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Segmentation in virtual colonoscopy using a geometric deformable model

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Abstract

The Geometric Deformable Model is developed for accurate colon lumen segmentation as part of an automatic Virtual Colonoscopy system. The deformable model refines the lumen surface found by an automatic seed location and thresholding procedure. The challenges to applying the deformable model are described, showing the definition of the stopping function as the key to accurate segmentation. The limitations of current stopping criteria are examined and a new definition, tailored to the task of colon segmentation, is given. First, a multiscale edge operator is used to locate high confidence boundaries. These boundaries are then integrated into the stopping function using a distance transform. The hypothesis is that the new stopping function results in a more accurate representation of the lumen surface compared to previous monotonic functions of the gradient magnitude. This hypothesis is tested using observer ratings of colon surface fidelity at 100, 000 randomly selected locations in each of four datasets. The results show that the surfaces determined by the modified deformable model better represent the lumen surface overall.

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1. Introduction

Virtual Colonoscopy (VC) [1] (also called CT Colonography [2]) is intended to augment conventional (endoscopic) colonoscopy as a screening method for colorectal cancer (CRC). Patients found to have polyps using VC still require a conventional colonoscopy/polypectomy. However, it has been estimated that as many as 75% of conventional colonoscopy screening procedures could be unnecessary if VC is successful as a prior screening tool [3]. Typically better tolerated by patients in terms of comfort and convenience when compared to conventional colonoscopy, VC will most likely lead to increased compliance with screening recommendations. It is particularly useful in those 5-10% of cases where incomplete examination of the distal colon (to the Cecum) cannot be accomplished with conventional colonoscopy or in cases of occlusion due to pronounced cancer. The identification of extra-colonic findings such as possible liver metastases is also a benefit of the procedure.

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Although Magnetic Resonance Imaging has been used to obtain data for CRC screening, X-ray Computed Tomography (CT) remains the dominant implementation due to its wide clinical availability, high spatial resolution, and high temporal resolution. The patient undergoes a bowel cleansing regime with a modified diet one to two days prior to the exam. Just before scanning, the now collapsed colon is typically inflated with CO₂ or NO gas via a rectal catheter to distend the lumen. Multi-row CT scanners are the recommended norm for VC data acquisition, in both prone and supine positions. A radiologist or trained technician then reviews the 2D slices, using 3D endoluminal renderings for problem solving. A recent summary of VC performance [4] shows that it can be used to detect lesions one centimeter and larger with a sensitivity varying between 50 and 100%, depending on the inclusion criteria and reader experience. The identification of patients with at least one lesion greater than one cm has a sensitivity between 80 and 100% and specificity between 74 and 100%. These patient detection results indicate that VC is effective for screening and referral to conventional colonoscopy within high risk and symptomatic groups. While the individual lesion detection statistics are less convincing, there is potential for VC to reach individual polyp detection rates comparable to that of traditional colonoscopy.

Several open issues remain, including: reader variability, the use of computer aided diagnosis software, the type and implementation of stool opacification (fecal tagging) [5,6], and the wide range of sensitivity to detecting individual lesions. The size and type of polyps that can be detected with VC is also debatable, with most studies reporting pedunculated polyps greater than 1 cm. However, polyps above 5 mm are considered to be potentially significant [7] and there is new evidence that VC can detect sessile lesions [8]. Reader variability has been primarily attributed to experience, the slice reconstruction size used, software used, and the reading technique. To aid data analysis the use of computer assisted polyp detection (CAPD) is an emerging area of research [9], motivated by the success of computer-aided diagnosis in mammography and lung cancer detection.

Since accurate identification of the colon wall is essential to the localization of polyps and cancerous lesions, one of the most important steps in CAPD is lumen segmentation. Previous work in this area has revealed three main points which make colon segmentation a difficult task:

- The colon is not the only gas-filled structure in the abdomen. For example, lower portions of the lung are often present in virtual colonoscopy data in order to fully image the transverse segment and splenic flexure. Portions of the small bowel and stomach may also be partially filled with gas (Fig. 1(a)).
- 2. Obstructions in the colon itself complicate automated segmentation and prevent a continuous colon segment. Possible obstructions include peristalsis, very large lesions, and residual feces. Such obstructions increase the likelihood of an incomplete segmentation by automated methods. Fecal tagging or contrast enhancement can be used to classify residual material along with the lumen air (Fig. 1(b)). In other protocols prone and supine scans are used to reposition the residual feces, and contrast enhanced areas may not be separately classified [9].
- 3. Partial volume and interpolation artifacts reduce the effective resolution of the CT scanner and are the focus of this paper. One artifact is a blurring and reduction of contrast in areas where the colon wall contacts air on

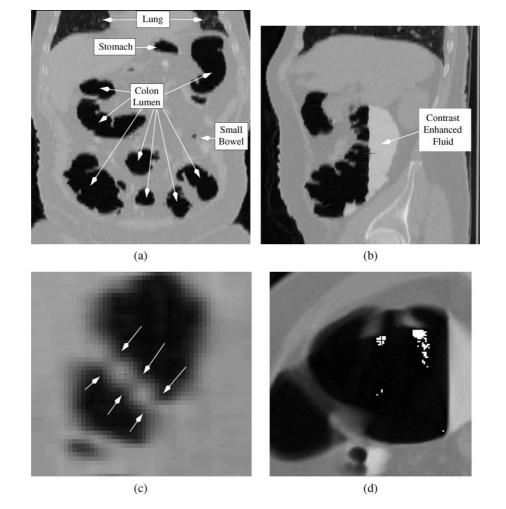


Fig. 1. Obstacles to VC data analysis: (a) Gas-filled structures in the abdomen. (b) Residual fluid breaking the colon into two sections. (c) Partial volume effect reduces contrast along haustral folds (arrows). (d) Null regions mapped to white pixels values in an axial slice.

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