



A CAD System Framework for the Automatic Diagnosis and Annotation of Histological and Bone Marrow Images

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Abstract

Due to ever increasing of medical images data in the world's medical centers and recent developments in hardware and technology of medical imaging, necessity of medical data software analysis is needed. Equipping medical science with intelligent tools in diagnosis and treatment of illnesses has resulted in reduction of physicians' errors and physical and financial damages. In this article we propose a computer – aided diagnosis system framework in order to automatic classification and annotation of histological and bone marrow images. The proposed method has been tested on two data set including cytological and histological images. Images context features are used to train support vector machine classifier and the accuracy of classifier is 96%. Results show that the proposed framework can be a software model in order to classify and annotate microscopic images in clinical routine functions.

Keywords: CAD, Supervised Learning, SVM Algorithm, Context Features

1. Introduction

Computer aided diagnosis (CAD) are medical procedures which help physicians interpret medical images. Visualization techniques with X-ray, Magnetic resonance image (MRI), ultrasound diagnosis and histology images provide physicians with high volume of information which should analyze them in a short period of time. CAD is a relatively new inter – disciplinary technology which combines artificial intelligent and image digital processing components with medical diagnostic and treatment procedures. CAD is based on diagnosing very complex patterns. Machine learning and visioning are the main components of computer diagnosis. Machine learning is related to manufacturing and studying systems which can learn from data. There are different algorithms for machine learning which the most important ones are learning with the supervisor, without supervisor and semi – supervisory algorithms [1]. Medical data can be inserted into CAD systems with different forms. Among different medical data forms are genes sequence, data gathered by biosensors and medical images. Machine visioning algorithms in computer diagnosis systems are used for receiving, pre – processing, quality promotion and segmentation of images.

Digital images in a CAD system are prepared and analyzed in several steps, including:

- Pre – processing step for reducing interruptions and promoting image quality

- Segmentation step in order to differentiate the structures and different areas of the image.
- Features determination and extraction step in order to describe considered areas quantitatively
- Structures analysis step in which each area is investigated separately to diagnose and examine the possibility of specific patterns [2].

Among methods used in diagnosis and classification of medical images, we can refer to studies which relate to the present article. In [3] the authors have used a blood cells segmentation framework in blood microscopic images using digital image processing, statistical pattern detection method and neural network in order to segment blood microscopic images. The framework obtained 92% accuracy for core segmentation and 78% accuracy for cytoplasm segmentation. In [4] cell core segmentation in heterogeneous microscopic images is proposed, a method based on changeable patterns in order to detect and segmenting cells core and histological heterogeneous images with 90% accuracy. In [5] powerful detection of white blood cells images is used. The method is based on statistical patterns detection and neural networks in order to detect 5 types of white blood cells with 98% accuracy. In above studies, most used images are homogenous.

In the present article, we propose architectural framework in order to detect based on bone marrow microscopic images content and chest tissue (histology). The advantage of the proposed method is in diagnosis of heterogeneous images (two types). Differentiating heterogeneous medical images from each other can be useful in content – based recovery, annotation or automatic information registration about image content in big databases of medical images which are necessary for treatment management in medical digital images databases. The rest of the article is arranged as follows. Section 2 presents the methodology. This section includes the definition of data set structure, proposed architecture, features extraction, reduction of features dimensions and classification. In the third section, we provide implementation results and findings examination. And finally, section 4 presents conclusions.

2. Methodology

2.1 Data Set

Data used in this article includes two types of microscopic images. First type includes chest histological images and the second type is related to bone marrow images. The data set consists of 120 images, 60 chest tissue images and 60 bone marrow images. The dimensions of the images are 1712*1368. Figure (1) is a sample image which is related to two classes.

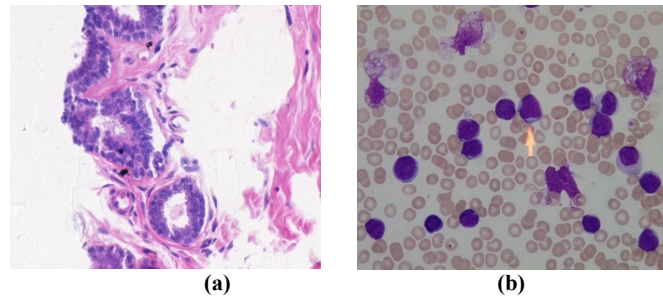


Figure 1. (a) a sample image of chest tissue histology (b) a sample image of bone marrow

2.2 Architecture of Proposed CAD

Figure (2) shows proposed CAD system in a block diagram.

