Abstract—With polyps being the main cause of colorectal cancer, accurate colon segmentation is a crucial step for polyp detection in a virtual colonoscopy system. This paper presents a fully automated segmentation framework for the colon which is based on convex formulation of the active contour model. Our approach is tested on 7 sets where the results are further validated for polyp detection. Results show the efficiency of the framework with an overall accuracy of 99%, and high sensitivity of polyp detection.

Index Terms—Mumford-Shah, convexification, polyps, shape index, region growing, haustral folds.

INTRODUCTION

Colorectal cancer is the second leading cause of death among cancers and the third common type of cancers in the United States [1]. The main cause of such type of cancer is colorectal polyps. A polyp is an abnormal growth on the surface of the colon, which if not detected early, might be cancerous. Virtual colonoscopy systems aim at early detection of polyps where colon segmentation has a significant impact on the results. Unfortunately, colon segmentation is a challenging problem due to 1) the complex winding structure of the colon, 2) the presence of other organs such as small bowels, and lungs that have similar intensity, 3) the partial volume (PV) effect due to lesions, resulting in an area that combines the intensity of both air and fluid and thus disconnecting colon parts appear, 4) injection of contrast agents (e.g. barium) to tag the colon that causes the lower concave parts of the colon to have an intensity similar to that of bones and ribs; see Figure 1 for an illustration of the segmentation challenges ([2]-[4]).

Colon segmentation problem has an extensive literature with a common feature of making use of the colon connectivity. In [5], a technique was proposed to remove contrast agents inside colon parts, but artifacts were generated. In [6], a region – growing based algorithm was used along with a special bowel preparation scheme. Mustani et al. [7] used anatomical features to discard non-colon parts, but results were not very satisfactory.

This paper presents a fully automated technique to segment the colon. The framework starts with a pre-processing stage to remove the PV effect. Then the convex formulation of the active contour model is applied as the main segmentation technique. 3D Region growing is finally incorporated with anatomical features to discard all non-colonic segments.

Results show the accuracy and the efficiency of colon segmentation while other extra colonic parts are removed. Also the polyps in ground truth data are not missed due to the segmentation, which further proves the accuracy of the proposed framework in keeping all details on colon walls without missing polyps.

MATERIAL AND METHODS

PV Removal

According to the anatomical knowledge, the contrast agent injected resides in the lower parts of colon segments and a boundary between air and fluid is established. From anatomical studies [6], one can observe the following: 1) thickness of this boundary does not exceed two voxels, 2) the region above it is air, while 3) the region below is fluid. In order to have a unified intensity for all colon parts, an air-fluid boundary filter is established to detect the region where such a boundary lies, whereas its intensity along with the intensity of the fluid-filled parts are set to zero.

3D Convex Formulation of the Active Contour Model for Primary/or initial segmentation

Our earlier work in [8] generalized the global minimization of the active contour model presented in [9] to the 3D case. The global minimization scheme avoids getting stuck in local minima, and is independent of the initial solution. The 3D generalization provides a fast scheme that is needed for colon
The convex, unconstrained minimization problem used for segmentation is:

$$\min_{u,\nu} \{ TV_g(u) + \lambda \int r_1(x, c_1, c_2) u + \alpha v(u) dx \}$$  \hspace{1cm} (1)

where $\nu(\xi) = \max \{ 0, 0.2 \left( \frac{\xi - 1}{2} \right) - 1 \}$ is a penalty function, with $\alpha$ being large enough compared to $\lambda$. $TV_g(u)$ is the weighted total variation of a function $u$ with a weight function $g$ that contains information concerning the boundaries of the image. $r_1(x, c_1, c_2) = ((c_1 - f(x))^2 - (c_2 - f(x))^2)$, where $f(x)$ is the given image, and $c_1$ and $c_2 \in \mathbb{R}$. Finally, $\lambda$ is a positive parameter controlling the tradeoff between regularization process and fidelity of solution with respect to $\nu$.

