Benefits of Centerline Analysis for CT Colonography Computer-Aided Polyp Detection

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ABSTRACT

The purpose of this paper is to assess colonic distension and length and to evaluate a polyp matching algorithm on prone and supine studies in CT colonography (CTC) computer aided diagnosis (CAD). Our CTC CAD software was used to reconstruct the colonic surface, to compute the colon centerline and to detect spatial positions of polyps. Normalized distance along the centerline (NDAC) and colon distension at each polyp were compared in prone and supine positions. 8 patients presented 12 polyps detected in both supine and prone positions and confirmed by colonoscopy. NDAC for all polyps were very similar in supine/prone positions. The average NDAC differences were 0.01 +/- 0.01 which indicates excellent agreement. Colon profiles (distension vs. DAC) were not similar in supine/prone positions due to high variability of colonic distension and mobility of the colon when the patient was repositioned. However the final colon lengths and average distension were very similar (average difference was 4.5%). Also, as could be expected from normal anatomy, the cecum and rectum tended to have the greatest distension and the rectum tended to be better distended on the prone exam. The colon centerline provides a natural coordinate reference and is a useful tool for CTC CAD.

1. INTRODUCTION

In the United States, cancers of the colon and rectum combined are the second most common cause of cancer death in both men and women. Many of new cases and deaths from colorectal cancer are preventable by improvement in nutrition and physical activity and by timely use of existing colorectal screening tests [1]. CT colonography (CTC) is a new diagnostic technique that can be very useful for screening since it is less invasive, more comfortable for the patient and is likely to be less expensive. CTC based on CT images of the patients rather than classical optical colonoscopy. CTC computer aided diagnostic (CTCCAD) uses the CT slices of the patient to reconstruct the colonic 3D surface and then, based on the computed features of the 3D surface and CT volume data, detects the polyp candidates that finally should be presented to the radiologist who has the final decision: polyp or non-polyp.

In order to evaluate our work we compare automatically our detections with the database of real polyps found by the colonoscopist and matched to the CT images by a radiologist. The sensitivity and specificity that are subsequently computed give us a measure of our CTCCAD performance. To each potential polyp detected by our CAD software we can assign a (normalized) distance along the centerline (NDAC) which is a natural way of localizing the detection along the colonic surface. Thus a complementary way to select a region as a potential polyp is the degree of matching between its NDAC values in supine and prone scanning conditions. Our motivation is to evaluate such a polyp matching algorithm on prone and supine studies and to assess colonic distension and length, using a computed centerline of the reconstructed colonic surface. Colon distension and NDAC could be also used for the evaluation of the performance of our polyp detector, i.e. analyzing number of detections as a function of local colon distension or as a function of colon regions.

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2. METHODOLOGY

2.1 Colon segmentation and polyp detection

Since there is a great amount of CT data (typically we have 150 images, 512x512 pixels each) a manual approach in which the physician should analyze each CT image is not feasible. Excessive interpretation time and inter-observer variability are actually the two main areas of concern regarding the CTC [2]. So we need to process automatically the 3D colonic surface and the volume CT data and select only a small volume/area which should finally be visually analyzed by the radiologist.

Our software uses a semi-automated interactive approach to segment the interior of the colon. The user interaction is minimal and consists only of placement of seeds inside the colon, performed by the radiologist. A region growing algorithm then extracts the colonic surface. We need more seeds only in the case of collapsed colons, when the region growing stops before the whole colon is segmented. If the colon is well distended a single "user click" (or "seed") is enough. The reconstructed 3D colonic surface together with the original CT data allow us to compute 2D/3D features like curvature, sphericity or wall thickness. We are thus able to eliminate a great part of the colonic surface (70% to 97%) by selecting for further analysis only regions having elliptical curvature and sphericity above certain thresholds. Other important features also included in our analysis are: lesion size, region density and wall thickness. The potential polyps' positions are computed based on these features and finally the user is able to analyze the 3D colonic surface colored according to polyp detections and the original CT images where the detections are also highlighted.

