

A Bayesian Approach for False Positive Reduction in CTC CAD

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Abstract. This paper presents an automated detection method for identifying colonic polyps and reducing false positives (FPs) in CT images. It formulates the problem of polyp detection as a probability calculation through a unified Bayesian statistical model. The polyp likelihood is modeled with a combination of shape and intensity features. A second principal curvature PDE provides a shape model; and the partial volume effect is considered in modeling of the polyp intensity distribution. The performance of the method was evaluated on a large multi-center dataset of colonic CT scans. Both qualitative and quantitative experimental results demonstrate the potential of the proposed method.

Keywords: colon CAD, colonic polyp detection, Bayesian framework

1 Introduction

Typical approaches to computed tomography (CT) colonography (CTC) CAD can be classified as shape-based. Shape-based methods typically rely on various shape features derived from either first-order differential geometric quantities [1] or from second-order quantities computed by use of Hessian matrices [2-4]. The shape features take advantage of the fact that polyps tend to have rounded shapes or at least contain local spherical elements, whereas colonic folds have elongated shapes. However, in practice, polyps are often abnormal growths that exhibit varying morphology, and shape-based methods may fail to detect polyps with sufficient reliability. Therefore, in addition to shape-based features, other features such as those based on appearance can also be used to improve detection performance. Appearance-based features include image intensity either directly or indirectly through intensity related features, which take advantage of the fact that polyps typically exhibit a slightly elevated intensity and inhomogeneous texture relative to the surrounding mucosal tissue.

Our goal in this paper is to incorporate shape features with appearance features in a unified Bayesian framework to reduce false positives (FPs) in colon CAD. For each voxel within the candidate region, our method estimates the probability that the voxel is contained within a polyp. The advantages of a Bayesian technique are as follows. First, statistical techniques are ideally suited to modeling the large uncertainty inherent in detection problems in medical imaging. Second, there often is useful medical knowledge (such as lesion density, size, shape, etc.) that can be utilized to constrain the solution of detection problems. This prior medical knowledge can be easily encoded into a Bayesian model. Finally, a Bayesian technique provides a unified framework for incorporating various features F into one statistical model.

Mendonca *et al.* [5] formed a probability distribution function for each *voxel* in the image based on simplified geometric models (ellipsoidal polyps, spherical colon wall, etc.), which

preclude a specific training step. However, these parametric models have limited capability to model the complexity of actual polyps in the human anatomy. Our approach uses a more expressive shape model that has been shown to model the variation in polyp shapes. Also, the proposed framework includes prior medical knowledge through explicit learning based on labeled examples. To our knowledge, this is the first time such a learning-based Bayesian approach for modeling the likelihood of polyp voxels has been proposed in a CTC CAD system.

The proposed method has been applied to the candidate regions found by our previous CAD algorithm [6]. Quantitative evaluation on a large multi-center clinical dataset of colonic CT scans shows the excellent performance of the method, which reduces the FPs by an average 16%, while keeping the same sensitivity.

2 Method

We are given a set of voxels $X = \{x_i, i=1, \dots, N\}$ in a 3D image, a set of features $F = \{F_j, j=1, \dots, M\}$ associated with each voxel x_i , and a set of labels $\Lambda = \{l_0 \dots l_{K-1}\}$. Here, we use $K=2$, where, l_0 is a non-polyp label, whereas l_1 is a polyp label. This paper focuses on assigning one of the labels to individual image voxels within a candidate region based on a probability calculation through a unified Bayesian framework. Two features are considered: the intensity I and shape S ; namely, $F_1 = I, F_2 = S$. Whereas we focus on these two features, the framework is extensible to other features as well.

Assuming that each feature F_j is conditionally independent, the probability of a polyp label at each pixel can be calculated based on Bayes' law:

$$P(X|F) = \frac{P(F|X) \cdot P(X)}{P(F)} = \frac{P(F_1|X) \cdot P(F_2|X) \cdot P(X)}{P(F_1) \cdot P(F_2)} \quad (1)$$

The posterior, likelihood, and prior terms are $P(X|F)$, $P(F|X)$ and $P(X)$. In this paper, a uniform prior is used.

