


A Comparative Study on the Performance of Classification Algorithms for Effective Diagnosis of Liver Diseases

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Abstract

In recent years, different approaches and methods have been proposed to diagnose various diseases accurately. Since there are a variety of liver diseases, till late-stage liver disease and liver failure occur the symptoms tend to be specific for that illness. Therefore, early diagnosis can play a key role in preventing deaths from liver diseases. In this study, we compare the accuracy of different classification methods supported by the SAS software suite, such as Neural Network, Auto Neural, High Performance (HP) SVM, HP Forest, HP Tree (Decision Tree), and HP Neural for the diagnosis of liver diseases. In this study, the Indian Liver Patient Dataset (ILPD) provided by the University of California, Irvine (UCI) repository is used. Experimental results show that based on the metrics of our study, in the training phase while HP Forest achieves the highest accuracy rate, HP SVM and HP Tree do the lowest accuracy rates. However, in the validation phase, Neural Network achieves the highest accuracy rate and HP Forest does the lowest accuracy rate. Our experimental results may be useful for both researchers and practitioners working in related fields.

Keywords: liver diseases, early diagnosis, data classifiers, data mining

1. Introduction

The liver is the largest internal organ in humans. Also, metabolically it is the most complex organ and is the only organ that can regenerate itself. When a portion of the liver is transplanted, the transplanted portion will grow to the appropriate size for the recipient while the donor's liver will regenerate back to its original size. It performs more than 500 different functions including neutralizing toxins, controlling blood sugar, manufacturing proteins and hormones, fighting off infection, and helping to clot the blood [1,2]. There are over 100 types of liver disease that affect men, women and children. Some of them like different types of hepatitis are caused by viruses. Others can be the result of drugs, poisons or drinking a lot of alcohol. If liver abnormality is suspected, jaundice is usually the first sign. In addition, many parameters should be reviewed by performing blood tests. Moreover, the liver is investigated for inflammation and relevant virus particles are scanned. [3].

Diagnosis and treatment of diseases are time-intensive procedures. Software-based solutions are a promising approach which may enhance the availability and cost-effectiveness of assessment and intervention. Surely, the early detection of diseases and the treatment is of so crucial to control the diseases and improve their prognosis. Nevertheless, establishing a diagnosis in early stages is really challenging since many diseases initially present with similar signs and symptoms. To address this important challenge, in recent years, several software-based solutions have been developed and some of those solutions are based on existing screening instruments. The incorporation of such solutions into clinical practice is one of the focuses of research efforts in health informatics.

Early diagnosis and treatment of diseases is crucial for human health. There are various symptoms and signs for detecting liver diseases in the early stages. Especially for general practitioners, it is a challenge to diagnose the disease. Diagnosing disease in computer science has made great progress in recent years [4-8]. Software-based practical solutions are actively used successfully. As a part of daily diagnosis, a huge amount of diagnostic data is generated everyday related to various types of disorders and diseases. Since they discover relationships in a huge amount of data automatically, data mining and analytics techniques and solutions play a key role for knowledge discovery from this diagnostic data. Various

data mining techniques, such as clustering, classification, association rules and regression, are available for predicting diseases [6-8]. Since classifiers, which are tools in data mining that take a bunch of data representing things to be classified and attempt to predict which class the new data belongs to, have received considerable attention for disease diagnosis, in this study we focus on and analyze the performance of different classifiers for the detection of liver diseases.

Although recently several novel contributions have been made in the use of classifiers for medical diagnosis, this study extends those contributions in mainly two directions: (i) presentation of the classifiers which have not been analyzed before but are natively supported by the SAS software suite; (ii) performance evaluation of the classification algorithms in the SAS software suite for liver diagnosis. The rest of the paper is organized as follows. Related works are given in Section 2. In Section 3, classification algorithms in the SAS software suite and materials are introduced. Experimental results are presented in Section 4. Finally, the paper is concluded in Section 5.

