A Novel CAD System for Detection and Classification of Liver Cirrhosis using Support Vector Machine and Artificial Neural Network

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Abstract
In this paper, a computer aided system is designed to determine the extent to which the blood indices, fibro-scan and liver biopsy can help diagnose liver cirrhosis in patients with Chronic Hepatitis C. A novel approach, for feature selection is created and used to reduce the extracted features to their best informative subset. The performance of three classifiers is investigated. One is the Support Vector Machine (SVM) with cross-validation, the second is a Multilayer Perception neural network (MLP), and the third is Generalized Regression Neural Network (GRNN). The system resulted in an accuracy of 100% in both training and validation phases for SVM and MLP and 99.50 % for GRNN.
Key words:
Liver Cirrhosis; Artificial Neural Network; Support Vector Machine; Accuracy.

1. Introduction

The main causes of chronic hepatitis are chronic hepatitis B (CHB) and C (CHC) [1]. Since Chronic liver disease is a major worldwide health problem, It is estimated that around 170 million individuals globally are chronic carriers of hepatitis C virus(HCV) [2]. Chronic hepatitis can lead to liver cirrhosis compensation. Compensated cirrhosis of the liver can then lead to liver failure and hepatocellular carcinoma with accompanying complications, such as hepatic encephalopathy and bleeding of the varix. Early detection of cirrhosis of the liver in patients with chronic hepatitis has therefore become an significant clinical problem for doctors [3] [4].
The term CAD is commonly used to refer both computer aided detection and computer aided diagnosis. Computer aided detection refers to locating or detecting anomaly, and computer-aided diagnosis related to liver cirrhosis assessment[5]. A Novel CAD scheme using techniques from lab, fibro-scan and liver biopsy processing for the detection of abnormal liver tissues, extracting almost all known features used in literature for classification of liver tissues into abnormal liver tissues (affected) or normal liver tissues (unaffected), aiming to help a physicians who would have already outlined suspected abnormalities by giving him/her a second opinion, leaving the final decision to him/her.
This study is done to compare the performance of SVM, MLP and GRNN in classification of liver diseases through the use of the measures accuracy, sensitivity, specificity and area under curve (AUC)on an actual dataset.

2. Literature Overview

CAD has now become one of the important research topics, especially in radiology, medical physics, and medical engineering [6]. Paul Mangiameli et al., [7] proposed model selection affects the decision support systems accurately. In their model selection, how to affects the accuracy of decision support system hydrides by single model and ensembles. They proposed single model is not more accurate than ensembles. Ahmed M. Hashem et al.,[8] suggested predicting a single phase classification model for Liver Cirrhosis or fibrosis and a multistage classification model. In their model based on Tree of Decision, Neural Network, Clustering Nearest Neighborhood and Logistic Regression. Ziol.M et al., [9] proposed to evaluated liver fibrosis with chronic hepatitis C for patients using liver stiffness measurement (LSM). Z. Jiang.Z., [10] proposed for discovering the corresponding degree of fibrosis by support vector machine (SVM). Dong-Hoi Kim et al., [11] proposed machine learning technique and decision tree(C4.5).In this method is used for to predict the susceptibility to two liver diseases such as chronic hepatitis and cirrhosis from single nucleotide polymorphism(SNP) data . They also used to identify a set of SNPs relevant to those diseases. Piscaglia et al.,[12] proposed to predict Liver cirrhosis and other liver-related diseases used by Artificial neural network. Chun-Ling Chuang et al.,[13] Proposed early diagnosis of liver disease and prediction of classification accuracy through integrated case-based reasoning in the classification and regression tree, back-propagation neural network (BPN), discriminatory assessment and logistical regression of data mining methods. Vaidya et al.,[14] proposed system is an expert system that uses Fuzzy C-Means to diagnose LDs in

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an environment characterized by Microsoft Window XP, Microsoft Access Database Management, Visual Basic Application Language and Microsoft Excel. The CLD classification was suggested using hybrid WOA-SA classifiers and ensemble classifiers. The results from clinical CT image datasets experimented with 3D VOIs indicate the usefulness of using WOA-SA to select features for the ensemble classifier optimally [15].