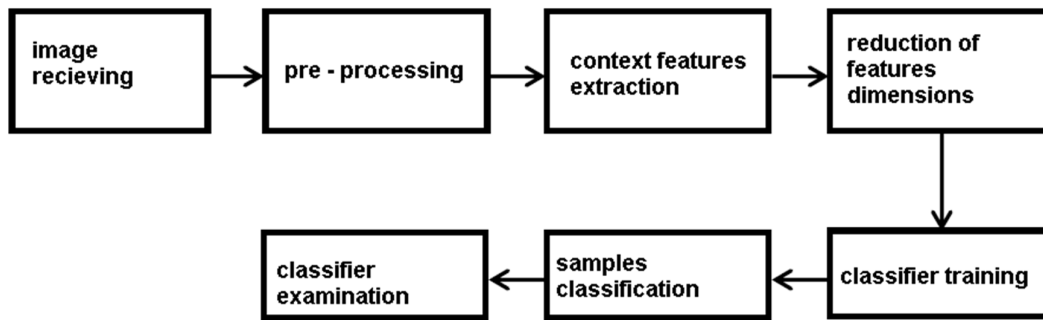


Figure 2. Architecture of proposed CAD

After receiving the image, pre – processing step is conducted which includes quantization of image brightness levels. Then, image context features are extracted. After features extraction, because the number of features are high, the dimension of features matrix is reduced. In the next step, support vector machine (SVM) is trained using experimental samples, and finally the remaining samples are classified and performance of the classifier is examined.

2.3 Features Extraction

For each image, there is one context description which is done using co – occurrence matrix of gray surfaces. In fact, co – occurrence matrix calculates the times which a pixel with value of surface – gray i places in horizontal or vertical vicinity of a pixel with j value. Then, some statistical features are extracted from co – occurrence matrix and hold on a feature vector. At the same time, the real class of the sample is kept in a matrix to be compared with classes which will be predicted in the future.

Co – occurrence matrix can numerically describe some statistical features of the image context. In this method, a matrix $p(i,j)$ is produced from neighborhood window of any image pixel. Harlic introduced co – occurrence matrix for the first time. This matrix shows the possibility of points with assumed brightness levels in certain distance and angle from each other in the image [6]. Image context includes non – static changes of brightness levels which can be iterative or non – iterative [7]. In fact, we can describe context as a function of spatial changes of pixels' brightness intensity. In this study, we use co – occurrence matrix statistical method to extract context features. Here we use 4 features, contrast, energy, entropy and homogeneity using Eqs (1) to (4) on co – occurrence matrix [8].

$$\text{contrast} = \sum_{i=1}^M \sum_{j=1}^N \left((i-j)^2 \times p(i,j) \right) \quad (1)$$

Where contrast returns light intensity between one pixel and its neighbor on the whole image in which the difference is one neighborhood. i shows the line and j represents column. In this equation, $p(i,j)$ is the number of light intensity vicinity.

$$\text{Energy} = \sum_{i=1}^M \sum_{j=1}^N \left(p(i,j)^2 \right) \quad (2)$$

Energy returns total square elements in co – occurrence matrix.

$$\text{Entropy} = \sum_{i=1}^M \sum_{j=1}^N \left(\log(p(i,j)) \times p(i,j) \right) \quad (3)$$

Entropy measures the degree of irregularity or randomness of data.

$$\text{Homogeneity} = \sum_{i=1}^M \sum_{j=1}^N \left(\frac{p(i,j)}{1+|i-j|} \right) \quad (4)$$

Homogeneity is a quantity that returns closeness degree of elements distribution in co – occurrence matrix to diagonal co – occurrence matrix.

2.4 Reduction of Feature Dimensions

Information from image features extraction usually have correlation. Thus, we must reduce such data redundancy. In fact, eliminating useless features leads to matrix dimensions' reduction and increases computations speed and finally improves detection system efficiency. There are different ways to reduce features and in this study we use principal component analysis. PCA is a transformation in vector space which is used to reduce data set dimensions. In this method we can select high energy features and ignore the rest using threshold marking on energy components obtained from PCA transformation [9, 10]. Extracted features are reduced to two main components using PCA techniques. In the next step, we should train transformed data with supervisory algorithm and then examine its performance for different states so for this purpose we use SVM.

