Tuberculosis Disease Prediction Using Chest Radiographs

Prof. Dr. Thispenswamy K., Nisha M.
Visvesvaraya Technological University, Computer Science and Engineering Department, Department of PG studies, VTU RC, Mysuru-570029.

Abstract: Tuberculosis is a major health threat in various regions of the world. Opportunistic infection in immune compromised HIV/AIDS patients and multi-drug resistant bacterial strains have exacerbated the problem, while diagnosing tuberculosis still remains a challenge. When left undiagnosed and thus untreated, mortality rates of patients with tuberculosis will be high. Standard detection still rely on methods developed in the last century. They are slow and mostly unreliable. In an effort to reduce the burden of the disease, this paper presents a automated approach for detecting tuberculosis in conventional chest radiographs. We first should extract the lung region using a graph cut segmentation method. For this lung region, we compute a set of texture and shape features, which will enable the X-rays to be classified as normal or abnormal using a binary classifier. We measure the performance of the system on two datasets: a set collected by the tuberculosis control program of our local county’s health department in the United States, and a set collected by Shenzhen Hospital, China.

Keywords: Image processing, Lung, Segmentation, Tuberculosis, X-ray Imaging

I. INTRODUCTION

TUBERCULOSIS (TB): is second leading cause of death from an infectious disease worldwide, after HIV, with a mortality rate of over 1.2 million people in 2010. With about one-third of the world's population having latent TB, and an estimated nine million new cases occurring each year, TB is a major world global health problem. TB is an infectious disease caused because the bacillus Mycobacterium tuberculosis, which typically affects the lungs. It spreads through the air when people with TB cough, sneeze, or otherwise expel infectious bacteria. TB is most prevalent in sub-Saharan Africa and Southeast Asia, where because of widespread poverty and malnutrition reduce resistance to the disease. And opportunistic infections in immunocompromised HIV/AIDS patients have exacerbated the problem. The increasing appearance of multidrug resistant TB had further created an urgent need for a cost effective screening technology to monitor progress during treatment.

Several antibiotics are there for treating TB. While mortality rates will be high when left untreated, treatment with antibiotics greatly improves the chances of survival. In clinical trials, cure rates over 90% had been documented. Unfortunately, diagnosing TB is still a major challenging problem. The definitive tests for TB is the identification of Mycobacterium tuberculosis in a clinical sputum or pus sample, which is the current gold standard. However, it may take several months to identify this slow-growing organisms in the laboratory. Another technique is sputum smear microscopy, in which bacteria in that sputum samples are observed under a microscope. This technique developed more than 100 years ago. In addition, many skin tests based on immune response are available for determining whether an individual has contracted TB. However, skin test are not always reliable. The new developments for detection are molecular diagnostic tests that are fast and accurate, and that are highly sensitive and specific. However, further financial support is required for this tests to become commonplace.

In this paper, we present an automated approach for detecting TB manifestations in chest X-rays (CXR), based on lung segmentation and lung disease classification. An automated approach to X-ray reading allows the mass screening of large populations that could not be managed manually. A post anterior radiograph (X-ray) of a patient’s chest is a mandatory part of every evaluation for TB. The chest radiograph include all thoracic anatomy and provides a high yield, given the low cost and single source. So, a reliable screening system for TB detection using radiographs would be a critical step towards more powerful TB diagnostics. HIV and TB like co-infections are very common due to the weakened immune system. It is therefore very important to detect patients with TB infections, not only to cure the TB infection itself but also to avoid drug incompatibilities. At risk individuals identified by our system are then referred to a major hospital for treatment. In this paper, we explain how we discriminate between normal and abnormal CXRs with manifestations of TB, using image processing techniques.
II. METHOD

A. Lung Segmentation

We can model lung segmentation as an optimization problem that takes properties of lung boundaries, regions, and shapes into account. In general, segmentations in medical images has to cope with poor contrast, acquisition noise due to hardware constraints, and anatomical shape variation. Lung segmentations is no exception in this regard. We therefore can incorporate a lung model that represents the average lung shape of selected training masks. And select these masks according to their shape similarity as follows. First linearly align all training masks to a given input CXR. Then, compute the vertical and horizontal intensity projections of the histogram equalized images. To measure the similarities between projections of the input CXR and the training CXRs, we use the Bhattacharyya coefficient.

B. Feature Computation

We can evaluate the performance of Feature Set A on the MC datasets. For each CXR in the MC datasets, we compute the descriptors in Feature Set A and concatenate them into a single feature vector. We can then apply a leave-one-out evaluation scheme, using the SVM-classifier described in Section IV-C. According to the leave-one-out schemes, we can classify each feature vector (CXR) in the MC dataset with a classifier trained on the remaining feature vectors (CXRs) of the MC dataset. We can thus train as many classifiers as there are CXRs in the MC datasets(138 altogether). To get a better understanding of the performance of individual descriptors and descriptor groups, we perform leave-one-out evaluation for all possible descriptor subsets. The following features are finding out based on the segmented lung image.

- Intensity histogram (IH)
- Gradient magnitude histogram (GM)
- Shape descriptor histogram (SD)
- Curvature descriptor histogram (CD)
- Histogram of oriented gradients (HOG)
- Local binary patterns (LBP)

C. Classification & Decision Support

We are classifying the segmented result with pre trained datasets. We can compute a set of shape, edge, and texture features as input to a binary classifier, which then classifies the given input image into either normal or abnormal. So finally we can produce the result as either normal x-ray or abnormal using this SVM classifier result.

CONCLUSION

We had developed an automated system that screens CXRs for manifestations of TB. When given a CXR as input, our system will first segments the lung region using an optimization method based on graph cut. This method is combining intensity information with personalized lung atlas models derived from the training set. We can compute a set of shape, edge, and texture features as input to a binary classifier, which then classifies the given input image into either normal or abnormal. In this paper, we are comparing two different established feature sets: one set typically used for object recognition and the other used in image retrieval applications. We can also experiment with different classifier architectures. Both of the feature sets and most of the classifier architectures we tested, provide a similar performance. To improve the performance further, we can try to improve the lung segmentation, which provides average performance compared to other systems in the literature. One approach would be to find optimal weights for the terms in the graph cut energy function. These comparison results had encouraged us to test our system in the field under realistic conditions.

REFERENCES


