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See also BibTeX entry below.

\begin{verbatim}
\bibitem{BRE11b}
  \textbf{author} = {Matthias Breier AND Sebastian Gross AND Alexander Behrens},
  \textbf{title} = {Chan-Vese-Segmentation of Polyps in Colonoscopic Image Data},
  \textbf{booktitle} = {Proceedings of the 15th International Student Conference on Electrical Engineering POSTER 2011},
  \textbf{address} = {Prague, Czech Republic},
  \textbf{month} = {May 12},
  \textbf{year} = {2011}
\end{verbatim}

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Chan-Vese-Segmentation of Polyps in Colonoscopic Image Data

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Abstract. Colon cancer is the third most common type of cancer in Germany. About 70,000 cases are newly diagnosed each year. Early detection of polyps is crucial for successful therapy. The standard screening procedure where physicians can find polyps and remove them if necessary is called colonoscopy. However, the removal of polyps can lead to side effects like severe bleedings or colon perforation. Thus, only polyps diagnosed as potentially malignant should be removed. This decision can be based on the inspection of the polyp’s surface structure including vascular patterns highlighted by Narrow-Band imaging (NBI). We investigate Chan-Vese-Segmentation for the localization of polyps in NBI image data which is a prerequisite for the subsequent classification. However, the shape of polyps, though roughly elliptical, is highly variable. The Chan-Vese-Segmentation was designed to offer the flexibility to adapt to shape variation well without using edge information. The results were evaluated using manually segmented polyps as ground truth data and were compared to Active Contours, to a template matching approach and to the Generalized Hough Transform. The Chan-Vese-Segmentation has a higher accuracy than all other evaluated methods but do not perform well in terms of sensitivity.

Keywords

Colonoscopy, colon polyps, chan-vese, active contours, NBI

1. Introduction

Colon cancer is one of the most common forms of cancer among the population of the western hemisphere. In Germany, roughly 70,000 people are newly diagnosed with colon cancer every year and about 30,000 people die as a result of this disease[1]. Colon cancer develops rather slowly (in the course of about 5–10 years). Complete recovery is often possible if cancer is diagnosed at an early stage.

Vogelstein showed that colon polyps usually turn into cancer in two major stages (adenoma-carcinoma-sequence)[2]. The key to cancer prevention is detecting potentially adenomatous polyps (adenomas).

The standard medical procedure for diagnosis of colon polyps and cancer is colonoscopy, an examination of the colon with a flexible video endoscope. Normally endoscopes have an integrated canal which allows the medical practitioner to insert tools into the focussed area and perform tasks like taking tissue samples or removing polyps. The removal of polyps may cause side-effects like severe bleedings or even perforation of the colon wall. Therefore medical practitioners seek to only remove adenomatous polyps and leave the benign ones (hyperplasias) in the colon. Visual inspection by a medical practitioner is necessary to decide whether a polyp is adenomatous or hyperplastic.

In a study by Tischendorf et al.[3] a special light source is used which is able to emit narrow band (NBI) light. NBI-light consists of two narrow frequency bands at 415 nm and 540 nm in contrast to white light which covers a wide range of frequencies from 380 nm to 780 nm. NBI-light is well absorbed by haemoglobin, thus, highlighting blood vessels. It was shown that the blood vessel structure can be used as an indicator for adenomatous tissue[3]. Stehle et al. [4] presented a computer-aided diagnosis system for the classification of colon polyps based on the analysis of vessel structure.

Delineation of polyps in colonoscopic images is the first step for automated classification of colon polyps. Any surface which is not part of the polyp has to be omitted before classification. Additionally, the detected area should cover most of the polyp’s area to gain as much polyp data as possible. The more data is captured the higher is the accuracy of the classification process.

