A NEW 3-D VOLUME PROCESSING METHOD FOR POLYP DETECTION

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Abstract- **Early diagnosis and removal of colonic polyps is effective in the elimination of subsequent carcinoma. This paper presents a new approach for computer-aided detection of polyps. The approach mimics the way the radiologists view CT abdomen images and utilizes several geometric attributes obtained from many triples of mutually orthogonal planes. The histogram of the attributes obtained from a sufficiently large number of perpendicular random images serves as a robust signature to represent the shape. We combine the new 3-D pattern recognition with a support vector machine classifier, and show that the number of the false positive detections in the initial polyp detection studies can be substantially reduced. One of the main contributions of this study is the thorough analysis of planar geometrical attributes. When an appropriate combination of planar attributes is used, the false positive rate is reduced by 87 percent beyond that of the initial stage detector, while maintaining a sensitivity level of 95 percent. Using such methods, radiologists should be able to view CTC data much more efficiently and accurately than without CAD.**

Keywords **- Computer aided diagnosis, vector quantization, support vector machine, polyp detection**

I. INTRODUCTION

Colon cancer is the second leading cause of cancer deaths in the USA [1]. Previous research has shown that adenomatous polyps have a high probability of developing into subsequent colorectal carcinoma [2]. Detection and removal of pre-cancerous polyps can prevent eventual cancer development. As such, a cost-effective and patient-comfortable screening procedure is desirable in order to diagnose the disease in an earlier stage.

CT colonoscopy (CTC) is a recently developed, non-invasive screening method that combines spiral CT data acquisition of the air-filled and cleansed colon with 3-dimensional imaging software to create endoscopic images of the colonic surface[9]. While initial results are promising, the method is limited partly due to the extensive amount of radiologist time involved in the interpretation process. Therefore, an automated computer-aided detection method for polyps is necessary to increase efficiency prior to the widespread use of CTC for screening.

Automated polyp detection is a new, but rapidly growing area of research. The problem of identifying colonic polyps is very challenging because they come in various sizes and shapes, and because thickened folds and retained stool may mimic their shape and density. Fig. 1 gives examples of the similar shapes rendered from polyps and normal tissue. Initial studies concerning automated polyp detection have been based on analysis of 3D shape. In [4], Summers *et al.* computed the minimum, maximum, mean and Gaussian curvatures at all points on the colon wall. In [22], Yoshida *et al.* use curvedness to distinguish polyps from healthy tissue. In [5], Paik *et al.* introduced a method based on the concept that normals to the colon surface will intersect with neighboring normals depending on the local curvature features of the colon. In [7], Gokturk and Tomasi designed a method where a sphere is fit locally to the isodensity surface passing through every CT voxel in the wall region and densely populated nearby sphere centers are considered as polyp candidates.

Due to the large number of false positive detections, all of the methods mentioned above can be considered more as polyp *candidate* detectors than polyp detectors. This paper presents a statistical method to differentiate between polyps and normal tissue amongst the candidate polyps. The input to the system is a set of small candidate volumes, derived from one of the methods just discussed. Our volume processing technique attempts to mimic the way radiologists view these shapes and generates shape-signatures for each candidate volume. The signatures are then fed to a support vector machine (SVM) classifier for the final classification of the candidate volume.

The paper is organized as follows: Section 2 describes our volume processing method in detail. Section 3 explains the experimental setup and describes results from initial clinical applications. Section 4 describes our early conclusions and possible directions for future work.

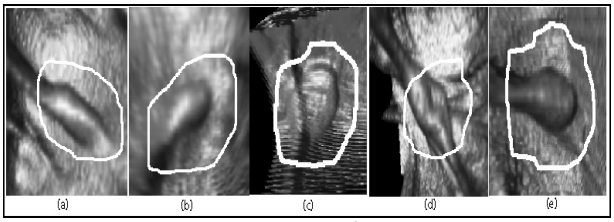

Fig. 1: Virtual endoscopic reconstructions from CTC data showing (a-c) true polyps, (d) a normal thickened fold (e) retained stool.

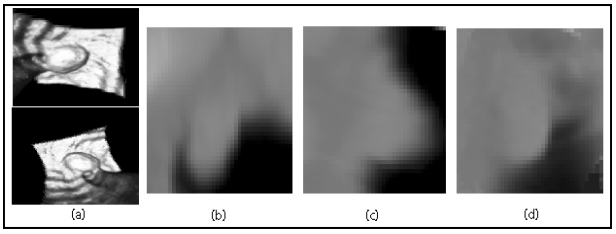

Fig. 2: (a) Two different volume renderings of a polyp. (b-d) Three mutually orthogonal tomographic planes through the same volume.

