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A MACHINE LEARNING APPROACH BASED ON SVM FOR CLASSIFICATION OF LIVER DISEASES

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ABSTRACT

The liver is an organ in the body that plays an important role in the production and secretion of the bile. Recently, the number of liver patients are increasing because of the inhalation of harmful gases, the consumption of contaminated foods, herbs, and narcotics. Today, classification algorithms are widely used in diverse medical applications. In this paper, the classification of the liver, and non-liver patients is performed based on a support vector machine (SVM) on two datasets. To this end, the dataset is normalized and then sorted based on a proposed algorithm. After that, the feature selection is performed in order to remove the outliers and missing data. Then, 10-fold cross-validation is used for the data partition. In the end, the classification models of Linear, Quadratic and Gaussian SVM are defined and performance evaluation of the proposed method is investigated by calculation of F1-score, accuracy, and sensitivity. The results show that ILPD data have maximum accuracy, sensitivity, and F1-score of 90.9%, 89.2%, and 94%, respectively, so that a minimum improvement of 17.9% is obtained in accuracy than previous works. Additionally, the highest accuracy, sensitivity, and F1-score of BUPA data is 92.2%, 89%, and 94.3%, separately.

Keywords: ILPD; BUPA; Liver patients; Classification; SVM.

INTRODUCTION

Liver-related problems are not readily detected early in life because the liver normally continues to function until it encounters with damages.[1] Prevention, or in other words, early detection of liver problems can increase the likelihood of rescue for these patients.

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Liver disease can be detected by analyzing the number of enzymes present in the blood and classification methods[2,3] as well as benefiting wearable technology.[4–10] The classification methods are a two-step process, the first phase is the training phase, in the form of the algorithm, makes an organized classification for training, a set of data and the second is a classification model and its performance is analyzed by testing a set of multiple data.[11] One of the most important algorithms for classification is the Bayesian algorithm which is a statistical classification based on the Bayesian theorem.[12] This classification is very simple and shows great speed and accuracy when applied to large databases. Also, this classification is based on the fact in which the effect of a given amount of feature is dependent on the other features.[12] Another algorithm for classification is the k-nearest neighbor (KNN) algorithm that accounts for one of the observation learning algorithms and is used in many data mining applications such as recognizing statistical patterns and many more.[13] Classification in the diagnosis of medical illness is accomplished with the help of another algorithm called the recurrence propagation algorithm, which is a multi-layered neural network for learning the rules. This algorithm provides instructions to initiate a set of a random set of synaptic weights. In such a way that the difference between the output of the neural network from the inputs and outputs with known inputs must be maximized in order to interconnect them.[14] The recurring propagation algorithm uses a calculated output error to change the weight values in the rear direction. To get this error network, it should be considered a propagating toward forward ahead. The neurons are activated by a complex function in propagation toward forward.[15] Linear Discriminant Analysis (LDA) is also used for classification. LDA is a statistical method that is used in machine learning and pattern recognition to find out the linear combination of features in which it distinguishes best way between two or more classes of objects.[16] LDA has a close relationship with variance analysis and regression analysis that attempts to express an independent variable as a linear combination of other features. This independent variable in the LDA is in the form of a class label. Also, the LDA has a close relationship with the analysis of the main components of the Principal Component Analysis (PCA).[17] Both methods are a linear combination of variables that describe the data in the best way. The LDA is used when observation values are continuous. The introduction should provide sufficient background information to make the paper understandable for readers in other disciplines, and provide enough context to ensure that the implications of the experimental findings are clear.[17] Another important classification algorithm is the support vector machine (SVM) algorithm. SVM places the data in two sections to carry out the classification as well as the construct of an n-dimensional super-page. These models are closely related to neural networks.[18] In fact, this model uses a nuclear ring structure that is equivalent to a perceptron neuronal dual-layer network. These models are closely related to the perceptron neural network. By employing the nuclear structure, these models are an alternative training method for polynomials, radial base functions, and multi-layered perceptron classification that their weight is found by solving the problem of a second-order program with linear constraints.[19]

In this paper, a proposed method based on Linear, Quadratic, and Gaussian SVM (G-SVM) is proposed for the classification of two communities of the liver and non-liver patients. In the proposed method, normalization, sorting, feature selection, and data partition are done on the datasets, and the mentioned classification algorithms are applied at the end for performance evaluation of the presented method. The performance evaluation of the datasets illustrates that the maximum accuracy and F1-score of Indian Liver Patient Dataset (ILPD) are 91.3%, 94.5%, respectively. While the values for the BUPA dataset are 92.2% and 94.3% in turn. The obtained results illustrate that the accuracy of the presented methods in liver and non-liver classification is more than the other works in Refs. 20–24.

