# Reduction of Pattern Search Area in Colonoscopy Images by Merging Non-Informative Regions

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## Abstract

*One of the first usual steps in pattern recognition schemas is image segmentation, in order to reduce the dimensionality of the problem and manage smaller quantity of data. In our case as we are pursuing real-time colon cancer polyp detection, this step is crucial. In this paper we present a non-informative region estimation algorithm that will let us discard some parts of the image where we will not expect to find colon cancer polyps. The performance of our approach will be measured in terms of both non-informative areas elimination and polyps' areas preserving. The results obtained show the importance of having correct non-informative region estimation in order to fasten the whole recognition process.*

## 1. Introduction

Colon cancer is considered as the second leading cause of death by cancer, behind lung cancer in men and breast cancer in women [1]. During the last years, colon cancer has seen an increase in its frequency of appearance in developed countries and, even considering its survival rate, it is necessary to detect it on its early stages.

Colon Cancer includes cancerous growths in the colon, rectum and appendix and it can be better identified by observing adenomatous polyps in the colon. Cancer polyps can be usually identified by its prominent (flat or peduncular) shape and are usually benign but some may develop into cancer.

Colonoscopy can help to diagnose colon cancer. This process consists of an endoscopic examination of the colon and the distal part of the small bowel with a CCD, CMOS, NMOS or fiber optic camera on a flexible tube passed through the anus. The doctor observes the patient status as the colonoscopy progresses, searching zones or structures that may indicate the presence of polyps.

And it is here where computer vision can aid. The objective of our project is to develop a tool that can help the doctor in identifying possible colon cancer polyp candidates by pointing out the areas in the image where he/she should pay more attention. In order to do so, a pattern recognition schema can be useful. First, we have to segment the image to obtain sub-images that we will later describe in order to get the higher possible amount of information that can help us to determine the likelihood of appearance of a cancer polyp in this area.

As it may seem, dealing with thousands of images (and even in real-time) can be very expensive in terms of computation time. In this document we present a pre-processing algorithm that will discard some parts of the image that we will denote as non-informative, that we will not use in any of the later stages of the process. The idea behind this approach is that it is very difficult to detect, even by direct sight, a cancer polyp located in the darkest areas of the image and there is no point on wasting computer resources on analyzing that part of the image when we can make the colonoscopy progress further and get a clearer vision of the colon.

The rest of the document is structured as it follows. After this introduction, we show in the Related Work section a summary of some of the sources of information that were consulted while developing our approach, that we will present in the Methodology section. Before closing with the Conclusions, we present the results of several experiments to show the performance of our method.

## 2. Related Work

The bibliographic references can be divided into the several groups: **medical information** and **image processing**. This latter group could also be divided into **image segmentation** and **image description**.

Belonging to the first group, **medical information**, the first reference that needs to be consulted is [1], which covers a lot of information about what colon cancer is and how to prevent and diagnose it. More related to the topic of our project, [2] is an interesting read about how to classify colon polyps in endoscopy and we can see in [3] a comparison between the polyp detection results obtained by using virtual or conventional colonoscopy.

As our work is focused on **image segmentation,** it is necessary to study which techniques are being applied nowadays, taking also into account the requirements of our project. One basic but yet very useful approach is the watershed transform [4] that is a region-based segmentation approach whose underlying idea comes from geography, where we can think of a landscape or topographic relief flooded by water, being watersheds the division lines of the domains of attraction of rain falling over the region. Another segmentation technique, more expensive in terms of computation cost, is *graph cuts* [5], where the segmentation process is taken as an energy minimization problem and therefore reduced as instances of the maximum flow problem in a graph. *Mean shift-based* approaches [6], that use a radially symmetric kernel to estimate local density, can be also a good alternative.