II. METHODOLOGY

Many radiologists prefer to view colon CT images using three perpendicular image planes aligned with the transaxial, sagittal, and coronal anotomical directions [3]. Our approach takes advantage of this observation. To be more accurate, we collect statistics over several random *triples* of

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Abstract

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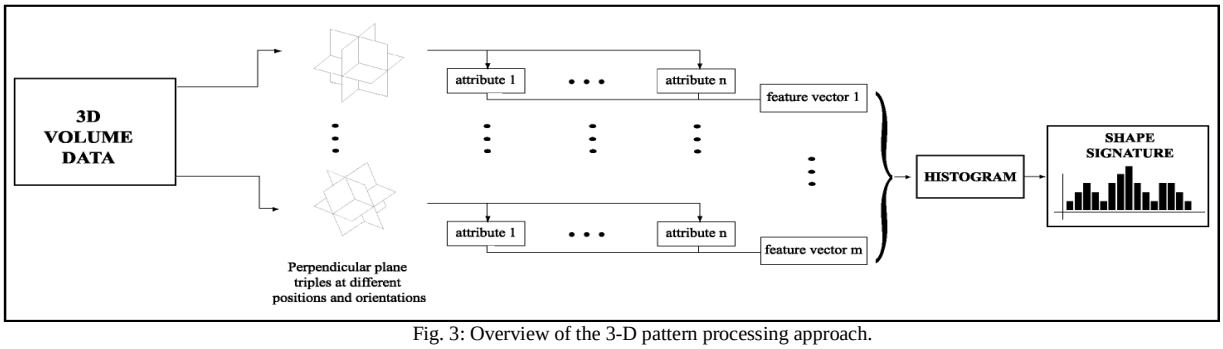

Fig. 3: Overview of the 3-D pattern processing approach.

mutually orthogonal planes rather than using only the principal directions (Fig. 2). Fig. 3 gives the overview of our volume processing approach. Having obtained many triples of planes, geometric attributes are obtained for each random plane. We use a histogram of these geometric attributes obtained from each triple as a feature-vector to represent the shape. Taking histograms of these geometric attributes over several random triples makes the resulting signatures invariant to rotations and translations. More details on such "signatures" are given in Sections *A* and *B*. Support vector machines, as described in Section *C*, are then trained with signatures computed from an initial set, and are subsequently used to classify new candidate volumes as containing polyps or normal tissue.

A. Image Processing

Once each candidate volume is sliced with several triples of perpendicular planes, the necessary region on the slice needs to be segmented. On each slice, a polyp may not occupy the resulting image entirely. As a consequence, images are segmented, so as to disregard tissues surrounding the putative polyp. By segmentation, we aim to discover the best square window that would capture the essentials of the shape as demonstrated on Fig. 4. We parameterize the segmentation task as an optimization problem for searching the optimum window size [3]. Shape and intensity attributes are computed in the resulting optimum sub-window.

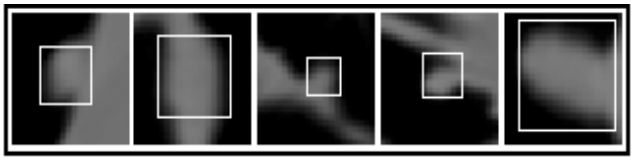

Fig. 4: 2-D images of five different suspicious lesions, with the size of the critical region varying from image to image.

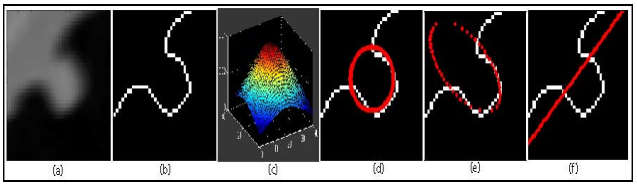

Fig. 5. (a) Sample image. (b) Edges. (c) Gaussian mask to weight the edge points on the image. (d) Circle, (e) ellipse, (f) line fitted to the weighted edge points.

The geometric attributes of the image should capture representative information about the candidate shape. In the following paragraphs, we describe the feature vectors derived to describe these geometric attributes. Primitive shapes such as circle, ellipse, line and parallel set of lines (Fig. 4. d,e,f,g) are fit to the largest connected edge component, *i.e.* the boundary of the shape.

A random slice of a sphere is a circle. Thus, fitting circles is a means of measuring the sphericity of the 3-D shape. While doing so, we first mask the boundary points by a Gaussian located at the center of the image in order to give more importance to the boundary points that are closer to the center of the image. Next, the least squares solution is found to minimize the residual of the Gaussian weighted circle. The residual to the least square solution is recorded as well.

