Deep Ensemble Stacked Technique for the Classification of Liver Disease using Artificial Neural Networks at the Base Level and Random Forest at the Meta Level

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ABSTRACT
Liver is the most noticeable and metabolically active organs in the human body. Damage to this organ might result in liver failure and a loss of life. The early detection of liver infection is critical for effective therapy. The main goal of the research is to identify liver illness using machine learning and deep learning classification algorithms. The proposed "Deep ensemble stacked model" is implemented on the “Indian liver Patient Dataset”. An attempt is made to analyze the data through various pre-processing and visualization techniques to understand which factors affect the liver. An artificial neural network is used as the model's primary training and testing tool. The new training set is created for the meta-level consisting of base-level predictions. The random forest classifier is used at the meta level which serves as a meta classifier for the final prediction. The deep ensemble stacked model performed better than the most recent research with 98.29% of classification accuracy, 97.43% of precision, 100% of recall rate, and 98.69% of f1-score. To evaluate the effectiveness of the suggested approach, the outcomes are also contrasted with well-known machine and deep learning models.

Keywords
Deep ensemble stacked model, Liver disease, meta-classifier, base-classifier, Indian Liver Patient Dataset, Pre-processing.

1. INTRODUCTION
An essential part of the human body is the liver, which aids in the digestion of protein, fat, and carbs as well as other vital life-sustaining processes like detoxification and vitamin storage. The structure of the liver is impacted by a variety of disorders, including cirrhosis, cancer, hepatitis, and fatty liver. These may cause major health problems, and if the appropriate steps are not done on time, they may even result in death [1]. The World Health Organization (WHO) ranks liver cancer as the second most common cause of cancer. Hepatocellular carcinoma (HCC) is the most common kind of primary liver cancer and the sixth most common cancer [2]. In addition, secondary tumors frequently develop in the liver. Software created for the healthcare industry is essential for providing effective services to doctors, which allows for improved patient care in the end. Effective algorithms may help with a variety of tasks, including illness prediction based on patient history, image processing for medical imaging, etc. [3].

To achieve this, machine learning has drawn a lot of attention from researchers and has been applied globally in many different areas. Machine learning (ML) has demonstrated its value in the field of medicine, where it has been applied to manage various emergencies [17]. On the other hand advanced machine learning model known as deep learning(DL), has recently surpassed traditional machine learning approaches by a large margin in the disciplines of speech recognition, image identification, and natural language processing [18]. Hence, ML and DL have made considerable advances in recent years and it is now being used in the medical sector for tasks like disease screening and intelligent diagnosis. The use of ensemble learning techniques for predictive modeling has lately gained prominence. The success of employing various learning methods to improve overall accuracy of predictions [31]. Many areas, including healthcare, economics, manufacturing, and bioinformatics, have successfully used ensemble stacking techniques.

This study uses the ensemble stacking method to forecast liver disease. The paper makes three contributions. First, ANN and random forest are provided as base and meta-classifiers. Second, the accuracy, precision, recall, and f1-score of the ensemble classifier's output are evaluated. The findings are then contrasted and analyzed with cutting-edge research conducted on the Indian liver patient dataset. [11].

2. LITERATURE REVIEW
Several methods for diagnosing liver illness have been created by researchers utilizing machine learning and deep learning techniques. Here is a brief summary of current research.

In their work, Rehman et al. [4] focused on the utilization of clinical data for the prediction of liver disease and alternative ways of showing this data through analysis. Six well-known machine learning algorithms were used to investigate and predict liver disease. Among these, linear regression has the best accuracy (75%). Fazle et al. [5] have conducted experiments on linear regression, decision trees, random forest, and extra tree in order to predict liver illness. The outcome of these algorithms are compared based on accuracy, ROC, precision, f1 score, and recall. They have got highest accuracy of 92.19% on boosting extra tree. They eliminated the irrelevant data based on the Pearson correlation coefficient. Mounitha et al. [6] evaluated the performance of several machine learning approaches such as logistic regression, XGBoost, random forest, AdaBoost, support vector machine, KNN, and decision tree. They observed that a random forest tree is the best algorithm for diagnosing liver disease, with an accuracy of 83.70%. Alaa et al. [7] used the JustNN tool to create and develop an artificial neural network to predict whether or not a person has liver disease. The model's performance is evaluated using the Indian liver patient dataset [11]. The simplest static neural network model has a 99% accuracy.

