

Detection of Anatomical Landmarks in Human Colon from Computed Tomographic Colonography Images

A.S. Chowdhury, J. Yao, R.L. VanUitert, M.G. Linguraru, R.M. Summers
*Department of Diagnostic Radiology, National Institutes of Health Clinical Center
Building 10, Room 1C368X, Bethesda, MD 20892- 1182, USA.
E-mails: chowdhuryas@mail.nih.gov, rms@mail.nih.gov*

Abstract

Colon cancer is the second leading cause of cancer-related deaths per year in industrial nations. Virtual colonoscopy is a new, less invasive alternative to the usually practiced optical colonoscopy for colorectal polyp and cancer screening. In this paper, we present some physics-based modeling and pattern recognition techniques to identify anatomical landmarks in the human colon like the haustral folds and the tenia coli to further exploit the benefits of virtual colonoscopy. A combination of heat diffusion field algorithm and fuzzy c-means clustering algorithm is used to detect the haustral folds in human colon from volumetric computed tomography (CT) images. Each voxel on the corresponding colon surface is parameterized using the colon centerline information and associated local Frenet frames. The parameterized fold information is utilized to establish the tentative location of one tenia coli. Preliminary results on automated detection of tenia coli are shown on the colon surface.

Keywords: Heat Diffusion, Fuzzy C-Means, Frenet Frame, Haustral Fold, Tenia Coli, Computed Tomography.

1. Introduction

Colon cancer is the second leading cause of cancer-related deaths in industrial nations [1]. Virtual colonoscopy (VC) is a new, less invasive alternative to the usually practiced optical colonoscopy for colorectal polyp and cancer screening [2]. By reconstructing a virtual endoscopic view within the colonic lumen, VC has led to high sensitivity of colonic polyp detection. As a part of increasing the effectiveness of virtual endoscopic navigation in the existing computer-aided-diagnosis (CAD) system, we

propose in this work, novel detection of anatomical landmarks in human colon viz. the haustral folds (colonic folds) and tenia coli. Teniae are longitudinal muscles which can serve as ideal references for guiding virtual navigation and polyp registration.

Existing techniques on fold detection use simple threshold-based curvature filter [3]. We propose a novel fold detection method that instead uses heat diffusion, fuzzy c-means clustering and label filtering. The motivation behind this approach is to get the folds in their entirety to facilitate subsequent important applications like tenia detection and prone-supine registration. In particular, the detection of folds help in detection of teniae as the teniae are a flat band perpendicular to the folds and they interrupt the folds. The published literature on tenia detection include substantial manual intervention [4], detection of discontinuous tenia (due to insufficient fold detection) [5] and tenia detection in some parts on a 2D instead of the actual 3D colon space [6]. We try to detect tenia automatically without changing the colon geometry. This makes the detection problem very complex. The current work presents initial results on tenia detection in addition to the fold detection.

The rest of the paper is organized in the following way: in section 2, we describe the detection of haustral folds. Section 3 discusses the detection of tenia. Section 4 illustrates the experimental results and section 5 presents the conclusion and future work.

2. Detection of Haustral Folds

The input to our problem for fold detection is the segmented colon volume shown in Fig. 1(A). The segmentation is performed using modified region growing and fuzzy connectedness [7]. We have so far used well segmented colons for this research. Different steps of the proposed colonic fold detection methodology are discussed below.

2.1 The Heat Diffusion

Every voxel inside the segmented colon is treated as a ‘hot’ voxel and every voxel outside the segmented colon is treated as a ‘cold’ voxel (see Fig. 1(A)). Thus, the segmented colon is set to a constant temperature $\theta_0 = 1$ and is then allowed to ‘cool down’ [8]. The heat diffusion equation is given by:

$$\partial\theta(r,t)/\partial t = \nabla \cdot D\nabla\theta(r,t) \quad (1)$$

where $\theta(r,t)$ represents the temperature at position $r = r(x,y,z)$ and time t and D is the diffusion coefficient. The temperature diffuses across the colon boundary and fills in the fold spaces after certain time. Perona-Malik’s gradient anisotropic diffusion is employed [9] to generate such candidate voxels for folds, which also includes voxels surrounding the edges. The rationale behind choosing gradient anisotropic diffusion over a standard distance transform (e.g. Danielson’s [10]) to generate the desired set of voxels for folds are to ensure some noise removal and preserve the fold structures better.

