

Lung CT Analysis and Retrieval as a Diagnostic Aid

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Abstract

Image retrieval is currently a very active research field due to the large amount of visual data being produced in most modern hospitals. Most often, the goal is to aid the diagnostic process. Unfortunately, only very few medical image retrieval systems are currently used in clinical routine. One of the application domains for image retrieval is the analysis and retrieval of lung CTs. A first user study in the United States shows that these systems allow improving the diagnostic quality.

This article describes the approach to an aid for lung CT diagnostics. The analysis incorporates several steps and the goal is to automate the process as much as possible for easy integration into diagnostics. Thus, several automatic steps are proposed from a selection of the most characteristic slices, to an automatic segmentation of the lung tissue and a classification on the segmented area into diagnostic classes. Feedback to the MD will be given in the form of marked regions in the images that appear to be different from the norm of healthy tissue. We are currently working on a small set of training images with marked and annotated regions but a larger set of images for the evaluation of our algorithm is in work. For this reason, the article does currently not contain much quantitative evaluation.

For several tasks we use existing open source software such as Weka and itk. This allows an easy reproduction of the search results.

Keywords

Content-based image retrieval; High-resolution lung CT; Diagnostic aid; Classification

1. Introduction

Content-based image retrieval (CBIR) has been an extremely active domain in the fields of computer vision and images processing for more than 20 years [1]. In the medical field, this domain is also starting to become active, as an increasing amount of visual data is being produced in hospitals and made available in digital form [2,3]. General medical image retrieval in PACS-like databases is in this context very different from specialized retrieval in a very focused domain. In the medical field, the main goal is the use as a diagnostic aid and for access to medical teaching files. Current medical use is on the retrieval of tumour shapes [4] as well as on histological images [5], and in other more specific fields (dermatology, pathology). A domain where textures play a very important role in the diagnostic process is the analysis of high-resolution lung CTs [6]. In [7], a user test shows that an image retrieval system can improve the diagnostic quality significantly, especially for less experienced radiologists. Still, most of these systems either rely on much

complicated interaction with the user, which makes them hard to introduce into a clinical context, or they are too broad to be used as a diagnostic aid in a specialized domain.

This article details a solution for helping with the interpretation of high-resolution lung CTs, which is a domain where diagnostics are fairly hard especially for non-chest specialists. The diagnostic result strongly depends on the overall texture of the lung tissue, so automatic analysis seems possible. Our project limits the direct interaction with the user and performs as many tasks as possible in an automatic fashion, so a minimum of time is needed to operate the system and get responses for feedback.

2. Steps for a diagnostic aid on lung CT interpretation

This section describes the various steps that are necessary for a complete diagnostic aid system for lung diagnostics and their degree of automation.

2.1 Generation of a test database and acquisition of representative samples

The first and most important part is the creation of a database of thin-section lung CTs. This database needs to include healthy cases as well as pathologic cases. Characteristic regions need to be marked by a radiologist to allow us learning the characteristics of a disease with respect to healthy tissue. Currently, we only have a fairly small database of 10 series containing around 50-60 images per series. 112 regions are marked in the images by a radiologist to represent the following classes of tissue for the further classification step:

- Healthy tissue (52 sample regions);
- Emphysema (21);
- Micro nodules (19);
- Macro nodules (3);
- Interstitial syndrome (5);
- Bronchiectasis (5);
- Ground glass attenuation (1);
- Fibrosis (6).

It is important to note that prototypically healthy regions have to be annotated by the radiologist as well so that a classifier can get a good idea of healthy tissue. Other systems in the literature often use only pathologic classes for the classification but the first step in the diagnostic process is to find out whether the tissue is abnormal or not. We are currently creating a larger database projected to contain at least 100 series of 50-60 images that will allow us a better representation of these classes. In Figure 1 you can see a screenshot of our tool for image annotation. It generates a simple XML file containing the regions of interests as a set of points (outline) and a label for each outline. These files are then fed into the system along with the images at the training step.

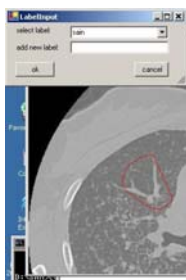


Figure 1 - A screenshot of our utility for the annotation of image regions.

