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Finding Corresponding Lung Nodules
in Sequential Chest CT Images for Follow-up Surveillance

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Abstract: It is important in human health care to surveil a patient's condition over the long term. We have developed a method to find corresponding nodules between previous and current CT images. To measure the curative effect of lung nodules quantitatively, it is necessary to find the corresponding nodules between images. These corresponding pairs and their accompanying statistics may be good indices for determining whether current medical treatment is effective. We employ relative distance for coarse matching and image correlation between volumes of interest for precise matching. Results show that this method can match correspondences to an accuracy of 97%. Because several features can be measured easily, such as the total number and volume of nodules, appearance of nodules, disappearance of nodules, it is expected that this method will be an effective diagnostic tool.

1 Introduction

It is important in human health care to surveil a patient's condition over the long term. CT imaging devices such as multi-detector row CT scanners are able to produce a huge number of high-resolution slice images for a patient; analyzing these slice images, however, is a heavy burden on medical doctors. To help ease this load we have developed a method to find corresponding nodules between previous and current CT images. To measure the curative effect of lung nodules quantitatively, it is necessary to find corresponding nodules between images. These corresponding pairs and their accompanying statistics may be good indices for determining whether current medical treatment is effective. To achieve this we have developed a computer-aided diagnosis algorithm to detect hundreds of small nodules from CT images and find corresponding pairs in order to evaluate the curative effect for comparative reading. Particularly, in the case of multiple metastatic lung nodules, it is necessary to analyze hundreds of nodules and evaluate curative effect, but this is an extremely difficult task for a doctor.

Several CAD systems have been developed to detect candidates for small lung nodules and to aid comparative reading by showing corresponding slices or nodules[1, 2, 3, 4, 5, 6]. In this work, we employ relative distance for coarse matching and image correlation between volumes of interest for precise matching in order to detect corresponding nodules. Our method includes the following features: extraction of lung area for reducing both false positives and computational time; detection of small nodules by using two types of shape features; coarse matching by using the relative position of each nodule in the lung area; and precise matching using local gray value features.

We applied the method to four chest CT images that were taken during successive examinations of the same patient over fourteen months. The proposed algorithm is presented in Section 2, and experimental results are shown in Section 3.

2 Method

In the proposed method, we assume that the entire lung region and lung nodules are extracted from each sequential CT image beforehand. To reduce the effect of lung deformation caused by a change in patient's condition, a nodule's position is represented as a relative coordinate appropriate to lung size. The whole procedure consists of two steps: (1) coarse matching using distance between relative position of nodules, and (2) precise matching using image correlation.

2.1 Coarse matching

2.1.1 Transformation of coordinates

In this step, the coordinates of a nodule center are transformed into coordinates represented by a relative position in the lung region. First, circumscribed quadrangles are set to left and right lung regions, respectively, in each axial and coronal section. The sets of nodules in previous and current images are defined as

$$A = \{A_i;\ i = 1, 2, ..., M\}, \quad B = \{B_j;\ j = 1, 2, ..., N\}.$$

Then, the relative position of nodule A_i in lung region, $P_{A_i}(x_{A_i}, y_{A_i}, z_{A_i})$, is defined as follows,

$$P_{[A_i]}(x_{A_i}, y_{A_i}, z_{A_i}) = (\frac{d_x}{W_a} + \delta, \frac{d_y}{D_a} + \delta, \frac{d_z}{H_c} + \delta) \tag{1}$$

$$\delta = \begin{cases} 1 & (A_i \text{ is in left lung}) \\ 0 & (A_i \text{ is in right lung}) \end{cases}$$

where the d_x and d_y are distances from the given quadrangle's origin to a nodule center along the x-axis and y-axis in the axial section, respectively, and d_z is defined in the same way in the coronal section. Here, W_a and D_a are ranges of the quadrangle along the x-axis and the y-axis in the axial section, and H_c is a range of the quadrangle along the z-axis in the coronal section (Fig.1). All nodules in A and B are transformed into relative coordinates in the lung region by Eq. 1.

2.1.2 Calculation of distance

The distance between nodule A_i in the previous image and nodule B_j in the current image is defined as follows:

$$d_{ij} = \sqrt{(x_{A_i} - x_{B_j})^2 + (y_{A_i} - y_{B_j})^2 + (z_{A_i} - z_{B_j})^2} \tag{2}$$

This distance is calculated for all possible pairs of nodules between previous and current images.

2.1.3 Determination of corresponding nodule candidates

Here, the candidates for corresponding nodules are determined for every single nodule. There may be many other nodules in the neighborhood of each nodule. The distance defined above is not stable because the volume of lung is varied by respiration. Therefore, we select the nodules for which the distance of separation is smaller than the predefined threshold value T_d.
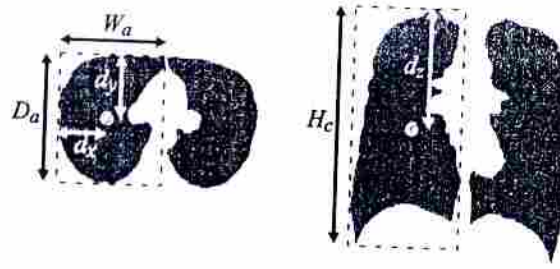
Figure 1. Parameters W_a, D_a, H_c and d_x, d_y, d_z. On the left is an axial section; on the right is a coronal section of the lung area.

