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AN EFFICIENT VISUALIZATION AND SEGMENTATION OF LUNG CT SCAN IMAGES FOR EARLY DIAGNOSIS OF CANCER

Preeti Aggarwal, H.K. Sardana, Renu Vig
pree_agg2002@yahoo.com

Abstract: Cancer is one of the most serious health problems in the world. Lung Computer-Aided Diagnosis (CAD) is a potential method to accomplish a range of quantitative tasks such as early cancer and disease detection, analysis of disease progression. For identifying the lung diseases, computed tomography (CT) scan of the thorax is widely applied in diagnose. DICOM [1] (Digital Imaging and Communications in Medicine) has become a standard for medical imaging. Its purpose is to standardize digital medical imaging and data for easy access and sharing. There are many commercial viewers that support DICOM image format and can read metadata, but image displaying is not always optimal. One of the problems with these DICOM viewers occurs when only a small portion of amplitudes is of interest to display. In this paper a recent developed DICOM viewer YaDiV [2] has been evaluated for identification of various lung tissues as well as for efficient visualization of lung images. Also MATLAB based tool MATITK [3] has also been evaluated for segmentation. This paper presents an interface for fully automatic method of visualizing and identifying the lungs in three-dimensional (3-D) pulmonary X-ray CT images. Various lung data sets from NCI (National Cancer Institute) of NBIA (National Biomedical Imaging Archive) have been tested. This paper reviews and suggest different methods that can be used for efficient visualization as well as automatically extracting the organ regions from abdominal CT (Computerized tomography) data especially from lung that can be further used in various medical diagnosis applications like CBMIR (Content-based medical image retrieval).

Keywords: CAD, DICOM, CBMIR, MATITK, YaDiv, NCI, NBIA

1. INTRODUCTION

Interpretation of medical images is often difficult and time consuming, even for experienced physicians. The aid of image analysis and machine learning can make this process easier. The medical service has been enriched with a lot of new techniques for diagnostic imaging during the last decades. As digital technologies are incorporated in every aspect of our lives, they are also the key part of medical diagnosis. DICOM standard was developed to make sharing of medical information safe and above all standardized. DICOM images can be viewed by various available DICOM viewers. Visual information retrieval is an emerging domain in the medical field as it has been in computer vision for more than ten years. It has the potential to help better managing the rising amount of visual medical data currently produced. One of the proven application fields for CBMIR as diagnostic aid is the retrieval of lung CTs. The diagnostics of these images depend strongly on the texture of lung tissue and automatic analysis can be a valuable help. The preprocessing step of most Computer-Aided Diagnosis (CAD) systems for identifying the lung diseases is lung segmentation.

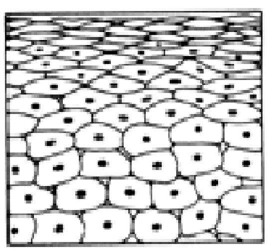
Segmentation of abdominal organs presents many challenges. In the Computer-Aided Detection (CAD) of lung nodules in x-ray computed tomography (CT) scans of the thorax, lung segmentation is the preliminary step. This paper suggests that a fast, fully automated lung segmentation method for application in X-ray computed tomography can enhance the diagnose process. Conventional methods of lung segmentation rely on large gray value contrast between lung fields and surrounding tissues. These methods fail on scans with lungs that contain dense pathologies, and such scans occur frequently in clinical practice.

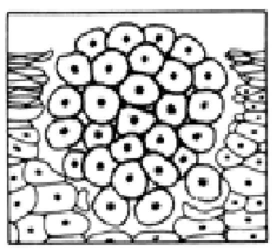
Recent advances in medical informatics enabled access to most of the radiological exams to all clinicians through the electronic health record (EHR) and the picture archival and communication system (PACS). This change of the medical workflow calls upon computer expert systems able to bring the right information to the right people at the right time. Most of the proposed systems aim at categorizing lung tissue to provide a second opinion to radiologists. This provides a quick and exhaustive scan of the large number of images and can draw the radiologist's attention on diagnostically useful parts of the images.

