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Research Article

Neuro-Opt: A Novel Multi-Stage Feature Selection and Classification Model for Accurate Liver Disease Detection

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ABSTRACT

Liver disease is a pervasive and pressing global health challenge whose conditions vary from viral infections, fatty liver disease, to more severe conditions such as cirrhosis and hepatocellular carcinoma. In order to detect liver disease at earliest stages, there is an urgent need of developing an accurate and efficient diagnostic model. Considering this, a novel and highly accurate NeuroOpt model is proposed in this manuscript for detecting and classifying stages of liver disease in patients. The proposed model utilizes Neural Network architecture for classifying disease whose performance is enhanced by self-tuning process through GWOA2 (Grasshopper and Whale Optimization Algorithm) method. Moreover, an effective three-stage Feature Selection method is also used in the proposed work for meticulously choosing vital attributes from given dataset. The key innovation of this work is the development of a dynamic self-tuned NeuroOpt liver disease detection model along with three-stage Feature Selection that not only predicts the presence and absence of liver disease in humans but also classifies them into multiple stages using two datasets instead of only one. Through the utilization of two datasets, the proposed model became dynamic due to its high accuracy rate for both binary and multi-stage classifications respectively. The efficacy of proposed approach is examined and validated on Indian Liver Patient Dataset (ILPD) and Cirrhosis Prediction Dataset (CPD) using MATLAB software for binary and multi-stage disease classifications respectively. Experimental outcomes determine that proposed model is able to detect disease in patients with an accuracy of 97% (binary classification) on ILPD dataset, whereas, it attained an accuracy of 98.9% for multi-stage disease classification of CPD dataset to prove its effectiveness.

Keywords: Liver Disease, Feature Selection, Optimization Algorithms, Machine Learning etc.

INTRODUCTION

Liver is considered as one of the most essential organs of our body that aids in bile production, detoxifying toxins and also serves as the supplier of crucial proteins necessary for blood coagulation [1, 2, 3]. It has a distinct self-regeneration process, making it the only visceral organ in humans with this ability. Nonetheless, the functionality of liver is quite intricate, therefore, it is necessary to main liver health because any abnormality in liver can results in fatal diseases [4,5,6] like liver cancers, Hepatitis, Fatty liver etc. A person's body may suffer serious harm if liver stops its basic functioning. Irrespective of the fact, whether the liver tissue gets damages by having chemical substances, viruses or by body's immunological system, the core risk is identical i.e., liver becomes so damaged that it cannot help in keeping person alive. Hepatotropic virus strains which trigger liver illness place a significant financial strain on medical care. Chronic liver disease (CLD) is brought on by recurrent infections with the hepatitis B, C and delta viruses [7, 8, 9, 10].As per the study, Asia accounts for 75–80% of all hepatocellular carcinoma (HCC) cases worldwide. While the risk factors differ greatly across Asia, hepatitis B virus and cancers are associated with higher

risks of HCC. Furthermore, the cases of HCC are higher in Japan than Asia, due to the exceptionally high frequency of hepatitis C [11].

Based on the type of liver disease, it is usually classified into two types of acute and chronic [12, 13, 14]. The disease is considered as acute if it has not exceeded six months from its date of origin and its typically caused by acute viral hepatitis and reaction of medicines [15, 16]. Some of the typical liver illness indications include weakness, tiredness, pain in upper right part of abdomen, and feeling nauseous [17, 18]. In addition to this, some other signs are also found in patients suffering from liver disease and these include jaundice, drowsiness, pain in the spine, swollen abdomen, decreased appetite, fluid intypical cavity, pale stools, increased spleenand gallbladder [19]. Although signs and indicators of liver illness vary among individuals, most tend to involve bloating, swollen legs, a tendency to bruise readily, different color of urine and stooland yellowness of skin and eyes. Nonetheless, it must also keep in mind that there are some cases that shows no signs of liver disease at all, making it challenging to treat patient at early stages [20, 21, 22]. As per the statistics, around 4.5% to 9.5% or 50 million individuals reportedly are having liver disorders. Out of these individuals, every year close to 2 million people die because of liver diseases [23]. The only ways to solve this issue are promptly identified and appropriate therapies. Some of widely adopted diagnostic methods for identifying liver disordersare liver biopsies, blood tests, CT scans, MRIs for checking damage in live or tumors [24, 25]. Medical professionals or specialists determine if an individual has been infected or not upon examining these tests. However, diagnosing liver problems remains daunting due to the expertise required by medical professionals and the prolonged duration it entails. In order to aid experts with accurate diagnosis of disease, Machine Learning (ML) algorithms are playing a pivotal role [26, 27]. These models could be utilised to draw out useful data from medical records so that patients can be categorized easily. Data gathering, preparatory processing, feature selection, and classification are all steps in the process of ML detection of liver disease [28, 29]. Among all these stages, feature selection and classification hold a central position. In the field of diagnosing liver conditions, feature selection plays a crucial role in improving the precision and efficacy of diagnostics techniques. Investigators and data analysts carefully analyse a range of diverse medical indicators like enzyme levels, bilirubin counts, and radiological features, to isolate the portion of the most pertinent and instructive traits. The likelihood of overfitting, in which the technique operates satisfactorily on training data but fails when presented with fresh, untested data, is reduced by careful feature selection in addition to lowering the computational complexity of the model [30]. Such selection methods allow diagnostic algorithms to produce precise and accurate outcomes by emphasising relevant traits. However, using only effective feature selection technique is not effective and hence it is important to use a good classier as well for identifying and forecasting liver illness. By utilizing the edge cutting techniques like ML, classification algorithms may carefully assess a wide range of clinical information, from medical imaging studies to different biochemical markers. Such algorithms may identify intricate trends and minute details in the information that could escape human observation. By doing so, they can accurately differentiate between healthy individuals and those afflicted with liver diseases, often at an early stage when intervention can be most effective. Moreover, the high accuracy generated by these techniques greatly minimizes the possibility of misdiagnosis, thereby ensuring patients receive prompt and effective medical care. Furthermore, the accuracy rates of liver condition identification are expected to increase further as technology develops and algorithms get more complex, resulting in more accurate diagnosis, tailored treatments, and eventually improved patient outcomes. Consequently, expanding the field of liver disease diagnosis and improving the standard of healthcare delivery depend greatly on careful selection and application of innovative Feature selection and classification algorithms.

Motivation

The imperative need for developing effective liver detection method stems from the escalating global burden of liver diseases and their profound impact on public health. Liver disorders, encompassing a wide spectrum from hepatitis to cirrhosis and liver cancers, are often asymptomatic in their initial stages, leading to late diagnoses and low treatment efficacy. Therefore, timely and accurate detection is pivotal, as it facilitates early intervention, which in turn can significantly improve patient outcomes and reduce healthcare costs associated with advanced disease management. In this realm, AI can help in revolutionizing diagnostic process for precise and reliable liver detection methods. These methods not only enhance the speed and accuracy of diagnoses but also assist healthcare professionals in developing targeted treatment plans tailored to individual patients. Keeping this in mind, an effective liver disease detection model is presented in this paper that is able to detect liver disease and its stage in patients as well.

Our Contribution

In order to detect liver disease and its stage in patients with high accuracy, an effective classification model is proposed in this research. The main contributions of proposed work are:

- Firstly, work has been done on resolving dimensionality and complexity issues, by proposing an effective three-stage feature selection technique.
- After feature selection, a novel tuned NeuroOPT model is designed by utilizing $GWOA_2$ for identifying and classifying liver diseases in ILPD and CPD datasets.
- Finally, efficiency of proposed approach is authenticated by comparing it with traditional models under different metrics for binary and multi-stage disease classifications.

