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Inherent Selection Of Tuberculosis Using Graph Cut Segmentation

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Abstract*—Tuberculosis (TB) is a major global health threat. An estimated one-third of the world's population has been exposed to TB, and millions of new infections are occurring every year. Tuberculosis naturally affects the lungs it also affects the other parts of the body. It is spread through air when infectious people cough, sneeze etc. The advent of new powerful hardware and software techniques has triggered attempts to develop computer-aided diagnostic systems for TB detection in support of inexpensive mass screening in developing countries. In this paper the medical background of TB detection in conventional posterior anterior chest X-rays has been described. In the first step the chest x-rays has been given as an input. In the second step, the selected images are segmented using graph cut segmentation method. In the last step a set of features such as area, dispersion, entropy, energy, correlation has been extracted and calculated. Lastly, the support vector machine is applied to classify the extracted feature vectors as normal or abnormal lungs and therefore it also reduced the false positive rate. It achieved 95.28% sensitivity with only 2.27 false positives per scan.

***Keywords*— Tuberculosis, Computer Aided Diagnostics, Segmentation, Graph cut, Support vector machine**

I. INTRODUCTION

Tuberculosis is an infectious disease caused by the bacillus Mycobacterium tuberculosis, which affects mainly the lung. While TB is less prevalent in industrialized nations, the death toll in developing countries is high. In 2011, 8.7 million people fell ill with TB, and 1.4 million died from TB (1). The emergence of new drug resistant strains is beginning to exacerbate the problem, rendering the existing drugs ineffective, and necessitating resolute action for any attempt to eradicate the disease to be successful. In addition, large numbers of patients with HIV/TB co-infections need to be X-rayed and screened for active TB to ensure a proper treatment of their infection(s). Taking standard chest X-rays (CXRs) is an inexpensive way to screen for the presence of TB. Unfortunately, the interpretation of CXRs is subject to human error and depends on the expertise of the reader (2-5). In addition, mass screening of a large population is a time-consuming and tedious task, which requires considerable effort when done manually. For this reason, there is considerable interest in developing computer-aided diagnostic systems (CAD) that can detect TB automatically in CXRs. These systems have the potential to reduce the risk of detection errors and increase the efficiency of mass screening efforts.

II. PROBLEM STATEMENT

However TB is a wide spreading disease and many tests such as skin test, sputum test, blood test has been conducted to test the occurrence of TB. Those test are very time consuming and unreliable therefore in this paper we use an automated approach for detecting tuberculosis in chest radiographs using Graph cut Segmentation method.

III. OVERALL DESIGN

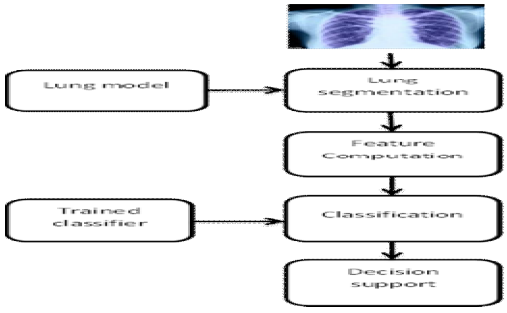


Fig 1: This takes chest X-ray as input and produces an output which indicates the degree of abnormality for the given chest X-ray.

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IV. ALGORITHM OUTLINE

A. Graph Cut Segmentation

It is employed to solve a computer vision problems such as image smoothening. This segmentation also takes the properties of lung boundaries, shapes and regions into account [4] currently we employ a modified version of Active Shape Models to extract the lung fields from a chest radiograph. This method is very robust and trainable, making it easy to adjust it to other databases with different image characteristics. The segmentation result is generally sufficiently accurate for our purposes. We align the entire training mask for the given input CXRs and then perform the horizontal and vertical histogram equalized images. We employ a graph cut approach in which three necessities a lung region has to fulfill: 1) the lung region should be reliable with distinctive CXR intensities expected in a lung region, 2) adjacent pixels should have reliable labels, and 3) the lung region requirements to be similar to the lung model we computed. Let $C=(C_1,C_2,C_3.....C_p,C_N)$ be a binary vector components and C_p is the foreground and background label, p€P is the pixel and N is the number of pixels