To the human eye, polyps are prominent objects in an image. Gross et al. [5] localize polyps in NBI-images by a template matching approach exploiting the ellipse boundary shape often exhibited by polyps. However, polyp images usually show a lot of detail. A simple edge detection approach would identify a vast number of edges. Thus, a non-linear diffusion filter[6] was put in place to reduce the number of edges found by subsequent Canny edge detection[7]. The resulting edges were filtered by a multi-scale dilation process after which only prominent edges remain. The residual edges were compared to a database containing elliptical
templates at different sizes, axis ratios, rotation angles, and at different positions. The best fitting ellipse is combined with the edge image of the polyp to determine the assumed position of the polyp in the image. Active Contours and Active Rays with a traditionell edge based approach were investigated in [10].

One of the biggest problems of colon polyp segmentation is the multitude of manifestations of the polyps. It is hard to find common properties which fit to all polyps encountered in the colon. The approaches mentioned above use edge information for localizing polyps on colonoscopic images. Unfortunately, polyps often show no clear edges on images as they originate from the same colon tissue. The Chan-Vese-Segmentation[8] offers a possibility to segment images without relying on edge information edges. The segmentation performance of this algorithm in conjunction with our polyp database is investigated in this paper.

The remainder of this paper is organized as follows. In section 2 we describe the background of Active Contours and the Chan-Vese-Segmentation algorithm used in this paper. The evaluation environment is described in section 3, while we discuss the results and future research in section 4.

2. Method

Segmentation of colon polyps is the first step of polyp classification. A standard approach to medical image analysis are parametric Active Contours[9], which were first described by Kass et al. [11]. The aim of this approach is to locate objects in an image by modifying contours until they represent the object’s boundary. To this end, a contour function \( C(s) \) has to be found which minimizes the energy functional

\[
E_{\text{active contour}} = \int_{s=0}^{1} E_{\text{internal}}(C(s))ds + \int_{s=0}^{1} E_{\text{external}}(C(s))ds. \tag{1}
\]

Two energy types \( E_{\text{external}} \) and \( E_{\text{internal}} \) define the energy state the contour is currently in. The internal energy \( E_{\text{internal}} \) is determined by the form of the contour (i.e. length, curvature, continuity, enclosed area). Normally an initial contour is set around the object to localize and moved iteratively to its boundaries. The external energy \( E_{\text{external}} \) controls this movement by guiding the contour towards the boundary and stopping the contour when it has reached the boundary.

Many implementation of active contours use energy terms based on the gradient of the image. An example is the snake energy functional

\[
E_{\text{snake}} = \alpha \int_{s=0}^{1} |C'(s)|^2 ds + \beta \int_{s=0}^{1} |C''(s)|^2 ds - \tau \int_{s=0}^{1} |\nabla u_0 (C(s))|^2 ds \tag{2}
\]

defined by Kass, Witkins and Terzopoulos[11] where \( \alpha, \beta \) and \( \tau \) are positive parameters, \( C(s) \) is the curve function and \( u_0 \) is the image. The first two terms belong to the internal energy while the last term comprises the external energy.

The gradient based approach encounters some drawbacks if the image data is noisy. To mitigate the effect of the noise the image is filtered by a low pass filter which weakens the edges and thus the accuracy of the localization. Another problem arises if there are not enough or too many edges on the image which is especially the case with colonoscopic NBI images. In these cases the contour will not find the right boundary of the object as it is distracted by artifacts.

It is rather difficult to cover several objects in an image with a single parametric active contour as there have to be discontinuities from object boundary to object boundary. A solution for this problems is using geometric active contours[9]. Geometric active contours use a level set function \( \phi(x,y,t) \) to define the contours implicitly. For each time step \( t \) the contour is defined by

\[
C = \{(x,y)|\phi(x,y,t) = 0\}. \tag{3}
\]

By introducing the artificial time parameter \( t \) the level set function can be changed to allow for cusps, corners a topological changes.

