Automated Breast Cancer Diagnosis based on GVF-Snake Segmentation, Wavelet Features Extraction and Neural Network Classification

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Abstract: Breast cancer accounts for the second most cancer diagnoses among women and the second most cancer deaths in the world. In fact, more than 11000 women die each year, all over the world, because this disease. The automatic breast cancer diagnosis is a very important purpose of medical informatics researches. Some researches has been oriented to make automatic the diagnosis at the step of mammographic diagnosis, some others treated the problem at the step of cytological diagnosis. In this work, we describes the current state of the ongoing the BC automated diagnosis research program. It is a software system that provides expert diagnosis of breast cancer based on three step of cytological image analysis. The first step is based on segmentation using an active contour for cell tracking and isolating of the nucleus in the studied image. Then from this nucleus, have been extracted some textural features using the wavelet transforms to characterize image using its texture, so that malign texture can be differentiated from benign on the assumption that tumoral texture is different from the texture of other kinds of tissues. Finally, the obtained features will be introduced as the input vector of a Multi-Layer Perceptron (MLP), to classify the images into malign and benign ones.

Key words: Breast Cancer, GVF-Snake, Segmentation, Wavelet feature extraction, Neural Network, MLP classification.

INTRODUCTION

Medical automatic diagnosis is still considered as a hard task. In fact, medical diagnosis requires an expert able to cope with the uncertain cases only by eyeing the visible symptoms. Such performances are difficult to achieve using an automatic system for diagnosis. Breast cancer is a vital problem needing quick handling and treatments. The cytological step of the diagnostic is the first step done to make a first approach of the case. It consists of the extraction of some cells of the lesion. Various histological tests are performed to make a first appreciation of the case but the ultimate diagnosis may be sometimes difficult to obtain, even for a medical expert.

This paper summarizes the current state of the Autonomous Diagnostic of Breast cancer Chip project, an ongoing interdisciplinary research effort begun at the University of Sciences of Monastir-Tunisia in the early 2000’s [29,30,31]. The project addresses an important problem in breast cancer treatment, that the diagnosis (determination of benign from malignant cases). This project is divided in two big parts of active research; the first is realization of solution software that permits the validation of the concept of the diagnosis of the breast cancer and the second is of built-in this process within a Hardware System “BioChips” for the detection extraction and classification typical of the cancerous cells of a breast cancer from a cytological image. The resulting software system provides accurate and interpretable results to both doctor and patient to aid in the various decision-making steps in the diagnosis and treatment of the disease.

Many studies have been oriented to do pattern breast cancer diagnosis processes such as Xcyt Project [2,4,32] is a software system that provides expert diagnosis and prognosis of breast cancer based on fine needle aspirates. The system combines techniques of digital image analysis, inductive machine learning, mathematical programming, and statistics, including novel prediction methods developed specifically to make best use of the cytological data available. The point is that the digitizing of the observed samples of lesions and their preprocessing leads to images on which the cells have different shapes and sizes, they are sometimes condensed and the edges and limits of each one can’t often be detected. There are also residual cells which hadn’t any thing to do with the lesion such as...
blood ones for example (Figure 2). This entire make the process of classification of the images into benign or malign cases very difficult because of the absence of an easy mathematical formalism that can characterize the objects in the observed images.

Considering these constraints, the adopted software solution in this work is performed in three steps: a first, an active contour cell detecting technique is used to approximately isolate nucleus in an observed image. Then a texture-analysis-based feature extraction is done to the obtained nuclei. In fact, the wavelet transforms has been widely used for description of images texture [3,7]. Numerous decompositions schemes have been proposed for the purpose of texture characterization [8], two approaches can be detected: the first is numerical description mainly based on second order or higher statistics of the wavelet coefficients. The second approach is quantification of the textures in the way human can see them as coarse, regular, directional, symmetric, etc.

In this paper, the work is organized as follows (Figure 1); the first part is given the description of segmentation results of the technique of cancerous cell detected to basis of the Active Contour Models "Snake" [6] and "GVF-Snake"[9,10]. The second part has led to nineteen textural features based discreet wavelet transform. Finally, the obtained features are used to achieve the classification of Images using their texture descriptions; in texture classification the goal is to assign an unknown sample image or an image block to one of a set of known texture classes. This last work is assured by the application of the Neural Network classification as MLP (Multi-Layer Perceptron).

