RESEARCH PAPER

A Hybrid Residual Network-Based Deep Learning Framework for Intelligent Liver Disease Prediction

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Abstract:

Liver disease is a huge health problem because by the time people are diagnosed, they may already have the disease in an advanced stage. Routinely available clinical and biochemical parameters can be used to predict early, to help facilitate timely screening, referral and management. In this study, a deep learning framework based on Hybrid Residual Network was proposed, which is hybrid liverNet, known as HRN-LiverNet, for predicting liver diseases intelligently. The framework adopted adopted a dataset similar to Indian Liver Patient Dataset (ILPD) that included demographic and laboratory data such as age, gender, total bilirubin, direct bilirubin, alkaline phosphatase, alanine aminotransferase, aspartate aminotransferase, total proteins, albumin, and albumin/globulin ratio. Data preprocessing, handling missing values, converting categorical variables into numeric, applying Robust Scaling, correcting class-imbalances, feature expansion, dense blocks with Residuals, global feature aggregation and Sigmoid Based Binary Classification were the steps in the proposed system.

The experimental results demonstrated that the proposed HRN-LiverNet model effectively outperformed the traditional machine-learning algorithms in terms of the predictive performance and a conventional deep neural network. The model obtained an accuracy of 94.2%, sensitivity of 95.6%, specificity of 91.8%, F1-score of 95.1%, and AUC of 0.972. The aforementioned factors—residual connections, class balancing, dropout, and batch normalization are all confirmed as crucial to the ablation analysis. The removal of residual blocks decreased the performance of the model and removal of class balancing lowered the model's sensitivity and raised the chance of missed liver disease cases. The results indicated that the proposed hybrid residual learning model has the ability to learn the nonlinear relationship between clinical biomarkers and it can be used as a clinical decision-support model in liver disease prediction.

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1. Introduction

Liver disease [1] is one of the major health problems worldwide because it involving many different forms of diseases such as viral hepatitis, Metabolic dysfunction-associated steatotic liver disease, cirrhosis, hepatocellular carcinoma, Drug induced liver injury and Alcohol Related liver damage [2]. The liver has a number of important metabolic, detoxification, digestive, immune and protein-synthesising roles and its progressive damage can impact on several physiological systems. Liver diseases in recent reviews, have been reported to cause death in almost 2 million people per year worldwide and are rising due to viral hepatitis, alcohol exposure, obesity, diabetes and metabolic liver diseases.

Routine laboratory test detection is important clinically because numerous liver disorders are undiagnosed in early stages and manifest at a later stage when significant liver damage has been completed [3]. Current screening is based on liver function tests, serum biomarkers, imaging, and in some cases also on biopsy; all methods of screening have specific limitations. Disease un-specific biomarkers may be present, between observer variability when imaging, and biopsy is still an invasive technique and not appropriate for population screening. There have been more recent reviews which focus on the diagnostic role of AI [4] and that traditional diagnostic concepts have some restricted ability to detect and differentiate certain diseases, particularly in early disease and in being applied to a heterogeneous group of patients.

AI is of greater relevance in predicting liver disease [5] because it can analyse demographic, laboratory, imaging and clinical data and identify unseen associations or trends that aren't apparent by manually sifting through these data. To date, machine-learning [6], [7] and deep-learning [8] techniques have been applied to early screening, risk stratification, fibrosis assessment, steatosis grading, detection of hepatocellular carcinomas, prognosis estimation, and planning of treatment. These are all findings from a 2025 research [9] wherein AI was found to assist in early screening, risk assessment, diagnosis, treatment selection, and long follow-up periods for hepatology-related articles, as well as a 2025 imaging review, which explained how AI can be useful for fibroscan staging, steatosis estimation and liver lesion detection.

The proposed liver disease prediction framework in this study takes Indian liver patient dataset (ILPD) [10] as the reference dataset. This is a patient dataset consisting of 583 patient records, of which 416 patients have liver disease and 167 patients do not have liver disease. These consists of 10 clinical variables: age, sex, total bilirubin, direct bilirubin, total proteins, albumins, albumin globulin ratio, SGPT, SGOT and alkaline phosphatase. The dataset would be suitable to be used for binary liver disease prediction as the important demographic and biochemical parameters that can be found in routine clinical practice were included.

1.1. Motivation

The research is motivated by three practical needs: Here is the need for availability of a low cost method of prediction that won't require any costly imaging or invasive biopsy. Second, most common available machine-learning models suffer from limited capacity to model complex nonlinear relationship between liver biomarkers. Specifically, if a medical dataset contains few data items and is highly imbalanced, then the desired architecture must learn discriminative patterns without being rapidly overwhelmed with overfitting each dataset. As a result, this paper presents a hybrid residual network-based deep learning framework, HRN-LiverNet, which integrates the dense features, class balancing, residual learning, batch normalization, dropout and sigmoid-based classification.