Chan and Vese[8] use the geometric approach to formulate their active contour model without relying on edges. The basic energy functional

\[
F(c_1,c_2,C) = \mu \cdot \text{Length}(C) + \nu \cdot \text{Area}(|\text{inside}(C)|)
+ \lambda_1 \int_{\text{inside}(C)} |u_0(x,y) - c_1|^2 dxdy
+ \lambda_2 \int_{\text{outside}(C)} |u_0(x,y) - c_2|^2 dxdy \tag{4}
\]

omits gradient information as \( c_1 \) and \( c_2 \) are the average values of the inside respectively outside region of the contour \( C \). The external energy terms (the last two integral terms of the energy functional) are minimal if the segmented regions
are entirely homogeneous. Using the level-set function $\phi$ the energy functional can be written as

$$F(c_1, c_2, C) = \mu \int_{\Omega} \delta(\phi(x, y)) |\nabla \phi(x, y)| dxdy + \nu \int_{\Omega} H(\phi(x, y)) dxdy + \lambda_1 \int_{\Omega} |u_0(x, y) - c_1|^2 H(\phi(x, y)) dxdy + \lambda_2 \int_{\Omega} |u_0(x, y) - c_2|^2 (1 - H(\phi(x, y))) dxdy \quad (5)$$

in which $H$ ist the Heavyside function

$$H(z) = \begin{cases} 1, & \text{if } z \geq 0 \\ 0, & \text{if } z < 0 \end{cases} \quad (6)$$

and

$$\delta_0(z) = \frac{d}{dz} H(z) \quad . \quad (7)$$

After minimizing this functional by using variational calculus and Euler-Lagrange-Differential-Equations[8] the update function is deduced to

$$\frac{\partial \phi}{\partial t} = \delta_0(\phi) \left[ \mu \cdot \text{div} \left( \frac{\nabla \phi}{|\nabla \phi|} \right) - \nu - \lambda_1 (u_0 - c_1)^2 + \lambda_2 (u_0 - c_2)^2 \right] \quad . \quad (8)$$

Unfortunately, the colonoscopic images show dark, artificial corners which originate from the imaging hardware (cf. Figure 1). Furthermore the illumination of the colon’s interior produces visible specular reflections on the images. Both effects result in homogeneous areas in the images which are very attractive for the Chan-Vese-Segmentation which is an obstacle for the correct segmentation of the polyps. To mitigate the effect too homogeneous regions are filled using exemplar-based image inpainting[12].

3. Evaluation

We compared the quality of the aforementioned localization methods in an evaluation. Five localization approaches were chosen for this comparison: Active Contours, Active Rays[10], Template Matching with ellipses[5], the Generalized Hough Transform (GHT) for ellipses[13] and Chan-Vese-Segmentation.

The evaluation was based on a test set of 184 polyp images, in which a polyp was present in the center of the image. Centering the polyps was requested of the medical practitioners before taking the still pictures. The images were accompanied by a set of binary masks of the same size, in which the position of the polyp was marked manually. These masks are regarded as ground truth data for the evaluation.

All localization methods return the designated position of the polyps in the images as binary masks. The localization can be considered as a pixel classification with two classes — polyp and background. Thus, a pixel by pixel comparison of the ground truth masks with the resulting masks of the localization methods yields the localization quality. The localization method has to decide for each pixel whether it belongs to the polyp or to the background. With respect to the ground truth data, this yields four possible result cases: true positive (TP), true negative (TN), false positive (FP) or a false negative (FN). "Positive" stands for a polyp pixel while "negative" denotes a background pixel. Summing up the pixels of these four cases, three characteristic values can be computed[14]:

$$\text{specificity} = \frac{TN}{TN + FP} \quad (9)$$

$$\text{sensitivity} = \frac{TP}{TP + FN} \quad (10)$$

$$\text{accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad . \quad (11)$$

The specificity is the number of correctly detected background pixels divided by all background pixels. A high value indicates a low number of pixels incorrectly regarded as polyp pixels. The sensitivity is the ratio of correctly detected polyp pixels to all polyp pixels. High values indicate a high number of pixels available for classification of the polyp. The accuracy is the fraction of all pixels which were classified correctly.