3. Components of the CAD System

A block diagram of the modules of the proposed system is depicted in Fig.1.

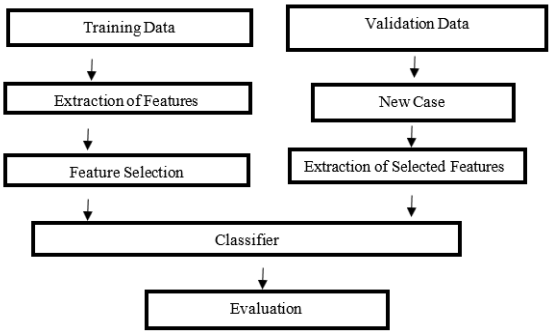

Fig. 1 A block diagram of the modules of the proposed system

3.1 Feature Selection

Any successful CAD depends mainly of a good choice of features. Feature selection has three major benefits:

a. Enhancing the prediction capabilities.
b. Representing highly correlated features by only a single feature, and
c. Providing faster and more cost effective predictors.

To enhance the efficiency of feature-discarding methods, I suggested a new measure, inspired by the hypothesis testing principle, using a score based on the distinction between the means of instances in the two groups (affected, unaffected) and then standardizing it by a pooled standard deviation. This measure, which we named the T-squared, and denoted by TSQR is used to discard less important features To this end, the TSQR score assumes that the target variable is categorical. The TSQR score does not throw away features that might be useful, but it determines the features that must be included. The inputs are: a matrix of predictors in the rows the features in the columns. TSQR determines the importance of each predictor in the diagnosis phase A feature is retained if only if its significance exceeds 2.

The TSQR score, for feature k, is calculated from:

$$TSQR(k)= \frac{(\bar{x}_j^{(+)}-\bar{x}_j^{(-)})^2}{\frac{1}{n_+-1}\sum_{i=1}^{n_+}(x_{i,j}^{(+)}-\bar{x}_j^{(+)})^2+\frac{1}{n_--1}\sum_{i=1}^{n_-}(x_{i,j}^{(-)}-\bar{x}_j^{(-)})^2} \quad (1)$$

where, $\bar{x}_k^{(+)}$ is the average of the k^{th} feature for the affected cases (k=1,…, 15), $\bar{x}_k^{(-)}$ is the average of the k^{th} feature for the unaffected cases (k=1,…, 15), $x_{i,k}^{(+)}$ is the i^{th} observation of the k^{th} feature (affected), $x_{i,k}^{(-)}$ is the i^{th} observation of the k^{th} feature (unaffected), n_+ is the number of affected case, and n_- is the number of unaffected cases. A total of 15 features were extracted for the work in this thesis. The extracted features were normalized to be between 0 and 1 and then used for classification.

3.2 Classifiers

Here I shall give a brief description of the classifiers used to obtain the results experimentation presented.

a. Multilayer Perception (MLP)

In this type of network, a forward direction is used in the signal propagation and there is no feedback [16]. A number of layers of neurons forms the input layer, ,one or more hidden layers besides the output layer. The structure of a feed forward network is shown in the Fig. 2 Feed forward networks are called universal approximations. It has been shown that feed forward networks can be used to approximate any feature with the suitable amount of concealed layers. This makes feed forward networks famous for applications such as time series prediction.