Fig. 1: The followed steps diagnostic of breast cancer to image classification into malign and benign images

Fig. 2: Examples of an observed Cytological Image of Breast Cancer samples: (a) Cytological Image for the malign case, (b) Cytological Image for the benign case
Background on Active Contour Models or "Snake" and "GVF-Snake"

Kass and al. [6] proposed active Contour Models, also called snakes, that since then have been successfully applied in a variety of problems in computer vision and image analysis, such as edge and subjective contours detection, motion tracking and segmentation[11]. Basically, there are two types of snake models: the implicit ones and the parametric ones.

Implicit models, such as the formulation used by R. Malladi.al [12], consist basically of embedding the snake as the zero level set of a higher dimensional function and to solve the corresponding equation of motion. Such methodologies are best suited for the recovery of objects with complex shapes and unknown topologies. However, due the higher dimensional formulation, implicit models are not as convenient as the parametric ones, for shape analysis and visualization, and for user interaction.

The parametric snake models consist basically of an elastic curve (or surface), which can dynamically conform to object shapes in response to internal forces (elastic forces) and external forces (image and constraint forces). These forces can be the result of a functional global minimization processor based on local information. Such approach is more intuitive than the implicit models. Its mathematical formulation makes easier to integrate image data, an initial estimated, desired contour properties and knowledge-based constraints, in a single extraction process [11].

However, parametric models also have their limitations. First, most of these methods can only handle topologically simple objects. The topology of the structures of interest must be known in advance since the mathematical model cannot deal with topological changes without adding extra machinery [11]. Second, parametric snakes are too sensible to their initial conditions due to the non-convexity of the energy functional and the contraction force, which arises from the internal energy term [17,18].

Several works have been done to address these limitations. The use of simulated annealing for minimization and dynamic programming [15] has been proposed to reduce problems caused by convergence to local minima. However, the utility of such techniques is limited by performance problems [16,17]. Levine. al. [19] used another approach by applying hierarchical filtering methods, as well as a continuation method based on a discrete scale-space representation. Basically, a scale-space scheme is first used at a coarse scale to get closer to the global energy minimum represented by the desired contour. In further steps, the optimal valley or contour is sought at increasingly finer scales. These methods address the no convexity problem but not the bad effects of the internal normal force. This force is a contraction force, which makes the curve collapse into a point if the external field is not strong enough.

In Cohen.al [20] and Gang Xu. al. [18] Problem this is addressed by the addition of another internal force term to reduce the bad effects of the contraction force. In both these works the number of parameters are increased and there are some trade-offs between efficiency and performance. Another way to remove the undesired contraction force of the snake model is to use the idea of invariance, which is well known, in the field of computer vision [21]. That idea has been applied for closed contours and consists in designing an internal smoothing energy, biased toward some prior shape, which has the property of being invariant to scale, rotation and translation. In these models, the snake has no preference to expand or contract but tends to acquire a natural shape.

Classical Snake Model: Parametric Active Contours: A parametric active contour or snake is a curve:
\[ \Omega = \{ \alpha, \beta \} \rightarrow R^2, s \rightarrow \nu(s) = (x(s), y(s)) \]  \hspace{1cm} (1)

With parameter \( s \in [0,1] \). The curve can move on the image plane under the influence of two types of forces internal and the external forces. The former constrains the snake to be smooth while the latter guides the snake to seek desirable image properties, such as edges. The external forces are computed from the image data. Such an active contour model seeks to minimize the following functional [6]:
\[ E_{\text{scale}} = \int_{\alpha} \left[ E_{\text{int}}(\nu(s)) + E_{\text{image}}(\nu(s)) \right] ds \]  \hspace{1cm} (2)

Where the first bracketed energy term define the internal energy of the snake. The non-negative constants \( \alpha \) and \( \beta \) are the resistance to stretching and bending of the active contour, respectively. The external energy term \( E_{\text{image}} \) is usually defined as [6]:
\[ E_{\text{int}} = \frac{1}{2} \left( \alpha \| \nu_x \|^2 + \beta \| \nu_y \|^2 \right) \]
\[ E_{\text{image}} = -\int I(x,y) \]  \hspace{1cm} (3)

