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Article

A DEEP LEARNING INSPIRED LIVER DISEASE PREDICTION MODEL WITH OPTIMAL WEIGHTED RBM KERNELS FOR FEATURE EXTRACTION AND HYBRID DEEP RESIDUAL NETWORK

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Abstract: - Since liver disease often presents no clear symptoms in its early stages, misdiagnosis by doctors can occur, putting patients' health at risk. Generally, liver disease does not show early-stage symptoms to the false diagnosis, which may lead to wrong treatment and cause a threat to the health of the patient. However, the traditional methods are very complex and expensive. Deep learning techniques are employed to solve challenges, enabling effective treatment of liver disease by leveraging vast amounts of data. Initially, the patient data on various liver diseases are collected for the dataset. The data is sent to data cleaning process for removing unwanted data. Then, the cleaned data is sent for accurate feature extraction, and the Weighted Restricted Boltzmann Machine (WRBM) kernels are considered for identification of the high dimensional features. Also, here the weights involved in the process are optimally generated by the newly developed Intellectual and Randomized Integer Amendment-based Starfish Optimization Algorithm (IRIA-SOA). Then, high dimensional features are trained using the proposed Hybrid Deep Residual Network (HyDRNet), which is a combination of both Convolution Extreme Learning Machine (Conv-ELM) and Echo State Network (ESN). The presented network can process large patient data records, and predict different liver disease types....

Keywords: Liver Disease Prediction; Weighted Restricted Boltzmann Machine; Randomized Integer Amendment-based Starfish Optimization Algorithm; Hybrid Deep Residual Network; Convolution Extreme Learning Machine; Experience Sampling Method; Feature Extraction

1. INTRODUCTION

In recent decades, the medical field has faced significant challenges due to the overwhelming growth of biomedical data (Rachna *et al.,* 2024). The continuous advancement of biotechnology and the increasing complexity of bio-data have driven the need for modern data mining and machine learning techniques to process and interpret this information efficiently (Saeed *et al.,* 2025). These computational approaches are increasingly being used to construct predictive and diagnostic models, supporting healthcare professionals in identifying diseases more accurately (Xiao & Ren, 2025). One of the major advantages of these models is their ability to improve clinical decision-making, which helps minimize medical errors and enhances diagnostic confidence (Allenki & Soni, 2024). Medical datasets often contain a wide range of features, many of which are crucial for disease identification, yet only a small portion is typically considered during analysis. This highlights the importance of careful feature selection and interpretation

(Priyadharshini *et al.,* 2024). The emergence of intelligent systems in bioinformatics has coincided with advancements in computing power, enabling the analysis of large-scale and complex medical datasets (Ali & Aljabery, 2024). However, the unclear and often ambiguous nature of medical data still poses a significant barrier for physicians seeking clear insights, potentially leading to misdiagnosis and inappropriate treatment decisions. By integrating intelligent algorithms capable of handling uncertainty and extracting meaningful patterns, medical experts can improve the precision of diagnoses, refine therapeutic approaches, and minimize expenses as well as clinical mistakes. (Ginting *et al.,* 2024).

Intelligent approaches like data mining can be used in liver disease diagnosis due to their accuracy rate and fastness in examining key determinant. The data mining process in the medical domain has a different approach when compared to other domains (Chen *et al.,* 2024). One to consider is poor-quality medical data while comparing others. Machine Learning is a technique to train machines and allow them to make or predict decisions (Sarkar *et al.,* 2024). An effective feature selection strategy identifies the most significant variables, thereby improving classification efficiency and reducing computational burden. The feature pruning problem is solved with the help of a hybrid optimization problem by selecting a criterion-optimized feature set (Güre, 2024). Data mining techniques are used to select features and ML techniques overcome high-dimensionality and identify best features. One of the reasons for the major mortality rate is liver disease. To enhance the control, care, and mitigation of its effects, early diagnosis of this disease is necessary (Xie *et al.,* 2024). The diagnosis typically starts with gathering patient history and performing a physical evaluation. The procedure includes checking the cardiac rhythm, the role of the lungs in respiration, and the presence of unusual masses in the abdominal region (Rahman *et al.,* 2024). The symptoms associated with liver disease often overlap with those of other conditions, making them unreliable as sole indicators for diagnosis. Hence liver disease can be diagnosed using ultra-sonography or Magnetic Resonance Imaging (MRI) (Shaheamlung & Kaur 2021).

The human liver plays many important functions and it is connected with other organs, therefore the symptoms of the liver disorder are more common, but the crucial liver problems symptoms are not shown until advanced stages (Topcu *et al.,* 2024). Due to this, the misdiagnosis of the condition could happen, which leads to the development of short-term and chronic effects linked to this disease or complications (Nakatsuka *et al.,* 2025). Therefore an early and accurate diagnosis is very much necessary for this organ. Multilayer Perceptron (MLP) network can work with large amounts of data; hence it can be used in the identification of concurrent deficiency disorders. Numerous traditional methods have been used to diagnose liver diseases which also include data mining techniques with intelligent systems (Manjunath *et al.,* 2024). But these traditional systems don't provide results with have high error rate and for converting and detecting values they are sensitive (Noor *et al.,* 2025). This work is deployed to overcome all the above-mentioned challenges with the help of a deep learning platform. The entire system is connected for reliable assistance to the treatment staff and smart diagnosis of liver disease in patients in clinics and medical science centres.

Contribution: The proposed model integrates multiple key contributions to form an advanced liver disease identification system. By leveraging deep learning alongside optimization algorithms, the system enhances early diagnosis and supports strategic management of liver diseases to ensure optimal treatment outcomes. By combining these approaches, the system achieves greater precision and reliability for diagnosing diseases, enabling early clinical intervention.

To enhance precision and effectiveness. of the liver disease identification system, Dl models are integrated with optimization algorithms. DL algorithms automatically extract discriminative features from medical images and clinical datasets, whereas optimization methods improve selection and tuning of these features. The advanced neural network architecture adopted in proposed system enhances classification capability, and optimization algorithms further refine model parameters for superior results. This combined strategy enables early and accurate diagnosis, promoting prompt clinical intervention. Furthermore, system adapts to newly acquired medical data, improving its robustness and reliability over time. Optimization also reduces computational time, making the model suitable for large-scale, real-world healthcare environments. Ultimately, these advancements support physicians in accurate diagnosis and effective treatment planning.

To optimize the disease detection process and enhance the feature extraction process, the WRBM is used. IRIA-SOA is used here to optimize the weights of the WRBM to obtain optimal results. By assigning adaptive weights to hidden layer connections, WRBM improves the representation of complex medical dataset and prioritizing important features during learning. It contributes to better feature selection by analyzing medically significant patterns, reducing noise in large datasets, and enhancing classification accuracy by refining the input for deep learning models.

Additionally, IRIA-SOA aids in optimizing weights, allowing the model to dynamically adjust to variations in liver disease characteristics, leading to more reliable early diagnosis and treatment planning.

To enhance liver disease identification, the IRIA-SOA is developed leveraging the Starfish Optimization Algorithm (SFOA) for optimizing the feature extraction process and improving prediction accuracy. By strategically refining weight parameters derived from clinical data, method reduces irrelevant variations and enhances computational performance. The IRIA-SOA algorithm incorporates randomized integer adjustments to continuously update feature weights, strengthening robustness of disease pattern recognition. Its adaptive optimization mechanism improves parameter calibration in DL approaches, thereby increasing diagnostic accuracy and consistency. In addition, IRIA-SOA accelerates processing speed, and suitable for large-scale medical datasets or real-time clinical applications.

To improve liver disease detection, the HyDRNet integrates the strengths of Conv-ELM and ESN. Conv-ELM enhances feature extraction from medical images, capturing spatial details crucial for identifying liver abnormalities while maintaining fast processing speed. This network makes residual connections with both the Conv-ELM and ESN. The input is collected by both the structure and the output from each block gets averaged to produce the final output. The integration of residual connections refines model's predictions, contributing to more robust and dependable diagnostic system.

Organization of paper: Section II presents review of related literature. Section III describes liver disease prediction framework developed using collected patient data. Section IV details optimization algorithm for weight tuning and feature extraction. Section V explains operational mechanism of proposed hybrid deep residual network for liver disease prediction based on extracted features. Section VI discusses experimental results and analysis, and Section VII concludes the study.

2. LITERATURE SURVEY

2.1 Related Works

In Mohamed *et al., (*2024) have worked on the Indian Liver Patient Dataset using single and ensemble machine learning methods and compared the same and existing studies with or without feature selection methods. The proposed two-tier stacking ensemble, combined with feature optimization techniques, significantly improved predictive accuracy, reaching 93.88% and 94.12% as the best outcomes. These results were noted when the system was trained with the feature selection method. The achievement level of high prediction was evident from the results.

In Kalaiselvi & Anusuya, (2023) have developed the convolutional Neural Networks (CNN) liver tumor prediction using a depth-based variant search algorithm incorporated with an attention mechanism (CNN-DS-AM). To predict liver tumours, the proposed work performed at a high accuracy compared with other conventional methods. The model was stacked with additional advanced attention methods along with the CNN model for predicting liver tumors at higher accuracy by highlighting the regions of the CT scans. This addition leads to higher accuracy and the development of a robust system. The system was used to assist the radiologist in predicting the disease and developing the treatment plan. 95.5% accuracy rate resulted from this system compared with conventional methods.

In Velu *et al., (*2022) have proposed steps for the preprocessing of data in this system. There were 30691 records along with 11 attributes within the collection. Data mining was used to predict liver diseases accurately because of the classification model used, which makes the practitioners capable of identifying liver diseases. The C4.5 model-based rules were used to develop the liver patient prediction system. As a result, the training set worked with 99.36% accuracy and the testing set worked with 98.40% accuracy. The enhanced accuracy for training data was 29.5 and with the testing data was 28.73. This was a machine learning-based liver disease predicting system. There was a framework that connected healthcare providers with patient information.

In Chunduru *et al., (*2024) have predicted seven diseases diabetes, cardiovascular disease, renal disease, hepatic disease, breast carcinoma, malaria, and respiratory infection. This work had a web app for disease prediction, the app was created using Flask. Deep learning CNN models were used to predict those diseases mentioned above. They were deployed to achieve higher accuracy.

In Dashti *et al., (*2024) have used data mining and Artificial Neural Networks (ANN) to analyze every parameter that created an impact on identifying liver failure. This included a software system, which was more helpful when attached to data mining and ANN for precise medical diagnosis. Liver patients' datasets were evaluated using MLP. This system created results in higher accuracy with intelligence. MATLAB was used to simulate this model to check out the accuracy criteria of 99.57% in comparison with traditional ones. The performance and efficiency of the system are evident from the accuracy rate of the system.

