SUPINE AND PRONE CT COLONOGRAPHY REGISTRATION BY MATCHING GRAPHS OF TENIAE COLI

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ABSTRACT

This paper proposes a registration method for supine and prone CTC scans. The method matches graphs built using the teniae coli, three muscles that run the length of the colon. The teniae are visible on CTC and were detected using fully-automatically software. Then key points of the teniae were obtained by non-uniformed sampling of the teniae. Graphs were built using these key points. The colon registration was formulated as a graph matching problem. Mean field theory was applied to match the graphs. The proposed method was tested on 10 pairs of supine and prone CTC scans. The average registration error was 2.5cm (±0.7 cm, 95% C.I. [2.1 2.9]), significantly improving the baseline graph matching method for CTC registration.

Index Terms— CTC, registration, graph, teniae coli

1. INTRODUCTION

Computed tomographic colonography (CTC) has been shown to be effective in the detection of colorectal polyps and for cancer screening [1]. Computer-aided detection systems (CAD) [2] have been shown to improve radiologist detection performance. In CTC, a patient will be scanned twice, once supine and once prone, to improve the sensitivity for polyp detection [3]. In Fig. 1 we show two typical 3D colon CTC surface reconstructions of a patient. Registering the supine and prone CTC scans is expected to improve CTC interpretation by reducing interpretation times and potentially improving detection sensitivity.

Many methods have been proposed for CTC registration. Li et al.[4] proposed a heuristic algorithm for the colon centerline registration that employed the coordinate information of the centerline. Summers et al.[5] used the normalized distance along the colon centerline (NDACC) to register prone and supine scans. Zeng et al.[6] employed teniae coli and quasi-conformal mapping to register flattened colons. Wang et al.[7] proposed a graph matching method for CTC colon registration which can be performed without centerline extraction. Suh and Wyatt proposed a deformable method [12] and volume registration under the topological change [13] for supine and prone colon registration.

In this paper we further develop the graph matching method [7] for CTC registration by incorporating the location of teniae coli to the graph. Teniae coli are three bands of longitudinal smooth muscle on the colon surface. They are anatomical important landmarks, which can be used as coordinate system to estimate the circumferential positions of polyps, enabling a more accurate detection, and can serve also as a reference for registration and synchronized virtual navigation of supine and prone CT scans. In our method, the graph of the colon was built on the key points selected from the teniae, rather than the entire colon surface. The matching of the graph was based on mean field theory.

The remainder of the paper is organized as follows: Section 2 describes teniae detection and formulation of CTC registration as a graph matching problem; Section 3 states the experimental results; Section 4 concludes the paper.

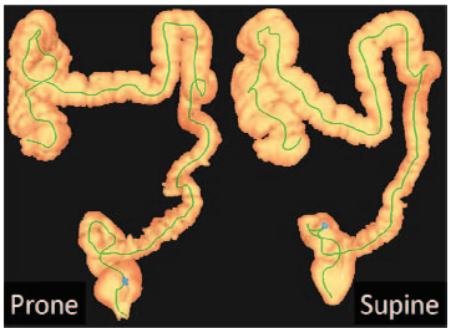


Figure 1: Prone and supine three-dimensional CTC surface reconstructions of the colon of a 65 year old man. Colon centerlines shown in green.

2. METHODS

2.1. Teniae coli detection

The three teniae coli are named tenia omentalis (TO), tenia mesocolica (TM) and tenia libera (TL), according to their position on the colon. Teniae coli were detected automatically using methods described in [8]. Fig.2 illustrates our teniae detection method. The 3D colon surface was first segmented and unfolded to a flattened view using a reversible projection technique [9]. Then the circumference of the colon was normalized to fixed length by stretching the flattened colon to a rectangular region (see Fig.2b). The flattened colon was converted to a 2D height map, where the intensity of the image reflects elevation of the 3D surface, shown in Fig.2c. Gabor filter banks were convolved with the height maps to extract haustral fold features, shown in Fig.2d. The Sobel operator was used to detect the edge of each haustral fold feature. The haustral fold centers were identified by detecting local maxima of the edge image (Fig.2e). Connecting the fold centers yielded the paths of the folds (Fig.2e). Teniae coli were extracted as lines running equidistant from a pair of fold paths (Fig.2f). Teniae detected on the 2D height map can be back-projected to the original 3D colon surface.

