

Prediction of Esophagitis and Z-Line from Wireless Capsule Endoscopy images using Fusion of low-level features



R. Ponnusamy, S. Sathiamoorthy

Abstract: Wireless endoscopy capsule (WCE) pictures are often used to recognize digestive tract illnesses as they enable immediate GI tract perception. In any case, it requires a clinician's long-lasting review because of an incredible number of pictures delivered by the system. In this manner, it might be valuable to devise an Automatic detection framework to enable clinicians to distinguish abnormal pictures. In this work, it is endeavour to plan an electronic plan intending to distinguish esophagitis in WCE pictures. The Esophagitis in WCE pictures show extraordinary variations in appearance. Scale-Invariant Feature Transform (SIFT) and Auto Color Correlogram (ACC) are two features that are used to coordinate the texture, color and shape characteristics collected from points of interest. Using Naïve Bayes, Support Vector Machine (SVM) and Random Forest, we assessed the performance with comprehensive tests on our current picture information consisting of 100 normal-z-line WCE pictures and 100 esophagitis. From the experimental analysis, it is promising to use the proposed plan to distinguish esophagitis and normal-z-line from WCE pictures.

Keywords : WCE, GI Tract diseases, SIFT, ACC, Naïve Bayes, SVM, Random forest.

I. INTRODUCTION

Wireless capsule endoscopy (WCE), a disposable tool in the form of a pill for the diagnosis of gastrointestinal disease [1,2]. There are many anomalies in human digestive track due to so many factors, such as hereditary, lifestyle, occupational dangers, and medical history. Some of the commonly seen abnormalities are the Ulcers, Polyps, Bleeding, Tumours, Esophagitis and Z-line, etc [3,4]. We developed an innovative method in this research using SIFT and ACC to detect Esophagitis and normal Z-line. In classification phase, we extensively evaluated various classification techniques such as SVM, Naïve Bayes and Random Forest in order to find the appropriate one for the GI tract image dataset. Esophagitis is defined as inflammation of the esophagus, which is the tube that joins the throat to the abdominal. According to the cause, there are several kinds of esophagitis. Esophagitis may be induced by infection, esophagus irritation, or esophagus

lining inflammation. Fig. 1(a), indicates an instance picture of esophagitis in white esophageal lining with red mucosal



Fig. 1. (a) Esophagitis (b) Normal Z-line

tongues. The rating of inflammation is defined by span of the mucosal disruptions and amount of the circumference intricate. Clinically, discovery of esophagitis is necessary for treatment initiation to prevent further development of possible difficulties. Automatic detection of esophagitis and normal-Z-line would be of special value in assessing severity of the diseases [5,6].

The Z-line denotes the progress site between the throat and the stomach. Endoscopically, it is obvious as a reasonable fringe where the white mucosa in the throat meets the red gastric mucosa. A case of the Z-line is appeared in Fig. 1(b). Acknowledgment and appraisal of the Z-line is significant so as to decide if diseases is available or not. For example, Z-line is where gastro-esophageal reflux signs may appear. The Z-line is likewise helpful as a kind of perspective moment that portraying pathology in the throat [5,6].

The manuscript has been organized in this way. Section 2, we discussed the method which is proposed. In Section 3, deals about the feature extraction where we introduced the SIFT algorithm and ACC features. Then the classifier we used in our method is discussed in section 4. We briefly discussed experimental results and performance in section 5 and finally Section 6 has the conclusion.

II. PROPOSED WORK

In the proposed method, the abnormalities of esophagitis and Z-line are detected from WCE images using the combined features SIFT +ACC. The SIFT captures local features based on the particular interest points. The ACC features capture the color and its spatial location. The extracted SIFT and ACC features are invariant against rotation and illumination and robustness to small scaling. Using Naive Bayes, SVM and Random forest techniques, the extracted characteristics are classified. By doing 10-fold cross validation the classifiers classified the two classes and their performance metrics like kappa statistic MAE, RMSE, RAE and RRSE are assessed. Fig. 2 shows our proposed method.