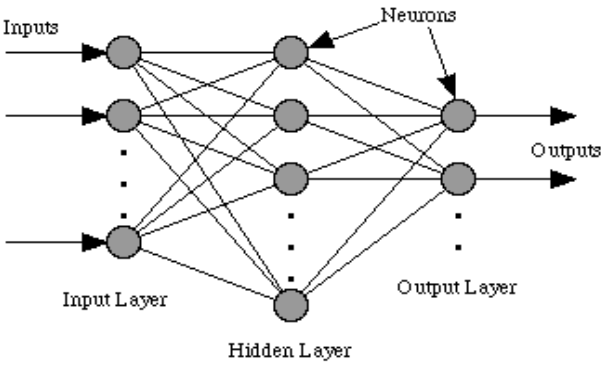

Fig. 2 Multilayer Perceptron (MLP)

Table 1. The extracted features &Categories

Category	No	Feature Name	Descriptions
Lab findings	1	Alanine aminotransferase (ALT) 0.98	Calculated from Blood test
	2	Aspartate transaminase(AST)	
	3	Bilirubin	
	4	Gamma GlutamylTranspeptidase (GGT)	
	5	Albumin	
	6	Alkaline Phosphatase	
	7	Alfafetoprotein	
	8	Hemoglobin	
	9	WBC	
	10	Platelets	
	11	International Normalized Ratio (INR)	
	12	Creatinine	
Imaging	13	Fibro-Scan	Calculated from normal and abnormal liver tissues
Liver biopsy	14	Metavir Activity	Calculated from histopathology of liver tissues
	15	Metavir Score Fibrosis System	

b. Generalized Regression Neural Network (GRNN)

A variant of neural networks [17] is the generalized regression one (GRNN), which uses a normalized basis function with a hidden layer for each training observation. Fig. 3 shows is a diagram of a GRNN network

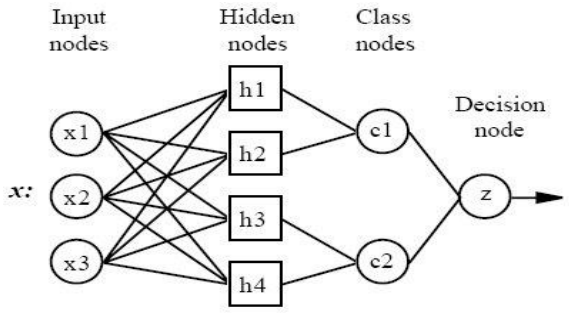

Fig. 3 Neural Network Implementation of GRNN

c. Support Vector Machines (SVMs)

A The SVM algorithm can be summarized in the following [18]:

For any set of observation ,i={1,2,…,n}. The SVM classifies the observations, Xi ϵ Rd, in one of two groups Y n ϵ {-1,1} , assuming a hyperplane W i . Φ (X) + b = 0, with W being a vector of weights perpendicular to the hyper plane and b is a bias. The two boundaries are W i. Φ (X) + b = ± 1.

Mathematically, the whole problem is a quadratic programming problem

$$Min\ \frac{1}{2}W^T.W + C\sum_{i=1}^{1}\vartheta_i \qquad (2)$$

with C being a classification error. I note that controlling C can minimize the classification error. Fig. 4 shown the classification error.

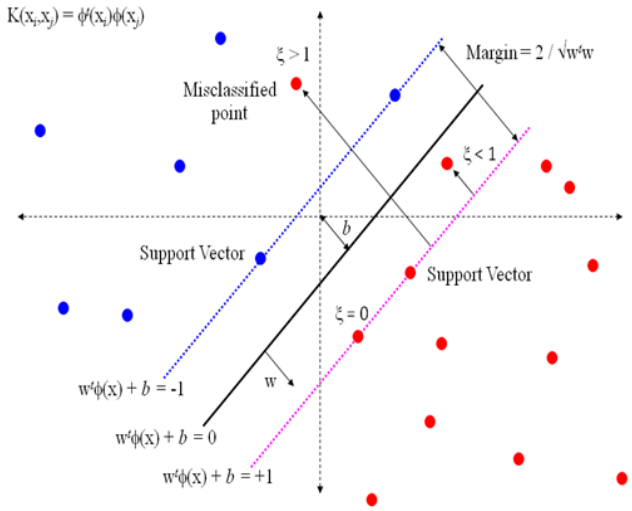

Fig. 4 Linear separation of two classes -1 and +1 (or 0 and 1) in two-dimensional space with SVM classifier

3.3 Evaluation

Several measuring tools are used to evaluate the performance of ANN and SVM models in classifying the detected liver tissues into affected or unaffected. They are accuracy, sensitivity, specificity and AUC. Each of them is used to measure different aspects of the classifiers performance.