2.2 Centerline computation

Detecting the centerline of the colon is a challenging problem. In one common approach, the radiologist has to manually trace the entire centerline or identify numerous centerline points (keyframing). There is of course a large inter- and intra-observer variability in this case but probably the biggest disadvantage is the huge amount of user effort necessary to build the centerline since there are 150 or more images per patient which need to be analyzed. To address this problem methods of centerline determination have been developed including computing center of mass for growing voxels [3], cell decomposition [4], topological thinning ("onion peeling"), skeletons and cost functions [5, 6], penalized distance from a source field ([7-11])and Dijkstra shortest path [12].

Unlike most of the other approaches, our centerline extraction method does not require any user interaction. Provided the colon is not collapsed, we can extract the centerline fully automatically. We do not use any rectangular grid to place the vertices so we provide flexibility in choice of the control points' position and consequently we need fewer computational and storage resources. Unlike skeletons (the most common approach for centerline computation) our method preserves the colon topology (no branches are added) so it is ideal for segmenting cylindrical shapes. The most important difference between existing methods and ours is that we do not want to use the whole 3D data but only the 3D surface that is generated by our existing CTC software. This approach allows us to keep the processes separable and reduce the amount of data that needs to be processed.

We start with the high resolution original colon surface (OC) and we compute a decimated colon surface (DC) and then a thinned version of the decimated colon (TDC). In this paper we use the term "rings" to define cross-sections of the (original or thinned) colon that are roughly small cylinders. Also by "perpendicular rings" we mean rings whose axes are parallel to the centerline of the original or thinned colon. By TDC we mean a 3D surface, obtained from the DC surface (which in turn is based on OC which was reconstructed using the parallel CT images). The TDC has the same number of vertices as the DC and the same graph structure – the connectivity of all vertices is the same. We will describe below all six operations applied sequentially in our algorithm:

1. Decimation: OC surface is preprocessed to reduce the number of triangles and vertices composing it. The result is DC. The triangle mesh of the original colon needs to be decimated because the thinning algorithm is computationally expensive. The decimation maintains the general appearance of the colon surface but reduces the number of vertices. We decimate the colon vertices by 80%. For decimation we use [13]. We only need the two surfaces (OC and DC) to be similar. We will use later (in step 6) a mapper that associates vertices in the OC with the vertices in the DC.

2. Thinning: The TDC is computed by iteratively averaging the distances between colon vertices in the DC. The thinning is equivalent to applying a Laplacian operator to each vertex Vi. If vertex Vi has N_V neighbors and all of these neighbors are in a neighborhood v*, we obtain the formula for thinning:

$$V_i = V_i + \frac{\sum_{v_i \in v^*} (v_j - V_i)}{N_V} = \frac{\sum_{v_i \in v^*} v_j}{N_V} \quad \textbf{(1)}$$

Thinning is done iteratively, e.g., typically 1000 iterations of thinning. Figure 1 shows a human colon thinned 250, 500 and 1000 times.

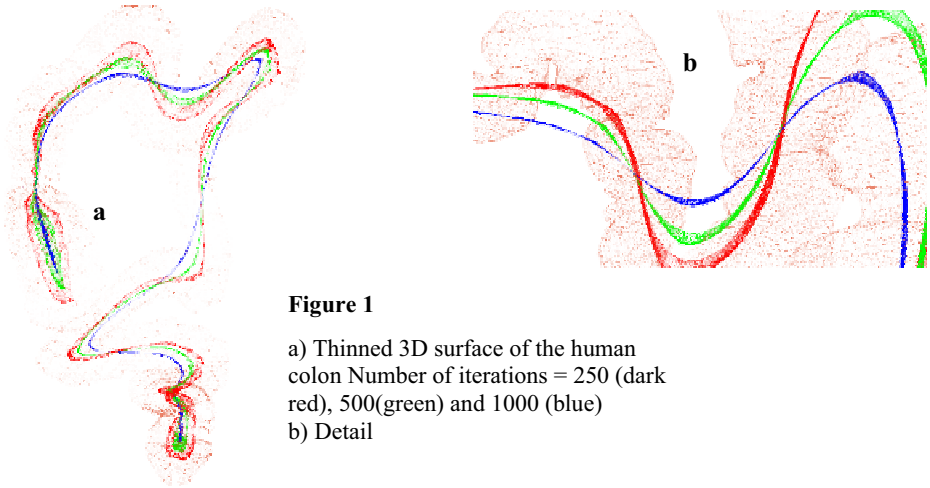


Figure 1

a) Thinned 3D surface of the human colon Number of iterations = 250 (dark red), 500(green) and 1000 (blue)
b) Detail