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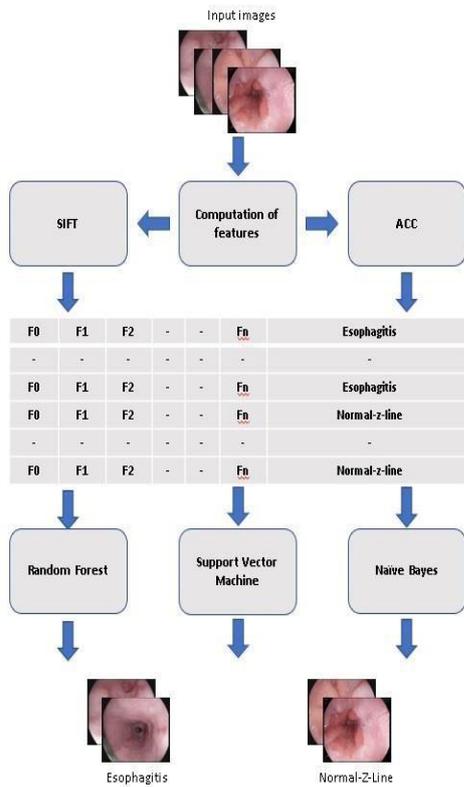


Fig. 2. Proposed method

III. FEATURE EXTRACTION

A. Scale Invariant Feature Transform (SIFT)

For the detection and identification of local characteristics in a picture, SIFT is used. SIFT features are used for reliable matching between dissimilar views of the same object. The separated highlights are invariant to scale, direction and are in part invariant to enlightenment changes [7]. The SIFT include extraction is a four-advance procedure. In the initial step, areas of the latent interest focuses are figured in the image by finding the extrema's in a lot of Difference of Gaussian (DOG) channels connected to the definite image at various scale-space. At the point those interest focuses which are situated at the zones of low brightness and along the edges are disposed of. From that point forward, a direction is distributed to the rest of the focuses dependent on local image gradients. Finally, local image features based on image gradient is calculated at the neighboring regions of each of the key points. Every feature is defined in the 4 x 4 neighborhoods of the key points and is a vector of 128 elements [7,8].

B. Autocorrelogram

The description of the correlogram is found in [9-11]. Let [D] portray a set of D fixed distances {d1... dD}, where the image correlogram It is defined for level pair (gi, gj) at a distance d.

$$\gamma_{g_i g_j}^{(d)}(I) \equiv P_{p_i \in I_{g_i}} p_i \in I_{g_i} [P_2 \in I_{g_j} | p_1 - P_2 = d] \quad (1)$$

Where

I - given image.

$\gamma_{g_i g_j}^{(d)}(I)$ - gives the probability, that a pixel at distance d away from the given pixel is of color g_j for a given any pixel g_i .

p_1, p_2 - any pixel in a image.

d - fixed distance.

g_i, g_j - level pairs.

ACC gives the possibility that given any pixel p1 of level gi, a pixel p2 at a distance d in certain way from the given pixel p1 is of level gi. Auto correlogram [9-11] finds the spatial correlation of identical levels only:

$$\alpha_g^{(d)}(I) = \gamma_{g,g}^{(d)}(I) \quad (2)$$

Where

I - given image.

$\alpha_g^{(d)}(I)$ – Auto correlogram of image I, which is from spatial correlation of identical levels.

d - fixed distance.

g_i, g_j - level pairs.

We get the probability of pixels p1 and p2, d away from each other, are of the same level gi. The distance measure among the histograms, auto-correlograms and correlograms is the L1- norm that is computationally light technique and used in [9-11].

IV. CLASSIFICATION

A.Support Vector Machine (SVM)

Support Vector Machines (SVMs) have been a standout amongst the best artificial intelligence (AI) methods for the past decade. SVM is a broadly utilized classifier that has a strong hypothetical establishment and performs well when contrasted with different calculations in numerous applications. SVM are today a well-known AI method that can be utilized in an assortment of utilizations. In those applications; SVMs perform at any rate in the same class as different techniques regarding the speculation blunder. SVM takes the capacity of the model into account, which is the flexibility of the learned model to represent any training dataset with a minimal error. SVM has the capability of convex optimization objective that ensures reaching a global optimum. The solution obtained through SVM is spares' which improves efficiency of this technique when compared to other kernel-based approaches. A generalization of the linear binary SVM classifier, $\gamma(x)$, classifying instances of $x \in X$ described by a vector of features (x_1, x_2), into classes $C = \{\text{tested_positive, tested_negative}\}$ can be expressed as follows

$$\gamma(x) = w \cdot x + b \quad (3)$$

Where w is a vector perpendicular to the boundary and where b determines the boundary offset from the origin. On the basis of this formalization, x instances will be classified as positively tested if $\gamma(x) \geq 0$ or tested negative if $\gamma(x) \leq 0$. The input data space is transformed into a higher dimensional feature space to make data linearly separable and suitable for linear SVM construction when classes cannot be divided linearly. Usually, a kernel function is used to accomplish this conversion. It makes it likely to determine a nonlinear decision boundary, which is linear in the higher dimensional feature space, without calculating the ideal hyper plane parameters in a possible elevated dimensionality feature space.

Therefore, the response can be written as a weighted sum of the values of certain kernel feature assessed in the support vectors [12].