Where \( I(x,y) \) is the image intensity at \( (x,y) \). The computing of variations [17] is applied to minimize (2) to obtain the following Euler or the motion equations [6],
\[ \alpha \nu_x(x,y) - \beta \nu_y(x,y) - \nabla E_{\text{image}}(\nu(x,y)) = 0 \]  \hspace{1cm} (4)

The Euler equations (4) are called snake evolution equations and can be essentially viewed as a force balance equation, where: \(- \nabla E_{\text{image}} \) can be...
thought of as an external force \( f(x,y) \) \[16\]. Then (4) takes the general form of force balance equations (5):

\[
\begin{align*}
 f_x(x,y) &= \frac{\partial E_{\text{image}}}{\partial x}(x,y) \\
 f_y(x,y) &= \frac{\partial E_{\text{image}}}{\partial y}(x,y)
\end{align*}
\] (5)

Unlike the finite element implementation, most implementations of snakes make use of finite differences in space. By sampling the snake at regular intervals into an ellipse curve with \( n \) vertices, a discretization of the snake's representation is achieved. This representation is used to approximate the derivatives used by means of central differences.

The minimizing of this energy functional gives rise to the following two independent Euler-Lagrange equations:

\[
\frac{\partial^2 x_i}{\partial s^2} = \frac{1}{h^2} (x_{i-1} - 2x_i + x_{i+1})
\] (6)

\[
\frac{\partial^2 y_i}{\partial s^2} = \frac{1}{h^2} (y_{i-1} - 2y_i + y_{i+1})
\] (7)

When assuming equidistant points, for each snake point \((x_i,y_i)\) the following equation must hold:

\[
\begin{align*}
-dx_{i-1} - 2x_i + x_{i+1} + \beta x_{i+2} - 4x_{i+1} + 6x_i - 4x_{i-1} + x_{i-2} &= -f_x[i] \\
-dy_{i-1} - 2y_i + y_{i+1} + \beta y_{i+2} - 4y_{i+1} + 6y_i - 4y_{i-1} + y_{i-2} &= -f_y[i]
\end{align*}
\] (8)

With \( f_x \) is the differential of energy external by \( x_i \). Using this approximation, we can write the Euler equations in matrix form as:

\[
\begin{align*}
A_{xx} &= f_x(x,y) \\
A_{yy} &= f_y(x,y)
\end{align*}
\]

If we deal with a closed snake (which has the advantage that central differences can be evaluated everywhere, since the snake has neither head nor tail), with \( A \) is matrix \( n \times n \) defined by the coefficients \( \alpha \) of elasticity and \( \beta \) of bending.

Since in practice \( E_{\text{image}}(v(s)) \) is a discrete function, and \( A \) is singular and cannot be inverted, neither be solved for \( x \) and \( y \) directly. Kass et al. (1987) have used a friction force in order to constrain the displacement of the snake setting as following:

\[
\begin{align*}
A_{xx} - f_x(x_{i-1},y_{i-1}) &= -\gamma (x_i-x_{i-1}) \\
A_{yy} - f_y(x_{i-1},y_{i-1}) &= -\gamma (y_i-y_{i-1})
\end{align*}
\] (10)

Where \( t \) is the iteration step (or a viscosity factor)? As a result, the discrete equation of the snake's motion can be written in the form:

\[
\begin{align*}
x_i &= (A + \gamma I)^{-1} (\gamma x_{i-1} - f_x(x_{i-1},y_{i-1})) \\
y_i &= (A + \gamma I)^{-1} (\gamma y_{i-1} - f_y(x_{i-1},y_{i-1}))
\end{align*}
\] (12)

Where the \( n \times n \) identity matrix is 1. The solution is found iteratively; in each time step, the image forces of the last position are used. Since \( A + \gamma I \) is constant over time, its inverse can be computed at the beginning using for example a LU-decomposition or Cholesky factorization.