MATERIALS AND METHODS

Data Required in Liver Disease

Liver blood tests are obtained from some blood tests. These tests can be used to evaluate liver function or liver damage.[25] The first step in detecting liver damage is a simple blood test to determine the level of certain enzymes (protein) in the blood. Under normal conditions, these enzymes are predominantly present in the liver cells. But when the liver is damaged for whatever reason, these enzymes are poured into the bloodstream. The enzymes are proteins that are present throughout the body, each of which has a unique function. The enzymes quickly help the chemical and normal reactions in the body. One of the most important liver enzymes is the use of aminotransferases which consists of aspartate aminotransferase (AST) and alanine aminotransferase (ALT). These enzymes are predominantly in the liver and to a lesser extent in muscle cells.[25] The most important enzymes in the liver comprise of bilirubin, albumin (ALB), serum glutamate-pyruvate transaminase

(SGPT), serum glutamic-oxaloacetic transaminase (SGOT) and alkaline phosphatase. Bilirubin is a substance that is formed by the breakdown of "Heme" in the red cell and muscle hemoglobin. "Heme" is the name of a combination in the blood that causes the exchange of oxygen. When the lifetime of red blood cells run over or muscle damage occurs, hemoglobin is converted to biliverdin in several steps and then to bilirubin. ALB is commonly referred to as a group of water-soluble proteins, but it is one of the most important proteins for the human body in the plasma and is not a glycosylated protein. SGPT is an enzyme that is found mostly in liver and kidney cells; much smaller amounts of them are found in the heart and muscle. In healthy people, its level is low in the blood. SGOT is an enzyme that is commonly found in the liver and heart cells. When the liver or heart is damaged for some reason, the enzyme is transmitted to the blood and its level increases in the blood. Alkaline phosphatase is an enzyme that is mainly produced in the liver and bone marrow, and the enzyme is extracted from the intestine and kidneys. Its values depend on the measurement method and the test. However, normal values are high in children and pregnant women.

As previously mentioned, two datasets of ILPD and BUPA are considered in this paper. ILPD dataset consists of various features such as age, gender, Total Bilirubin (TB), direct bilirubin (DB), total protein (TP), A/G ratio, and the ratio of alkaline phosphatase (ALKphos), SGPT, SGOT, and ALB.[26] Another dataset called BUPA comprises seven parameters corpuscular volume, alkaline phosphatase, SGOT, SGPT, gamma-glutamyl transpeptidase, number of half punch alcohol drink per day, selectable by patients is liver and non-liver.[27]

The Proposed Method

In this paper, a proposed method is used in order to classify liver and non-liver patients employing the datasets (Fig. 1). To this end, it is mandatory pre-processing the data. First, the data is normalized by dividing the raw data on maximum value for any raw data. As a result, all data are put in a specific range 0 to 1. Then, the normalized data are sorted by a proposed algorithm (Fig. 2). As shown in Fig. 2, at first maximum value of the normalized data (s) is taken and then is put in a M. Then, all of the normalized data (s_i) are compared with M and if s_i is equal with M, s_i is put in the maximum vector that is defined in order to sort the data. Also, the target related to the s_i is put in new matric called a new target. Then, s_i is removed of the s and 1 unit is increased to j. If j is lower than 584, the procedure is performed with a new s. Otherwise, the sorted data are prepared for classification. If s_i is not equal with M, i increases 1 unit until the condition exists ($i < 584$).

In the next step, feature selection is carried out. There are some outliers in two datasets. In order to remove the outliers, some features of the dataset are removed. For this reason, backward selection is used. Backward selection starts with all features contained in the dataset. It then runs a model and calculates an observed significance level (p-value) associated with the test of the model for each feature. The feature with the largest insignificant observed significance level will then be removed from the model, and the process starts again. This continues until all features with the insignificant observed significance level are removed from the model. Accordingly, five features of the ILPD dataset remains and remnants are removed. The five features consist of the age of the patient, TB, Sgot, TP, and ALB are considered as predictors or input. Also, the response or output is selected being patient or not (the feature of 11th in ILPD dataset). In another dataset (BUPA), feature selection is performed with five features comprise of corpuscular volume, ALKphos, SGOT, SGPT, gamma-glutamyl transpeptidase as input and being patient or not as output data.