In Amin *et al., (*2023) have created a liver disease diagnosis work using the Indian Liver Patient Dataset (ILPD). Notable machine-learning algorithms were used here. Feature extraction method was used to analyze the patients to diagnose the disease. As a result, the accuracy rate was obtained as 88.10% and an AUC score of 88.20%. This system worked 10-18.5% greater than the conventional methods. This approach assists medical professionals in diagnosing liver disease at early stage.

In Aswini *et al., (*2024) have suggested a way to predict liver disease using modified Mask-regional CNN (MR-CNN). The difference between the laboratory measurement and diagnoses was done by Pelican Optimization Algorithm (POA)-modified MRCNN algorithm. The deployed system has screened with an accuracy rate of 98% in predicting liver disease and it was also used to assist the physicians.

In Mostafa *et al., (*2021) have predicted liver disease by medical diagnosis using machine learning algorithms with the help of the health data from 615 people. The proposed system used Data visualization techniques. The system used a binary classifier to make better analysis and help the experts in accurate predictions. The deployed system results in a 98.14% accuracy rate and helps in predicting liver disease in a precise manner.

2.2 Problem statement

Data mining techniques have been well-versed in handling medical data records. Still, the dimensionality offered in large datasets requires effective feature extraction techniques. Deep learning strategies can process large data records, and arrive at a timely diagnosis. Recent works developed in liver disease prediction considered different techniques and strategies as pointed out in Table 1. Still, the following points have to be considered for developing an effective liver disease prediction platform.

Patient data records have a lot of unnecessary data records not related to disease diagnosis, and this adds a burden to the training process. Removing unwanted data records before subsequent processing leads to better effectiveness in data training and feature extraction.

Large data records, particularly medical data contain high-level and low-level features. While processing this information, it is necessary to obtain significant features more relevant to disease prediction. Optimization techniques with rapid convergence can strengthen feature extraction process, enabling selection of significant features that enhance prediction efficiency and speed up disease diagnosis.

Deep learning models process large information through their deep interconnected layers. However, the liver disease dataset has different disease types, and complex information relating to different medical terms. Developing hybrid networks is promising in processing high dimensional datasets, and also improves the prediction efficiency.

Table 1. Advanatges and drawbacks of Traditional Liver Disease Prediction Models

Author [citation]	**Techniques**	**Advantages**	**Drawbacks**
(Mohamed *et al.,* 2024)	Ensemble machine learners	Optimized data encoding ensures high data balancing and better stability. Ensemble stacking achieves better feature selection and ensures high prediction accuracy.	This technique's application in large scale datasets is not suitable. Cannot be considered for large scale imaging platforms. Cannot be extended into a multi-class prediction model.
(Kalaiselvi & Anusuya, 2023)	CNN-DS-AM	Can be applied to diverse datasets, and medical prediction models. Model's robustness to medical noise is high and better handled through CNN training.	Used under specific medical settings. Model has low generalizability. Limited to certain tumor types.

(Velu *et al.,* 2022)	Naïve Bayes, C4.5 Decision Tree	Can be used in predicting different liver disorders. Offers different data visualization techniques in prediction.	Integration of different techniques can result in high prediction but can increase the computational time while handling large datasets.
(Chunduru *et al.,* 2024)	CNN, and random forest	Deep learning enhances the prediction of different types of diseases. Suitable in handling large scale medical history.	Even though CNN offers a high prediction rate, its performance speed can be compensated due to less divergence flow between its layers.
(Dashti *et al.,* 2024)	ILDP and ANN	High diagnosis rate through backpropagation strategy. The high success rate in predicting different liver disorders.	Lacks feature selection mechanism, and hence faces high computational cost.
(Amin *et al.,* 2023)	Ensemble voting classifier	Integrates feature extraction with pre-processing techniques, for obtaining significant information. Results are easily interpretable by medical professionals.	Feature dimension has to be reduced for better stability during training. Non-linear features are not obtained.
(Aswini *et al.,* 2024)	MRCNN, POA	Allows for automatic screening and diagnosing of different liver disorders. Balances bound box regression.	High Feature dimension can hinder the training accuracy.
(Mostafa *et al.,* 2021)	Statistical Machine learning	Better balances the missing data points during training, and achieves high training efficiency. Regulates the overfitting problem.	Can be employed only for a small sample group.

3. DETAILED VIEW OF THE DEVELOPED INSPIRED LIVER DISEASE PREDICTION METHOD WITH COLLECTED PATIENT DATA AND THE EXISTING CHALLENGES

3.1 Existing Challenges in Liver Disease Prediction

Traditional approaches to liver disease prediction often face obstacles such as ambiguous symptoms, reliance on invasive techniques, constraints in non-invasive testing, overlapping risk factors, and delayed diagnosis. Symptoms like fatigue or loss of appetite usually occur as symptoms of stress or diet changes, so this confuses whether to consider this symptom for liver disease or not. This makes it harder to recognize the disease by doctors earlier. A liver biopsy involves risks such as pain, infection, and bleeding. It's not always feasible for frequent monitoring or in patients with other health complications. Techniques like ultrasound or fibro-scan can detect liver stiffness and fatty liver, but they might miss milder forms of liver dysfunction or early-stage diseases. The diagnostic accuracy can fluctuate depending on clinician's experience and patient's health status. Conditions including hepatitis, alcohol-induced liver disorders, and non-alcoholic fatty liver disease may exhibit overlapping symptoms. This overlap often requires complex testing and sometimes educated guesswork to determine the exact cause. Asymptomatic progression is a major problem. Many liver diseases like cirrhosis or hepatocellular carcinoma are diagnosed only when significant damage has already occurred, limiting treatment options.

3.2 Proposed System Overview

The deep learning algorithms surpass the traditional methods for liver disease detection. It can analyze complex patterns thereby producing a higher accuracy rate. It helps in personalizing treatment by predicting the disease and making treatment plans and decisions to cure the disease. It also helps in automating data analysis to focus on patient care. The very first step is data collection, the patient's data on their symptoms, health status, and scanned images are served as data. The data plays a prominent role in detecting the liver disease. The collected data may have interferences or noise or even may be corrupted so the model cannot straightly process the raw data. Therefore, dataset undergoes a cleaning process to ensure that only meaningful and required information is retained for further processing. It is very helpful in removing erroneous data, which may affect the precision of the model. Once data has been cleaned, it is prepared for analytical processing. The next phase focuses on identifying essential features, which are vital for accurate decision-making. To identify high-dimensional features, the WRBM kernels approach is used. This is mainly used for identifying key attributes and minimizing data complexity. The structure consists of visible and hidden layers, with weighted connections between them. The main advantage of using WRBM is to analyze complex medical data to identify patterns indicative of liver conditions. The IRIA-SOA is used along with WRBM to improve its accuracy and efficiency in detecting liver diseases. IRIA-SOA is mainly used to optimize the weight of the WRBM. This could lead to a precise diagnosis of liver disease by providing importance to certain features. Once features are extracted, they are fed into HyDRNet prediction model. Residual connections between Conv-ELM and ESN strengthen learning performance. Conv-ELM captures spatial representations through convolutional operations, and ELM ensures high training speed with minimal computational cost. It uses a single hidden layer with randomly assigned weights, which eliminates the need for iterative weight updates. By combining convolutional feature extraction with ELM's rapid training, Conv-ELM ensures that the model can quickly and effectively learn from large datasets. The system is tested with multiple datasets with deep learning algorithms to increase robustness and reliability. The HyDRNet model is central to proposed approach, as it strengthens performance, flexibility, and efficiency. A schematic overview of architecture is shown in Fig. 1.

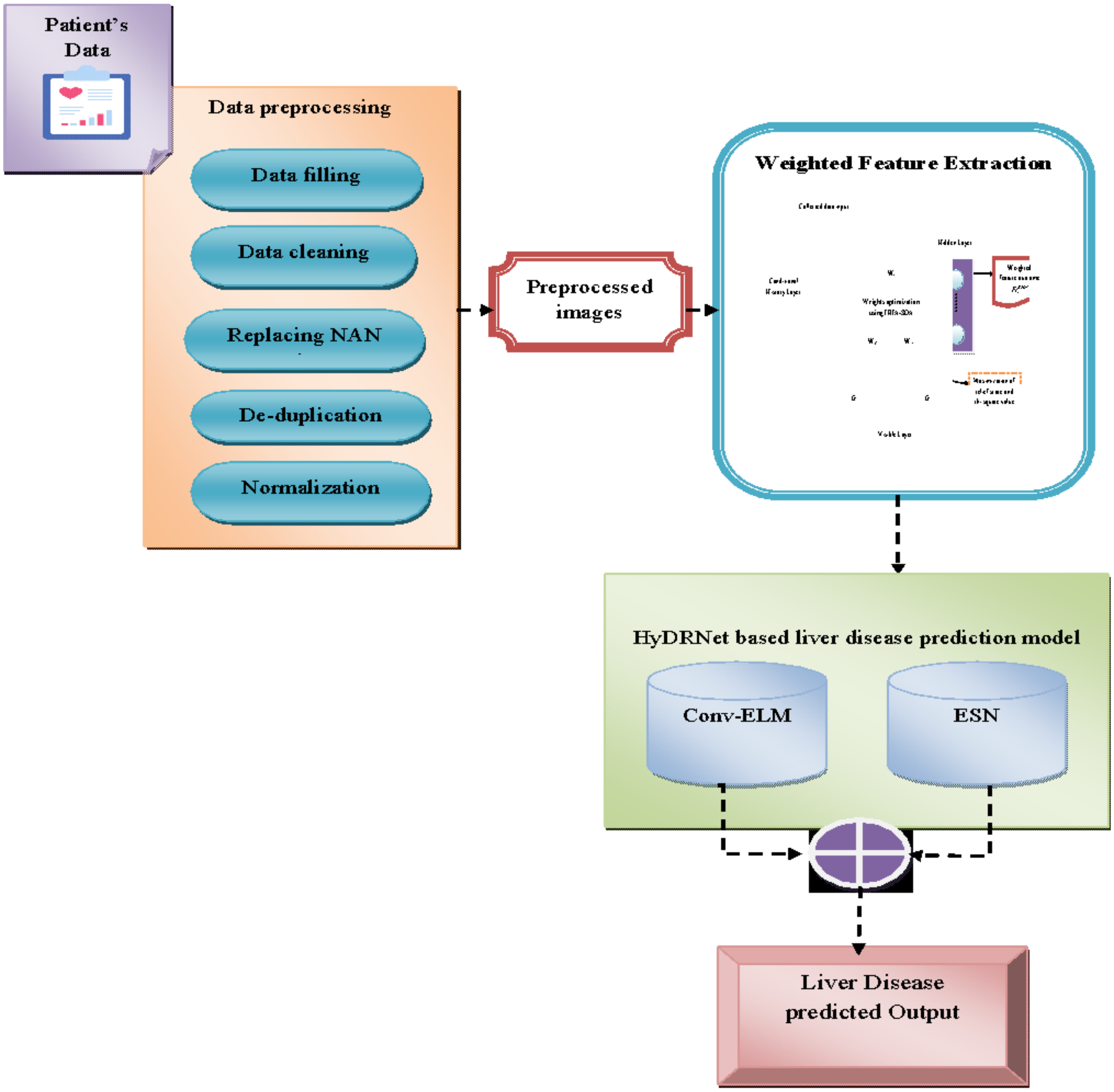


Fig 1. Architectural Depiction of the Proposed System

3.3 Data Collection Details

This section presents details of dataset employed to develop liver disease prediction model.