The rest of the paper is divided into following sections. Section II reviews some of the latest methodologies presented for detecting liver disease, followed up by problem statement. Section III gives detailed overview of proposed work. Experimental results for binary and multi-stage disease classificationsare added in section IV and finally the conclusion of paper is given in Section V.

LITERATURE REVIEW

In this section, we delve into a comprehensive analysis of recently proposed methods for predicting liver diseases. This review is meticulously conducted, employing relevant keywords such as "Liver disease," "DL-based Liver disease methods," and "ML-based liver disease detection methods." This exploration spans esteemed platforms including "IEEE," "Hindwai," "Springer," "Elsevier," and other reputable sources. Through this rigorous examination, we aim to provide an insightful overview of the cutting-edge advancements in liver disease prediction techniques, synthesizing knowledge from top-tier academic and research publications.

In [31], proposed a DL based light CNN liver diagnostic model in order to categorize given CT scan image as malignant or benign. Their model had a total of eight layers along with 1 convolutional layer. Moreover, they implemented their model in two different tracks wherein a DL classifier was used in first case and achieved 95.6% accuracy rate. Also, SVM was used along with features extracted automatically in second case, which attained an accuracy score of 100% on LiTS17 dataset.

On the contrary, the authors in [32], utilized Liver patient data as input which was fed to 7 ML classifiers which include, LR, DT, RF, KNN along with Gradient boosting, Extreme GB and Light GBfor making the prediction whether a person is infected or not. Their results showcased all classifiers achieved good accuracy because of the Feature selection technique they implemented. Similarly, in [33], again a ML based liver disease detection approach was presented in which RF, Extra Tree, SVM, KNN and MLP was used for classifying liver disorders. They implemented two imputed techniques for handling the null values in dataset. Simulating results attained demonstrated that Extra Tree classifier was attaining highest accuracy of 98.37% and 99.18% on two imputed databases. In addition to this, the classifier attained an F1-Measure and AUC of 98.3% & 99.17% and 99.3% & 99,4% respectively. Another ML model was proposed in [34], wherein a hybrid classification module was developed in order to detect and classify liver disorders on ILPD database. They implemented their model on Python along with Spyder tool, upon which it attained an accuracy score of 77.58%. Furthermore, data mining approaches in which ANN, LR, LR-SGD were used in [35] along with passive aggressive, Ada Boost and Voting classifiers for detecting and categorizing liver disorders. They implemented every classifier in two scenarios, one with LDA and another without LDA to calculate their efficiency. According to the results, DT model was showing improved accuracy rate of 99.5% to prove its superiority over other classifiers.

Moreover, in [36], Modified CNN-LDPSwas proposed with the aim of producing highly accurate results for liver disorders among patients. They improved their model by using a modified PCA technique for solving dataset dimensionality issues. Also, only important and pertinent features were selected by employing Score based AFSA technique. By implementing their model on ILPD database, their model improved accuracy by around 4.05%. Additionally, f1-score, precision and recall score were improved by approximately 21.23%, 4.22% and 34.26% on same database.

Again, in [37], utilized two ML algorithms i.e., SVM and KNN for predicting the liver disorders on ILPD database. Through extensive experimentation, they were able to attain an accuracy of 82.90% and 72.64% for SVM and KNN respectively. These scores suggested that SVM was outperforming KNN by achieving high accuracy results on given dataset. Also, in [38], proposed ML liver disease detection model in which 14 important features were attained from

clinical data 525 patients. They used 5 ML classifiers which include, RR, LR, RF, DT ad XGBoost for categorizing liver diseases. Experimental results revealed that out of above-mentioned classifiers, RF was generating highest accuracy score of 0.762 along with an AUC of 0.999 respectively. Moreover, the recall rate and F1-Score values were also attained for RF whose values were 0.843 and 0.775 respectively. Furthermore, authors in [39], makes use of 4 data mining techniques which included NB, RF, SVM and Bagging that were implemented on R platform for identifying and categorizing normal and abnormal patients. They also proposed a hybrid model in which SVM and FFANN classifiers were utilized, namely as NeuroSVM model in order to enhance the accuracy further. Results attained from the experiments showed that their suggested model attained an accuracy of 98.83%. In addition to this, authors in [40] proposed a CNN approach for detecting liver disorders. To check the efficiency of their model they used two databases namely as BUPA and ILPD and compared their model with few standard ML models on these two databases. Results attained showcased that their CNN model was able to generate an accuracy of 75.55% on BUPA and 72% on ILPD datasets correspondingly.

After analysing the above literatures, it is observed that over the years a significant number of techniques have been proposed by various researchers for detecting liver diseases. These models were giving moderate results, but we observed there is still a scope of improvement.A prevalent challenge in current liver disease detection methodologies lies in the inadequate implementation of effective feature selection techniques coupled with suboptimal classification methods. Insufficient attention to the selection of pertinent features results in the incorporation of irrelevant or redundant data, leading to skewed analyses and diminished accuracy. Additionally, the absence of optimized classification techniques further exacerbates the problem, as it prevents the models from discerning intricate patterns within the selected features. Moreover, very few models are available currently that depict the stage of liver disease in patients to get proper treatment. Addressing these issues is imperative for the advancement of liver disease detection, ensuring the creation of models that are not only accurate but have ability to depict the stage of disease as well, thereby improving patient outcomes and optimizing healthcare resources.

PROPOSED WORK

This portion of paper gives detailed information about proposed model. In this study, a pioneering approach NeuroOpt has been introduced for the early detection of liver disease, focusing on the crucial stages where timely intervention can significantly enhance patient outcomes. Our proposed work combines the power of three phased feature selection technique with an NeuroOpt, marking a significant advancement in the field of medical diagnostics.Here, features are selected in the three phases rather than only one phase, opted by majority of traditional disease detection models. During the first phase relevance score of every feature present in the dataset is determined through entropy, Eigenvector centrality and Enhanced IFS techniques, which are later combined to form a single set. This set is then passed to RF classifier for evaluating the accuracy score for each feature set in second phase. The relevance score in this phase is updated by adding the accuracy along with entropy weight of best features with the feature weights obtained in first phase. In the third phase of FS, a fuzzy based model is introduced for analysing the second feature set with some defined fuzzy rules to determine final feature set. However, utilizing only effective feature selection is not enough for improving the detection rate of liver diseases. Therefore, it is pertinent to propose an effective classification model that can easily discern patterns from featured data to detect diseases with high accuracies. Several researchers in the literature were using neural network for identifying liver diseases, however, they did not tune its parameters which leads to poor accuracy, overfitting, and complexity issues. Inspired from this, a self-tuned NeuroOpt classification module is proposed in our work for detecting liver disease and its stages. Because of its capability to learn from huge and high-dimensional datasets and its ability to handle complicated, non-linear interactions within data, Feed Forward based NN is used in the proposed work. However, the parameters of FFNN are very sensitive and any small change in these parameters can lead to low accuracy rates. Therefore, to improve performance of FFNN two effective optimization algorithms i.e., GOA and WOA are hybridized as $GWOA_2$, for tuning the hyperparameters of FFNN. The key notion behind using GOA is its ability to adjust its parameters while searching for optimal solution but it converges prematurely to a local optimum, especially in complex and high-dimensional search spaces leading to increased complexity. To overcome this limitation, number of other optimization algorithms were studied in proposed work. During our study, we found that WOA's prey searching strategy can effectively mitigate this issue by diving deeper into the solution space, allows for a more profound exploration. Furthermore, we introduced diversification and personal influence factor in proposed $GWOA_2$ method for balancing exploration and exploitation phases during tuning process. The two techniques are implemented on ILPD and CPD datasets whose description is given in subsequent sections.