2. Related Works

Although in the past different techniques and approaches were proposed to work with disease databases and diagnosis data, nowadays, data mining techniques, especially classification, have been widely utilized in this domain [9]. In this section, we give a literature survey and present the results of the papers covered in the literature survey. Due to the focus of our study, we mainly concentrate on studies handling the use of data mining techniques proposed for liver diseases and by presenting their advantages and disadvantages outline our study.

Literature survey confirms that some researchers focused on comparing the performance of different classifiers. Alfisahrin and Mantoro in [10] proposed the use of Decision Tree, Naive Bayes and NBTree algorithms for accurate diagnosis of liver diseases and showed that compared to the others, NBTree algorithm provides the highest accuracy whereas Naive Bayes algorithm requires the least computation time. Bahramirad et. al., [11] introduced the use of data mining for disease diagnosis and disease prediction using two different liver disease datasets, namely Andhra Pradesh state of India (AP dataset) and BUPA dataset from California State of USA. The authors mainly focused on the algorithms, including Logistic, Linear Logistic Regression, Simple Logistic, Bayesian Logistic Regression, Logistic Model Trees (LMT), Multilayer Perceptron, K-STAR, Repeated Incremental Pruning to Produce Error Reduction (RIPPER), Neural Net, Rule Induction, SVM, Classification and Regression Tree (CART) and Bayesian Boosting, and proved that using the AP dataset the authors achieved higher accuracy owing to the higher number of features involved in the AP dataset. On the other hand, in some cases, the algorithms performed better when the BUDA dataset was used.

Kim, Sohn, and Yoon in [12] focused on the use of logistic regression, DT and NN for analyzing risk factors in liver diseases. The authors showed that the use of growth curve estimator increases sensitivity value dramatically. In that study, Neural Network model achieved 72.55% accuracy and 78.62% sensitivity.

In the last decade, especially in the last couple of years, hybrid approaches drew the attention of research community. Karthik et al. [13], proposed the use of different methods in three steps: ANN to classify, Learn by Example (LEM) algorithm to create classification rules, and fuzzy rules.

In [14] J-48, Multi-Layer Perceptron (MLP), Support Vector Machine (SVM), Random Forest and Bayesian Network were used by Gulia, Vohra, and Rani for the same goal. The authors evaluated the results in two phases: before and after applying feature selection. While before applying feature selection SVM achieved the highest accuracy, 71.3551%, after applying feature selection Random Forest achieved the highest accuracy, 71.8696%.

Liang and Peng in [15] presented the integration of AI and GA for the same goal and showed the outcome of their approach using two different liver disease datasets in the UCI machine learning repository: Liver Disorder dataset and Indian Liver Patient Dataset (ILPD) dataset [16]. They achieved an average accuracy of 88.7% when the Liver Disorder was used. However, the average accuracy rate

they achieved was 98.1% when the ILPD dataset was used. For both of the datasets 20-fold cross-validation was performed.

Bashir, Qamar, and Khan in [17] introduced an ensemble model with multi-layer classification called HM-BagMoov which utilizes enhanced bagging and optimized weighting. The authors applied the proposed model on several datasets and proved that it performed better compared to the single classifiers used in that study in terms of accuracy, sensitivity and F-measure metrics. The authors also developed an application called IntelliHealth, currently used in hospitals and by doctors.

Another focus of the researchers in this domain was to compare the performance of simulation platforms. For instance, in [18], Abdar compared the performance of Rapid Miner and IBM SPSS Modeler using a liver disease dataset. The author applied Linear regression, K-Nearest Neighbor (KNN), C4.5, C5.0, Naïve Bayes, Chi-square Automatic Interaction Detector, SVM, Neural Network and Random Forest algorithms in Rapid Miner and CHAID, Logistic Regression, Bayesian net, SVM, Neural Network, KNN, C5.0 and Decision List algorithms in IBM SPSS Modeler. It was shown that although Neural Network achieved the highest accuracy rate in Rapid Miner, in IBM SPSS Modeler, C5.0 achieved the accuracy rate of 87.91% and was the best algorithm in the performance evaluation study.

