Nodule detection in 3D chest CT images using 2nd order autocorrelation features

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Abstract—We have developed a new recognition approach using 2nd order autocorrelation and multi-regression analysis to detect a small (<7mm in diameter) lung nodules in chest 3D CT images. By combining our previous detection method of the template matching based on genetic algorithm, the detection performance was 94% true-positive rate at 2.05 false-positive marks per case using leave-one-out study.

I. INTRODUCTION

Chest CT images provide the most common information for chest diseases. Lung nodules are typical findings for lung cancer to be detected in clinical examination.

The purpose of this work is to develop a new image recognition method using 2nd order autocorrelation features in 3D space and apply it to detect lung nodules appeared on 3D chest CT images. The template matching technique using genetic algorithms (GATM), we have already developed [1], was also employed as a part of this detection approach. In this paper, we describe the new technique and estimate the whole detection rate employing 139 nodules in 35 clinical cases.

I. MATERIALS AND METHODS

Our detection approach includes the training and recognition phase. In the training phase, the nodule patterns were analyzed using our original approach of the 2nd order autocorrelation features in 3D space and the multi-regression analysis. The 2nd order autocorrelation features in 3D space

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as a feature vector calculated from the combination of voxel value in a 3x3x3 region. The number of combination patterns in the region was 235 excluding the same combination when the center of the region was parallel moves. The voxel values in a combination were multiplied each other, and the result was to be a one of the elements of

the feature

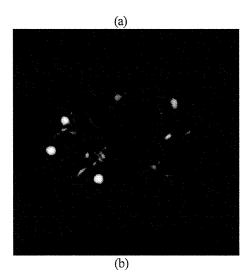


Fig. 1. Original image (a) and filtered image(b).

| | True positive rate | False positive marks per case |
|------------------------------------|-------------------------|-------------------------------|
| New method with 2nd OAFs (7-10mm) | 95% (55 / 58 nodules) | 1.1 (37 marks / 35 cases) |
| Previous method with GATM (10- mm) | 93% (75 / 81 nodules) | 1.0 (35 marks / 35 cases) |
| Combined method | 94% (130 / 139 nodules) | 2.05 (72 marks / 35 cases) |

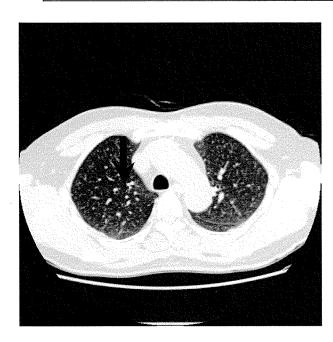


Fig. 2. Original image with 5mm nodule [black arrow] in diameter

For example, if the center of the region was given as fn(i,j,k), one of the elements of the feature vector was a multiplied result of three voxel as $f-1(i-1,j-1,k-1) \times f0(i,j,k) \times f+1(i+1,j+1,k+1)$. The number of the combination was upto 235 patterns when the f-1 and f-1 will be at any positions around the center pixel of f0.

The feature vector for a small region was defined with 235 elements summarizing the each 235 patterns in a 3D space moving the center voxel within a small region. Using the multi-regression analysis, the weighting factor for the 235 elements and one constant value were determined to indicate training values. The training value was defined as a likelihood of nodules. A nodular shadow gave a 3-D Gaussian distribution for the training output, on the other hands; a normal shadow gave a flat plane.

In recognition phase, the following steps were performed:

- 1. 3D matched filtering using 3D Fourier Transforms
- 2. Estimated image using the multi-regression analysis from 235 features
- 3. Calculation of mutual correlation between the training pattern and the estimated

image

- 4. Elimination of false-positives
- 5. Combination of detection results from GATM approach[1]
 - 6. Final detection results

The matched filter is a kind of band-pass filter emphsizing special frequency band, and Katsuragawa et al. [2] also proposed to employ to detect lung nodules employing the filter technique. In this work, the shape of nodules can be defined as a sphere shape with 3D Gaussian distribution, the frequency pattern was determined by 9 pixel nodules (5.4mm in diameter). Fig.1 shows an original image with a small nodule (upper right) and processed image with the band pass filter.

The estimated image was calculated from the results of the multi-regression analysis with 235 features. The features were extracted from the region with higher values on the image after matched filter.

The output of multi-regression will be a continuous value, so, the comparison between the training pattern for multi-regression and the output also emphasize the nodular shadows. The false-positives were eliminated by using the correlation value and the volume [mm3].

Our previous method based on genetic algorith template matching (GATM) [1] also applied to detect large nodules larger than 10 to 20mm in diameter. Logical OR technique are employed to combine two results.

II. RESULTS

We employ the leave-one-out method to estimate our

detection performance.

The detection approach using 235 features focuses on small nodules 7mm in diameter or less. The GATM approach was designed to detect the nodules from 7mm to 10mm in diameter. The larger nodules than 10mm in diameter was omitted in this work.

Thirty-five cases with 16824 images (resolution: 0.585 - 0.703mm, slice thickness: 0.62 - 0.63mm) were employed. A hundred thirty nine nodules were less than 10mm in diameter and were not along the chest walls. Fifty-eight nodules were less than 7mm in diameter, and 81 of nodules were larger than 7mm in diameter.

55 of 58 small nodules (=<7mm) and 75 of 81 large nodules (7 - 10mm) were detected correctly. The number of false positive in 35 cases in the two-detection approach was 37 marks and 35 marks, respectively.

By combining the two detection results taking logical OR operation, the final detection rate was 94% (130/139) true positive fraction with 2.05 (72/35) false positive marks per case. Figure 2 shows an example of a 5mm detected nodule in diameter.

III. CONCLUSION

We have developed a new recognition approach using 2nd order autocorrelation and multi-regression analysis to detect a small (<7mm in diameter) lung nodules in chest 3D CT images. By combining our previous detection method of the template matching based on genetic algorithm, the detection performance was 94% true-positive rate at 2.05 false-positive marks per case using leave-one-out study.

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