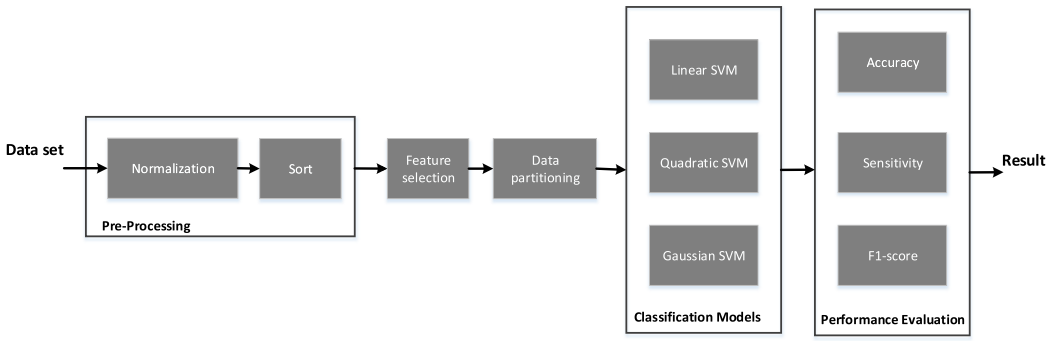

Fig. 1 Diagram of the proposed methodology to classify liver patients.

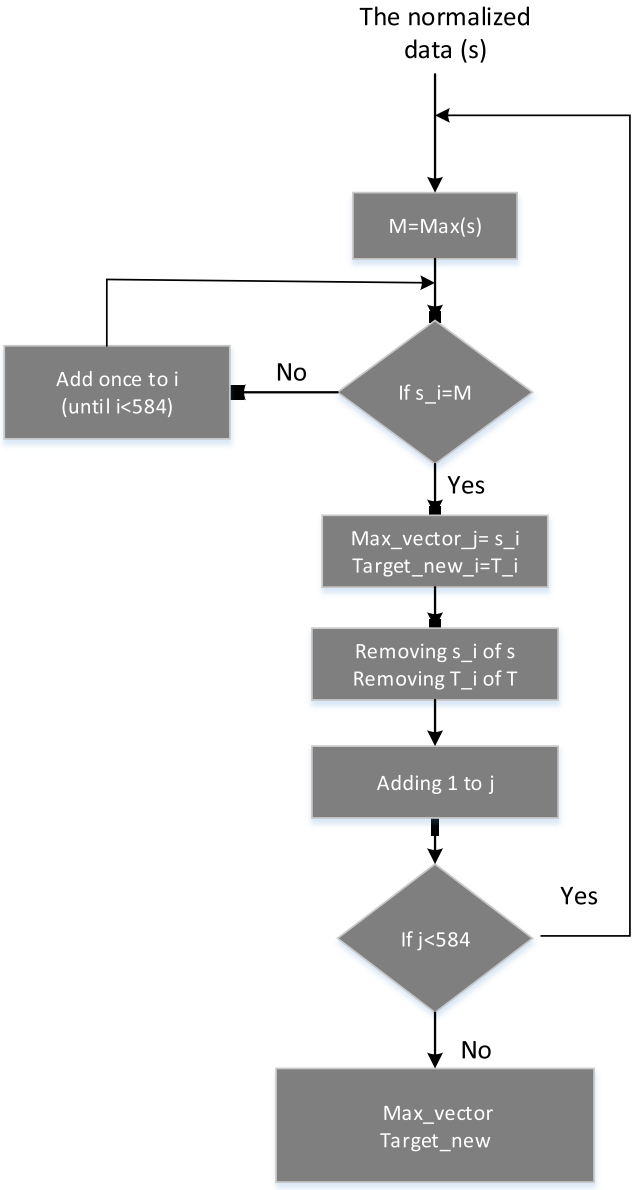

Fig. 2 The proposed algorithm for sorting the dataset.