Prerequisite for the successful application of snakes is their initialization close to the object to be interpreted. Snakes have the tendency to shrink, since the inner energy is minimized (vanishing) when the active contour is reduced to a single point. We took advantage of the characteristics in \[8\], since at potential causes weak image forces only; the snake shrinks to a size where it meets the edge of the objects. As such, shrinkage is welcome, since it makes the snake move when no image forces exist. On the other hand it causes contours to be rather convex. Serves is parameter for the magnitude of oscillation. The higher is the slower of the evolution and the higher the inertia of the snake. If a large value of \( \gamma \) is chosen, then \( A + \gamma I \approx \gamma I \) which proves the contour to be quasi stationary (the same considerations are valid with respect to the \( y \)-direction).

In this section, the parametric active contour models are applied to the segmentation of cytological breast cancer images. The application uses cytological images, representing samples of breast cancerous cells, selected from a medical database \[22\] (Figure 2). In order to detect the pathology in cytological images, we must proceed initially by an operation of pre-treatment; that consists on the application of the Gaussian filter to the initial image (Figure 3). The Gaussian filter blurs the edges, thus increasing the snake’s capture range as it spreads the force vectors along the potential field.

![Original Image](a).jpg) ![Filtered Image](b).jpg)

**Fig. 3:** Elimination of the attached noise to the Image Cytological by the application of a Gaussian filtering
As shown in Figure 4, the edge map shows higher values where the image gradient is larger, and low values over homogeneous regions. Using a traditional snake model and a fair initial position, we can see that it correctly evolves towards the desired contour, in figure 4, we show for adequate choice of snakes parameter $\alpha$ and $\beta$. For several experiments, a fixed set of pair $(\alpha, \beta)$ has been used. The experiments where done for $\alpha = 0.0001$, and $\beta = 0.000125$. This pair of $(\alpha, \beta)$ has drawn agree results. And isolate correctly the tumors.

**Gradient Vector Flow "GVF-Snake" (Parametric GVF-Snake Model):** The convergence of Snakes contours depends on the interaction of internal and external forces, where the minimum energy can be found \cite{6}. The internal force is based on the assumption that the contour is continuous and smooth, while the external force is used to extract the desired characteristics, for example a line or an object boundary. In other hand, the conventional classical Snakes model has some limitation in that the initial contour must be placed close to the object to prevent it from converging to a local minimum. To solve these problems the method of GVF-Snake is currently also most efficient to the point of view precision in the tracking breast cancer cells.

C. Xu and J.L. Prince\cite{9,10} proposed to generate a more general field by allowing the possibility that it comprises both an irrotational component and a solenoidal component. They designed a new force field that has both the desired properties of both a large capture range and the presence of forces that point into boundary concavities.

The gradient vector flow field $F_{ext}$ is derived from the following energy functional in \cite{9,10},

\[
E_{ext} = \iint \left[ \mu \left( \nabla f \right)^2 + f_x^2 + f_y^2 \right] dxdy \tag{13}
\]

Where $V(x,y)$ is the field Vector Flow of image:

\[
V(x,y) = (v(x,y), u(x,y))
\]

In this context, $f$ is the edge map, and $\mu$ is a decreasing function of the gradient magnitude defined as \cite{9,10}:

\[
f(x,y) = \sqrt{\nabla G_{\alpha}(x,y)^2 + 1}
\]

\[
\mu = \exp \left( - \left( \frac{\nabla f}{K} \right) \right)
\]

$K$ is a positive constant controlling the smoothness of the resulting field \cite{9,10}. Calculus of variations is once again applied to Minimize (13) leading to the following Euler equations \cite{10}:

\[
\mu \nabla^2 u(x,y) - (u(x,y) - f_x)(f_x^2 + f_y^2) = 0 \tag{17}
\]

\[
\mu \nabla^2 v(x,y) - (v(x,y) - f_y)(f_x^2 + f_y^2) = 0 \tag{18}
\]

One solves (9) and (10) to obtain the GVF force field $(u,v)$ that minimizes (13). The resolution of these equations can be iterative to basis to transform it of Euler-Lagrange for the differential equations. Of which this method is adapted for the numeric treatment while considering $u$ and $v$ iterated data, with $t$ is the indication of iteration:

\[
u_t(x,y) = \mu \nabla^2 v_t(x,y) - (v_t(x,y) - f_y)(f_x^2 + f_y^2)
\]