1.2. Research Paper Organization

The remaining paper is organized as follows. The literature review is provided in Section 2 and research gap identified. Details of the dataset, preprocessing strategy, and proposed architecture of HRN-LiverNet is explained in Section 3. All experimental setup, the training of the model and the evaluation metrics are described in Section 4. The comparative result, ablation analysis, graphical interpretation of performance, the findings, and discussions are provided in Section 5. The paper on the hybrid intelligent prediction model for liver disease is concluded in section 6.

2. Literature Review

Data driven Machine learning and Deep learning methods have replaced the conventional statistical prediction methods in liver disease prediction according to recent literature. Manual selection of thresholds or linear relationship between laboratory values and patient characteristics is usually the method of modeling, whereas AI models may be able to uncover nonlinear interactions between laboratory values and patient characteristics. In their 2025 review, Gao and Duan [11] pointed out that leveraging AI to help predict, diagnose, stratify, and support treatment of liver diseases is increasingly common in the field and will be more prevalent as clinical data grows more complex and intensive.

There has been significant use of machine-learning models to structured clinical liver datasets. According to a study [12] published in the Journal of BMC Medical Informatics and Decision Making in 2024, machine learning could be used to find patterns in patients' demographics, lab results, medical history and other clinical variables that link to liver disease. The same study lacked common classifiers like support vector machines, random forests, artificial neural networks, etc., which are available for the prediction of liver disease, along with bagging and boosting methods and stacking approach.

One of the most commonly used benchmark datasets for the classification of liver diseases has been the Indian Liver Patient Dataset [13]. It has biochemical characteristics indicative of hepatocellular damage, cholestasis and liver synthetic function. The associated class imbalance is clinically and computation relevant since more liver disease suffers exist than non-liver disease controls. This disproportion may lead to a poor performance on the minority examples and the control examples, unless some sampling, weighting or threshold optimisation is done [14]. Few research works [15], [16] are based on traditional machine-learning models for data sets similar to ILPD. Logistic regression is easy to interpret but likely to fail when there are any nonlinear feature relationships. Support vector machines can be used to learn a nonlinear boundary, but may need to select the kernel and SVM's parameters carefully. Usually, random forest and gradient boosting models work better, as they are able to capture inter-relationships between features

and non-linearities. Yet, they remain heavily reliant on the preprocessing, feature selection, class distribution, and hyperparamters tuning. An ensemble-learning study [17] carried out in 2024 validated the data quality, feature selection and model parameters to impact the performance of liver disease prediction.

Several weak/medium learners are combined to enhance the stability and generalization in predicting liver disease; ensemble learning has gained popularity in this context [18]. Random forest, gradient boosting (sequential error correction), and stacking (stacking multiple classifiers to form a meta-model) are several examples of bagging methods that reduce variance, improve sequential error correction based on boosting, and combine multiple classifiers to create a meta-model, respectively. The 2024 BMC study indicated that ensemble models are becoming popular for disease prediction and found the results of applying different ensembles to the liver disease prediction problem using clinical data. Predicting liver diseases has been expanded to be modelling by deep learning [19]. In contrast with shallow classifiers, deep NN networks have the ability to learn several layers of feature representation. The significance of this is for liver disease as these liver enzymes (AST, ALT, alkaline phosphatase, and albumin) may have nonlinear interactions with each other and with the other biomarkers of liver disease (bilirubin and albumin/globulin ratio). Deep learning has been recently found to be beneficial in addition to tabular clinical prediction, for imaging-based fibrosis staging, steatosis grading, cirrhosis detection and HCC classification.

The relevance of the residual neural networks [20] is in the context of study of the training degradation in deeper networks. The original form of residual learning added shortcuts to skip any one layer or multiple layers to help the model learn deeper. Residual Dense Blocks are used in the model HRN-LiverNet for adapting the dense blocks for clinical data format tabular, not for image format. This is accomplished by these shortcut connections that help preserve clinically useful information, as well as the ability of the network to learn deeper nonlinear transformations. AI use is also starting to move into clinical use in hepatology [21], with recent advances in the field. The European Medicines Agency (EMA) [22] approved the use of an AI tool in clinical trials to assess the severity of MASH, AIM-NASH, in 2025, while in 2024, the FDA [23] qualified AIM-NASH for liver disease drug development, as reported by Reuters. They highlight the potential for AI to go beyond theoretical research and into the realm of regulated clinical and pharmaceutical applications.

Although there has been progress, many limitations in current studies of prediction of liver disease exist [24]. The high accuracy rates reported for many models are accompanied by weak explainability capabilities, limited external validation, minimal ablation analysis of the model, and limited capabilities to deal with a class imbalance. Few works [25]-[27] have been carried out for comparing classifiers without reporting their performance justifications for using the particular architecture suitable for the clinical laboratory data. Some work on the AI of imaging; that might not be available in low resource areas. Hence, it's still necessary to create a systematic deep learning platform that utilizes regular biochemical data and supports imbalance, deep feature learning, and component-wise performance impact reporting.