Liver disease dataset: The liver disease dataset was sourced from Kaggle on the following link: https://www.kaggle.com/datasets/uciml/indian-liver-patient-records, (Access date: 2025-04-29). It includes 416 records of liver disease patients and 167 instances without liver disease. The data were gathered from the northeastern region of Andhra Pradesh, India. The attribute labeled "Dataset" acts as the class indicator, separating liver disease cases from non-disease cases. In addition, the dataset contains records of 41 male patients and 142 female patients. For patients aged above 89, their age is recorded as "90."

The collected data are represented by the term In_k^{data} .

4. DATA PRE-PROCESSING AND OPTIMAL FEATURE EXTRACTION PROCESS WITH OPTIMIZED WEIGHTS USING THE INTELLECTUAL AND RANDOMIZED INTEGER AMENDMENT-BASED HEURISTIC APPROACH

4.1 Data Pre-Processing

Data preprocessing a crucial process of liver disease prediction model. Sometimes the collected data may be inaccurate or inconsistent, hence the data are preprocessed. It makes the model work efficiently by preprocessing the data and making them suitable for analysis.

Data filling: Data filling refers to the process of addressing missing values to ensure the dataset maintain its accuracy and usability. It begins with identifying gaps and analyzing the extent and patterns of missing data from the collected data In_k^{data} . Simple methods like replacing missing values with averages (mean, median, or mode) or using nearby sequential values (forward or backward fill) are often used. For more complex cases, techniques like interpolation, which estimates values based on trends or predictive modelling using relationships between data points, can be applied. Once the gaps are filled, the updated data In_k^{fill} is reviewed for accuracy and reliability.

Data Cleaning: The process focuses on correcting flawed data, addressing inconsistencies, and managing missing values to enhance overall dataset reliability. This involves removing duplicate entries, addressing missing values through techniques like imputation or deletion, and fixing incorrect or inconsistent data points from the data-filled input In_k^{fill} . Standardizing formats, such as dates and units, helps create uniformity across the dataset, while outliers are either adjusted or removed to maintain meaningful analysis. Finally, the cleaned data In_k^{clean} is validated to confirm its accuracy. This structured approach guarantees data integrity, reliability, and well-organized for analysis.

Replace Nan Values: Replacing NaN values handles missing data by inputting the cleaned data In_k^{clean} to ensure its quality and consistency for analysis. It begins by identifying NaN values and understanding the context of the affected data. Simple methods like replacing NaN with the mean, median, or mode of the column, or using forward or backwards filling in sequential datasets, are commonly used. Once NaN values were replaced, In_k^{Nan} ensure logical consistency and reliability, making it ready for further analysis or modelling.

Deduplication: Deduplication is a structured process that helps identify and remove duplicate entries in NaN value-replaced data In_k^{Nan} , improving data quality and efficiency. The process begins by scanning the data for repetitive entries, which may be exact copies or slight variations of the same record. Once duplicates are identified, the process involves determining which version of the data to retain usually based on criteria like completeness, accuracy and eliminating the redundant entries. After cleaning, the updated data In_k^{DD} is reviewed for consistency and validated to ensure no relevant information is lost. This process not only saves storage space but also enhances database performance and ensures more accurate analysis or system operations.

Normalization: Normalization is the procedure of transforming data into a uniform structure to improve its coherence and reliability, comparability, and efficiency for analysis of the deduplicated data In_k^{DD} . Numerical attributes are normalized using methods like Min–Max scaling to map values within a fixed range, typically between 0 and 1, and Z-score normalization to rescale data based on a mean of zero and unit variance. It also includes removing redundancies in data by organizing data into related tables to minimize repetition and standardizing formats such as date structures or text cases across datasets. Once normalized, the data In_k^{Norm} is validated to ensure accuracy.

4.2 Developed IRIA-SOA

In this work, a metaheuristic optimization algorithm named IRIA-SOA is deployed to optimize the weight. The IRIA-SOA is the advanced version of the SOA algorithm. It performs weight optimization to increase predictive performance, reduce errors, and enhance processing efficiency. The optimizer enhances convergence speed, reducing the time required to find optimal weight values. It ensures optimal balance between searching new solutions and refining existing ones for enhancing weight optimization outcomes.

The stochastic search optimization algorithm, known as SOA (Zhong *et al.,* 2025), is inspired by the exploration, predation, and regeneration behaviors observed in starfish. Like other popular metaheuristic algorithms, the algorithm comprises an exploration phase, inspired by the starfish's search patterns, and an exploitation phase, which leverages preying and regenerative actions to fine-tune optimal solutions. In the initialization stage of SOA, the starfish positions are given as Eq. (1) and it is represented as:

$$Y_{kl} = m_l + r(V_l - m_l)\,;\, k = 1,2,.....,P,\ l = 1,2....,E, \tag{1}$$

Here the term Y_{kl} denotes the l^{th} coordinate location of k^{th} starfish, random number as r and it ranges from $(0,1)$. A term V_l m_l are used to represent lower bound and upper bound value of l^{th} dimension design attributes. Since randomness introduces variability, ensuring consistent results across different runs can be challenging. Poorly managed randomness can slow down the convergence rate in SOA, making optimization less efficient. Poor management of stochastic elements may lead to premature convergence to suboptimal solutions. As a result, modifying random number generation process in SOA is essential for better global search performance. So, IRIA-SOA is developed in this work by updating the random number in Eq. (1) using Eq. (2).

Novelty: The enhanced IRIA-SOA framework revises randomization process of conventional SOA through an adaptive formulation presented in Eq. (2). The improved stochastic control increases model resilience to uncertainty, resulting in more trustworthy diagnostic outcomes.

$$r = \frac{Bestfit}{Worstfit + Currentfit} \tag{2}$$

The term r represents the updated random number $Currentfit$ $Bestfit$ and $Worstfit$ represents the fitness value rate as current, best, and worst respectively. The optimized randomization strategy strengthens exploration–exploitation balance for supporting an effective search adaptive diagnostic solutions. It also reduces impact of initial parameter settings, improving model robustness across varying patient datasets. Additionally, improved randomness enhances diversity in analyzed medical data, preventing biases and ensuring comprehensive coverage of potential disease indicators. This refined method adapts better to dynamic physiological variations, allowing detection algorithms to respond efficiently to changes in liver function patterns.

In liver disease prediction, IRIA-SOA assists in optimizing the weight values of WRBM. The modified randomization strategy in IRIA-SOA improves equilibrium between exploration and exploitation, leading to faster convergence and mitigating the likelihood of being trapped in local optima. This enhancement allows for more precise optimization of RBM weights, thereby strengthening effectiveness of liver disease detection. By avoiding premature convergence to suboptimal solutions, the method improves predictive performance. The refined weight adjustment process also boosts classification accuracy, producing consistent and reliable results across different models. A working flow process of proposed IRIA-SOA algorithm was presented at Fig. 2.

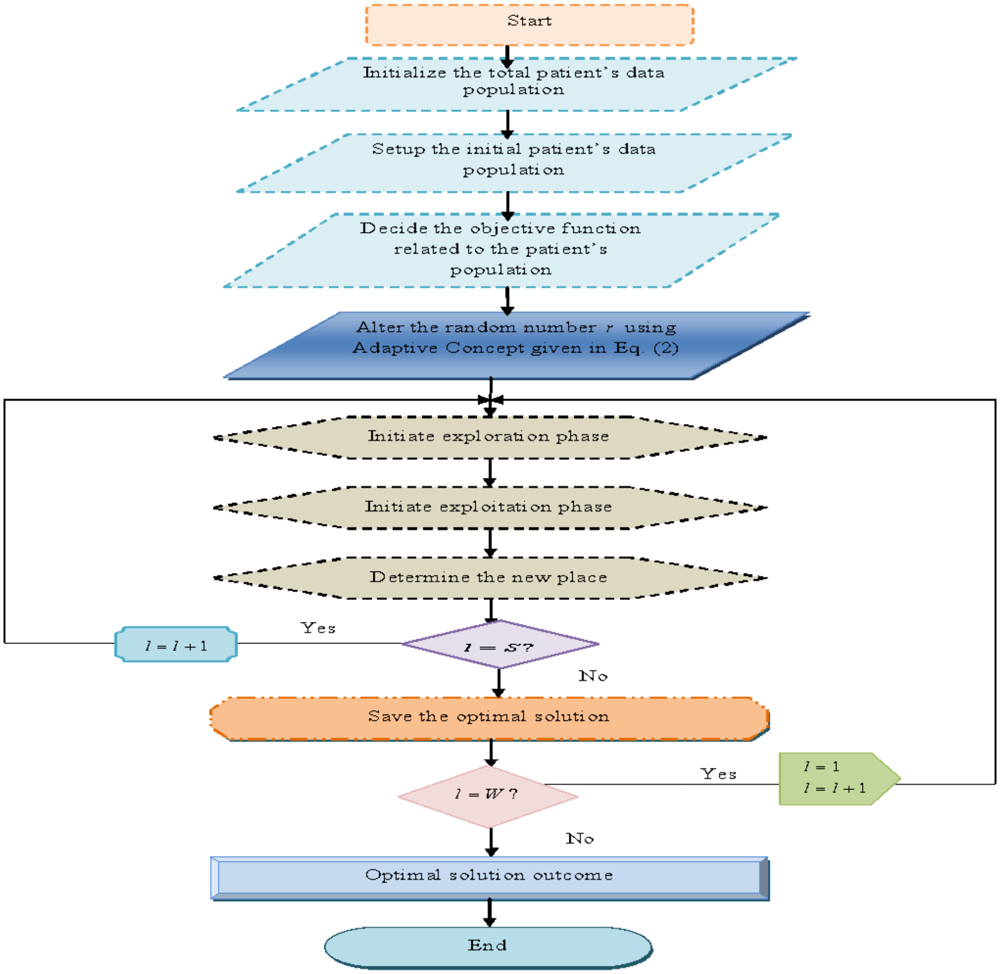


Fig 2.Flow Chart of IRIA-SOA Algorithm

4.3 Weighted RBM-based Feature Extraction

The feature extraction is optimized using WRBM Kernels and enhanced by the IRIA-SOA algorithm. The feature extraction process begins by mapping clinical input vectors into higher-dimensional spaces using kernel functions. This allows the model to captures non-linear biomarker relationships. This model differs from standard RBM by applying specific weights to ensure that the most important liver biomarkers have a greater impact on the final result. The IRIA-SOA algorithm acts as a powerful weight-tuning engine to govern the optimal extraction of features in a RBM. By modeling the foraging, preying, and regenerative behaviors of starfish, the algorithm intelligently refines potential weight configurations (search agents) for effectively avoiding the trapping in local optima. This optimization process ensures the RBM energy function reaches a global minimum and allows the reconstructed input to align perfectly with the latent features. Consequently, this produces a set of highly distilled high-dimensional features for representing the most significant pathological markers, which are then used to train the subsequent HyDRNet. Furthermore, the IRIA-SOA-tuned WRBM kernel enhances data quality by significantly improving the signal-to-noise ratio. This approach optimizes input for the Conv-ELM while preserving complex, high-dimensional data essential for the ESN. Consequently, the system produces compressed and highly discriminative features for enabling accurate automated classification of various liver disease types.