The goal is to use Eq. 1 to model the probability of a polyp label existing at each voxel within each candidate region. A block diagram of the proposed method is illustrated in Fig. 1. Below each stage is described in detail.

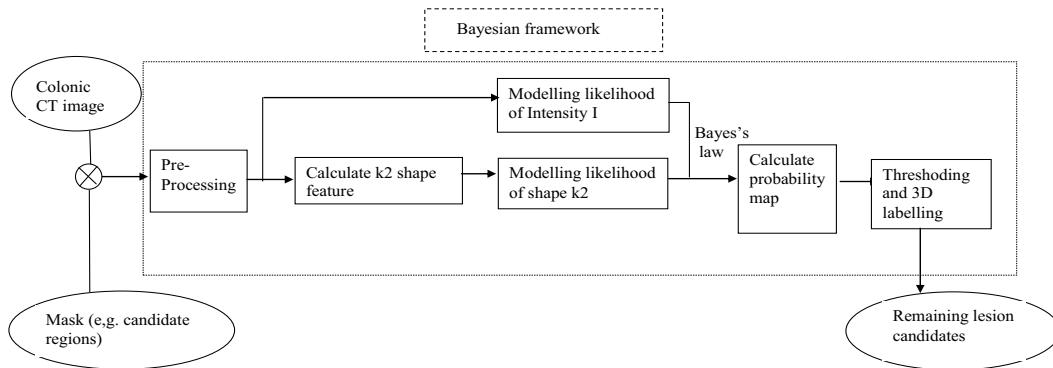


Fig. 1. Block diagram of the proposed Bayesian method for FP reduction

2.1 Modeling the likelihood term

In the Bayesian framework, the likelihood term indicates the joint density distribution of all features for class l_1 . It is noted that, to calculate each feature accurately, during the pre-processing step, a Gaussian filter is applied to remove noise.

2.1.1 Intensity model

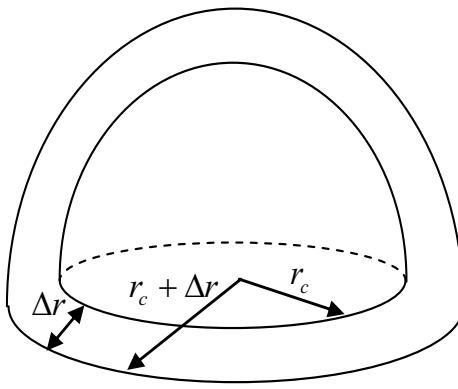


Fig. 2. A schematic diagram of colonic polyp

For each candidate region, a sub-image is extracted. The polyp intensity model varies for each polyp region and can be given by a Gaussian function:

$$P(F_1|X) = \exp\left(-\frac{(F_1 - \mu_I)^2}{\delta_I^2}\right) = \exp\left(-\frac{(I - \mu_I)^2}{\delta_I^2}\right) \quad (2)$$

where μ_I can be defined as a function of potential polyp size (e.g., radius r), namely, $\mu_I = f(r)$. Given the whole polyp radius as $r = r_c + \Delta r$, the mean intensity of a polyp is adaptively determined as:

$$\mu_I = f \cdot \mu_{lc} + (1 - f) \cdot \mu_{lp} \quad (3)$$

where f is the fraction of the core part's volume compared to the whole polyp's volume, namely, $f = r_c^3/r^3 = (r - \Delta r)^3/r^3$.

When a polyp is very small, there might be no core part, namely $r_c = 0$ and $f = 0$, so the mean intensity μ_I depends on the mean intensity of PVE μ_{lp} . In contrast, when a polyp is very large, e.g., $r \rightarrow \infty$, we have $f = 1$, and the mean intensity μ_I depends on the mean intensity of the core part.

2.1.2 Shape model

The second principal curvature (K2) partial differential equation (PDE, or *flow*) for polyp detection was recently introduced by van Wijk *et al.* [4]. Our aim in this section is to model the K2 flow feature's distribution and combine it into the joint statistical likelihood term of the Bayesian framework.

The vast majority of polyps are raised objects protruding on the colon surface, which means that their first and second principal curvatures have positive values. In contrast, colonic folds are elongated structures, bent only in one direction, and correspondingly exhibit a positive first principal curvature and a close-to-zero second principal curvature. Therefore, for detection of polyps, a flow based on the second principal curvature can be designed that affects only points with a positive second principal curvature in such a way that the second principal curvature decreases. Repeated application of the PDE on an image will gradually deform the image, reducing and then removing surface protrusions.