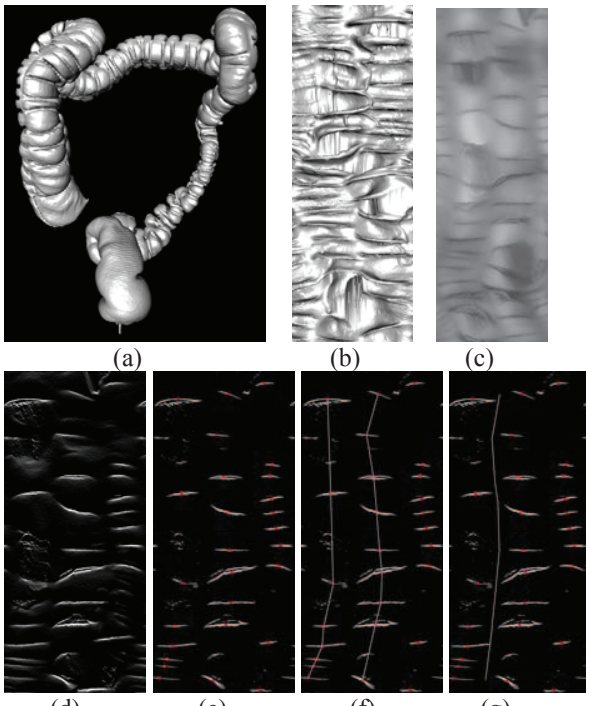


Figure 2. Illustration of the detection process of one tenia. (a) 3D colon surface. (b) 3D flattened colon surface with normalized circumference. (c) 2D height map image. (d) Gabor filters response to height map image. (e) Detected fold centers. (f) Fold center path. (g) A detected tenia.

2.2. Graph representation of teniae coli

Given the teniae coli of a colon, non-uniformed sampling was used to obtain the key points of the teniae. To preserve the shape of the colon, regions with denser point cloud were down sampled by a larger factor and with sparser point cloud were down sampled by a smaller factor. With the key points on both the prone and supine teniae, we built graphs using a K-nearest neighbor criterion.

Graph construction is similar to the method described in [7]. Given two graphs from supine and prone teniae to be matched, we define the prone graph as model graph G_M and the supine graph as data graph G_D. Each graph is depicted by a set of vertexes and edges: $G_M=G(V_M,E_M)$, $G_D=G(V_D,E_D)$, where V denotes the vertex set and E denotes the edge set. The matching of two sets of vertexes can be described by a binary matrix U, with size $|V_D|\times|V_M|$. We assume that the data graph G_D has fewer vertices than the model graph G_M and each vertex in G_D has one and only one correspondent vertex in graph G_M. The above constraints can be formulated as:

$$\sum_{\alpha\in V_M} U(a,\alpha)=1,\ \forall a\in V_D \text{ and } \sum_{a\in V_D} U(a,\alpha)\le 1,\ \forall \alpha\in V_M .$$

The matching quality between G_D and G_M can be depicted by vertex similarity and link compatibility. We use a matrix W, with size $|V_D|\times|V_M|$, to depict the similarities of each vertex in V_D and V_M. The link compatibility is equivalent to the co-existing probability of a pair of links between G_D and G_M. We use a matrix Q to represent the link compatibility whose size is $|V_D||V_M|\times|V_D||V_M|$. We convert matrices U and W into one dimensional vectors u and w whose elements are taken column-wise from U and W, respectively. The objective of the graph matching problem can be formulated as follows:

$$\max_m \ u^T\times w+u^T Q u \qquad (1)$$

$$s.t. \quad A_R\times u=e_R,\ A_C\times u\le e_C, \text{ and } u\in\{0,1\}^{|V_D||V_M|},$$

where e_R (size $|V_D|\times1$) and e_C (size $|V_M|\times1$) are vectors whose elements are all one. $A_R=I_{|V_D|}\otimes e_C^T$ and $A_C=e_C^T\otimes I_{|V_D|}$. I_n is an $n\times n$ identity matrix.

