

A ROBUST METHOD FOR TUBERCULOSIS TRACKING AND SPARSE CLASSIFICATION OF FEATURES IN CHEST RADIOGRAPH IMAGES

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Abstract - Tuberculosis is an infectious disease caused by bacillus *Mycobacterium tuberculosis* which mainly affects the lungs. Mortality rates of the patients with tuberculosis are high. When left undiagnosed and thus untreated. Standard diagnosis still remains slow and often unreliable. In this paper a new approach is proposed for the detection of tuberculosis. This approach is aimed at finding abnormal signs of a diffuse textural nature, such as they are encountered in mass chest screening against tuberculosis (TB). Before classification, geometric features of tuberculosis cell image are found from its binary image. The geometric features of tuberculosis cell image are extracted using the t-test algorithm. The extracted shape and texture features from test image are compared with the trained features. The sparse classifier classifies whether the case is TB or NON-TB. Results presented for several images show that the sparse classifier classifies the presence of tuberculosis bacteria image accurately. Moreover the classification accuracy and the effectiveness of the proposed approach are validated through MATLAB.

Key Words— classification, chest screening, T-test algorithm, sparse classifier, Tuberculosis

1. INTRODUCTION

Gliomas are the most frequent primary brain tumors that originate in glial cells. Glial cells are the building-block cells of the connective, or supportive tissue in the central nervous system. According to World Health Organization (WHO), gliomas are classified into four grades that reflect the degree of malignancy. Grades 1 and 2 are considered low-grade and grades 3 and 4 are considered as high-grade. Grades 1 and 2 are the slowest-growing and least malignant; Grade 3 tumors are considered malignant and grow at a moderate rate. Grade 4 tumors, such as Glioblastoma multi form, are the fastest growing and the most malignant primary brain tumors. Classification of glioma tumors is important for clinical understanding of tumor biology, clinical response and for assessing overall prognosis with brain tumors. Conventional MR imaging is the standard technique for diagnosis, treatment planning, and monitoring of CNS lesions, with superior sensitivity compared to alternative modalities. It is routinely used for the non-

invasive assessment of brain tumors, but its ability to define the tumor type and grade of gliomas is limited.

A biopsy and surgical resection is usually required to establish the diagnosis and subtype of a brain tumor after conventional MR imaging, but variations in tissue sampling may produce erroneous result during biopsy. In this work, only conventional T2-weighted MR images are considered and this modality highlight tissues with higher concentration of water in which border definition and tumor heterogeneity are best observed. Most of the segmentation technique in literature such as fuzzy c-means clustering, Markov random fields, level set method model based techniques are time consuming or complex or need human intervention. Accurate segmentation of glioma is also very important in this work because entire portion of tumor texture is considered for classification of tumor. Hence a new method for accurate detection of glioma tumor is described here.

Texture features have proved useful in differentiating normal and abnormal tissues in different organs using different types of imaging modalities. Texture analysis is very important in the brain tumor detection, as it is difficult to differentiate between various tissues using shape feature alone. 2D textural features have been previously employed for MRI brain tumor characterization and pattern recognition systems. Classification of primary and secondary brain tumors using first and second order statistics from MRIs have also been developed. Statistical analyses of texture from brain CT images for quantifying tumor heterogeneity and thereby differentiate high and low grade glioma are there in literature. Texture analysis using statistical quantification has proposed in literature for differentiating glioneuronal tumors as a subclass of grade III and IV. Malignant gliomas. Gray level co-occurrence (GLCM) based texture analysis is widely used in the detection of breast cancer in mammograms, detection of abnormal liver in CT images and detection of primary and secondary tumor in brain MRIs. Several approaches are developed in the literature for classification and grade detection of glioma tumors.

Classification of glioma from metastatic and grading of glioma from conventional MRI and perfusion MRI, using support vector machines (SVM), Artificial Neural Network

(ANN) and linear discriminant analysis (LDA) is cited in literature. The features used for their study were tumor shape, intensity characteristics as well as rotation invariant Gabor texture features. Determination of degree of malignancy of glioma using SVM is also developed in the literature. The degree of malignancy was determined in their work using the features from clinic al data before operation and findings from conventional T1 and T2 weighted MRI such as age, shape, gender etc. The objective of this work is automatic detection and classification of low and high grade glioma from T2 weighted brain MRI. The framework of the method consists of detection of region of interest (ROI) using Adaptive Gray level Algebraic set Segmentation Algorithm (AGASA), feature extraction from detected tumor texture based on first order and GLCM based second order statistics, feature selection using t-test and its corresponding p-value, and classification of low and high grade glioma, based on p-values of selected features, training and performance evaluation of results using receiver operating characteristic curve (ROC).

