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Pulmonary nodule registration in serial CT scans using global rib matching and nodule template matching

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ABSTRACT

We propose an automatic nodule registration method between baseline and follow-up chest CT scans. Initial alignment using the center of the lung volume corrects the gross translational mismatch, and rigid registration using coronal and sagittal maximum intensity projection images effectively refines the rigid motion of the lungs. Nodule correspondences are established by finding the most similar region in terms of density as well as the geometrical constraint. The proposed nodule registration method increased the nodule hit rate (the ratio of the number of successfully matched nodules to total nodule number) from 26% to 100%.

1. Introduction

Chest computed tomography (CT) techniques are screening methods for lung cancer in high-risk individuals, as these techniques have the ability to identify early lung cancer [1–5]. With follow-up CT study, nodule growth assessment is the most reliable method for differentiating benign from malignant nodules [6–11]. For nodule growth analysis, the establishment of correspondence between nodules in sequential CT scans is necessary. However, this is difficult due to the possible variations of the lung volume in different respiratory and changes of the nodule size and shape in the sequential CT scans. Furthermore, thin-section CT scans of the entire thorax with a large number of slices require radiologists to spend a considerable amount of time interpreting the images [12]. Therefore, an automatic registration of pulmonary nodules in serial CT scans is necessary to match corresponding nodules.

Several methods of nodule registration have been suggested, and these methods generally fall into two categories: global and local registrations. A global registration is when corresponding nodules are matched through registration of the lungs. This type includes rigid and affine registrations [13–19]. Kubo [20] proposed a lung registration method that corrects coarse differences of the lungs using the apexes of the lungs and the backbone, subsequently refines the rigid motion of the lungs using lung boundary and pulmonary blood vessels. Betke [21] developed an automated registration technique that initially aligns sequential images using landmarks such as the trachea, sternum and spine and then refines the initial surface alignment using the iterative closest point (ICP) [22]. Correspondences of nodules are established by computing the Euclidean distances between all nodule pairs in sequential CT scans. To improve the long processing time of the ICP, Hong [23] proposed multilevel 3D registration of the lung surface that reduces the original number of points and aligns them using an iterative surface registration method. This process is repeated until the surfaces are registered at their original resolution. As another method for the improvement of the processing time of the original ICP algorithm, Betke [24] used Elias' nearest neighbor algorithm to establish the correspondence of lung surface points. This method reduces the processing time from $O(kn\log n)$ to $O(kn)$. Hong [25] extracted the lungs using an automatic segmentation method and initially aligned using the optimal volume of the segmented lungs. Affine registration using narrow-band distance propagation from the lung surface was then performed to correct the remaining errors in the transformations. Gurcan [26] proposed a rigid registration method using coronal maximum intensity projection (MIP) image without the detection of any anatomical landmarks.

Although global registration can establish the nodule correspondence by globally correcting translational, rotational and scale

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differences between two lungs, errors in nodule correspondences still remain due to the local deformation caused by respiration. To solve this problem, local registration for the nodule region has been suggested as successive step after the global registration of the lungs. The local registration involves corresponding nodules to match using meaningful local information such as the nodule shape and relative position from the chest wall and vessels near the nodule. Mullally [27] developed a registration algorithm that matches the nodules using nodule information such as the size, location, and shape. Kusanagi [28] represented the position of each nodule as a relative coordinate in the lung region and determined the nodule correspondences by measuring the distance from the origin of the lung volume to the nodule center. Sun [29] proposed a nodule registration method using a semi-rigid model that considers only the nodule and its principal surrounding structures, treating the semi-rigid model as individual rigid bodies. Shi [30] proposed nodule template matching that finds correspondence among detected nodule candidates through a Hessian analysis in all images. As contrasted with this method, we focus on nodule template matching using density similarity and geometrical constraint within limited search volume without nodule detection.

In this paper, we propose an automatic nodule registration method that can globally align the lungs and locally search for nodule correspondences. The lungs in the follow-up CT scan is aligned to that in the baseline CT scan by global rib matching, involving the initial alignment using the center of the lungs and rigid registration using coronal and sagittal MIP images. The initial alignment corrects the gross translational mismatch without any anatomical landmarks, and the rigid registration process effectively corrects the rigid motion (translational, rotational, and scale differences) of the lungs using the ribs, which undergo movement most similar to that of the lungs. The nodule template matching can refine the mismatch of the nodule correspondences by considering not only density similarity of nodules but also geometrical constraint, which accentuates the correlation between nodule and its neighboring structures such as the chest wall and vessels.