In [19], a set of individual classifiers involved in an ensemble classifier, solo classifiers and neural network classifiers was applied on 4 datasets provided by UCI: the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, the ILPD, the VCDS and the HDDS. Different from the similar studies, the focus of [20] was Fatty Liver Disease (FLD) and several methods such as Decision Tree, SVM, AdaBoost, KNN, Probabilistic Neural Network (PNN), Naive Bayes and Fuzzy Sugeno were used to work with normal and abnormal liver images through linear and quadratic discriminant analysis. According to the results, PNN achieved the best performance in terms of accuracy, sensitivity, specificity, and Area under Curve (AUC) metrics.

In [21] used Levenberg–Marquardt Back Propagation Network classifier through random partitioning approach to process 124 ultrasound images in order to diagnose FLD and evaluated the results using five metrics: accuracy, sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV). In terms accuracy, the authors achieved 97.58%.

Baitharu and Pani [22] used Decision Tree J48, Naive Bayes, Neural Network, ZeroR, 1BK, and Voting Feature Intervals (VFI) algorithms to process a liver disorder dataset. The authors proved that Multilayer Perceptron achieved higher accuracy rates.

In [23] two well-known decision tree algorithms including CHAID and C5.0 have been applied. According to the results, the best performance was related to C5.0 when it applied with boosting technique.

In [24] three decision tree algorithms including C5.0, CHAID, and CART applied with boosting technique on liver disease data set. They have then combined with Multilayer perceptron Neural Network (MLPNN). Their results indicated that MLPNNB-C5.0 with 94.12% had the best performance compared with other methods.

In literature, there are many research papers about diagnosis of some diseases. In this article studies, machine learning methods were used for the effective diagnosis of Heart Disease [25], Parkinson [26], Tuberculosis [4], Diabetes [5] and Chest [6].

3. Materials and Methods

The classification process in Artificial Intelligence applications is widely used in data mining to identify groups within a given population. When the literature is reviewed, different classification methods and algorithms are used effectively in the detection of many diseases. The SAS-based software platform is a scalable, powerful, integrated software environment designed for data access, conversion, and reporting [27]. The Java-based platform includes data mining algorithms, artificial intelligence methods and many methods and algorithms used in data processing applications. In this sense, it is an effective

and very powerful data processing platform that can be used for many applications such as a new generation programming language, data processing, information storage and retrieval, descriptive statistics and web mining [28]. In this study, we used SAS Enterprise Guide 7.1 [27] for data pre-processing and SAS Enterprise Miner 14.1 [27] for analyzing and diagnosing liver diseases through combining multiple classification algorithms using model comparison node. The performance of Decision Tree, Neural Network, AutoNeural, HP SVM, HP Forest and HP Neural algorithms were compared as shown in Fig. 1. The following subsections explain the main steps of how we implemented the algorithms in the SAS software suite and presents information about our simulation study.