B. Naïve Bayes

It is a technique of classification based on the theorem of Bayes with a predictor hypothesis of independence [3]. Simply put, a Naive Bayes classifier assumes that any other characteristic is unrelated to the presence of a particular function in a class. For example, if it is red, round, and about 3 inches in diameter, an apple can be considered as a fruit. Even if these features depend on each other or on the presence of the other features, all these features contribute individually to the probability that this fruit is an apple, which is why it is called 'Naive.'

Naive Bayes model for very big information sets is simple to construct and especially helpful. Naive Bayes is recognized to outperform even very advanced techniques of classification, along with simplicity.

Bayes theorem offers a way to calculate P(c) from P(c), P(x) and P(x|c) and is described as follows [3]

$$P(c|x) = \frac{P(x|c)P(c)}{P(x)} \quad (4)$$

$$P(c|X)=P(x_1|c)*P(x_2|c)*.....*P(x_n|c)*P(c) \quad (5)$$

where,

P(c|x) - later probability of the predictor (x, attributes) class (c, target).

P(c) - class's previous likelihood.

P(x|c) - probability of the class provided predictor.

P(x) - predictor's previous likelihood

C. Random Forest

Random Forests is a group of untrained decision trees trained using a version of the random subspace method or feature bagging method [13]. The random forest training method is not as easy as applying bagging to many individual decision trees and then simply aggregating the yield. The technique for practicing random forests is as follows [13]. Select p characteristics from characteristics D at the present node. Usually the amount of characteristics p is much lower than the amount of characteristics D overall.

1. Use the given splitting measure to calculate the best split point for tree k and divide the present node into daughter nodes and decrease the amount of characteristics D from that node.
2. Repeat steps 1 to 2, until either a maximum tree depth l is reached or the dividing metric reaches a certain extreme.
3. For every tree k in the forest, repeat steps 1 to 3.
4. Vote or aggregate each tree's production in the forest.

V. EXPERIMENTAL RESULTS

Experiments are performed using datasets collected from the Kvasir datasets. We have taken 200 images of Z-line and esophagitis and each class contains of 100 images. The suggested scheme uses fusion of SIFT and color auto correlogram characteristics to detect defects with the more frequently used classifiers such as SVM, Naive Bayes and

Random Forest.

A. Performance Measure

The classification error is measured by Kappa statistic, Mean Absolute Error (MAE), Root Mean Square Error (RMSE), Relative Absolute Error (RAE) [13], Root Relative Squared Error (RRSE) and Mean Absolute Relative Error (MARE).

Kappa statistics: The kappa of Cohen measures the agreement between two raters that classify N products into mutually exclusive classifications. The agreement is defined as in [3] between two raters.

$$k = \frac{p_o - p_c}{1 - p_c} = 1 - \frac{1 - p_c}{1 - p_c} \quad (6)$$

where p_o is the relative contract observed among raters and p_e is the hypothetical probability of chance agreement, by means of the experimental data to compute the chances of each observer arbitrarily sighting each category.

Mean Absolute Error (MAE): It is used to assess how carefully forecast the possible outcomes. The MAE is computed as defined in [14]

$$MAE = \frac{1}{n} \sum_{i=1}^n |s_i - t_i| = \frac{1}{n} \sum_{i=1}^n |u_i| \quad (7)$$

where u represents the average of absolute error, s_i is the prediction and t_i is the true value.

Root Mean Square Error (RMSE): The square root of Mean square error (MSE) gives the RMSE. The RMSE is the square root of variance known as Standard deviation [14]

$$RMSE = \sqrt{\sum (x - x_1)^2} \quad (8)$$

Where x is the original value and the x_1 is the obtained value.

Relative Absolute Error (RAE): It is defined as the proportion of mean absolute error to the mean value of measured quality and defined as in [14].

$$MAPE = MSE / \text{Measured Quality} \quad (9)$$

Root Relative Squared Error (RRSE): The relativesquared error takes the total squared error and standardizes it by dividing by the total squared error of the simple predictor. By taking the square root of the relative squared error one reduces the error to the same dimensions as the quantity being predicted Mathematically, the root relative squared error E_i of an individual program i is evaluated by the equation as follows

$$E_i = \sqrt{\frac{\sum_{j=1}^x (p_{(v)} - T_j)^2}{\sum_{j=1}^x (T_{(j)} - \bar{T}_j)^2}} \quad (10)$$



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Table-1: Performance measures for SVM, Naive Bayes and Random forest

measures	SVM	Naive Bayes	Random forest
Correctly classified instance	191	185	190
Incorrectly classified instance	9	15	10
Kappa statistic	0.91	0.85	0.9
MAE	0.06	0.135	0.05
RMSE	0.17	0.270	0.22
RAE	12.4	27.1	10
RRSE	35.5	54.1	44.7

In Table.1, the performance of SVM, Naïve Bayes and Random forest using various measures like kappa statistic MAE, RMSE, RAE and RRSE are shown. While classifying the abnormalities, it is noted that the classification error is lower for SVM when compared with other two methods.

