Current Challenges on Polyp Detection in Colonoscopy Videos: From Region Segmentation to Region Classification. A Pattern Recognition-based Approach

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Abstract. In this paper we present our approach on selection of regions of interest in colonoscopy videos, which consists of three stages: Region Segmentation, Region Description and Region Classification, focusing on the Region Segmentation stage. As part of our segmentation scheme, we introduce our region merging algorithm that takes into account our model of appearance of the polyp. As the results show, the output of this stage reduces the number of final regions and indicates the degree of information of these regions. Our approach appears to outperform state-of-the-art methods. Our results can be used to identify polyp-containing regions in the later stages.

1 Introduction

Colon cancer, with an approximate number of 655.000 deaths worldwide per year, has become the fourth leading cause of death by cancer in the United States and the third leading cause in the Western world [1]. Colon cancer includes cancerous growths in the colon, rectum and appendix. Colon cancer arises from adenomatous polyps in the colon which can be identified by its prominent (flat or peduncular) shape.

Colon cancer has four distinct stages along with a fifth stage that is called 'recurring'. Its survival rate (measured in five-year survival rate) decreases according to the higher the stage the polyps are detected on, going from a 95% in stage I to a 3% in stage IV [2], hence its importance to be detected on its early stages. There are several types of screening techniques grouped according to the principles of functioning (depending on if they need the on-line intervention of a physician or consist of introducing some particle into the patient). One of the most used is colonoscopy. Colonoscopy [3] is a procedure used to see inside the colon and rectum and it is able to detect inflamed tissue, ulcers, and abnormal growths [4]. During colonoscopy, patients lie on their left side on an examination table. The phyisician inserts a long and flexible tube called colonoscope into the anus and guides it slowly through the rectum and into the colon. A small camera is mounted on the scope and transmits a video image from inside the large intestine to a computer screen, allowing the doctor to examine carefully the intestinal lining. During this process the physician can remove polyps and later test them in a laboratory to look for signs of cancer. Colonoscopy allows a direct visualization of the intestinal

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surface but it has some drawbacks, such as the risk of perforation, the intervention cost, or visualization difficulties among others.

The global objective of our project is to develop a tool that can indicate the doctor which areas of the colon are more likely to contain a polyp by means of computer vision techniques. The results of this tool can be used in several applications such as: 1) real-time polyp detection, 2) off-line quality assessment of the colonoscopy, 3) quantitative assessment of the trainee skills in training procedures, only to mention a few.

In order to achieve this goal we base our approach on a common Pattern Recognition scheme (see Figure 1). The input to the scheme is a frame from a colonoscopy video and the output will be this same image annotated in terms of polyp detection.

Fig. 1. General scheme of our approach.

The first stage, Region Segmentation, consists of segmenting automatically the image in order to end up with a reduced number of relevant regions, one of them containing a polyp. So the objectives are twofold: reduce the number of regions that should be analyzed and indicate which are the non-informative regions on where not even the human eye can distinguish anything and therefore there will be no need to analyze them later.

The second and third stages (Region Description and Classification) are closely related one to the other. Once we have a few regions from the segmentation stage, we need to find which features in these regions can denote the presence or not of a cancer polyp. The objective of the second stage will be to find a series of descriptors that describe better what is a polyp region and what is not and, in the third stage, using the knowledge acquired from the examples, classify the input regions into polyp-containing candidates or not.

In order to develop and test our approach we rely on a database of thousands of images extracted from 15 different videos of colonoscopy interventions.

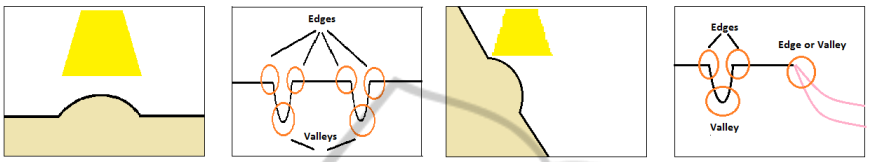
The structure of this paper is as follows: In Section 2 we present our Region Segmentation stage. In Section 3 we introduce the Region Description and Region Classification Stages. In Section 4 we present our preliminary experimental results. Finally, in Section 5 we expose the main conclusions that have been extracted from this work along with a presentation of the Future Work that we plan to do.