How Proposed NeuroOPT is Better?

The proposed NeuroOPT model stands out as a highly effective method for liver disease detection, addressing key limitations in existing approaches. Our model's superiority lies in its comprehensive design and practical implementation, which surpasses current methods commonly found on the Kaggle site, where the ILPD and CPD datasets are sourced. Unlike the majority of existing models that perform binary classification using a single dataset, NeuroOPT incorporates a multi-stage classification system and leverages both ILPD and CPD datasets, significantly enhancing its versatility and applicability.

While reviewing existing liver disease detection models revealed that most achieve an accuracy range of 70% to 93% on the ILPD dataset, which is suboptimal for a reliable binary classification system. Although a few models approach 99% accuracy, they lack dynamism and are limited to predicting disease presence or absence within a single dataset. Recognizing these shortcomings, we aimed to develop a more dynamic and practical model by integrating two datasets and addressing both binary and multi-stage classification challenges.

However, the CPD dataset, in particular, posed a significant challenge for existing models, which demonstrated an accuracy range of only 40% to 67% for multi-class classification, highlighting their ineffectiveness for categorizing multiple stages of liver diseases. To overcome these issues, we introduced a three-stage feature selection technique, enhancing the model's ability to extract relevant features efficiently. Furthermore, we employed the NeuroOPT model, which utilizes a neural network optimized with $GWOA_2$ to fine-tune hyperparameters and improve predictive accuracy. By implementing these advancements, our proposed NeuroOPT model not only increases the accuracy rate for both binary and multi-class classification but also offers a dynamic and practical solution that addresses the limitations of current liver disease detection models. It is pertinent to mention here that $GWOA_2$ tuned FFNN is proven out to be highly effective than conventional approaches on both kaggle datasets, as proven by accuracy rates discussed in results section of this paper.

Datasets Used and their Pre-Processing

In the proposed work, two widely used datasets i.e., ILPD and CPD are used for examining the efficacy of proposed method in detecting disease (binary classification) and its stages (multi-stage disease) classification. Here, ILPD dataset model is used to determine presence of absence of liver disease in patients (Binary Classification), while as, CPD dataset is used because it contains information about four different stages of liver disease and hence is useful for performing multi-stage disease classification in patients.

- **ILPD Dataset [41]:**The given repository consists of 583 liver specimens which are obtained from 441 and 142 male and female patients respectively. Among of these specimens, 416 specimens are associated with liver illnesses, whereas the balance of 167 specimens are associated with healthy people. Additionally, Selector class label is used in this database to divide people into two categories: liver patients and normal people. Moreover, this database constitutes of 10 attributes along with 1 target feature whose detailed description is given in Table 1.
- **CPD Dataset [42]:** This dataset comprises 424 PBC samples taken from Mayo clinic trials out of which 312 samples were gathered by following complete trails and remaining 112 participated in main measurements only. The dataset contains information about four stages of liver disease, having 20 features, mentioned in Table 1.

Table 1: ILPD and CPD dataset information

S.no	ILPD Dataset Features	CPD Dataset Features
1	Age	ID
2	Gender	N_Days
3	TB	Status
4	DB	Drug
5	Alkphos	Age
6	Sgpt	Sex
7	Sgot	Ascites
8	TP	Hepatomegaly
9	ALB	Spiders

10	A/G Ratio	Edema
11	Selector (Target)	Bilirubin
12	-	Cholesterol
13	-	Albumin
14	-	Copper
15	-	Alk_Phos
16	-	SGOT
17	-	Triglycerides
18	-	Platelets
19	-	Prothrombin
20	-	Stage

However, the information present in these datasets cannot be used directly in proposed model, because our classifier is dealing with numerical data and dataset information is available in string format. Furthermore, the given dataset contains some null or missing values which may cause biased results. To tackle these challenges, following methods are employed for creating a refined dataset.

- **Label Encoding:** Initially, label encoding technique is implemented on raw dataset for converting string attributes into numeric values like 0 and 1.
- **Mean Imputation Method:** This technique is implemented to handle the missing or null values in given dataset. By employing this technique, the null cells in dataset are filled by calculating the mean of columns from given data points.

These steps were successful in making sure that the processed datasets is devoid of any NAN values, which has improved our algorithm's general resilience and applicability.

Three-Phase Feature Selection Technique

The importance of selecting only crucial features from the available feature set is of utmost importance as it significantly improves the efficiency of algorithms by focusing on the most relevant features, reducing computational complexity, and ensuring faster training and prediction times [43]. For identifying key characteristics in datasets, scientists have historically employed different technique wherein, feature weights were determined by using single technique. This leads to increased complexity and processing time which automatically deteriorates performance of these models.Considering this, a hybrid feature selection technique is proposed in this work wherein relevance score of features is calculated in three phases.The reason for doing so is to reduce processing time and complexity of proposed approach while simultaneously increasing its detection accuracy rate. During the first phase of FS, relevance of every feature present in the processed dataset is calculated by employing three techniques i.e., Entropy, Eigenvector centrality and entropycorrelation-based IFS (ECIFS).The entropy-based feature weights are calculated by using equation 1, with the aim to determine uncertainty in each feature. The feature values are calculated using this equation, and are subsequently placed in descending order according to their weight values to help choose the more useful traits. The traits that have lower entropy values are given a better ranking and are therefore more pertinent to our task.

$$H(f) = \sum_{i=1}^{n} p_i \log_2 p_i \qquad (1)$$

Next, Eigenvector centrality technique is implemented on processed dataset to calculate the weights of features by using equation 2. In this stage only central features of the graph are considered and rest are discarded.

$$x_v = \frac{1}{\lambda} \sum_{t \in M(v)} x_t = \frac{1}{\lambda} \sum_{t \in G} a_{v,t}\, x_t \qquad (2)$$

After this, standard IFS is improved in this phase by incorporating entropy and correlation factors in it, to form the third feature set of phases one. For calculating entropy, equation 1 is used and for calculating correlation, between features and target variables information factor (I) is used, whose mathematical formula is given in equation 3.

$$I = \sum_{x \in X} \sum_{y \in Y} p(x,y) \log_2 \left(\frac{p(x,y)}{p(x)p(y)} \right) \quad (3)$$

The final first feature set is obtained by taking the mean value of three methods i.e., entropy, ECFS and ECIFS by employing equation 4.

$$RelevanceScore\ 1 = \frac{Entropyscore + ECFSscore + EIFSscore}{3} \quad (4)$$

The feature whose relevance score1 came out to be highest are put in the final list and rest are discarded.

During the second stage of proposed FS technique, RF classifier is used for calculating the accuracy of feature set formed in first stage. But before training the RF classifier with given features, it is mandatory to initialize some of its basic parameters for its appropriate working. The list of RF parameters is given in table 2.