3. Modeling: The TDC is modeled by an ordered group of 3D points by taking approximately equally-spaced vertices from the thinned colon (see Figure 2). We start with a random vertex V0, and then moving from neighbor to neighbor (and marking each visited vertex) we find another random vertex V1 at a certain distance. These first 2 vertices (V0 and V1) give us a direction $\vec{D}1$. We then select the third vertex (V-1) at the same distance from the first one (V0) but in the opposite direction to $\vec{D}1$. From that moment, we have two models of the same thinned colon, each covering its distinct part of the colon. We only check new (unmarked) vertices to see if the distance is appropriate: we add vertex V2 at a certain distance from V1 and V-2 at a certain distance from V-1, without checking any direction information. Since we go from neighbor to neighbor and the colon is thinned the resulted models cover the entire colon. When we cannot find any new model vertices we stop and merge the two resulted models.

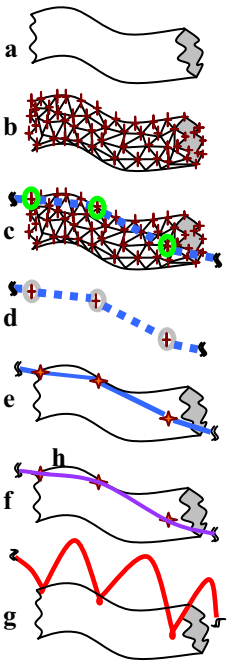
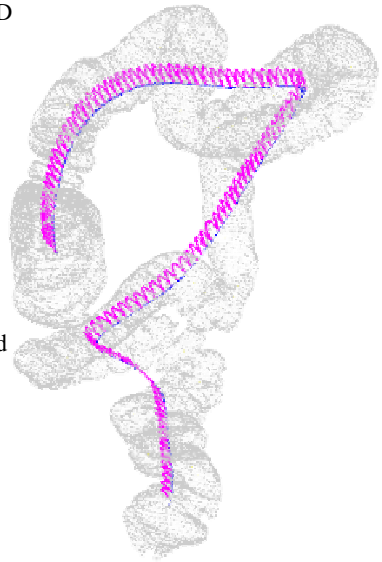


Figure 2

Modeling the colon by an ordered set of 3D points
a) portion of the (thinned) colon
b) same portion, but vertices and their connectivity are also displayed
c) some vertices are selected to model the thinned colon
d) model of the thinned colon
e) portion of the (thinned) colon and its model
f) portion of the (thinned) colon and its spline interpolated model
g) In this paper we display the position and order of the model vertices using a red curve
h) Human colon – thinned (blue) and original colon OC (grey). The violet curve shows the position of the thinned colon model points.



4. Remapping: We use the model to compute rings perpendicular to TDC. Using the one-to-one mapping of the vertices on the TDC and DC, the indices of the vertices from the same ring are used to get a slice (or a ring) in DC.

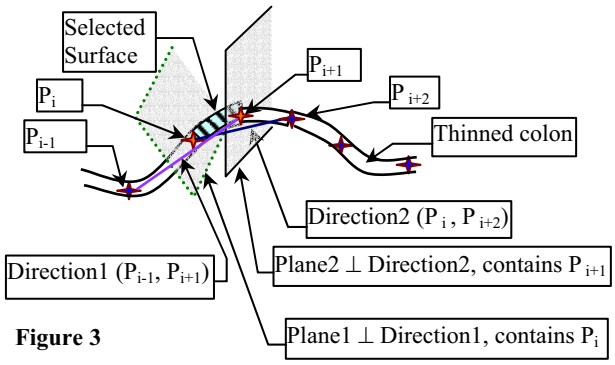
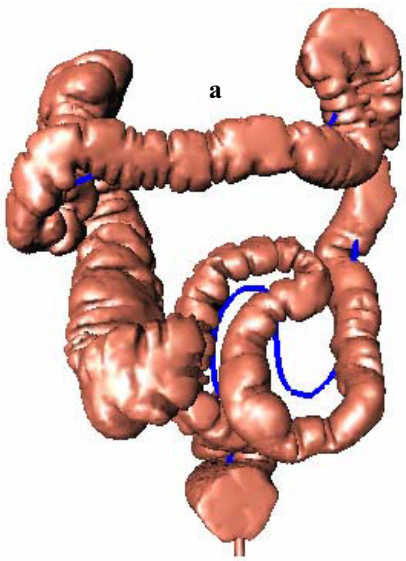