2.3. Graph matching based on mean field theory

The graphs are matched using the same method in [7]. The matching problem in Eq.1 is a quadratic integer program which is non-deterministic polynomial-time hard (NP-hard) and has no known polynomial-time solver. To solve this problem efficiently, we temporary ignore the one-to-one constraint and treat the problem in a probabilistic manner. The objective function can be expressed by the following probabilistic model:

$$p(u)=\frac{\rho(u)}{Z(w,Q)}\exp\left[\sum_{i<j}u_iQ_{ij}u_j+\sum_i w_iu_i\right], \quad (2)$$

where $\rho(u)=\prod_i \rho(u_i)$ models the distribution for each single variable in which we can encode all the constraints to be satisfied by u_i, such as discreteness and bounds on the range; $Z(w,Q)$ is called the partition function where:

$$Z(w,Q)=\int\prod_j\left(du_j\rho(u_j)\right)\exp\left[\sum_{i<j}u_iQ_{ij}u_j+\sum_i w_iu_i\right].$$

The binary constraint of the matching problem can be encoded in the following way by using the Delta function: $\rho(u_i)=\frac{1}{2}\delta(u_i-1)+\frac{1}{2}\delta(u_i+1)$.The probabilistic model shown in Eq.2 with binary constraint is an Ising model where $w_i, i=1,2,...,|V_D||V_M|$ is called the external field. An Ising model is a probabilistic energy model describing ferromagnetism with variables called spins that have only two energy states. Mean field theory provides an effective way to compute approximate values for the moments of the spins u_i and for the free energy $-lnZ$ [11].

According to mean field theory, the expectation of u_i can be approximated as $\langle u_i\rangle=\partial\ln Z_0^{(i)}/\partial w_i$, where $Z_0^i=\int dh_i du_i\rho(u_i)e^{u_i(h_i+w_i)}p(h_i\setminus u_i)$. Here $h_i=\sum_j Q_{ij}u_j$ is called the "cavity" field and its distribution $p(h_i\setminus u_i)$ at the location of vertex i can be approximated by a Gaussian distribution with mean $\langle h_i\rangle_{\setminus i}=\sum_j Q_{ij}\langle u_j\rangle-V_i\langle u_i\rangle$ and variance V_i.

With the mean field approximation, Eq.1 without matching constraints can be solved in a probabilistic manner. The expectation of matching variables $\langle u_i\rangle, i=1,2,...,|V_D||V_M|$, can be viewed as confidence that a vertex in graph G_D is matched to a vertex in graph G_M. To incorporate the one-to-one matching constraint in the mean field solution, we use an iterative technique for mean field calculation and for adding the matching constraints. Our algorithm first matches the most prominent points in the data and model graphs, less similar points are matched with guidance from the prominent points previously matched. We keep the external field w_i corresponding to variable u_i having the highest expectation value and set all other external fields which conflict with u_i to zero in order to develop a one-to-one matching constraint. The algorithm can be summarized as:

1. Given two sets of teniae to be match, build the data graph G_D and the model graph G_M.
2. Construct matching link compatibility matrix Q and vertex similarity matrix W based on G_D and G_M.
3. Find $u^*=\arg\max_{i\in L}\langle u_i\rangle$ using the mean field method. L is the set of all possible links between G_D and G_M.
4. Remove all the constraints in L which conflict with u^* by fixing the external fields of these links to zero. The external field of u^* will be kept.
5. If all vertices in G_D have been processed and L is empty, return the solution u^* found in each iteration; otherwise go back to step 3.

3. EXPERIMENTAL RESULTS

Our evaluation dataset consists of CTC examinations from 10 patients collected from two medical centers. Each patient was scanned in the supine and prone positions. Each scan was done during a single breath hold using a 4 or 8 detector row CT scanners. CT scanning parameters included 1.25- to 2.5-mm section collimation, 15 mm/s table speed, 1-mm reconstruction interval, 100 mAs, and 120 kVp. Each patient had one or more polyps. We randomly picked a single polyp for algorithm evaluation if a patient had more than one polyp. We selected a total of 10 polyps 6-25 mm in size. The polyps were confirmed by both traditional optical colonoscopy and CT colonography.