A fast minimization technique was proposed in [9] to solve Eq. 1, and was extended in [8] to the 3D case. This technique is based on the dual formulation of the TV norm. Eq. 1 can be regularized according to:

$$\min_{u,v} \{ E(u,v,c_1,c_2,\lambda,\alpha,\theta) \} = TV_g(u) + \frac{1}{2\theta} \left\| u - v \right\|^2_{L^2} + \lambda \int r_1(x, c_1, c_2) v + \alpha v(u) dx, \hspace{1cm} (2)$$

As the function in Eq. 2 is convex, its minimizer can be computed by minimizing its parameters $u$ and $v$ separately according to the following:

$$\min_{u} \{ TV_g(u) + \frac{1}{2\theta} \left\| u - v \right\|^2_{L^2} \} \hspace{1cm} (3)$$

$$\min_{v} \{ \frac{1}{2\theta} \left\| u - v \right\|^2_{L^2} + \lambda \int r_1(x, c_1, c_2, v) + \alpha v(u) dx \} \hspace{1cm} (4)$$

with $u$ being fixed, and iterating of these two functions is done till convergence [9].

Extending this solution to the 3D case is performed with the parameters of Eq. 3 and Eq. 4 set as follows: $\lambda = 0.35$, $\theta = 0.1$. The constants $c_1, c_2$ are updated each 10 iterations.

The output of this phase of the framework is the colon with all other non-colonic parts that have the same intensity (lung, ribs, and small bowels). The next and last phase is to remove all those parts and keep only the colon parts that were obtained from the segmentation approach. Figure 2 shows a sample output of this phase.

**3D Region Growing with anatomical features**

Region growing is a well-known segmentation technique that has been widely used in the literature. It is applied here on the volume of the colon with a starting seed point that is selected automatically, using the anatomical fact that the last slice of the colon contains the rectum. Advancing through the volume, each new object that appears is detected, and by recursively applying region growing, the objects are classified as colon or non-colon by applying the following criteria:

**Size:** structures, such as the lung portions appear at the end of the set and the ribs are much smaller in size than colon parts. Even in case of a well-distended colon part, bowels - which have similar tomographic segments - should be much smaller in size. In our earlier work [8], a template with the size of the smallest possible well-distended colon part size was used to discard non-colon structures from the segmentation output. Nonetheless, this criterion is noticed to provide weak classification result, since for poorly-distended colons, some colon parts would be falsely interpreted as small bowels. In this paper, we add more robust geometric descriptors in order to detect non-colon parts.

**Shape index:** The volumetric shape index characterizes the topological shape of the volume in the vicinity of a voxel. The haustral folds of the colon have a shape index (SI) of values that usually lie in the ridge class (Figure 3). While those folds are absent in small bowels, SI value could be a good discriminator between colon and bowels [10]. Using the principal curvatures, SI can be computed as:

$$SI(p) = \frac{1}{2} \frac{1}{\pi} \arctan \frac{k_1(p) + k_2(p)}{k_1(p) - k_2(p)} \hspace{1cm} (5)$$

where $k_1$ and $k_2$ are maximum and minimum principal curvatures, respectively. All shapes could be mapped to the
interval \( SI \in [0,1] \). Figure 3 shows the most representative associated local shapes of SI according to [11].

**Curvedness:** It is considered to be a dual feature to the shape index that provides scale information about how much shape the neighborhood of a voxel includes. It is given by:

\[
CV(p) = \sqrt{\frac{k_1(p)^2 + k_2(p)^2}{2}}
\]  

Maximum and minimum principal curvatures for each voxel on the iso-surface of the set are calculated, and based on the calculated shape index values; the haustral folds are proved to have high SI values (> 0.5), as they fall in the ridge class, Figure 3. The same procedure is conducted for small bowels, and much lesser points on the bowel surface satisfy that criterion of having that high shape index value. The small bowels usually fall in the same class of shapes for the colon walls, with SI values of less than 0.3. Also haustral folds have high curvedness values (> 0.3), whereas small bowels, like colon walls have small curvedness values (<0.1). Accordingly, a criterion for colon/small bowel separation is established based on the number of points of each object which lie in the ridge class, and with high CV value. Values which meet such criterion are stored in an array for each object. The array length for each object is found a good discriminator between colon parts and small bowels. For the 7 data sets used for this study, the mean of the ratio between colon object array length and small bowel array length is ~3. Figure 4 shows a comparison between color maps of SI and CV of haustral folds of a colon part and for a small bowel part.