2.1. Research Gaps Identified

This paper work is trying to solve the problem that there is no clear hybrid residual deep-learning framework for routine tabular clinical data-based liver disease prediction. Many previous machine-learning methods [28]–[30] have involved shallow classifiers or ensemble models, while many studies for deep learning neglect utilization of residual learning for structured variables related to liver function. This gap is filled by the proposed HRN-LiverNet which integrates powerful preprocessing, class balancing, dense feature expansion, residual blocks, dropout, batch normalization, feature aggregation, and sigmoid based classification layer. The design here's to enhance the prediction rates of accuracy, sensitivity, specificity as well as to enhance the robustness of the model whilst simultaneously retaining the input requirement to be meaningful for clinical screening.

3. Proposed Methodology

The proposed Hybrid Residual Network-Based Deep Learning Framework for Intelligent Liver Disease Prediction (HRN-LiverNet) is shown in figure 1. This architecture is based on a comprehensive prediction pipeline from clinical input features to a probability-based liver disease classification. A similar dataset appropriate for this kind of architecture is the Indian Liver Patient Dataset that consists of demographic and biochemical details like age, gender, bilirubin, alkaline phosphatase, aminotransferases, albumin, total proteins and albumin/globulin ratio. The mentioned variables are preprocessed, followed by deep feature learning layers, residual blocks, and finally, a sigmoid classifier to classify the patients as either having liver disease or not.

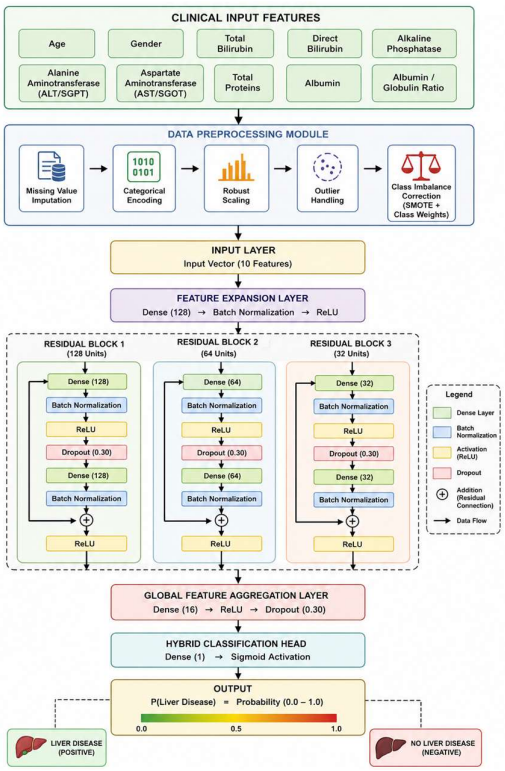

Figure 1. Proposed Hybrid Residual Network-Based Deep Learning Framework for Intelligent Liver Disease Prediction

3.1. Clinical Input Features Module

The clinical input features for liver disease prediction are included in the first module.The first module includes the clinical input features which relate to liver disease prediction. The parameters checked are the age, gender, levels of total bilirubin, direct bilirubin, alkaline phosphatase, alanine aminotransferase, aspartate aminotransferase, total proteins, albumin and the albumin/globulin ratio. They are easily available in routine liver function tests and basic patient record and makes the proposed framework feasible for early screening.

These features give useful clinical information regarding the functioning of the liver in a relatedLiver dataset, for instance, the Indian Liver Patient Dataset. The amount of bilirubin is a measure of how well the liver is functioning normally to remove bile pigments from the blood. The level of alanine aminotransferase (ALT) and aspartate aminotransferase (AST) are markers of hepatocellular damage. Albumin and Total protein indicates liver synthetic function and nutritional status.

This module is the first one of the system. The performance of these clinical features directly influences the performance of the deep learning model. When the input variables are incomplete, noisy or not very well scaled, that later network layers may learn unstable patterns. Hence the clinical input module is the base for the whole prediction framework.

3.2. Data Preprocessing Module

The second module is called data preprocessing module, which preprocesses the raw clinical data before it is fed to the neural network. Medical data sets are often class-imbalanced, included with outliers, inconsistent units, categorical variable and missing values. Therefore, it is necessary to put the raw data into a clean and model ready form, so it is called preprocessing.

In this model the missing values are dealt with appropriately by means of imputation. Laboratory values like bilirubin, enzymes, albumin or total proteins can be imputed by median values, as they are usually skewed. Categorical encoding is used to transform gender into numbers. Then robust scaling is used to make sure that numbers with a magnitude of several orders are not dominating numbers of a rather small magnitude.

This module also includes the treatment of outliers and class imbalance. Occasionally, the levels of liver enzymes can be very high in a patient so that the result can be an outlier. These values are carefully managed to not take the weight of the learning process. Class imbalance correction methods like SMOTE and class weighting can assist the model to learn the liver disease and non-liver disease class in a balanced way. This is significant because a significant number of liver disease data sets have more patients with liver disease than healthy controls.