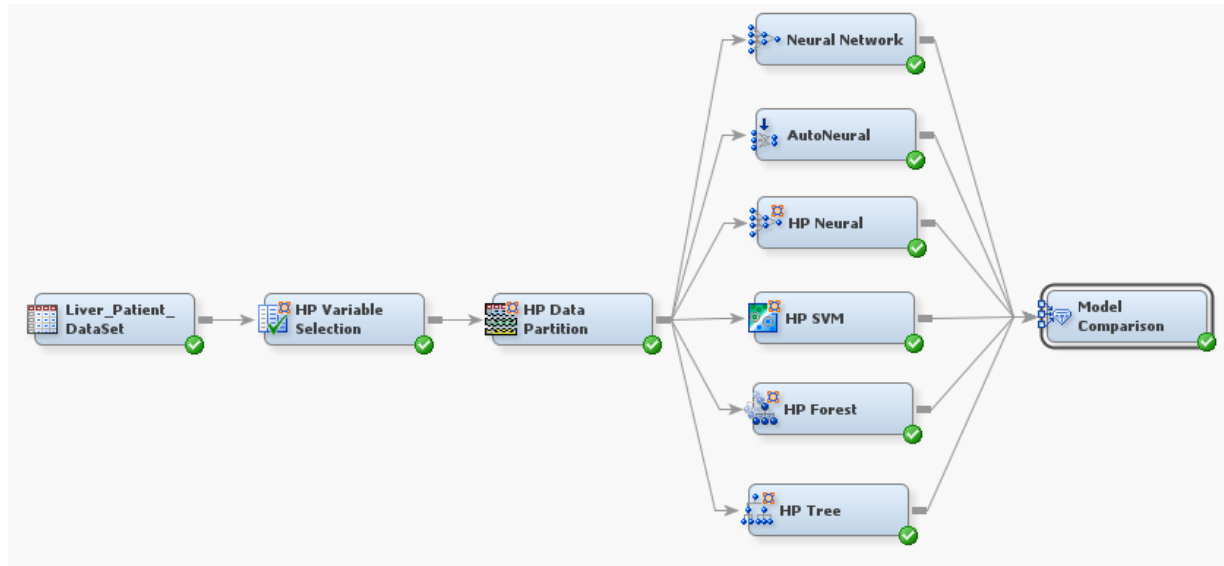


Figure 1 Algorithms used in this study and how they are implemented

3.1 Dataset

Nowadays, there are many different datasets for liver diseases. In our study, the ILPD was used. The IPLD consists of data collected by Ramana et al. in 2012 from the North East of Andhra Pradesh region [29,30]. It includes 583 rows and has two classes. While the first class is related to liver disease patients records (PR) and includes 416 records, the second class is for non-liver (PR) and includes 167 records. Overall, the dataset has 11 columns for 441 male and 142 female patients. The details are given in Table 1.

Table 1 Attributes of the ILPD

No.	Attribute name	Type	Range
1.	Age : Age of the patient	Interval	[4-90]
2.	Gender : Gender of the patient	Nominal	[Male-Female]
3.	TB: Total Bilirubin	Interval	[0.4-75]
4.	DB :Direct Bilirubin	Interval	[0.1-19.7]
5.	Alkphos : Alkaline Phosphotase	Interval	[63-2110]
6.	Sgpt Alamine : Aminotransferase	Interval	[10-2000]
7.	Sgot Aspartate : Aminotransferase	Interval	[10-4929]
8.	TP : Total Protiens	Interval	[2.7-9.6]
9.	ALB : Albumin	Interval	[0.9-5.5]
10.	A/G Ratio : Albumin and Globulin Ratio	Interval	[0.3-2.8]
11.	Selector field *	Binary	[1-2]

* utilized to divide the dataset into two groups (class-1: includes 416 LPR and class-2: includes 167 non-LPR).

3.2 HP Variable selection

Our dataset has 11 features include 10 features are inputs and 1 feature (selector field) is the target. Although all of the features have some effect on the diagnosis of liver diseases, some of them are much more important rather than the others. HP Variable Selection node was used to identify unimportant or

less important ones relative to the target. In this regard, it is an appropriate solution to find the best set of input variables from the whole of possible input variables in order to achieve the highest possible prediction accuracy through training by these inputs [27].

3.3 Data Partition

In our liver study, the data partition node was used to process the liver disease dataset and then randomly partition it into two sub-groups: training and validation datasets. This way it helps to reduce running time spent for preliminary modeling of the simulation study [27].

3.4 Classification Algorithms Used in Applications

This subsection briefly introduces the algorithms used in this study and describes how they can be applied. *Neural Network* is used to classify the feature space, and one of the most popular NN models is multi-layer feed-forward. It consists of three main layers connected to each other including an input layer, an output layer, and one or more hidden layer(s), which are placed between input and output layers. Each of the layers consists of a number of neurons in this model. Even though there are various types of the algorithms such as the Pola–Ribiere Conjugate Gradient (CGP) and the Scaled Conjugate Gradient (SCG) algorithms, in this study the Levenberg–Marquardt algorithm was preferred.