2.2 Fuzzy C-Means Clustering

The generated diffusion map identifies a set of voxels as candidates for folds. However, the candidate set contains some non-fold voxels also. This calls for applying the fuzzy c-means (FCM) algorithm [11] to classify the set of voxels into folds and non-folds. The classification for Q such voxels is done in the two-dimensional feature space \mathfrak{R}^2 , constituted by the number of ‘hot’ (having temperature > 0.9) and the number of ‘cold’ (having temperature < 0.0001) neighbors (within a spherical neighborhood of radius 6 voxels). Number of clusters C for the present problem is 2; one corresponds to the fold and the other to the non-fold. Let $u_{ij} \in [0,1]$ be the membership of a voxel v_j to belong to cluster c_i . Then, u_{ij} is given by [12]:

$$u_{ij} = \left(\sum_{k=1}^C \left(\frac{\|v_j - c_i\|}{\|v_j - c_k\|} \right)^{2/(m-1)} \right)^{-1} \quad (2)$$

where $1 < i < C$ and $1 < j < Q$. Let U be the fuzzy partition matrix and V be the cluster center vector. Then the objective function, which is minimized in the FCM algorithm, is given by:

$$J_m(U, V) = \sum_{i=1}^C \sum_{j=1}^Q (u_{ij})^m \|v_j - c_i\|^2 \quad (3)$$

The weighting exponent m is chosen as 2. The intuition behind applying the clustering algorithm in the above feature space is as follows: a fold voxel would have more hot neighbors than cold neighbors

and similarly, a non-fold voxel would have more cold neighbors than hot neighbors. This pattern can be visually observed by looking at the diffusion map in figure 1(B). Table 1 shows different parameters used in the heat diffusion and the FCM algorithm.

Label filtering, based on concept of connected pixels labeling, is employed next to isolate some misclassified voxels to further improve the above clustering process. For the present work, we use a 6-connected neighborhood for the 3D voxels under consideration [13].

3. Detection of Tenia Coli

The folds detected on colon volume are first converted on colon surface. This is because a tenia can be visualized better on a colon surface. A component labeling procedure is applied at this stage to identify the different folds.

3.1 Parameterization of the Colon Surface

We parameterize all the voxels on the colon surface including the detected folds using localized Frenet frames [14] and the centerline of the colon. The centerline serves as the approximate axis of the colon and has been previously extracted using level sets [15]. The level set-based centerline is further smoothed by fitting B-Spline. Tangent (T), normal (N) and binormal (B), which constitute a Frenet frame, are computed for each centerline voxel using the fitted B-Spline. If we consider a curve $p \in \mathfrak{R}^3$ from any colon voxel to the closest centerline point with arc-length s , then T , N and B are respectively given by the following equations:

$$T = dp/ds \quad (4a)$$

$$N = (dT/ds)/|dT/ds| \quad (4b)$$

$$B = T \times N \quad (4c)$$

For each colon voxel, we find the closest centerline vertex and then use the appropriate local Frenet frame to compute the circumferential angle (α). This angle α is the angle of a voxel projected in the plane containing the normal and the binormal [5].

3.2 Analysis of Fold Patterns for Tenia Angle

After the parameterization is complete, we first filter out incorrect folds based on certain anatomical characteristics like elongation and size. Then the extremities of each of the filtered folds are detected based on their α -values [5]. Next, we study the orientation of the detected fold extremities using a

histogram in the transverse colon. The extremities of the folds serve as anatomical landmarks/ markers for the detecting the tenia. A tenia essentially passes between these markers. The histogram has 36 bins, each of 10 degree width. A histogram peak represents a group of markers. We choose the mean angle between the highest and the nearest peaks by considering both their widths and heights. Intuitively, a tenia should consistently subtend this angle, with respect to the centerline in the section of the colon, for which the histogram has been constructed. Once this angle is determined, we pick all the voxels on the colon surface at this angle to be the constituent points for a tenia in that particular section of the colon.

4. Experimental Results

Figure 1(A) is a 2D slice of a segmented volume of a colon, obtained using modified region growing and fuzzy connectedness on the original CT volume. Figure 1(B) shows the result of diffusion map. All the voxels in gray represent the candidates for folds. It is evident from this figure that only some of these voxels, part of thin protruding structures into the segmented colon, actually constitute the folds. Figure 1(C) indicates the final fuzzy membership values of the previously identified voxels (in figure 1(B)) to belong to the cluster ‘fold’, after stable clustering is achieved. The higher the fuzzy membership value of a voxel to belong to the class ‘fold’, the brighter is the intensity of that voxel in this figure. Figure 1(D) shows the effect of thresholding the fuzzy membership values followed by a label filtering operation. All the fold voxels are represented in gray on a white colon in figure 1(D). After the connected component labeling algorithms and certain anatomical constraints are employed, incorrect folds are filtered out. Figure 2 shows a histogram of the markers in the transverse colon where the x-axis represents angles in multiples of 10° and the y-axis represents the number of markers. There are 7 markers each at angles 350° and 0° constituting the first peak and 4 markers at an angle 90° forming the nearest peak. Thus, the weighted starting angles for the highest peak and the closest second peak are 355° (equivalent to -5°) and 90° respectively. As a result, for this section of the colon we choose 42.5° as the angle for the points on a tenia. Table 2 shows the accuracy of this extraction in terms of the average and RMS physical and pixel distances between the detected tenia using the proposed methodology and the one extracted manually, for 5 different cases. The overall matching error is 0.31 ± 0.14 (cm.) in terms of physical distance and 4 ± 2 in terms of the pixel distance. Figures 3 and 4 show the

visual comparison of the same for dataset 1 and dataset 2 respectively.