2. SYSTEM ANALYSIS

In this paper a new approach is proposed for the detection of tuberculosis. This approach is aimed at finding abnormal signs of a diffuse textural nature, such as they are encountered in mass chest screening against tuberculosis (TB). We first extract the lung region using a graph cut segmentation method. For this lung region, we compute a set of texture and shape features. Before classification, geometric features of tuberculosis cell image are found from its binary image. The geometric features of tuberculosis cell image are extracted using the t-test algorithm. The extracted shape & texture features from test image are compared with the trained features. The X-rays are classified as normal or abnormal using a sparse classifier. This system provides high accuracy and low feature size. Figure 4 shows the overview of the system.

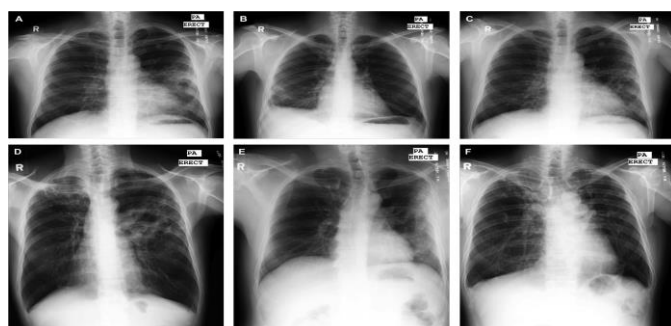


Fig. 1: Examples of abnormal CXRs in the MC dataset.

3. GRAPH CUT SEGMENTATION

Lung segmentation is modeled as an optimization problem that takes properties of lung boundary, region and shapes into account. A lung model is to be incorporated that represents the average lung shape. As training mask publicly available JSRT set are used. First, we linearly align all training mask to a given input CXR and compute the intensity projections and measure the similarity between projections of input CXR and the training one, then we use average mask computed on the subset of similar training mask as a lung model. The pixel intensity of the lung model is the probabilities of the pixel being part of the lung field

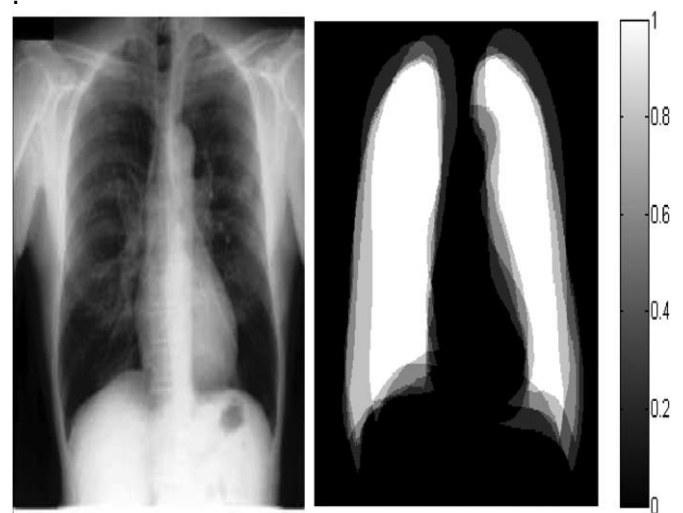


Fig. 2: CXR and its lung model

Segmentation procedures partition an image into its constituent parts or objects. In general, autonomous segmentation is one of the most difficult tasks in digital image processing. A rugged segmentation procedure brings the process a long way toward successful solution of imaging problems that require object to be identified individually. Representation and description almost always follow the output of the segmentation stage, which usually is raw pixel data, constituting either the boundary of a region or all the points in the region itself

