A Novel Technique for Reducing False Positive Detections in CAD-CTC

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Abstract

Computed tomography colonoscopy (CTC) is an emerging alternative to conventional colonoscopy for colorectal cancer screening. A series of *computer assisted diagnosis* (CAD) techniques have been developed for use in CTC. Although high levels of accuracy for polyp detection have been reported, the problem of excessive false positive detections still warrants attention. We present a CAD-CTC technique that has been developed specifically to reduce the number of false positive detections without compromising polyp detection accuracy. The technique incorporates a novel intermediate stage that restructures initial polyp candidates so that they conform more closely to the shape of actual polyps. The restructuring process causes false positives to expand to include more false positive characteristics, whereas, actual polyps retain their original polyp-like characteristics. An evaluation of the documented technique demonstrated that it can be successfully applied to the majority of polyp candidates, and that its use can reduce the number of false positive detections by up to 57.8%.

Keywords: Colon cancer, polyp, CTC, curvature, CAD

1 Introduction

Colorectal cancer is the second most common cause of cancer-related death in developed countries. Regular screening can reduce the level of mortality associated with this type of cancer. Colonoscopy is typically used for colorectal cancer screening and involves a thorough endoscopic examination of the large intestine. *Computed tomography colonography* (CTC) [1] is a minimally invasive alternative to conventional colonoscopy. A CTC examination involves obtaining an abdominal CT scan of a suitably prepared patient. One of the most active areas of CTC research deals with the *computed assisted detection* (CAD) of colorectal polyps. A number of CAD techniques have been proposed in the literature. Early techniques identified polyps as regions of abnormal colon wall thickness [2]. More recently, the surface curvature characteristics of mesh based [3] and voxel based [4] representations of the colon surface have been used for initial polyp candidate detection. CAD techniques have also been proposed that are intended to identify polyps based on the methods and techniques that radiologists use to identify polyps at conventional, manually read, CTC [5, 6]. Current CAD-CTC techniques typically consist of two stages: Initial polyp candidate detection, followed by false positive reduction. Although high levels of accuracy have been reported, the problem of excessive false positive detections still warrants attention. This paper describes a CAD-CTC technique that has been developed specifically to deal with the problem of false positive detections. The documented technique includes a novel intermediate stage that restructures polyp candidates so that they conform to an elliptical model. The restructuring process causes false positive regions to include more false positive characteristics, whereas, actual polyps retain their original polyp-like characteristics. An evaluation of the restructuring process demonstrates that it can be successfully applied to the majority of polyp candidates, and that its use significantly reduces the level of false positive detections.

2 Methods

A cohort of 37 patients underwent CTC in the prone and supine positions followed immediately by conventional colonoscopy. The details of the patient preparation and the CTC protocol are outlined elsewhere [7]. In four cases patients were only scanned in a single position and in two cases only

partial data sets were supplied. Consequently, a total of 68 valid data sets, containing an average of 263 slices, were available for use in this study. All of the polyps contained in the data sets were identified by a radiologist who had experience in CTC, and who was unblinded to the conventional colonoscopy results. The size and location of each polyp, i.e. the gold standard information, was recorded and ultimately used for system training and evaluation. An isometric representation of each data set was obtained using trilinear interpolation. The colon lumen was segmented from the isometric data sets using 6-connected, 3-D region growing. A modified version of the original marching cubes algorithm [8] was used to generate a mesh representation of the colon surface. The modifications ensured the generation of airtight surfaces; facilitated mesh based region growing; and determined the shape and density characteristics of the colon surface at each vertex location. A total of six vertex level shape characteristics were calculated. The mean curvature H and Gaussian curvature K were obtained using the technique described in [9]. These values were subsequently used to calculate the principle, i.e. minimum $\kappa_{\min}$ and maximum $\kappa_{\max}$, curvatures at each vertex location:

$$\kappa_{\min}, \kappa_{\max} = H \pm \sqrt{H^2 - K}, \quad \kappa_{\min} \geq \kappa_{\max} \qquad (1)$$

The principle curvatures were in turn used to calculate for shape index SI and curvedness C values as outlined in [10]:

$$SI = \frac{1}{2} - \frac{1}{\pi} \arctan\left(\frac{\kappa_{\min} + \kappa_{\max}}{\kappa_{\min} - \kappa_{\max}} \right) \qquad (2) \qquad C = \frac{2}{\pi} \ln \sqrt{\frac{\kappa_{\min}^2 + \kappa_{\max}^2}{2}} \qquad (3)$$

Initial polyp candidates were identified from the mesh representation of the colon surface using a hysteresis thresholding technique derived from the voxel based approach outlined in [3]. A candidate level feature, sphericity S, was subsequently calculated for each candidate region.