Figure 3

The selected area is between Plane1 and Plane 2.
These planes are computed based on selected vertices

The remapping algorithm uses each 3D point Pi (see Figure 3) of the model and the adjacent points Pi and Pi+1 of the model to compute two planes perpendicular to the thinned colon model, one passing through each of the corresponding points Pi and Pi+1. These planes define a perpendicular ring of TDC. We then select all the vertices of TDC that lie between these two planes and map these vertices one-to-one to DC. We can perform the one to one mapping because the TDC has the same number of vertices as the DC and the same graph structure – the connectivity of all vertices is the same.



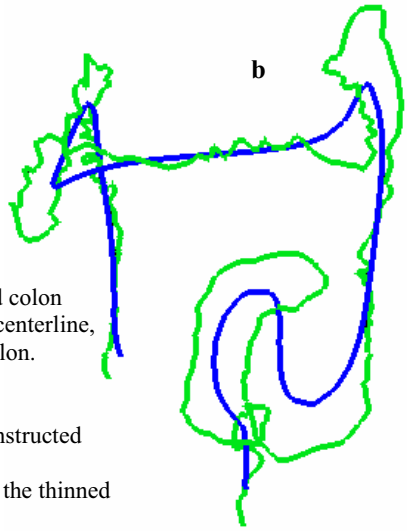


Figure 4

a)Human Colon, thinned colon model (blue line) AND centerline, not visible, inside the colon.

b) Final results:
- green curve = the reconstructed centerline of the colon
- blue curve = model of the thinned version of the colon

5. Centerline computation: The ring-like areas in the DC are averaged to compute the local centerline point (see Figure 4).

6. Mapping DC to OC: We built a mapper that associates vertices in the OC with the vertices in the DC. This mapper is based on the minimum distance between the vertices in the two surfaces. This mapper gives us the rings in the OC. The centerline of the OC is the same as the centerline of the DC (obtained at step 5). If the colon surface was collapsed we used a minimum distance criterion and user supervision to link disconnected colon segments.

4. RESULTS

11 patients underwent CT colonography after having a classic colonoscopic inspection. 12 polyps (visible in both supine and prone) were present in 8 patients, detected by our CTCCAD software and confirmed by colonoscopy.

The centerline algorithm was tested by visual inspection of the resulting colonic surfaces. We obtained a centerline that stayed inside the colon except in extreme cases such as nearly collapsed segments having a wall convex to the lumen. The programs were run on a Dell Workstation PWS530 PC with 1500 MHz processor running the Windows 2000 operating system. The total average execution time was less than 1 minute (maximum time was 90 sec).

We also build a colon model and computed the error between 100 computed centerline points and corresponding points along the axis of a cylindrical colon phantom (see Figure 5). The average error was 1.1 mm which is appropriate for clinical use.