Related to **region merging** (because we will start with a high number of regions that needs to be reduced), and enclosed into the **image description** group, we can go through different routes. One of them can be to analyze the frontiers between regions in order to merge those whose frontier can be considered as weak. To measure frontier weakness we can consider 'edginess' (or the probability of having an edge in the considered frontier) and then use some of the more common edge detector algorithms, such as Canny [7] or Sobel edge detector [8] (and even use Harris corner detector [9] as an edge detector). Another interesting measure could be the presence of valleys and ridges in the image [10], paying attention to the boundaries that separate them. Also related to **region merging,** we have [11], where a hierarchical segmentation process is done by considering contour dynamics or [12] where watershed image segmentation algorithm is used as a primal step into an iterative segmentation process.

# 3. Methodology

The processing schema can be divided in two basic steps that will be explained separately. The general chain of processes can be seen in Figure 1.
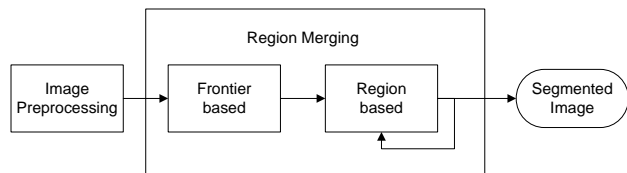


*Figure 1. Processing Schema*

## 3.1. Image Preprocessing

As part of image preprocessing, and as we have to deal with high definition images from an interleaved video, the first operation will be to deinterleave the image. After that we will invert the resulting image that we will use as source for the next steps.

Once the preprocessing is done a basic watershed image segmentation algorithm is applied followed by a morphological closing in order to reduce the number of regions that watershed returns.

One important point of our approach is that we have considered the use of alternative image sources to the watershed algorithm, apart from the already mentioned preprocessed image. We have explored the use of gradient images with two different methods of calculation.

The first one is obtained by calculating the modulus of the output of the gradient function on each pixel position, and it is able to follow better the edges structure of the image. The second method corresponds to the morphological gradient (i.e. calculated by subtracting two versions of the image, one dilated and the other eroded), which can give us a first representation on the valley structure of the image. The results of watershed segmentation by using gradient approaches suit better the structure of the image, as it can be seen in Figure 2 although they lead to deal with a higher number of regions.
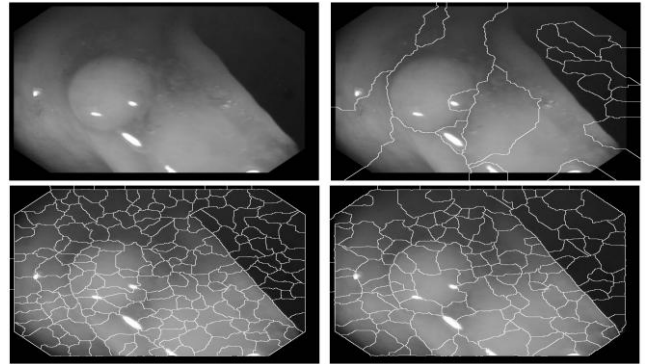


*Figure 2. (up-left) Original Image Preprocessed (up-right) Original Image Segmented (down-left) Gradient Modulus Image Segmented (down-right) Morphological Gradient Image Segmented*

## 3.2. Region Merging

In this step we use two different ways to merge regions. The first one is based solely on a measure of frontier weakness while the second adds some degree of region information to the merging process.

### 3.2.1 Frontier-based Region Merging

In order to consider a frontier as weak, it has to be weak in each one of the categories that we have considered. For each of the first three categories we calculate first, to assess the degree of weakness, a mask which will act as a filter (different for each case). Second, we superimpose the mask to the original image and we calculate, for each frontier from the original segmentation, the proportion of pixels from the frontier that will not be eliminated after applying the mask. Finally, if this proportion is higher than a certain threshold value, the frontier is labeled as weak for this concrete category.

