Abstract

We previously proposed a recognition method of lung nodules based on experimentally selected feature values (such as contrast, circularities, etc.) of pathological candidate regions detected by our Quoit filter. In this paper, we propose a new recognition method of lung nodule using each CT value itself in ROI (region of interest) area as a feature value. In the clustering stage, first, the pathological candidate regions are classified into some clusters using Principal Component (PC) theories. A set of CT values in each ROI is regarded as a feature vector, and then eigen vectors and eigen values are calculated for each cluster by applying Principal Component Analysis (PCA). The eigen vectors (we call them Eigen Images) corresponding to the 10 largest eigen values, are utilized as base vectors for subspaces of the clusters in the feature space. In the discrimination stage, correlations are measured between the testing feature vector and the subspace which is spanned by the Eigen Images. If the correlation with the abnormal subspace is large, the pathological candidate region is determined to be abnormal. Otherwise, it is determined to be normal. By applying our new method, good results have been acquired.

1. Introduction

In Japan, mass screening for lung cancer is widely performed by simple chest X-ray films with spectrum cytology. At present, however, the detection ability of the observation by the simple X-ray films is not sufficient yet for early detection of lung cancer. It is known that the false negative ratio of the observation is considerably high. From such a viewpoint, we proposed a lung cancer screening system by CT for the mass screening [1]. By using the new screening system, the false negative ratio can be decreased. But it had one problem that the number of generated images was increased to about 30 slices per patient. In order to make the system more practical, we need to develop a Computer-Aided Diagnosis (CAD) system which detects pathological candidate regions in X-ray CT images automatically, and informs the doctor of the shadow positions in the images as a second opinion.

First, to detect cancer shadows, we proposed an image filter called Quoit filter which is a type of mathematical morphology filter [2,3]. This filter can automatically detect abnormal shadows with the sensitivity over 95%, but it detects many false positives, which are mainly related to blood vessel shadows.

In order to reduce such false positives, we developed a discrimination method of cancer shadows based on feature values obtained from pathological candidate regions [4] detected by our Quoit filter. In this method, we experimentally choose about 15 types of the feature values such as average CT values, modified circularity, and X-ray attenuation. However, it could not be guaranteed that they were the optimal combination for recognizing the pathological candidate regions.

In this paper, we propose a new recognition method using each CT value itself in a ROI area as a feature value. By applying PCA to these CT values, essential information can be extracted from CT images, and the accuracy of our CAD system is increased drastically.

Fig.1 shows the outline of our new method. This method is composed of two stages; clustering stage and discrimination stage. In the clustering stage, normal shadows are classified into 50 - 200 clusters, and abnormal cluster are classified into 2 - 3 clusters based on PC theories. The difference of the cluster number between normal and abnormal shadows comes from the difference of the ROI number between normal and abnormal shadows.

In the discrimination stage, one normal cluster and one abnormal cluster are selected which correspond to an unknown input image (assuming as normal shadow for normal cluster, and an abnormal one for abnormal cluster). Final discrimination between two clusters is performed by a subspace method described later.

2. Clustering stage

2-1. Clustering

Fig.2 shows the clustering stage. First, the ROI regions are detected by our Quoit filter. A set of CT values in each ROI (N x N[pixel]) is regarded as a N^2-dimensional feature vector. In this paper, the ROI size is set as N=33[pixel].
The pathological candidate regions contain many kinds of shadows (if it is a normal organ group, it is big blood vessel, small blood vessel, pleurae and etc). So, the essential information cannot be extracted, if the subspace is calculated by using all the pathological candidate regions without any clustering operation.

We developed the automatic clustering method using PC theories to classify the pathological candidate regions(Fig.1). Normal shadows are classified into two sub-clusters according to Principal Component Score(PCS) calculated from their feature vector. After that, each sub-cluster is further classified into two sub-sub-clusters calculated from the feature vectors in the sub-cluster. Repeating this process, normal shadows are also classified into 2 - 3 clusters. The abnormal shadows are classified into 50 - 200 clusters. The abnormal shadows are classified into 2 - 3 clusters.

2-2. Calculation of the subspace

A set of the feature vector \( \mathbf{x} \) of each cluster \( \mathbf{c} \) is Eq.(1). And \( \mathbf{x} \) is \( N^2 \)-dimensional vector.

\[
\begin{align*}
\mathbf{e}_1^{a-1} &= (x_1^{a-1}, x_2^{a-1}, \cdots, x_{N-1}^{a-1}) \\
\vdots \\
\mathbf{e}_p^{a-1} &= (x_1^{a-1}, x_2^{a-1}, \cdots, x_{N-p}^{a-1}) \\
\mathbf{e}_1^{a-p} &= (x_1^{a-p}, x_2^{a-p}, \cdots, x_{N-p}^{a-p}) \\
\vdots \\
\mathbf{e}_q^{a-q} &= (x_1^{a-q}, x_2^{a-q}, \cdots, x_{N-q}^{a-q})
\end{align*}
\]

"p" is the number of the abnormal clusters, and "q" is the number of the normal clusters.

"n_i" (\( 1 \leq i \leq p \)) is the index of the i-th abnormal cluster, and "n_j" (\( 1 \leq j \leq p \)) is the index of the j-th normal cluster.

"l_i" is the number of the learning samples classified into the i-th abnormal cluster and "J_j" is the number of the learning samples classified into j-th cluster.