In this paper it is shown that the automated lung classification in CT data is complementary to case–based retrieval, both from the user's viewpoint and also on the algorithmic side. Then, based on the volumes of the segmented tissues and a set of selected clinical parameters, similar cases can be retrieved from a medical database.

2. LUNG CANCER

Cancer is a group of diseases characterized by an abnormal and unregulated growth of cells. Tissue with abnormal cell growth is called a tumor and can be malignant or benign, which is the same as cancerous or non-cancerous as shown in Fig 1. The main differences are that a benign tumor grows slower, will not spread and will usually not come back if it is surgically removed. Lung cancer is, in competition with prostate and breast cancer, the most common type of cancer and the leading cause of death. Lung cancer is a very deadly disease and has an inclination to spread to other parts of the body, e.g. the brain, liver, bone and bone marrow. In most cases this occurs before it is discovered. Usually, lung cancer happens after the age of 50. There are two major groups of lung cancer, Small Cell Lung Cancer (SCLC) and Non-Small Cell Lung Cancer (NSCLC), which together cover more than 90% of all cases. The methods for diagnosing lung cancer include CT scan (Computed Tomography), PET scan (Positron Emission Tomography), MRI (Magnetic Resonance Imaging), bronchoscopy (examination of the airways with fiber optics) and biopsy (examination of lung tissue sample).





Normal cells Cells forming a tumor

Fig: 1 Normal and Benign cells

The staging of lung cancer is an important step for deciding the right treatment. An international staging system (TNM classification) is often used, based on three characteristics.

- Growth of the primary tumor
- Extent of lymph node involvement
- Metastases in distant part of the body

Identification of lung cancer stages by analyzing the patient record with CAD systems can fasten the process of treatment. This paper suggests some of the automatic methods and DICOM viewers which can enhance the overall diagnosis of lung cancer.

2.1 Computed Tomography (CT)

Computed Tomography, also known as computed axial tomography, or CAT scan is a medical technology that uses X rays and computers to produce three-dimensional images of the human body. Unlike traditional X rays, which highlight dense body parts, such as bones, CT provides detailed views of the body's soft tissues, including blood vessels, muscle tissue, and organs, such as the lungs. While conventional X rays provide flat two-dimensional images, CT images depict a cross-section of the body. Fig. 2 shows a typical CT scan image.

Fig: 2 Typical CT scan image of Lung

The CT scanner contains an X-ray source, which emits beams of X rays; an X-ray detector, which monitors the number of X rays that strike various parts of its surface; and a computer. The resulting data are sent to the computer, which interprets the information and translates it into images that appear as cross-sections on a television monitor. This series of slices is then analyzed to understand the three-dimensional structure of the body.

3. SEGMENTATION OF THE LUNG REGION

In medical imaging, segmentation is important for feature extraction, image measurements, and image display. In some applications it may be useful to classify image pixels into anatomical regions, such as bones, muscles, and blood vessels, while in others into pathological regions, such as cancer, tissue deformities and multiple sclerosis lesions. The purpose of the segmentation of the lung region in the CT image is to achieve a better orientation in the image. A lot of articles can be found regarding segmentation of the lung region in CT images. Hu et al. [4] describe a method of global thresholding for that purpose. Pohle and Toennies [5] suggest adaptive region growing for segmentation of medical images. In this paper both region growing and thresholding are discussed using automatic tools. Segmentation of pulmonary X-ray computed tomography (CT) images as one shown in Fig 3 is a precursor to most pulmonary image analysis applications [6].

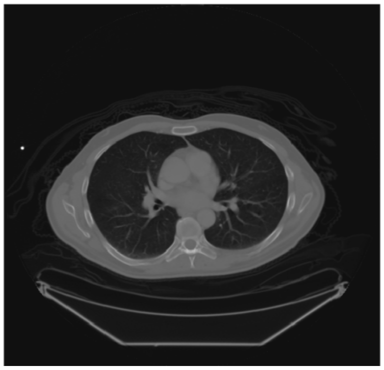


Fig 3: The lung region which is to segment the lung seen as the dark region in the body. The surrounding tissue appears with a higher intensity.