A PDE flow to remove protruding objects can be defined as

$$\frac{\partial I}{\partial t} = \begin{cases} -k_2(x_i) \cdot |\nabla I| & (k_2(x_i) > 0) \\ 0 & (k_2(x_i) \leq 0) \end{cases} \quad (4)$$

where $k_2(x_i)$ is the second principal curvature at image voxel x_i , and $|\nabla I|$ is the gradient magnitude of the input image.

Based on Eq. 4, the image intensities exhibit a small (if any) change for folds, and a large change for protruding objects (such as polyps). During each iteration, only at locations of protruding objects is the image intensity reduced by an amount proportional to the local second derivative k_2 . After the PDE reaches a steady state, the difference image D between the input and the deformed images indicates the amount of protrusion. By design, it discriminates between polyps and folds and is robust to different polyp morphologies and sizes. A truncated Gaussian function is used to model the polyp likelihood as a function of the intensity difference $F_2^{k^2} = D$. The truncated Gaussian function allows a larger range of voxels with high K2 flow have high probability of being polyp labels.

$$P(F_2^{k^2} | X) = \exp\left(-\frac{(F_2^{k^2} - \mu_{k^2})^2}{\delta_{k^2}^2}\right), \text{ when } F_2^{k^2} > \mu_{k^2}, P(F_2^{k^2} | X) = 1 \quad (5)$$

where μ_{k^2} and δ_{k^2} are the mean and standard deviation (std), respectively, determined through a training dataset.

We compared this K2 flow to other second-order shape features such as the shape index [2]. Fig.3 shows a comparison applied to two polyps (a) (with one polyp attached to the colonic wall, whereas the other polyp is attached to the colonic fold). It can be seen that both the intensity likelihood map (b) and the shape likelihood map (c and e) are highlighting the polyps. However, compared to the shape likelihood map calculated based on the shape index (c), the proposed K2 difference map (e) shows a superior performance with very few false regions in the entire sub-image. Fig. 3(f) is the final polyp probability map from the intensity and K2 flow likelihoods (Eq.1). It is noted that, by use of the proposed Bayesian method with the K2 flow shape model, both polyps can be detected and properly segmented from the surrounding tissues.

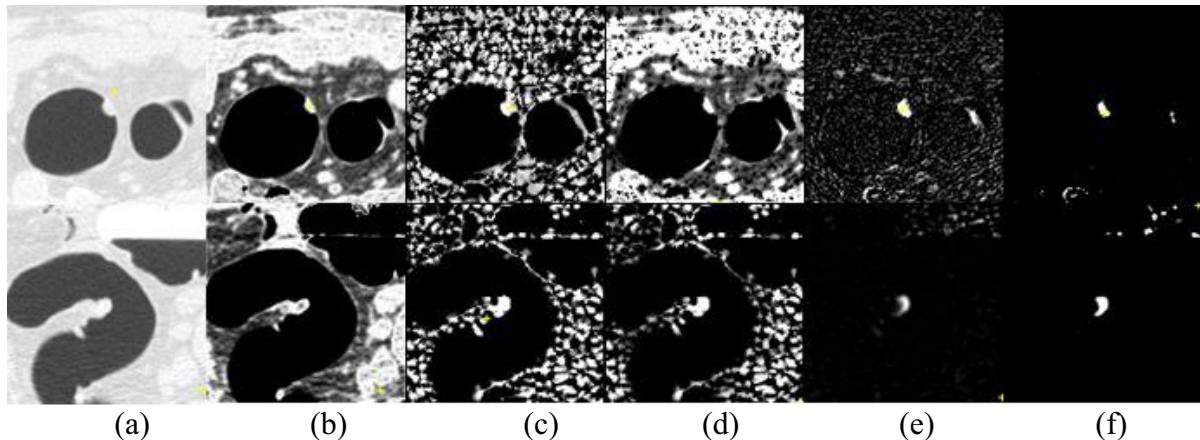


Fig. 3. Results of the Bayesian method comparing two different shape features on two polyps (a) CT sub-image; (b) intensity probability; (c) shape index probability; (d) joint (Bayesian) probability based on intensity and shape index probability; (e) K2 flow difference image; (f) joint (Bayesian) probability based on intensity and K2 probability.