$$S = \frac{\overline{\kappa}_{\min} - \overline{\kappa}_{\max}}{\overline{H}} \qquad (4)$$

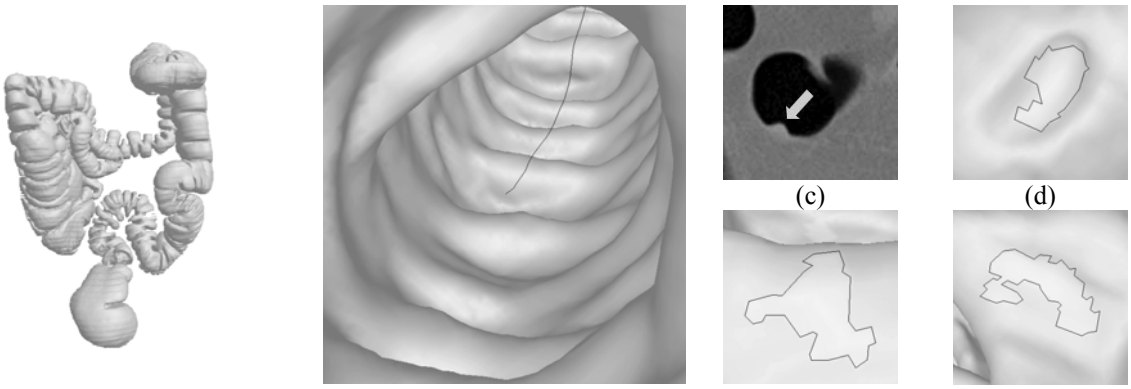
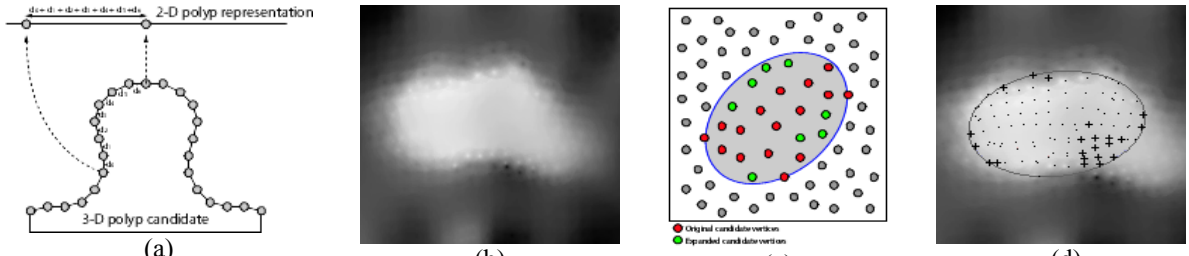


Figure 1: Segmentation and initial candidate detection. A surface rendering of the exterior of the colon (a). A surface rendering of the interior of the colon (b). 2-D and 3-D representations of the same polyp (c) & (d). Typical false positive detections (e) & (f), note the irregular shape of the boundary.

An alternative 2-D representation of each candidate was obtained by projecting the candidate region and its surroundings onto a plane perpendicular to the normal of the central candidate vertex. This projection preserved the direction of each vertex with respect to the central vertex and also preserved the geodesic distance, along the surface of the colon, from each vertex to the central vertex. The projection process is illustrated in Figure 2(a) and the projected version of the polyp candidate from Figure 1(d) is illustrated in Figure 2(b). Candidate expansion was achieved by identifying the *minimum bounding ellipse* (MBE) for the projected candidate points using [10] and adding any additional points enclosed by the MBE to the candidate region. The candidate expansion process is

illustrated in Figure 2(c) and the expanded version of the candidate from Figure 2(b) is illustrated in Figure 2(d). Three additional features; expansion, eccentricity and protrusiveness; were calculated during the candidate projection and expansion processes. A minimum distance classifier was ultimately used in the final stage of the system to compare the use of original and expanded candidates for the detection of colorectal polyps. In each case the candidate feature vector consisted of *S* and mean values *H*, *K*, *SI* and *C*.