2 Region Segmentation

2.1 Our Model of Appearance of a Polyp

As we have mentioned before, we are dealing with colonoscopy images obtained from real interventions videos. While observing the videos, we have found out that the lighting of the probe can give us hints about what is a polyp in an image. As the light

falls perpendicularly to the walls of the colon, it creates shadows around the surfaces at which it is. More precisely, when the light falls into a prominent surface, it creates a bright spot (with high grey-scale value) surrounded by darker areas, which are the shadows, generating edges and valleys in the intensity image. This can be better understood by looking at Figure 2, where we show an indication of the effect of light in the intensity profiles, that depend on how the polyp appears (cenital or lateral view).



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

Fig. 2. (a-b) Simulation of an overhead prominent surface and its correspondent grey-scale profile (c-d) Simulation of a lateral prominent surface and its correspondent grey-scale profile.

Even considering this evidences of prominent surface appearance, there are some challenges that need to be overcome:

- Non-uniform Polyp Appearance: first, the appearance of the polyp by itself is not uniform, going from peduncular to flat shapes. Second, in most of the images we will not have a clear vision of the polyp, viewing them from an overhead or lateral views, which makes difficult a shape-based recognition scheme work.
- Uniform Colour Pattern: as all the tissues in the image present a very similar color distribution, a segmentation scheme based purely on color will have difficulties to segment correctly the image.
- Effect of the Reflections, which makes segmentation algorithms create artificial regions in the image.
- Over and under Segmentation: We can have two problems related to the number of segmented regions. Oversegmentation is related to having a large number of very small regions, which implies a high computation cost to analyze them all) and under-segmentation to the fact of having a smaller number of bigger regions, but still higher than the number of structures that a human could identify on the image).

Taking these considerations into account, we base our segmentation method on a model of appearance of a polyp that we have defined as a prominent shape enclosed in a region that can be identified by the presence of edges and valleys. But we have to take this as an indication, and we also should try to overcome the challenges we have presented.

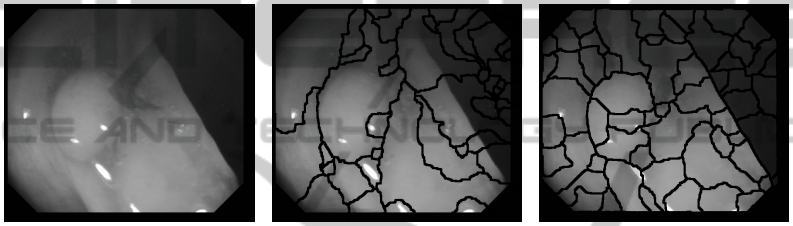
2.2 Region Segmentation Algorithm

In this subsection first we present the basics of each step of our segmentation approach and at the end we show in Figure 4, step by step, a complete graphical example.

1. Image Preprocessing: Before applying any segmentation algorithm there are some operations that should be done to the input image (Figure 4 a) in order to overcome

some of the challenges that were presented before. These preprocessing operations include: converting to gray-scale (Figure 4 b), image deinterleaving (as our images come from a high definition interleaved video), correction of the reflections (Figure 4 c) and obtaining the complemented version of the image (Figure 4 d).

2. Segmentation: In this step we have several alternatives. We can use either simpler (in terms of computation cost) methods such as watersheds [5] or go with algorithms that are more powerful in terms of segmentation such as Mean-shift or Normalized Cuts. We use watersheds to reduce the computation cost and also because more complex approaches are generally color-based which do not seem so useful in our case. Another point of our approach is that, instead of using the preprocessed image obtained in the first step, we use gradient information, which, as it can be seen in Figure 3, encloses better the structure of the shapes that appear on the image. After this step our image will be divided in a large number of regions (Figure 4 e) that we will reduce by merging them.