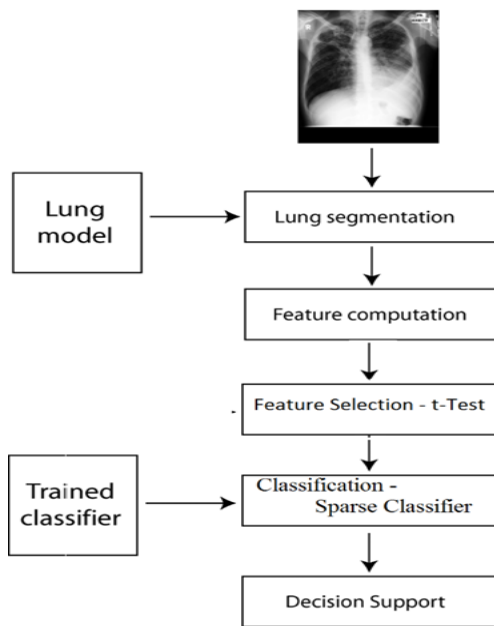


Fig.3: System Overview

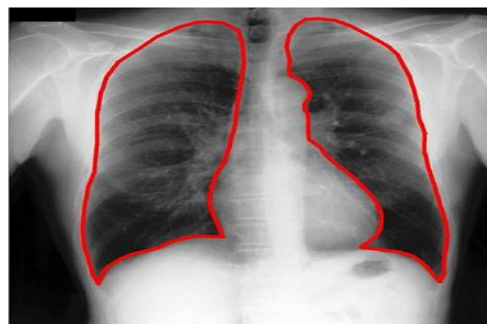


Fig. 4: Segmented lung region

Next employs the graph cut segmentation and formulates the objective function

Image is firstly divided into multiple blocks.

- Each block features are calculated.
- Each block is considered as a node and features as graph
- Assign seeds randomly as source and destination.
- Divide into groups based on the weight value.

To formulate the objective function, we define three requirements a lung region has to be satisfied; the lung region should be consistent with typical CXR intensities expected in a lung; neighbouring pixels should have consistent label; the lung region should be similar to the lung model. Let $f = \{f_1 \dots f_p \dots f_N\}$ be a binary vector whose component f_p correspond to foreground (lung

region) and background label assignments to pixel $p \in P$, where P is the set of pixels in the CXR, and N is the number of pixels. According to our method, the optimal configuration of is given by the minimization of the objective function. The objective function is given by,

$$E(f) = E_d(f) + E_s(f) + E_m(f)$$

Where E_d , E_s , and E_m represent the region, boundary and the lung model properties of CXR



Fig.5: Segmented CXRs

4. FEATURE EXTRACTION

To describe normal and abnormal patterns in the segmented lung field, different features are to be extracted.

Object Detection Inspired Features

It is a combination of shape, edge and texture descriptor. for each descriptor a histogram that shows the distribution of the different descriptor values across the lung field are computed. Each histogram is a feature and all the descriptor are put together form a feature vector ,that we input to a classifier.

4.1. Intensity Histogram

Graphical representation of the image is the histogram. Histogram is a graph showing the number of pixels in an image at each different intensity value in that image.

4.2. Gradient Magnitude Histogram

First apply the gradient filter to the image (sobel filter) and convolute with the original image .Two images will be obtained $g(x)$ & $g(y)$

4.3. Shape Descriptor Histogram

It is used to analyses the shape. Hessian matrix is calculated, which is the partial derivative of the gradient image. Then, take the Eigen values of the hessian matrix

$$g(x)=\lambda_1 \ \& \ g(y) = \lambda_2$$

$$SD= \tan^{-1}(\lambda_1/\lambda_2)$$

Where λ_1 & λ_2 are the eigen values of the hessian matrix with λ_1 less than or equal to λ_2 Graph λ_1 less than or equal to λ_2

4.4. Curvature Descriptor Histogram

$I(x,y)$ is the pixel intensity for pixel (x,y) . In this Normalization with respect to intensity make the descriptor independent of image brightness.

$$CD= \tan^{-1} [(\lambda_1*\lambda_1+\lambda_2*\lambda_2)]^{0.5} / 1 + I(x,y)$$

4.5 Histogram of Oriented Gradients

HOG is a descriptor for gradient orientation weighed according to gradient magnitude .The image is divided into small connected region and for each region a histogram of gradient direction for the pixel within the region is computed .the combination of these histogram represents the descriptor

4.6. Local Binary Pattern

Local binary pattern is a texture descriptor that codes the intensity difference between neighbouring pixels by a histogram of binary patterns. LBP is thus a histogram method in itself. The binary patterns are generated by thresholding the relative intensity between the central pixel and its neighboring pixels. Because of its computational simplicity and efficiency, LBP is successfully used in various computer vision applications

