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XAIHO: explainable AI leveraging hybrid optimized framework for liver cirrhosis detection

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Abstract

This study introduces an explainable AI leveraging hybrid optimized framework for liver cirrhosis detection (XAIHO) with deep learning (DL) to address the critical challenges of low interpretability and diagnostic inefficiency in traditional and AI-driven liver cirrhosis detection systems. Conventional approaches often rely on invasive procedures and lack transparency, while existing DL models, although accurate, function as black boxes and limit clinical trust. To bridge this gap, the research initially explored machine learning (ML) models and then integrated XAI techniques to improve model explainability. Subsequently, DL approaches were employed using fine-tuned pre-trained models such as VGG16, VGG19, ResNet50, ResNet101, Xception, Inception-V3, EfficientNetB1, EfficientNetB2, Vision Transformer (ViT), and InceptionResNetV2. While these models showed strong classification performance, their limited interpretability remained a barrier for clinical deployment. To address this, the proposed XAIHO framework was developed in two phases: first implementing XAI without optimizers, and then enhancing it with advanced optimizers (Adam, NAdam, RMSProp) to improve both predictive accuracy and interpretability. The proposed XAIHO framework achieves a peak accuracy of 92.35%, representing a 4% improvement over standard DL models and an 8% increase compared to traditional ML baselines. Additionally, transparency and interpretability are significantly improved using SHAP values and attention-based visualizations, providing meaningful insights into critical features such as bilirubin, albumin, and age. Empirical results, validate through multiple performance metrics, confirm the framework's potential for accurate, transparent, and clinically applicable liver cirrhosis diagnosis.

Keywords Liver cirrhosis disease, Machine learning (ML), Deep learning (DL), Convolutional neural network (CNN), eXplainable AI (XAI)

1 Introduction

Liver cirrhosis is a progressive, severe condition by widespread scarring of liver tissue consequential from protracted liver damage. Common causes include persistent alcohol use, viral hepatitis (particularly Hepatitis B and C), non-alcoholic fatty liver disease



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(NAFLD), and autoimmune disorders [1]. As cirrhosis advances, it impairs the liver's functionality, leading to complications such as liver failure, portal hypertension, and a significant risk of liver cancer [2, 3]. The disease typically develops steadily over several years and is often asymptomatic in its early stages. Early recognition is essential to prevent strict complications and enhance patient outcomes [4]. Liver cirrhosis is an enduring liver disease characterized by the scarring of liver tissue, frequently caused by alcohol consumption, viral hepatitis, or NAFLD. As liver function declines, it leads to complications such as jaundice, fluid buildup, fatigue, bleeding, and a delicate risk of liver cancer [5]. Without appropriate treatment, cirrhosis can progress to liver breakdown and is a significant cause of death worldwide [6]. Early judgment and involvement are critical for better supervision and prediction. The stages of liver disease are shown in Fig. 1. There are four distinct phases of liver disease progression, each of which reflects the severity of liver damage.

The incidence of liver cirrhosis has risen significantly, touching millions worldwide and accounting for around 2 million deaths in 2023 [8]. Figure 2 highlights a dependable increase in liver cirrhosis cases and deaths worldwide (2000–2024), mainly recognized as alcohol expenditure, viral hepatitis, and NAFLD, underscoring significant global health distress. It is also a severity sign for liver disease that is exponentially increasing cases along with deaths.

Table 1 shows a comprehensive list of acronyms and their meanings used throughout the paper.

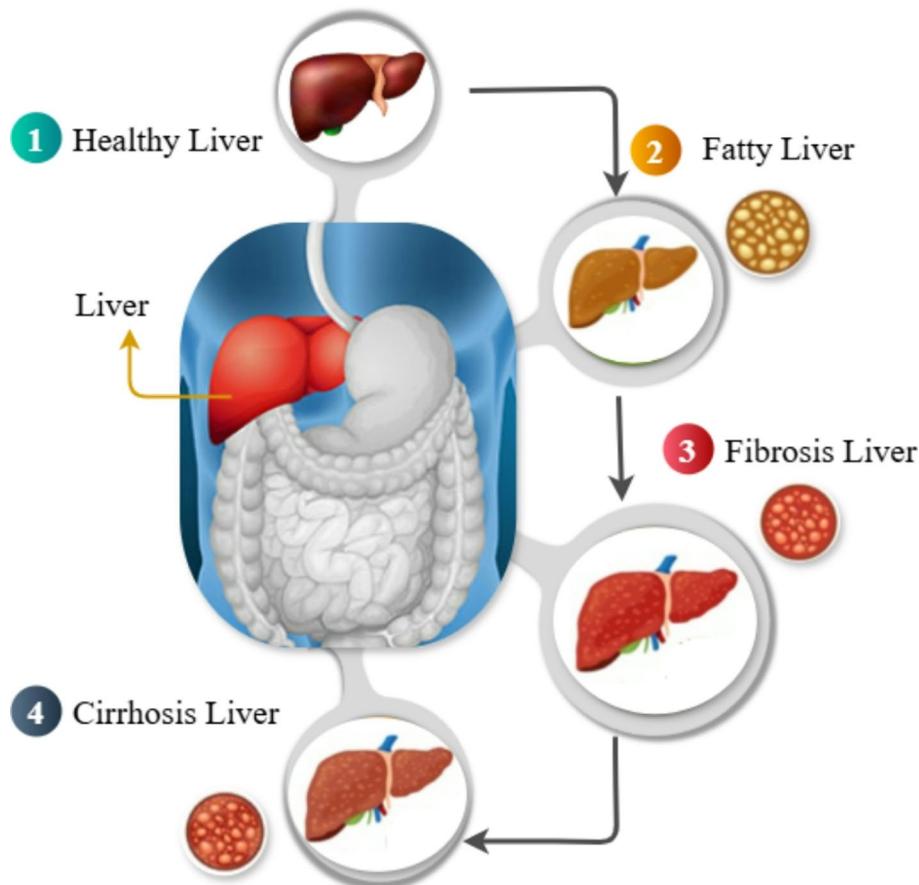
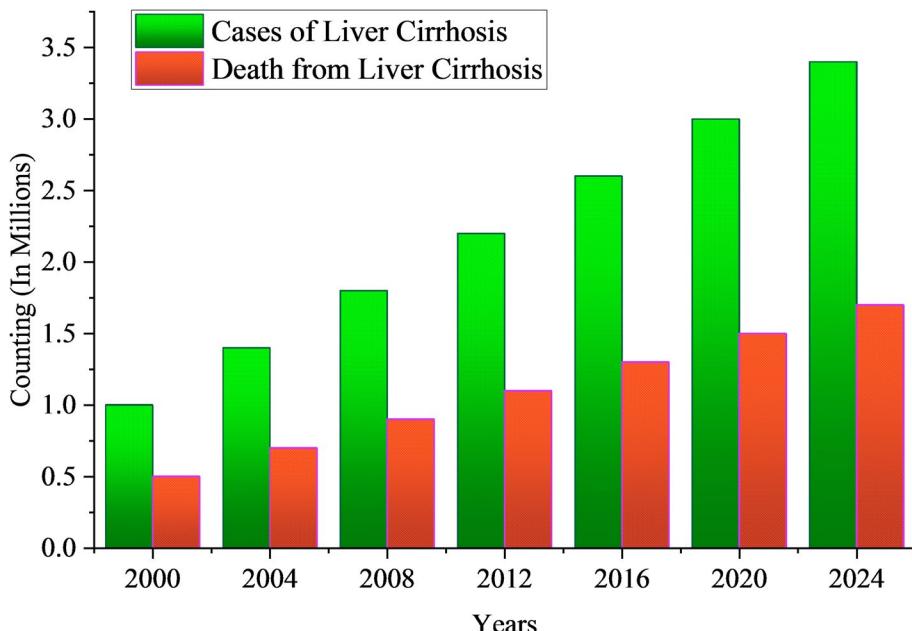


Fig. 1 Stage of Liver Cirrhosis [7]

**Fig. 2** Liver Cirrhosis Cases and Death [8]**Table 1** Acronyms referenced in the Article

S. No.	Acronym	Definition
1	NAFLD	Non-alcoholic fatty liver disease
2	DL	Deep Learning
3	CNN	Convolutional neural networks
4	TL	Transfer learning
5	ML	Machine learning
6	XAI	Explainable Artificial Intelligence
7	SNN	Siamese neural network
8	RoC	Receiver operating characteristic
9	US	Ultrasound images
10	CT	Computerized tomography images
11	MRI	Magnetic resonance imaging
12	Adam	Adaptive Moment Estimation
13	NAdam	Nesterov-accelerated Adam
9	RMSprop	Root Mean Square Propagation
10	NB	Naive Bayes

In India, liver cirrhosis cases and deaths have also shown a stable rise in Fig. 3, attributed to factors such as alcohol use, hepatitis infections, and NAFLD, highlighting an increasing public health worry. The fraction of patients with alcohol-related cirrhosis and nonalcoholic patients is 63% and 19%, respectively. Moreover, patients with viral hepatitis-related cirrhosis is 16% [9] in a single state.

Early recognition is indispensable to slowing disease development and thwarting supplementary liver damage. However, diagnosing liver cirrhosis often involves costly and persistent measures like liver biopsies or sophisticated imaging techniques, making an appropriate and truthful diagnosis unreachable for many, predominantly in low-resource settings.

Recent therapeutic imaging and deep learning (DL) advancements have smoothed the way for computerized, non-invasive, and cost-effective liver cirrhosis recognition.

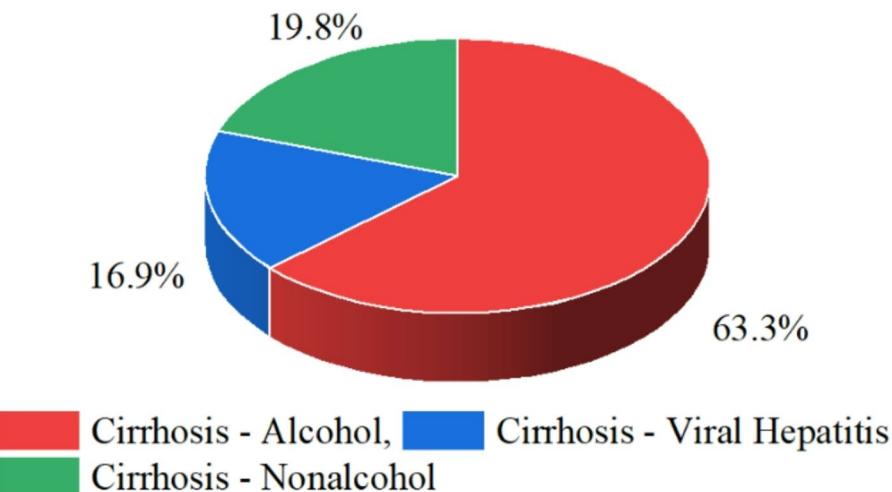


Fig. 3 Liver Cirrhosis Cases in India

Techniques such as convolutional neural networks (CNN) and other DL models have shown hopeful accuracy and competence in classifying liver cirrhosis. In spite of this enhancement, challenges like data imbalance, model robustness, and computational demands persist. This learning aims to improve liver cirrhosis diagnosis using transfer learning (TL) and data amplification. TL leverages pre-trained models to extract features from liver descriptions, which are fine-tuned for classifying cirrhosis stringency [10] and [11]. Data intensification generates varied image variations, addressing data patchiness and refining model presentation. A pervasive appraisal of TL approaches will be conducted, optimizing hyperparameters and comparing model presentation using different metrics.