(a) (b) (c)

Fig. 3. (a) Original image (b) Original image segmentation (c) Gradient image segmentation.

3. Frontier-based Region Merging: in this step we focus on merging small neighbor regions that are separated by weak frontiers (Figure 4 f). We denote as weak those frontiers which present a low value of the weakness function (1).

$$\begin{aligned} FrontierWeakness = \alpha * edginess + \beta * valleyness \\ + \gamma * anisotropic + \eta * orientation \end{aligned} \quad (1)$$

This weakness function is calculated using the response of the image to four different weakness criteria: edges (by using a Canny detector the the image), valleyness (using a ridges and valleys detector [6]), anisotropic filtering and gradient-based orientation. For each one of the criteria we create a binary mask and take as first measure the percentage of pixels that fall under the dark side of the mask. Once we have this percentage for each of the criteria, we can decide if a frontier is weak according to a weakness criteria by setting up a threshold.

We merge regions until there are no weak frontiers between regions (up to a threshold value of the weakness function) or until the number of regions is stabilized.

4. Region-based Region Merging: in this step, as it did not happen in the previous one, we consider when merging not only the weakness of the frontiers (by using a different weakness function (2)) but also the grey-level content of the regions. In this

case the weakness measure takes into account which frontiers are kept after applying consecutively two order-increasing median filters and a botton-hat mask.

$$FrontierWeakness = \mu * median + \rho * bottom - hat \quad (2)$$

Then we categorize the regions and frontiers, in terms of the amount of information that they contain (i.e., low information means a region with a very high or very dark mean grey level and very low standard deviation) and then merge compatible (same kind of information) regions that have compatible weak frontiers. The objective here is to end up with a reduced number of large regions as uniform as possible.

We merge regions until there are no weak frontiers between compatible regions (up to a threshold weakness value) or until the number of regions is stabilized.

The objective of our segmentation and region merging sub-steps is twofold: first obtaining a good segmentation of the image that fits the structure of the several objects that appear in it, such as polyps, and second, join and label those parts of the image where we know we will not find a polyp inside and therefore, we should not process them in order to save resources. We show in Figure 4 one complete segmentation process.

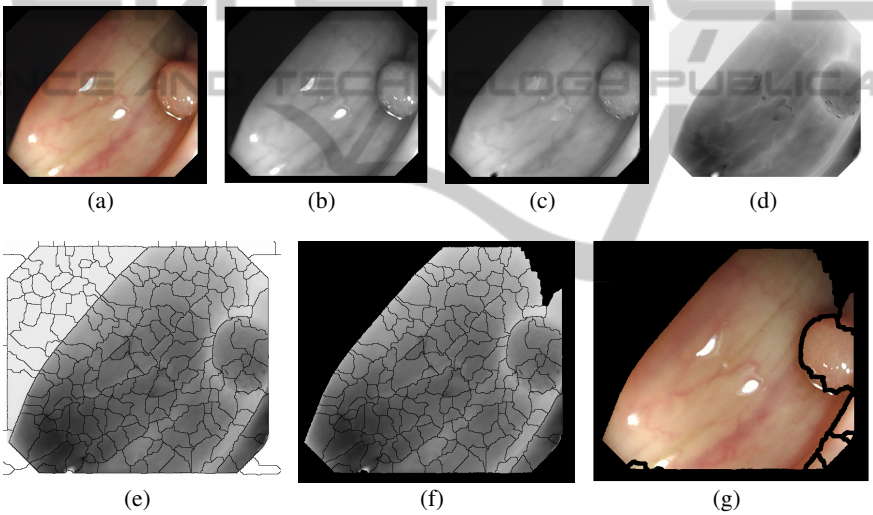


Fig. 4. (a) Original image (b) Grey-scale (c) Reflection corrected (d) Preprocessed image (e) First segmentation (184 regions) (f) Before region-based merging (136 regions) (g) Final image (9 regions).