We analyze the performance of abnormalities using SIFT+ACC features with SVM, Naive Bayes and Random forest. When comparing with each class, the performance of combined SIFT+ACC with SVM shows a better accuracy of 95.5% as overall. The Naïve Bayes and Random forest methods produce 92.5% and 95%. Table.2 shows the confusion matrix for SVM, Naïve Bayes and random forest. It is revealed from Table 2 that the highest accuracy is attained by the SVM for Esophagitis and Z-line and are 96% and 95% respectively.

Kappa statistic is a metric used to denote how closely the classes classified by the proposed classifier matched with actual classes. Henceforth kappa statistic for one method is comparable for the other methods which are used for the classification of the similar data. The interpretation of kappa statistic according to [3] is the values from 0.8 to 1 is almost perfect. From the Table 1, we observed that all the three methods of kappa statistic are almost perfect but the kappa statistic for the MLP is 0.91 which is substantially best among the other two methods.

Table 2 displays the confusion matrix of esophagitis and normal-z-line classes using Naïve bays, SVM and Random forest. From the confusion matrix, it is found that SVM predicts well esophagitis and normal-z-line when compared with two other techniques and Compared to other methods, it also has a minimum quantity of false positives.

Table-2: Confusion Matrix for SVM, Naive Bayes and Random forest

Naive Bayes		
	Esophagitis	Z-line
Esophagitis	93	7
Z-line	8	92
SVM		
	Esophagitis	Z-line
Esophagitis	96	4
Z-line	5	95
Random Forest		
	Esophagitis	Z-line
Esophagitis	93	7
Z-line	3	97

Table 3. displays classification performance using our techniques. It demonstrates recall, f-measure, and accuracy. Fig. 3 demonstrates the performance measurement in visual

representation. It demonstrates that Random Forest does a very good job of detecting Normal-z-line, but many pictures of Esophagitis are mistakenly predicted as Normal-z-line. The SVM is doing well with 95.5 precision in a general output.

Table-3: Precision, Recall and F-measure of the proposed model

Classification model	Classes	Precision	Recall	F-measure	Accuracy (in %)
Naive Bayes	Esophagitis	0.921	0.93	0.925	92.5
	Z-line	0.929	0.92	0.925	
SVM	Esophagitis	0.950	0.96	0.955	95.5
	Z-line	0.960	0.95	0.955	
Random Forest	Esophagitis	0.969	0.93	0.949	95
	Z-line	0.933	0.97	0.951	

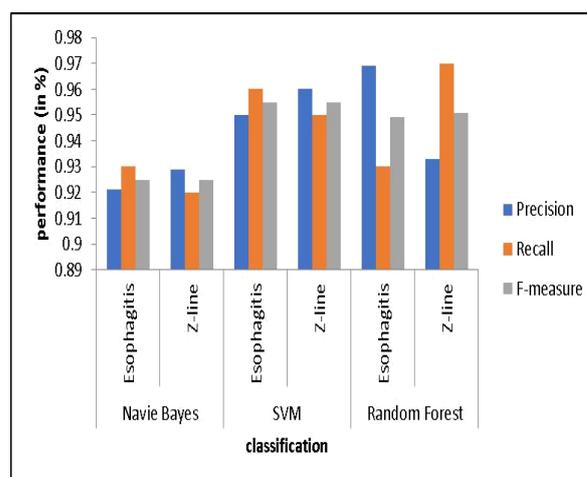


Fig.3. Classification performance for Esophagitis and Z-line

VI. CONCLUSION

The proposed scheme uses two features to portray WCE pictures specifically SIFT (Scale Invariant Feature Transform) and auto color correlogram, which coordinates points of interest of color, texture and shape highlights. Comparative experiments with three classifiers namely Naïve Bayes, SVM and Random Forest is carried out and results demonstrate that SVM outperforms the others. The findings also obviously demonstrate that the suggested system is promising in identifying esophagitis and z-line in WCE pictures and achieves the highest detection precision of 95.5 percent despite the reality that esophagitis shows excellent differences in appearance in WCE pictures. There remains, however, some room for improving detection precision. One possible path of our imminent job along this path is to do some pre-processing for WCE images to examine images that are excessively dull or visually unsettling.

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