In the next step, 10-fold cross-validation is used to partition data. Then, the classification models are defined based on a SVM. An optimal hyperplane is made by SVM as a decision surface such that the margin of separation between the two classes in the data that is maximized.[28] Support vectors allude to a small subset of the training observations that are employed as support for the optimal location of the decision surface. SVMs fall under a class of machine learning algorithms that are called kernel methods.[29] Training for SVMs has two phases: The first phase that is commonly known as the kernel trick is to transform input data into a high-dimensional feature space. It is enough to just determine the kernel for this step and the data is never clearly transformed to the feature space. The second phase is to solve a quadratic optimization problem for fitting an optimal hyperplane to classify the transformed features into two classes.[29] The number of transformed features is specified by the number of support vectors. In the presented method in this paper, the classification is performed by Linear SVM, Quadratic SVM, and G-SVM that their kernels follows, respectively:

$$K(x_1, x_2) = x_1^T x_2, \tag{1}$$

$$K(x_1, x_2) = (x_1^T x_2 + 1)^\rho, \tag{2}$$

$$K(x_1, x_2) = \exp\left(-\frac{\|x_1 - x_2\|^2}{2\sigma^2}\right), \tag{3}$$

where x_1 and x_2 are vectors in the input space, σ is the width of the kernel and ρ is the order of the polynomial. Quadratic programming is the mathematical problem of finding a vector x that minimizes a quadratic function.[30]

$$\min_x \left(\frac{1}{2} x^T H x + f^T x\right). \tag{4}$$

In order to solve Eq. (4), subject to the constraints of inequality constraint, equality constraint, and bound constraint is defined[30] and are as follows, respectively.

$$\begin{cases} Ax =< b \\ A_{\text{eq}} x = b_{\text{eq}} \\ lb < x < ub. \end{cases} \tag{5}$$

Two common algorithms are used to solve quadratic programming problems consist interior-point-convex, which is used for solving convex problems with any combination of constraints, and trust-region-reflective, which is utilized to solve bound-constrained or linear equality constrained problems.[31] Finally, the F-score, accuracy and sensitivity are determined as follows.[24]

$$F1 - \text{score} = \frac{2T_p}{2T_P + F_p + F_n}, \tag{6}$$

$$\text{Accuracy} = \frac{T_p + T_n}{T_P + T_n + F_p + F_n}, \tag{7}$$

$$\text{Sensitivity} = \frac{T_p}{T_P + F_n}. \tag{8}$$

F1-score is a measure of the accuracy of datasets that are properly categorized. The accuracy of classification is the percentage of the multiplicity of datasets of the subject that are properly categorized. Sensitivity also returns to the number of true positives that are correctly identified. It should be noted that the true positive (T_p), the true negative (T_n), the false positive (F_p) and the false negative (F_n) of the confusion matrix. Also, every feature is considered with output separately and the

proposed method is performed five times. In the end, the mean F-scores, accuracy, and sensitivity are calculated.

RESULTS

In this section, the dataset of ILPD in Ref. 26 and BUPA in Ref. 27 are classified by benefiting the proposed method. The purpose of classification is the prediction of the liver and non-liver patients. As previously mentioned, ILPD data have 11 specifications consist of age, gender, GB, DB, TP, ALB, A/G ratio, SGPT, SGOT and ALKphos, and whether liver patients are or not. The number of features is 11, and the total number of data is 583. Another data, which is called BUPA whose total number of data is 345, including seven features mean corpuscular volume, ALKphos, SGOT, SGPT, gamma-glutamyl transpeptidase, number of half-punch drinks per day, liver-chooser and non-liver. Here, the ILPD dataset and then BUPA dataset was classified.

Analysis of ILPD Data

In the first test, the ILPD dataset is called. Then, the data is normalized and then sorted by the proposed algorithm. After feature selection, and data partitioning (10-fold cross-validation), the classification models are applied. In feature selection, five specifications consist of the age of the patient, TB, Sgot, TP, and ALB are considered as the predictor and the liver and non-liver patients as responses. Accordingly, the classification models, which are Linear SVM, Quadratic SVM, and G-SVM, are trained based on five inputs and one output. The obtained results of the method are shown in Fig. 3 that comprises confusion matrix (top in Fig. 3) and Receiver Operating Characteristic (ROC) curve (bottom in Fig. 3).

As Fig. 3 in Model 1 showed (Confusion Matrix), 156 non-liver patients of a total of 167 non-liver patients were classified in this category, and the rest were not included in this category. Accordingly, 93.4% of them were classified in the class, while 6.4% did not fall into this category. On the other hand, only 327 patients of