2.2 Precise matching

2.2.1 Calculation of image correlation

To find the corresponding nodule accurately, it is important to evaluate the sameness of the distribution of blood vessels around the nodule. Image correlation is one suitable method for this. However, both the timing of a patient's respiration and a change of posture make it impossible to calculate correlation in a three-dimensional image directory. Moreover, the size and shape of the nodules are varied by illness. Consequently, we compute image correlation c_{ij} between maximum intensity projection(MIP) images around the nodule A_i and B_j. In this projection, the nodule region is not projected to avoid its volume change. Here, c_{ij} is defined as an average of the correlation of three MIP images projected along each axis.

$$c_{ij} = (c_x + c_y + c_z)/3 \tag{3}$$

where c_x, c_y, c_z are cross-correlations of each MIP images.

2.2.2 Determination of corresponding nodule candidates

Here, corresponding nodules are determined in consideration of 1-to-1, 1-to-0, 0-to-1 correspondence[7]. First, a pair of A_i and B_j nodules that has the largest correlation value c_{ij}, is determined to be the corresponding pair. Next, all pairs except the pairs selected already are employed and the pair having the largest correlation value is selected. This process is iterated until all pairs are selected or the correlation value of the present selected pair is smaller than the predefined threshold T_c. Threshold T_c is used to identify nodules that have no corresponding nodules in another image.

3 Experiment

We applied the proposed method to four chest X-ray CT images taken in different examinations of the same patient. The interval between acquisition of data 1 and data 2 was two months, that between data 2 and data 3 was one month, and there was a 10-month interval between data 3 and data 4. Acquisition parameters of the CT images are shown in Table 1. The lung region used here was extracted based on thresholding for CT values and a dilation and erosion (fusion) operation. A medical doctor identified nodules that have voxels whose CT values are greater than -600 H.U. in data 1 ~ 4, respectively (Table 2). These nodule regions were marked manually. The experimental results when $T_d = 0.10$ and T_c 0.4 are shown in Table 3. In this experiment, the size of MIP image around each nodule was 35

Table 1. Acquisition parameters of CT images.

Slice size	512 × 512 [pixels]
Number of slices	193 ~ 209 [slices]
Pixel size	0.469 [mm]
Reconstruction pitch	1.25 [mm]
Slice thickness	2.5 [mm]

Table 2. Number of nodules that have the regions whose CT values are greater than -600 H.U. in each data set.

Data	Number of nodules
1	378
2	91
3	53
4	50

$5mm$ and the projected range was $5mm$. The scattergram of two criteria for this method is shown in Fig.2. The examples of correspondence are shown in Fig.3. Prior to the automated check, 265 pairs of corresponding nodules were detected through a visual check of all combinations of the four images. The experimental results showed that 260 pairs of corresponding nodules were found automatically, of which 258 pairs agreed with visual correspondence results, while only two pairs were false positive correspondences. This result provided a correct correspondence rate of 0.97. The volume change of corresponding nodules was measured for evaluation of the curative effect. The result of the ratio of volume change between corresponding nodules is shown in Fig.4.

Table 3. Results of correspondence in each combination of data 1 ~ 4 ($T_d = 0.1$, $T_c = 0.4$).

Data	Correct pairs	False pairs	Missing pairs	Correct pair rate
1 & 2	88	0	1	0.99 (88/ 89)
1 & 3	52	1	0	1.00 (52/ 52)
1 & 4	30	1	3	0.91 (30/ 33)
2 & 3	46	0	1	0.98 (46/ 47)
2 & 4	23	0	1	0.96 (23/ 24)
3 & 4	19	0	1	0.95 (19/ 20)
Total	258	2	7	0.97 (258/265)

4 Discussion

The proposed method showed good performance and could find corresponding nodules accurately, even if there was another nodule approximately 10 mm from it (Fig.3). In fact the accuracy is improved remarkably in comparison with using relative distance only[6]. The proposed method worked well even when the volume of the specified lung region changes by up to about 15%. False correspondences occurred when the lung volume changed significantly by pleural effusion, as seen in Fig.5. In these cases, the relative distance tended to be too small for the nodules to be deemed candidate corresponding
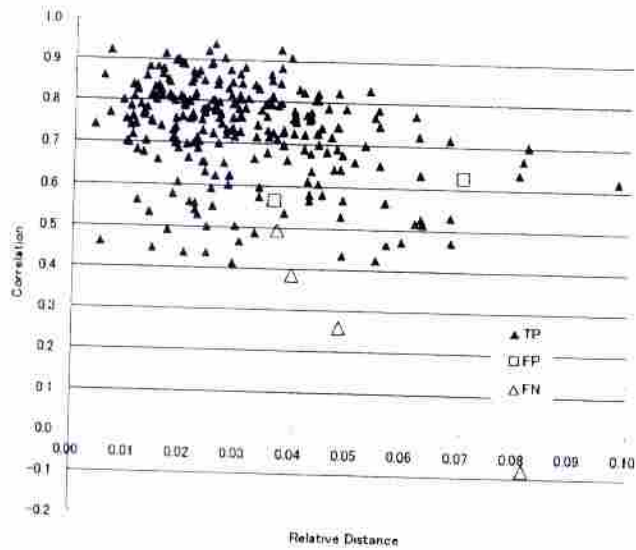
Figure 2. Distribution of relative distance vs. image correlation. Three cases have greater relative distance than 1.0