Table 1. Parameters for diffusion and FCM

Diffusion (implementation using ITK) [16]	Conductance Parameter: 3.0 No. of iterations: 10 Time Step: 0.0625
FCM clustering	Convergence Criterion: 0.1 (i.e. maximum fuzzy membership difference < 0.1) No. of iterations: 3

Table 2. Accuracy of Tenia Extraction

Dataset	Average Dist. \pm RMS Dist. (cm)	Average Dist. \pm RMS Dist. (pixel)
1	0.44 ± 0.13	7 ± 2
2	0.24 ± 0.16	3 ± 2
3	0.26 ± 0.13	3 ± 2
4	0.43 ± 0.11	6 ± 1
5	0.17 ± 0.17	2 ± 2

5. Conclusions and Future Scope

We presented a novel method of detecting folds in human colon using a combination of heat diffusion and FCM clustering. These anatomically meaningful patterns are used to identify tenia coli. The later phase of identification is based on colon parameterization using Frenet frames and studying the orientation histogram of fold extremities.

As part of the future work, we plan to detect all the three teniae using the anatomical markers and do a more thorough quantitative comparative analysis. In addition, we will use the detected folds for (a) prone-supine colon registration and (b) improving colonic polyp detection, especially for the polyps on folds.

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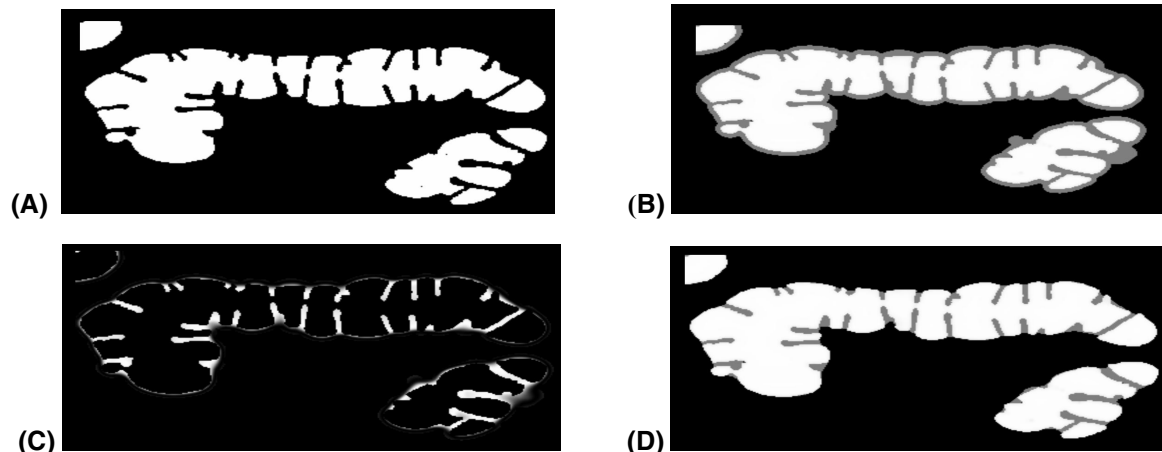


Figure 1. Stages in processing of dataset 1. A single CT colonography slice through the transverse colon is shown. (A) Segmented colon. (B) Diffusion map. (C) Fuzzy C-means clustering. (D) Label filtering and thresholding of fuzzy membership values.

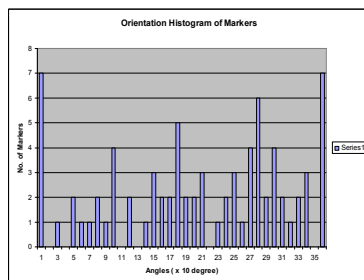


Figure 2. Orientation histogram for fold markers in transverse colon for dataset 1.

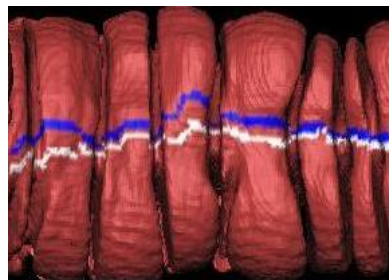


Figure 3. Detected Tenia (blue) vs. ground-truth (white) on a zoomed transverse colon (red) for dataset 1.

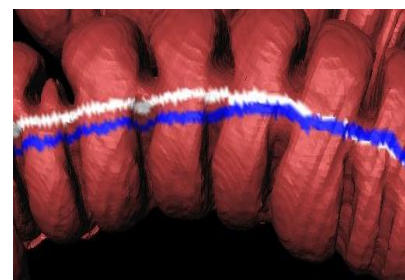


Figure 4. Same as in figure 3 for dataset 2.