Novelty: WRBM-based feature extraction model is derived from a conventional method known as RBM. To achieve higher predictive precision, IRIA-SOA is employed to refine the RBM weights, giving rise to WRBM model. A preprocessed data In_k^{Norm} processed as input to RBM to extract the best features. RBM (Gao *et al.,* 2016) consists of two units, one visible unit and a hidden unit the visible unit is represented $z \in \{0,1\}^F$ and the hidden unit is represented as $i \in \{0,1\}^R$. It is to be noted that every hidden unit is linked with all hidden units using a matrix of weight x. However, the units do not get connected with other units inside the same layer.

Increasing the value of the likelihood makes a clear view of RBM parameters. The log-likelihood derivative is given in Eq. (3).

$$\frac{\partial}{\partial\theta}K(\theta) = -\left\langle \frac{\partial G(z;\theta)}{\partial\theta} \right\rangle_{data} + \left\langle \frac{\partial G(z;\theta)}{\partial\theta} \right\rangle_{\mathrm{mod}el} \tag{3}$$

Here, the free energy function has $z \in \{0,1\}^F$ RBM. The terms $\langle\cdot\rangle_{data}$ $\langle\cdot\rangle_{\mathrm{mod}el}$ represent the expected value of visible vector, and data and z are the distribution of the model. When the exponential term arrives, then the computation becomes complex. The parameter θ_1 is invariable, and on the other hand, the probability $p(z_1 \mid G;\theta_1)$ is declared as inputs z_1 Extracted from the concealed nodes of the lowest layer. Then the features of the collected data are extracted for further liver disease prediction analysis. However, RBM training can suffer from vanishing gradients, where lower layers receive minimal updates due to gradient decay during backpropagation. The IRIA-SOA algorithm is employed to optimize weights and overcome this limitation. In context of liver disease prediction, weighted RBM is particularly useful for analyzing large datasets, such as patient records or imaging data, to identify patterns indicative of liver diseases. By assigning weights to features using IRIA-SOA, the model can prioritize relevant attributes, such as biomarkers or imaging characteristics, while minimizing the influence of irrelevant data. Finally, the extracted features are represented as Fr_k^{WRBM}.

The algorithm's two-phase approach ensures a balance between exploring the solution space and exploiting the best solutions, which can lead to better weight optimization. It performs well even with high-dimensional problems, which is crucial for RBMs that often deal with large datasets. IRIA- SOA has demonstrated superior computational efficiency compared to other optimization algorithms, making it suitable for complex tasks like RBM for weight tuning.

Objective Function: The goal of this objective function is to maximize the relief score and chi-square statistics by optimizing the weight distribution in WRBM using the IRIA-SOA algorithm to enhance learning efficiency and feature selection. By refining weight parameters, the WRBM improves its ability to capture essential data patterns, ensuring better classification and prediction accuracy. The IRIA-SOA algorithm dynamically adjusts weights, balancing exploration and exploitation while minimizing sensitivity to initial conditions. This optimization process strengthens robustness against noisy or incomplete data, leading to a more reliable and adaptive WRBM framework for complex tasks. Eq. (4) defines the optimization criterion for the WRBM-driven feature extraction framework.

$$Zuh = \underset{\{W_m^{RBM}\}}{\arg\min}\left(\frac{1}{sT_{Dg} + \chi^2}\right) \tag{4}$$

Here, the weight is represented by the term W_m^{RBM} and it ranges from $[-0.20, 0.20]$. The expression for relief score sT_{Dg} and chi-square statistics value χ^2 is given in Eq. (7) and Eq. (8), respectively.

$$sT_{Dg} = \Sigma\left[I_{it}\left(g, U_C^G\right) - miss\left(g, U_Z^G\right)\right] \tag{5}$$

The term $I_{it}\left(g, U_C^G\right)$ is the Variation in feature scores among classes sharing the same label concerning a specific feature g, and the divergence in feature scores among classes with differing labels relative to the same feature g $miss\left(g, U_Z^G\right)$.

$$\chi^2 = \sum_{j=1}^{n}\frac{(P_j - F_j)^2}{F_j} \tag{6}$$

The term P_j represents the observed feature and F_i represents the expected feature. The illustration of the feature extraction process based on WRBM is given in Fig. 3.

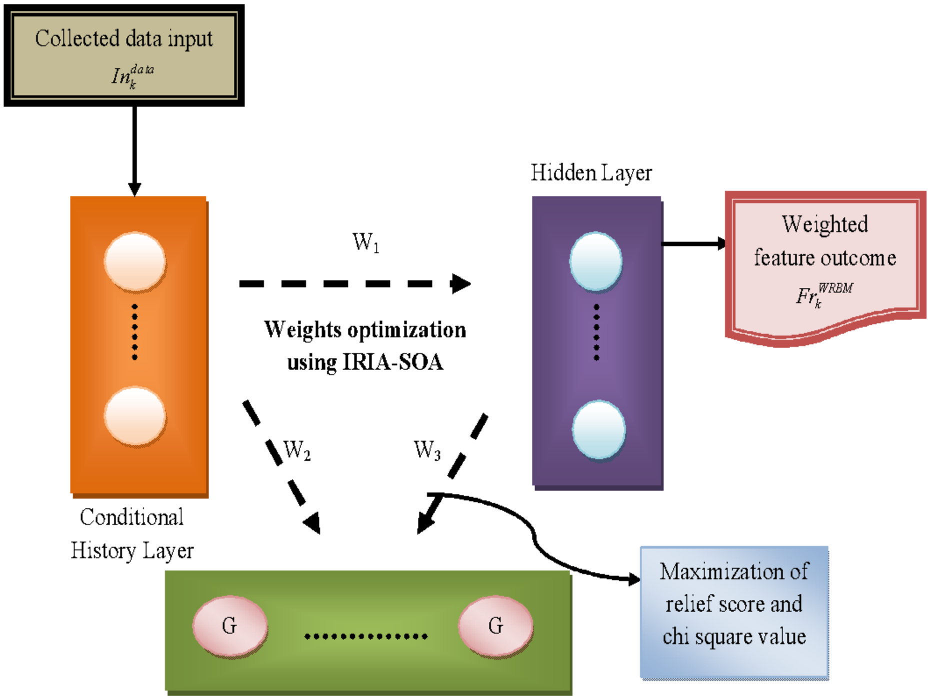


Fig 3. Illustration of Feature Extraction Process based on WRBM

5. .HYBRID DEEP RESIDUAL NETWORK FOR LIVER DISEASE PREDICTION FROM THE EXTRACTED FEATURES BY CAPTURING COMPLEX PATTERNS

5.1 Basic Conv-ELM

Generally, prediction tasks are done with the help of Conv-ELM (Racca & Magri, 2021). The fast training by ELM and the feature extraction factor of CNN are combined in this method. The hidden layers are arranged alternately with a convolutional layer and that is continued with one pooling layer. There are a few important points to be noted while structuring this design. Initially, high level features are extracted with the help of the multiple number of hidden convolution and pooling layer, followed by the regional dependencies are understood by the local receptive weights. The convolutional layer performs feature extraction by convolving filters over input data or feature maps obtained from preceding pooling layers. A kth feature map for coordinates (l,m) is given in Eq. (7).

$$E_{l,m,n}(x) = \left(\sum_{p=1}^{s} \sum_{q=1}^{s} x_{l+p-1,m+q-1} . c_{p,q}^{k} \right) \quad l,m = 1,........,(f - s + 1), \tag{7}$$

The term x denotes the input image. The map is connected to the pooling layers and feature maps in previous layers. The calculation is started by convoluting feature maps with their weight and they are added together to get a pooled feature map.

5.2 Basic ESN

ESNs (Van Berkel *et al.,* 2017) are useful for predicting liver disease by analyzing time-series medical data. They capture patterns in patient records and biomarker trends to assess disease progression. ESNs use a fixed reservoir of neurons to process inputs, while only the output weights are trained, making them computationally efficient. Their ability to model dynamic health changes suggests they could enhance liver disease prediction and diagnosis.

At any given time I_t, the input vector $V_{in}(I_T) \in R^N$ is transformed to reservoir state through input matrix $X_{in} \in R^{N_s \times N_t}$, with reservoir neurons N_s is greater than or equal to number of input neurons N_t. A reservoir state $s \in R^{N_s}$ modified at each time step based on both the present input and its preceding state is given in Eq. (8).

$$s(I_{t+1}) = \tanh(X_{in} V_{in}(I_t) + X_s(I_t)), \tag{8}$$

Here, the term $X \in R^{N_s \times N_t}$ is the state matrix. The final predicted outcome is obtained as

$$V_p(I_{t+1}) = \hat{s}(I_{t+!})^U X_{out}, \qquad \hat{s}(I_{t+1}) = h(s(I_{t+!})); \tag{9}$$

In Eq. (9), $h(.)$ represents a nonlinear transformation, with $\hat{s} \in R^{N_{\hat{s}}}$ denoting the updated reservoir state $X_{out} \in R^{N_{\hat{s}} \times N_v}$ serving as the output matrix. An input matrix X_{in} and the state matrix X generated in a random manner remain unchanged, whereas output matrix W_{out} were determined through network processing.

This method proves valuable in studying real-time liver disease development, supporting conceptual models rooted in personalized and behavioral health tracking. The ESN is a research approach used to collect real-time data on people's symptoms, behaviors, and environmental influences in their everyday lives. When applied to liver disease prediction, ESN collects data on symptoms, lifestyle factors, and environmental conditions that impact liver health. By prompting individuals to report their health status at various intervals, ESN helps track variations in symptoms, monitor medication effectiveness, and identify behavioural patterns affecting liver functionality. This approach minimizes recall bias, providing continuous and personalized insights into liver disease development and progression, ultimately aiding in early detection and tailored treatment plans.