\[
u_t(x,y) = \mu \nabla^2 v_t(x,y) - (v_t(x,y) - f_y)(f_x^2 + f_y^2)
\]
The deformable models are used extensively in image processing, computer vision, and medical imaging applications, particularly to delineate object boundaries. Problems associated with initialization and poor convergence to boundary concavities, however, has limited their utility. This section presents an external force for deformable models, largely solving both problems in cytological image segmentation. This external force, which we call gradient vector flow (GVF), is computed as a diffusion of the gradient vectors of a gray-level or binary edge map derived from the image. It differs fundamentally from traditional deformable model external forces in that it cannot be written as the negative gradient of a potential function, and the corresponding deformable model is formulated directly from a dynamic force equation rather than an energy minimization formulation (equation 13). Using several two-dimensional examples, we show that GVF has a large capture range and is able to move deformable models into boundary concavities.

In this part, we present results of this new technique of detection of the cancerous cells in cytological image of breast cancer (Figure 5). All while touching the success of the GVF algorithm to converge the active contour toward the concave limits in the majority of cytological Image types and even for the one diving's in the noise or who contains some dark parts, values of regulation $\mu$ and although the couple $(\alpha, \beta)$ is permitting to control it of the contour at the time of the growth initialized by hand. Outrages, this method is founded in the majority of applications of the image segmentation and treatment, as the medical domain, but remains no adaptable for the treatment to the real time.

Our objective has been performing a comparative study of traditional [6] and gradient vector flow [9] snake models for tracking cancers cells from cytological image of breast cancer [23]. First, we have evaluated the accuracy of the shape descriptions obtained by these snake models in gray–level images, showing that gradient vector flow snakes outperform traditional snake models. Next, we have evaluated the robustness of the two snake models with respect to changes of model parameter values, i.e., regularization, elasticity and weight of the external force parameters. Finally, we have evaluated the robustness of the snake models with respect to changes of user–defined parameters, such as the position, size and shape of the initial snake. Our experimental results have shown that, the gradient vector flow snake model outperforms other snake models in terms of robustness with respect to both model and user–defined parameters, followed closely by the classical snake model.

Particular advantages of the GVF deformable model over a traditional deformable model are its insensitivity to initialization and its ability to move into boundary concavities. As we show in Figure 5, its initializations can be inside, outside, or across the object's boundary (cancers cells). Unlike deformable models that use pressure forces, a GVF deformable model does not need prior knowledge about whether to shrink or expand toward the boundary. The GVF deformable model also has a large capture range, which means that, barring interference from other objects, it can be initialized far away from the boundary. This increased capture range is achieved through a spatially varying diffusion process which does not blur the edges themselves, so multi resolution methods are not needed.

Finally, in this section the isolation of the cells in breast cancer cytological image has been achieved, by the use of parametric active contour models. The obtained cells will be used to make the classification of the case into benign or malign breast lesion. In the next section, we introduce the step of Textural Feature Extraction based Discreet Wavelet Transform.
Analysis Texture Method based on Discrete Wavelet Transform

Introduction: Texture features provide a measure of the underlying texture within a given region. A variety of methods are used to extract texture characteristics. Some of the commonly used approaches include the use of spatial frequencies, edge frequencies, run lengths, pixel’s joint probability distribution, and special masks such as Law’s masks. It has been demonstrated in different studies that different feature extraction methods yield different results based on the application domain and it is for this reason that a diverse range of techniques were investigated.

The evaluation of texture feature is an important step in the image processing of the studied images. The texture analysis is the basis of pattern recognition and classification especially in medical domain. The ability of classifiers depends on the quality of feature used as well as the amount of the data available to them [24]. There are many texture extraction methods such as autocorrelation based texture features, Co-occurrence matrices texture features [25], edge-frequency based texture features, etc.

In this work, the texture analysis has been done using a based transform method of feature extraction. The used transforms in this paper, are discrete wavelet transforms. In all this work the obtained results have been achieved using two kinds of transforms: the first one is the Daubechies wavelet at level 2 (db2) which is an orthogonal and compactly supported wavelet, and the second one is the B-splines biorthogonal wavelet (bior) which is a biorthogonal and compactly supported pairs of wavelets. In the two cases the Fast wavelet transform (FWT) is used, with finite impulse filters (FIR filters), the first one is however an asymmetric wavelet with poor regularity and orthogonal proprieties while the biorthogonal wavelet is symmetric but without orthogonality [26].

