnormality; (b) segmentation result of the masses

The table below provides the precision percentage of segmentation of masses that can be found on each class of abnormality. As you can see in some cases the precision percentage is higher than 90%. As regards the mean precision of all cases, the percentage reaches 83,96%.

V. CONCLUSION

In this work we presented an approach for segmentation of masses in digital mammograms. This approach, consists of three main stages which are the (ROI) detection, edge extraction and mass segmentation. We start by Hunting the regions of interest by using the iterative thresholding algorithm, then the (BEMD) decomposition and egde linking algorithms are used to segment the masses lesions. The testing results proved that, the algorithm is efficient for segmentation of masses in mammography with a mean precision of 83,96 %. From this results, we believe that the proposed approach can play an important role in improving the quality of the computer-aided diagnosis.

TABLE I

THE PRECISION PERCENTAGES OF SEGMENTATION OF MASSES

class of abnormality	the precision percentage of segmentation of masses
CALC	90.9%
CIRC	86.3%
SPIC	89.47%
MISC	71.42%
ARCH	78.94%
ASYM	86.66%

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