Similarly, the residual to the optimum fitting line gives information on the flatness of the surface. Quadratic curves include any second order equation system of two variables. By fitting a quadratic curve to the boundary of the image, the ellipsoidal structure of the shape can be measured, thereby helping to capture similarity to a pedunculated polyp.

The projection of a fold onto the image plane contains parallel lines. In order to capture this structure, we apply parallel lines analysis, which includes fitting lines to the two largest connected components of the boundary points. The residual to these lines and the angle between the parallel lines are also recorded as a feature vector.

In order to extract information regarding the higher order frequency characteristics of the boundary, 3rd order moment invariants are computed as well [10]. This gives information regarding the curviness of the boundary points. In addition to these shape features, intensity features are extracted from the tissue part of the image. These features include the mean and and standard deviation of the intensity of the tissue in the volume.

All the attributes mentioned so far are calculated for each random triple of images. The three images in each triple are sorted in the order of increasing radius of curvature, and the features above are listed into a vector in this order. Often, one plane out of the three planes does not contain useful geometric information, *i.e.* it might represent uniform tissue or air-containing voxels. In these cases, features from the non-contributing plane are not considered further. The remaining vector represents the signature of the candidate volume relative to that particular triple of perpendicular planes.

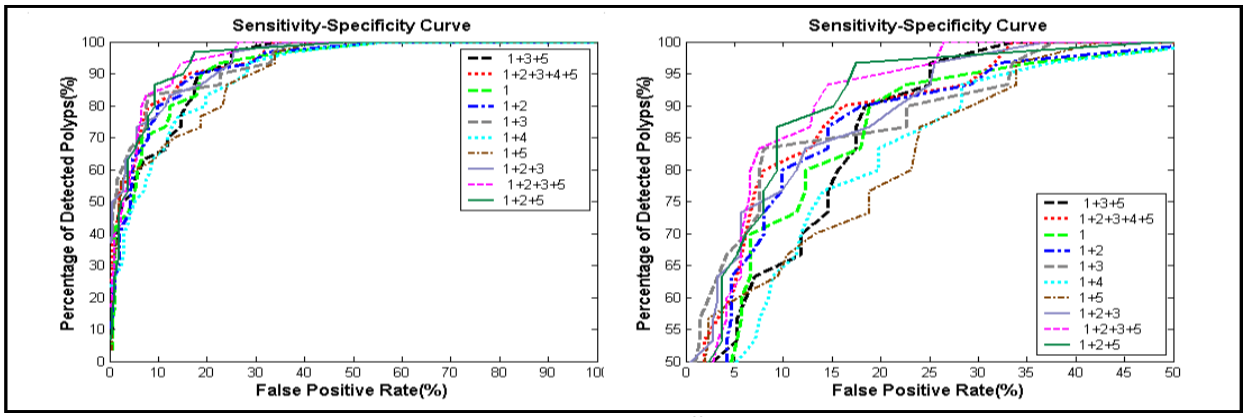

Fig. 6: The results obtained with different planar attributes

B. Vector Quantization

The features computed from each triple of perpendicular planes depend on the position and orientation of that particular triple. However, if histograms of feature distributions are computed from sufficient numbers of triples with random positions and orientations, the histograms themselves become invariant to position and orientation. Representing the histograms of these attribute vectors is non-trivial, as uniformly oriented histogram bin centers are not possible due to the high dimensional space of the underlying vectors. An alternative method is necessary to obtain histogram bin centers that would represent the data accurately. We use vector quantization for this purpose. First, the representative histogram bin centers are obtained using a k-means clustering algorithm[11]. This algorithm starts with a random selection of feature vectors as histogram bin centers and iterates to find the optimum bin centers. Having obtained the bin centers, each feature vector partitions a unit vote into fractions that are inversely proportional to the vector's distances to all cluster centers. The histograms thus obtained, one per candidate volume, are the final shape signatures used for classification as described in the next section.