Although there are several survey studies on medical diseases using machine learning (ML) & CNN, this manuscript propose a new loom to enhancing the accuracy and transparency of healthcare systems by integrating Explainable Artificial Intelligence (XAI). We have also explored the key properties of XAI, such as fidelity, completeness, and compactness. By combining XAI with feature selection, our approach aims to improve the detection accuracy of Cirrhosis and ensure that the decision-making process is transparent and understandable to the patients and doctors.

1.1 Motivation

Liver cirrhosis is a degenerative illness in nature that has a significant effect on health worldwide, increasing mortality and medical expenses. Improved patient outcomes and effective treatment depend on early identification. However, traditional diagnostic methods, such as biopsy and imaging, are often invasive, expensive, and subject to interpretation variability among clinicians. The inability of existing AI-driven models to be explained is a significant issue, which makes it challenging for medical personnel to trust automated diagnostic tools and interpret forecasts. The “black-box” nature of AI models impedes their use in healthcare by preventing transparent decision-making. Medical professionals often resist adopting opaque systems that lack transparency, as they cannot rationalize outcomes to patients or integrate model outputs into personalized treatment plans. For example, two patients with identical bilirubin levels may require vastly different clinical interventions depending on additional risk factors. Hence, XAI becomes

a bridge between complex AI models and human understanding, empowering doctors with visual and statistical justifications of model predictions. Guo et al. [16]. present a real-world case study, which developed an interpretable ML framework to predict liver cirrhosis complications using plasma metabolomic data. Their approach, which included model explainability via a nomogram, outperformed traditional fibrosis scoring systems and allowed better risk stratification across patient groups. To address the concern, the research initially explored ML models and integrated XAI techniques to improve model transparency. Using XAI and DL models in liver cirrhosis research improves indicative precision and enables modified care. XAI pinpoints the specific spike of cirrhosis datasets, ensuring intelligibility. At the same time, DL analyzes intricate data for early revealing and treatment, tackling this serious health issue with accuracy and improvement. Therefore, developing an XAI Leveraging Hybrid Optimized Framework for Liver Cirrhosis Detection depiction is exceedingly annoyed with an hybrid approach that can significantly burden healthcare.

In nutshell, this work is driven by the dual goals of clinical effectiveness and interpretability. The integration of explainable AI into liver cirrhosis detection frameworks not only enhances model trust and adoption but also improves patient care through actionable insights—a necessity in the age of intelligent healthcare.

1.2 Contribution & novelty

The primary assistance of this work focus on integrating and enhancing transparency and performance within XAI with the DL model and optimizers for liver cirrhosis analysis, enabling accurate disease localization in datasets with more excellent intelligibility. Merging interpretability with sophisticated algorithms enhances investigative accuracy, supports custom-made treatments, and provides clinicians with actionable insights, addressing a noteworthy healthcare challenge with meticulousness and improvement. The key contributions are as follows:

- We propose XAIHO, a hybrid optimized framework that integrates explainable AI (XAI) techniques with DL models for liver cirrhosis detection.
- XAIHO utilizes SHAP to improve model transparency, enabling medical experts to understand AI-based liver cirrhosis predictions.
- A comparative analysis was performed by applying XAI without optimizers and then XAI with optimizers, demonstrating notable improvements in classification performance.
- A hybrid feature selection approach, combining DL-based methods and statistical techniques, was utilized to extract the most relevant features and enhance model transparency.
- A random forest classifier is used to classify extracted features into different liver cirrhosis stages, ensuring high reliability and computational efficiency.
- The model was trained on a publicly available liver disease dataset, leveraging clinically significant features to enhance decision support and interpretability.
- The proposed XAIHO framework achieved an accuracy of up to 92.35%, with interpretability further improved using SHAP values and attention-based visualization techniques, fostering clinical trust and aiding medical decision-making.

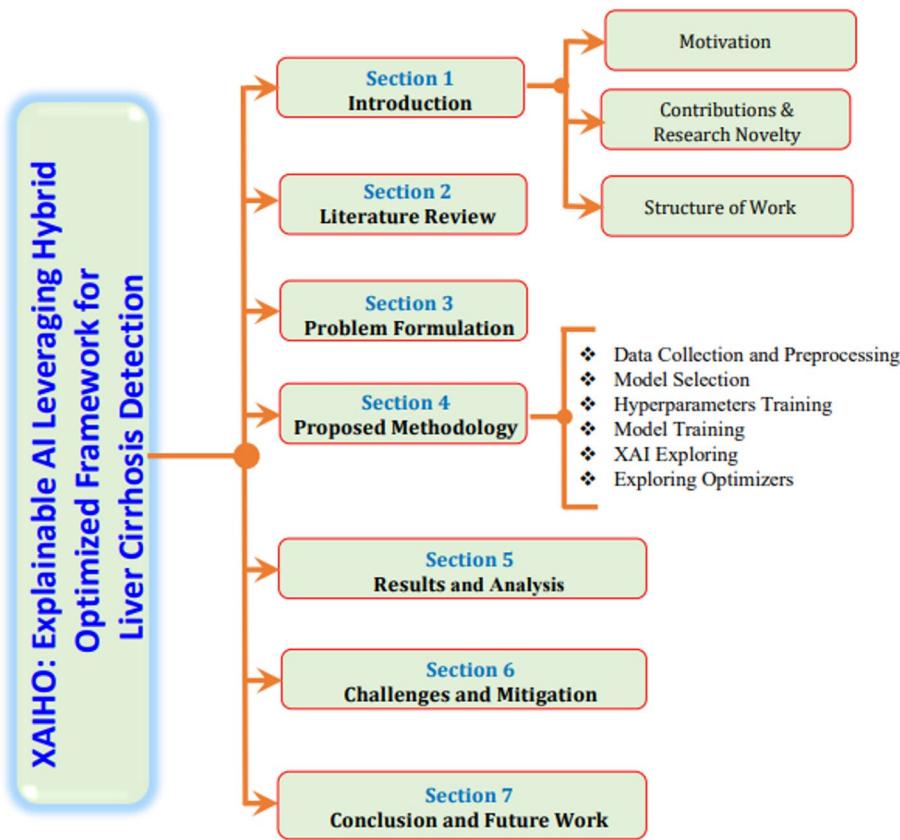


Fig. 4 Detailed organization of the content flow used in the paper

Table 2 Comparative analysis of existing schemes

S.No.	Authors	Methods	Accuracy & Findings
1	Kiran et al. [12]	CNN	98.43% & Categorization of fatty liver
2	Zhang et al. [13]	IVW, MR-Egger	95% & predicted MASLD
3	Zhou et al. [14]	CEUS-LI-RADS LR-5	96% & Evaluated the performance of LR-5
4	Theerthagiri et al. [15]	(HGBoost) MLP, GBoost, Adaboost	95.78% & HGBoost outperformed other Models
5	Guo et al. [16]	AUC & Decision curve	86% & AUC:0.84 outperforming fibrosis-4 index (time dependent AUC diff: 0.06
6	Mohit et al. [4]	SNN	99% & categorize fatty liver grade 1,2,3 & chronic liver diseases.
7	Ramachandran et al. [17]	PCA	96.54% & Extract features analyzes Principal components
8	Makram et al. [3]	CNN Techniques	98% & predicting liver cancer variant
9	Khaled et al. [20]	VGG16,19, ResNet50,101, Xception	98% & predict liver cirrhosis variant
10	Moumin et al. [23]	ML Techniques	97.4% & categorize the liver cirrhosis

1.3 Structure of paper

The residue of this manuscript is prearranged as illustrated in Fig. 4. Section 2 presents correlated work. Section 3 presents a quandary formulation. Section 4 provides into detail about the planned methodology. The conclusion and investigation of the projected

transfer-learning (TL)-based computation are accessible in Sect. 5. The Sect. 6 provides a termination and prospect compass of the work.

2 Related work

Numerous researchers have focused on classifying liver cirrhosis diseases, leading to a miscellaneous variety of momentous contributions accredited in this explicit field. Kiran et al. [12] focus on the analysis and treatment of fatty liver conditions during the development of a convolutional neural network (CNN). By evaluating its recognition performance against several pre-trained deep CNN models, the study aims to accomplish strong simplification capability, especially in accurately categorizing fatty liver. The work utilized synopsis statistics from genome-wide involvement studies to execute a two-sample Mendelian randomization (MR) investigation [13]. Five corresponding MR methods, including contrary variance weighting (IVW), MR-Egger, weighted median, undemanding mode, and weighted mode, were applied to scrutinize the causal affiliation between MASLD and GH and PE. The hereditarily predicted MASLD was found to increase the risk of GH appreciably (IVW: OR = 1.138, 95% CI: 1.062–1.220, $p < 0.001$), whereas there was minimal confirmation of a fundamental link between MASLD and PE (IVW: OR = 0.980, 95% CI: 0.910–1.056, $p = 0.594$). Zhou et al. assigned CEUS-LI-RADS categories (LR-5 for predicting HCC) by six blinded readers and compared these to the confirmed HCC diagnoses in liver cirrhosis patients according to the 2017 China Liver Cancer Guidelines (CLCG) [14]. Contrast-enhanced ultrasound (CEUS) features were recorded for 96 patients, each with histology-proven lesions. The analytical performance of LR-5 was evaluated based on sympathy, specificity, and accuracy. Multi-reader agreement was assessed using intraclass correlation coefficients (ICC). Theerthagiri et al. aim to forecast liver disorders using feature selection and categorization methods [15]. The paper introduces the Histogram-based Gradient Boosting categorization Tree with a recursive feature assortment algorithm (HGBoost). This loom combines recursive feature selection with Gradient Boosting to envisage liver disease. The planned HGBoost method was evaluated using data from Indian liver patient records. The study involves implementing and comparing various categorization techniques, including Multi-layer Perceptron (MLP), GBoost, AdaBoost, and the proposed HGBoost, with concert assessed based on accuracy, confusion matrix, and area under the curve. The HGBoost method, aided by recursive feature selection, outperformed other existing algorithms. Guo et al. defined liver cirrhosis complications as hospitalization due to liver cirrhosis or the appearance of HCC [16]. They applied an interpretable machine-learning framework to analyze metabolomic data imitative of 168 circulating metabolites in the training cohort. An integrated nomogram was developed and compared to conventional and genetic risk scores. The cohort was separated into three groups—low-risk, middle-risk, and high-risk—based on selected cutoffs from the nomogram. The predictive performance was validated using a time-dependent area under the receiver operating characteristic curve (time-dependent AUC), calibration curves, and decision curve investigation. The metabolomic state outperformed the fibrosis-4 index (time-dependent AUC difference: 0.06 [0.03–0.10]) and the polygenic risk score (0.25 [0.21–0.29]). The model precisely predicted the 10-year risk of liver cirrhosis complications in the training cohort.