- Valleyness: in order to obtain the valleyness mask we binarize the morphological gradient image (emphasizing the valley values) by applying a Canny edge detector. The resulting image can be seen in Figure 3 where we show in green the pixels with high valleyness measure.
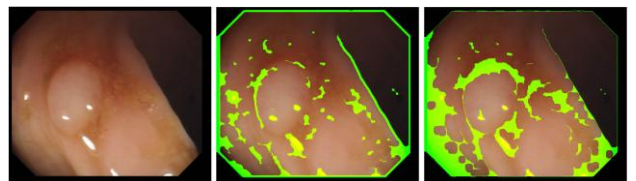


*Figure 3. (left) Original Image (center) Valleyness image (right) Edginess Image*

- Edginess: in this case we apply a Canny edge detector to the original image and the result is used as the mask for this criteria. We also show in Figure 3 in green the areas of the image with great edginess value.

- Anisotropic Filtering: is a method that enhances the image quality of textures on surfaces that cannot be seen properly as well as it removes

aliasing effects and reduces blur while preserving detail. After the filter, and in order to obtain the mask, we apply some morphological operations to enhance the areas where the response of the filter has been high, which denote stable regions.

- Gradient-based Frontier Orientation: we denote as weak frontiers those which does not follow what we can call a 'logical gradient succession', that is, when we are in an intersection of three regions the more logical path will be the one that follows one same gradient orientation.

We combine these four methods to create a 'frontier weakness' measure and we merge, two by two, the regions that have a very weak frontiers.

### 3.2.2 Region-based Region Merging

Once we have reduced the number of regions after the first Region Merging step, we can characterize them in terms of mean and standard deviation of both regions and frontiers between regions, following the criterion that is shown in Table 1 and Table 2.

| Name | Mean Grey Value | Standard Deviation |
|---|---|---|
| Non-Informative Bright | 230-255 | < 10 |
| Non-Informative Dark | 0-25 | < 10 |
| Slightly Informative Bright | 195-230 | < 10 |
| Slightly Informative Dark | 25-60 | < 10 |
| Informative | 60-195 | < 10 |

*Table 1. Region Profiling*

| Name | Mean Grey Value | Standard Deviation |
|---|---|---|
| Non-Informative Bright | 230-255 | < 10 |
| Non-Informative Dark | 0-25 | < 10 |

*Table 2. Frontier Profiling*

In short, we denote as non-informative regions or frontiers those whose mean grey value is very high (or very dark) and the standard deviation is low. With this definition we can label very dark regions and frontiers (that will cover the borders of the image and the darker areas of the colonoscopy image) and very bright regions and frontiers (mainly reflections).

When joining we consider, along with the new frontier measure that will be explained in a few lines, some degree of region compatibility, for example, we merge bright regions with bright frontiers.

The measure of frontier weakness that is used in this step is a combination of the following measures:

- Scale-space Filtering: we pass our image through two order-increasing median filters in order to discard some frontiers (in our case it works well with the frontiers that are located in the veins).

- Bottom-hat: in this case, applying a bottom-hat morphological operation will let us connect objects close to each other.

In this case we merge, two by two, compatible regions with weak frontiers until the number of regions is stable. In order to obtain the final image we categorize again the regions and consider the darker regions that will remain as non-informative (borders of the image + dark areas).

## 4.    Experiments and Results

- **Experimental Setup**

Before showing some results, we have to define both the database that has been used and the performance measure:

- **Database:** In order to test the performance of our method, we have created a database that consists of 20 different images where there is a colon cancer polyp (covering different shapes, sizes or degree of visibility). We have manually segmented the images and, as result of this segmentation we have two masks per image: one for the polyp and one for the whole non-informative area (darker areas + borders).

- **Performance measure:** For each of the masks we will consider as performance measure the number of pixels that have been labeled correctly (i.e. number of pixels labeled as non-informative that are really non-informative pixels).