C. Support Vector Machine Classification

A classifier learning algorithm takes a *training set* as input and produces a *classifier* as its output. In our experiment, a training set is a collection of candidate volumes that a radiologist has individually labeled as polyps or non-polyps. A Support Vector Machine classifier finds the best discriminating hypersurface between the two classes in the training set, *i.e.* polyps and non-polyps [8]. This hypersurface not only classifies the two subsets correctly but also maximizes the margin between the closest points. The points closest to the hypersurface are termed the "support vectors". This problem of finding the optimal hypersurface is illustrated to be a quadratic programming problem in [8]. Suppose that vector x_i in the training set is given (by the radiologist) a label y_i =1 if it is a polyp and y_i =-1 if it is not. Then the optimal classifier has the form:

$$f(x) = \sum_{SV's} \alpha_i y_i K(x_i, x) + b \qquad (1)$$

Where SV denotes the set of support vectors, K is a kernel function used to transform the data from its original space to a higher space where it is easier to discriminate the two classes, and α_i and b are constants computed by the classifier-learning algorithm.

SVMs minimize the structural risk, given as the probability of misclassifying previously unseen data. In addition, support vectors are inherently the vectors that carry the differentiating characteristics of each class. Identification of these vectors exploits all of the information in the training set optimally, and eliminates the guess work from the task of defining appropriate discrimination criteria.

III. EXPERIMENTS

We used a data set consisting of small candidate volumes from the CT scans of subjects enrolled in our CT colonography study comprising 30 known colonic polyps and 212 other regions containing tissue from non-polyp or normal mucosal surfaces. These non-polyp structures were obtained by taking the false positive detection outputs of the algorithms presented in previous work [5,7]. These areas typically represented thickened haustral folds, convergent folds, or foci of retained stool.

100 random triples of perpendicular images were extracted from each candidate volume. A 24-element vector was obtained for each triple. These vectors incorporate all the geometric attributes from each particular plane. For analysis purposes, we divided these attributes in to five different categories: (1) {radius of best fitting circle, residual to the best fitting circle, residual to best fitting line}, (2) {moment invariants}, (3) {quadric invariants}, (4) {intensity based features}, and (5) {parallel line features}. We divided our experiments into different groups where subsets of these five categories were evaluated. This way, one can judge the relative importance of each attribute. The optimum selection of these geometric attributes not only would have computational affectivity but also could give valuable feedback to radiologists.

The results are summarized in Fig. 6. The numbering on the legend is the same as the numbers of the attributes mentioned above. An exponential radial basis function [8] was used as kernel function with support vector machine classifiers. A 10-fold cross validation was applied in order to obtain the results given in Figure 6. Here, sensitivity is given as the ratio of the detected polyps over all of the 30 polyps.

False positive rate is the ratio of uneliminated false positives in the initial set. Observe that, on average, the false positive rate occurs as 35%, 23%, 18%, 15% and 13% at polyp detection sensitivity levels of 100%, 95%, 90%, 85%, and 80% respectively. The combination of attributes {1, 2, 3 and 5} served as the optimal set in these initial experiments. In geometric terms, these results show that searching for circular and elliptical structures in the image, then searching for parallel lines and 3rd order curved structures is the most discriminating strategy for polyp detection. When these planar attributes are used, the false positive rate can be further reduced to 28%, 15%, 13%, 9% and 8% for sensitivity levels of 100%, 95%, 90%, 85%, and 80% respectively.

In the current experimental design, we search for the optimum set of planar attributes by trial and error, i.e., by searching the space of all possibilities one by one. While the current results are considerably improved compared with our earliest implemenation, we desire more targeted methods to replace the exhaustive search strategy for obtaining the optimum choice and combination of attributes.

IV. CONCLUSION

Virtual colonoscopy is a promising new medical imaging technique to evaluate the human colon for precancerous polyps. Due to the large amount of radiologist time involved in reviewing hundreds of images in a search for small lesions, computer aided diagnosis is necessary to make the approach efficient and cost-effective. Previous automated detection methods had a high sensitivity for polyp detection, but relied on human observations to differentiate polyps from normal folds or retained fecal material. To be more accurate, we need a method that is capable of differentiating polyps from other normal healthy structures in the colon. In this study, we proposed a learning approach that yields a good polyp detection rate with a reasonable number of false positives, thereby showing the feasibility of computer-based screening. One of the main contributions of the paper is the new 3-D pattern analysis approach, which combines the information of planar attributes from many random images to generate reliable shape signatures. We present an experimental setup to obtain the best combination of these planar attributes by exhaustive search. We also show that the use of support vector machines allows to implicitly distinguish the differentiating characteristics of polyps and healthy tissue, thus improving classification rates.

There are many possible directions for future investigation. First, we would like to analyze support vectors to observe the differentiating characteristics of polyps and healthy tissue. Using the features in these support vectors, we would like to find an automated way to obtain the optimum combination of planar features to be used in polyp detection. In addition, studies integrating these computer-aided detection schemes with radiologist readers will be used to measure potential improvements in sensitivity and efficiency compared with unassisted radiologist interpretation.

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