AutoNeural can handle multiple network configurations, and after finding the best one it captures the relationship in the dataset and trains its model based on previous experiences and training. It is used in order to carry out the automatic configuration of the Neural Network Multilayer Perceptron model [27].

HP Neural is a procedure without a lot of parameters for some individuals who have minimal experience related to the neural networks to achieve good and acceptable outcomes. One of its distinct features is the need for limited memory relying on Broyden–Fletcher–Goldfarb–Shanno (LBFGS) optimization approach by proprietary enhancements [27].

HP SVM is a procedure which supports various dataset as inputs in both continuous and categorical types of data. In addition, it supports the classification of a binary target, the interior-point method, and the active-set method, cross-validation for penalty selection, and the scoring of models [27].

HP Forest provides an ensemble of hundreds of decision trees in order to forecast a unique target in two types that are as follows: interval or nominal measurement level. In fact, HP Forest looks for those rules which maximize the worth measurement which has associated with the splitting criterion [27].

HP Tree is creating and visualization a decision tree and define input variable importance. This node includes so many of the tools and results found. There are two different targets as interval and taxonomical.

In addition, in this node, standard visualization and assessment plots, such as the tree diagram, tree map, leaf statistics, subtree assessment plot, and node rules are available [27].

3.5 Model Comparison

In the SAS software suite, using the expected and actual profits the model comparison node provides the standard charts and tables to clearly show the performance of compared algorithms [26], [27]. As shown in Fig. 1, all of the algorithms were connected to this node so that the performance of the algorithms could be compared and the best algorithm could easily be identified. The ROC and CL functions were provided for visual representations and fit statistics were presented, too.

4. Experimental Results

The liver disease dataset was randomly divided into two different groups: the first group was created for training and was 80% of the whole dataset, and the second group was created for testing and was 20% of the whole dataset. Initially, the adjustable parameters related to each classifier were tuned. In

Neural Network algorithm, Levenberg–Marquardt algorithm was the optimization algorithm and classical feed-forward Back Propagation learning algorithm was used. The neural network consisted of single hidden layer with 10 neurons where the initial weights were also selected randomly. For Decision tree node, default value was selected and for regression node logistic regression algorithm was used. Although there are several different metrics to evaluate the performance of classification algorithms, similar to the literature [5-8] and [25-27] in this study we used 7 parameters shown Table 3 and Table 4. The Confusion Matrix for each algorithm is given in Table 1 and the metrics are as follows formulas (1)-(8). These formulas and calculations used in classification processes are known general rules. Therefore, in this context, it is possible to see these equations related to classification in many different articles. The important thing is to use effective methods to ensure that these equations are correct, understandable and real results are obtained.

$$\text{Specificity} = \text{TNR} = \text{TN} / (\text{TN} + \text{FP}) \quad (1)$$

$$\text{Sensitivity} = \text{TPR} = \text{TP} / (\text{TP} + \text{FN}) \quad (2)$$

$$\text{Precision} = \text{TP} / (\text{TP} + \text{FP}) \quad (3)$$

$$\text{FPR} = \text{FP} / (\text{FP} + \text{TN}) = 1 - \text{TNR} \quad (4)$$

$$\text{FNR} = \text{FN} / (\text{FN} + \text{TP}) = 1 - \text{TPR} \quad (5)$$

$$\text{F1} = 2\text{TP} / (2\text{TP} + \text{FP} + \text{FN}) \quad (6)$$

$$\text{Accuracy} = (\text{TP} + \text{TN}) / (\text{TP} + \text{TN} + \text{FP} + \text{FN}) \quad (7)$$

where TP, FN, FP and TN are as follows:

True Positive (TP) is the number of positive samples correctly classified.

False Negative (FN) is the number of negative samples misclassified as positive.

False Positive (FP) is the number of positive samples misclassified as negative.

True Negative (TN) is the number of negative samples correctly classified.