Most of segmentation methods are based on morphological operations as [7]. But the results as seen are not so efficient to be judged by physicians. Watershed algorithm provides good results in case of lung segmentation especially for high volume dataset as [8] but can lead to over segmentation sometimes. In this paper there is no need to find the optimal threshold to separates the left and right lung.

4. SEGMENTATION USING YaDiV

Segmentation of the lung volumes is a required preliminary step to lung tissue categorization. Since the geometries and shapes of the lungs are subject to large variations among the cases, semi–automatic segmentation based on region growing and mathematical morphology is used. The range and region growing routine contained in YaDiv is used. The resulting binary mask *Mlung* describes the global lung regions well but contains many holes where the region growing algorithm was stopped by denser regions. To fill these holes, a closing operation is applied to *Mlung* using a spherical structuring element.

Then, based on the volumes of the segmented tissues and a set of selected clinical parameters, similar cases are retrieved from a multimedia database of ILD cases as shown in Fig4 (a) and (b).

5. SEGMENTATION USING MATITK

ITK is an open source medical imaging processing library written in C++. While MATLAB also has many medical imaging algorithms, it is nice to be able to make use of the algorithms available in ITK. Precisely for this purpose, MATITK is written, allowing users to access certain ITK algorithms in Matlab. With the help of MATITK, biomedical image computing researchers familiar with MATLAB can harness the power of ITK algorithms while avoiding learning C++ and dealing with low-level programming issues.

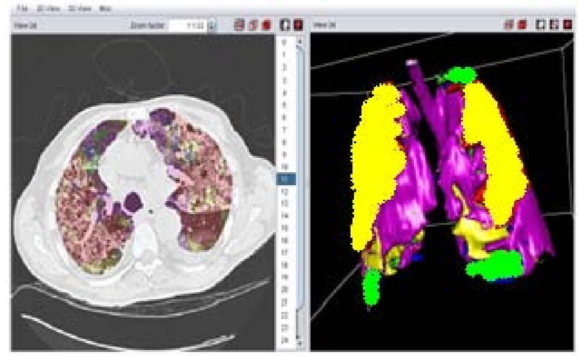


Fig: 4 (a) Automated region growing segmentation of the lung tissue patterns of a patient affected with pulmonary fibrosis. The 3D segmented regions are displayed to the clinician using YaDiV.

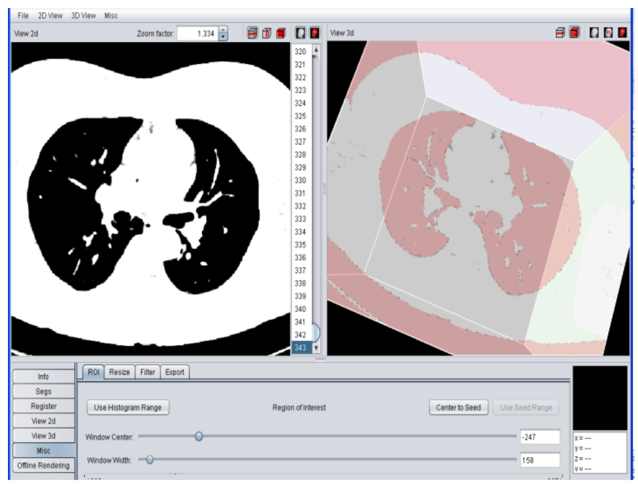
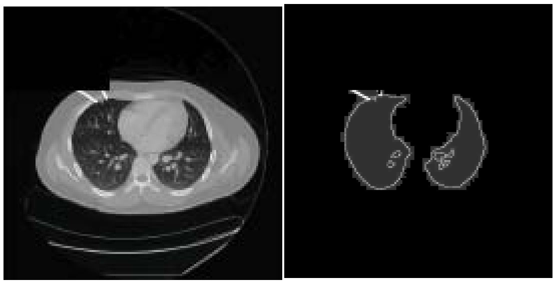
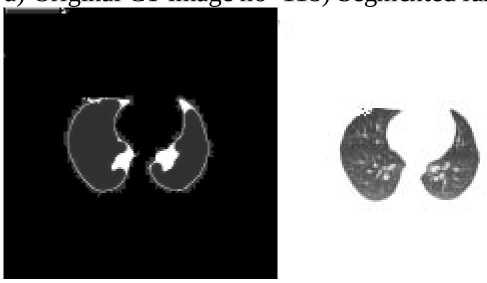


Fig: 4 (b) Automated thresholding of the lung tissue patterns using YaDiv.