Usually, it is not an easy job to identify liver lesion from fibrosis. Decision based on the detection can be summarized in following table 2:

Equations can be easily written in equation environment. See Equation 1 for example.

Table 2: Confuse Matrix

		True (T)	False (F)
Reality	Positive (P)	T P	F P
	Negative (N)	T N	F N

- TP (TN): Number of unaffected (affected) livers correctly identified.
- FP (FN): Number of affected (unaffected) livers correctly identified.

Sensitivity and specificity are the two measures that separately estimate a classifier's performance on different classes [19] [20].

$$Sensitivity\ (\%) = TPR = \frac{TP}{(FN+TP)} * 100 \quad (3)$$

$$Specificity\ (\%) = TNR = \frac{TN}{(FP+TN)} * 100 \quad (4)$$

AUC represents a common measure of sensitivity and specificity over all possible thresholds and it can be done as follows [21]:

$$AUC(\%) = \frac{1}{2}\left(\frac{TP}{(FN+TP)} + \frac{TN}{(FP+TN)}\right) * 100 \quad (5)$$

Accuracy assesses the overall effectiveness of the classifiers. It is given by

$$Accuracy\ (\%) = \frac{(TP+TN)}{(TP+FN+TN+FP)} * 100 \quad (6)$$

Sometimes a series of equations are needed. See Equation 1 for details.

4. Methodology

4.1 Development of SVM and ANN Classification Model

The SVM and ANN algorithms are used for classifying the detected liver tissues into affected or unaffected. With every classifier used, the data is portioned into 70% of the dataset were used for training and the remaining 30% were used for testing the classifier.

To avoid the possibility of not having a significant portion of the data as the testing set, 5- fold cross-validation has been used. Leave-one-out (LOO) is a special case of the k-fold cross validation where k is selected to be the size of the data; therefore only a single sample is used to estimate the error rate in each step. In our analysis the LOO approach (k=199), is also used for validation. As mentioned in Sub- Section 15 features were reduced to only the best 7 features. These features were entered to the LDA component for classification.

A 5-folding scheme is applied (using K-folding means dividing the dataset to k sets and use k-1 of them for training and one for testing. This is repeated k times and then the average of the result is taken).

The data mining module in the DTREG version 10.7.18 software is used to obtain the results in this research.

5. Results and Discussion

In this research, two different classification models have been built using three different classifiers which are SVM, MLP and GRNN. The following set of tables (3, 4,5) present the optimal configuration and accuracy of the SVM, MLP and GRNN used. Accuracy is used to approximate how effective the classifier is by showing the percentage of the true value of the class label. In this case, the accuracy of SVM and MLP are better (100%) than GRNN (99.50%). Thus, it means that SVM and MLP classifiers could correctly classified more data than GRNN classifier.

Table 3: Confusion Matrices SVM, training data followed by validation data

	Training Data		**Validation Data**	
	Predicted Category		**Predicted Category**	
Actual Category	affected	Unaffected	affected	Unaffected
Affected	99	0	99	0
unaffected	0	100	0	100

Overall accuracy = 100.00%

Table 4: Confusion Matrices MLP, training data followed by validation data

	Training Data		**Validation Data**	
	Predicted Category		**Predicted Category**	
Actual Category	affected	Unaffected	affected	unaffected
Affected	99	0	99	0
unaffected	0	100	0	100

Overall accuracy = 100.00%

Table 5: Confusion Matrices GRNN, training data followed by validation data

	Training Data		**Validation Data**	
	Predicted Category		**Predicted Category**	
Actual Category	affected	unaffected	affected	Unaffected
Affected	99	0	98	1
unaffected	0	100	0	100

Overall accuracy = 99.50%.