2.2 Analysis of blocks of lung tissue

In Figure 3 you can see the partitioning of the lungs into smaller blocks (size 16x16 pixels in the image) for further detailed texture analysis. A block is taken into account if it is by more than 80% inside of an area marked by the expert or automatically segmented by the system. These lung blocks are stored as references together with the original image. This avoids artefacts of the filters that can occur due to missing border pixels as we can take into account the entire block environment.

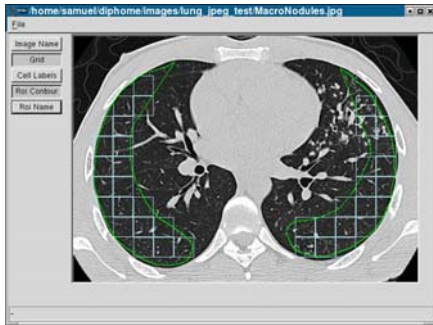


Figure 2 - The partitioning of the lung tissue into small blocks for classification and feature extraction.

The framework is designed to facilitate finding the optimal block size for analysis and classification. From each block we extract and store the following visual features:

- average grey level and standard deviation of the grey levels in the block;
- grey level histogram using 32 grey levels;
- features derived from co-occurrence matrices (four directions, two distances);
- responses of Gabor filters in four directions and at three scales;
- Tamura texture features.

A small number of grey levels in the histogram is sufficient for this kind of classification as has been shown in image retrieval applications, where they often perform better.

2.3 Training

Then, the features together with the region label become a sample in a classification problem [8]. Based on the acquired training data, the weights of the features for classification are calculated. To develop an optimal classification strategy, several classifiers are tested and their performance is evaluated on the currently available data. An open source utility allowing us to compare several classifiers is Weka1, which has also the advantage of being able to connect directly to the feature database (MySQL). We perform cross-validation using various classifiers to get an idea of how discriminant our features are. While Weka is an external tool, we have also included libsvm [9] into, an easy-to-use Support Vector Machine (SVM) classifier. We also plan to integrate torch [10] to discover connections between the various features and the classes of our system. Torch is a fast data-mining tool. In the final version, only the best classifier will be integrated but as for the testing phase we need several to find out the optimal solution.

¹ <http://www.cs.waikato.ac.nz/~ml/weka/>

2.4 Lung segmentation as data preparation for classification

When submitting a new image for analysis and as diagnostic aid, we concentrate on the part of the image that we are interested in, the lung tissue. While manual region selection of the image is still possible (using the tool described in 2.1 – only without a label), automatic segmentation is desired to minimize user interaction in the final diagnostic aid step. To this aim we use an algorithm described in [11] to find an optimal threshold for lung tissue segmentation, which works on DICOM images having a full 12-bit resolution (or more) as well as on the jpeg images from our radiology teaching file. As basis for the segmentation we use itk2. In Figure 2, a lung CT, its segmented version and a view of the outline discovered by the software can be seen.



Figure 3 - A lung CT and the tissue of the two lung halves segmented.

For the final texture classification we do not plan to take into account the entire lung tissue but rather the diagnostically interesting part, which is the outside part of the lung with less vessels that can change the texture strongly and introduce noise for the classification. The inside part with the vessels is automatically removed from further analysis.

2.5 Classification of lung blocks

For the classification step of a new lung image, a partitioning of the image into blocks is performed. Then, the features of each block in the (manually or automatically) marked regions corresponding to lung tissue are extracted. The samples are created by the block's features and have no label attached to them, yet. The integrated classifier (currently libsvm) now performs the classification and attaches a label to each block of the lung tissue based on previous learning data. We use the parameters (kernel type, gamma factor, stop criterion, etc.), which performed best at cross-validation (see step 2.3).

2.6 Slice selection from a CT lung volume

This step is currently not implemented and will likely be the last part to be done, as its development is not crucial. Goal is basically to perform the task of the medical doctor to find the slice(s) that best characterize a disease. Once a large database of labelled tissue samples is ready, it will be fairly easy to process the entire volume slice by slice and select those slices with the largest part of the tissue being marked as non-healthy for further inspection. To select several slices, we can give the system a combination of maximum number of slices and a threshold of unhealthy tissue. Selected slices can also be marked in the volume data by highlighting the volume part that contains the most pathologic blocks.

