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Interactive registration between supine and prone scans in computed tomography colonography using band-height images

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ABSTRACT

In computed tomographic colonography (CTC), a patient is commonly scanned twice including supine and prone scans to improve the sensitivity of polyp detection. Typically, a radiologist must manually match the corresponding areas in the supine and prone CT scans, which is a difficult and time-consuming task, even for experienced scan readers. In this paper, we propose a method of supine-prone registration utilizing band-height images, which are directly constructed from the CT scans using a ray-casting algorithm containing neighboring shape information. In our method, we first identify anatomical feature points and establish initial correspondences using local extreme points on centerlines. We then correct correspondences using band-height images that contain neighboring shape information. We use geometrical and image-based information to match positions between the supine and prone centerlines. Finally, our algorithm searches the correspondence of user input points using the matched anatomical feature point pairs as key points and band-height images. The proposed method achieved accurate matching and relatively faster processing time than other previously proposed methods. The mean error of the matching between the supine and prone points for uniformly sampled positions was 18.41 ± 22.07 mm in 20 CTC datasets. The average pre-processing time was 62.9 ± 8.6 s, and the interactive matching was performed in nearly real-time. Our supine-prone registration method is expected to be helpful for the accurate and fast diagnosis of polyps.

1. Introduction

Computed tomographic colonography (CTC) has been accepted as a promising procedure for the noninvasive screening of colon cancer [1–5], which is one of the five most common types of diagnosed cancer [6]. Although optical colonoscopy (OC) is considered the most sensitive and most specific procedure for colon examination [5], OC is an invasive procedure, which is uncomfortable for the patient [5,7,8]. CTC is able to mimic the invasive OC navigation procedure, however, by looking for polyps via fly-through in a virtual colon model reconstructed from abdominal computed tomography (CT) images [9,10]. CTC offers safety, lower cost, and better patient compliance compared to OC, and has the potential to become a mass screening modality [3,11–13].

In CTC, a patient is commonly scanned twice including supine and prone scans to improve the sensitivity for polyp detection [14]. Typically, a radiologist must manually match the corresponding areas in the supine and prone CT scans. Interpretation of CTC scans is a difficult and time-consuming task, even for experienced readers owing to the distortion that occurs during patient repositioning for multiple scans [15]. Hence, the computed registration between the supine and prone CTC scans is expected to improve CTC interpretation by reducing interpretation times and potentially improving poly detection sensitivity.

Numerous methods have been proposed to find correspondence between supine and prone CTC scans. The basic method was non-rigid iterative closest point (ICP) algorithm proposed by Fitzgibbon [16]. However, this method doesn't guarantee correct matching of all the diagnosis regions. There are supine-prone registration methods based

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on the extracted centerlines of the segmented colon areas in both CT datasets [17–21]. These methods make the virtual center path along the colon lumen from the anus to the cecum. Then, a registration algorithm is performed utilizes geometric information, such as the local extreme points [19]. However, these methods only consider the local geometries of the extracted centerlines. When the patient changes positions, the centerline matching between the supine and prone scans is constrained by these characteristics. Näppi [22] used several anatomical landmarks such as the anus or recto-sigmoid junction for registering the supine and prone datasets. However, the number of these landmark points is insufficient to match all positions with colonic deformation. Some recent studies use *teniae coli* (three discrete muscles running longitudinally along the exterior colonic surface) as the features [23,24]. However, teniae coli only partially exist on the colon [25].

Voxel-based methods were developed by Suh and Wyatt [26,27]. These approaches lack robustness since these methods require the assumption that there is no fluid occlusion or collapse. Fukano et al. [28] proposed a registration method based on haustral folds extracted from supine and prone data. However, it can be very difficult to establish correct correspondences between haustral folds. Correct registration results were reported for 65.1% of large folds and 13.3% of small folds. Zeng et al. [29] presented a method based on conformal mapping combined with feature matching in order to establish correspondences between the supine and prone surface. They mapped the supine and prone colon surface onto five rectangle pairs, and then established correspondence between supine and prone surfaces for each rectangular segment. This method relies on the ability to determine the same segments on the prone and supine surfaces accurately, which can be very difficult even for fully distended colons, and may not be possible for cases with local colonic collapse. The method proposed by Roth et al. [30] aims to overcome these limitations by mapping the entire endoluminal surface to a cylinder. However, this method can be sensitive to mis-registration of continuous areas due to the similarities of neighboring features. Recently, Wang et al. [31] used a graph matching algorithm to register a set of features, which were detected by n-SIFT algorithm. The main advantage of this method is that colon center path definition is unnecessary. However, the reported mean registration error for this method was 37.6 mm. Most recently, Hampshire et al. [32] proposed a method to establish correspondence between the supine and prone based on matching haustral folds. This method matched haustral folds using a Markov Random Field (MRF) model. The mean error of the algorithm of this method was 6.0 mm. However, this method only considers fold areas for matching.