5.3 HyDRNet-based Liver Disease Prediction Model

The proposed HyDRNet framework combines deep residual learning with hybrid modules, including Conv-ELM and ESN, to enhance representation learning and prediction performance. By employing shortcut connections, ResNets mitigate vanishing gradients and enable stable training of deep architectures. In a hybrid approach, these residual connections are integrated with other architectures, such as Conv-ELM and ESN to improve efficiency in complex tasks like liver disease diagnosis. The HyDRNet model combines both Conv-ELM and ESN. Conv-ELM accelerates training by integrating extreme learning principles with convolutional layers, enabling efficient extraction of spatial and temporal features in data-rich environments. Meanwhile, the ESN refines decision processes by dynamically collecting and analyzing relevant samples, improving real-time adaptability in complex scenarios.

Novelty: The feature extracted from the data Fr^{WRBM} is given as input to HyDRNet. Then it is processed through both the Conv-ELM and ESN models simultaneously. Conv-ELM processes liver disease data by first cleaning and organizing patient records to ensure accuracy. It then uses convolutional layers to extract key features, identifying abnormalities such as lesions or fibrosis. Once the relevant features are gathered, ELM quickly classifies liver conditions, making the diagnosis process more efficient. This approach reduces bias, ensures consistent detection across different cases, and adapts to variations in disease progression. By combining deep learning for feature extraction with rapid classification, Conv-ELM enhances liver disease diagnosis, allowing for more precise and timely medical decisions. Conv-ELM applies residual connections to refine and preserve important information. These connections help maintain key details while bypassing unnecessary transformations, ensuring the integrity of the extracted features.

Deep ResNet (Shehab *et al.,* 2021) helps deep neural networks to learn better by solving the vanishing gradient problem, where early layers struggle to update as training progresses. It does this using residual learning blocks, where each layer's output is combined with its input before moving to the next layer. This shortcut connection allows information to flow smoothly, preventing important details from getting lost. The process is represented as

$G(y) = I(y) + y$, meaning the network learns the residual part while keeping the original input intact. Since these shortcuts don't add extra parameters, training becomes faster and more efficient, making it possible to build very deep networks. Improved versions of ResNet add more identity connections, further boosting performance and stability in the developed HyDRNet-based framework for forecasting liver disease outcomes. Using convolutional operations, the model strengthens feature representation by analyzing spatial dependencies and patterns in the medical data. This enhances its ability to detect liver abnormalities more effectively. Conv-ELM dynamically adjusts weight distributions to improve generalization, ensuring reliable detection across different patient cases. This reduces bias and enhances adaptability to variations in liver disease progression. Finally, the predicted output $\mathrm{Pr}1$ is obtained from the Conv-ELM model with the residual connection.

The same extracted features are fed into the ESN model. ESN dynamically refines feature representations by continuously sampling and analyzing relevant data points in real time. It ensures that essential features are effectively weighted and adjusted based on evolving patterns in liver disease detection. Through systematic sampling, ESN fine-tunes the weight distribution of extracted features, emphasizing the most critical indicators while minimizing noise. This enhances classification accuracy and improves the reliability of predictions. After refining features, ESN strengthens classification by ensuring optimal mapping to various liver disease conditions. Unlike traditional deep learning methods, ELM assigns weights randomly and learns in a single step, making classification much faster while maintaining high accuracy. Residual connection is made in ESN to improve the speed of the training phase and increase the convergence rate. The use of residual networks reduces the problem of overfitting problem in ESN and helps to analyze the patient's data in a precise manner. It improves predictive performance by capturing variations in disease progression across different patient cases. The output obtained from ESN with residual connection is indicated by the term $\mathrm{Pr}2$.

Finally, the output of these two models is then collected and averaged to obtain the final liver disease predicted F_o output. The final predicted output F_o is obtained using Eq. (10).

$$F_o = \frac{\mathrm{Pr}1 + \mathrm{Pr}2}{2} \tag{10}$$

The term F_o denotes the final liver disease predicted output from the HyDRNet model. The deployed HyDRNet model is very helpful in the early detection of the disease. It also can analyze varieties of data with different patterns, thereby enhancing the output. It is an adaptable model that could work on different types of liver diseases like fatty liver, and cirrhosis. The model analyzes complex liver disease patterns and can work with large datasets with accurate results. Fig. 4 presents architectural diagram of proposed HyDRNet-driven liver prediction framework.

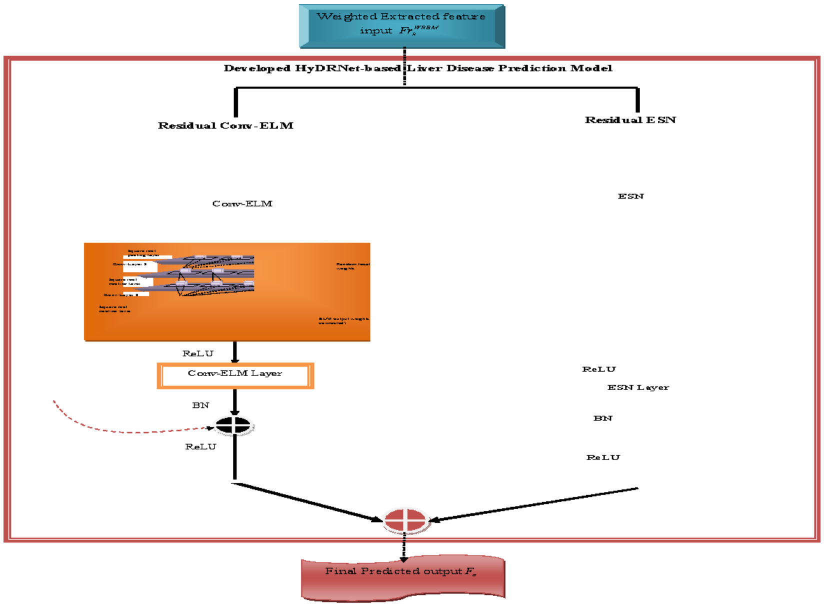


Fig 4.Diagrammatic Representation HyDRNet-based Liver Disease Prediction Model

The HyDRNet architecture is a sophisticated dual-pathway system designed for high-precision liver disease diagnosis by integrating spatial and temporal feature processing. The process begins with the weighted extracted feature input Fr^{WRBM}, which is extracted using optimized RBM kernels and then fed into two specialized residual components such as Residual Conv-ELM and Residual ESN. This structural allows the model to simultaneously handle both the immediate spatial characteristics of patient biomarkers and the deeper, sequential patterns found in extensive clinical history records. In the initial processing stage, the system passes input data through a sequence of specialized residual layers to generate the Conv-ELM layer. This component leverages a Conv-ELM to provide rapid feature extraction without the need for intensive backpropagation, while the residual skip-connections ensure signal stability as data moves through the network. Simultaneously, the ESN processes the data stream to produce its corresponding reservoir-based output layer. The ESN acts as a reservoir computing approach, which is highly efficient at identifying complex dependencies and temporal trends within large patient datasets. The final stage of the architecture involves the refinement and fusion of these two distinct streams. Following layer-wise computation, a ReLU activation is applied to each component to incorporate non-linear transformations, enabling the network to model intricate patterns more effectively. These processed streams are then merged and directed towards a final prediction node. Overall, this HyDRNet integartion produces the final predicted output F_o, which classifies liver disease types with high accuracy for effectively combining the computational speed of ELM with a robust pattern-recognition capabilities of ESN.

6. RESULT AND ANALYSIS

6.1 Implementation configuration

Implementation of liver disease prediction approach was carried out in Python platform. Optimization settings included 10 individuals in population, chromosome size of 64, and allow up to 50 iterations to achieve better predictive outcomes. The proposed system was then compared with different disease diagnosis models to assess its performance, such as CNN-DS-AM (Kalaiselvi & Anusuya, 2023), Naïve Bayes (Velu *et al.,* 2022), CNN (Chunduru *et al.,* 2024), and ANN (Dashti *et al.,* 2024), optimization algorithms such as SFOA (Zhong *et al.,* 2025) Coati Optimization Algorithm (COA) (Qi *et al.,* 2024), Red Kite Optimization Algorithm (RKOA) (Gunasekaran *et al.,* 2024), and Northern Goshawk Optimization (NGO) (Yang *et al.,* 2024), were used in this study for the effective comparison with the developed liver disease prediction.

6.2 Evaluation Metrics

The evaluation criteria utilized in the simulation are discussed in this section.

In these expressions, Tj_p and Td_n represents true positive and true negative values respectively as well as Fj_p and Fd_n refer false positive and false negative values.

(a) Accuracy:

$$Ae_{cc} = \frac{Tj_p + Td_n}{(Tj_p + Td_n + Fj_p + Fd_n)} \tag{11}$$

The terms Tj_p, Td_n, Fj_p and Fd_n denotes true positive, true negative, false positive and false negative values respectively.

(b) Sensitivity:

$$Si_n = \frac{Tj_p}{Tj_p + Td_n} \tag{12}$$

(c) Specificity:

$$Sc_p = \frac{Td_n}{(Td_n + Fd_p)} \tag{13}$$

(d) F1 Score:

$$Fk_1 = \frac{(2 \times Tj_p)}{(2 \times Td_p + Fj_p + Fd_n)} \tag{14}$$

(e) False Negative Rate (FNR):

$$Fk_{NR} = \frac{Fd_n}{(Tj_p + Fd_n)} \tag{15}$$

(f) False Discovery Rate (FPR):

$$Fk_{DR} = \frac{Fj_p}{(Tj_p + Fj_p)} \tag{16}$$

(g) False Positive Rate (FPR):

$$Fk_{PR} = \frac{Fj_p}{(Fj_p + Td_n)} \tag{17}$$

(h) Matthews Correlation Coefficient (MCC):

$$Mr_{CC} = \frac{(Tj_p \times Td_n) - (Fj_p \times Fd_n)}{\sqrt{((Tj_p + Fj_p) \times (Tj_p + Fd_n) \times (Td_n + Fj_p) \times (Td_n + Fd_n))}} \tag{18}$$

(i) Negative Predictive Value (NPV):

$$Ns_{PV} = \frac{Td_n}{(Td_n + Fd_n)} \tag{19}$$

(j) Precision:

$$Ps_{rec} = \frac{Tj_p}{(Tj_p + Fj_p)} \tag{20}$$

(k) False Omission Rate (FOR):

$$Fa_{OR} = \frac{Fd_n}{(Fd_n + Td_n)} \tag{21}$$

(l) Prevalence Threshold (PT):

$$Pv_t = \frac{\sqrt{Fk_{PR}}}{\sqrt{Si_n} + \sqrt{Si_n}} \tag{22}$$

(m) Balanced Accuracy (BA):

$$Bv_A = \frac{(Si_n + Sc_p)}{2} \tag{23}$$

6.3 Convergence behaviour analysis

Fig. 5 presents convergence study of proposed model. The evaluation of multiple loss functions confirms model's stability and generalization capability on new datasets. Here, developed IRIA-SOA algorithm provides the least cost function value, followed by the COA, NGO, SFOA, and RKOA methods. When evaluated over multiple iterations, proposed model exhibits a cost function reduction of 62%, 13%, 31%, and 59% compared to COA, NGO, SFOA, and RKOA. This indicates that IRIA-SOA framework delivers improved predictive accuracy and performance. The IRIA-SOA algorithm ensures optimal tuning, which results in more efficient training and superior performance. By effectively reducing loss during the training phase, the IRIA-SOA model attains superior predictive performance, with higher accuracy and fewer errors. The model's increased sensitivity reduces false negatives, facilitating early diagnosis and timely treatment. Additionally, the algorithm is robust against variations in data and environmental conditions, delivering reliable results across multiple scenarios. This makes the IRIA-SOA model a more effective and reliable solution for liver disease prediction, providing substantial benefits in enhancing both computational efficiency and clinical precision.