Sensitivity and specificity assess the effectiveness of the classifier on a single class. As mention earlier, sensitivity measured the performance of the classifier on the amount of correctly classified unaffected liver while specificity examined the performance of the classifiers on the amount of correctly classified affected liver. SVM, MLP and GRNN achieved higher value of sensitivity (100%). SVM and MLP achieved (100%) in specificity compared to GRNN (98.99%). Since the purpose of the liver cirrhosis detection is to detect whether the patient has cirrhosis or not, which is represented by the existing of the affected liver; the highest precision in specificity is more important in this research. Because patients that are detected as cirrhosis can be further investigated to prolong their survival but patients that are classified as normal will remain undetected. Therefore the capability of classifier to classify the affected liver correctly is more important than

unaffected liver. AUC evaluates the ability of the classifiers to correctly classify the true positive (unaffected liver) and true negative (affected liver) classes. It can be seen that the AUC value of all classifiers with percentage of (1.00%). Based on the AUC values obtained by both classifiers, it can be said that SVM, MLP and GRNN classifiers could determine the class of the data. The summary of the results obtain liver disorder are shown in Table 6. Fig. 5 and 6 show the features importance based on MLP and GRNN, respectively.

Table 6: Summary of the Results obtain Liver Disorder Dataset

Classifier	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC (%)
SVM	100	100	100	1.00
MLP	100	100	100	1.00
GRNN	99.50	100	98.99	1.00

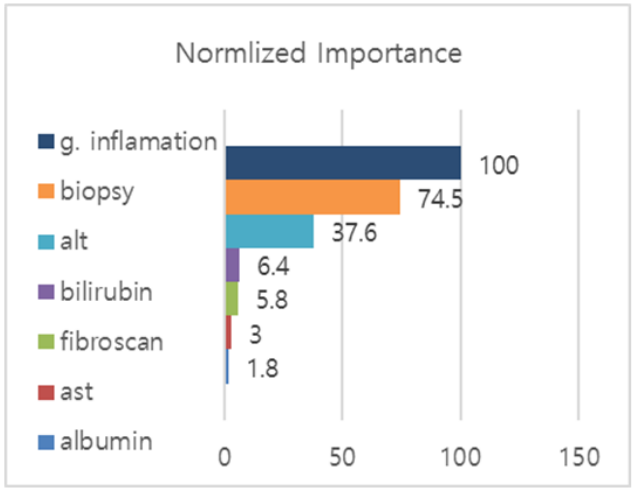

Fig. 5 Feature Importance in the GRNN classifier

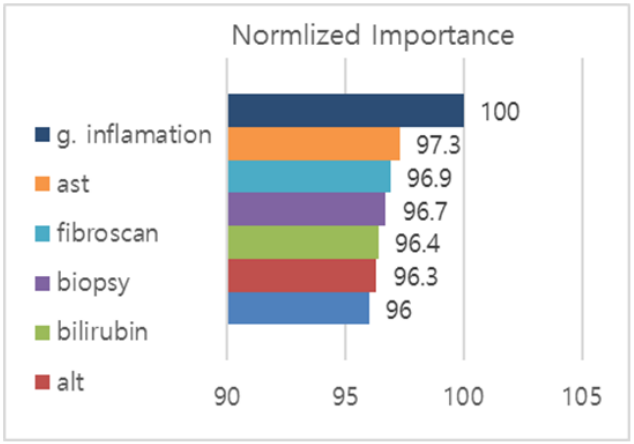

Fig. 6 Feature Importance in the MLP classifier

6. Conclusion

In this research, the performance of SVM, MLP and GRNN has been examined in classifying the liver tissues (affected or unaffected) dataset. Experimental results shows that SVM and MLP classifiers gives better performance than GRNN for liver cirrhosis classification in terms of accuracy and specificity value of (100%). This shows that using the best 7 features listed in Table 1. This work indicates that SVM and MLP can be effectively used to help the medical experts to diagnose liver cirrhosis.

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