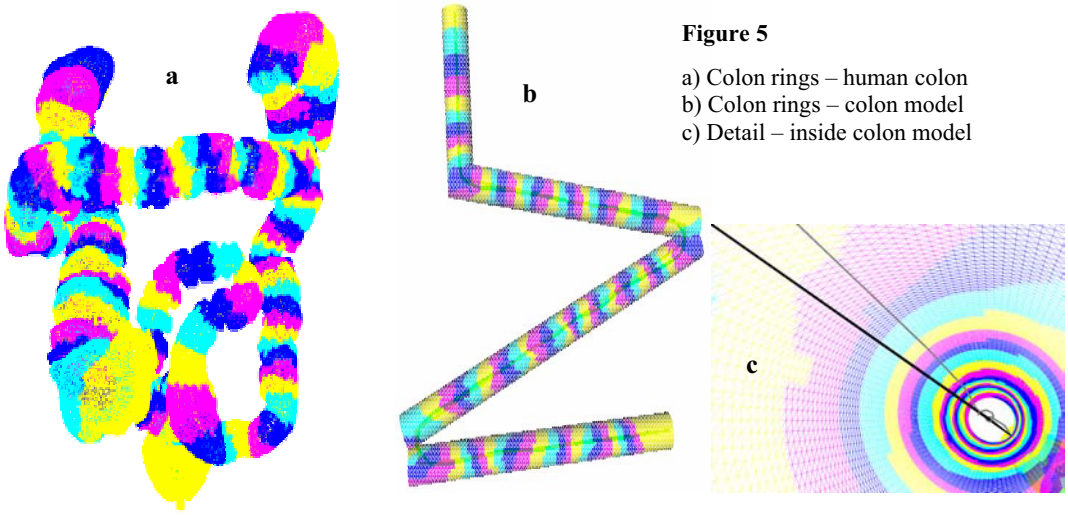


Figure 5

a) Colon rings – human colon
b) Colon rings – colon model
c) Detail – inside colon model

3.1 Colon profiles

Using the computed centerline as a coordinate system we assigned to each colon vertex a local distension and a distance along the centerline (DAC). Spatial positions of polyps were obtained using existing CTC CAD software. Normalized (to final colon length) DAC and colon distension of each polyp were compared in prone and supine positions. We constructed colon profiles (distension vs. DAC) for all the patients and compared final length and average distension for supine/prone colons.

We built colon profiles by plotting colon distension versus normalized distance along the colon centerline (NDAC). The plots in Figure 6 show local colon profiles as a thin violet curve and rolling averages in dark blue. The rolling averages were performed with a mobile window of 5 samples to provide a smoother curve and show the local trend. The horizontal axis values are given by the normalized distance along the centerline for each ring while the vertical axis values are given by the average distension of the colon ring.

Usually colon profiles are not similar in the supine and prone positions due to high variability of the colon and different scanning conditions (air is typically lost and re-insufflated between the scans). However the final colon lengths and average distension were very similar, as expected.

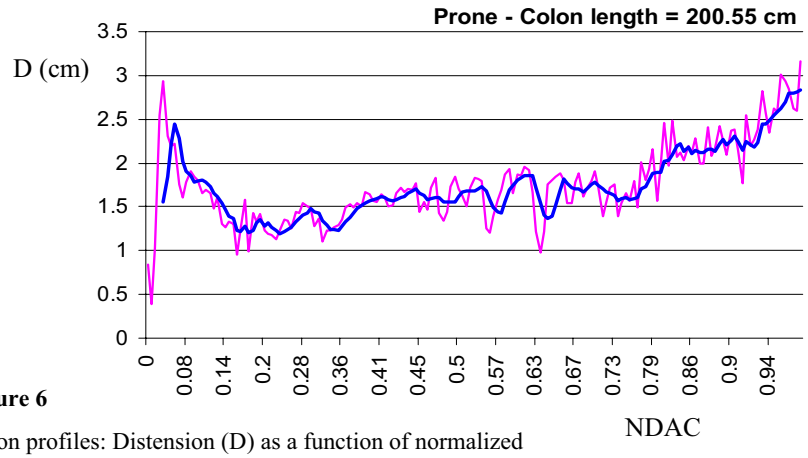
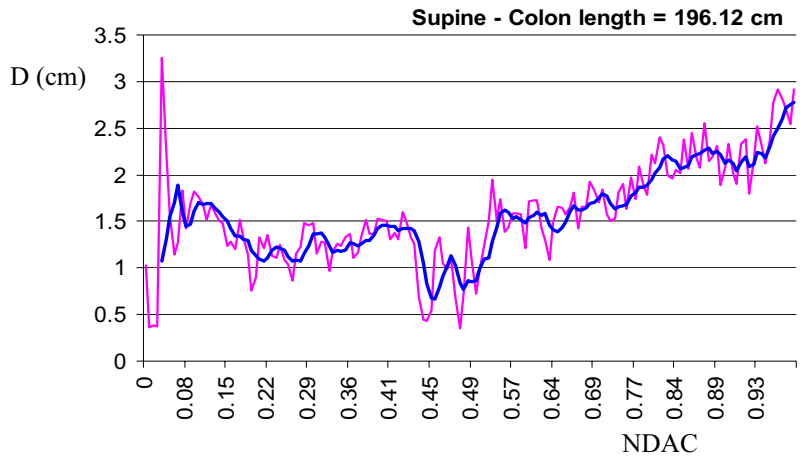