For the db2 transform the high pass filter is \( h_0 \) and the low pass filter is \( h_1 \); given by:
\[
\begin{align*}
   h_0 &= [-0.483 0.8365 -0.2241 -0.1294] \\
   h_1 &= [-0.1294 0.2241 0.8365 0.483]
\end{align*}
\]
For the bior transform the high pass filter is \( h_2 \) and the low pass filter is \( h_3 \); given by:
\[
\begin{align*}
   h_2 &= [0 0 0 0.3536 0.7071 0.3536 0 0 0 0] \\
   h_3 &= [0 0.03315 -0.06629 -0.1768 0.4198 0.9944 0.4198 -0.1768 -0.06629 0.03315]
\end{align*}
\]
In this section, we will expose the 2D wavelet transform method and show the features extracted by this analysis are shown.

2D Discrete Wavelet Transforms (2D DWT Method): The classical 2D wavelet transform is performed by two separate 1D transforms along the rows and the columns of the image data, resulting at each step of decomposition in a loss pass image or the coarse scale approximation and tree detail images as shown in the Figure 6.

<table>
<thead>
<tr>
<th>LL (_0)</th>
<th>LH (_0)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HL (_0)</td>
<td>HH (_0)</td>
</tr>
</tbody>
</table>

Fig. 6: 2D Discrete Wavelet Transforms after one application

So, the two-dimensional wavelet transforms decomposes an image into four frequency bands called subbands, each one quarter the size of the original as shown in Figure 2. LL subband contains the original image filtered and sub sampled by a factor of 2; the HL, LH and HH subbands contain details in the horizontal, vertical and diagonal orientations [27]. LL subband is a coarse scale approximation of original image and the rest of frequency bands are detail signals. The transform can be applied recursively to the LL sub image to obtain decomposition at coarser scales, yielding a hierarchical decomposition or pyramid representation. The number of levels to apply depends of the original image size. The last LL band is a coarse approximation to the original image corresponding to low frequency, and all the others bands, the most part in the decomposition, are detail information corresponding to high frequency. The high frequency bands have small magnitudes and become zero if the quantization step of a loss coder is applied. So, the high frequency bands are very easy to compress [27].

Features extracted using DWT: The extracted features obtained by the DWT on the studied images are statistical ones and based upon the wavelet coefficients. In this section we are selected four cytological Image from Data Base [22] (2 malign and 2 benign), for the experimental studied.
The obtained results show for benign cases the maximum values of the mean of the approximated coefficients is bigger than the one for malign cases. Besides, for benign distribution of the mean of these coefficients there is some regularity in the obtained shapes; which is not the case of the malign samples.

**Second central moment:** The second central moment is the variance computed using a divisor of \( n \) rather than \( n-1 \), where \( n \) is the number of rows in the matrix \( X \). In this case, the variance is computed for all the obtained subband coefficients using Daubechies wavelet transform at level 2 and biorthogonal wavelet transform.

\[
m_m = E(x - \mu)^2
\]

(21)

Where \( m \) is the central moment of order 2 of the matrix \( x \), and \( \mu \) is the mean value.

**Entropy:** Entropy is a common concept in many fields, mainly in signal processing. There are different entropy criteria, many others are available and can be easily integrated. In the following expressions, \( s \) is the signal and \( (s) \). Its coefficients are an orthonormal basis.
The entropy $E$ must be an additive cost function such that $E(0) = 0$ and $E(s) = \sum_i E(s_i)$.

- The normalised Shannon entropy is given by:
  \[
  E_1(s_i) = s_i \log(s_i) \quad (22)
  \]
  \[
  E_1(s) = -\sum_i s_i \log(s_i) \quad (23)
  \]
  With the convention $0 \log 0 = 0$

- The log energy entropy is given by:
  \[
  E_2(s_i) = \log(s_i^2) \quad (24)
  \]
  \[
  E_2(s) = \sum_i \log(s_i^2) \quad (25)
  \]

Energy:

This section consists in the computing of the energy percentage corresponding to the approximations vectors and the details vectors. In the following table are shown the computed values of entropy and energy obtained using a biorthogonal transform on the image for a malign sample and a benign one.