Therefore

$$E(C)= Ed(C)+Es(c)+Em(C) \quad (1)$$

Ed, Es, Em represents the region, boundary and the lung model

$$Ed(C)= 1/Imax(\sum p,s\in F)|Ip-Is |+\sum p,t\in F|Ip-It | \quad (2)$$

Ip is the intensity of pixel P and F is the set of edges. Is, It represents the intensities of foreground and the background images. Imax is the maximum intensity values.

$$ES(C) = \sum(P,q\in F)exp(-(Ip-Iq) ^2) \quad (3)$$

Therefore we compare the segmentation algorithm with the lung boundary detection and obtain

Ω = TP/(TP+FP+FN)Where TP is the True Positive and FP is the False Positive and FN is the False Negative.

TABLE I
0VERLAP SCORES ON DATASET

Method	Avg ± std	Min	Median	Max
Hybrid Voting [22]	0.949 ± 0.020	0.818	0.953	0.978
Human Observer [22]	*0.946 ± 0.018*	*0.822*	*0.949*	*0.972*
PC postprocessed [22]	0.945 ± 0.022	0.823	0.951	0.972
Hybrid ASM-PC [22]	0.934 ± 0.037	0.706	0.945	0.968
Hybrid AAM-PC [22]	0.933 ± 0.026	0.762	0.939	0.966
MISCP [69]	0.930 ± 0.045	-	-	-
ASMOF [70]	0.927 ± 0.032	0.745	0.936	0.946
ASM-SIFT [71]	0.920 ± 0.031	0.783	0.928	0.961
ASM [22]	0.903 ± 0.057	0.601	0.924	0.960
GC [4], [5]	**0.901 ± 0.054**	**0.541**	**0.911**	**0.969**
ASM [71]	0.870 ± 0.074	0.608	0.892	0.954
AAM [22]	0.847 ± 0.095	0.017	0.874	0.956
Mean shape [22]	0.713 ± 0.075	0.460	0.713	0.891

V. IMPLEMENTATION

A. Texture Feature Extraction

A filter-bank texture analysis method that extracts multi-scale texture features from local histograms is used (see e.g. [4]). The set of filters is given by the Gaussian and its derivatives up to second order, at multiple scales. The histogram per region of the filtered image is computed, from which the first four moments are extracted. Density features are added and the difference between corresponding regions in the left and right lung field is used to construct additional 'difference' features, in order to mimic right-left comparisons as they are made routinely by radiologists.

B. Region Classification

The features are each scaled to zero mean and unit variance. A simple k-nearest neighbour classifier is used to estimate the probability that a region is abnormal. Different sets of features (different scales, different moments, whether or not to include the difference features, etc.) have been tested on several databases. A selection of features for each region separately could be

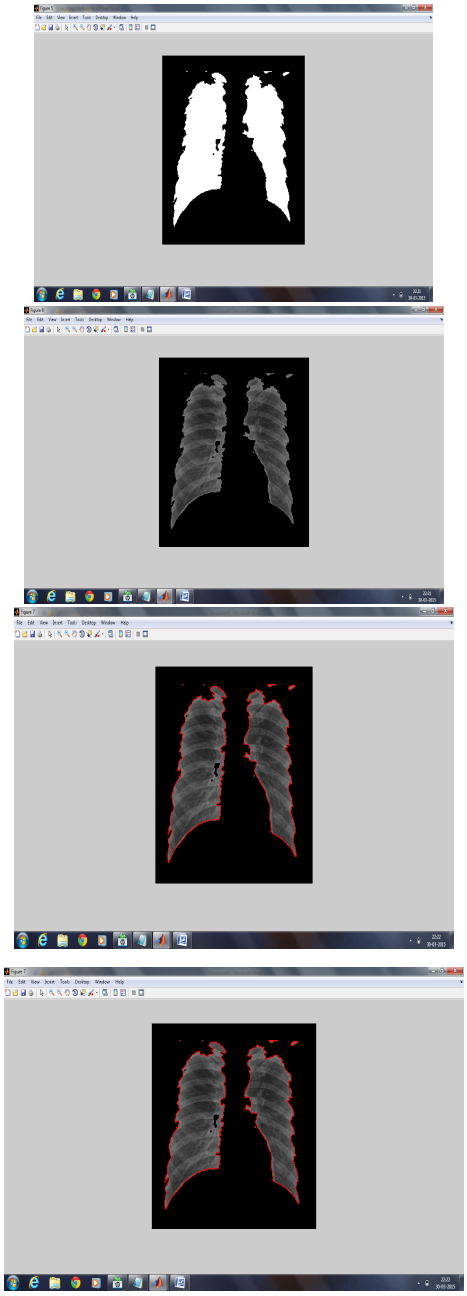
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employed, but the size of our databases is currently rather small (for some regions the number of features is much larger that the number of abnormal cases), therefore we currently do not perform feature selection.