Mohit et al. recommend a self-supervised Siamese neural network (SNN) for identifying fatty liver [4]. The SNN leverages the model optimization properties of unsupervised learning and the physical footnote properties of supervised learning. This technique is based on contrastive learning within a joint embedding network. It enables it to learn delicate representations from unlabeled medical images for categorization tasks, requiring only one or a few labeled images per class for training. The planned model's competence was validated using liver ultrasound images, classifying them as normal, fatty liver grade-I (mild), grade-II (moderate), grade-III (severe), and chronic liver diseases. The model achieved remarkable categorization accuracy of 99.90% for a two-class classifier (normal/abnormal) and 99.77% for a five-class classifier by minimizing contrastive loss. Ramachandran et al. notice liver tenderness using principal component analysis (PCA) for feature extraction and random forest for categorization. A hybrid model is urbanized for feature extraction, which analyzes liver cirrhosis's principal components and categorization [17]. The model's performance is evaluated on various datasets, and its efficiency is assessed using the receiver operating characteristic (RoC) curve. Desai et al. investigate ML algorithms for disease calculation based on symptoms [18]. The learning proposes the implementation of supervised ML algorithms to calculate liver cancer in patients. The model's accuracy is evaluated and compared to recognize the most suitable model for liver cancer prophecy. Wang et al. aim to undertake the serious healthcare challenge of liver cirrhosis categorization by attracting the correctness of ultrasound imaging and aiding medical professionals in early diagnosis and interference [2]. The article introduces a novel multiscale feature fusion network model (MSFNet), which employs a feature extraction module to capture multistage features from ultrasound images. This move allows the neural network to influence richer information for more precise categorization of cirrhosis stages. In [19], widespread research on liver disease investigation uses machine learning, emphasizing advancements in disease exposure and diagnosis accuracy. By leveraging machine learning, computers can attract knowledge and make inferences from historical data, enabling them to appoint themselves to self-learning processes without explicit programming by human developers. This study provides a general idea of machine learning techniques applied to liver disease, utilizing various datasets such as liver function test data, ultrasound (US) images, computerized tomography (CT) images, and magnetic resonance imaging (MRI). Khaled et al. make several contributions. First, they made considerable effort to create a multi-class liver tumour dataset sourced from Ain Shams University Specialized Hospital (ASUSH) in Egypt, annotated by two specialists [20]. The dataset consists of 8,237 CT images categorized into eight different classes. Furthermore, the article benchmarks this dataset against abundant deep learning models, including a premeditated CNN and fine-tuned pre-trained models such as VGG16, VGG19, ResNet50, ResNet101, Xception, and Inception-V3. The investigational results demonstrate that the projected CNN outperforms the fine-tuned models, achieving a typical precision of 99.76% in predicting the eight dissimilarities of liver cancer. Makram et al. currently use the ASUSH, an inventive resource, as Egypt's first multi-class liver cancer dataset with eight divergent classes [3]. Furthermore, the article benchmarks this dataset against a multiplicity of deep learning models, together with the projected CNN, as well as fine-tuned pre-trained models such as VGG16, VGG19, ResNet50, ResNet101, EfficientNetB1, EfficientNetB2, Xception, Vision Transformer (ViT), Inception-V3, and InceptionResNetV2. The experimental

results, evaluated across numerous routine metrics, demonstrate that the models achieved an accuracy of 98% in predicting liver cancer variants.

The other application of ViT applies on eye disease and skin cancer discussed in [21, 22], respectively. Moumin et al. spotlight mounting an AI system, supported by ML algorithms, to support professionals in diagnosing liver cirrhosis at its untimely stages [23]. The paper presents four dissimilar models built using experimental parameters from patients and machine learning techniques. Among these models, the random forest model achieved the highest accuracy, with a score of 97.4% using the 10-fold cross-validation process. Da Silva et al. present a fully automated platform designed for high-throughput sorting of 3D spheroids through label-free analysis of bright field images [24]. The compressed platform is well-matched with standard biosafety cabinets and features a commissioned microscope along with two fluidic systems that optimize the treatment of individual spheroids to recover sorting speed. ML is utilized to categorize spheroids based on their bio printing compatibility, enabling intricate morphological analysis, including viability estimation, without the need for enveloping fluorescent labels. Additionally, the learning demonstrates the efficacy of transfer learning in biological applications, addressing the deal with acquiring large datasets.

Some recent studies in broader medical domains have begun to incorporate explainability.

This study introduces a novel and effective learning framework for accurately identifying liver disease patients [33]. The proposed approach combines multiple feature ranking and projection techniques, leveraging deep learning to detect early indicators of liver disorders. To enhance interpretability, SHAP are employed for global interpretation analysis, enabling optimal feature selection by evaluating each feature's contribution to the model's predictions. Experimental evaluations reveal that the proposed model consistently outperforms conventional machine learning algorithms, demonstrating superior accuracy. Through cross-validation and comprehensive testing, our deep neural network (DNN) achieves an accuracy of 90.12%, exceeding the performance of other classifiers. A novel XGBoost-based liver disease prediction model that integrates diverse feature selection techniques, including ranking methods and statistical projection strategies, to effectively identify early signs of liver disorders is presented in [34]. The Fisher score is utilized to perform global interpretation, enabling the selection of the most relevant features by evaluating their contributions to the overall model. The proposed model's performance is thoroughly assessed using k-fold cross-validation. The evaluation is conducted in three phases: first, by analyzing the model's effectiveness with both individual and hybrid feature sets; second, by comparing its performance with commonly used classification algorithms; and third, by benchmarking it against existing state-of-the-art computational models. The experimental outcomes demonstrate that the proposed model consistently outperforms existing approaches, achieving an average accuracy of 92.07%.

This study proposes an explainable AI-based model for accurate and rapid brain tumour diagnosis using two widely recognised datasets: the four-class Kaggle dataset (Dataset I) and the three-class Figshare dataset (Dataset II) [35]. DenseNet201 is a pre-trained feature extractor, and Grad-CAM is used for tumour localisation. Features are selected using the Iterative Neighborhood Component Analysis (INCA) method and classified using a Support Vector Machine (SVM) with 10-fold cross-validation. The

proposed model achieved high accuracy, reaching 98.65% on Dataset I and 99.97% on Dataset II. The Greylag Goose Optimization (GGO) algorithm to enhance heart disease classification accuracy is introduced in [36]. The algorithm effectively selects optimal features in its binary form (bGGO), outperforming six other binary optimization methods. Multiple classifiers were tested, with Long Short-Term Memory (LSTM) delivering the best results. GGO was also used to tune LSTM hyperparameters, leading to a significant improvement. The GGO-LSTM model achieved the highest accuracy of 99.58%, demonstrating its superiority over alternative optimizers. The primary aim of this work is to propose a novel framework, CVD-SO, for analyzing cardiovascular disease (CVD) data using the Snake Optimization (SO) algorithm [37]. The framework integrates SO with five ML classifiers to effectively select and classify relevant medical data. By combining machine learning and optimization within a unified model, the study achieves highly accurate CVD detection, reaching an impressive accuracy of 99.9%. The proposed MBER algorithm was evaluated against five competing optimizers—BER, PSO, WAO, GWO, and GA—using predefined assessment criteria [38]. Statistical significance was verified through ANOVA and Wilcoxon signed-rank tests, while visual analyses confirmed the algorithm's robustness. MBER outperformed others on most unimodal benchmark functions. For classification, various machine learning models were tested, with KNN delivering the best results, achieving top metrics in precision (0.959), NPV (0.965), F1-score (0.963), accuracy (0.961), sensitivity (0.971), and specificity (0.950). This study focuses on improving mechanical ventilation prediction using the MIMIC-III dataset, analyzing patient data across 6-, 12-, and 24-hour windows, with a 6-hour gap before forecasting outcomes over the next 48 h. The proposed two-layer model [39] uses multilayer multitask LSTM networks—Layer 1 predicts the need for ventilation and mortality risk, while Layer 2 estimates the duration of ventilation—enabling timely and accurate ICU decision-making. This study employs four feature selection methods—BBFS, BPSO, BGWO, and BWAO—where BBFS demonstrated superior performance with an average error reduction of 47.29% compared to others [40]. Six ML models (RF, SGD, NBC, DC, QDA, and ET) were then applied to a dataset containing 310 instances and six features. Among them, the Random Forest (RF) model achieved the best results, reaching an accuracy of 91.4%. Some other recent advancements in XAI have significantly improved transparency in medical DL systems. Several researchers have combined interpretable techniques with deep models to enhance clinical trust. For instance, the DeepXplainer framework [41] has been used to detect lung cancer by coupling deep learning with layered explanations, providing high predictive accuracy alongside feature-level interpretability. Similarly, efforts in IoMT-driven healthcare diagnostics [42] have been advanced through explainable AI fusion frameworks, as seen in the work on Explainable AI-driven IoMT fusion, highlighting the integration of multi-modal medical data sources for transparent decision-making. In breast cancer diagnostics, recent work utilizing interpretable AI through fusion modelling [43] has demonstrated that coupling different modalities and providing localized feature explanations can significantly improve clinical acceptance. Additionally, synergistic fusion approaches [44] have shown promise in cardiac disease prediction by integrating multiple classifiers and XAI modules to enhance accuracy with a more apparent rationale. To tackle these challenges, we introduce OPT-CO, an innovative approach that integrates stochastic configuration networks (SCNs) with pre-trained transformer models for efficient COVID-19 classification [46]. This method

includes two distinct optimization strategies: sequential optimization (SeOp), which applies optimizers in a step-by-step fashion, and parallel optimization (PaOp), which utilizes multiple optimizers simultaneously. OPT-CO improves model performance effectively while minimizing the need for additional parameters. CTBViT, designed for more efficient and accurate tuberculosis (TB) classification in CT and X-ray images, is discussed in [47]. We introduce a Patch Reduction Block (PRB) that eliminates less significant tokens to enhance computational efficiency. Additionally, they incorporate a randomized classifier to address the overfitting challenges often associated with large pre-trained models on TB datasets. The model is rigorously evaluated across multiple datasets to assess its generalization capabilities, and the results demonstrate that CTBViT outperforms. The approach [48] enhances computational efficiency in brain MRI analysis by selectively identifying and merging less critical tokens, ensuring diagnostic accuracy is maintained. It dynamically adjusts the token structure during inference, focusing on regions most relevant for diagnosis. Furthermore, integrating randomized learning regularization improves learning stability and model robustness. Evaluations on two brain MRI datasets from the Alzheimer's Disease Neuroimaging Initiative (ADNI) reveal that LRAD-ViT achieves a diagnostic accuracy of 93.41% for distinguishing Alzheimer's Disease (AD) from cognitively normal (CN) individuals and 90.95% for differentiating CN from mild cognitive impairment (MCI), while reducing computational overhead by approximately 40%. Despite the advancements in existing models, certain limitations persist. To address these challenges, we introduce a novel DLBCNet network [49] for the multi-class classification of blood cells. As part of this framework, a specialized generative model, BCGAN, is developed to produce synthetic blood cell images. The architecture utilizes a pre-trained ResNet50 as the backbone for feature extraction. These extracted features are passed through the proposed Enhanced Transformer-based Recognition Network (ETRN) to boost classification performance. Experimental results show that the proposed model achieves an average accuracy of 95.05%, sensitivity of 93.25%, precision of 97.75%, specificity of 93.72%, and an F1-score of 95.38%.