2.5 Classification

Supervisory learning algorithm of support machine vector (SVM) is used to classify the samples. Based on this, for each image, 4 effective contextual features (contrast, energy, entropy and homogeneity) are selected and extracted. These feature are applied in the form of a vector to support machine vector. 50percent of the two classes images is used for training and the remaining 50percent is used to test and validate classification algorithm.

It should be noted that supervisory algorithms consist of two training (learning) and classification steps. In training step, we use training data set to develop a model for mapping new samples to considered classes. The shape of the model or the functions depends on the type of learner algorithm. In classification step, experimental data set is used to validate and calculate model accuracy.

Support machine vector is a binary classifier which separates two classes using a border line [11]. SVM has been used successfully in many problems pertaining to data classification and pattern recognition, such as texts classification, face detection in images, handwriting figures distinguishing and bioinformatics. Important feature of SVM is data classification based on structural error minimization or experiment error. Most other classifiers work based on experimental error minimization or training error. Figure (3) shows the simplest state of SVM which is called SVM with hard margin; where data of the two class are linearly separable [12].

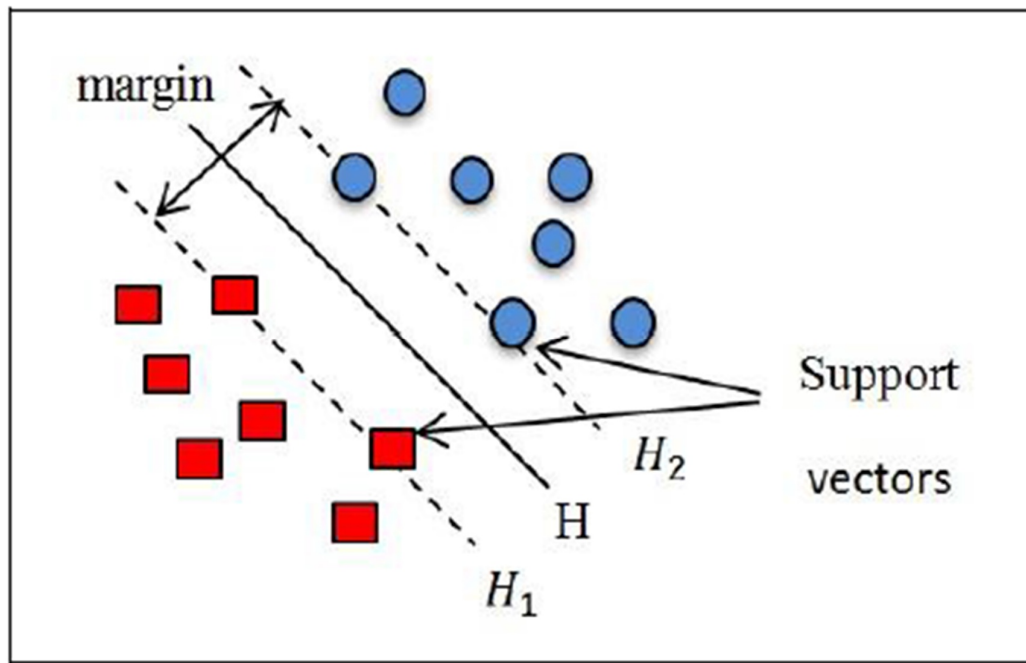


Figure 3. Linear SVM with hard margin

H is the decision border which separates two classes' data. H1 and H2 are parallel to H in the same distance and pass through the nearest points to H which are called support vectors. The distance between H1 and H2 shows decision border margin and totally the aim of SVM is to find decision border which has the most margin in addition to data classification of the two class with minimum error.

2.6 Examination Measure

After classification, we used two criteria to examine the classification results. Confusion matrix is used to calculate correctness and accuracy and ROC diagram is used to calculate system sensitivity. In signal detection theory, ROC diagram is a curve that show sensitivity ratio to the system index value [13]. In learning algorithms with supervisor, confusion matrix is a table which shows classification algorithm performance. In this matrix, each column shows predicted class for the samples while each row shows the real classes.

In medical diagnosis, the accuracy of patients is more important than detection of healthy people; it means that if we consider a healthy person as a patients, it is not harmful but if we consider a patient as a healthy person, it is very dangerous and lethal [14].