Table 2: Initialization parameters of RF

Parameter	**Values**
Alpha	0.5
No of Bagger	100
No of trees	10
Method to work	Classification
Prediction method	OOB

The sorted collection of attributes produced in the preliminary level is passed to RF classifier after initialization for the purpose of training. For calculating the weight of features at this stage, OOB prediction technique is employed which determines the impact of each feature on models' accuracy rate. Unless the optimum accuracy values are attained, the iterative procedure is continued. The correctness of the RF model is evaluated after every iteration and compared to the preceding one. The accuracy is updated if the current accuracy is greater than the prior accuracy; else, it is left intact. The feature scores are updated while maintaining the feature set that is most accurate. The procedure of upgrading scores at this level is given by equation 5.

$$RSu = RSp + Nacc * ENwgt \quad (5)$$

Where, updated relevancy score of features and previously determined score is represented by *Rsu* and *Rsp* respectively. Also, accuracy is depicted by Nacc and entropy-based weights are depicted by *ENwgt*. The updated feature list obtained is depicted by *Rsu*.

In the third and final stage, fuzzy model is utilized for calculating feature weights. Here, features in Rsu serve input to proposed fuzzy model which analysed the mean, min and max scores of features for determining their membership function and introducing contextual relevancy across different features. This implies that feature weights whose scores are entirely different from mean or are close to min or max scores will have unique membership score to reflect their relevance. The fuzzy framework evaluates each feature's weight by considering the values of the membership function, producing a unified membership score that fluctuates between 0 to 1. The weighting or relevance of each characteristic in relation to the earlier feature sets is indicated by this score. These membership scores are then combined with the initial feature set to create the final set. Equation 6 is used to determine the final feature weights.

$$Feature\ Weight = membership\ degree\ or\ score\ \times feature\ weights\ of\ RSu \quad (6)$$

In the last step of proposed FS technique, a filtration mechanism is introduced in which threshold of 0.7 is used for selecting final features. All features whose weight is greater than 0.7 are included in the final list and rest are removed. The mathematical formula for finalizing the feature sets is shown in equation 7.

$$FfeatSet = FetureWeight > thershold\ 0.7 \quad (7)$$

Where, *FfeatSet* depicts the last and updated feature set, that is utilized for training the proposed classification model. The final feature set is then categorized into training and testing phase in the ratio of 70:30.

Classification by NeuroOpt

Classification is a fundamental task in machine learning models which holds immense importance in deciphering patterns within featured data and making informed decisions. In light of this, different ML classifiers were used by

researchers for predicting liver disorders but still the accuracy rate in these models were not optimum. In order to improve the detection accuracy rate for binary and multi-stage disease classifications, NeuroOpt model is proposed for identifying and classifying liver diseases into different stages. This NeuroOPt signifies that proposed model utilizes FFNN and $GWOA_2$ algorithm for tuning process. The reason for using FFNN is its excellent ability of capturing complex, nonlinear relationships within datasets, making them ideal for modelling the intricate patterns often found in medical data. However, the success of an NN model hinges greatly on the careful tuning of its parameters. The performance of the network is greatly influenced by parameters such as learning rate, number of hidden layers, and number of neurons in each layer. Improperly tuned parameters can lead to issues such as slow convergence, overfitting, or underfitting, impairing the model's accuracy. Considering this, an improved GWOA technique is implemented for tuning the hyperparameters of FFNN classifier. The main reason for using WOA along with GOA is because GOA tends to converge prematurely to local optima, especially in intricate and multidimensional search spaces, which significantly escalates complexity.To address this limitation, we explored various other optimization algorithms. Our investigation led us to the Whale Optimization Algorithm (WOA), where we discovered a distinctive prey searching strategy that adeptly navigates the solution space, enabling a deeper and more comprehensive exploration. What makes WOA particularly effective is its ability to delve deeper into the complexities of the problem, offering a robust solution to the premature convergence problem observed in GOA. Additionally, the exploration phase is enhanced by integrating diversification and personal influence factors. This integration effectively balances the exploration and exploitation processes, ensuring a thorough exploration of the solution space while leveraging the algorithm's capacity for exploitation.The proposed classification module is different from other models in the fact that not only exploration ability of GOA is improved by using WOA, but strengths of both algorithms are utilized for creating a proper balance between exploitation and exploration phase to effectively tune parameters of FFNN, which in turn results in improved accuracy. The pseudo code for tuning the parameters of FFNN using improved GOA-WOA is given in Algorithm 2.

Algorithm 2: Pseudo code for tuning parameters of FFNN

Initialize the population in terms of network weights Wi (i = 1, 2, ..., n)

F=Calculate the fitness of each set

W*=Best solution set

Lb, Ub= Lower and Upper Limit of solution set

Miter=Maximum iterations

while (t < Miter)

for each solution set (i,j)

Update C, p, and V

if (p<0.5) (50% chance to GOA method)

$$W(t+1) = C\left(\sum_{j=1\ (j\neq i)}^{n} C\,\frac{Ub-Lb}{2}\,S(|W_j - W_i|)\,\frac{W_j - W_i}{dij}\right)+W^*$$

elseif (p>0.5) (Rest 50% chance to update using velocity factor)

V(t+1)=cV(t) + aU(W*-Wi);

W(t+1)= Wi + V(t+1)

end

Fnew=Calculate the fitness of each new solution set

If Fnew<F

F=Fnew

W*=Best new solution set

else (improving exploration phase)

Generate a1, r1, r2

```
                    Calculate A1, C1
                    D=C1 * W(t+1)-W*
                    W(t+1) = W(t+1) – A1D
                end
            end
        t=t+1
        end
```

The process of classification begins by defining some parameters of proposed FFNN model, that are listed in Table 3.

Table 3: FFNN Initialization Parameters

Parameters	Values
Network	Feed Forward
No of neurons	15
Iterations	100
Population count	5
LB	Min (Network wight)
UB	Max (Network Weight)
CMin	0.00004
CMax	1
Alpha	1

As per the configuration given in the above table, network type is feed forward which indicates that the model is structured in layers where information travels in one direction, from the input layer through hidden layers to the output layer. Moreover, number of neurons is kept 15 in the proposed model because given dataset is not that vast and we were getting good results at this range. Similarly, experiment was carried out for 50 to 500 iterations and at 100th iteration there was no significant improvement in fitness value and hence its value is kept 100. Additionally, the population count is kept smaller because population weight is higher in our model, creating various data combinations. If the population count is increased then processing ability of proposed model also increases which can downgrade its performance, therefore, we kept the population count only 5. Also, LB and UB represent the minimum and maximum values for the network weights. These values are crucial in weight initialization to ensure that the weights are within a certain range, preventing issues like exploding or vanishing gradients during training. Additionally, *CMin* and *CMax* represent certain coefficients or constants used in the optimization process. These values likely affect how the optimization algorithm explores the solution space, balancing between exploration and exploitation. Meanwhile, Alpha, with a value of 1, represent a regularization parameter or a learning rate in proposed optimization algorithms.

Once the classifier is initialized, weights are extracted from it by corresponding each input feature to a node in input layer of FFNN. The initial weights connecting these input nodes to the neurons in the first hidden layer are established during the initialization process. These initial weights essentially determine how much influence each input feature has on the hidden layer neurons. In order to check the efficiency of given weights, fitness value “F” is calculated for each set. Here, fitness function is inverse of accuracy, implying that fitness value should be least so that accuracy is increased. The best fitness value is stored in W*, depicting best solution set generated by FFNN.