Arya et al. [29] applied SHAP values to enhance understanding of liver cirrhosis biomarkers, and Aswin et al. [32] combined ResNet with LIME for liver cancer prediction. Still, most of these models do not optimize for accuracy and interpretability simultaneously, nor do they address the data imbalance, high computational cost, or lack of hybrid feature selection strategies. The research gap in the existing literature is a lack of explainable deep models for liver cirrhosis specifically. Very few works optimize for both performance and transparency in one hybrid framework. Existing models often neglect feature relevance interpretation (e.g., bilirubin, albumin), which is vital for medical trust. Limited integration of optimization techniques (Adam, RMSProp, etc.) with XAI frameworks in the medical domain. The section is also summarized in research gaps and findings in Table 2. We have also summarized the performance of existing XAI-enabled models for medical application approaches for a more robust comparison in Table 3.

3 Problem formulation

Liver cirrhosis is a progressive and severe circumstance that often goes undetected in its early stages due to the limitations of traditional diagnostic methods. Conventional techniques, such as biopsies and imaging, are prolonged, susceptible to creature error, and may lead to delayed or inaccurate diagnoses. Furthermore, existing AI-based models

Table 3 Comparative analysis of existing XAI schemes

S. No.	Authors & Years	Application Area	Methodology	XAI Techniques	Accuracy (In%)	Limitations
1	Arya et al. [29]	Liver Cirrhosis Biomarkers	ML with feature selection	SHAP	91.5	No DL or hybrid optimization
2	Guo et al. [16]	Cirrhosis Risk Prediction	Interpretable Nomogram	Nomogram	86	Long-term risk, not stage-wise
3	Aswin et al. [32]	Liver Cancer	ResNet + CNN	LIME	90.5	Limited clinical interpretability
4	Ali et al. [30]	Hepatitis B, Fatty Liver	ML models with insights	LIME, SHAP	88	No optimizer integration
5	Makram et al. [3]	Liver Cancer	Fine-tuned CNN models	None	98	No explainability
6	Wang et al. [2]	Liver Cirrhosis Classification	MSFNet with multiscale features	None	88.7	No feature attribution

for liver cirrhosis detection face challenges such as poor dataset quality, imbalanced data distribution, and high computational complexity, which restrict their real-world applicability in healthcare settings.

A primary concern with current AI-driven models is their lack of explainability, making it difficult for medical professionals to interpret predictions and confidently rely on automated diagnostic systems. Many AI models' "black-box" nature prevents transparent decision-making, hindering their adoption in clinical practice. Additionally, accurately classifying the different stages of liver cirrhosis remains challenging due to variations in imaging quality, limited labeled data, and the complexity of disease progression. XAI and DL liver diagnosis frameworks are used only with DL models with XAI for transparency; however, the accuracy and performance of other parameters are also issues with existing schemes. So, the hybrid model is needed to address existing problems and challenges. We have worked on the XAIHO framework, a collection of DL, XAI, and optimizations, to enhance performance and address the above-cited concerns.

4 Proposed methodology

This segment present an indication of the workflow of the projected eXplainable AI Leveraging Hybrid Optimized (XAIHO) framework for liver cirrhosis detection, the datasets used, the activation functions used, the hyper parameters used to develop the performance of the sculpt, and the accomplishment background.

This fragment illustrates the hybrid AI framework with optimizers such as Adam, NAdam, RMSProp and XAI for liver cirrhosis detection. In addition, we have also analyzed Naïve-Bayes, K-NN, SVM, Decision Tree, CNN, VGG16, ResNet-50, and XAI with optimizers and without optimizers. In Fig. 5, the proposed XAIHO framework encompasses six phases: data compilation, preprocessing, model conception, preparation, and valuation. The meticulous depiction of each division is as follows:

4.1 First segment of XAIHO framework

The first segment is Data Collection and Preprocessing as shown in Fig. 5. In this segment, the data anthology process involves assembling dissimilar datasets, including instances of liver cirrhosis disease. Subsequently, methodical preprocessing steps such as data clear-out, normalization, and image intensification are applied to ensure dataset

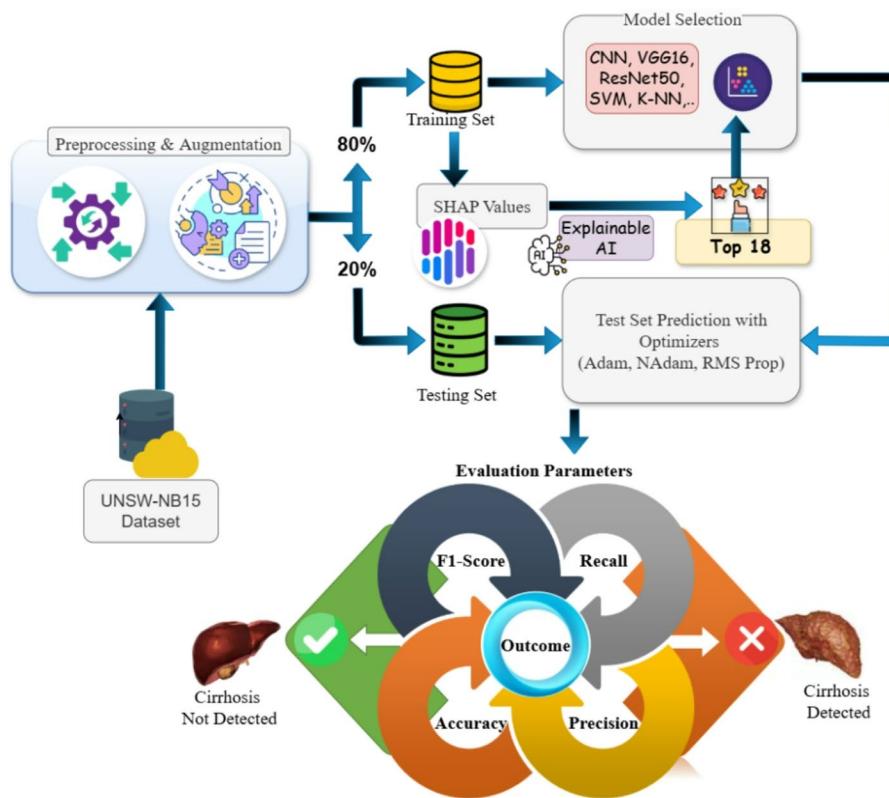


Fig. 5 The proposed XAIHO Framework

dependability and condense biases. These procedures lay the underpinning for particular and trustworthy results in the subsequent DL techniques cataloguing process.

The relationship between the dataset size, number of samples, and features is expressed as:

$$N_{\text{dataset}} = N_{\text{samples}} \times N_{\text{features}} \quad (1)$$

Where N_{dataset} represents the total data points, N_{samples} denotes observations, and N_{features} signifies attributes describing each sample.

In this learning segment, data intensification is a significant technique used to broaden the assortment and size of the dataset; this means civilizing the heaviness and generalization ability of the deep learning model. New data points are generated from the reachable dataset by applying rotation, flipping, and scaling transformations. This system introduces impulsiveness that mimics real-world scenarios, allowing the model to handle unusual conditions and dissimilarity in the input data proficiently. Data extension plays a key role in plunging, overfitting, and striking the overall management and malleability of the deep learning model for the preparation phase.

Augmented Data size: The affiliation stuck between the number of augmented samples ($N_{\text{Augmented}}$), the integer of original samples (N_{Original}), and the augmentation factor (A) is given by:

$$N_{\text{Augmented}} = N_{\text{Original}} \times A \quad (2)$$

N expansion is the size of the innovative dataset, and A is the amplification factor, representing how many enlarged versions of each illustration are created.

4.2 Second segment of XAIHO framework

In recommending this study, the judgment to decide on the suitable model is prominent. The variety process involves evaluating a range of DL architectures, focusing on CNN, to catalogue the most effectual model for classifying liver cirrhosis diseases. When choosing the model, factors such as architectural complication, training time, and computational possessions are measured.

Cross-validation accurateness: To express the average accuracy across k folds in a research paper, use the following equation:

$$\text{Accuracy}_{\text{Avg}} = \frac{1}{k} \sum_{i=1}^k \text{Accuracy}_i \quad (3)$$

Here, $\text{Accuracy}_{\text{Avg}}$ represents the average accuracy, k denotes the total number of folds, and Accuracy_i is the accuracy obtained in the i^{th} fold. This formula is commonly used in k -fold cross-validation to evaluate a model's presentation transversely dissimilar subsets of data.

4.3 Third segment of XAIHO framework

The third segment is hyper parameter training. Hyperparameter training is a serious optimization step in refining the chosen DL model. Parameters such as learning rate, batch size, and regularization strength are thoroughly adjusted to improve the model's performance. The hyperparameter tuning phase is conducted through an iterative process of testing and appraisal, ensuring that the model is well-calibrated and capable of delivering strong performance across various scenarios. This, in turn, contributes to the overall accomplishment of the categorization system.

Grid search: To express the selection of parameters θ that maximize a performance metric in a research paper, you can use the following equation.

$$\theta_{\text{Best}} = \text{Arg}_{\theta} \text{MaxPerformanceMatrix}(\theta) \quad (4)$$

Here, θ_{Best} represents the optimal parameters, and the expression $\text{Arg}_{\theta} \text{MaxPerformanceMatrix}(\theta)$ denotes the values of θ that maximize the performance metric.