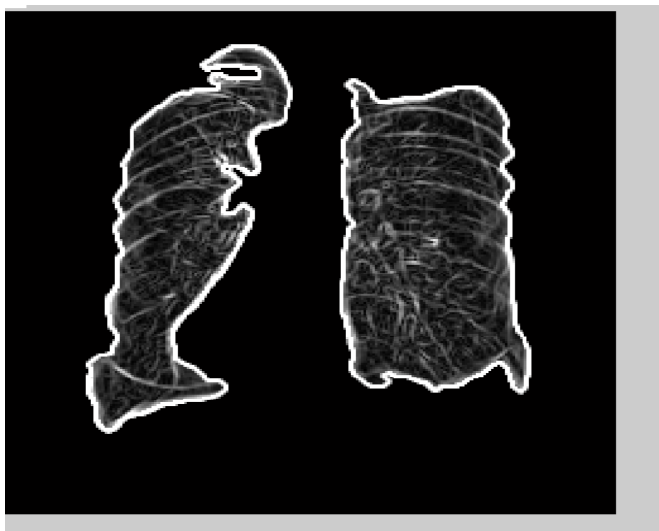


Fig.6: Feature extracted CXR

5. FEATURE SELECTION

To reduce the feature size, complexities and time consumption after feature extraction feature selection is performed. Here feature selection is accomplished using the t-test algorithm. The most type of t-test is often used to assess whether the means of two classes are statistically different from each other by calculating a ratio between the difference of two class mean and the variability of the two classes. The t-test has been used to rank features for microarray data and for mass spectrometry data. The uses of t-test are limited to two-class problems. For multi-class problems, a t-statistics value is calculated for each gene of each class by evaluating the difference between the mean of one class and the mean of all the classes, where difference is standardized by the within –class standard deviation. T-test is based on a ranking based on the t-score. Here t_{ic} is the t-statistics value for the i-th gene (feature) of the c-th class.

$$t_{ic} = \frac{\bar{x}_{ic} - \bar{x}_i}{M_c \cdot (S_i + S_0)}$$

$$S_i^2 = \frac{1}{N - C} \sum_{c=1}^C \sum_{j \in c} (x_{ij} - \bar{x}_{ic})^2$$

$$M_c = \sqrt{1/n_c + 1/N}$$

And \bar{x}_i is the mean of the i-th feature for all classes; x_{ij} refers to the i-th feature of the j-th sample; N is the number of all the samples in the Cclasses and n_c is the number of samples in class c; S_i is the within-class standard deviation and S_0 is set to be the median value of S_i for all the features

$$t_i = \max \left\{ \frac{|\bar{x}_{ic} - \bar{x}_i|}{M_c S_i}, c = 1, 2, \dots, C \right\}$$

Therefore, we generalize the t-score of each feature as; suppose the feature set is $F = \{f_1, \dots, f_i, \dots, f_g\}$ and feature i has different nominal values represented as $f_i = \{x_i^{(1)}, x_i^{(2)}, \dots, x_i^{(m_i)}\}$. Transform each nominal feature value into a vector with the dimension m_i . $x_i^{(1)} \Rightarrow \vec{X}_i^{(1)} = (0, \dots, 0, 1)$, $x_i^{(2)} \Rightarrow \vec{X}_i^{(2)} = (0, \dots, 1, 0), \dots, x_i^{(m_i)} \Rightarrow \vec{X}_i^{(m_i)} = (1, \dots, 0, 0)$.

Replace all the numerical features with those vectors.

$$t_i = \max \left\{ \frac{|\bar{X}_{ic} - \bar{X}_i|}{M_c S_i}, c = 1, 2, \dots, C \right\}$$

$$S_i^2 = \frac{1}{N - C} \sum_{c=1}^C \sum_{j \in c} (\bar{X}_{ij} - \bar{X}_{ic})(\bar{X}_{ij} - \bar{X}_{ic})^T$$

Feature selection depend on ranking based on a t-score. t-test calculates the t-value .from this, probability values are assigned by the t-value. T-value obtained by evaluating the difference between the mean of one class and the mean of all the classes, where the difference is standardized by within the class standard deviation. If the difference is relatively small then the corresponding t-score of the feature is small. Hence the feature significant is also less. If the difference is large, then t-score is also high. High t-score indicate that a particular feature is dominant. Then the p values are sorted and selected. From the probability value cumulative distributive function is obtained and a graph is plotted using MATLAB. Indicates feature size decreased.