The relationships in examination criteria of a classifier in medical diagnosis problems can be presented in Eqs (5) to (7) [15]:

1) Accuracy:

$$\text{Acc} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \times 100 \quad (5)$$

Accuracy is defined as the ratio of classes which are predicted correctly (with and without error) to total number of classes. Accuracy measure (or success degree) is for measuring total accuracy of prediction correctness.

2) Sensitivity or positive samples detection capability:

$$\text{Se} = \frac{\text{TP}}{\text{TP} + \text{FN}} \times 100 \quad (6)$$

Sensitivity show the correctness of prediction model and is defined as percent of classes were correctly predicted to be error-prone. In fact, it is correct detections to real positive samples ratio.

3) Specificity or ability to detect negative samples:

$$\text{Sp} = \frac{\text{TN}}{\text{TN} + \text{FP}} \times 100 \quad (7)$$

Specificity is used to measure model correctness which is defined as the percentage of classes that are properly predicted as non – error – prone. It means that it calculates the negative samples which are detected correctly to negative samples number ratio.

3. Implementation Results

In this section, we provide implementation details, influential parameters in experiments results and obtained results. 50% of the images are used for training and 50% are used to test the classifier. Finally, we used RBF kernel due to better performance and less experimental errors to train the model. Due to reduction of images gray surfaces (quantization), another influential parameter in experiments is the number of gray surfaces. Depending on selecting the number of gray surfaces, results of confusion matrix and ROC diagram can be different. In the experiment we tested image brightness level parameter with degrees of 256, 128, 32, 16, 8 which the best results obtained for sensitivity, specificity and the area under ROC curve for 8 brightness levels. In order to avoid classifier bias to specific training samples, we randomly selected test and training vectors and the steps of training and test are conducted with selected vectors. Implementation results are shown in table (1) and figures (4 and 5).

Table 1. Classifier results with 8 brightness surface

| | |
|--------------------|------|
| Sensitivity | 0.98 |
| Specificity | 1 |
| AUC | 0.96 |

As we can see, the value of sensitivity is 0.98. In fact, this value shows that the algorithm could detect considered class images (histology) up to this level. Although,

this result can be acceptable because the closer this value to 1, the better performance of the algorithm.