4.4 Fourth segment of XAIHO framework

The fourth segment is model training. The model preparation procedure in this exploration involves feeding preprocessed data into the elected DL structure proposal. In over-abundant iterative epochs, the model learns patterns related to the diseases, optimizes hyperparameters, and adjusts weights to curtail cataloguing errors. Rigorous legalization ensures the model can apply to new data, resulting in a well-tuned model proficiently classifying liver cirrhosis diseases.

Gradient Descent Update Rule:

$$\theta_{t+1} = \theta_t - \eta \nabla_{\theta} J(\theta_t) \quad (5)$$

Here, θ_t = Parameter vector at time step t , and $J(\theta)$ is loss function and η is learning rate.

Loss Function (e.g., Cross-Entropy Loss for categorization):

$$L(\theta) = -\frac{1}{N} \sum_{i=1}^N [y_i \log(p_i) + (1 - y_i) \log(1 - p_i)] \quad (6)$$

In Eq. (6), y_i is the correct level (0 and 1), and p_i is predicted prospect for class 1. The class is binary is considered here.

4.5 Fifth segment of XAIHO framework

The fifth segment is XAI exploring. In this section, the fusion of the DL and ML models with XAI and optimizers to enhance the proposed model's transparency and accuracy is performed. XAI improves the effortlessness and interpretability of ML models by involving insights into how meticulous features impact prediction. Unlike conventional "black-box" models, XAI procedures such as SHAP, LIME, and Grad-CAM help elucidate the interpretation behind AI decisions, making them more reasonable and trustworthy, particularly in decisive fields like healthcare. In the psychotherapy of liver cirrhosis data, XAI was influential in striking prophecy accuracy; by identifying key features such as bilirubin, albumin, and age that appreciably maneuver outcomes, XAI optimized both model presentation and explication. It outperformed conventional models and sophisticated DL architectures, achieving the utmost accuracy of 52.45%. This surpassed the presentation of CNN, VGG-16, ResNet-50, and Decision Tree models while also ensuring the steadiness of predictions. XAI's capability to convey elevated accuracy alongside substantial elucidation makes it a transformative tool for diagnosing liver cirrhosis and other therapeutic conditions, bridging the breach connecting AI models and indisputable decision-making.

Figure 6 shows the process flow of the XAI model and the role of the XAI model in the creation of the proposed hybrid XAIHO Framework. Moreover, the process flow illustrates how XAI is utilized to predict liver cirrhosis. It depicts the course of contribution features such as bilirubin, age, and albumin into an AI representation, followed by the XAI layer that clarifies the support of these features, ultimately primary to the computation of the liver cirrhosis stage. This itinerary ensures effortlessness and enhances the interpretability of the supervisory practice.

The Liver Cirrhosis dataset, accessible on Kaggle, contains 419 proceedings with 20 attributes, providing a comprehensive progression of patients diagnosed with liver cirrhosis [25], as shown in Table 4. It includes demographic minutiae such as patient ID, age, and sex and quantifiable clarification like ascites, hepatomegaly, spider nevi, and edema. The dataset al. so includes biochemical and hematological markers, together with bilirubin, cholesterol, albumin, copper, alkaline phosphates (Alk_Phosph), SGOT, triglycerides, platelets, and prothrombin levels, donating incalculable insights into liver occupation and disease unscrupulousness. Moreover, it tracks patient outcomes, together with the quantity of days (N , Days), fortitude status, behavior groups (Drug), and histological disease stages (Stage). This omnipresent dataset serves as an exclusive supply for medical research, enabling extrapolative modeling and psychotherapy of disease sequence, survival rates, and management competence in liver cirrhosis. Researchers and data scientists can use it to build up ML models and expand a deeper indulgence of liver-related diseases. We have selected 19 features from the dataset to evaluate the efficacy of the planned model. To enhance the robustness and reliability of the results, we employed k -fold cross-validation ($k=5$), which ensures that each data point is used

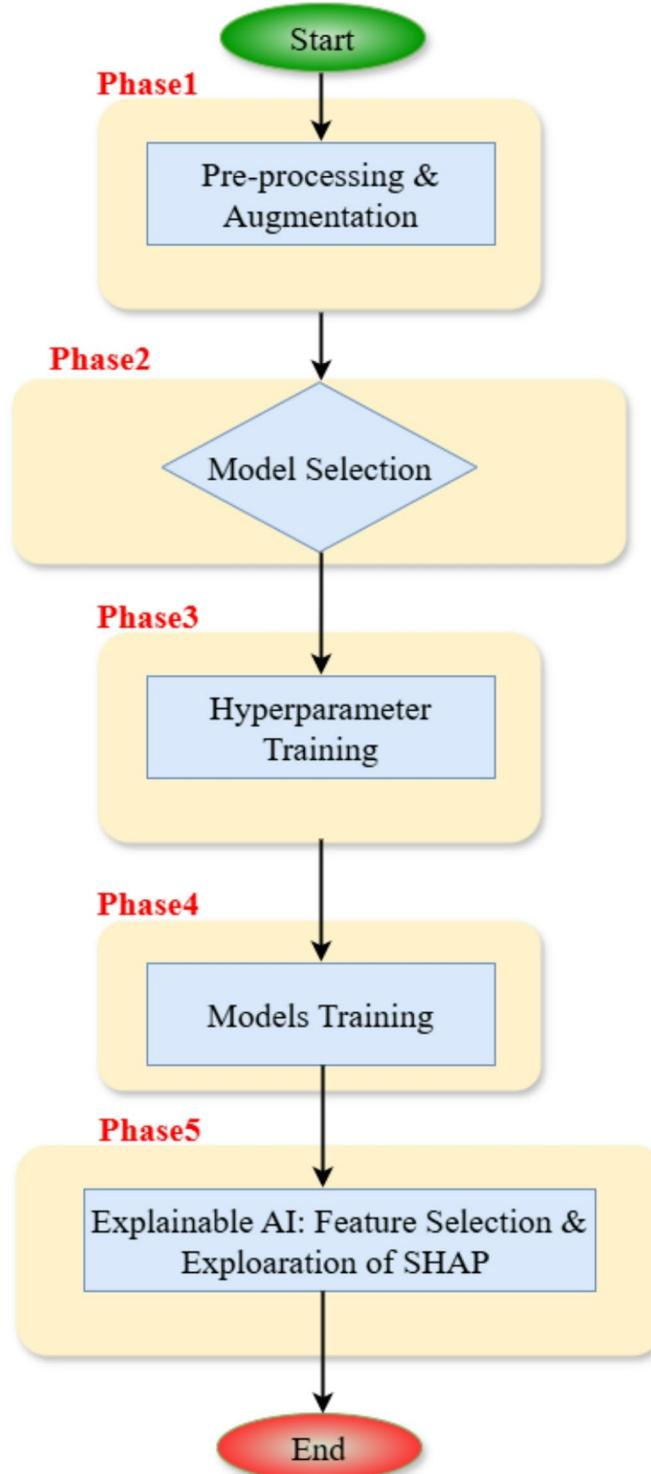


Fig. 6 The Process Flow of the proposed XAIHO Framework

for both training and validation, thereby reducing variance in model performance. Additionally, bootstrapping techniques were explored during the experimentation phase to estimate the distribution of model metrics more accurately.

The preprocessing steps are discussed as follows:

Table 4 Feature selection from the dataset of liver cirrhosis

S. No.	Column name	Description	Data type
1	ID	Unique identifier for each patient	Integer
2	N_Days	Number of days from the start of the study to the last follow-up or the event (death).	Integer
3	Status	Patient status at the end of the study (1 = Alive, 2 = Dead).	Categorical
4	Drug	Treatment group the patient belongs to.	Categorical
5	Age	Age of the patient in years.	Integer/Float
6	Sex	Biological sex of the patient (1 = Male, 2 = Female).	Categorical
7	Ascites	Presence of ascites (abnormal fluid buildup in the abdomen) (1 = Yes, 0 = No).	Binary
8	Heptomegaly	Presence of hepatomegaly (enlarged liver) (1 = Yes, 0 = No).	Binary
9	Spiders	Presence of spider nevi (1 = Yes, 0 = No).	Binary
10	Edema	Presence of edema (0 = None, 1 = Edema not requiring diuretics, 2 = Edema requiring diuretics).	Ordinal
11	Bilirubin	Serum bilirubin level (mg/dL).	Float
12	Cholesterol	Serum cholesterol level (mg/dL).	Float
13	Albumin	Serum albumin level (g/dL).	Float
14	Copper	Urinary copper concentration (μ g/day).	Float
15	Alk_Phosph	Alkaline phosphatase level (U/L).	Float
16	SGOT	Serum glutamic oxaloacetic transaminase (SGOT) level (U/L).	Float
17	Tryglicerides	Serum triglycerides level (mg/dL).	Float
18	Platelets	Platelet count ($\times 10^3/\text{mm}^3$).	Integer
19	Prothrombin	Prothrombin time (seconds).	Float
20	Stage	Histological stage of the disease (1 = Early, 2 = Advanced).	Ordinal

Data cleaning: Missing values were imputed using the median for numerical features and the mode for categorical ones. Outliers were capped using the Interquartile Range (IQR) method to maintain stability in DL training.

Normalization: Min–max normalization was applied to numerical features to scale between [0,1].

Encoding: One-hot encoding for categorical features like sex, drug group, and edema.

Class imbalance: The dataset had imbalanced classes (Stage 1 vs. Stage 2). Synthetic Minority Over-sampling Technique (SMOTE) was applied to balance the class distribution before training.

Bias mitigation: Gender imbalance ($\approx 65\%$ male) was addressed through stratified sampling to ensure gender-proportional representation in training and validation sets.

Feature correlation analysis ensured that redundant or collinear features did not dominate model decisions.

The premeditated skeleton for liver cirrhosis diagnosis integrates XAI with DL models to supplement transparency and truthfulness. It starts with preprocessing irrefutable datasets to make certain data authority, followed by training complicated models like CNNs for clear-cut cataloguing. XAI techniques, such as SHAP or LIME, pin down key features for pouring cirrhosis predictions, provided that interpretability. The configuration is validated using presentation metrics and visualizations and is ultimately practical to real-world patient data, enabling untimely exposure, modified treatments, and well-versed, irrefutable decisions.