The MCNN-LDPS technique, proposed by Jayalakshmi et al.

[8], offers higher outcomes in terms of precision and accuracy. According to this study, MCNN-LDPS achieves 4.05% more accuracy, 4.22% precision, 21.23% F-measure, and 34.26% recall. For the performance study, this research methodology was contrasted with the current multilayer perceptron neural network (MLPNN).

Maria et al. [9] have made an analysis and research to predict liver disease. In their study they have used a variety of approaches including median imputation for missing values, label encoding to turn categorical data into numerical data, duplicate values are removed and outliers are removed by using isolation forest. A genetic algorithm and XGBoost are used to determine the best features for predicting liver illness.

Jagadeep et al. [10] used custom-built software to predict disorders of the liver using several classifiers on a dataset of liver patient illnesses. The dataset was processed and distributed using feature selection processes and the 10-fold cross-validation testing option on the WEKA tool. After implementing several classifiers, the proposed work is compared in terms of execution time and accuracy with and without feature selection processes.

3. ENSEMBLE STAKING MODEL

The ensemble stacked model is incorporated into the proposed model. Ensemble techniques use many classifiers to provide better prediction efficiency than a single classifier. The ensemble model's main idea is to combine a set of weak learners to produce a powerful learner, hence enhancing the model's accuracy [16]. Using the stacking ensemble learning approach, a meta-classifier may merge numerous classification models. A meta-classifier is trained using several classifier predictions, also known as level one or base-classifiers. Any classifier can serve as a meta-classifier [19]. A meta-learner attempts to find out how to best combine the input predictions to make a greater output prediction by utilizing the predictions as features and the ground truth values as the target, as illustrated in the Fig 1.

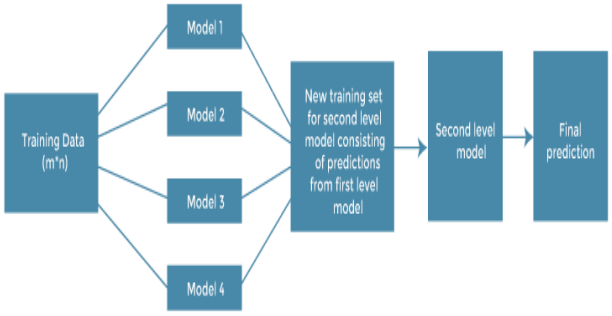

Fig 1. General structure of stacked ensemble model

The purpose of the stacking technique is to solve a machine-learning problem by combining different model types that can learn to some extent rather than learning the full problem space. These models may be used to create intermediate predictions, and then a new model that can learn based on the intermediate predictions can be added, with the final model layered on top of the intermediate models and trained using the intermediate predictions

4. METHODOLOGY

The strategy used in this work is broken down into six key steps, which are shown in Fig 2. Data collection is the initial phase. The collected data is then pre-processed and divided into training and testing data. The model is then developed by adding training data layers. Utilizing testing data, the model is assessed. The final step compares a model to state-of-the-art studies. These stages are detailed in the following subsections.