The output of this part was just the entire colon with all of its parts got from the previous stage of the convex active contour model. Sample result is shown in Figure 2. The segmentation framework was applied to 7 sets, including cases of broken and poorly-distended colons. Five of the seven sets are supine scans, and the remaining two are prone scans. One of the sets has been provided by the 3DR Inc., Louisville, KY, and the rest of them were received from the Virtual Colonoscopy Center, Walter Reed Army Medical Center, Washington, DC. The patients underwent standard 24- hour colonic preparation by oral administration of 990 ml of sodium phosphate and 10 mg of bisacodyl; then consumed 500 ml of barium (2.1 percent by weight) for solid stool tagging. The CT scanner was either GE LightSpeed or LightSpeed Ultra. The CT protocol included 1.25 mm to 2.5 mm collimation, 15mm/second table speed, and 100 mAs and 120 kVp scanner settings. A dataset contains 400 ~ 500 slices, and the spatial resolution for 1.0 X 1.0 X 1.0 mm. The 7 sets used had a total number of 5 polyps, 4 of which are large (> 10 mm), and one was small (<9 mm).

**RESULTS AND VALIDATION**

Results are validated using the ground truth data which were segmented by the aid of physicians, and the accuracy is measured based on,

\[
\text{Accuracy} = \frac{TP + TN}{TP + FP + FN + TN}
\]  

where TP is the number of true positives (e.g. an existing colon segment that is correctly identified), TN is the number of true negatives (a segment that is correctly rejected, as it is not colon), FP is the number of false positives (an incorrectly identified segment as colon), and FN is the number of false negatives (a segment is rejected while it is colon). The proposed framework has an overall accuracy of 99%. 

![Figure 4](image-url) - (a) Color map of colon and bowels from a section of a data set, where folds of the colon (SI> 0.5 and CV>0.3) are colored in dark blue, and bowels that did not meet the criteria are not colored. (b) colon parts of (a) are shown without the small bowels for clarity, where parts that met the criteria of SI and CV for folds are in dark blue, and the colon walls are in red.

![Figure 5](image-url) - (a) sample result of a color map of a colon polyp inside the yellow ellipse, where it met the criteria of polyp detection (SI> 0.7, CV between 0.1, 0.2, and SP < 1.2).

Further validation of results is assessed by detecting polyps of the colon sets segmented with the proposed framework and comparing to the ground truth to see if the segmentation step missed polyps on the colon walls. Polyps usually lie in the cap class (SI≈1, Figure 3), with small to medium curvedness values (> 0.1, and < 0.2). This accounts for automated detection of polyps in the segmented colons where we color-coded these voxels that meet the shape index criterion in both ground truth data and segmented data. Finally the percentage of polyp detection is computed by
dividing the number of polyps detected from the segmentation by the number of polyps that are present in the ground truth. In order to be able to detect all polyps, SI threshold is relaxed to be > 0.7. Another important feature a polyp has is the sphericity ratio which measures how much the shape is rounded. It is defined as,

\[ SP(p) = \frac{\text{abs}(k_1 - k_2)}{H} \]  

(8)

where \( H \) is the mean curvature. In this experiment, we used SP < 1.2 for polyps.

Applying the thresholds of SI, CV, and SP, Figure 5 shows a sample of a color map of a polyp detected from one of the sets used in this paper using the proposed segmentation framework. To further assess the segmentation framework in terms of polyp detection ability, the fly-through technology (a widely used technique in virtual colonoscopy systems) was used to navigate inside the colon. Fly-through primarily depend on a virtual camera with a specific field of view moving along a special planned path inside the colon, usually its centerline, to render its internal views. Figure 6 shows results of navigating inside a segmented colon set, while a polyp was detected.

The segmentation framework is able to detect all of polyps present in the used data sets with an overall sensitivity of 100% (where 5/5 of the polyps were detected).

CONCLUSIONS

This work introduces a fully automated segmentation framework using the convex formulation of the active contour model with incorporation of some anatomical features. We introduced the use of robust geometrical descriptors to aid the classification of colon versus non-colon part in the segmentation output. The system achieved highly accurate results, with accurate detection of polyp. Future work will be focusing on the detection of more challenging polyps’ cases, such as detection of smaller polyps and polyps in harder areas. This will test the accuracy of the segmentation framework and will require relaxation of the ranges put for the polyp’s geometry without having any errors at the same time.

REFERENCES