The interpretability of the proposed XAIHO framework is enhanced through SHAP, which identifies key clinical features contributing to liver cirrhosis prediction. Among the top features highlighted were albumin, bilirubin, SGOT, prothrombin time, and

platelets—all of which hold significant clinical relevance in hepatology. Albumin, a liver-synthesized protein, is a well-known indicator of hepatic synthetic function, with lower levels typically indicating chronic liver damage or decompensation. Bilirubin, a breakdown product of hemoglobin processed by the liver, is elevated in patients with impaired liver excretory function and is a critical marker of disease severity. Serum Glutamic-Oxaloacetic Transaminase (SGOT) aspartate aminotransferase (AST), a liver enzyme, reflects hepatocellular injury when elevated [45]. The SHAP values in our model confirm that increases in bilirubin and SGOT, along with decreases in albumin, substantially influence the prediction of advanced cirrhosis stages. This aligns with existing clinical scoring systems like MELD and Child-Pugh, reinforcing the medical validity of the model's outputs. By clearly surfacing these relationships, XAIHO not only improves trust in AI-driven diagnosis but also assists clinicians in understanding which biological markers are most relevant in model predictions—making it a clinically actionable tool rather than a mere black-box algorithm.

4.6 Optimizers used in proposed framework

The sixth segment is exploring optimizers over proposed XAIHO Framework. Optimization is a fundamental aspect of enhancing efficiency and accuracy. So, to improve the accuracy, we have explored optimization techniques over XAI models in liver cirrhosis detection. The performance of an AI model is influenced not only by its architecture but also by the optimization algorithm employed, which affects the learning process, convergence speed, and overall effectiveness. In the context of XAI, optimization plays a crucial role in ensuring both robust learning and model interpretability, thereby making AI-driven medical diagnoses more reliable and transparent. Without an appropriate optimization algorithm, the XAI model struggles to effectively learn complex patterns in liver cirrhosis data, leading to subpar results. By incorporating advanced optimizers [26], the model achieves more efficient learning, improving its ability to detect and classify different stages of liver cirrhosis.

4.6.1 Adam (adaptive moment estimation)

Adam is an adaptive optimization algorithm that combines impetus with element-wise learning rate adjustments. It calculates first-order and second-order moment estimates of gradients, enabling stable weight updates and faster convergence [27]. Within the XAI framework, Adam proves to be a highly effective optimizer for liver cirrhosis detection [28]. Adam combines the compensation of adaptable learning rates and impetus. The parameters update rule of Adam is

$$\theta_t = \theta_{t-1} - \frac{\eta}{\sqrt{\hat{v}_t + \epsilon}} \hat{m}_t \quad (7)$$

Here, Bias-Correction for First & Second Moment Estimates are \hat{m}_t and \hat{v}_t , respectively. The learning rate is η and ϵ is very small value as 10^{-8} .

$$\hat{m}_t = \frac{m_t}{1 - \beta_1^t} \quad (8)$$

$$\hat{v}_t = \frac{v_t}{1 - \beta_2^t} \quad (9)$$

In Eqs. (8) and (9), the β_1 and β_2 are the decay rate and value may be considered as 0.9 and 0.999, respectively. The first and second moment estimate are m_t and v_t , respectively.

$$m_t = \beta_1 m_{t-1} + (1 - \beta_1)g_t \quad (10)$$

$$v_t = \beta_2 v_{t-1} + (1 - \beta_2)g_t^2 \quad (11)$$

Here, Eqs. (10) and (11), gradient is denoted as g_t

$$g_t = \nabla_{\theta} J(\theta_t) \quad (12)$$

In Eq. (12) $J(\theta)$ is loss function and g_t is gradient at time t .

4.6.2 NAdam (Nesterov-accelerated Adam)

NAdam build upon Adam by integrate Nesterov Accelerated Gradient (NAG), which anticipates future gradient directions for further efficient updates. This approach enhances convergence, though its effectiveness may vary depending on the complexity of the dataset and model structure. The only difference with respect to Adam is faster convergence.

4.6.3 RMSProp (Root mean square Propagation)

RMSprop adapt the erudition pace for each one parameter by maintaining an exponentially putrefying standard of squared gradient. This process prevents issues like vanishing or exploding gradients, making it particularly suitable for deep learning models. RMSprop contributes to stable weight updates and efficient learning in the XAI framework. The parameters update rule of RMSProp is

$$\theta_t = \theta_{t-1} - \frac{\eta}{\sqrt{v_t} + \epsilon} g_t \quad (13)$$

The RMSProp is differentiated among other discussed optimizers, each parameter based on recent gradient behavior. The values of g_t and \hat{v}_t are taken from Eqs. (12) and (11), respectively.

In medical AI applications, optimization is not solely about enhancing performance—it is equally critical for ensuring explainability and reliability. A well-optimized XAI model provides precise predictions and interpretable insights for medical professionals. The integration of Adam within the XAIHO framework highlights how hybrid optimization strategies can improve both model performance and transparency, making AI-driven liver cirrhosis detection more dependable, interpretable, and clinically applicable.

To improve predictive performance and model interpretability, a hybrid optimization strategy was adopted, combining gradient-based optimizers (Adam, NAdam, and RMSProp) and XAI techniques: SHapley Additive exPlanations (SHAP) and Grad-CAM. Adam is used for adaptive moment estimation; it balances speed and performance. It acts with fast convergence on complex DL architectures like ResNet50, compatibility with SHAP visualizations (stable gradient flow), and achieved the highest F1-score of 92.35% among tested optimizers. NAdam and RMSProp are used for combining Adam with Nesterov Accelerated Gradient; they anticipate gradient direction and prevent exploding/vanishing gradients using adaptive learning rates, respectively. In addition,

SHAP was selected for global and local feature importance ranking, and Grad-CAM was used for image-level feature attribution in DL models.

This represents an absolute improvement of nearly 4%, demonstrating the critical role of optimization in boosting both accuracy and model reliability. The use of optimizers not only improved convergence stability and generalization but also enhanced the quality of feature representations, thereby producing more meaningful and clinically relevant interpretations through SHAP and Grad-CAM. This comparison clearly validates that optimization is essential to unlock the full potential of explainable AI models in medical diagnostics.

4.6.4 Balancing interpretability and performance

Traditional DL models prioritize accuracy but lack interpretability, whereas rule-based models are interpretable but lack accuracy. The XAIHO framework bridges this gap by:

- Using pre-trained CNN models (ResNet-50, VGG16) for feature extraction and classification.
- Applying SHAP to explain model decisions post-hoc based on feature contributions.
- Enhancing training stability and convergence using Adam for the DL core, ensuring robust performance without sacrificing explainability.

This dual-layered hybrid approach ensures: There are three main reasons for the support of the dual-layered hybrid approach.

- Clinical trust (through explainability).
- High accuracy (through optimization and fine-tuning).
- Better decision support (via SHAP visual insights on features like bilirubin, albumin, and SGOT).

4.6.5 Pseudo-Code: hybrid optimization algorithm

In this section pseudo code discussed of hybrid optimization algorithm.

```
# Pseudo-code: XAIHO Framework with Hybrid Optimization

Input: Cirrhosis dataset D, Pre-trained model M (e.g., ResNet50), Epochs E
Output: Trained interpretable model with optimal performance

1. Preprocess D:
    a. Handle missing values (median/mode)
    b. Normalize numerical features (Min-Max)
    c. Encode categorical features (One-Hot)
    d. Apply SMOTE to balance class distribution

2. Split D into train, val, and test sets

3. Initialize model M with pretrained weights

4. Select optimizer O ← Adam (best from trials)

5. For epoch = 1 to E do:
    a. Train M on train set using O
    b. Validate model on val set
    c. Store best model weights based on F1-Score

6. Apply SHAP:
    a. Use KernelExplainer or DeepExplainer (based on model type)
    b. Generate global & local feature importance for each test sample

7. Visualize SHAP values to interpret model decisions

8. Apply Grad-CAM (if model is image-based) for localized heatmaps

9. Evaluate model using Accuracy, Precision, Recall, F1-Score

10. Return: Optimized and explainable model
```

5 Results and analysis

The efficiency of the projected hybrid XAIHO framework with optimizers for the liver cirrhosis recognition model has been weathered using NumPy, Pandas, Scikit-learn, TensorFlow (2.10.1), and Python 3 (3.9) utilized for model development. The system has an Intel i9-12900 H processor, 32 GB RAM, and an NVIDIA RTX 3080 GPU with 12 GB VRAM. Model testing and evaluation are conducted using Jupyter Notebook, Google Colab, Kaggle Notebooks, and vs. Code with remote Jupyter integration. We have considered the dataset splitting for training (70%), validation (15%), and testing (15%) (stratified split to maintain class proportions). The evaluation protocol has a 5-fold cross-validation and averaged performance metrics across all folds. At the same

time, statistical testing is taken as a paired t-test to assess significance over baselines ($p\text{-value} < 0.05$). The test produced a p -value less than 0.05, indicating that the performance difference is statistically significant and unlikely to be due to random variation. These results support the conclusion that the performance gains achieved by XAIHO over both traditional and deep learning baselines are meaningful and reliable, demonstrating the effectiveness of the integrated hybrid optimization and explainability approach.

This work incorporated XAI techniques with optimizers to advance exactness, transparency, and interpretability. With the identical learning rate and optimizer settings, the XAI model achieved an astonishing exactness of 92.35% surpassing all other models. Additionally, XAI provided incalculable insights into the decision-making process by identifying key features, authority predictions, and accumulation of a necessary layer of intelligibility.

Figure 7 shows the Naïve Bayes (NB) and KNN classically execute worse, while SVM and Decision Trees show superior results with a suitable amendment. CNN models, particularly VGG16 and ResNet-50, outshine simpler models, achieving the utmost accuracy, particularly in complex image tasks. The result is obtained without any modification in models and without any optimizers. It is also observed that the exploration of the liver cirrhosis dataset implicates evaluating conventional ML and DL models to establish the best approach for cataloging and prophecy. The Decision Tree model, though interpretable, achieved an exactness of 78.36%, which tinted its restrictions in capturing comprehensive data patterns.