Table 2 Confusion matrix in this study

Actual	Predicted	
	Disease (positive)	No-disease (negative)
Positive	TP	FP
Negative	FN	TN

Tables 3 and 4 list the accuracy rates of all the applied algorithms in the training and validation phases. In addition to the metrics, the ROCs of the algorithms are given in Fig. 2. The ROCS provide valuable information about the training and validation phases. As can be seen in the figure, in the training phase HP Forest algorithm achieved the accuracy rate of 100%. On the other hand, in the validation phase Neural Network algorithm performed better than the others. CL graph is given in Fig. 3. in the training phase HP Forest algorithm obtained the highest classification score while the others obtained almost the same scores. But in the validation phase, Neural Network obtained a better predictive model with the highest CL.

Table 3 Classification rates in the training phase (%)

Description	FN	TN	FP	TP	Specificity	Sensitivity	Precision	FPR	FNR	F ₁	Accuracy
HP Tree	0	0	134	333	0.00%	100.00%	100.00%	100.00%	0.00%	83.25%	71.31%
Neural Network	11	13	121	322	9.70%	96.70%	96.70%	90.30%	3.30%	82.99%	71.73%
Auto Neural	32	42	92	301	31.34%	90.39%	90.39%	68.66%	9.61%	82.92%	73.45%
HP Neural	17	20	114	316	14.93%	94.89%	94.89%	85.07%	5.11%	82.83%	71.95%
HP Forest	0	134	0	333	100.00%	100.00%	100.00%	0.00%	0.00%	100.00%	100.00%
HP SVM	0	0	134	333	0.00%	100.00%	100.00%	100.00%	0.00%	83.25%	71.31%

Table 4 Classification rates in the validation phase (%)

Description	FN	TN	FP	TP	Specificity	Sensitivity	Precision	FPR	FNR	F ₁	Accuracy
HP Tree	0	0	33	83	0.00%	100.00%	100.00%	100.00%	0.00%	83.42%	71.55%
Neural Net	4	7	26	79	21.21%	95.18%	95.18%	78.79%	4.82%	84.04%	74.14%
Auto Neural	10	10	23	73	30.30%	87.95%	87.95%	69.70%	12.05%	81.56%	71.55%
HP Neural	4	6	27	79	18.18%	95.18%	95.18%	81.82%	4.82%	83.60%	73.28%
HP Forest	11	10	23	72	30.30%	86.75%	86.75%	69.70%	13.25%	80.90%	70.69%
HP SVM	0	0	33	83	0.00%	100.00%	100.00%	100.00%	0.00%	83.42%	71.55%