pairs. As shown in Fig.4, it is considered that the proposed method is applicable for quantifying the curative effect of individual nodules.

5 Conclusion

In this paper, we proposed a method of find pairs of corresponding nodules for evaluating the interval change in sequential chest X-ray CT images. We applied the method to four chest CT images that were taken during successive examinations of the same patient over a period of 14 months. By representing the nodule position as a set of relative coordinates in a lung region and the similarity index as an average of image correlations for three MIP images of nodules, corresponding nodules could be accurately located, even when the lung volume changed. The experimental results showed that 258 pairs out of 265 pairs
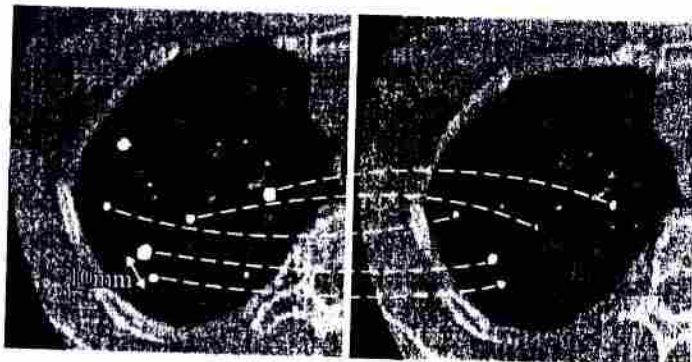

Figure 3. Examples of corresponding nodules between data 1 (left) and data 2 (right).
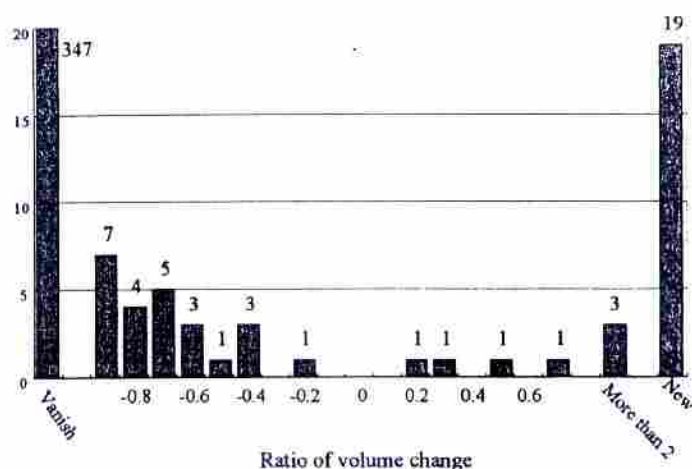
Figure 4. Histogram of ratio of volume change between corresponding nodules. The volume was measured in the regions whose CT values are greater than -600 H.U.

were correct and nine pairs were false correspondences (seven false negatives and two false positives), meaning our method could match correspondences to an accuracy of more than 95%. Because several features could be measured easily, such as the total number and volume of nodules, appearance of nodules, disappearance of nodules, it is expected that this method will be an effective diagnostic tool. Future work includes accuracy improvement when the lung volume changes remarkably and application to many other medical situations.

Acknowledgment

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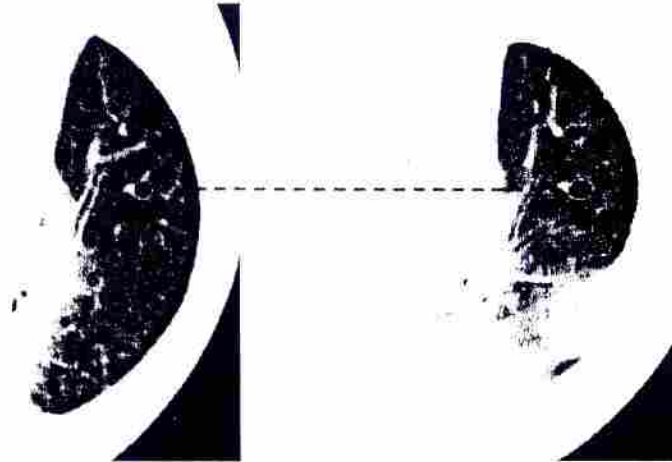
Figure 5. Example of false correspondence

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