| Table 1: Entropy and Energy for a malign and a benign case for db2 transform. |
|-----------------------------|-----------------------------|
|                           | Malign sample               | Benign sample               |
| Entropy shannon            | -1.39 $10^6$                | -6.031 $10^5$               |
| Entropy log energy         | -1.72 $10^6$                | -4.96 $10^5$                |
| Energy app                 | 99.341                      | 99.923                      |
| Energy h                   | 0.05228                     | 0.0076                      |
| Energy v                   | 0.0527                      | 0.0060                      |
| Energy d                   | 0.2568                      | 1.0232                      |
|                           | 0.0045                      | 0.0006                      |
|                           | 0.0360                      | 0.0040                      |

From the obtained results, we deduce that the entropy of Shannon, the log energy entropy and the energy of approximated coefficients are greater for the benign cases.

Discrete Wavelet packet decomposition of cytological images (DWPD method):

The wavelet packet decomposition is a method based on algorithms tests the replicability in computer graphics applications. It’s a generalization of the method of multi-resolution decomposition and comprises the entire family of the subband-codded tree [28]. The decomposition leads finally to a complete wavelet tree. The original discrete texture image $I[m,n]$ characterize only the original space $V_0$, while the set of approximation spaces $\{V_j\}$ is $V_{j+1} = V_j \otimes W_j$, where $W_j$ is the detail space. In the case of wavelet packet decomposition each projection space is denoted by the relation $W_{j^p,q}^{r,s}$, where $j$ is the resolution and $p,q$ are subband indices, each space is a sum of four subspaces [28]:

\[
W_{j^p,q}^{r,s} = W_{j+1,q}^{r,s} \otimes W_{j+1,q}^{r,s} \otimes W_{j+1,q}^{r,s} \otimes W_{j+1,q}^{r,s} \quad (26)
\]

The figure 10 shows the subspaces as the outputs of band-pass filters used to extract detail coefficients and detect image edge orientations along different orientations. With $A_\alpha$ is an approximation subband while $D_\alpha$ is corresponding to detail subband.

**Fig. 10: Separable 8-subband filter bank**

Feature extraction using DWPD of the cytological images: The objective of the feature extraction from this decomposition is to compute the vector:

\[
f = [\eta, \xi, \eta_m, \xi_m, \eta_s, \xi_s, \eta_r, \xi_r] \quad (27)
\]

Where $\eta$ and $\xi$ are measures of horizontal and vertical directionality, $\eta_m, \xi_m$ and $\eta_r, \xi_r$ are regularity features along the horizontal axis and $\eta_s, \xi_s, \eta_y, \xi_y$ are regularity features along the vertical axis.

Directionality: Directionality function along the $x$ denoted by $\eta_x$ is based on the correlation between the wavelet coefficients of the successive columns in the horizontal subbands. Similarly the directionality functions along the $y$ axis $\eta_y$ is based on the correlation between wavelet coefficients in the successive rows in the vertical subbands. To obtain the $\eta_x$ and $\eta_y$ parameters we compute in a first step the normalized lag0 -correlations $c(i,j)$ between the rows (respectively the columns) of detail coefficients:

\[
c(i,j) = \frac{E(d_i d_j) - E(d_i) E(d_j)}{\sigma(d_i) \sigma(d_j)} \quad (28)
\]

Where $d_i$ and $d_j$ are sequences of the wavelet coefficients within the row $i$ (or the column) and $j$. $E[.]$ is the expected value and $\sigma[.]$ is the standard deviation. The texture is a phenomenon that depends on the region, so the edge variation estimates must be...
considered in a region of size $k$ in the image. So that, the function $c_i(\tilde{f})$ measuring the correlation between the rows (columns) of detail coefficients within a region of size $k$ is computed [28]:

$$
c_i(\tilde{f}) = \frac{1}{k} \sum_{j=1}^{k} c_i(j)
$$

(29)

For this experiment $k=2^l$ where $l=1,2,3,4,5$ has been applied on 3 horizontal subbands (packet (2,1) or 6, packet (2,4) or 9, packet (2,5) or 10) and 3 vertical ones (packet (2,2) or 7, packet (2,8) or 13, packet (2,10) or 15). In figure 6, is shown the obtained tree of a malign image using db2 wavelet packet decomposition with the Shannon entropy criterion for the optimization of the tree.