Figure 6

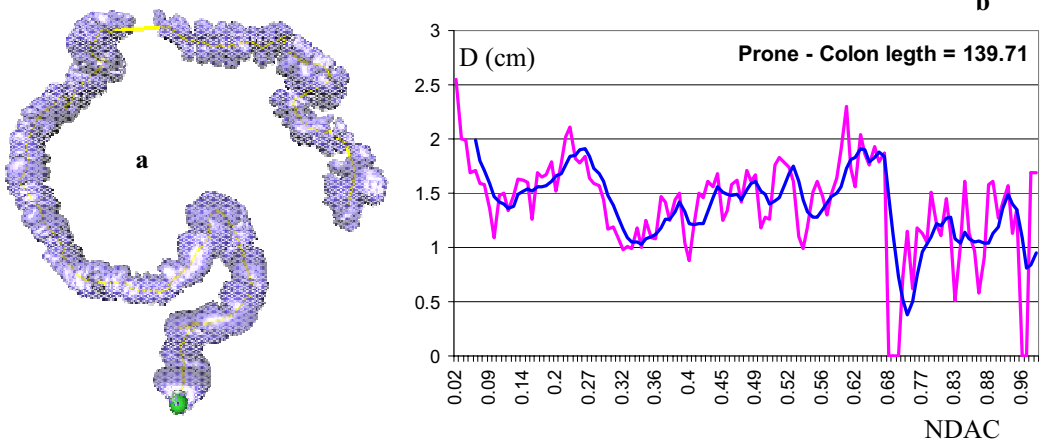
Colon profiles: Distension (D) as a function of normalized distance along the centerline (NDAC)



Also, as could be expected from normal anatomy, the cecum and rectum tended to have the greatest distension and the rectum tended to be better distended on the prone exam. Future improvements in surface reconstruction and more distended CTC exams should allow us to avoid collapsed colon surfaces (see Figure 7) which affect the final colon length and the corresponding normalized DAC.

Figure 7

Collapsed colon:
a) 3D surface and centerline b) Colon profile



3.2 Comparison of NDAC values in supine and prone positions

In our study, 12 polyps (visible in both supine and prone) were present in 8 patients, and for 11 polyps colon lengths and average distension were very similar in supine and prone modes. In the 12-th case the colon was collapsed in different parts in supine and prone modes so its values were discarded.