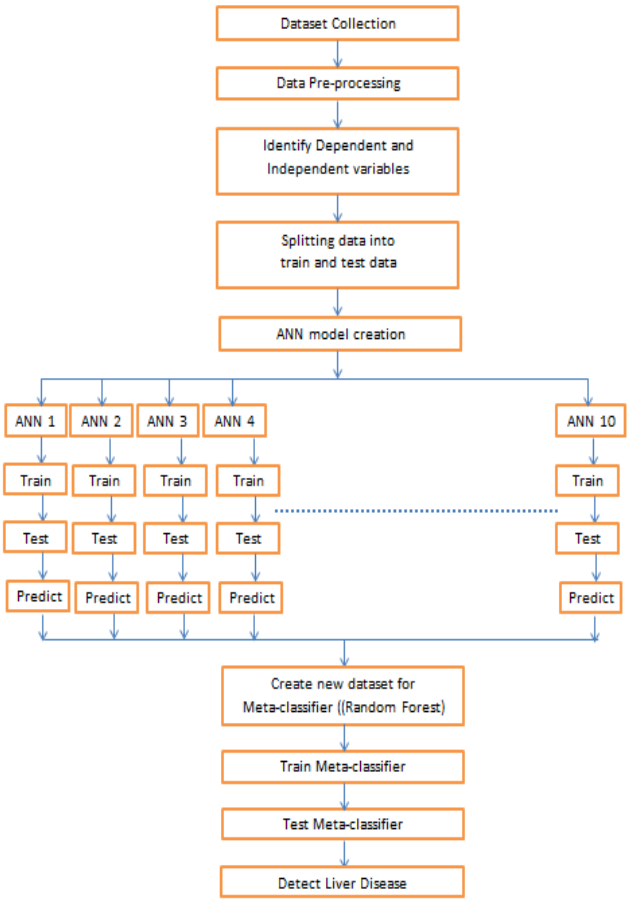

Fig 2. Flowchart illustrating the proposed approach

4.1 Data Source

To meet the goals of the proposed study, 583 examples with eleven distinct attributes are retrieved in CSV format from the UCI Repository utilizing the ILPD (Indian Liver Patient Dataset) [11]. The attribute "outcome" is used to characterize the disease, and the values "1" and "2" represent the disease's presence and absence, respectively. The features and values of the liver disease database are described in Table 1. The database contains 167 occurrences of non-liver disease and 416 instances of patients with liver disorders.

Table 1. ILPD dataset description [11]

Sl. No	Name of the Attribute	Type of the attribute	Description of the attribute
0	Age	Numeric	Patient's Age
1	Gender	Nominal	Patient's Gender
2	Total_Bilirubin	Numeric	Patient's total bilirubin level
3	Direct_Bilirubin	Numeric	Patient's direct bilirubin level
4	Alkaline_Phosphotase	Numeric	Patient's ALP enzyme level
5	Alamine_Aminotransferase	Numeric	Patient's SGPT level
6	Aspartate_Aminotransferase	Numeric	Patient's SGOT level

7	Total_Protiens	Numeric	Patient's total proteins level
8	Albumin	Numeric	Patient's albumin level
9	Albumin_and_Globulin_Ratio	Numeric	Patient's albumin and globulin ratio
10	Outcome (Dataset)	Numeric [1, 2]	Patient's Status of liver disease

4.2 Pre-processing

To increase the model's performance and training stability, following pre-processing techniques like missing value replacement, converting categorical data into numerical data, normalizing data, removal of outliers, etc.

- Albumin and Globulin Ratio had four null values, which were replaced by the mean value of its occurrences, as shown in Fig 3.

```
df.isnull().sum()
```

```
Age                         0
Gender                      0
Total_Bilirubin             0
Direct_Bilirubin            0
Alkaline_Phosphotase        0
Alamine_Aminotransferase    0
Aspartate_Aminotransferase  0
Total_Protiens              0
Albumin                     0
Albumin and Globulin Ratio  4
Dataset                     0
dtype: int64
```

```
avg=df['Albumin_and_Globulin_Ratio'].mean()
df=df.replace(to_replace = np.nan, value = avg)
```

```
df.isnull().sum()
```

```
Age                         0
Gender                      0
Total_Bilirubin             0
Direct_Bilirubin            0
Alkaline_Phosphotase        0
Alamine_Aminotransferase    0
Aspartate_Aminotransferase  0
Total_Protiens              0
Albumin                     0
Albumin_and_Globulin_Ratio  0
Dataset                     0
dtype: int64
```

Fig 3. The null values and their occurrences are replaced with the mean value

- Categorical data is translated into numerical data. The Fig 4 and Fig 5 represent the transformation of 'gender' feature from categorical to numerical respectively

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Ar
0	65	Female	0.7	0.1	187	
1	62	Male	10.9	5.5	699	
2	62	Male	7.3	4.1	490	
3	58	Male	1.0	0.4	182	
4	72	Male	3.9	2.0	195	

Fig 4. Gender data as categorical data before numeric transformation

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase
0	65	0	0.7	0.1	187
1	62	1	10.9	5.5	699
2	62	1	7.3	4.1	490
3	58	1	1.0	0.4	182
4	72	1	3.9	2.0	195

Fig 5. After translation, gender data is represented numerically

- Normalization is performed to bring the data into the same scale. To standardize the range of functionality of the input dataset, Standard Scalar is a crucial technique that is applied as a preprocessing step before constructing machine learning models. Fig 6, Fig 7 demonstrates data before and after normalization respectively.

