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Automated Approach for Detecting Tuberculosis using Chest Radiographs

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ABSTRACT

Tuberculosis is one of the major health problems in many parts of the world. Due to multi-drug-resistant bacterial strains have increased the problem, tuberculosis still remains a challenge. Mortality rates of patients with tuberculosis are high when left undiagnosed and untreated. Standard diagnostics depends on methods developed in the last century which are slow and unreliable. In an effort to reduce the complexity of the disease, this paper presents our automated approach for detecting tuberculosis using chest radiographs. At first we extract the lung region using a graph cut segmentation method. From this extracted lung region, we compute a set of texture and shape features, which enable the X-rays to be classified as normal or abnormal using a binary classifier.

Keywords: Computer-aided detection and diagnosis, lung, pattern recognition and classification, segmentation, tuberculosis (TB), X-ray imaging.

I. INTRODUCTION

Tuberculosis (TB) is the second leading cause of death due to an infectious disease worldwide, after HIV; with a mortality rate of over 1.2million people in 2010[1].TB is a major global health problem [2]. TB is an infectious disease caused by the bacillus Mycobacterium tuberculosis, which typically affects the lungs. It spreads through the air when people with active TB cough, sneeze, or otherwise expel infectious bacteria. The increasing appearance of multi-drug resistant TB has further created an urgent need for a cost effective screening technology to monitor progress during treatment. Several antibiotics exist for treating TB. While mortality rates are high when left untreated, treatment with antibiotics greatly improves the chances of survival. In clinical trial, cure rates over 90% have been documented [1].Unfortunately, diagnosing TB is still a major challenge. The definitive test for TB is the identification of Mycobacterium tuberculosis in a clinical sputum or pus sample, which is the current gold standard [2], [3]. However, it may take several months to identify this slow-growing organism in the laboratory. Another technique is sputum smear microscopy, in which bacteria in sputum samples are observed under a microscope are not always reliable. The latest development for detection are molecular diagnostic tests that are fast and accurate, and that are highly sensitive and required for these tests to become commonplace [1]–[3].. In this paper, we present an automated approach for detecting TB manifestations in chest X-rays (CXRs). An automated approach to X-ray reading allows mass screening of large populations that could not be managed manually.(X-ray)of a patient's chest is mandatory part of every evaluation for TB[7].The chest radio- graph includes all thoracic anatomy and provides a high yield, given the low cost and single source [8]. Therefore, a reliable screening system for TB detection using radiographs would be a critical step towards more powerful TB diagnostics.. It is therefore important to detect patients with TB infections, not only to cure the TB infection itself but also to avoid drug in compatibilities.

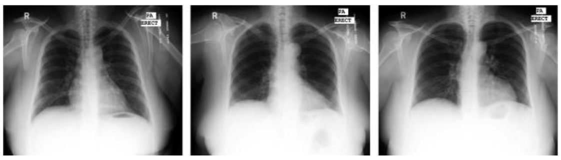

Figure1.

II. METHODS AND MATERIAL

This section presents our implemented methods for lung segmentation, feature computation, and classification.

Fig. 4 shows the architecture of our system with the different pro- cessing steps, which the following sections will discuss in more detail. First, our system segments the lung of the input CXR using a graph cut optimization method in combination with a lung model. For the segmented lung field, our system then computes a set of features as input to a pre-trained binary classifier. Finally, using decision rules and thresholds, the classifier out puts its confidence in classifying the input CXR as a TB positive case, for example.

A. Graph Cut Based Lung Segmentation

We model lung segmentation as an optimization problem that takes properties of lung boundaries, regions, and shape into account [4]. In general, segmentation in medical images has to cope with poor contrast, acquisition noise due to hardware constraints, and anatomical shape variations. Lung segmentation is no exception in this regard. We therefore incorporate a lung model that represents the average lung shape of selected training masks. We select these masks according to their shape similarity as follows. We first linearly align all training masks to a given input CXR. Then, we compute the vertical and hori- zontal intensity projections of the histogram equalized images. To measure the similarity between projections of the input CXR and the training CXRs, we use the Bhattacharyya coefficient. We then use the average mask computed on a subset of the most

Block Diagram

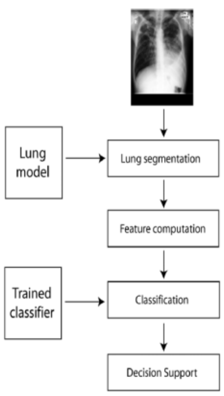

Figure 2. Lung Model

System Overview

The system takes a CXR a input and outputs a con- fidence value indicating the degree of abnormality. Increasing the subset size to more than five masks will decrease the lung model accuracy because the shapes of the additional masks will typically differ from the shape of the input X-ray. As training masks, we use the publicly available JSRT set [35] for which ground truth lung masks are available [22].The pixel intensities of the lung model are the probabilities of the pixels being part of the lung field. Fig. 5 shows a typical lung model we computed. Note that the ground-truth masks do not include the posterior inferior lung region behind the diaphragm. Our approach, and most segmentation approaches in the literature, exclude this region because manifestations of TB are less likely here. In a second step, we employ a graph cut approach [36] and model the lung boundary detection with an objective function. To formulate the objective function, we define three require- ments a lung region has to satisfy: 1) the lung region should be consistent with typical CXR intensities expected in a lungregion,2)neighboring pixels should have consistent labels, and 3)the lung region needs be similar to the lung model we computed.