3 Experimental Results and Discussion

The proposed Bayesian method has been trained and evaluated on CT colon images. The entire dataset is divided into a training set and an independent testing set. There are 68 scans containing 70 polyps in the training set. The training set is used to optimize model parameters. In this paper, each feature likelihood term in Eq. 1 is associated with one rule for polyp detection. The parameters for each model that provide good cut-off in a ROC curve are chosen.

In our previous work, we have developed an entire automatic CT colonic polyp detection algorithm [6]. The aim of this experiment is to use the proposed Bayesian method for further removal of false regions. For each candidate region, a polyp probability map based on a Bayesian framework (Eq.1) is calculated, where, the intensity model is based on Eq.2 and the K2 feature is used for the shape model. Hysteresis thresholding and 3D labeling are then applied on each probability map. If a candidate region contains a set of 3D connected voxels with high probabilities of “polypness”, the region is kept as a potential polyp region. Otherwise, the region is considered to be a non-polyp region and is removed from the polyp candidates.

For a quantitative evaluation of the performance, the method has been tested on our latest independent dataset of 59 patients (118 CT volumes) of prone and supine volumes collected from 4 institutions, with a total of 75 polyps. Fig. 4 shows FROC curves based on our previous CAD algorithm only and the further FP reduction based on the proposed Bayesian method. It can be seen that, with the same sensitivity, the Bayesian method reduces the FPs by an average of 16%. For example, with a sensitivity of 93.3%, the FP rate can be decreased from 6.2 per volume to 5.2 per volume after applying the Bayesian method. As we keep the same sensitivity for the proposed method, the improved curve looks a shift compared to the previous curve. This demonstrates the effectiveness of the proposed algorithm in the false-positive reduction. (It is noted that, in this experiment, the sensitivity is measured per polyp, that is, if a polyp is detected on either or both volumes, it is considered a true positive, and false positives are measured per volume, as is the convention in CTC).

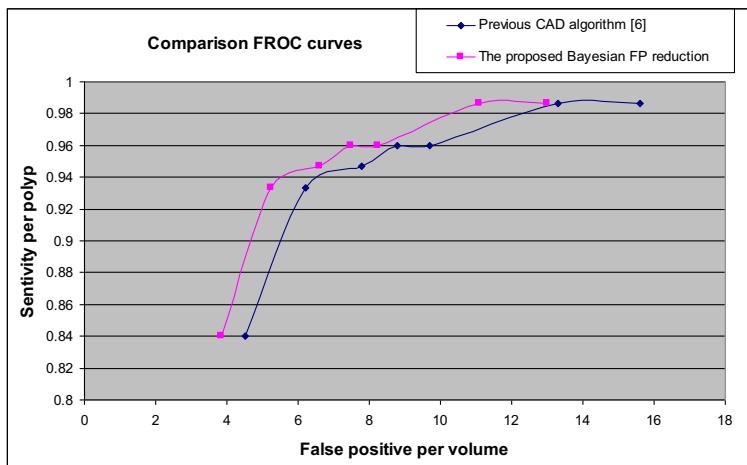


Fig. 4. FROC curves demonstrating the improvement of the Bayesian approach compared to our previous CAD algorithm.

4 Conclusion

We have presented a Bayesian approach to the reduction of false positives in CTC CAD. For each candidate region, the polyp likelihood is modeled by use of a combination of shape and intensity features. The second principal curvature flow is used as a shape model, while PVE is considered into modeling of the polyp intensity distribution. The proposed method has been applied on the candidate regions obtained from our previous CAD algorithm [6] on a multi-center dataset of colonic CT, and it shows an average 16% reduction of FPs while keeping the same sensitivity. The method provides a robust and consistent performance.

The Bayesian framework is general and can be flexibly extended to incorporate other features. Indeed, one could imagine incorporating other image features (location, texture) as well as patient informatics (age, family history of colorectal disease) for robust detection. The algorithm can also be easily adapted to candidate generation step of CAD system.

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