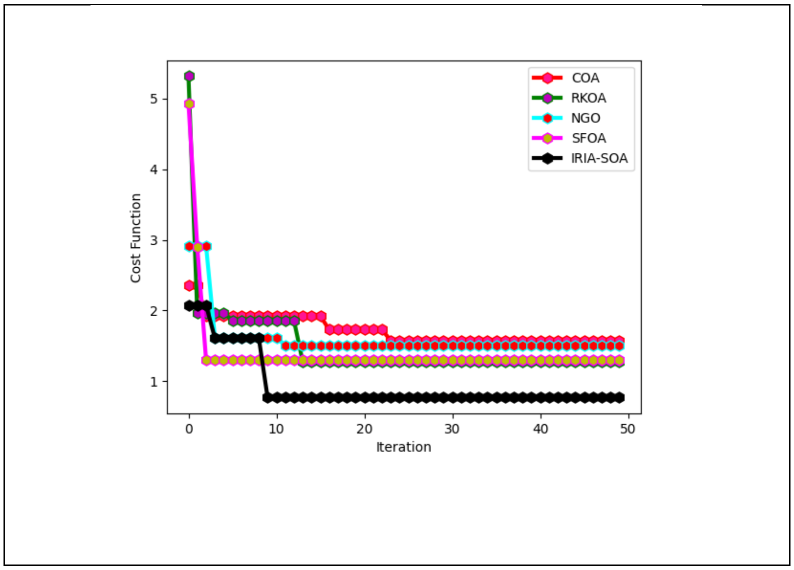
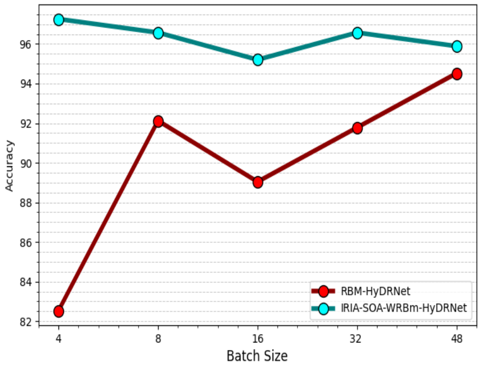


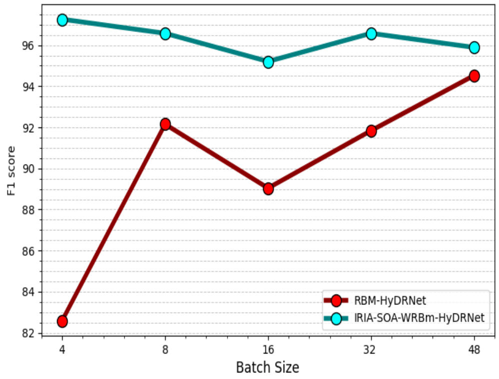
Fig 5. Convergence characteristics evaluation of implemented method

6.4 Effect of Weight Optimization on Model Performance

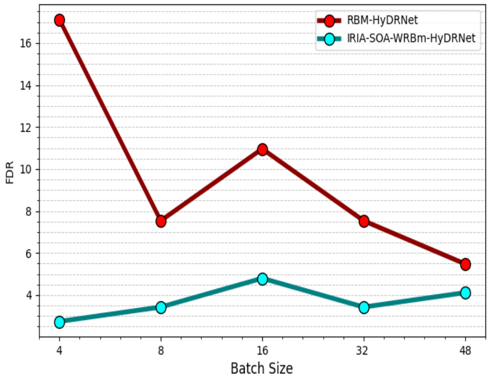
Fig. 6 depicts comparative analysis of the model with and without weight optimization. The assessment of weighted features evaluates the predictive capabilities of RBM-HyDRNet and IRIA-SOA-WRBM-HyDRNet. The RBM with HyDRNet model provides an accuracy of 92% at the 8th batch size without optimized weights. But with the same batch size, the IRIA-SOA with HyDRNet provides 98% accuracy with optimized weights. Therefore, the proposed model IRIA-SOA-HyDRNet analyzes the patterns in an optimized way than RBM-HyDRNet. The optimized framework exhibits enhanced accuracy relative to other approaches. A high performance paves the way for better diagnosis of liver diseases. Due to the optimization of weights, the diseased features are well analyzed by the developed model and provide better results. The IRIA-SOA-based WBRM has 19.5% higher accuracy compared to conventional RBM-based HyDRNet. The IRIA-SOA algorithm optimizes the weights and improves the feature extraction process. Consequently, the model demonstrates enhanced adaptability and provides more precise prediction outcomes.


Accuracy
96
94
92
90
88
86
84
82
4
8
16
32
48
Batch Size
RBM-HyDRNet
IRIA-SOA-WRBm-HyDRNet

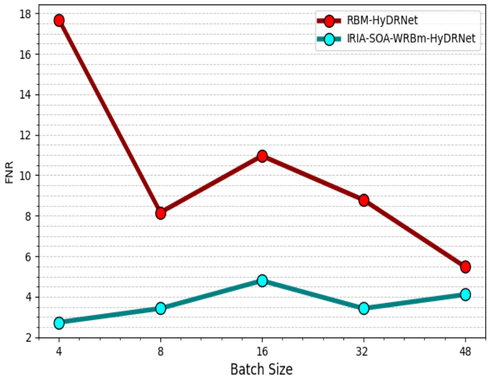
(a)


F1 score
96
94
92
90
88
86
84
82
4
8
16
32
48
Batch Size
RBM-HyDRNet
IRIA-SOA-WRBm-HyDRNet

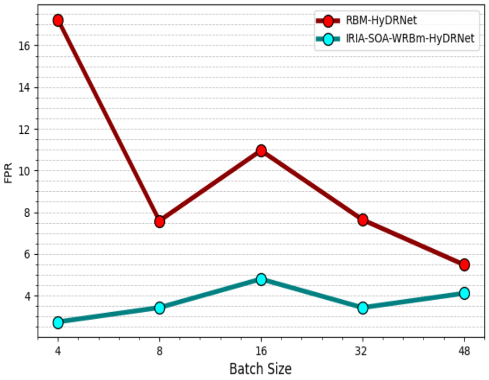
(b)


FDR
16
14
12
10
8
6
4
4
8
16
32
48
Batch Size
RBM-HyDRNet
IRIA-SOA-WRBm-HyDRNet

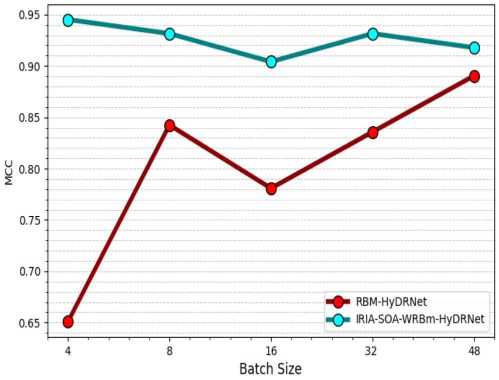
(c)


FNR
18
16
14
12
10
8
6
4
2
4
8
16
32
48
Batch Size
RBM-HyDRNet
IRIA-SOA-WRBm-HyDRNet

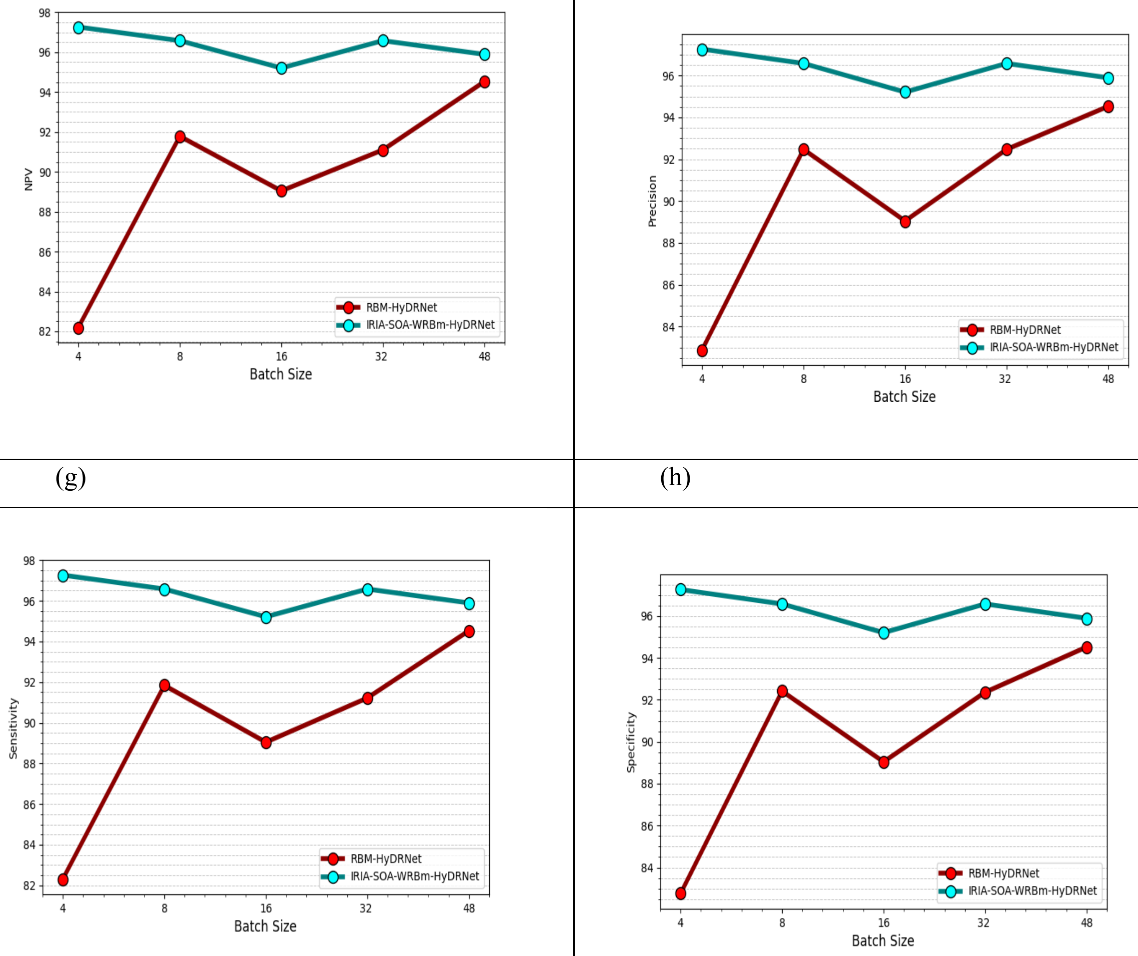
(d)