The Chan-Vese algorithm is controlled by several parameters. Preliminary experiments showed that $\mu = 0.2$, $\nu = 0$ and $\lambda_1 = \lambda_2 = 1$ form the best parameter set for our colonoscopic NBI images. The algorithm iterated 100 steps for each image.

The results of the evaluation are shown in table 1. Examples for the localization results are presented in Figures 2, 3, 4, 5 and 6. The localization method with the highest specificity is active contours, while the highest sensitivity can be achieved with the Chan-Vese approach. The Template Matching approach offers a compromise between specificity and sensitivity thus having the high accuracy results. Using the Chan-Vese Algorithm results in the highest accuracy while suffering under the lowest specificity.

4. Conclusion

We have investigated Chan-Vese-Segmentation as method for the localization of polyps on colonoscopic NBI images. The Chan-Vese algorithm offers the highest accuracy compared to the other evaluated methods. Although the specificity of the Chan-Vese-Segmentation is rather low it is a promising approach if the specificity can be increased. The sensitivity results for all localization methods may appear low in comparison to specificity results. However, for diagnostic purposes a background pixel mistakenly taken as polyp pixel is worse than vice versa since the background
Fig. 1: Filling dark corners and specular reflections with similar parts of the image.

<table>
<thead>
<tr>
<th>Method</th>
<th>Specificity $\varnothing$</th>
<th>Specificity $\sigma$</th>
<th>Sensitivity $\varnothing$</th>
<th>Sensitivity $\sigma$</th>
<th>Accuracy $\varnothing$</th>
<th>Accuracy $\sigma$</th>
</tr>
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<tbody>
<tr>
<td>Active Contours</td>
<td>0.9989</td>
<td>0.0050</td>
<td>0.0331</td>
<td>0.0258</td>
<td>0.4537</td>
<td>0.2311</td>
</tr>
<tr>
<td>Active Rays</td>
<td>0.9680</td>
<td>0.0623</td>
<td>0.3151</td>
<td>0.2441</td>
<td>0.5769</td>
<td>0.2285</td>
</tr>
<tr>
<td>Template Matching</td>
<td>0.9809</td>
<td>0.0448</td>
<td>0.3043</td>
<td>0.2550</td>
<td>0.5872</td>
<td>0.2326</td>
</tr>
<tr>
<td>Hough Transform</td>
<td>0.9931</td>
<td>0.0225</td>
<td>0.0930</td>
<td>0.1145</td>
<td>0.4765</td>
<td>0.2341</td>
</tr>
<tr>
<td>Chan-Vese-Segmentation</td>
<td>0.8555</td>
<td>0.1625</td>
<td>0.4814</td>
<td>0.2051</td>
<td>0.6154</td>
<td>0.1641</td>
</tr>
</tbody>
</table>

Tab. 1: Quality of the localization methods summed up for all polyp images. $\varnothing$ stands for the mean value and $\sigma$ for the standard deviation.

Fig. 2: Localization result of active contours.

Fig. 3: Localization result of active rays.
Fig. 4: Localization result of the Generalized Hough Transform.

Fig. 5: Localization result of the Template Matching approach.

Fig. 6: Localization result of the Chan-Vese approach.
pixels normally belong to healthy tissue. Thus, an inclusion of background pixels would weaken the accuracy of the diagnosis and therefore, a high specificity is a prerogative.

The Chan-Vese-Segmentation uses the images’ gray values to determine the segmented region’s boundaries. This is suboptimal if the regions are highly textured as is the case for polyp images. Therefore an approach using the texture information combined with color as data source might produce better results and should be considered in future research.

Acknowledgements

We would like to thank Prof. Dr.-Ing. Til Aach, Institute of Imaging and Computer Vision, RWTH Aachen University, Germany for supervising this project.

References


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Matthias BREIER was born in 1981. He studied Computer Engineering with a focus on Media Engineering at the RWTH Aachen University. Since his graduation in 2010 he has been working towards a PhD degree and is a research scientist at the Institute of Imaging & Computer Vision at RWTH Aachen University. His research interests are in industrial image processing, pattern recognition and computer vision.

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