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase
0	65	0	0.7	0.1	187
1	62	1	10.9	5.5	699
2	62	1	7.3	4.1	490
3	58	1	1.0	0.4	182
4	72	1	3.9	2.0	195

Fig 6. Data before normalization

	0	1	2	3	4	5	6	7	8	9
0	0.301754	0.56909	0.219835	0.347050	0.739591	-0.076322	-0.204795	0.446231	-0.207163	-0.807889
1	-0.191208	0.56909	5.194443	4.855197	0.002215	-0.096581	0.050788	-1.195430	-1.345882	-1.134320
2	-0.376068	0.56909	0.673791	0.612235	-0.310611	0.536534	2.670513	-2.289872	-1.851979	-0.807889
3	-1.608471	0.56909	-0.309782	-0.221204	-0.475961	-0.359957	-0.281470	1.358266	1.817226	1.150694
4	-0.560929	0.56909	-0.253037	-0.334855	-0.355300	-0.243464	-0.255912	0.537435	0.931556	0.824264

Fig 7. Data after normalization

- Data has been represented graphically to provide some fundamental understanding of the target feature (label) based on some of the features.
- According to Frequency distribution of age as shown in the Fig 8, middle-aged adults are the most severely affected, and liver diseases can affect people as old as 60 to 80.

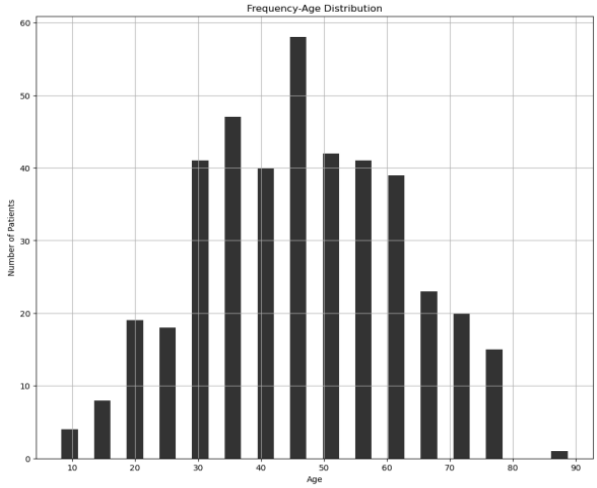

Fig 8. Frequency distribution of age

- The outcomes in Fig 9 indicate that the Albumin to Globulin ratio is greater in the non-patient group, implying that liver patients have a lower Albumin to Globulin ratio than non-diseased persons. As a consequence, it has been determined that this variable is important.

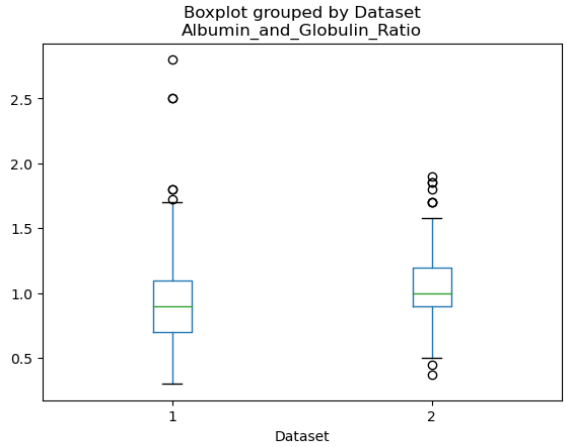

Fig 9. Box plot grouped by Dataset and Albumin and Globulin ratio

- Direct and total bilirubin levels in the male and female groups were compared. The visualization from Fig 10 shows that increasing Direct Bilirubin promotes liver disease since it is obvious that at some point there are more patients and more Direct Bilirubin present at the same time. These elements could be very important in liver illness.