FPR
16
14
12
10
8
6
4
4
8
16
32
48
Batch Size
RBM-HyDRNet
IRIA-SOA-WRBm-HyDRNet

(e)


MCC
0.95
0.90
0.85
0.80
0.75
0.70
0.65
4
8
16
32
48
Batch Size
RBM-HyDRNet
IRIA-SOA-WRBm-HyDRNet

(f)



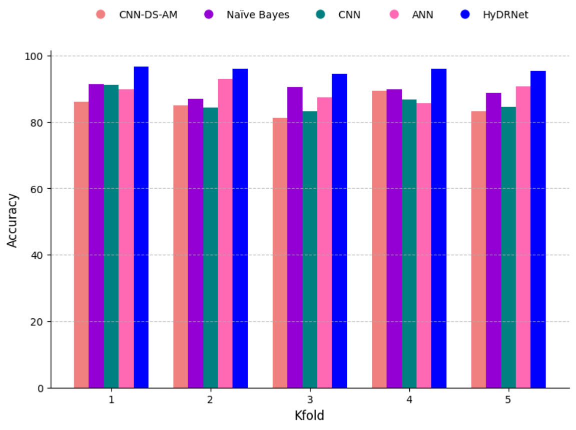
(g) (h)

(i) (j)

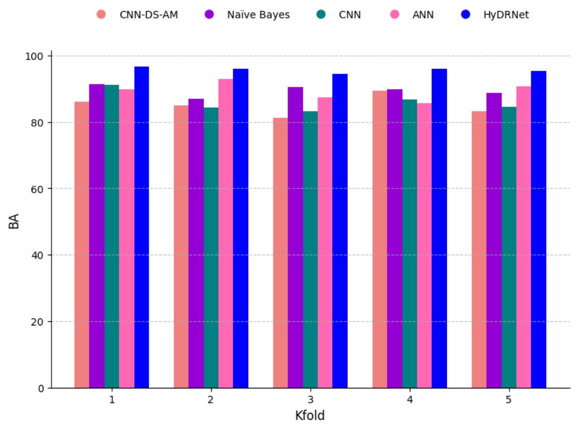
Fig 6.With and Without Weight Optimization of proposed approach regarding to metrics such as (a) Accuracy, (b) F1-Score, (c) FDR, (d) FNR, (e) FPR, (f) MCC, (g) NPV, (h) Precision, (i) Sensitivity, and (j) Specificity

6.5 Liver Disease Prediction Evaluation

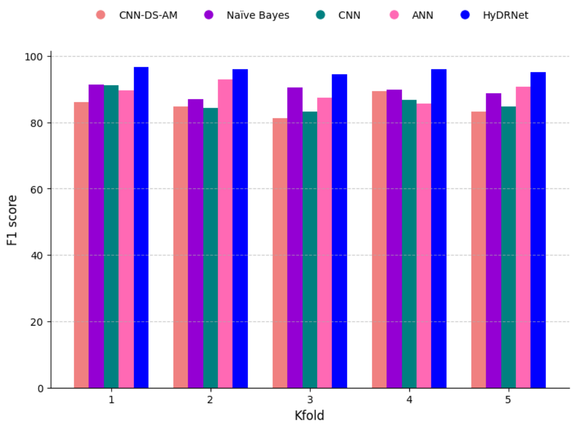
Fig. 7 presents evaluation of liver disease prediction using proposed HyDRNet model. The performance of HyDRNet is assessed and compared with other models, including CNN-DS-AM, Naïve Bayes, CNN, and ANN. The proposed model demonstrates superior accuracy and reliability, achieving improvements of 14.28%, 5.49%, 6.66%, and 10.34% over CNN-DS-AM, Naïve Bayes, CNN, and ANN, respectively, at 1 K-fold. A K-fold analysis confirms that HyDRNet consistently maintains higher accuracy. The model's high accuracy enables it to effectively capture patterns in liver disease images and predict conditions at an early stage, minimizing false predictions. HyDRNet also exhibits increased sensitivity, allowing for detection of mild or early-stage liver disease and supporting timely treatment. Furthermore, the model shows high specificity, accurately distinguishing between healthy and diseased cases. Overall, these results highlight the robustness and effectiveness of the HyDRNet framework in early and reliable liver disease diagnosis.


CNN-DS-AM
Naïve Bayes
CNN
ANN
HyDRNet
Accuracy
0
20
40
60
80
100
1
2
3
4
5
Kfold

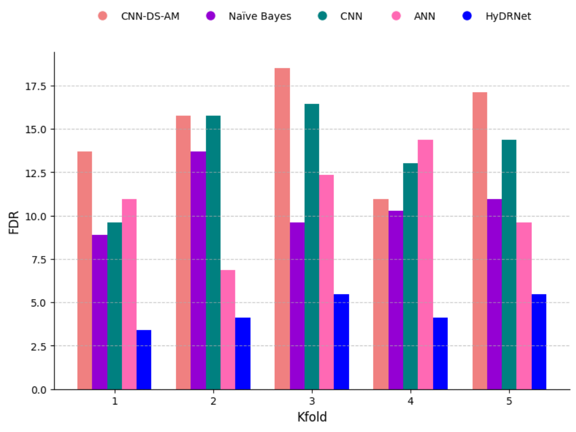
(a)


CNN-DS-AM
Naïve Bayes
CNN
ANN
HyDRNet
BA
0
20
40
60
80
100
1
2
3
4
5
Kfold

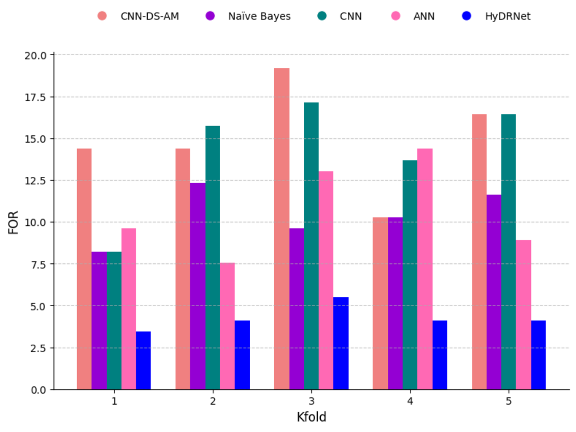
(b)


CNN-DS-AM
Naïve Bayes
CNN
ANN
HyDRNet
F1 score
0
20
40
60
80
100
1
2
3
4
5
Kfold

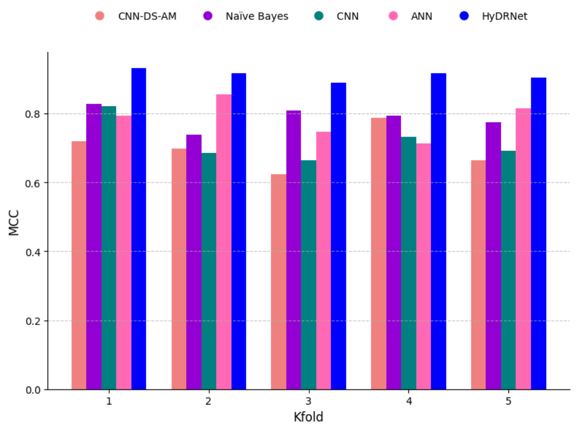
(c)


CNN-DS-AM
Naïve Bayes
CNN
ANN
HyDRNet
FDR
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
1
2
3
4
5
Kfold

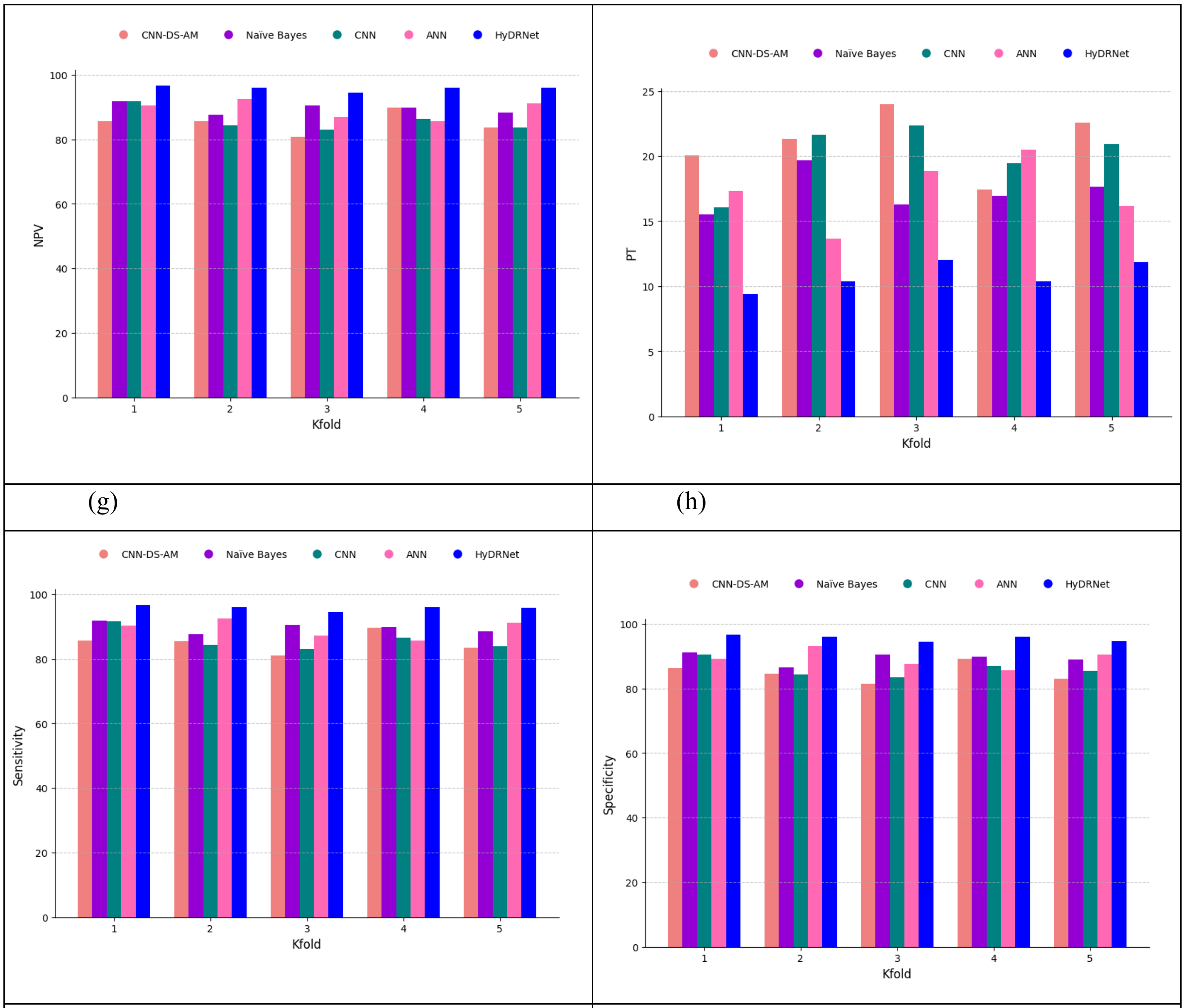
(d)