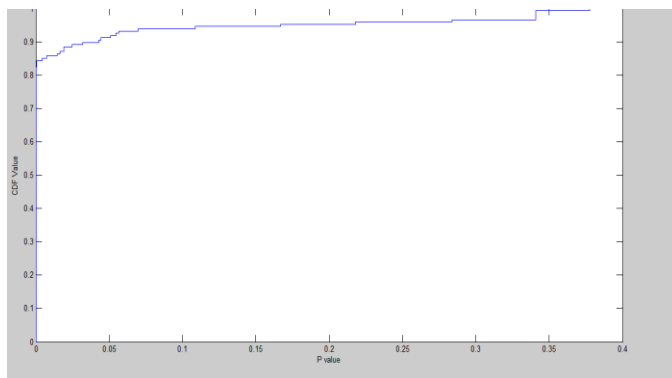


Fig.7: Graph plotted between cumulative distribution function and the probability value

6. CLASSIFICATION

Next step is the classification of chest X-rays to TB positive case as well as the negative ones. Here for classification a well-known classifier called sparse classifier is being used. The advantage of sparse classifier is that it classifies both linear as well as the non-linear data points. Let define sparse estimate that is degree of sparseness α_1 and β_1 as in which irrelevant or redundant components are exactly zero. Sparseness is desirable feature in classifier learning for several reasons namely; sparseness leads to a structural simplification of the estimated function; in kernel classifiers, the generalization performance increases with the degree of sparseness.

Firstly Training is considered and the trained o/p is given as $Y = xa + \alpha_1 f_1(a) + \beta_1 f_2(a)$, where Y is the training output, x denotes the transpose of the input feature values and a is the weight value. From training weight values and degree of sparseness is obtained. These parameters are applied for the classification of the sparse data. And from the known parameters actual output can be obtained that is TB positive or negative. The actual output is given by

$$y = xa + \alpha_1 f_1(a) + \beta_1 f_2(a)$$

7. RESULTS

The paper proposed a system which efficiently and accurately classifies the chest x-rays to tumor positive as well as negative. The time consumption decreased in a high rate by employing T-test algorithm. T-test algorithm reduces the feature size thereby decrease the time consumption and complexities. The sparse classifier which classifies both linear as well as the non-linear data enhances the system accuracy. Existing system employs graph segmentation and classification using SVM which are being modified using t-test and the sparse classifier. Time consumption comparison graph of modified system with the existing one is being shown below

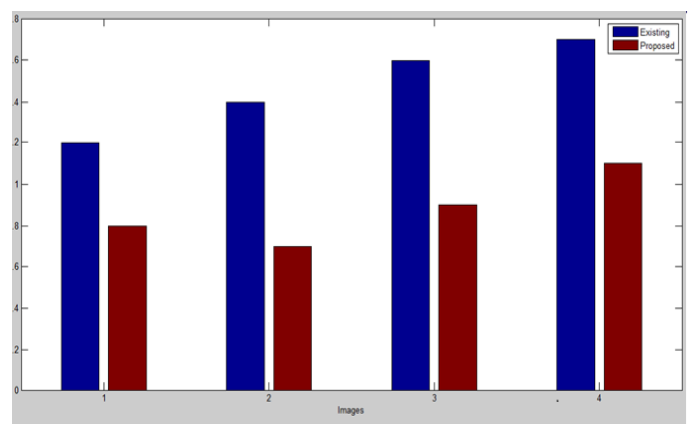


Fig.9: Time consumption graph

8. CONCLUSION

A model that can segment the chest radiographs effectively and detect TB manifestations accurately is implemented successfully. A novel method is presented for automatic detection and classification of low and high grade TB from conventional chest x-rays. It is important to detect tumor texture accurately, because entire portion is considered for further analysis and classification. Firstly, the input CXRs is segmented using Graph cut segmentation which is having high precision. This method combines intensity transformation with personalized lung model

derived from the training set. Then computing a set of shape, edge and texture features. Then the feature complexities and size is reduced by feature selection using t-test. Statistical significance of these features for low and high grade TB was determined using t-test and corresponding P-value is computed, and then input to a classifier called sparse classifier which classify linear as well non-linear data points. Efficient and accurate TB detection and classification can be obtained.

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