After this, main process of tuning parameters of FFNN is initiated for each solution set. As mentioned earlier, $GWOA_2$ is used in proposed work for this process. However, tendency of GOA to get trapped in local minima could lead to deteriorated results and hence, WOA is used in proposed work. The novelty contribution of our work is this phase is that exploration phase of GOA is improved by using WOA exploration abilities. Moreover, the addition of diversification and personnel influence factor further improves the exploration phase. By doing so, we can improve the local as well as global search of WOA algorithm.The proposed $GWOA_2$ updates weights for every possible solution

set by defining three factors i.e., C (coefficient for reducing comfort zone for new solution), p (Probability to update local solution set) and v (initial velocity factor generated randomly). The value of WOA's "p" factor is kept 0.5 in order to give 50:50 chances to GOA and velocity factor for updating weights. If the value of p is less than 0.5, then chance to update weights is given to GOA algorithm using equation 8.

$$W(t+1) = C\left(\sum_{j=1\ (j\neq i)}^{n} C\frac{Ub-Lb}{2}S(|W_j - W_i|)\frac{W_j - W_i}{dij}\right) + W^* \quad (8)$$

In the other case, if value of "p" is greater than 0.5, then chance is given to Velocity factor "V" for updating FFNN weights, by employing equation 9 and 10.

$$V(t+1) = CV(t) + aU(W^* - Wi) \quad (9)$$

Wherein CV represents the inertia factor,$aU(W^* - Wi)$ depicts the personnel influence factor for next possible solution. The value of a is set to 2 and U is random value between 0 and 1.

$$W(t+1) = Wi + V(T+1) \quad (10)$$

Once the weights are updated by using above equations, the fitness value of new solution set is calculated. If new fitness value is less than previous fitness, then value is updated and best solution is stored in W*. However, in case this new fitness value is greater than current fitness, the WOA's exploration phase is utilized for updating weights. The WOA exploration phase in improved by generating three random vectors a_1, r_1 and r_2, wherein, a_1 can be calculated by using equation 11.

$$a_1 = 2 - t^*\left(\frac{2}{maximum\ number\ of\ iterations}\right) \quad (11)$$

Also, r_1 and r_2 depict two random vectors whose range lies in between 0 and 1.

Moreover, instead of using only one coefficient vector A_1, we have used another coefficient vector "C_1" of GOA, to improve its performance. The value of $A_1$and C_1 is calculated by using equation 12 and 13 respectively.

$$A_1 = 2 * a_1 * r_1 - a \quad (12)$$

$$C_1 = 2 * r_2 \quad (13)$$

The final weights are updated by using equation 14 and 15.

$$D = C_1 * W(t+1) - W^* \quad (14)$$

$$W(t+1) = W(t+1) - A_1 D \quad (15)$$

This same process is followed for next iterations and the solution with best fitness is used for training the FFNN classifier.

Experimental Setup and Performance Metrics

In this section, the performance of the proposed approach is examined and validated in MATLAB using a number of metrics, including Accuracy, Recall, Precision, and F1-Score.The software was run on a system equipped with an i5 Core processor and 8GB of RAM. Additionally, the operating system utilized was Windows 10, and the system had a 500GB HDD. Also, it is pertinent to mention here that results are obtained and discussed separately for binary and multi stage disease classification using ILPD and CPD datasets respectively. The mathematical equations used for calculating each factor is given below.

$$Accuracy = \frac{TN + TP}{TN + TP + FN + FP} \quad (5)$$

$$Recall = \frac{TP}{TP + FN} \quad (6)$$

$$Precision = \frac{TP}{TP + FP} \quad (7)$$

$$F1 - score = 2 \times \frac{Precision * Recall}{(Precision + Recall)} \quad (8)$$

- **Binary Classification Using ILPD Dataset**

In this case, information given in proposed model is used for determining the presence or absence of liver disease in patients (binary classification). It is important to mention that efficacy of proposed approach is also examined with ensemble learning model that was proposed in our previous work. First, the accuracy of the proposed approach is compared with standard models to validate its efficacy. Fig. 1 displays the results obtained for the same. The x and y-axis of the given graph corresponds to the different algorithms and their respective accuracy values. The given graph reveals that logistic classifier is showing least accuracy rate of 55.4% only, whereas, it was 67.9% in KNN and SVM model. Moreover, the range of accuracies attained by standard RF, MLP and previously proposed Ensemble model was 88%, 83% and 82% respectively. On the contrary side, accuracy rate was higher in proposed model at 97.15%which is around 9.059% higher than standard RF model.

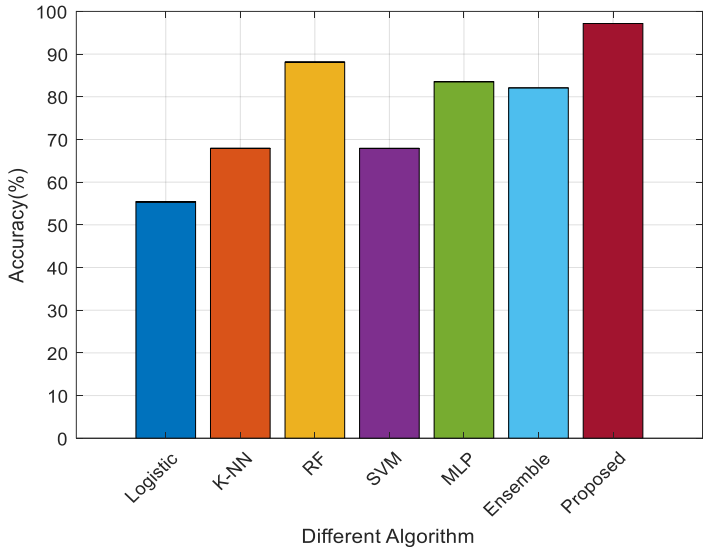

Fig 1. Comparative Analysis for Accuracy

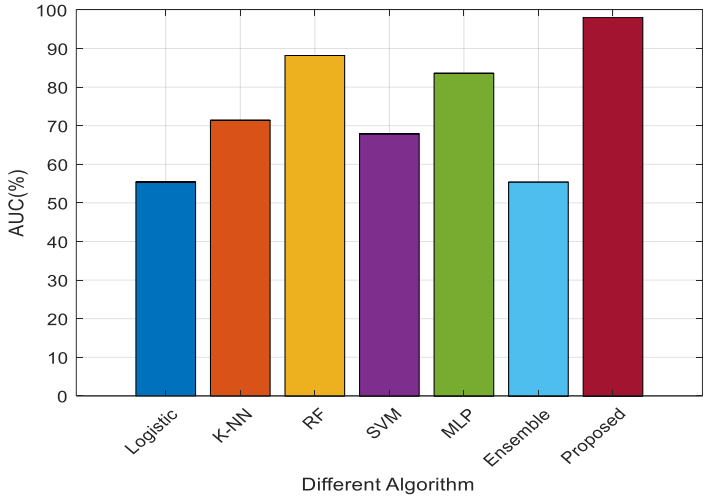

Fig 2. Comparative analysis for AUC

Moreover, proposed approach is also examined and validated by contrasting it with conventional approaches and previously proposed ensemble approach in terms of their AUC score. Fig 2 shows the comparative graph for AUC on given ILPD dataset. It must be noted that value of AUC must be close to 1 to depict model's efficacy. As per the given graph, AUC value came out to be 98.016% in proposed model, while as, it was only 55.4% in logistic and previously proposed ensemble model and 71.39%, 88.2%, 67.9% and 83.5% in KNN, RF, SVM and MLP models respectively. These results clearly show that AUC score is highest and close to 1 in proposed model, which signifies that it can effectively distinguish liver infected and non-infected.