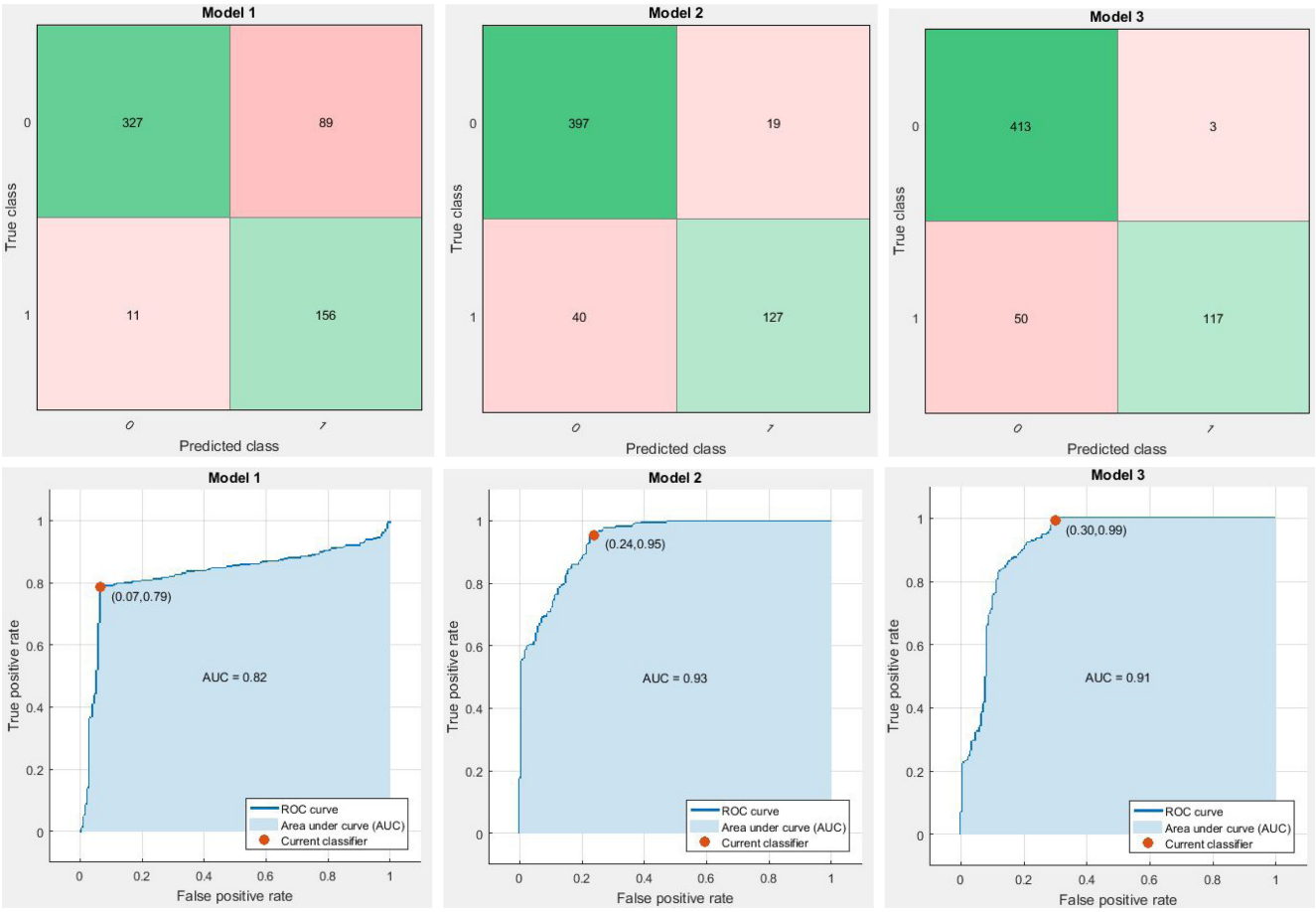

Fig. 3 (Color online) The obtained confusion Matrix (top) and ROC curve (bottom) of ILPD data based on the proposed method; Model 1 is Linear SVM, Model 2 is Quadratic SVM and Model 3 is G-SVM.

the 416 patients in the liver were classified in this category and 89 patients were not included in this category. In other words, 78.6% of liver patients were in this class, while 21.4% were not categorized. Totally, considering to these Fig. 3 and Linear SVM (Model 1), if all the classified data of patients are considered into a single category which consists of liver and non-liver, and all the non-classified data of non-liver and liver patients are placed in a different category, then 483 patients were classified in the category (82.8%) and 100 patients were not classified in this category, which is equivalent to 17.2%.

For further investigation, the ROC curve is demonstrated in Fig. 3 (bottom). As the curve of linear SVM (Model 1-Bottom) shows, the red circle is the false positive rate (FPR)/true positive rate (TPR) classification point. The point shows that the false positive rate of 0.07 is non-classified for non-liver patients and the true positive rate was 0.79, which was the percentage of the classified liver patients. It should be noted that the positive and negative classes were defined as the liver and non-liver patients, respectively. Moreover, Fig. 3 shows the relationship between FPR and TPR is not linear. Also, the area below the curve is an example of this fact and its value is 0.82. These steps were repeated for two other methods and accuracy of Quadratic, and G-SVM are acquired 89.9% and 90.9% in turn. Also, the area below the curves is 0.93 and 0.91, respectively.