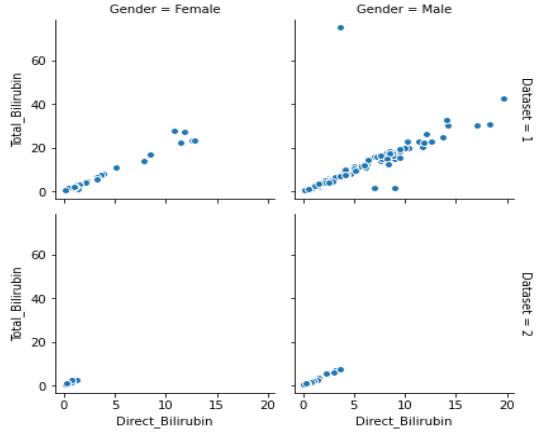

Fig 10. Comparison of direct and total bilirubin in male and female

- Fig 11 visualizes the high correlation between albumin and total protein

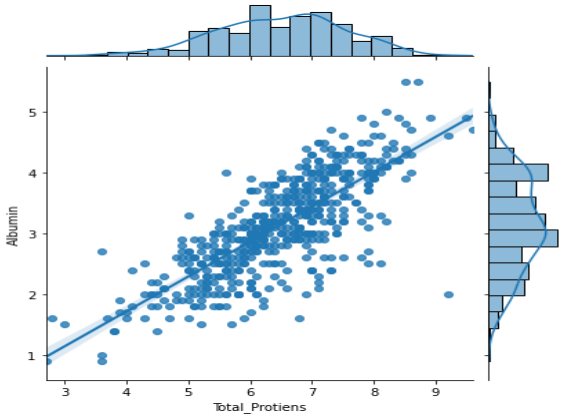

Fig 11. Relation between Albumin and Total Protein

4.3 Splitting of data

After the feature portion, the dataset is arbitrarily split into training and testing sets in an 80:20 ratio. The testing set comprises 117 samples, whereas the training set has 466 samples. To control the unpredictability of the model, the hyper parameter random state is used.

4.4 Ensemble stack model construction

In the deep ensemble stacked model ANN (Artificial neural networks) is used as base learners. An established machine learning method known as ANN was influenced by the biological neural network of the human brain [21]. Stacking and other ensemble learning algorithms that learn how to incorporate predictions from ensemble members are sometimes referred to as meta-learning algorithms. The final prediction is obtained by using the random forest classifier as a meta learner. A variety of tree predictors are put together using the decision tree-based classification method known as Random Forest. The following algorithm provides the foundation for building a deep ensemble stacked model for categorizing liver disease.

Liver disease classification algorithm:

Step 1: Collection of ILPD dataset

Step 2: Pre-processing data using preprocessing techniques

Step 3: Identifying dependent (features) and target(label) variable

Step 4: Create an ANN model

Step 5: Divide data into train data and test data

Step 6: Train and save the model

Step 7: Test the model

Step 8: Repeat step 5 to step 6 to train and test required number of models

Step 9: Create new dataset from the predictions of ANN models

Step 10: Train the meta classifier

Step 11: Test the meta classifier to make prediction

4.5 Evaluation of deep ensemble tacked model

The ensemble model is evaluated using the test dataset. The model's performance is measured using the f1-score, accuracy,

precision, and recall.

4.6 Comparison of deep ensemble stacked model

The procedure is completed with a comparative study of the full ensemble model, which is used in this work with state-of-the-art techniques.

5. RESULT AND DISCUSSION

In this part, the deep ensemble stacked model's performance is examined. The method is implemented on a computer running the 64-bit Windows 10 operating system with an Intel Core i3 CPU and 4GB of RAM. The implementation of the research methodologies in the Jupyter Notebook uses the Python programming language (version 3.9.7). To get unbiased results and training stability, null values are removed, categorical data is converted into numerical, and normalization is performed. Following feature selection, the dataset is randomly divided into training and testing sets in an 80:20 ratio. The training set has 466 samples, whereas the testing set contains 117 samples. The unpredictability of the model is controlled by the hyper parameter random state. Accuracy, precision, recall, and F1-measure are some of the performance indicators used in the proposed study. The Fig 9 depicts the performance of ANN models which is used as a base learner in the deep ensemble stacked model.