3 Region Description and Region Classification

The objective of the Region Description stage is to choose a series of descriptors that represent better what is a polyp region and what is not. We have made an study of the bibliography of Feature Descriptors [7], dividing them into four groups: Shape Descriptors, Color Descriptors, Texture Descriptors and Motion Descriptors. Our approach to this stage is not to rely on one only type of descriptors and, as possible, try to use really informative descriptors.

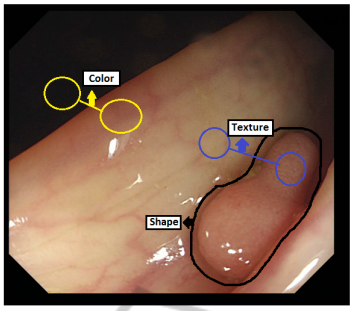


Fig. 5. Example of the need to use several types of descriptors.

If we take a look at the example, we can see that each of the types of descriptors may have a role in our system. For example, we can see that the polyp is enclosed by a closed contour and could be approximated by an ellipsoidal shape, so here we could use Shape Descriptors. Color as it can be seen can be an important cue when defining what is clearly not a polyp and we can also observe the difference of Texture between the polyp (more granular) and non-polyp regions (more plain). In Table 1 we show some of the most important ones of each group.

Table 1. Examples of several feature descriptors.

Type	Methods
Shape	Contour-based: Global (Wavelets [8], Fourier [9], Shape Signature [10]) or Structural (Chain Code [11], Blurred Shape Model [12], Shape Context [13]). Region-based: Global (Angular Radial Partitioning [14], Zernike Moments [15], Shape Matrix [16]) or Structural (Skeletons).
Color	Scalable Color Descriptor [17], Color Structure Descriptor [18], Color Constant Color Indexing [19].
Texture	SIFT [20], SURF [21], Texture Browsing Descriptor [22], Local Binary Patterns [23], Co-ocurrence Matrices [24].
Motion	Optical Flow [25], Angular Circular Motion [26].

Once we have described our regions we can start classifying them. As happens with the Region Description step, this stage has not been implemented yet in our method because of two reasons: first, time constraints (since we just started the development of our approach) and secondly, and more important, because we have a strong belief in that the classification system is good as long as its inputs (outputs from the previous stages) are good. As in many Pattern Recognition-based methods, we will use a machine learning approach [27]. A learner can take advantage of examples (in our case, descriptions of polyp and non-polyp containing regions) in order to capture characteristics of interest of their unknown underlying probability distribution.

We will provide the system examples of regions that contain polyps and examples of regions that no contain polyps. These example regions will be described and incorporated into the machine learning algorithm of choice in order to learn a polyp and

non-polyp pattern. New input images will be automatically segmented, described and incorporated into the testing step with the objective of finding out if they are more near to be a polyp candidate region or non-polyp candidate region. In our case our success will be measured not only on terms of how many true positives we get but also on the number of false negatives. It seems clear that it is harmless to identify one non-polyp region as a polyp region that the opposite.

4 Experimental Results

4.1 Experimental Setup

In order to test the performance of our segmentation algorithm (because we have only implemented the Region Segmentation stage until now) we have created a database which consists of 150 different studies of polyp appearance in colonoscopy videos. We have also a set of masks for each image (one that indicates the polyp position for each image and another that indicates the non-informative regions) that will be used to calculate the different performance measures.

We will use two different performance measures: Annotated Area Covered (AAC) and Dice Similarity Coefficient (DICE). The first one indicates the maximum percentage of polyp that is contained on a single region while the second indicates, for the region that covered more the polyp, the percentage of polyp information out of all the region information. We will compare our method with Normalized Cuts [28] for both polyp detection and non-informative region characterization.