In this paper, we present a method of the supine-prone registration based on band-height images, which are directly constructed from the supine and prone CT scans using a ray-casting algorithm in every centerline position. We first detect anatomical feature points and establish correspondence using local extreme points on centerlines [19], called by prior-key points. Our algorithm constructs the band-height image of each point on the supine and prone centerlines. The band-height images are generated using a ray-casting algorithm [33] to detect surrounding colon wall from each centerline point. So, each band-height image of its centerline position has neighboring shape information. We use the band-height images to correct the correspondences of anatomical feature points. We set additional feature points as sub-key points, between prior-key points to improve robustness. Then, our algorithm searches for correspondence of user input points on a real-time basis using key points and band-height images.

Our proposed method using the band-height images solves many issues of the previous study. We use the band-height images for matching between points on centerline using local shape information with geometric information. By using the band-height images, our method does not require the transformation of original CT data into another data type, such as triangle meshes, and does not require mapping CT data into other planes using complex algorithms. This leads the acceleration of processing time. Also, we consider not only the positions of neighboring polyps but all positions on the centerline of colon for establishing matching pairs. It might be a problem that is sensitive to mis-registration of continuous areas due to the similarities of neighboring features. We use prior-key points determined by global geometric information to prevent the spread of error of local mis-registration. We set additional key points, called as sub-key points, to maintain sufficient landmarks to improve robustness.

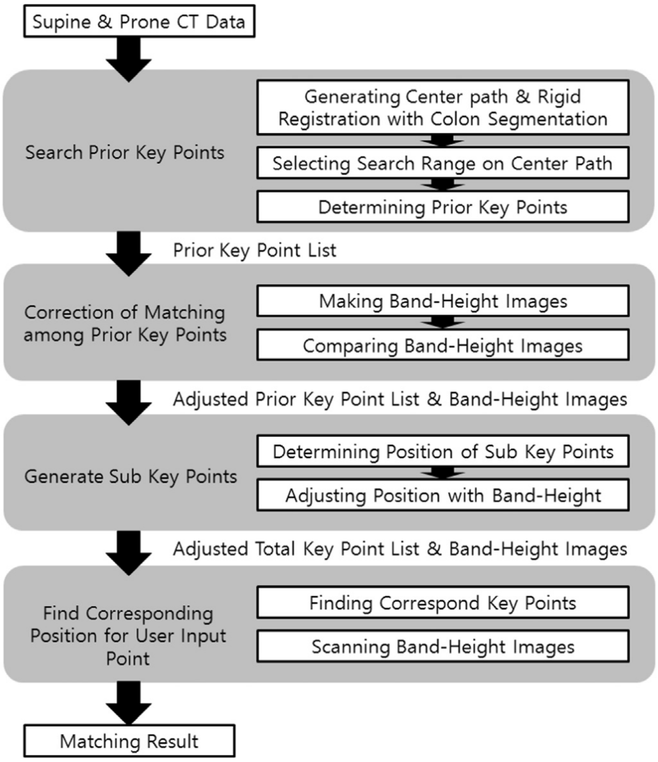

Fig. 1. A proposed matching algorithm process between the supine and prone center paths.

The remainder of this paper is organized as follows. In Section 2, we describes the supine-prone center path registration method using band-height images with user interaction. Section 3 presents our experimental results, followed by our conclusions and future work in Section 4.

2. Method

The proposed method is implemented in four main steps (see Fig. 1.). First, we search prior-key points on the centerline of supine and prone CT data. The prior-key points are anatomically important features searched by their geometric information such as position and gradient. Second, we find correspondence relations between prior key points of supine and prone data by exploiting band-height images. Third, we set sub-key points between prior-key points and find matching relations among them. The sub-key points are placed by proper distance among the prior key points to accelerate matching speed and reduce matching error in interactive matching process. Finally, the corresponding position of prone CT data is automatically identified according to the input position of the center path of supine CT data.

2.1. Search for prior-key points

In this step, we find anatomically important feature points on a center path. We define the correspondence of feature points using supine and prone volume data and supine-prone center path data. We

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