B. Features

To describe normal and abnormal patterns in the segmented lung field, we experimented with two different feature sets 1) Object Detection Inspired Features—Set A: As our first set, we use features that we have successfully applied to mi- cross copy images of cells for which we classified the cell cycle phase based on appearance patterns[38],[39]. The first set is a combination of shape, edge, and texture de- scriptors [6]. For each descriptor, we compute a histogram that shows the distribution of the different descriptor values across the lung field. Each histogram bin is a feature ,and all features of all descriptors put together form a feature vector that we input to our classifier. In particular ,we use the following shape and texture descriptors [38], [39]. • Intensity histograms (IH).

- Gradient magnitude histograms (GM).
- Shape descriptor histograms (SD)
- Curvature descriptor histograms (CD)
- Histogram of oriented gradients (HOG) is a descriptor for gradient orientations weighted according to gradient mag- nitude[43].The image is divided into small connected regions, and for each region a histogram of gradient directions or edge orientations for the pixels within the region is computed. The combination of these histograms represents the descriptor. HOG has been successfully used in many detection systems [40], [43]–[46].

- Local binary patterns (LBP) is a texture descriptor that codes the intensity differences between neighboring pixels by a histogram of binary patterns[47],[48].

CBIR-Based Image Features—Set B: For our second feature set, Set B, we use a group of low-level features motivated by content-based image retrieval(CBIR)[54],[55].This feature collection includes intensity, edge, texture and shape moment features, which are typically used by CBIR systems. The en- tire feature vector has 594 dimensions, which is more than three times larger than the feature vector of Set A, and which allows us to evaluate the effect of high-dimensional feature spaces on classification accuracy. We extract most of the features, except for moments and shape features, based on the Lucene image retrieval library, LIRE [56]–[58]. In particular, Feature Set B contains the following features.

- Tamura texture descriptor:The Tamura descriptor is motivated by the human visual perception[59].The descriptor comprises a set of six features. We only use three of these features, which have the strongest correlation with human perception: contrast, directionality, and coarseness.
- CEDD and FCTH: CEDD (color and edge direction descriptor) [60] and FCTH (fuzzy color and texture his- togram) [61] incorporate color and texture information in One histogram. They differ in the way they capture texture information. • Hu moments: These moments are widely used in image analysis. They are invariant under image scaling, transla- tion,and rotation[62].We use the DISCOVIR system (dis- tributed content-based visual information retrieval) to ex- tract Hu moments [63].
- CLD and EHD edge direction features: CLD (color layout descriptor) and EHD (edge histogram descriptor) are MPEG-7 features [64]. CLD captures the spatial layout of the dominant colors on an image grid consisting of 8 8 blocks and is represented using DCT(discretecosine transform) coefficients. EHD represents the local edge distribution in the image, i.e., the relative frequency of occurrence of five types of edges (vertical, horizontal, 45 diagonal, 135 diagonal, and nondirectional) in the sub-images.
- Primitive length, edge frequency, and autocorrelation: These are well-known texture analysis methods, which use statistical rules to describe the spatial distribution and relation of gray values [65].
- Shape features:We use a collection of shape features pro- vided by the standard MATLAB implementation (region- props)[66],such asthe area or ellipticalshape featuresof local patterns.

Figure:-3

C. Classification

To detect abnormal CXRs with TB, we use a support vector machine (SVM), which classifies the computed feature vectors into either normal or abnormal. An SVM in its original form is a supervised nonprobabilistic classifier that generates hyper- plane to separate samples from two different classes in a space with possibly infinite dimension [67], [68]. The unique char- acteristic of an SVM is that it does so by computing the hy- perplane with the largest margin; i.e., the hyperplane with the largest distance to the nearest training data point of any class. Ideally,the feature vectors of abnormal CXRs will have appositive distance to the separatinGhyperplane, and feature vectors of normal CXRs will have an egative distance.The larger the dis- tance the more confident we are in the class label.We therefore use these distances as confidence values to compute the ROC curves in Section

III. RESULTS AND DISCUSSION

This section presents a practical evaluation of our work .We show lung segmentation example and we evaluate our features both in combination and individually.We also compare the performance of our proposed TB detection system with the perfor- mance of systems reported in the literature, including the performance of human experts.

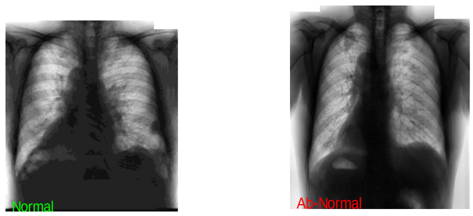

Figure 4. a)TB Negative b)TB Positive

IV. CONCLUSION

Tuberculosis is one of the major health problem in many parts of the world. We presents our automated approach for detecting tuberculosis using chest radiographs. At first we extract the lung region using a graph cut segmentation method. From this extracted lung region, we compute a set of texture and shape features, which enable the X-rays to be classified as normal or abnormal using a binary classifier.

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