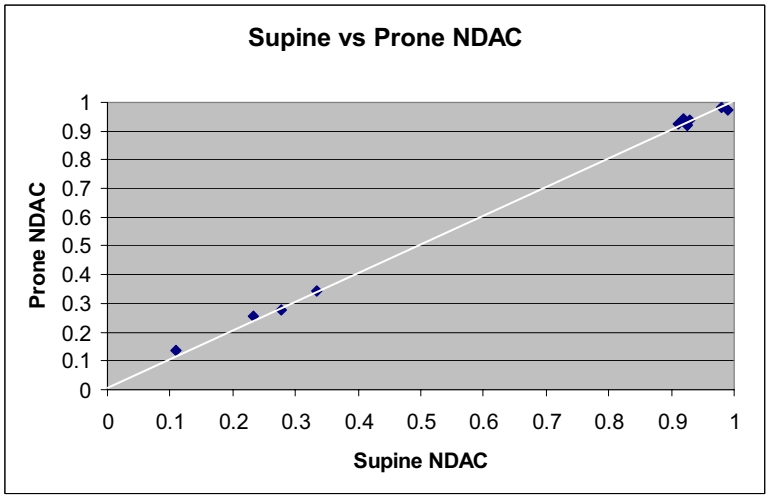


Figure 8

Comparison of NDAC for 11 supine/prone pairs

Normalized DAC (NDAC) for all polyps were very similar in supine and prone positions for all patients except one. In this last case the surface was not correctly reconstructed (rectum was collapsed in the supine position which lead to an incorrect origin of the normalized DAC). Without this last abnormal case, the average NDAC differences were 0.01 +/- 0.01 which indicates excellent agreement. The slope in Figure 8 is 45^0. The NDAC values give points close to the diagonal, as expected. More studies are necessary to fill the above plot and prove the method's accuracy.

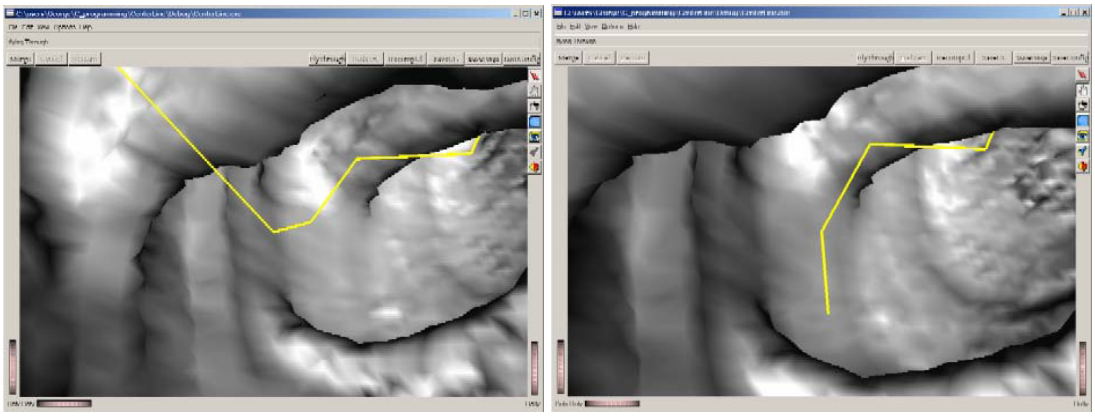
3.3 Virtual fly-through path

We also use the computed centerline to compute the path for a a virtual fly-through which can be used to access the polyps in a natural way – navigating inside the colon along the centerline. Having the centerline points, the virtual fly through engine is easy to build using a "camera" – a standard element in every 3D library. For each 3D point Pi of the centerline, camera position is given by Pi while camera orientation is given by (Pi+1, Pi) direction. Open Inventor's camera even provides the convenient pointAt and position methods. To perform the automated fly-through we only need a "timer" (another standard element) to update the index of the current centerline point "i". Thus, the pseudo-code for the timer subroutine becomes:

```
{
        (camera->position).setValue (Pi);
        camera->pointAt(Pi+1);
        i++;
}
```

Figure 9

Consequent virtual fly through (inside the colon) images,
obtained by navigation along the computed centerline (yellow curve).



5. CONCLUSIONS

The colon centerline provides a natural coordinate reference for colon elements and is a useful tool for CTC CAD. We have developed a novel method to segment topologically cylindrical shapes such as the colon. Our method is fully automated for well-distended colons and fast for large colonic surfaces (500000 triangles). Our method is quick: the processing times average only 1 min (maximum 90 seconds). Our algorithm provides virtual fly-path elements (projection of the rings onto a plane perpendicular to their axis).

We use the centerline as a reference along which to measure distance along the colon and differentiate polyp candidates, for validation of polyp detection by matching detections on the supine and prone exams and for virtual fly-through path planning. Provided we can reconstruct the 3D colon surface from the colonoscopy images, a challenging application would be to perform image registration and polyps' matching from CTC CAD detections to optical colonoscopy results. The computed centerline could also be used to split the colon into natural segments and allow conduction of per region polyp studies.

ACKNOWLEDGMENTS

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