CNN-DS-AM
Naïve Bayes
CNN
ANN
HyDRNet
FOR
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
1
2
3
4
5
Kfold

(e)


CNN-DS-AM
Naïve Bayes
CNN
ANN
HyDRNet
MCC
0.0
0.2
0.4
0.6
0.8
1
2
3
4
5
Kfold

(f)



(g) (h)

(i) (j)

Fig 7. Liver Disease Prediction analysis of Proposed approach based on Metrics such as (a) Accuracy, (b) F1-Score, (c) FDR, (d) FNR, (e) FPR, (f) MCC, (g) NPV, (h) Precision, (i) Sensitivity, and (j) Specificity

6.6 Confusion Matrix Assessment

The proposed HyDRNet model’s performance is analyzed using a confusion matrix, as shown in Fig. 8, which provides a clear comparison between predicted and true values. This assessment highlights areas for improvement, such as reducing false positives and missed detections. crucial factors in medical diagnostics. The combination of IRIA-SOA and HyDRNet has demonstrated superior performance in liver disease prediction. The IRIA-SOA algorithm optimizes the cost function, ensuring precise training leading to enhanced model efficiency. Through effective error minimization during training, the IRIA-SOA-HyDRNet model attains higher accuracy, reduced error rates, and superior generalization relative to earlier approaches. Thus, the proposed approach provides a trustworthy and efficient solution for predicting liver disease by providing significant benefits in terms of optimized computational performance and enhanced clinical accuracy.

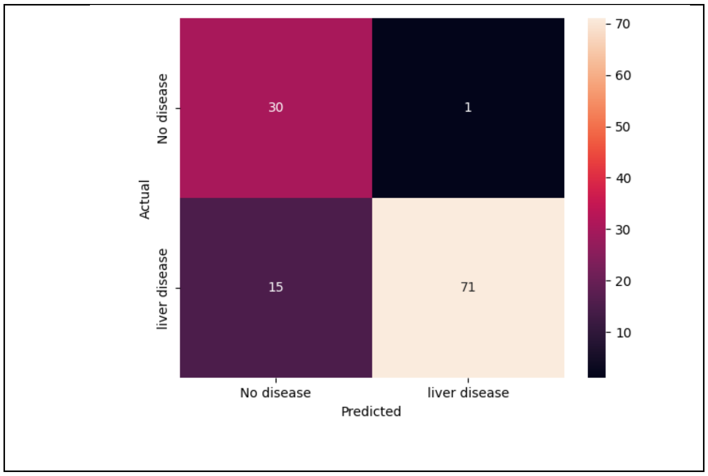


Fig 8.Confusion Matrix Evaluation on the Proposed Model

6.7 Accuracy performance of proposed method

Table 2 illustrates performance of IRIA-SOA-based HyDRNet model in terms of accuracy across multiple activation functions. The accuracy of the proposed model is evaluated by various activation functions. Activation functions used are linear, ReLu, Tanh, sigmoid, and Softmax. This evaluation shows that a higher metric value corresponds to improved accuracy. The proposed model is evaluated alongside alternative models, including CNN-DS-AM, ANN, CNN, and Naïve Bayes. The proposed HyDRNet model results in 3.32%, 14.65%, 2.19%, and 6.83% more than the other ANN, CNN, Naïve-Bayes, and CNN-DS-AM models when evaluated with a linear activation function. This proved that the accurate predictions given by the proposed model enable the identification of liver diseases at early stages, ensuring timely medical intervention and preventing complications. High accuracy reduces false positives and false negatives to guarantee accurate patient diagnosis and treatment. diagnoses and avoid unnecessary treatments or missed conditions.

Table 2.Accuracy analysis of implemented approach against various methods

Activation Function	**CNN-DS-AM (Kalaiselvi & Anusuya, 2023)**	**Naïve Bayes (Velu *et al.,* 2022)**	**CNN (Chunduru *et al.,* 2024)**	**ANN (Dashti *et al.,* 2024)**	**Proposed HyDRNet**
Linear	88.462	92.308	82.479	91.453	94.017
Relu	82.051	94.444	84.615	87.179	94.872
Tanh	80.342	91.453	91.453	85.897	95.726
Sigmoid	78.632	90.598	88.889	91.880	96.581
Softmax	83.761	87.607	82.051	90.598	94.872

6.8 Statistical Evaluation

Table 3 shows statistical analysis of developed model for liver disease detection. The evaluation highlights best and worst performances and includes key metrics such as mean, median, and standard deviation, which are essential for accurate decision-making. From the table, it is noted that the proposed IRIA-SOA performs 41.10%, 49%, 39.57%, and 51.20% better than SFOA, NGO, RKOA and COA. The IRIA-SOA algorithm has superior performance than others. This improvement strengthens both accuracy and stability of proposed model in diagnosing liver disease. An IRIA-SOA algorithms help in identifying varieties of patterns in liver disease images and provide accurate results. The model explains the overall accuracy, sensitivity and specificity and declares the efficient performance.

Table 3. Statistical perfromance of suggested framework against existing methods

Statistical	COA (Qi *et al.,* 2024)	RKOA (Gunasekaran *et al.,* 2024)	NGO (Yang *et al.,* 2024)	SFOA (Zhong *et al.,* 2025)	Proposed IRIA-SOA
BEST	1.574	1.271	1.506	1.304	0.768
WORST	2.354	5.318	2.917	4.937	2.077
MEAN	1.724	1.501	1.609	1.408	0.947
MEDIAN	1.574	1.271	1.506	1.304	0.768
STD	0.197	0.607	0.333	0.551	0.394

6.9 ROC Experimental analysis

Fig. 9 presents ROC evaluation of proposed model. The ROC curve is a key tool for model assessment, highlighting balance between sensitivity and specificity. This balance is critical in liver disease prediction to ensure accurate detection of true cases while minimizing false positives. The results indicate that HyDRNet model, enhanced with IRIA-SOA algorithm, significantly outperforms conventional models. Its true positive rate is 2.9%, 7.6%, 4.4%, and 16.6% higher than CNN, ANN, CNN-DS-AM, and Naïve Bayes, respectively. With a superior AUC score, HyDRNet-IRIA-SOA framework demonstrates excellent predictive performance. By optimizing key parameters using IRIA-SOA algorithm, the model achieves an effective trade-off between sensitivity and specificity, ensuring reliable and accurate predictions. This reduces diagnostic errors such as false positives and false negatives, improving clinical reliability. Furthermore, model's scalability allows it to process large datasets efficiently. Achieving a high true positive rate while maintaining a low false positive rate is essential for maximizing diagnostic performance.

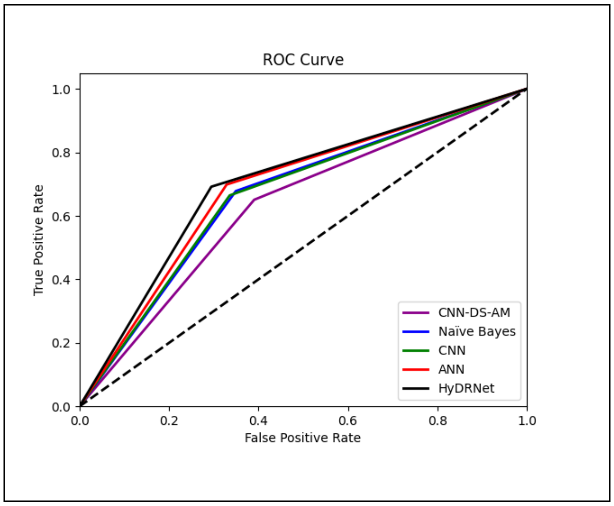


fig 9. ROC analysis of implemented approach

7. CONCLUSION

In this work, HyDRNet-based model is proposed for liver disease prediction, utilizing deep learning to process medical data and identify liver conditions at an early stage. It selected the most important features, like biomarkers, to improve prediction accuracy. The model worked well with large datasets, making it reliable and scalable for different medical scenarios. The reliable performance of model facilitates prompt diagnosis, contributing to better patient management and cost efficiency. Liver disease prediction with HyDRNet starts with preprocessing medical data. Features were extracted from the preprocessed data using WRBM, which optimized the weights with the help of the IRIA-SOA method for detecting and recognizing patterns. Best features were collected from the dataset for disease prediction. The derived attributes from the dataset were then sent to the HyDRNet model to obtain the output. These features were fed into the Conv-ELM and ESN blocks within HyDRNet simultaneously, and the predicted output from each block was averaged to produce the final output. The suggested model HyDRNet surpassed existing methods such as CNN, ANN, CNN-DS-AM, and Naïve Bayes, proving its efficiency in achieving precise liver disease prediction.

Achieving an accuracy rate of 98%, IRIA-SOA-WRBM-based HyDRNet outperformed all other approaches in the evaluation. Comparatively, CNN achieved 89%, ANN recorded 87%, CNN-DS-AM obtained 85%, and Naïve Bayes achieved 90%. The superior performance of IRIA-SOA-WRBM-based HyDRNet underscores its ability to accurately analyze and classify data, making it suitable for precision-driven tasks. Feature extraction is improved through weight optimization using IRIA-SOA algorithm in WRBM. The averaged output of the model HyDRNet increases the accuracy rate of predicted output. Thereby it predicted the presence of liver disease in early stages.

Limitation and Future Scope: The proposed model struggles with the intricacy and computational challenges involved in a process or system of liver disease data, which often includes diverse and intricate features that can be difficult to capture accurately. The use of Conv-ELM and ESN alone may not reliably capture most important features, impacting prediction accuracy. Employing hybrid or ensemble-based algorithms can address these challenges and increase model's precision.

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Data Availability Statement:

The data underlying this article are available in Liver disease dataset, at https://www.kaggle.com/datasets/uciml/indian-liver-patient-records

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