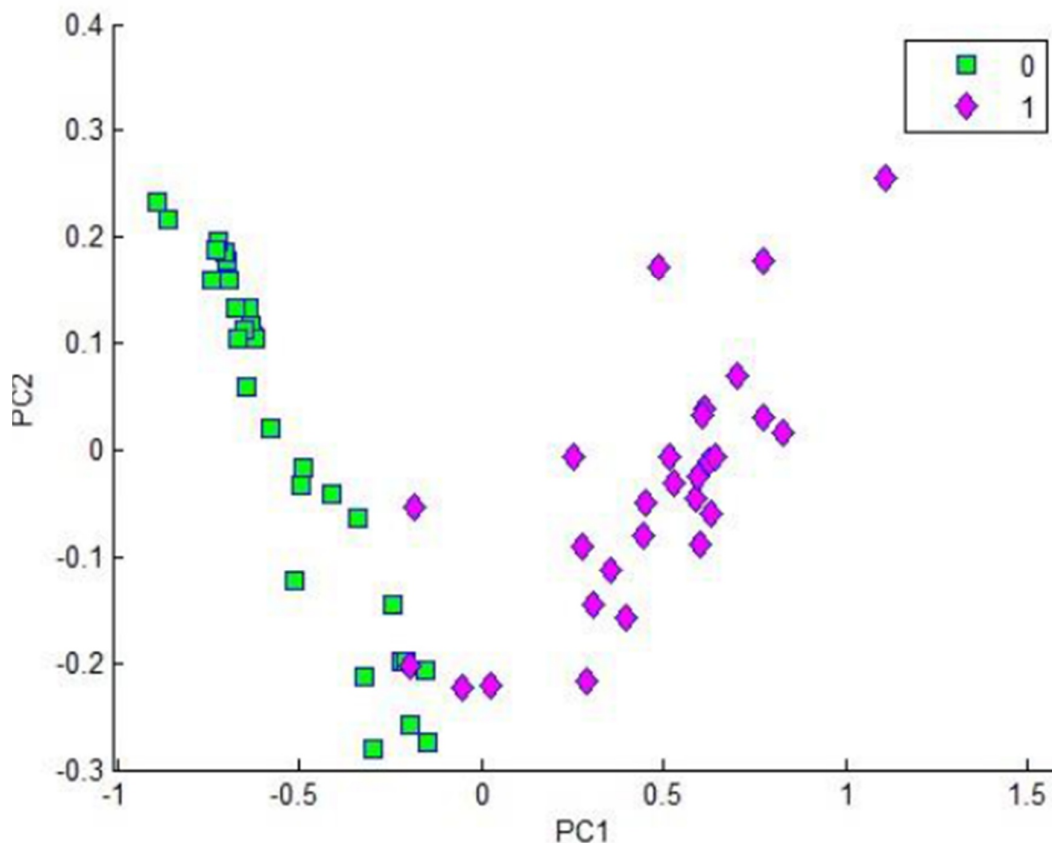


Figure 4. Two classes samples in reduced features space. 0 tag shows bone marrow images class and tag 1 shows the class of histology images.

Figure 4 shows samples of histology and cytology classes in reduced features space. In this diagram, diamonds represent histology samples and squares are bone marrow samples. Due to the fact that the samples of two classes in features space have significant distance or are separable, thus we use linear classifier to separate these samples.

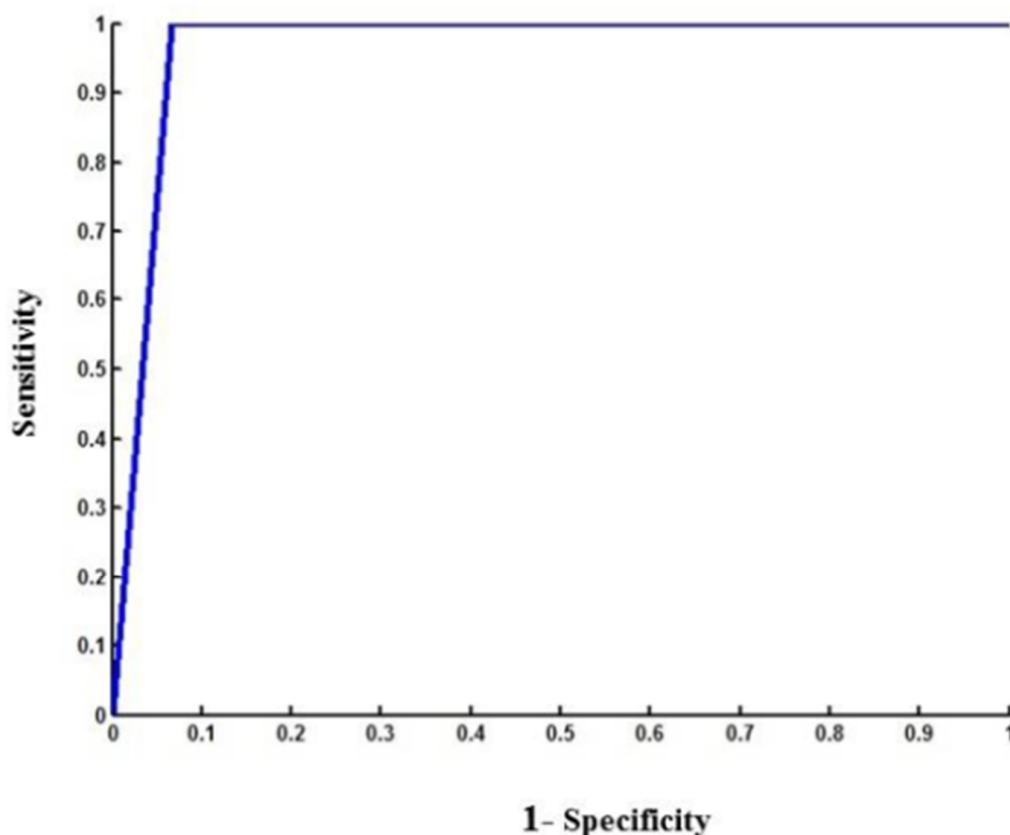


Figure 5. AUC or area under ROC curve shows detection system performance and samples classification

AUC or area under ROC curve shows detection system performance and samples classification which is equal to 0.96. It means that the algorithm could detect most positive samples because in the ideal form, the value is equal to 1 in which all samples are detected correctly.

4. Conclusions

A CAD system framework for the automatic diagnosis and annotation of histological and bone marrow images is proposed in this article. Results (AUC = 0.96) shows that the proposed CAD is a reliable system and can be used as a software pattern in order to classify and annotate microscopic images in clinical routine functions.

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