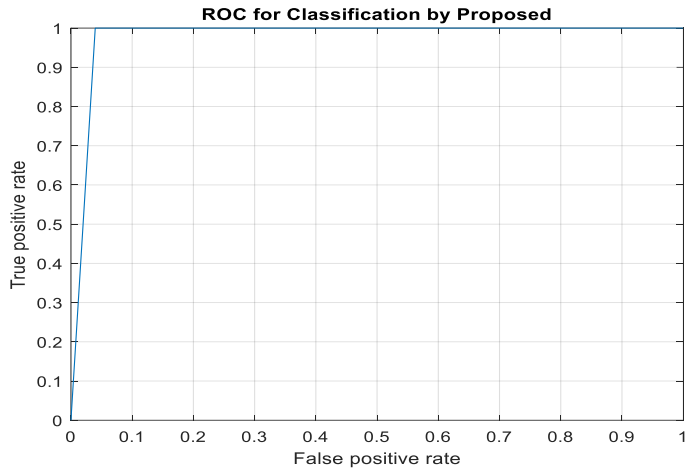

Fig 3. ROC curve of proposed Model

Furthermore, the efficacy of proposed approach is also analysed in terms of its ROC curve, whose line graph is shown in Fig 3. The given graph plots the true positive rate (sensitivity) versus the false positive rate (1-specificity) at different threshold settings to demonstrate the diagnostic ability of a proposed classifier. Following a thorough analysis of the given graph, it is observed that the proposed approach's ROC curve is hugging the upper left corner of the graph, meaning it achieves 100% sensitivity with a 0% false positive rate. This indicates that proposed model doesn't misclassify any negative cases as positive and thereby giving enhanced performance.

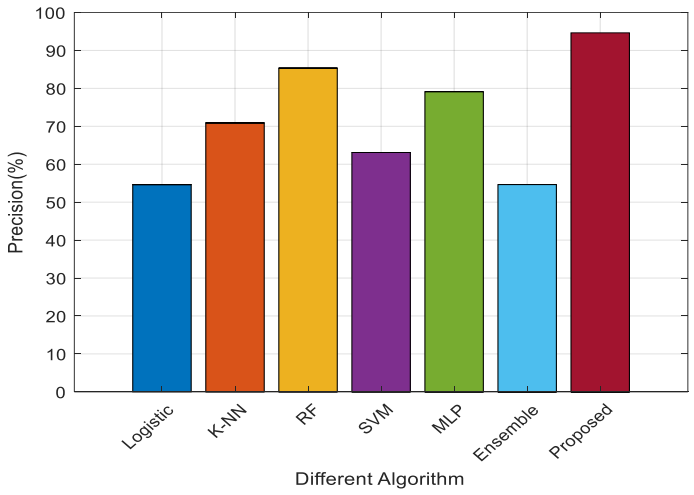

Fig 4. Comparative analysis for Precision

Also, the superiority of proposed liver disease detection approach is proved by comparing precision value of traditional models with proposed model. The comparative graph for Precision is shown in Fig 4. Graph revealed that logistic regression and the ensemble model both achieved a lowest precision of 54.63% on given dataset, while as, SVM exhibited a respectable performance with a precision of 63.09%, indicating a moderate level of accuracy.The MLP and kNN algorithm demonstrated a significant improvement by achieving a precision of 79.12% and 70.89% respectively. Moreover, RF outperformed the previous models substantially, achieving a precision score of 85.33%. However, the most noteworthy result comes from the "Proposed" model, which achieved an exceptionally high precision score of 94.624%, which is approximately 9.29% than standard RF model.

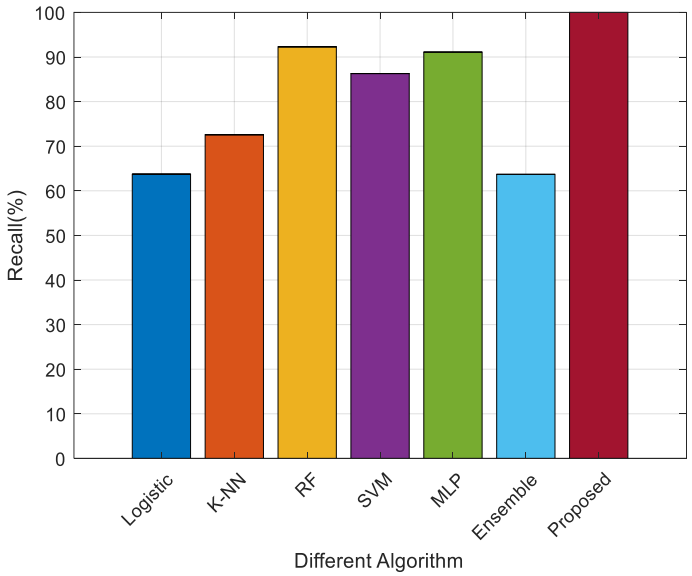

Fig 5. Comparative analysis for Recall

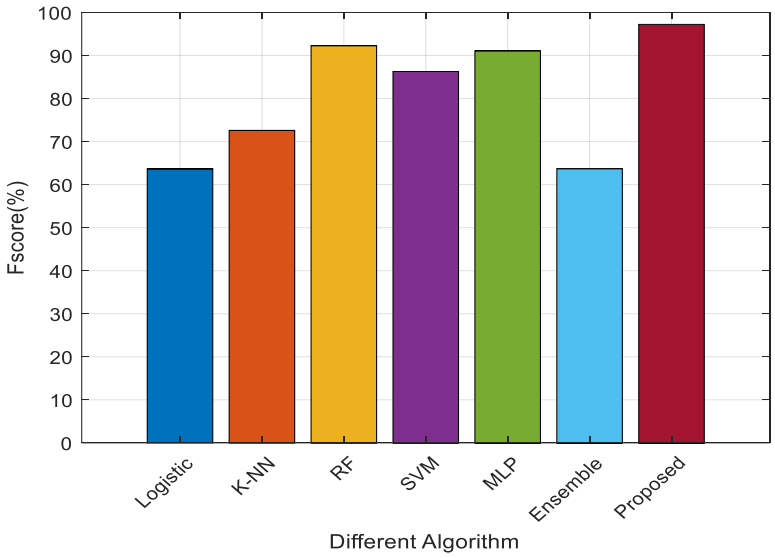

Fig 6. Comparative analysis for F1-Score

In addition to this, we also compared the performance of proposed approach with few standard models in terms of their recall score, whose graph is shown in Fig 5. The different classifiers are demonstrated on x-axis while their recall score is shown on y-axis respectively. After carefully observing the given graph, it is observed that proposed model outperforms all traditional and previously proposed ensemble models by achieving a recall score of 100%. On the other hand, recall score came out to be 63.7 in traditional Logistic and previously proposed Ensemble model, while, it was 72% in KNN, 92% in RF, 86% in SVM and 91% in MLP respectively. The results attained demonstrated that recall rate is improved by around 8% in proposed model, when compared with traditionally best performing classifier.

Finally, results are also attained by contrasting proposed approach with conventional approaches and previously proposed ensemble approach in context of their F1-Score. The simulating bar graph obtained for the same is shown in Fig 6. Results obtained from the given graph showcase that logistic and Ensemble learning were continuously showing lowest performance here as well, as they attained F1-Score of only 63.7%. However, this value was slightly improved by traditional KNN and SVM model which attained 72.5% and 86% F1-score respectively. Also, the F1-Score came out to be 91% and 92% in standard MLP and RF models, which shows significant improvement than previous models. Nevertheless, the proposed model demonstrates its superiority for this case as well, as it clings to an F1-Score of 97.2%, which is highest of all the similar models. The specific values obtained in proposed and traditional models are listed in Table 4.