Analysis of BUPA Data

The mentioned method in the previous section is also performed for the classification of BUPA dataset. However, five features are selected as the predictor and the liver and non-liver patients as responses. The main reason for removing one of the features is to have outliers. Thus, five features are chosen. Also, 10-fold cross-validation is applied for the partitioning of the dataset. In the end, the dataset is classified based on the classification models. The obtained results are shown in Fig. 4. As the Confusion Matrix of Linear SVM (Model 1) in Fig. 4 demonstrates, 192 of 200 the non-liver patients were classified in this category, and others did not include in this category. Consequently, 96% were classified in the class, while 4% were not in this category. On the

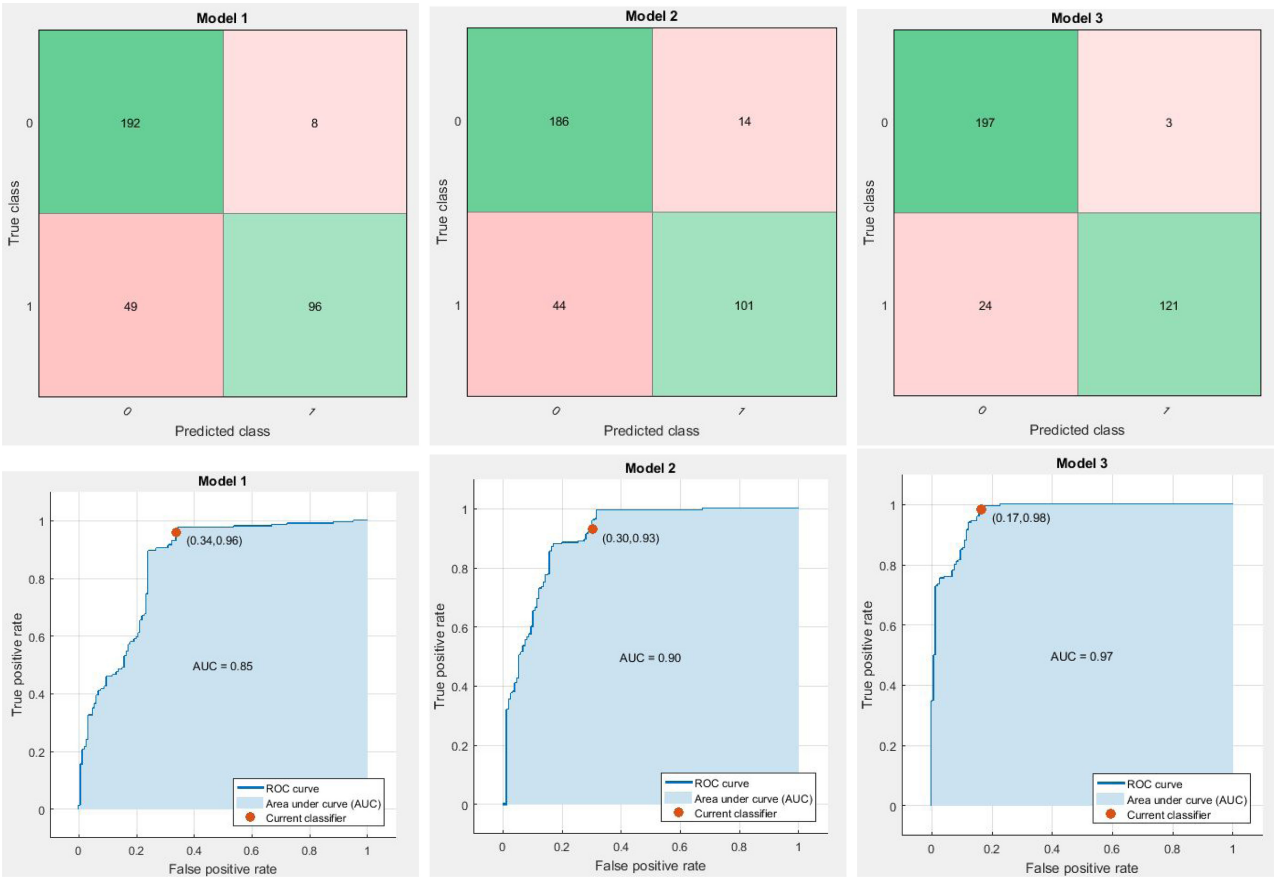

Fig. 4 (Color online) The obtained confusion Matrix (top) and ROC curve (bottom) of BUPA data based on the proposed method; Model 1 is Linear SVM, Model 2 is Quadratic SVM and Model 3 is G-SVM.