Thus, the autocorrelation matrix \( \mathbf{R} \) of each cluster is calculated as Eq.(2).

\[
\begin{align*}
\mathbf{R}^{a-1} &= (\mathbf{c}_1^{a-1})(\mathbf{c}_1^{a-1})^T \\
\vdots \\
\mathbf{R}^{a-p} &= (\mathbf{c}_p^{a-p})(\mathbf{c}_p^{a-p})^T \\
\mathbf{R}^{a-1} &= (\mathbf{c}_1^{a-1})(\mathbf{c}_1^{a-1})^T \\
\vdots \\
\mathbf{R}^{a-q} &= (\mathbf{c}_q^{a-q})(\mathbf{c}_q^{a-q})^T
\end{align*}
\]

Then, the eigen values (\( \lambda_1^{a-1}, \lambda_2^{a-1}, \lambda_3^{a-1}, \cdots, \lambda_{10}^{a-1} \)) and the eigenvectors (\( \mathbf{e}_1^{a-1}, \mathbf{e}_2^{a-1}, \mathbf{e}_3^{a-1}, \cdots, \mathbf{e}_q^{a-1} \)) (\( n = 1, \cdots, \kappa \)) are calculated from Eq.(3).

\[
\begin{align*}
\mathbf{R}_n^{a-1} \mathbf{e}_n &= \mathbf{R}_n^{a-1} \\
\vdots \\
\mathbf{R}_n^{a-p} \mathbf{e}_n &= \mathbf{R}_n^{a-p} \\
\mathbf{R}_n^{a-1} \mathbf{e}_n &= \mathbf{R}_n^{a-1} \\
\vdots \\
\mathbf{R}_n^{a-q} \mathbf{e}_n &= \mathbf{R}_n^{a-q}
\end{align*}
\]

In this paper, we use \( \kappa = 10 \) as the number of eigen values (See Fig.2, right column). The eigen vectors corresponding to these ten eigen values are selected.

And these eigen vectors are used as the base vectors, in order to span the subspaces \( L \) of each cluster. (as \( L_{a_1}, \cdots, L_{a_2}, L_{a_3}, \cdots, L_{a_5} \)) The eigenvectors which are base vectors for subspace have same dimension number with the feature vectors.

So, we can observe the eigen vector as a image by rearranging the eigen vector's elements. We call this image "Eigen Image". The Eigen Image expresses most important information of the feature vectors in a cluster.
3. Discrimination stage

Fig. 3 shows the discrimination stage. In the discrimination stage, one normal subspace $L_n$ and one abnormal subspace $L_a$ are selected which correspond to an unknown input image $Y$.

Then, correlation $\cos \theta^n$ between $Y$ and $L_n$, and $\cos \theta^a$ between $Y$ and $L_a$ are calculated. Eq.(4) shows the ratio of these $\cos \theta^n$ and $\cos \theta^a$.

$$\gamma = \frac{\cos \theta^n}{\cos \theta^a} \ldots (4)$$

Finally, if the result of Eq.(4) is larger than a certain threshold $\alpha$ ($\alpha$ is decided at the end so that the best result may be obtained), the testing vector is determined to be abnormal. Otherwise, it is determined to be normal.

4. Experimental results

Table.1 shows the experimental materials. We use actual CT images for the experiment from 3 facilities. The facilities are Hitachi Health Center(HHC), Osaka Medical Center(OMC) and Shinshu University(SU). One slice cross section has $512 \times 512$ [pixel], (the resolution of 0.625 [mm/pixel]) and slice thickness of 10[mm]. And the images have about 30 slices. And all samples have cancers which were diagnosed by medical doctor. SU has 2 kinds of samples. One is the samples found correctly by the doctor(Accepted), and the other is the samples which were missed by the doctor in the first examination and found later(Missed).

Fig.4 and Fig.5 show examples of abnormal Eigen Images, big nodule case in Fig.4 and small nodule case in Fig.5.Fig.6 and Fig.7 show examples of normal Eigen Images, big blood vessel case in Fig.6 and branching blood vessel case in Fig.7. In the figures, Eigen Images corresponding to first PC to tenth PC are displayed from upper left to lower right sequentially.
Fig.8-1 shows f-ROC curves of the experimental result. In this figure, X-axis is a number of false positives per slice and Y-axis is a true positive ratio. In case of HHC and OMC, learning samples are used as testing samples. But in case of SU, learning sample are “Accepted” ones, and testing samples are “Missed” ones.

Fig.8-2 shows another experimental result. In this case, all samples(HHC, OMC, SU) are equally divided to 2 groups. And one group is used for training and the other group is used for testing.

The results of experiments, the big difference occurred in the results between facilities(HHC, OMC, SU). One of the reasons is that the quality of CT image such as signal to noise ratio is different. The other reason is the difference of the doctor’s judgment standard.

### Table.1 Experimental Materials.

<table>
<thead>
<tr>
<th>Facilities</th>
<th>Number of samples</th>
<th>Number of cluster</th>
</tr>
</thead>
<tbody>
<tr>
<td>HHC</td>
<td>38</td>
<td>Nodule: 2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Normal: 45</td>
</tr>
<tr>
<td>OMC</td>
<td>46</td>
<td>Nodule: 2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Normal: 64</td>
</tr>
<tr>
<td>SU</td>
<td>Accepted: 73</td>
<td>Nodule: 2</td>
</tr>
<tr>
<td></td>
<td>Missed: 42</td>
<td>Normal: 101</td>
</tr>
</tbody>
</table>

4. Conclusion

We proposed a new method for pathological candidate regions in CT images using subspace method. By applying our new method to actual CT images, good results have been acquired.

References