2.7 Result presentation to the medical doctor

The goal of the results presentation is not to make the decision for the radiologist but rather to highlight parts of the lung tissue that were classified as pathologic. A highlighting of the

² <http://www.itk.org/>

background in coloured shades is planned instead of the grey scales in the parts of the images that were classified as pathologic. Each colour presents one of the classes that we are detecting in the classification step. Currently, we only present the results in a 2D view and one image at a time, meaning that the slices with the largest pathogenic parts are taken and displayed. It can also be imagined to present the results in 3D, where the entire pathogenic area over several slices can be highlighted within the volume. Retrieval of similar cases from the reference database will enable the MD to verify his diagnosis. This is easily possible through an image retrieval application using features from the currently active case and comparing them those stored and labelled for past cases in the database.

3. Results

We currently have a framework in place that allows us to acquire knowledge from the radiologists in the form of marked regions and annotations within images. Our database is still small but a larger number of cases are planned. The acquired data with labels is used to train our classifiers. This means that with a growing number of judged cases from the radiologist, the system is expected to perform better. The lung segmentation phase works reliably and stable as well as the partitioning of the lung tissue into small blocks and the feature extraction. All these steps work in a completely automated fashion. The medical doctor can simply feed a volume of lung CT images into the system. The images are segmented and portioned into smaller blocks automatically. These blocks are then classified and unhealthy tissue is marked in a different colour in the images so the medical doctor has a feedback for regions that he needs to inspect further.

Current results when using the 112 regions and block sizes of 32x32 pixels (corresponding to ~1000 blocks) are 84%, when using cross validation between healthy and non-healthy tissue using SVM classifiers. Nearest neighbours lead to roughly 74% correctly classified. When classifying into the 8 available classes, the nearest neighbour classifier reaches 85.5% correctly classified. Problems occur especially for classes with a very small number of representative blocks. Another problem is that the radiologist marked regions with a margin, leading to several blocks that are actually healthy tissue but close to a pathologic region and labelled as pathologic. This explains part of the errors.

We currently run the framework on a simply desktop computer with a Pentium IV processor with 2,8 GHz and 1 MB of RAM. On this computer, the segmentation takes around 5 seconds per slice and the subsequent cutting into blocks, feature extraction and classification another 2 seconds. Thus the analysis of a single slice is almost interactive whereas an entire volume takes a few minutes before results can be displayed. We still need to experiment with the classification part and also with the features that we extract from the images to obtain an optimal feature set for classification. The current framework is by now a research tool, designed to ease experimentation of features, classifiers, parameters, etc. The final system will probably discard a lot of these options, be much simpler and focus more on the user interface and the results display to the user.

4. Conclusions

This article presents a framework to aid the diagnostic process for lung diseases using lung CTs. The domain has shown its potential in studies and our current cross validations leads to good results. The steps of the diagnostic process are performed in an automatic way. Abnormalities are highlighted in the original images by a change of colour. Once we have a larger database accessible, more quantitative evaluation is needed to evaluate the algorithm quality and show the usefulness of the application in a clinical environment. Many parameters need to be optimized, from the feature extraction phase to the training step and

the classifiers employed. We also need to think about optimal block size of lung tissue and whether we should rather take overlapping blocks to avoid misclassifying small parts of the texture and reduce false positives.

Lung CT analysis has shown its usefulness in practice by improving the diagnostic quality especially of non-experts. Now it is important to create large reference databases and evaluate the many visual descriptors and techniques available to create a robust framework for routine use that needs to have as many steps of the process in an automatic way as possible. Several questions still need to be solved before routine use, for example the handling of other available data on the patients. The age can play an important role for the texture of the lung tissue. For the classification we need to integrate all these data into the framework. The possibility to compare the images with annotated cases from the reference databases is expected to further increase acceptance of the technology because the system does not make a decision by itself but rather points out interesting areas of the lung tissue and gives evidence on these areas by supplying similar past cases.

5. References

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