Table 4: Specific values of different parameters in different models

Algorithm	Accuracy	AUC	Precision	Recall	F1-Score
Logistic	55.4	55.4	54.63	63.7	63.7
kNN	67.9	71.39	70.89	72.59	72.59
RF	88.1	88.2	85.33	92.3	92.3
SVM	67.9	67.9	63.09	86.29	86.29
MLP	83.53	83.59	79.12	91.1	91.1
Ensemble	82.09	55.4	54.63	63.7	63.7
Proposed	97.159	98.016	94.624	100	97.238

- **Multi-Stage Disease Classification Using CPD Dataset**

In this section, results obtained by proposed model for determining the disease's stage in patient are discussed using CPD dataset that contains information about 4 stages. As mentioned earlier, proposed model utilizes optimization algorithms, therefore, we have first validated its effectiveness for multi-stage disease classification phase. The fitness curve is depicted in Fig 7, with iterations on x-axis and fitness on y-axis respectively. Through the given graph, it is observed that initially fitness curve is higher because model is not fully trained yet, but as soon as iterations increase, the fitness curve comes down below 0.05 and remains constant thereafter.

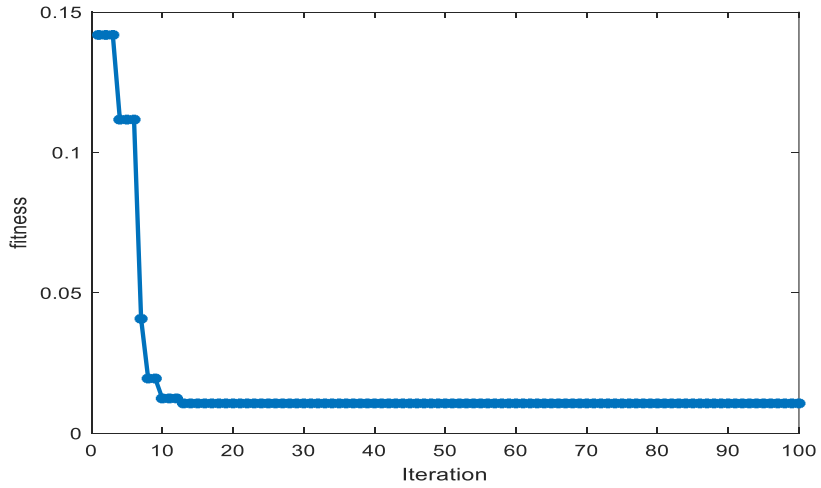

Fig 7. Fitness Curve of ProposedNet model for multi-stage Disease Classification

COMPARATIVE RESULTS

Moreover, to prove the efficiency of proposed approach, we have also compared our approach with several traditional models for multi-stage disease classification by implementing non-ensemble learning (case 1), bagging ensemble (case 2) and boosting ensemble learning (case 3) techniques on CPD dataset. The comparative results obtained for each case are discussed in this sub-section.

Case 1 (Non-Ensemble Learning Technique)

In first case, performance of proposed approach is examined and compared with traditional models for categorizing different stages of diseases using CPD dataset. The comparative graph obtained for this case is depicted in Fig 8, with different models labelled on x-axis and their percentage values for different parameters on y-axis respectively. After carefully examining the graph, it is found that standard GB model is giving best accuracy of 72.74%, however, proposed model is attaining accuracy of 98% for multi-stage disease classification. Similarly, traditional SVC model attained better precision of 70.17% than other similar models, while as, proposed model is outperforming it by attaining 96% respectively. Furthermore, proposed model is outperforming all traditional models in terms of recall

and F1-Score (97.2% and 96.8%) which is far better than standard best performing models like DT and GB which attained recall of only 50% and F1-score of 54% respectively. The precise values obtained by different models in this case are mentioned in Table 5.

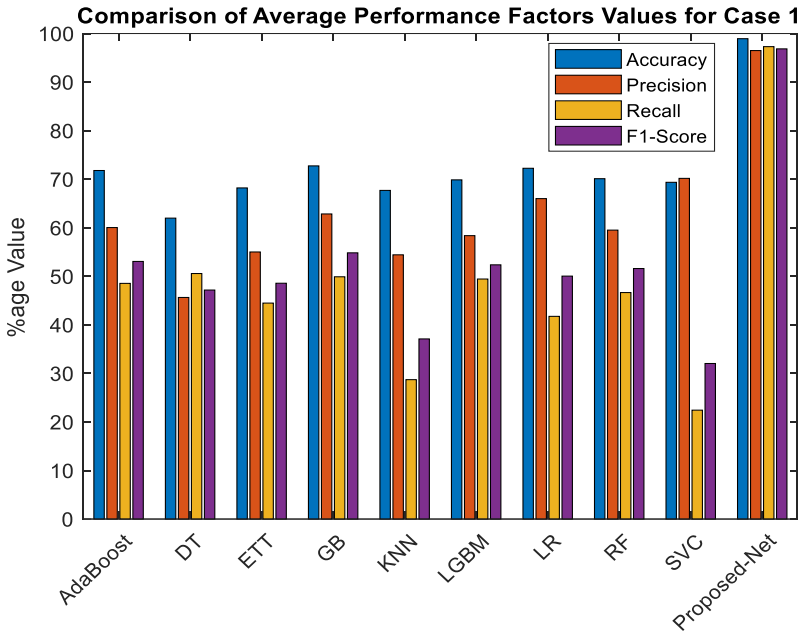

Fig 8. Comparative resultsof Case 1 for multi-stage Disease Classification

Table 5: Comparative Analysis for Case 1 Multi-stage disease classification [44]

Parameter	AdaBoost	DT	ETT	GB	KNN	LGBM	LR	RF	SVC	ProposedNet
Accuracy	71.79	61.98	68.2	72.74	67.69	69.86	72.25	70.1	69.36	98.93617021
Precision	60.04	45.64	55.01	62.84	54.42	58.37	66	59.51	70.17	96.49165875
Recall	48.54	50.57	44.48	49.9	28.71	49.44	41.75	46.65	22.43	97.29803998
F1-Score	53.06	47.17	48.57	54.83	37.1	52.36	50.04	51.6	32.04	96.84117278

Case 2 (Bagging Ensemble Learning Technique)

In second case, bagging ensemble learning technique is implemented to analyse the performance of proposed approach for determining different stages of disease in patients using CPD dataset. The comparative graph is demonstrated in Fig 9. From the given graph, it is clear that proposedNet model continuously outperforms standard models by achieving accuracy of 98%, precision of 96%, recall of 97% and F1-Score of 96% respectively. However, this is not the case in standard models wherein highest accuracy was attained by AdaBoost (73%), which is around 25% less than proposed model. Likewise, traditional models were able to generate highest precision, recall and F1-Score of 68%, 50% and 55% by AdaBoost model, which are still far less than scores obtained by proposed approach. The precise values obtained for each parameter is mentioned in Table 6.