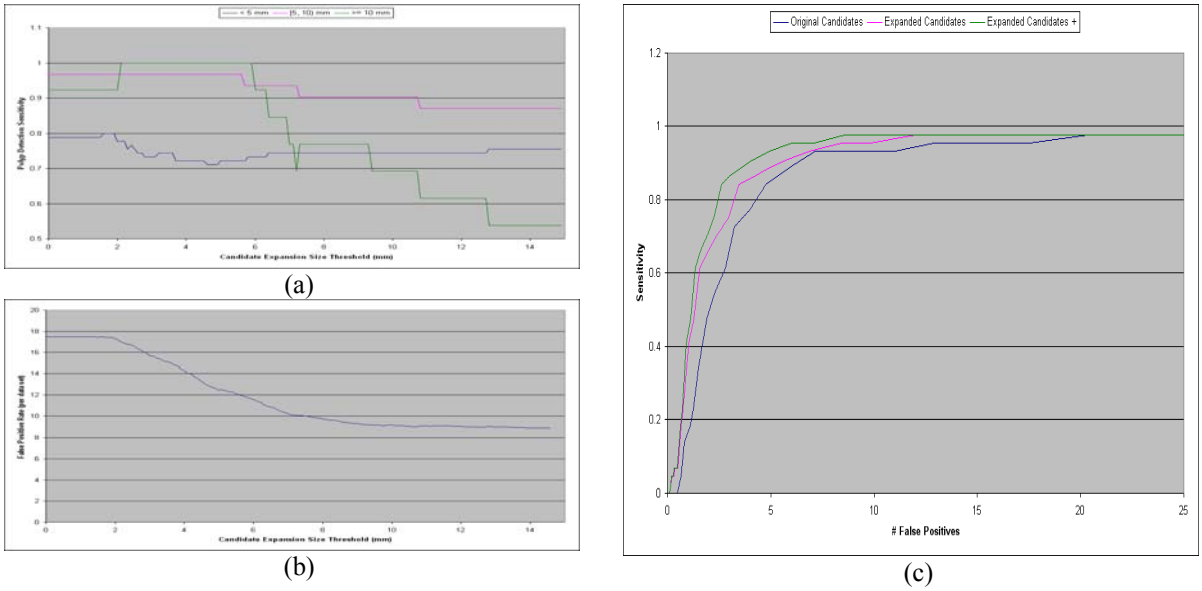


(a) (b) (c) (d)

Figure 2: The polyp projection and polyp expansion processes. (a) A crossectional illustration of the candidate projection process. (b) The projected version of the polyp candidate from Figure 1(d). (c) An illustration of the candidate expansion process. (d) The expanded version of the candidate illustrated in (b).

3. Results

There were a total of 155 colorectal neoplasia present in the 68 CTC data sets that were used in this study. Forty four of these were clinically significant polyps (i.e. ≥ 5 mm in), 11 were colorectal masses, two were flat polyps (both < 5 mm) and the remaining 98 were all < 5 mm in size. The leave-one-out approach was used for system evaluation. The decision boundary for the classifier was initially set to lie midway between the mean feature vectors for true polyps and the mean feature vector for false positives. The threshold for candidate expansion was varied from zero to the size of the maximum candidate region. The size of a candidate region was taken to be the length of the major axis of its MBE. A plot of polyp detection sensitivity versus candidate expansion threshold is illustrated in Figure 3(a) and a plot of the number of false positives per data set versus candidate expansion threshold is illustrated in Figure 3(b). The optimal operating threshold for the candidate expansion process was found to be 5.6 mm (Note that a candidate region of this size may be representative of a much larger underlying polyp).



(a) (b) (c)

Figure 3: Parameter selection and performance characterisation. (a) A plot of polyp detection sensitivity versus candidate expansion size threshold. (b) A plot of false positive rate versus polyp detection sensitivity. (b) A ROC curve illustrating the polyp detection sensitivity versus false positive rate for regular candidates, expanded candidates and expanded candidates plus additional features.

At this level 10,900 (87%) of the 12,250 initial polyp candidates were successfully expanded without adversely affecting polyp detection sensitivity. In fact, the sensitivity for the detection of large polyps (≥ 10 mm) was found to increase. The performance of the system was characterised by moving the decision boundary of the classifier between the mean true polyp feature vector and the mean false positive feature vector. The resulting series of ROC curves are illustrated in Figure 3(c). At a sensitivity of 97% original candidates generated 20.4 false positive per data set, whereas expanded candidates generated 12.0 (a reduction of 41.2%). The use of the additional features calculated during the candidate projection and expansion processes was found to reduce the number of false positive detections further to 8.6 per data set (an overall reduction of 57.8% compared to the use of original candidates).

4. Conclusions

This study demonstrated that the use of polyp candidate expansion can significantly reduce the number of false positive detections in CAD-CTC. Candidate expansion was applicable to 87% of all of the initial polyp candidate regions, and reduced the level of false positive detections by 41.2% without adversely affecting polyp detection sensitivity. When the additional features calculated during the candidate projection and expansion processes were also used, the total reduction in false positive detections was found to be 57.8%. Candidate expansion was not applicable in the case of large candidate regions (i.e. 13% of candidates) due to inaccurate candidate coverage. However, further research dealing with the refinement of the initial candidate detection process should enable polyp candidate expansion to be applied in all cases.

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