4.2 Experimental Results

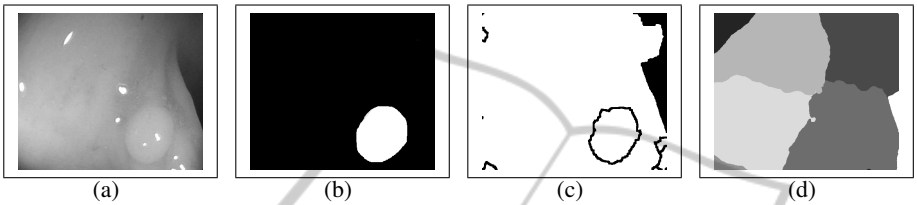
We show in Table 2 experimental results for both our method and Level Sets. The results show that our approach is better than Normalized Cuts in terms of AAC but it is worse than Normalized Cuts in terms of DICE, although our results for peduncular studies are similar than the ones achieved by Normalized Cuts.

Table 2. Summary of the results.

	Our Method			Normalized Cuts		
Measure / Database	Whole	Flat	Peduncular	Whole	Flat	Peduncular
Polyp AAC	96.5%	97.96%	92.79%	76.88%	79.33%	70.75%
Polyp DICE	22.07%	14%	42.23%	35.38%	28.10%	51.67%
Non-informative	96.86%	96.46%	97.88%	80.38%	77.83%	86.71%

The reason for the great difference in DICE results lie on the fact that our method divides the polyp area into smaller regions while Normalized Cuts fits the polyp area in a smaller number of regions. So in order to improve our results we should find a way to merge small polyp regions into bigger ones. We get better results than Normalized Cuts in terms of AAC because our regions are smaller so they contain less both polyp and non-polyp information and, in the case of a polyp region, as they are smaller, they

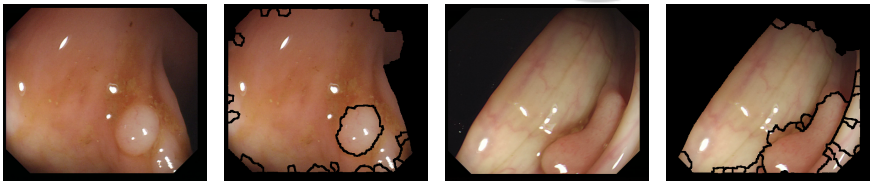
contain more polyp information. We show in Figure 6 qualitative segmentation results (which have been calculated, for the sake of comparison, not taking into account the black borders of the image). In general, the regions segmented by our method fit better the structure of the polyp but as they are smaller, they can miss some of the polyp information. Normalized Cuts regions, as they are bigger, cover more polyp information but they do not approximate well the shape of the polyp. Our method also gives better results in terms of detecting which regions of the image are non-informative.



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

Fig. 6. (a) Original images (b) Polyp mask (c) Final regions with our method (c) Final regions with Normalized Cuts.

So, taking into account that Region Segmentation is only the first stage of our approach (and that it is not finished yet) it seems clear that, if we are going to describe later our regions to decide if they contain a polyp or not, our method is more suitable than Normalized Cuts because our regions approximate better the polyp. To finish this section we show in Figure 7 we show some preliminary qualitative segmentation results, that show that first, we are reducing the search area of the image by eliminating non-informative regions and second, that we end up with a low number of regions.



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

Fig. 7. (a-c) Original images (b-d) Segmented images.

5 Conclusions

Our objective is to detect polyps in colonoscopy videos. To do so, we propose a Pattern Recognition scheme divided in three main stages. The first one, Region Segmentation, is done with two objectives: reduce the size of the problem (as one of our possible applications can be real-time polyp detection) as much as possible, and provide as result to the later stages of the process chain a set of regions of interest. In order to segment the image we have studied in depth the structure of several polyp-containing images from our video database, with the aim of finding cues that can let us discern which regions have some evidence of containing polyps and which not (in this case, we will not analyze again these regions). So far, our method reduces greatly the number of

regions, offering as output a small number of them that, in some cases, cover the whole shape of the polyp in just one region and, as the experimental results show, we identify well the non-informative regions of the image.

Once we have this subset of regions of interest, the next step, Region Description, will consist of describing them in terms of features to characterize them. This step will be the seed to the final stage, Region Classification, where our plan is to implement a machine learning approach. The ideal output will be a mask superimposed to the image that indicates the region of the image that more likely contains a polyp. The segmentation results give us hope that, after some improvements, we will be able to start with the description step.

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