Table 1. The result of the performance evaluation of the proposed methods for the classification of BUPA and ILPD datasets.

Data	Methods	Accuracy	Sensitivity	F1-Score
ILPD	Linear SVM	82.9	96.7	86.7
	Quadratic SVM	89.9	90.8	93.1
	G-SVM	90.9	89.2	94
Bupa	Linear SVM	83.5	80	87.1
	Quadratic SVM	83.2	81	86.5
	G-SVM	92.2	89	94.3

Table 2. The comparison between the proposed method and other works in ILPD dataset.

Reference	Classification model	Outcome of selected features	Accuracy
22	NBTree	TB, DB, ALKphos, Sgot, Sgpt, A/g	67.01
23	Decision Tree	—	69.40
24	ANN with $K = 3$	—	68.49
21	K-Nearest Neighbor	Alkphos, Sgpt and Sgot	—
20	KStar	—	73
The proposed method	G-SVM	Age, TB, Sgot, TP, ALB	90.9

other hand, 96 of 145 liver patients were classified in this category and 42 were not included in this category. In other words, 66% of liver patients are in this class, while 34% were not categorized. Totally, all the classified data of liver and non-liver patients are considered into a category and place all uncategorized liver and non-liver patients in a different category. Accordingly, 288 liver and non-liver patients were classified in the category (83.5%) and 57 were not classified in this category, which is 16.5%.

Furthermore, the ROC curve is obtained and has been shown in Fig. 4 (bottom) for Linear SVM (Model 1). As the curve shows, the red circle is the FPR/TPR classification point. In the current classifier in Fig. 4, the FPR is 0.34 for the non-classified non-liver patients and the TPR is 0.96 for the liver patients that were classified. The positive and negative classes in Fig. 4 were defined as the liver and non-liver patients, separately. The area under the curve is 0.85. These steps were repeated for other methods which are Quadratic and Guassin SVM. The results show the accuracy of the Quadratic and G-SVM are 83.2% and 92.1%, respectively (Table 1). Also, the area under the curves is 0.90 and 0.97. Therefore, the best accuracy is acquired by the G-SVM in the proposed method.

DISCUSSIONS

According to Table 2, the best method for classification of ILPD dataset based on the proposed method is G-SVM with an accuracy of 90.9%, the sensitivity of 89.2% and F1-score of 94%. Also, in another classification method which is Linear SVM, these values are 82.9%, 96.7%, and 86.7%, respectively, while the accuracy, sensitivity, and F1-score in Quadratic SVM are 89.9%, 90.8% and 93.1% in turn. In order to investigate the effect of the kernel on the accuracy in the ILPD dataset, the kernel scale of the mentioned classification models are varied from 0.5 to 5 and the corresponding accuracy is obtained and the results are shown in Fig. 5(I). As Fig. 5(I) illustrates, the best kernel is 1 for Guassin SVM with accuracy 90.9 while the best kernel of Quadratic SVM is 1 with an accuracy of 89.9. For linear SVM, the best kernel is 1 with an accuracy of 82.9. As it can be seen in Fig. 5(I), variations of the kernel affect