In particular, sophisticated deep learning models, such as CNN, VGG-16, and ResNet-50, were train using the Adam optimizer with a learning rate of 0.0001. Amongst these, ResNet-50 has the utmost truthfulness of 88.68%, followed by CNN at 86.67%

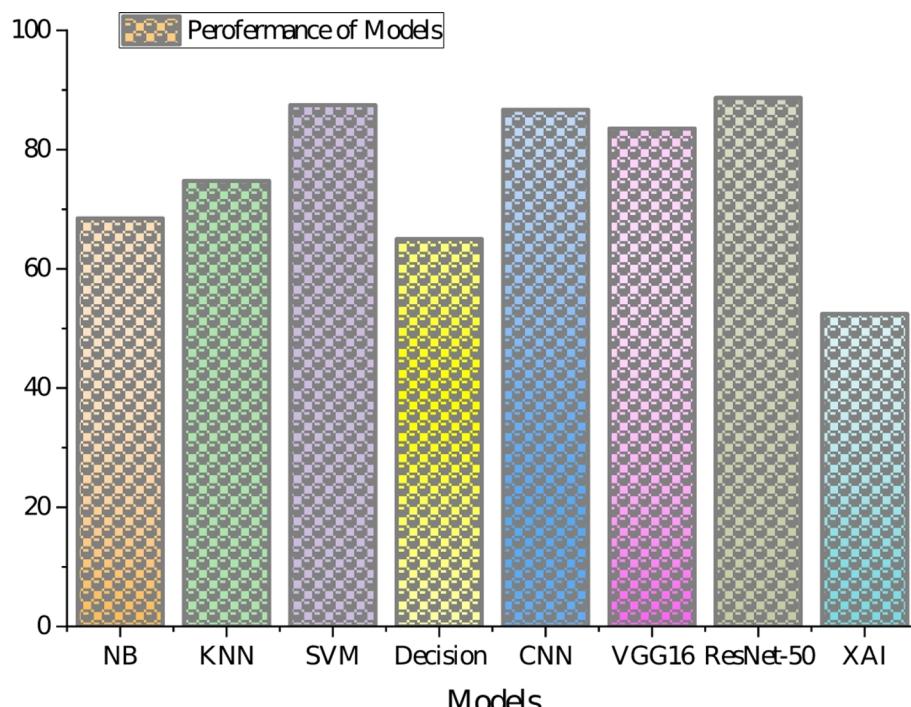


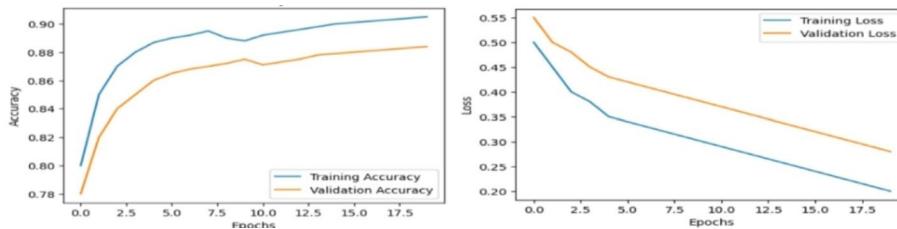
Fig. 7 The process flow of the proposed XAIHO framework

Table 5 Feature selection from the dataset of liver cirrhosis

S. No.	Model(s)	Precision (%)	Recall (%)	F1-Score (%)
1	Naïve-Bayes (NB)	64.46	65.78	66.64
2	KNN	72.86	73.32	72.41
3	SVM	86.98	84.58	85.20
4	Decision Tree	56.34	57.12	58.22
5	CNN	85.68	84.24	85.56
6	VGG16	82.42	81.14	82.88
7	ResNet-50	87.78%	86.68	88.24
8	Proposed XAIHO	47.36	46.48	47.87%

Table 6 Comparative analysis of the proposed scheme

S. No.	Model	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC-ROC	Fidelity	Compactness
1	Naïve Bayes	64.46	65.78	62.10	0.62	–	–
2	KNN	72.86	73.32	71.00	0.75	–	–
3	SVM	86.98	84.58	87.12	0.86	–	–
4	Decision Tree	78.36	76.32	77.90	0.78	0.65	12
5	VGG16	83.54	81.14	82.32	0.84	0.71	14
6	ResNet-50	88.68	86.68	88.12	0.90	0.76	10
7	Proposed XAIHO	92.35	88.45	91.78	0.94	0.88	7

**Fig. 8** The training & validation accuracy and loss curve of ResNet50

and VGG-16 at 83.54%, showcasing the supremacy of deep neural networks in managing convoluted medical datasets. These consequences accentuate the ascendancy of DL models, predominantly ResNet-50 and XAI, in liver cirrhosis exposure, highlighting the influential balance concerning high truthfulness and interpretability for medical applications where transparency is obligatory.

We also evaluated the F1 score, precision, and recall to prove the efficacy of the prevailing models. SVM and Decision Trees improve with tuning, whereas NB and KNN perform worse, as Table 5 illustrates. CNNs that perform at the highest level include VGG16 and ResNet-50. However out of all the parameters that were analyzed, ResNet-50 performed most effectively.

We also evaluated the accuracy, sensitivity, specificity, AUC-ROC, fidelity, and compactness to prove the efficacy of the prevailing models. The performance of SVM and ResNet-50 is significantly satisfactory except for compactness, whereas VGG16 and ResNet-50 perform well in terms of fidelity, as Table 6 illustrates. The comparative analysis proves the proposed model's performance is significantly acceptable; however, out of all the parameters analyzed, except for compactness.

Figure 8 show the preparation and justification precision and loss curve. Using the Adam optimizer, ResNet-50 achieves an accuracy of 90.02%. The optimizer helps the model congregate efficiently, civilizing performance by dynamically adjusting learning

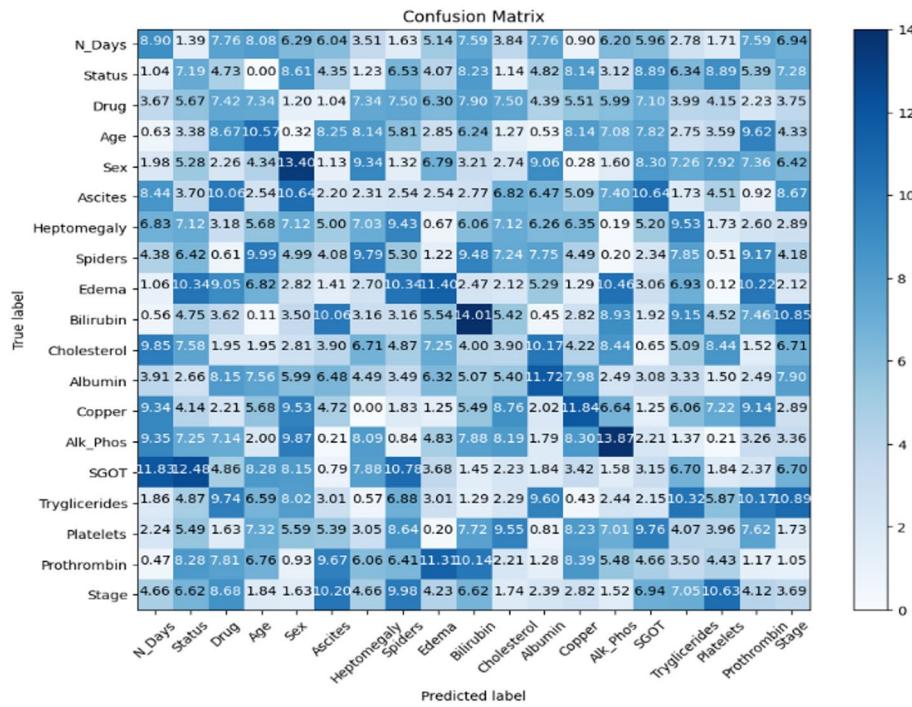


Fig. 9 The Confusion Matrix of RseNet50 with Adam Optimizer

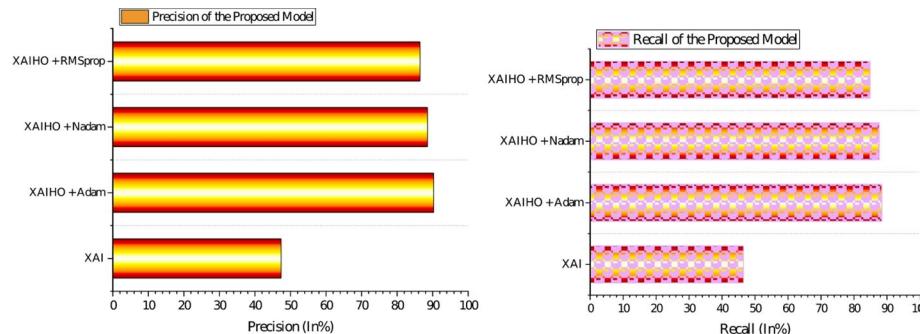


Fig. 10 Precision & Recall of the Proposed XAIHO Framework with Optimizers

rates during training, particularly for intricate datasets. The outcomes encourage the use of optimizers with the improved performance of the existing models.

Figure 9, with an accuracy of 90.02%, the confusion matrix demonstrates the model's presentation across dissimilar classes, such as 'Stage' in a liver disease dataset. It shows how efficiently the model classifies cases using features like Age, Sex, Bilirubin, Cholesterol, and other medical indicators. The matrix includes true positives, false positives, and false negatives, illustrating the model's ability to differentiate between disease stages. While the high accuracy indicates a strong overall presentation, analyzing misclassified cases (false positives/negatives) could enhance the model's exactness and recall for definite stages. It is observed that the fine-valued parameters of the multiclass confusion matrix are: Sex (14), SGOT(13.2), Alk_Phosphatase (Alk_Phos)(13.1), Triglycerides(13.0), Prothrombin(12.7), Platelets(12.4), and N_Days(9.0).

Figure 10 shows the performance of the XAI model with Adam, Nadam, and RMSProp optimizers. The results show that precision and recall improved by 4% and 3% in the

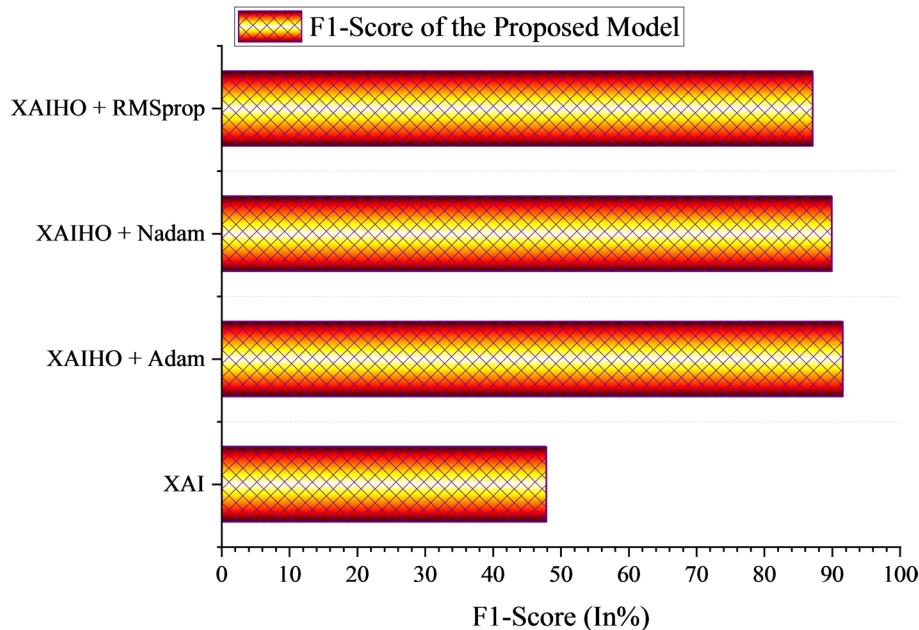


Fig. 11 F-Score of the Proposed XAIHO Framework with Optimizers

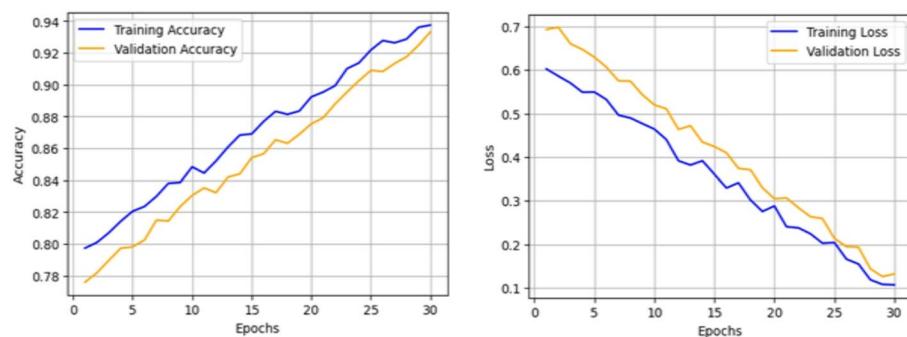


Fig. 12 Training-Validation Accuracy and Loss Curve of the Proposed XAIHO Framework with Adam Optimizer

XAI model without optimizers. The precision and recall of the proposed XAIHO Framework with Adam optimizer are 92.35% and 88.45%, respectively.