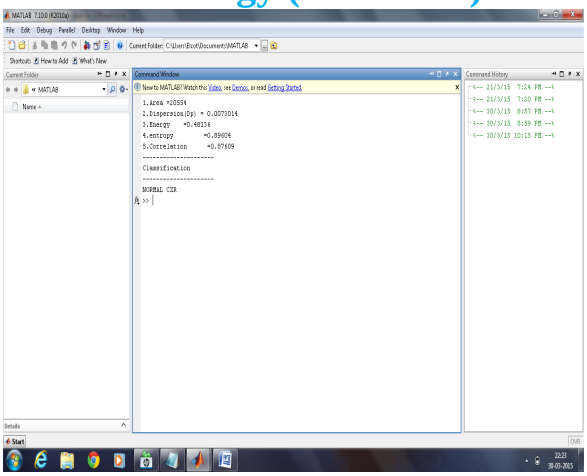
C. Region Pooling

For each region, the performance of the system can be measured in terms of A_z, the area under the ROC curve. Using A_z, we perform a weighted average of all regions to arrive at a final abnormality score of the complete image. The exact way in which the weighting is implemented is ad hoc, but turns out to have little effect on the overall performance of the system. The weighting procedure ensures that regions for which no reliable estimate can be made have only a small influence on the total abnormality estimate.

VI. IMPLEMENTATION RESULTS



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VII. EXPERIMENTAL RESULTS

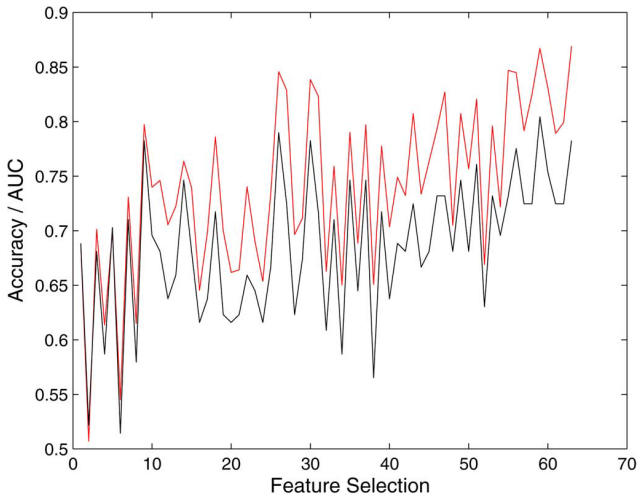


Fig2 The red curve shows the performance of using SVM classifier for 5 features and the blue curve shows the performance of Binary classifier for 2 features

VIII. CONCLUSIONS

We have developed an automated system that screens CXRs for manifestations of TB. When given a CXR as input, our system first segments the lung region using an optimization method based on graph cut. This method combines intensity information with personalized lung atlas models derived from the training set. We compute a set of features such as area correlation energy entropy as input to a SVM classifier, which trains the dataset and then classifies the given input image into either normal or abnormal.