3.3. Input Layer Module

Data pre-processing: The output of the data processor will be forwarded to the input layer of the network -a processed feature vector. The proposed structure is that the input layer has 10 nodes (corresponding to the 10 parameters in the data set). The nodes correspond to the clinical or biochemical characteristics. These features are given to the neural network as a vector (a tuple of numbers) in a structured representation.

The input layer does not have complex learning functions. Its main purpose is to transfer the processed patient information into the deeper layers of the model. For instance, a single patient's health

record might include values for children's age, gender, coded (as a numeric value instead of a text string), bilirubin levels, enzyme levels, levels of albumin, and the ratio of albumin to globulin. These values are all aggregated into one input vector which is meant to be the patient's clinical profile.

This layer is significant since it helps to maintain the structure of the tabular clinical data. The prediction of liver disease typically relies on a handful of clinically relevant blood laboratory tests, whereas image-based deep learning relies on thousands of pixels as inputs. Thus, the number of selected predictors should closely match with the number of features in the input layer and no dimensional mismatch should occur to avoid certain training errors.

3.4. Feature Expansion Layer

By mapping the original 10-dimensional input vector into a higher-dimensional feature space, the feature expansion layer transforms it. This is illustrated as a dense layer containing 128 neurons, then followed by a layer of batch normalization, and then ReLU activation. This is the layer that gives the model the ability to make more detailed depictions with less clinical data.

This module will be useful because relationships between liver function variables were often not linear. Bilirubin, AST, ALT, albumin or alkaline phosphatase, for instance, can exhibit different interactions in different patients. These interactions may not all be described by a simple linear model. The feature expansion layer facilitates an identification of hidden patterns that cannot be “viewed individually from the laboratory values”.

The key of batch normalization is to normalize intermediate activations during training in order to make it more stable. ReLU activation is nonlinear which enables learning of complex decision boundaries. Both these operations introduce the data for the more profound residual learning. This layer thus serves as a connection to the more sophisticated residual blocks.

3.5. Residual Block 1

The first Residual block has dense layers of 128 units, Batch Normalization, ReLU activation function, Dropout and Shortcut Connection. This block serves mainly to learn the (deep) feature interactions whilst maintaining the original transformed input with these added on in the form of residuals. This enhances the movement of information in the network.

Some patterns in liver disease prediction could be simple while others could be deep representation. As an example, if a bilirubin level is very abnormal, this will strongly indicate liver dysfunction; on the other hand, some modest changes in the levels of albumin, AST, ALT, and alkaline phosphatase may only be interpretable when all these tests are considered together. Residual Block 1 is used to encode these early nonlinear interactions.

Shortcut connection plays the most crucial role in the residual block. It lets the original input of a block pass through the dense transformations such that the original input is added to the output from the dense transformations. This minimizes the hazard of loss of information and vanishing gradients. This, in turn, enables learning of more subtle patterns and the retention of lower-level clinical cues that are helpful.

3.6. Residual Block 2

The second residual block is also a 64 unit block, and is used to keep refining the features again. The second block compresses and rearranges the learned information following the first block that has expanded the clinical representation. This helps the model pay attention to the important disease related patterns, and remove unwanted noises this way.

In a liver disease dataset, some variables might contain repeating information. For instance, there is a correlation between total bilirubin and direct bilirubin, and there is a correlation between AST and ALT, both of which indicate damage to liver cells. Residual Block 2 contributes to giving the model a sense of how these two sets of variables work together to affect the likelihood of liver disease. Can recognize that some associations of values may be more significant than singular abnormalities.

This block will prevent overfitting, by randomly stopping some of the neurons from firing in training. This is particularly true for medical data, which tend to be quite small. The advantage of batch normalization is to bring a stabilization effect during learning, and the advantage of ReLU activation is that it allows to learn in a nonlinear manner. The residual shortcut is also useful for keeping relevant information into the model while it learns more abstract representations.

3.7. Residual Block 3

The third Residual Block adds 32 and further compresses features. This is when the model has already acquired many levels of clinical representation. These representations are then fed into the third block for further converting them into

a small set of features relevant to disease before making the final classification.

This is a crucial block as deep learning models need to be both complex and generalized. Care must be taken to prevent overfitting on the training set if the model is too large at the end. The framework has been shrunk to 32 units, making it more simple to keep only the most relevant information for the prediction of liver disease within the network.

Gradient flow and gradient preservation are still supported in the residual connection in this block. In this way, if over the course of learning the size of the features drops, the model is able to learn and keep its responses steady. From a practical point of view, Residual Block 3 is useful to the architecture to generate a focused internal representation whose cases are likely liver disease cases, and whose cases are not likely liver disease cases.

3.8. Global Feature Aggregation Layer

The output of the residual blocks goes to the global feature aggregation layer which warps the learned features into a final condensed representation. For this module, a dense layer of 16 units, ReLU activation and dropout are used. This layer is a last summarization stage prior to classification.