Fig. 11: Packet Wavelet Decomposition of a malign sample (1-a) using db2 wavelet transform.

The directionality $d$ is obtained by integrating each sequence of $c_i(\tilde{f})$ along the three regions of sizes 2, 4, and 8 pixels.

$$
d = \sum_{i=1}^{n} \sum_{j=1}^{k} c_i(j)
$$

(30)

The estimates vertical edge correlation and horizontal edge correlation for a benign sample and a malign one has been done, in the figure13, an example of the obtained results.

Fig. 13: - malign case db(1-a) vertical and horizontal edge correlation for a region of size 8 using db2; bi(1-a) vertical and horizontal edge correlation for a region of size 8 using bior transform.

- benign case db(1-b) vertical and horizontal edge correlation for a region of size 8 using db2; bi(1-b) vertical and horizontal edge correlation for a region of size 8 using bior transform.

The obtained results for the malign sample using both the wavelet transforms are similar. The values of vertical edge directionality are very low in the case of malignity and benignity. For horizontal edge directionality the directionality varies between 0.5 and -0.2. This is the fact that the studied image has a non-directional texture or a very limited one. In benign samples, the obtained results for vertical edge correlation and horizontal edge correlation are higher than the ones obtained for malign samples.
Regularity: Regular textures have a structural element that is repetitive in the image. The correlation $c_k$ has a dominant spectral component corresponding to the frequency of the structural element’s repetition, so it can be used to detect the regularity of a texture. The first step is finding the maximum component of the power spectrum given by $|c_k|^2$ and the computing of the ratio, between the energy contained in the maximum component and the overall spectrum of energy; with $N$ is the resolution used for power spectrum estimation. $K=2^l, l=1,2,3,4,5$.

$$e_i = \frac{\max_k |c_k|^2}{\sum_k |c_k|^2}$$

(31)

To estimate regularity the following parameters are computed for the same previous horizontal and vertical subbands which lead to six parameters.

$$r_m = \max_i e_i$$

(32)

$$r_r = \arg \max_i e_i$$

(33)

$$r_f = \frac{2}{N} \left( \arg \max_k |c_k| \right) - 1$$

(34)

Where $r_m$ is the maximum value of $e_i$, $r_r$ is the region for which the maximum value is obtained and $r_f$ is the normalized frequency at which $r_m$ is obtained.

Table 2: Regularity parameters for a benign and a malign case

<table>
<thead>
<tr>
<th></th>
<th>benign</th>
<th>malign</th>
</tr>
</thead>
<tbody>
<tr>
<td>$r_m$</td>
<td>0.6829</td>
<td>0.927</td>
</tr>
<tr>
<td>$r_f$</td>
<td>0.0024</td>
<td>-0.006</td>
</tr>
<tr>
<td>$r_s$</td>
<td>0.6829</td>
<td>0.927</td>
</tr>
</tbody>
</table>

Finally, the obtained regularity parameter $r_m$ is more important in the case of benign samples than in the malign ones. At the end of this work, eighteen textural features have been computed using methods based on Daubechies wavelet transform at level 2 and biorhogonal wavelet transform. The step of feature extraction is the first one; the next step of this project would be the classification of cytological images based on evolutionary methods such as neural networks (Multi-Layer Perceptron (MLP)).

MLP Neural Network Classification

MLP are multilayered neural network having either threshold or sigmoid activation function. The used networks in this section are three layered one, with sigmoidal activation function; the weights updating is done using mean square error minimization. The input vector to the network is a feature of parameters obtained in the later section, and the output layer has one neuron which takes is the tumor is a benign one and 1 if it’s a malign one.

Fig. 14: Multi-Layer Perceptron Method of Neural Network Classification textural Feature of cancer cell from cytological image of Breast cancer

The used database [22] is composed of 200 cytological images. The obtained results, has show a rate of 98% of good classification process.

DISCUSSION

In this work, the segmentation of cytological breast cancer images has been done using an active contour models process to find the tumor cell; when this step is achieved and cell is isolated a wavelet feature extraction approaches applied to the cell led to a vector of textural parameters. This vector is then introduced as the input vector to the MLP neural network, which is classifier in this work. Good rate of classification of the images in the database has been obtained at the end of this process.

REFERENCES