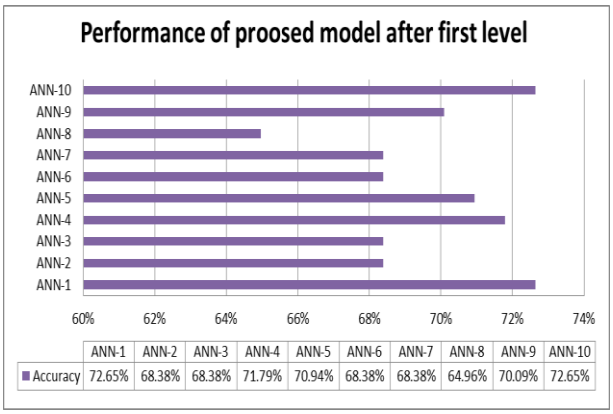

Fig 12. Performance analysis of base (ANN) models

From the above Fig 12, it is noticed that the average accuracy of all the ten ANN models is approximately 70%. To improve classification accuracy these results are inputted to meta-classifier. The performance of the deep ensemble stacked model after training with a meta-classifier is shown in the Fig 13.

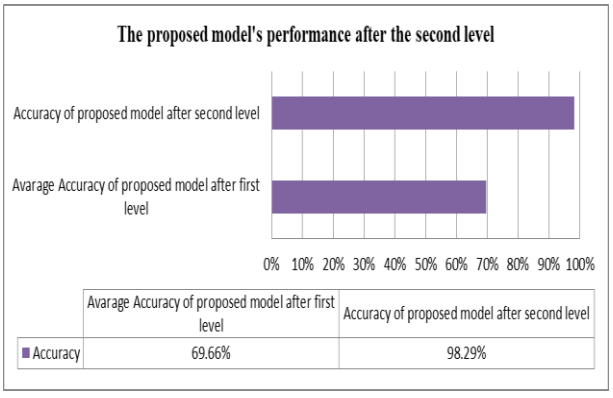

Fig 13. Performance of deep ensemble stacked model at first and second level

Table 2 also provides information on the accuracy, precision, recall, and f1-score of the deep ensemble stacked model

Table 2. Results obtained for the proposed deep ensemble stacked model

Performance measures	Percentage
Accuracy	98.29%
Precision	97.43%
Recall	100%
F1-score	98.69%

Table 2. depicts that there is a 28% of huge improvement in classification accuracy. These findings are contrasted with those of several machine learning and deep learning classification methods, which are listed in the Table-

Table 3. Performance evaluation of the suggested deep ensemble stacked model against cutting-edge research

Reference	Algorithm	Accuracy (%)
Al Telaq et al. [25]	KNN+RF+SVM	88
Veena et al. [26]	K-nearest neighbor	70.68
	C5.0	71.43
	K-mean	69.47
	Naïve-bayes	66.17
	Random forest	72.18
	C5.0 Boosting	75.19
Hossen et al. [27]	Linear regression	72.89
	Decision tree	81.32
	Multi layer perceptron	60.24
	Random forest	86.14
	Artificial neural network	75.61
	K-nearest neighbor	65.52
Jagdeep et al. [28]	Linear regression	74.36
	Naïve-bayes	55.9
	Sequential minimal optimization	71.36
	IBk	67.41
	J48	70.67
	Random forest	71.87
Adil et al. [29]	Linear regression	74
	Artificial neural network	71.59
	C 4.5	68.69
	K-nearest neighbor	62.89
	Support vector machine	58.26
	Naïve bayes	56.52
Rohini A. Bhusnurmath and	Linear regression	86.9

Shivaleela Betageri [30]	Gaussian naïve bayes	82.6
	Random forest	92.69
	Artificial neural network	79
	Convolution neural network	73
Proposed Model	Deep Ensemble Stacked Model	98.29

It is observed from Table 4 that the projected deep ensemble stacked method performs better than other methods in the literature [14,15,16,17,18,19] in terms of classification accuracy.

6. CONCLUSION

The stacking classifier algorithm was used in this work to forecast liver illness in a patient. To diagnose liver illness using a single classifier, various research has been done in the past. However, a deep ensemble stacking classifier is used in this work to categorize liver illness. For effectively predicting samples of liver illness, model performance is assessed using metrics including accuracy, precision, and recall. The model is evaluated in comparison to other deep learning and machine learning classifiers. The deep ensemble stacked model outperforms existing current techniques for liver disease classification and prediction. The reason for this is that deep ensemble stacking classifier's greatest performance in terms of classification accuracy. Additionally, the suggested model used ANN as a basic classifier, which led to successful results for the model's usage of random forest as a meta-classifier. This is how the model was able to attain this accuracy. It suggests that using deep learning and machine learning models in an ensemble improves classification accuracy.

7. ACKNOWLEDGEMENT

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