This block is used to gather all the very crucial learned information from the residual blocks. The earlier layers could identify some simple relationships between the various lab values, and the deeper the residual blocks learn more abstract clinical patterns. The aggregation layer combines all these signals with lower dimensionality in order to process the data by a classifier.

We add dropout again to enhance generalization in this layer. This helps to avoid overfitting your model to a particular neuron or learning a pattern from the training set. This is crucial for any clinical prediction system—it needs to work on the set of patients that it is meant to predict on.

3.9. Hybrid Classification Head

The last and the most important section of a neural network is the classification head function.The classification head function is the last one of the neural network that makes decisions regarding its classification. It has a dense layer having 1 output layer neuron and a Sigmoid activation function. The last learned representation is passed through the sigmoid function which transforms the representation into a probability score in the interval [0,1].

This probability score is an indication of the accuracy of the model - what is the probability the patient does have liver disease. For instance, a probability of 0.87 would be a high predicted risk, and a probability of 0.18 would be a low predicted risk. This classification threshold may be adjusted for the clinical use. A lower cut-point can be employed for screening to minimize false “negatives”.

This module is referred to as hybrid because it uses a number of integrated features: preprocessing, feature expansion, residual learning, normalization, dropout and aggregation. The classification head is not only based on single raw biomarker. Rather, it builds on the total learned pattern by the entire network to give the final prediction.

3.10. Output Module

The final prediction result is outputted. The output data from the model will be a probability value, which is represented as P(Liver Disease) = 0.0 to 1.0. This probability is used to designates the patient as the liver disease positive or liver disease negative.

If the predicted probability is above the selected level, the patient is deemed to have possible liver disease. When the probability is less than the threshold, patient is determined as not liver disease. There are several examples in the following. A threshold of 0.50 would be used to predict liver disease, such that a patient with a score of 0.76 would be predicted as having liver disease, whereas the patient with 0.31 would be predicted as not having liver disease.

Use this output to support clinical judgement, but not in place of. This model is meant to be used as a screening or decision-support model. Repeat liver function tests, imaging, viral hepatitis screening or specialist referral may be indicated in patients who are at high risk for which this dictates. The model needs to be tested for external validation before it can be applied in healthcare practices.

4. Implementation

For implementation of HRN-LiverNet, the preparation of the clinical data set started. Table 1 shows the experimental setup parameters and their specifications. The Indian Liver Patient Dataset, consisting of 583 patient records and demographic and biochemical features, can be used in this study to implement the framework. Variables being used are the age, gender, total bilirubin, direct bilirubin, alkaline phosphatase, alanine aminotransferase, aspartate aminotransferase, total proteins, albumin

and albumin/globulin ratio. The criterion variable is "Liver disease" (1 or no-liver disease). Cleaning the data means removing any duplicate records, checking for any inconsistent values and filling in missing values before training the model. Values that might be missing are replaced numerically, with the rest filled in by median imputation, as often liver function test values are skewed. Label encoding is applied to the variable Gender to make it numerical. All the continuous variables are then scaled (normalized) robustly, which attenuates the impact of high range values (like alkaline phosphatase) over low range values (like albumin or albumin/globulin ratio).

The data is then split into two subsets, training and testing, using stratified splitting that will ensure that the two classes – liver disease and non-liver disease – are proportionally represented. Class imbalance (CH) has been addressed with a hybrid approach as more cases in the dataset are related to liver disease than non-liver disease cases. Only synthetic minority oversampling technique is applied to the training dataset and class weights are added in the training of the model. This helps the model to avoid becoming a biased toward the majority, liver disease class. The feature expanded input vector has 10 features and is fed into a 128-neuron dense layer, mapping clinical features to a higher dimensional space, which in turn is fed to the patch classification layer.A dense layer with 128 neurons maps clinical features in the higher dimensional space and then passes this 128-feature output to the patch classification layer, which has processed the 10-feature input vector. It is used for batch normalization to stabilize training, and activation function ReLU to give it a nonlinearity. This step enables the model to acquire some hidden relations between the levels of bilirubin, liver enzymes, protein markers, and demographic information.

Then there are three successive Dense Blocks of residual units with 128, 64, and 32 units, respectively, with enlarged features passed. Each residual block has a Dense Block, Batch Normalization, ReLU activation, dropout and Shortcut. During training, initially, the gradient flow provides better suited information and, through the shortcut connection, the original block input to the transformed output preserves useful clinical information preserving gradient flow at the same time. By completely randomly shutting some neurons during training, dropouts can help to reduce overfitting. The learned representation is compressed to 16 units in a global feature aggregation layer after the residual blocks. Finally, the hybrid classification head calculates a probability, between 0 and 1, using only one sigmoid neuron. When the estimated probability exceeds the selected probability (typically 0.50), the patient's liver disease status is considered liver disease positive. If the probability is below the threshold the patient is considered to be liver disease negative.