IX. FUTURE ENHANCEMENT

To improve the performance further, we could try to improve the lung segmentation, which provides average performance compared to other systems in the literature. One approach is that we can make use of fuzzy classifier for SVM. Another approach would be to find optimal weights for the terms in the graph cut energy function.

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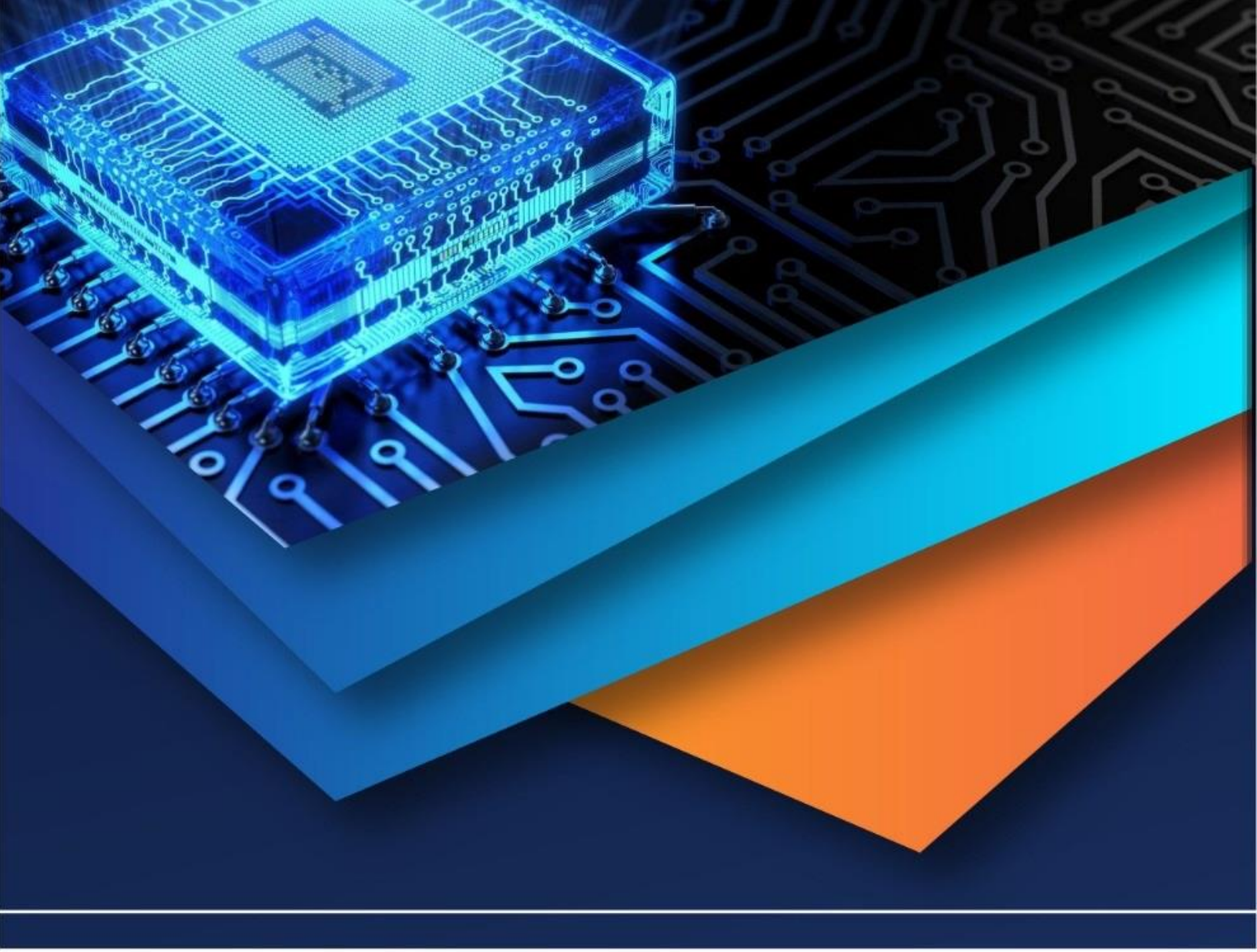
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