- **Results**

- **Variation of the performance results with respect to the input source**

    As we can see in Figure 4, there is an improvement in terms of performance rate if we choose as initial source to the watershed either any of the presented gradient-based images. For all the cases, the performance rate for the Polyp pixels is almost 100%.
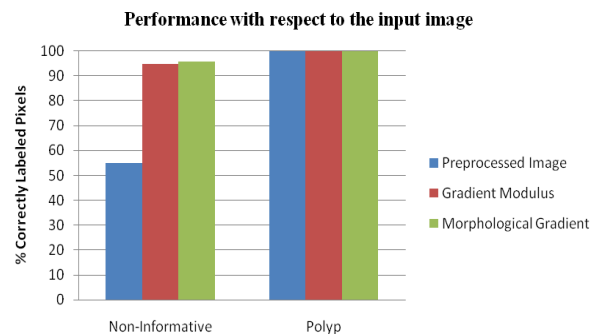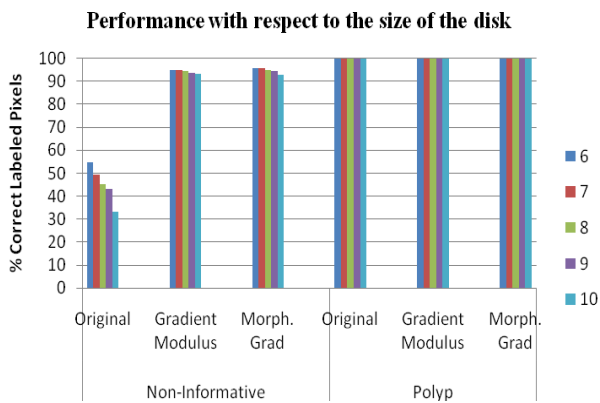


*Figure 4. Performance rate with respect to the input image*

- **Variation of the performance results with respect to the size of the initial closing**



**Performance with respect to the size of the disk**

*Figure 5. Performance rate with respect to the size of the disk*

By observing Figure 5 we can state that the smaller the size of the disk, the better the results. The reason behind the global worsening of the results lies on the fact that the higher the size of the disk, we have different frontiers and less (and bigger) initial regions which are less uniform and more difficult to categorize or merge.

- **Qualitative Results**

We show in Figure 6 a comparison between a pair of hand-made masks and the masks that our method will provide. We can see that, although there are some little differences, they are almost identical and that in no case polyp area is labeled as non-informative (white areas in masks).
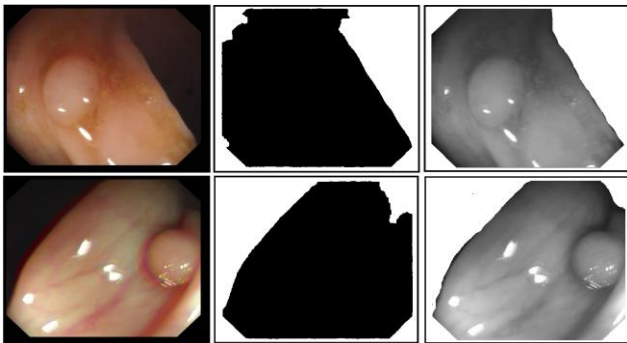


*Figure 6. (left column) Original Images (middle column) Hand-made Mask (right column) Output of our Method*

## 5. Conclusions

As we mentioned in the Introduction, dealing with thousands of images and process them in real-time can be quite difficult (even with an easy image processing algorithm). In this paper, in the context of Colon Cancer polyp detection, we have presented an approach that eliminates successfully some portions of the image where we do not expect to find a polyp. At the same time our method does not label any part of the image that contains a polyp as non-informative. The approach is based on exploring the characteristics of the frontiers between previously segmented regions and, on a second step, in the relationship between regions and frontiers with some degree of characterization. The next step will be to improve the region merging between the remaining regions before starting with the description of the areas of the image with the aim to search to polyp candidates.

## Acknowledgements

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