The organization of this paper is as follows. Section 2 presents experimental datasets and section 3 demonstrates how to register the lungs in sequential chest CT images and how to match corresponding nodules. Section 4 describes how our registration method accurately and rapidly matches corresponding nodules, and Section 5 discusses the effects of the proposed method. Finally, the paper is concluded in Section 6.

2. Material

Fifty pairs of serial chest CT scans with pulmonary nodules were obtained for lung screening and the 50 subjects have 73 pulmonary nodules of less than 3 cm in diameter, which have several types such as isolated nodule without any connection with other pulmonary structures, perivascular nodule connected to the vessels, pleural nodule attached to the chest wall, and pleural tail nodule connected to the vessels and attached to the chest wall at the same time. Twenty nodules showed isolated type, 17 nodules showed pleural type, 30 nodules showed perivascular type, and 6 nodules showed pleural tail type. One subject had 8 nodules and the other subjects had from one to four pulmonary nodules. The number of detected nodules of four subjects was different between baseline and follow-up CT scans and that of the other subjects was same between both CT scans. Five standard-dose CT scans were acquired on a Philips Mx8000 scanner, and 45 low-dose CT scans were acquired on a Siemens Sensation 16 scanner. The time interval between baseline and follow-up CT scans ranged from 1 to 25 months. The 5 subject scans had a thickness of 2 mm, and the other subject scans had a thickness of 1 mm. Each image had a matrix size of 512×512 pixels with in-plane resolutions ranging from 0.54 to 0.71 mm. The number of images per scan ranged from 270 to 454.

To show respiratory differences between baseline and follow-up CT scans, absolute volume differences of the lungs in the both CT scans were estimated, as shown in Fig. 1(a). Patients were suggested to be at maximal inspiration during the scanning. The left and right lungs were segmented using in-house software [31–32]. In this software, the lungs were extracted from chest CT images by an automatic segmentation method using 3D region growing, and the segmented lung boundary was corrected for the inclusion of pleural nodules and pulmonary vessels by lung smoothing. The lung volume differences ranged from 1.6 cc to 967.4 cc and an average difference of the lung volumes was 252.6 ± 209.6 cc. The lung volume difference of 43 out of 50 subjects was 187.9 ± 129.4 cc on average, whereas the other seven subjects showed a relatively large difference of 650.2 ± 164.4 cc on average.

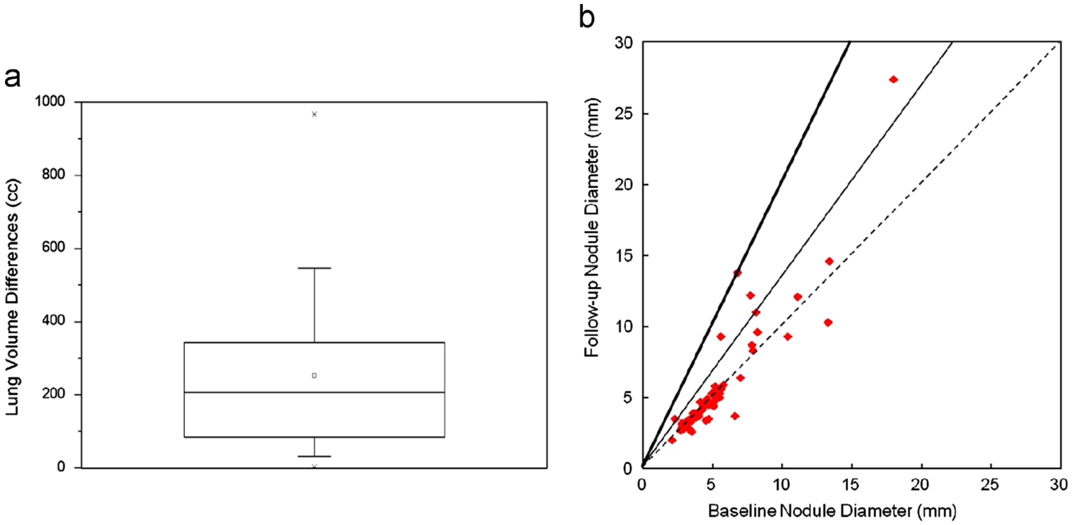

Fig. 1. Analysis of experimental datasets: (a) absolute volume differences of the lungs between baseline and follow-up CT scans of 50 subjects and (b) diameter changes of corresponding nodules in baseline and follow-up CT scans. In figure (b), dotted line means that there is no significant difference of diameter between both CT scans, and nodules on thin and thick solid lines indicate an increase of 50% and 100%, respectively.