We have implemented the volumetric segmentation by using the MATLAB environment. We obtained datasets from NCI of NBIA, USA. In this work, we have studied the performance of different segmentation techniques that are available in MATITK and used in CAD (Computer Aided Diagnosis) systems using thorax CT Scans. Figure 5 a)-d) gives the result of watershed segmentation of slice no=10 using MATITK. Though MATITK can be used only on 3D images, but in Fig 5 only slice no 10 is shown with its segmentation. Using VIEW3D function we can see the segmentation of all the slices. It is evident through observation that the proposed system produces much smoother results than the schemes that have been used earlier. There is also no loss of lung nodules in this method. This is a good advancement for next stage of CAD system employed in lungs nodule detection and classification system as MATITK is open source and accordingly can be modified.



a) Original CT image no=11b) Segmented lung borders



c)Smoothed lung borders d) Lung regions

Fig: 5 Watershed Segmentation of lung CT using MATITK for slice=10.

MATITK provides various other segmentation methods also like Levelset, Gardient Vector Flow and many more and all present comparable results. There is no mechanism available to see all the 3d slices in MATITK. View3d function has been used for the same as shown in Fig 6.

6. CONCLUSION AND FUTURE WORK

In the context of medical image analysis, providing quick and precious information to the clinician is not limited to automatic recognition of abnormal tissue and/or structure. Conventional methods of lung segmentation that rely on large gray value contrasts between lung fields and surrounding tissues fail on dense pathologies. The proposed study shows that automatic segmentation eliminates the tasks of finding an optimal threshold and separating the attached left and right lungs, which are two common practices in most lung segmentation methods and require a significant amount of time. We have applied segmentation tools on several pulmonary CT images. Experiments results show that the proposed method can improve the speed, robustness and accuracy of diagnosis as physician can judge a particular case in right time and with full information of pathology. Content–based medical image retrieval (CBIR) aims at finding objectively visually similar images in large standardized image collections such as PACS [9]. The notion of similarity is usually established from a set of visual features describing the content of the images.

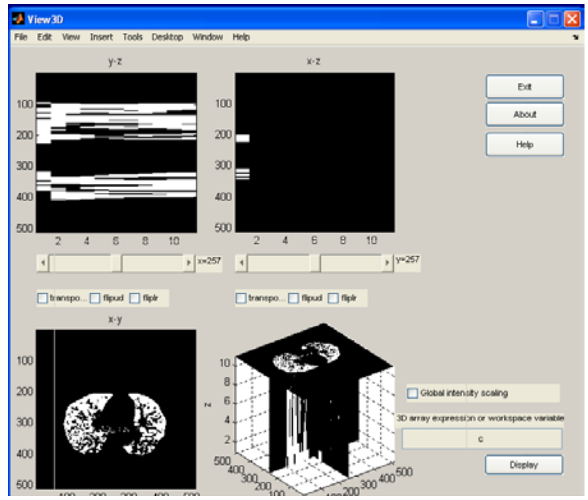


Fig: 6 3D view of MATITK result for ten slices.

Few CBIR systems have been evaluated in clinical practice but some of them showed that they can be accepted by the clinicians as a useful tool [10] [11]. The use of a CBIR system clearly increased the number of correct diagnoses. A possible extension to CBIR is to carry out case–based retrieval. In this paper we show that automated lung classification in CT data is complementary to case–based retrieval, both from the user's viewpoint and also on the algorithmic side. Based on the volumes of the segmented tissues and a set of selected clinical parameters, similar cases can be retrieved from a database of lungs.

Future work will include incorporation of segmentation results in CBMIR system and modification of similar segmentation tools to develop a more consistent definition of the lung contours.

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