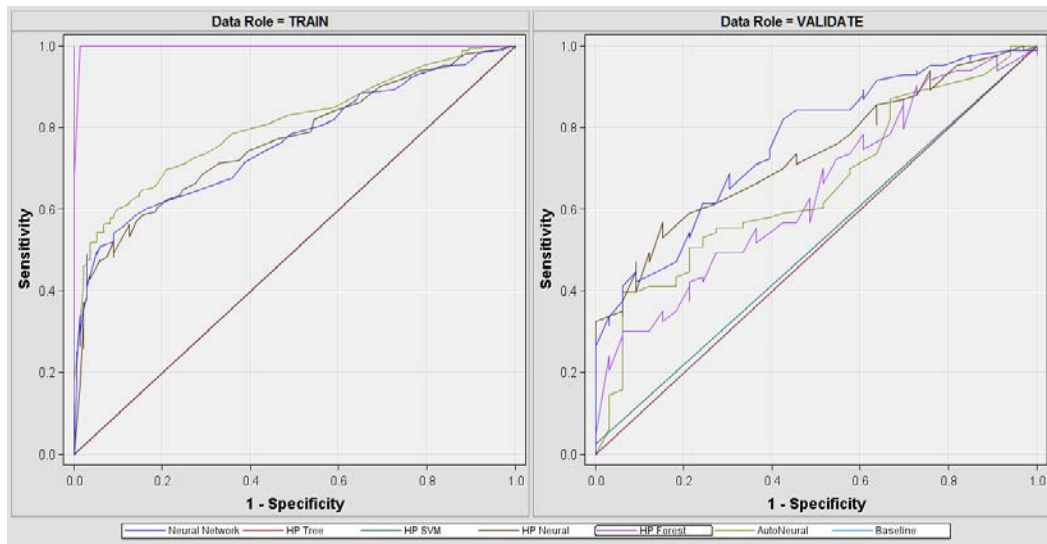


Figure 2 ROCs for the classification algorithms

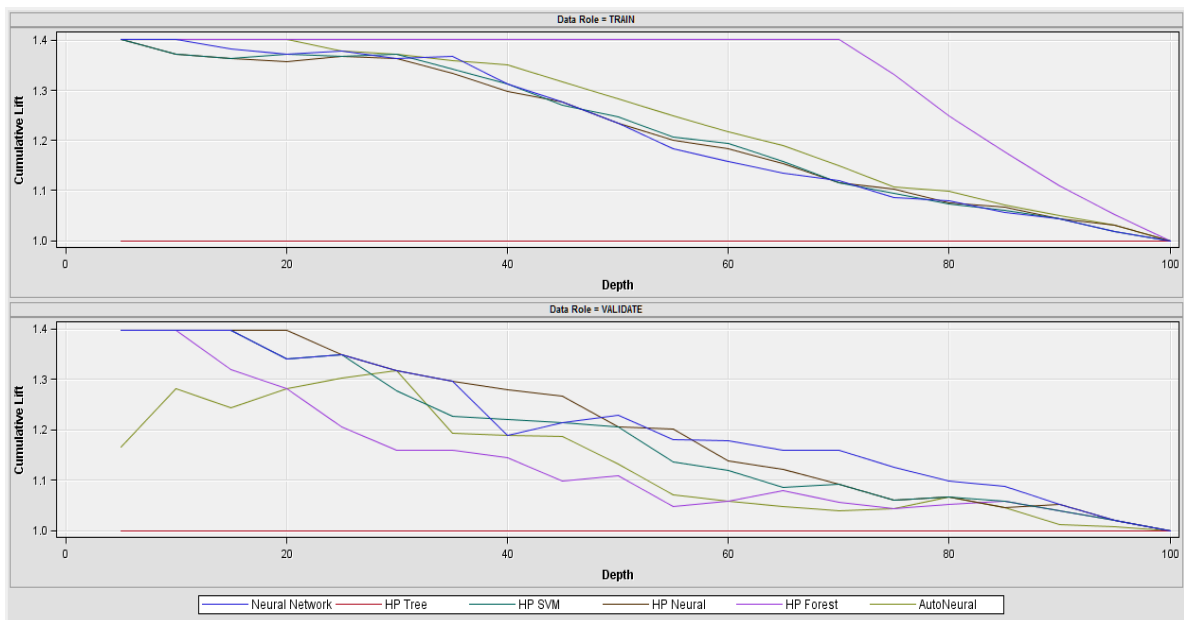


Figure 3 CL curves in the training and validation phases

4. Conclusions

Since their symptoms can be vague and easily confused with other health problems, Liver diseases can be difficult to diagnose. There are over a hundred different types of liver diseases and symptoms can vary widely. Sometimes, a person may have no symptoms but the liver may already have suffered serious damage. It is not easy to diagnose liver diseases in their early stages using traditional approaches;

hence, software-based tools could aid in early detection and thereby increase the chance of treatment. It is not possible that the diagnosis of liver diseases is always accurate. In the proposed software-based approaches, accepted diagnostic criteria should be applied to increase the general validity of the diagnostic process. In this study, we used ILPD provided by the UCI repository and compared the accuracy of different classification algorithms supported by the SAS software suite, includes Neural Network, Auto Neural, HP SVM, HP Forest, HP Tree and HP Neural, for the application. The metrics simulation results showed that in the training phase HP Forest provided the highest accuracy rate, and HP SVM and HP Tree did the lowest accuracy rates. On the other hand, in the validation phase Neural Network provided the highest accuracy rate, and HP Forest did the lowest one. Our experimental results verify that classification algorithms can provide the accuracy requirements of diagnosis tools if they are properly applied.

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