Table 6: Comparative Analysis for Case 2 Multi-stage disease classification [44]

Parameter	AdaBoost	DT	ETT	GB	KNN	LGBM	LR	RF	SVC	ProposedNet
Accuracy	73.21	69.15	71.05	71.54	69.37	70.81	72.01	72.02	68.39	98.93617021
Precision	68.28	58.06	65.23	66.56	59.01	65.67	67.23	66.37	60.33	96.49165875
Recall	50.39	44.34	43.33	49.38	31.13	49.62	41.75	43.09	16.24	97.29803998
F1-Score	55.73	51.55	53.12	55.51	41.82	54.1	49.06	54.18	29.15	96.84117278

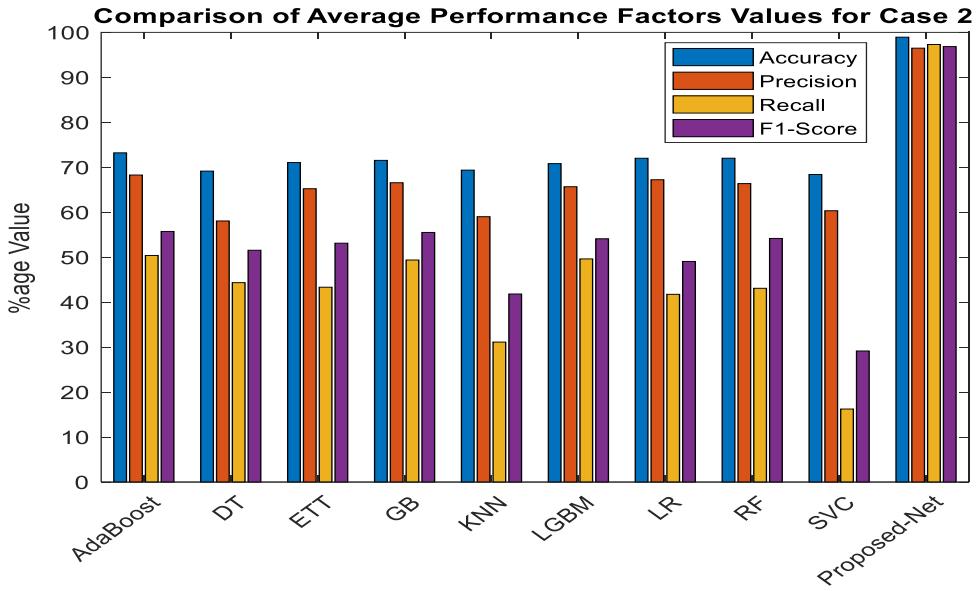

Fig 9. Comparative results of Case 2 for multi-stage Disease Classification

Case 3 (Boosting Ensemble Learning Technique)

In the third and final case of proposed work, we have examined and compared proposed model's effectiveness with several previous models by implementing Boosting ensemble learning technique on CPD dataset, (as shown in Fig 10). After closely analysing the graphs, it is clear that ProposedNEt model attains highest accuracy of 98% while as, it was only 66% in AdaBoost, 67% in GB and 67% in LGBM models. Similarly, precision rate was only 50%, 52% and 53% in these models (AdaBoost, GB and LGBM), while as proposedNet model attained 96% precision score for determining different stages of liver disease in patients. Also, proposedNet model attained highest recall and F1-score of 97% and 96% in this case to outperform traditionally best performing LGBM model respectively. The comparative results are recorded in Table 7.

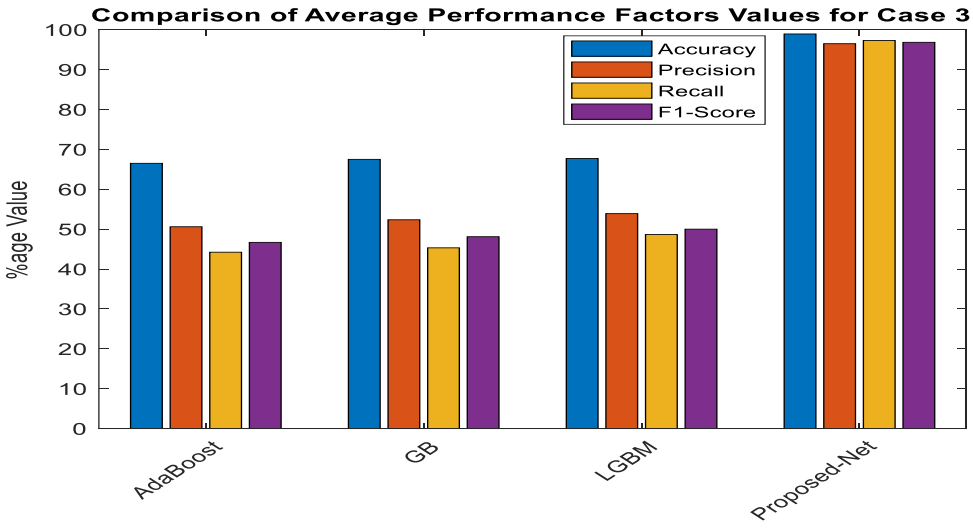

Fig 10. Comparative results of Case 3 for multi-stage Disease Classification

Table 7: Comparative Analysis for Case 3 Multi-stage disease classification [44]

Parameter	AdaBoost	GB	LGBM	ProposedNet
Accuracy	66.51	67.5	67.72	98.93617021
Precision	50.6	52.35	53.89	96.49165875
Recall	44.22	45.32	48.65	97.29803998
F1-Score	46.69	48.1	50	96.84117278

Observations

After analysing the given graphs and tables, it is observed that during binary classification, standard RF was giving good results for all metrics among the algorithms provided. Therefore, in order to validate supremacy of proposed approach, we compared its results for all metrics with standard RF model. The proposed model improves accuracy rate by around 9.059% when compared with best performing RF model. Similar trend is observed for other parameters in proposed model wherein an improvement of 9.186% was observed for AUC, 9.294% for Precision, 7.7% for recall and 4.938% for F1-Score respectively.

Similarly, for multi-stage disease classification, proposedNet approach outperformed all conventional models to achieve an accuracy of 98.9% for case 1, 2 and 3, showing an improvement of around 26.65% than LR (in Case 1) and 25.69% than AdaBoost (in case 2). Moreover, the proposed model showed an accuracy improvement of 31.18% for case three wherein LGBM had accuracy of 67.72%. In addition to this, proposed approach continuously outperformed conventional models in terms of precision, recall and F1-Score as well to show its supremacy for effectively determining stage of liver disease in patients. These results prove that by employing effective feature selection technique along with tuned classifier, liver disease can be detected easily at earlier stages.

CONCLUSION

This study presents a significant advancement in the field of liver disease detection by proposing an optimization-based Feedforward Neural Network (FFNN) model for accurately classifying liver-infected and non-infected patients as well as determines the stage of disease. Using MATLAB software, the efficiency of proposed approach is examined and validated on ILPD and CPD datasets. Results obtained showcased that proposed model achieves an impressive accuracy of 97.159%, while as, it was only 55% in Logistic, 67% in KNN, 88% in RF, 67% in SVM, 83% in MLP and 82% in ensemble learning model for binary classification. Moreover, the high AUC score of 98.016% attained by proposed model along with precision of 94.624%,recall of 100%, and F1-score of 97.238% during binary classification on ILPD dataset proves its superiority over other similar models.Additionally, proposedNet approach proved out to be effective for multi-stage disease classification as well wherein it achieved an accuracy of 98.9% for non-ensemble learning, bagging ensemble learning and boosting ensemble learning techniques. Moreover, proposedNet method also attained higher precision, recall and F1-Score rate of 96.4%, 97.2% and 96.8% in all three cases to prove its effectiveness. This high accuracyand precision scoreshighlight the potential of our approach in clinical applications.

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