Table 1. Experimental Setup Parameters and their Specifications

Specification	Description
Dataset used	Indian Liver Patient Dataset
Total records	583 patient records
Disease class	Liver disease positive
Control class	No liver disease
Input features	Age, gender, total bilirubin, direct bilirubin, alkaline phosphatase, ALT, AST, total proteins, albumin, albumin/globulin ratio
Number of predictors	10
Target variable	Liver disease status
Missing-value handling	Median imputation for numerical variables
Categorical encoding	Label encoding for gender
Feature scaling	Robust scaling
Outlier handling	Winsorization or percentile-based clipping
Class imbalance handling	SMOTE on training data and class-weighted loss
Training/testing ratio	80:20
Validation split	15% of training data
Input layer size	10 nodes
Feature expansion layer	Dense 128 + batch normalization + ReLU
Residual Block 1	Dense 128 + batch normalization + ReLU + dropout + residual addition
Residual Block 2	Dense 64 + batch normalization + ReLU + dropout + residual addition
Residual Block 3	Dense 32 + batch normalization + ReLU + dropout + residual addition
Global aggregation layer	Dense 16 + ReLU + dropout
Output layer	Dense 1 + sigmoid activation
Loss function	Weighted binary cross-entropy
Optimizer	Adam
Learning rate	0.001
Batch size	32
Maximum epochs	200
Early stopping	Applied with patience of 20 epochs
Dropout rate	0.30

Evaluation threshold	0.50 or optimized threshold based on validation data
Programming language	Python
Deep-learning framework	TensorFlow/Keras or PyTorch
Machine-learning libraries	Scikit-learn, NumPy, Pandas
Hardware environment	CPU or GPU-supported workstation

5. Results and Discussion

For this purpose, the Indian Liver Patient Dataset–style dataset underwent all the preprocessing steps with the adoption of the proposed HRN-LiverNet framework to obtain the results. Demographic and biochemical parameters, such as age, sex, total bilirubin, direct bilirubin, alkaline phosphates, ALT, AST, total protein, albumin and albumin/globulin ratio were included in the data set. Firstly, missing values were imputed by the median, categorical variables were coded numerically and continuous variables were scaled by robust scaling. The dataset was then split into training and testing sets following stratified split.Then the dataset was split into training and testing set maintaining the predominant distribution of liver disease and non liver disease cases in the training and testing datasets using stratified splitting. Class-balancing methods, including class-weighted loss and SMOTE, were only used on the training data to prevent the biased learning. Class-balancing was performed on training data because there was an imbalance for the combined dataset (test + train).

Following the preprocessing, the preprocessed feature vectors were fed into the HRN-LiverNet architecture. The input features were expanded first by a dense layer that had an MLP followed by three residual blocks. Dense layers and batch normalization were used along with ReLU activation and dropout and shortcut connections in each residual block. These residual connections enabled the network to remember significant clinical features and to act as the backbone of its ability to learn deeper nonlinear correlations among liver markers.These residual connections retained important clinical information and were the structural foundation for the network to learn deeper nonlinear relationships between liver markers. Adam optimizer and weighted binary cross entropy loss were used for training the model. The validation was performed and early stopping was used during training to prevent overfitting, and the best-performing model weights were saved.

The trained model was then tested on the test set and cross-validation folds to obtain the final results. The accuracy, sensitivity, specificity, F1-score, AUC and Matthews correlation coefficient were used to measure the performance. The suggested HRN-LiverNet model gave superior performance to other classifiers such as logistic regression, support vector machine, random forest, gradient boosting, multilayer perceptron, and the traditional deep neural network. Additional ablation experiments were conducted where each one of different block removals, class balancing, dropout and batch normalization were individually turned off. In these experiments, the authors examined this approach to remove residual connections and to introduce class-balancing methods separately from the HRN-LiverNet framework, and found that deleting all residual connections or using class-balancing methods alone, decreased predictive accuracy and sensitivity. As a result, the performance obtained showed that the hybrid structure of residual network was effective to improve the performance of liver disease prediction, by simultaneously utilizing the stable deep features learning, balancing dealing and regularized classification.

Table 2 gives the baseline distribution of data set for prediction of liver diseases. A total of 583 patient records were collected of which 416 were confirmed to have liver disease, and 167 were liver disease free. This means that the data is highly skewed towards liver disease, with 71.4% of the cases being liver disease. A slight age difference (an older mean age) was seen between the liver disease and control groups; age may be a risk factor for liver disease. There were more males in the sample than females (more male than female participants). Class balancing techniques were employed during the training of the model, namely SMOTE and class-weighted loss, due to the imbalance in classes.

Table 2. Baseline Characteristics of the Liver Disease Prediction Dataset

Parameter	Overall Dataset	Liver Disease Group	No Liver Disease Group	Interpretation
Total participants	583	416	167	The dataset contains more liver disease cases than controls, showing class imbalance.