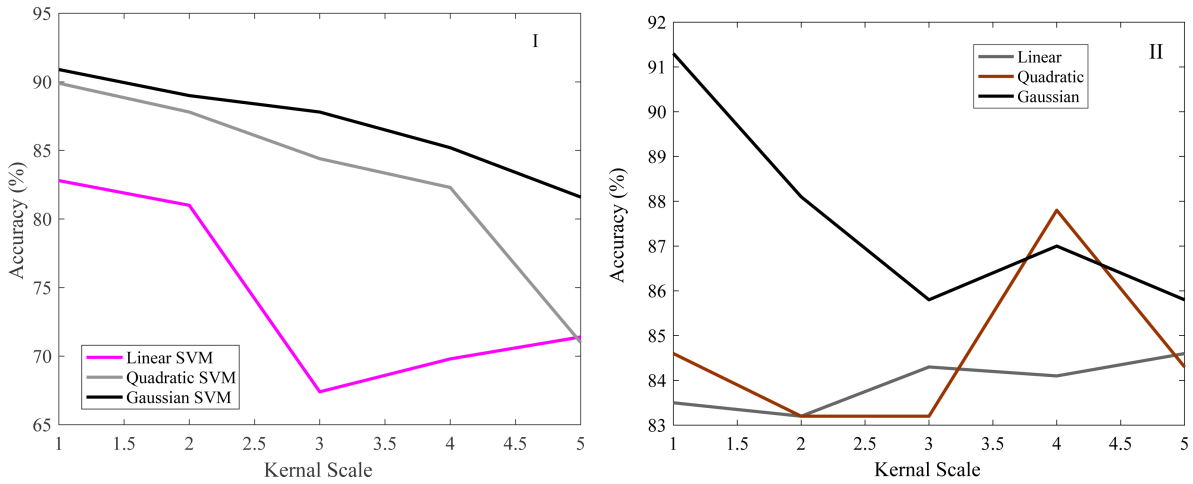

Fig. 5 The variation of kernel scales versus accuracy.

accuracy. The variations are associated with a mild slope in G-SVM while the accuracy varies with a steep slope in Linear and Quadratic SVM. Nonetheless, the Linear SVM experiences an intense decrease and then a mild increase in accuracy by the increase of the kernel.

Furthermore, the proposed method based on G-SVM predicts the best accuracy, sensitivity, and F1-score in the BUPA dataset than two other methods, whose values are 92.2%, 89%, and 94.3%, respectively. In Quadratic SVM, these values are estimated 83.2%, 81% and 86.5% in turn while for Linear SVM are 83.5%, 80%, and 87.1%, separately. A similar procedure with the ILPD dataset is carried out in the BUPA dataset in order to determine the effect of the kernel on the accuracy and the results have been shown in Fig. 5(II). As can be illustrated, the best accuracy is extracted with the kernel of 1 for the G-SVM while the best accuracy of Linear SVM is also in the kernel of 5 with a value of 84.6%. However, the best accuracy of Quadratic SVM is in kernel 4 with a value of 87.8%. Additionally, the accuracy of G-SVM experiences an intense slope with increasing kernel from 1 to 3 and after that a mild increase and decrease. The plot of accuracy-kernel in Linear SVM has a mild increase. In Quadratic SVM, a chaotic is seen with increasing the kernel. First, a decrease is observed from 1 to 3 and then an increase from 3 to 4 and at the end a decrease. According to Fig. 5 and other results in the paper, the G-SVM is the best-proposed method for classification models in the paper because the maximum accuracy and F1-score are obtained and also the plot accuracy-kernel owns a mild slope with minimum variations by increasing the kernel.

In the end, the G-SVM is compared with other methods in Refs. 20–24 for the ILPD dataset and the results have been shown in Table 2. It can be seen, the accuracy improved 17.9% than Kstar in Ref. 20 that is the maximum value of accuracy among the previous works in Refs. 20–24. In the proposed method, features that contain outliers and also, one of the features had a missing data (A/G ratio) were removed. Ultimately, five features of age, TB, Sgot, Tp, and ALB was considered. Moreover, the proposed method reached an improvement of 23.89% than Ref. 22 that was implemented with NB Tree, an increase of 21.5% than Ref. 23 that was implemented with decision tree, and an improvement of 22.41% than Ref. 24 that was done with Artificial Neural Network (ANN) with $K = 3$. In Ref. 22 that was performed by NB Tree, the feature of A/g owned four missing data and also DB, ALKphos and Sgpt have outliers, result in low accuracy. However, the presented method improves accuracy by considering to remove the outliers and sorting the datasets and also by benefiting Gaussian and Quadratic kernels and minimizes their functions.

CONCLUSIONS

In this paper, a machine leaning approach based on SVM was presented in order to classify the liver patient in two datasets. First, the dataset were normalized and sorted. In order to sort the data, a proposed algorithm was presented. Then, the data with outlier was removed and the remnant data was partitioned in a 10-fold cross-validation. The datasets were classified based on classification model of Linear, Quadratic and Gussian SVM that their kernel is defined and then minimized. After, training and testing the proposed method, evaluation performance was performed on two datasets and the obtained results illustrated the proposed algorithm which estimated the classification of patient by accuracy 90.9% and F1-score 94% in ILPD dataset and 92.2% and 94.3% for BUPA dataset, respectively. The results showed a minimum improvement of 17.9% than previous methods for classifying the ILPD dataset.

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