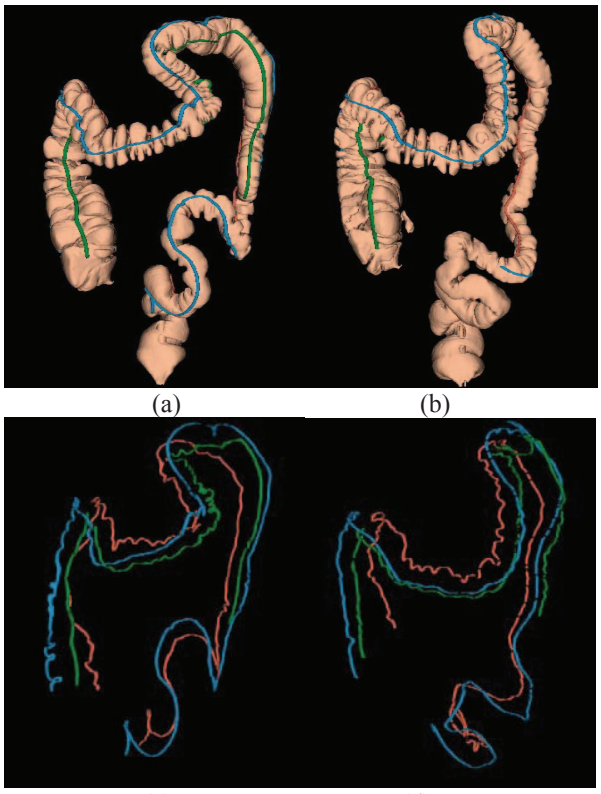
Fig.3 shows a pair of supine and prone CTC with the detected teniae coli highlighted on 3D colon surface. Fig.4 shows a pair of supine and prone teniae coli which are detected by our method. To quantitatively evaluate our registration method, we conducted an experiment based on the correspondence in the polyp location between supine and prone teniae. The baseline algorithm for comparison was graph matching using the colon surface without teniae detection [7]. For each case, 50 key points were selected for building the graph. Fig.5 compares graphs created from the colon surface versus the teniae coli. We measured the error as the Euclidean distance in the original 3D space. The average registration error (standard deviation, [95% confidence interval]) of polyps of the baseline method is 4.3cm (±1.1cm, [3.6 5.0]), of our method is 2.5cm (±0.7 cm, [2.1 2.9]). The improvement of our method was statistically significant ($p<0.01$). Fig.6 shows the performance of our method compared to the baseline method.

4. CONCLUSION

We have proposed a method of supine and prone CTC registration that uses graph derived from the teniae coli. By restricting the key points on where the teniae located, the graph represents the colon better compared to selecting the key points from the original colon. The proposed method significantly improves the original method that derived the graph from the colon surface.

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(a) (b) (c) (d)

Figure 3. A pair of supine (a, c) and prone (b, d) CTC with teniae highlighted on 3D colon surfaces. Blue: TO; red: TM; green: TL.

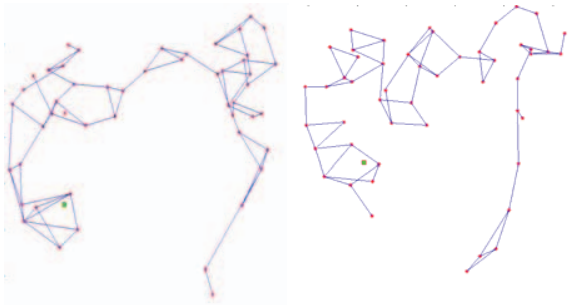


Figure 5. Comparison of graphs of one CTC that were built on colon surface (left) vs. built on teniae coli (right).

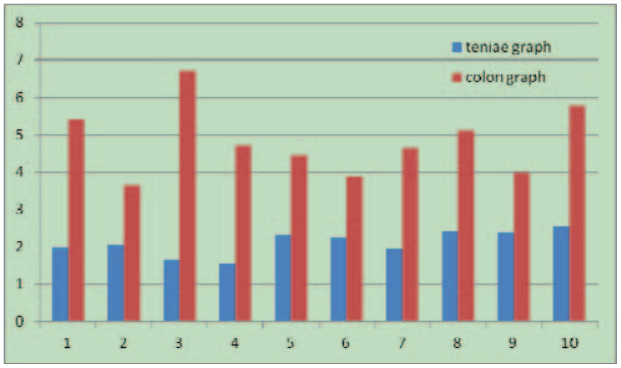


Figure 6. Performance of our method (teniae graph) compared to the baseline method (colon graph).

11. REFERENCES

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