Segmentation And Detection Of Polyp Using CT Colonography

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ABSTRACT

Todays Automated Detection System For Computed Tomography colonoscopy enables easy detection and segmentation of colorectal polyps . We present a new method that measure the protrudness of a body in adaptive fashion The performance of candidate detection is depends only on one parameter, amount of protrusions We calculated the implementation of method on 90 patients with total 57 polyps larher than or equal to 6mm. we obtain a performances of 95% sensitivity.

Keyword: Biomedical Image processing, Polyp detection, Colorectal cancer, Capsule Endoscopy

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1. INTRODUCTION

Colorectal cancer is one of the most commonly diagnosed types of cancer. Specifically, the American Cancer Society predicts 145,000 new cases and 56,000 deaths from colorectal cancer for 2005 [3]. Polyps are a well-known precursor to such carcinoma. Not surprisingly, it has been shown that early removal of polyps ensures a decrease in incidence [121]. In recent years, CT colonography has been proposed as a non invasive alternative to traditional polyp detection by colonoscopy. In CT colonography, the colon structure is often visualized from an endoluminal perspective by means of surface or volume rendering. Recently, methods have been proposed to support the inspection by a computer aided detection (CAD) system indicating suspect locations [106,141]. The size of a detected polyp is an important aspect for diagnosis and decision making. It is generally accepted that polyps with diameter < 5mm require no direct further action, whereas larger polyps should be removed via colonoscopy. Typically, the size of polyps is measured in colonoscopy by comparison with an open biopsy forceps. In CT colonography, it is usually measured in reformatted images, in which the largest polyp diameter is selected for size measurement. . polyp sizes thus measured by human experts can show significant inter- and intra-observer variability. Clearly, an automated method is needed to enable more accurate measurement of polyp size. As a side effect, such a procedure is also useful in CAD algorithms Automated Polyps detection is usually based on sophisticated pattern recognition techniques that take into account many features measured on tentatively selected candidates (e.g. size, area, average shape index etcetera). Proper segmentation is crucial to perform reliable feature measurement. The existing methods for colonic polyp segmentation (such as Summers et al. and Yoshida et al. are especially designed to work directly on the 3D CT data. Such an approach is hindered by not operating on a specifically defined region of interest c.q. the colon surface. Hence, segmentation of polyps which are by definition protrusions of the colon surface is not a trivial task.

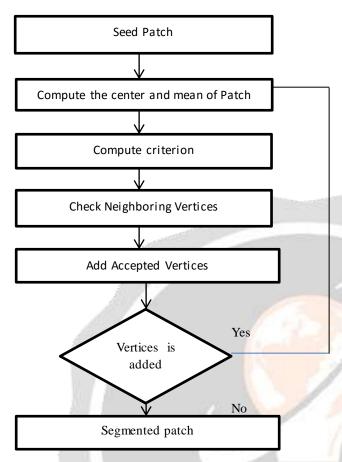


Fig:1 Schematic overview of segmentation procedure

In this paper we present a new method for semi-automatic segmentation of polyp-like structures. Additionally, a technique is described to automatically measure polyp sizes I Additionally, a technique is described to automatically measure polyp sizes using this algorithm. Our method assumes that the colon surface has been identified as a region of interest. Moreover, it is asserted that a candidate location has been identified; in our system by a vertex detection step based on the measured shape index [128]. We will compare the size measurement by our algorithm with that of physicians in a set of phantom objects (in which the size is known a priori)..

2. POLYP SEGMENTATION

Ideally, a polyp could be described as a rather spherical, symmetric mound on a background shape (see e.g. Figure 2a). One could intuitively delineate a polyp by the inflection points on both sides. However, these points may not be easily identifiable due to the curvature of the background shape (e.g. a fold). Hence, we model a polyp to have a symmetry axis that goes through the center point (Pc) in which the apical surface normals converge, and the mean position (Pm) calculated from the polyps surface points. The edge of the polyp is defined by the points at which the surface normals tend to deflect from the center point (we will formalize this below). Initially, a single position or a small patch indicates a point on the polyp candidate Since the center and mean points may not be robustly determined from such a seed patch, the polyp segmentation procedure is set up as an iterative process. During each cycle of this process neighbouring vertices are added if certain criteria are met. The process terminates when no more points are added. An overview of the procedure is shown in figure 1.

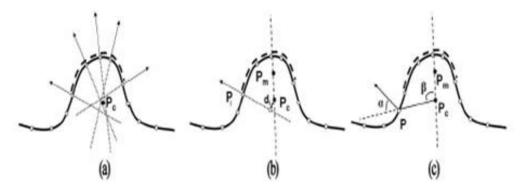


Fig 2: Schematic representation of a patch (dashed curve) on the colon wall. Figure (a) shows how convergent normals define a center point; figure (b) shows how the minimized distance di is defined for surface point Pi; figure (c) shows how the angles a and b are defined