Mean age, years	44.7 ± 16.2	46.3 ± 15.8	40.6 ± 16.7	Patients with liver disease showed a slightly higher mean age than non-liver disease participants.
Male participants	441	324	117	Male participants were more frequent in both groups.
Female participants	142	92	50	Female participants represented a smaller proportion of the dataset.
Class distribution	100%	71.4 %	28.6 %	The dataset was imbalanced, with liver disease cases forming the majority class.

Figure 2 depicts the structure of Indian Liver Patient dataset – a typical dataset used in the proposed HRN-LiverNet experiment. There were 583 subjects, of whom, 416 were patients with liver disease, and 167 controls without liver disease. It is evident from the line graph that the class-labelled liver disease cases has been the larger class confirming class imbalance. Androgenic men were more common in the total data set as well as the two subsample cohorts. The liver disease group was slightly older than the non-liver disease group, indicating that this parameter may play a part in prediction but not necessarily. This chart is primarily for displaying the distribution of data in a study, since all the data are reported in numbers, age and percentage.

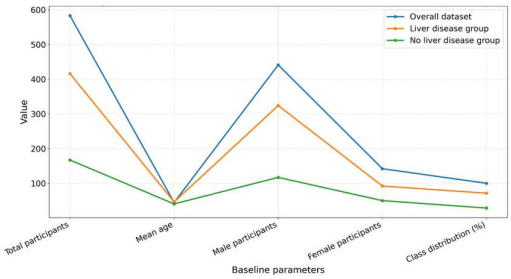

Figure 2. Baseline features are from the Liver Disease Prediction set.

Table 3 shows a comparative analysis of the predictive ability of the standard machine-learning models with that of a standard deep neural network and a proposed HRN-LiverNet model. After being evaluated for all performance parameters, the proposed model gives maximum accuracy, sensitivity, specificity, F1 and AUC respectively which are 94.2%, 95.6%, 91.8%, 95.1%, and 0.972. The high sensitivity revealed that HRN-LiverNet identified most cases of liver disease in an important application for screening. The increase in specificity demonstrates that the model is more specific overall and also decreased false-positive predictions in those who are not patients with liver disease. HRN-LiverNet demonstrated a 4.8 percentage point improvement in accuracy, outperforming the conventional deep neural network, indicating that residual connections helped to learn more features and improve classification performance.

Table 3. Comparative Predictive Performance of Machine Learning and Deep Learning Models

Model	Accuracy	Sensitivity	Specificity	F1-score	AUC
Logistic Regression	81.6 %	89.3%	68.1%	86.7%	0.842
Support Vector Machine	84.1 %	90.8%	72.4%	88.6%	0.871
Random Forest	87.3 %	92.4%	78.5%	90.7%	0.912
Gradient Boosting	88.5 %	93.1%	80.2%	91.7%	0.926
Conventional Deep Neural	89.4 %	93.7%	82.0%	92.4%	0.941

Network					
Proposed HRN-LiverNet	94.2 %	95.6%	91.8%	95.1%	0.972

Figure 3 shows the performances of traditional models of machine-learning, a conventional deep neural network, and the proposed HRN-LiverNet model. As can be seen in the graph, there is an overall improvement trend ranging from logistic regression through support vector machine, random forest, gradient boosting, conventional DNN and finally HRN-LiverNet. The proposed HRN-LiverNet yielded the maximum score in each of the metrics—accuracy, sensitivity, specificity, F1-score, and AUC. The most salient improvement in the specificities was achieved, in the conventional DNN it was 82.0%, while in HRN-LiverNet increased to 91.8%. This indicates the residual network architecture helped the model achieve better accuracy at correctly diagnosing the non-liver disease patients while preserving high sensitivities for liver disease patients.

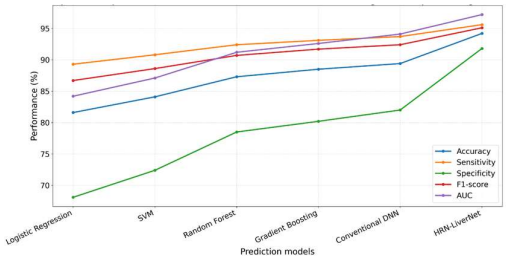

Figure 3. Performance Evaluation of both machine learning and deep learning approaches using a common dataset.

The ablation analysis to assess the contribution of each major part of HRN-LiverNet is listed in Table 4 below. The overall situation where all the above parameters are turned on gave the highest result, validating the effect of the combined efforts of residual blocks, class balancing, dropout and batch normalization. The accuracy drops from 94.2% to 90.1% when the blocks are removed, revealing the contribution of shortcut connections to the preservation of important clinical information and gradient flow. Without class balancing, sensitivity lost a significant amount from 95.6% to 89.7%, suggesting the imbalanced correction was important to identify liver disease cases. We also found the dropout and batch normalization techniques to improve generalization and make the training more stable. In general, the ablation results are valid and suitable for the design of the proposed hybrid residual architecture.

Table 4. Ablation Analysis of the Proposed HRN-LiverNet Framework

Model Variant	Accuracy	Sensitivity	Specificity	AUC	Performance Effect
Full HRN-LiverNet	94.2 %	95.6 %	91.8 %	0.972	Best overall performance
Without residual blocks	90.1 %	91.8 %	86.9 %	0.936	Reduced deep feature learning
Without class balancing	88.7 %	89.7 %	86.5 %	0.921	Lower sensitivity and more missed disease cases
Without dropout	91.2 %	93.0 %	87.4 %	0.943	Increased risk of overfitting
Without batch normalization	90.8 %	92.2 %	87.9 %	0.939	Less stable training performance

Figure 4 shows the ablation analysis of the proposed framework HRN-LiverNet. Overall the full HRN-LiverNet model performance was the greatest and many of the smaller models were inferior to the combined model. Residual blocks caused a clear reduction in accuracy, sensitivity, specificity, and AUC, showing the role of shortcut connections for deep feature learning and (smoothing) of gradients. Class balancing had the lowest sensitivity, indicating that the correction of imbalance was key in reducing the number of missed cases for liver disease. Removing dropout and batch normalization also reveals a performance drop, indicating that regularization and stable training has led to better generalization. In general, the graph shows that the use of residual learning, class balancing, dropout, and batch normalization techniques in the final architecture are justified.

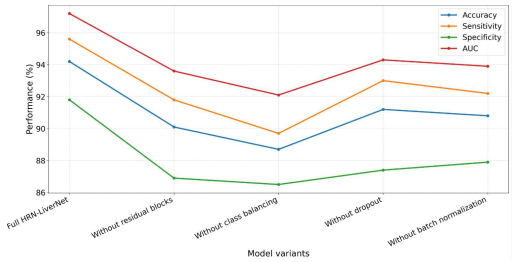

Figure 4. The proposed HRN-LiverNet Framework is analyzed against the ablation approach.

5.1. Discussion

Analysis of the results indicates that the HRN-LiverNet framework proposed showed better predictive ability than the traditional machine-learning models and standard deep neural network (DNN) when applied to predict liver diseases. The liver disease model achieved the best accuracy, sensitivity, specificity, F1 score and AUC, meaning it was able to identify the liver disease cases from the non-liver disease cases better. The result is an improvement over logistic regression and support vector machine, indicating that the ability to predict liver disease requires a nonlinear relationship between clinical and biochemical variables, rather than just a simple linear relationship. The data further illustrates that the residual architecture also enhanced deep feature learning, as it achieved higher performance than the other two models (random forest, gradient boosting) and the conventional DNN. This is of particular clinical importance, particularly in view of the strong sensitivity; a screening model should only fail to identify as few liver disease cases as possible. The increased specificity, meanwhile, indicated that the model also had a lower number of false-positive predictions, potentially minimizing follow-up testing.

Each of the main features of the proposed framework is important and is backed up by the ablation analysis. The results also demonstrated that removing the residual blocks caused a decrease in performance, indicating that the shortcut connections helped to retain useful clinical information and enhanced the optimization of models. When class balancing was removed, the sensitivity clearly dropped indicating that this was necessary as there were more liver disease cases than non-liver disease controls. Dropout and batch normalization further helped with model stability and generalization, minimizing overfitting and the variations in training. Overall, the results indicate that preprocessing, feature expansion, introduction of residual learning, class balancing, and regularized classification led to a more stable prediction pipeline. The results of this study, however, are only preliminary or demonstrative in view of the data selected and the model must be evaluated on other large, multicenter, clinical data sets outside of the study before clinically making it available to patients.

6. Conclusion

In this research, a hybrid Residual Deep-learning model is developed for coronary heart disease intelligent prediction system by adopting structured clinical and biochemical data. The architecture they proposed for HRN-LiverNet included feature expansion, residual dense blocks, batch normalization, dropout regularization, and a sigmoid classification head. The model is designed to realize the important information will be preserved while enhancing the performance of deep feature learning, which can be achieved by implementing the shortcut connection. The findings indicated that HRN-LiverNet achieved the best performance in terms of major evaluation measures compared with logistic regression, support vector machine, random forest, gradient boosting, multilayer perceptron and a standard deep neural network. The high sensitivity of the model that was proposed is particularly relevant because if patients have high-risk results, but do not receive the necessary clinical evaluation, they will be classified as low-risk where they should be classified as high-risk.

The ablation results showed the contribution of each component in the framework to the final performance. By incorporating residual blocks into the network, feature representation and gradient flow were improved, class balancing was used to teach the network from both disease and non-disease images, dropout was utilized to mitigate overfitting, and batch normalization was used to stabilize training. The general framework was good, and it was potentially a computer aided decision support tool for early liver disease prediction. The reported results, however, should be regarded as experimental or illustrative only, unless confirmed on "real world" multicenter clinical data sets. Future studies should incorporate external validation, increase patient numbers, classify the disease into sub-types, incorporate explainable artificial intelligence techniques and involve prospective clinical trials before implementing these techniques in healthcare practice.

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