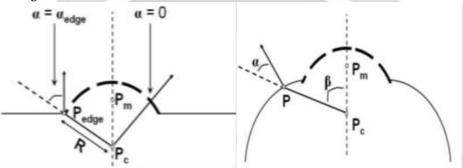


Fig 3: Schematic representation of a polyp (dashed curve) on a flat background

2.1 computing The Center and mean point

As depicted in Figure 2a, the surface normals on the polyp apex tend to converge in a center point. This point (Pc) is found by minimizing the sum of the distances (di) to all normals $(\sim ni)$. The surface normals are calculated by Gaussian derivatives the underlying 3D CT data at a scale of 2mm. This scale was determined experimentally such that no polyps are missed. The distances can be computed according to

$$d_i = \left\| \vec{n}_i \times (P_i - P_c) \right\| / \left\| \vec{n}_i \right\|$$

where Pi is a point on the patch and x denotes the vector outer product. Additionally, a mean point (Pm) is associated with a patch. The position of the mean is simply computed by averaging the positions of all vertices: Pm = $1/N \sum Pi$. The mean and the center point define a centerline (dashed in Figure.2b). Henceforth it is called the polyp axis. An important aspect that is used in deciding on a patient's treatment is the polyp size. It is measured from the largest object diameter in cross sectional views or in volume renderings. A role of CT colonography in screening is to pre-select patients with polyps such that only patients with polyps are sent to colonoscopy. Another advantage of CT colonography that it aids colonoscopy by localizing the lesion and hence increasing the overall sensitivity.

2.2 Adding Point To Seed Patch

Points are to be added to a seed patch until the local surface normal tends to deviate from Pc. To formalize the stopping criterion, consider first a sphere on a flat background. Let us define a as the angle between the line from the center point (Pc) to the vertex (Pi) and the normal at the position of the vertex (see Figure 2c). Clearly, on top of the polyp a is small (exactly zero on a spherical cap, see Figure 3). The angle a increases while moving to periphery of the polyp. Right outside the polyp the angle is given by (compare with Figure 3): Introduction related your research

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in which Pedge is defined as in Figure 3.3 and $\sim n$ is the normal at point Pedge. We assume that the ideal threshold value lies somewhere between these extreme value The required midway point is closely approximated by the angle calculated via (compare with Figure 3.3):

$$lpha_{edge} = arccosl \left[rac{P_{edge} - P_c) \cdot \vec{n}}{\left\| P_{edge} - P_c \right\| \cdot \left\| \vec{n} \right\|}
ight]$$

$$\alpha_{mid} = \arccos\left[\left(P_m - P_c\right)/R\right]$$

Thus, a < amid yields a safe stopping criterion for adding neighboring vertices to a polyp on a flat background. On a fold, however, the angle a remains small (see Fig.3) Let us define b as the angle between the polyp axis and the line between the vertex and the center point (as in Figure 2c): At the edge of the polyp b is given by bedge = aedge. Typically, b continues to increase while moving onto the fold Consequently, b < bedge yields a logical stopping criterion for a polyp on a fold Consequently, b < bedge yields a logical stopping criterion for a polyp besides a polyp on flat background do not fulfill b < bedge. Also, the angles amid and bedge are both dependent on the shape of a polyp. Flatter polyps tend to have lower values for amid and bedge than on a fold. It should be noticed that the two posed criteria are mutually exclusive: the side points of a polyp on a fold do not meet the criterion of a < amid. On the other hand, points more protruding polyps. In other words, the threshold values automatically depend on the polyp shape.

All vertices neighboring a seed patch that match the conditions are accepted and added at once to yield a new seed. Consequently, the outcome does not depend on the order in which points are processed. Clearly, if none of the vertices match the criteria, no points are added and the current patch is considered the final, segmented polyp. Otherwise all steps are iterated

$$\beta = \arccos \left[\frac{(P - P_c) \cdot (P_m - P_c)}{\|P - P_c\| \cdot \|P_m - P_c\|} \right]$$

3. AUTOMATED SIZE MEASUREMENT

The size measurements for polyps are based upon the segmented patches. The edges of these patches are projected along the polyp axis onto a plane. An ellipse is fitted to these points in 2D space by computation of the first and second order moments. This is in accordance with the current medical practice in the Academic Medical Center where the polyp size is characterized by its largest diameter

4.RESULT

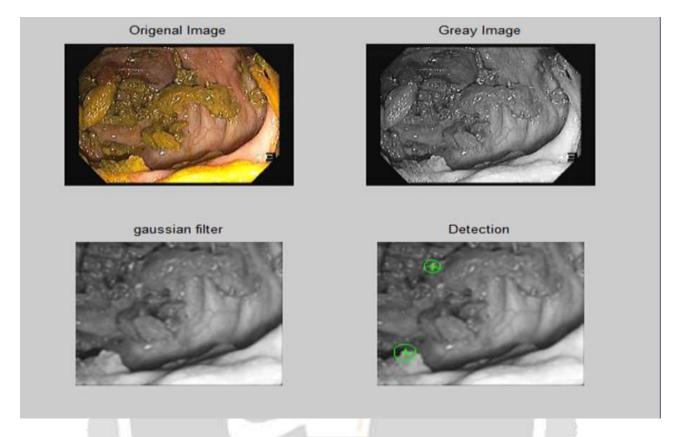


Fig 4 Polyp Detection Steps

4. CONCLUSIONS

The size of a colonographically detected polyp is important for diagnosis and decision making. The size measurement by human observers is generally considered to be imprecise and inaccurate. In this paper we presented a method for the automatic segmentation of polyp-like structures. The polyp size was automatically derived from the segmentation result. It was shown that our algorithm yields a smaller bias than the measurements from radiologists: on average 1mm or less for the automatic method and between 1 and 7mm for the radiologists, depending on the irregularity of the object. Even more important, the algorithm is consistent irrespective of the polyp shape. As opposed to that, the radiologists show a four times larger variation for the irregularly shaped objects. It is this irregularity which occurs in practice. A good polyp segmentation algorithm is also useful for automatic polyp detection algorithms. It allows for extraction of features such as volume, surface area, average grey-value etcetera. Such features may improve the specificity of CAD algorithms

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6. REFERENCES

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