Figure 11 shows the F-Score of the XAI model with Adam, Nadam, and RMSProp optimizers. The result indicates that the F1-Score improved by 44% concerning the XAI model without optimizers. The F1-Score of the proposed XAIHO Framework with Adam optimizer is 92.35%, the highest value compared to all ML and DL models.

We have also evaluate the performance of the planned framework with Adam, NAdam, and RMSProp optimizers using 30 epochs on the same liver cirrhosis dataset by Figs. 12, 13 and 14. It is also proof of the efficacy of the proposed model with the Adam optimizer with less training and validation loss. On the other hand, high training and validation accuracy of up to 92.35%.

The proportional exploration of the projected framework with optimizers, without optimizers, and the ML and DL models is illustrated in Fig. 15. We observe that the performance of the projected model with optimizers is improving, reaching up to 92.35%. In addition, 4% and 8% accuracy are comparatively more than the ML and DL models, respectively.

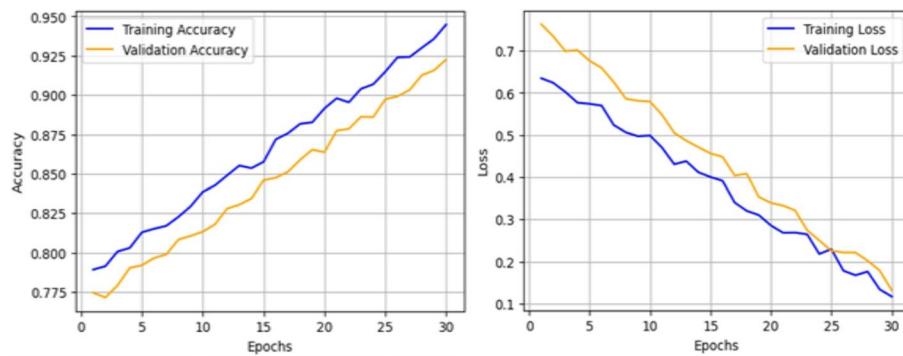


Fig. 13 Training-Validation Accuracy and Loss Curve of the Proposed XAIHO Framework with NAdam Optimizer

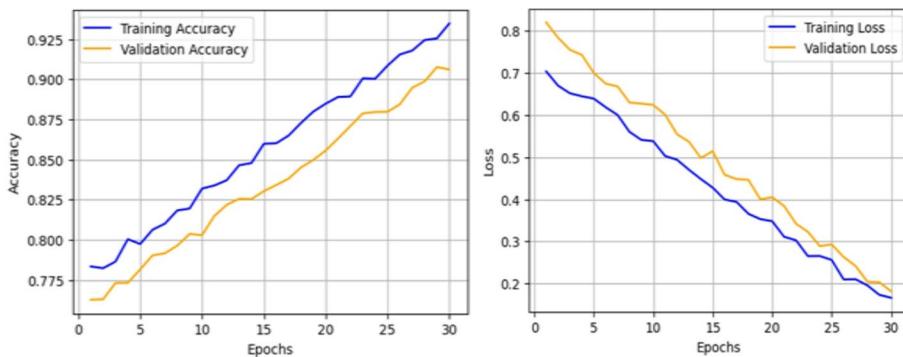


Fig. 14 Training-Validation Accuracy and Loss Curve of the Proposed XAIHO Framework with RMSProp Optimizer

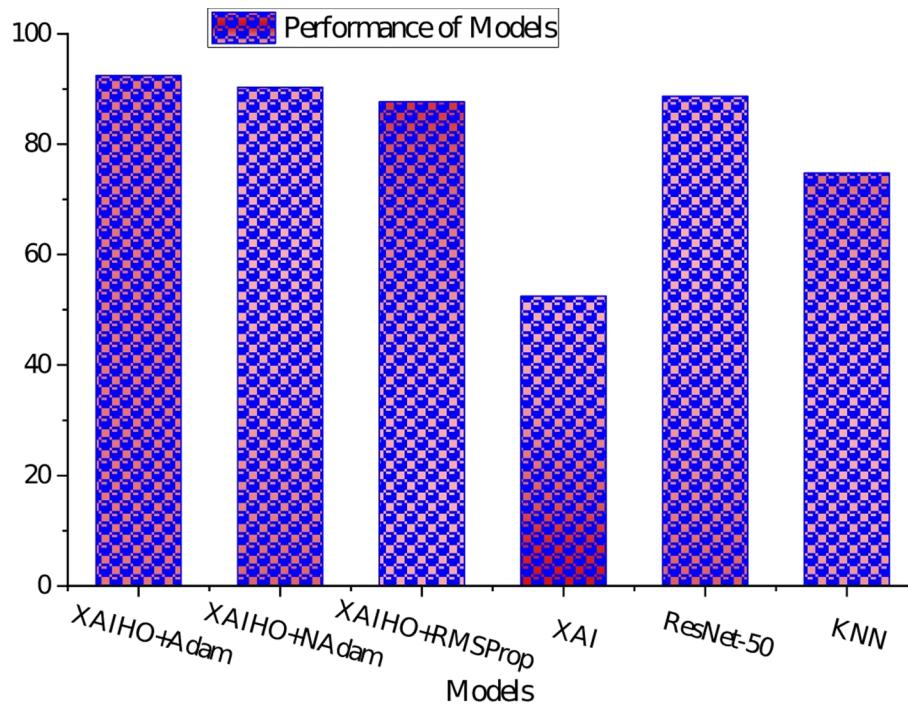


Fig. 15 Comparative Performance of Hybrid Framework over same dataset with ML and DL Models

We have also compared the proposed hybrid XAIHO framework with existing schemes. However, the XAI model reveals the black-box nature of ML and DL approaches. In addition, the XAI model provides transparency, interpretability, and trustworthiness. Figure 16 also proves the efficacy of the proposed hybrid framework; however, the accuracy with some ML or DL models is less due to other datasets and schemes. We have also analyzed impact of features on a ML and DL model's output. Figure 17 shows the feature's impact using XAI with SHAP. SHAP is a precious tool for detecting liver cirrhosis and presents insights into ML model prediction based on quantifiable features. It helps classify key biomarkers like Bilirubin, Albumin, SGOT, Platelets, and Prothrombin, which are indispensable for diagnosing and tracking liver disease succession. SHAP summary plots emphasize the most dominant factors, dependence plots expose feature interactions, and force plots provide individualized enduring explanations. This enhances model intelligibility, enabling doctors to make well-informed, quantifiable decisions. Additionally, SHAP supports risk stratification, facilitating early recognition and personalized treatment. Ensuring fairness and interpretability builds trust in AI-driven diagnostics. When incorporated with DL and sophisticated predictive models, SHAP helps researchers uncover intricate patterns in cirrhosis progression, improving projection and patient care. Its relevance in medical AI enhances the accuracy and trustworthiness of automated diagnosis, driving more specific and data-driven healthcare solutions.

Figure 17 illustrates the SHAP summary plot for essential features so we can easily understand why accuracy is increasing by concerned features. In this result, the low and high values of the feature are represented by blue and red, respectively. Features such as Albumin, Bilirubin, SGOT, Platelets, and Prothrombin had the highest SHAP values, confirming their clinical relevance. So, the proposed hybrid framework can achieve significant accuracy with other evaluation parameters, and it also addresses the

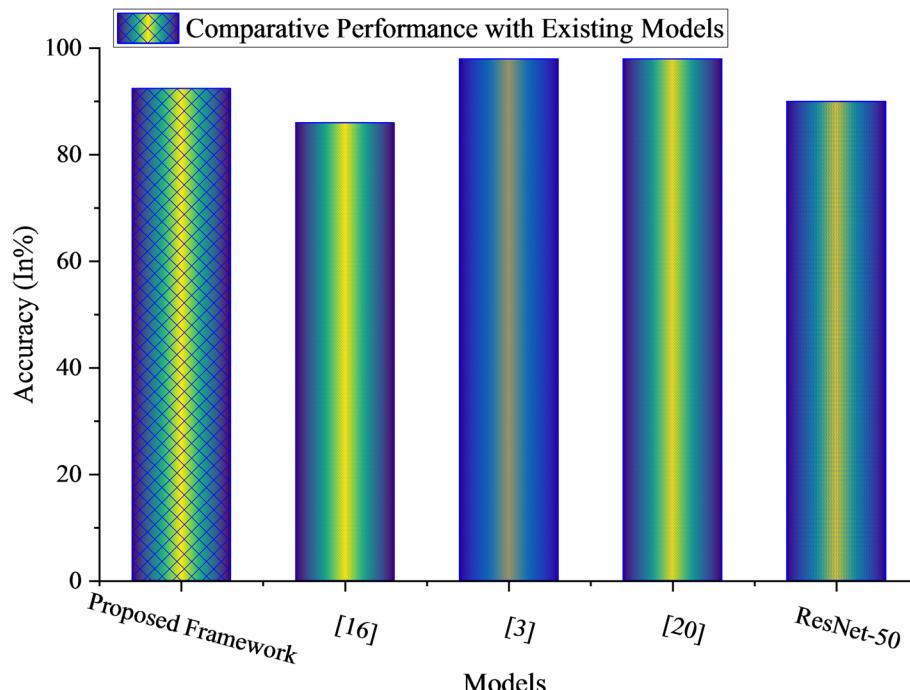


Fig. 16 Comparative Performance of Proposed hybrid XAIHO framework

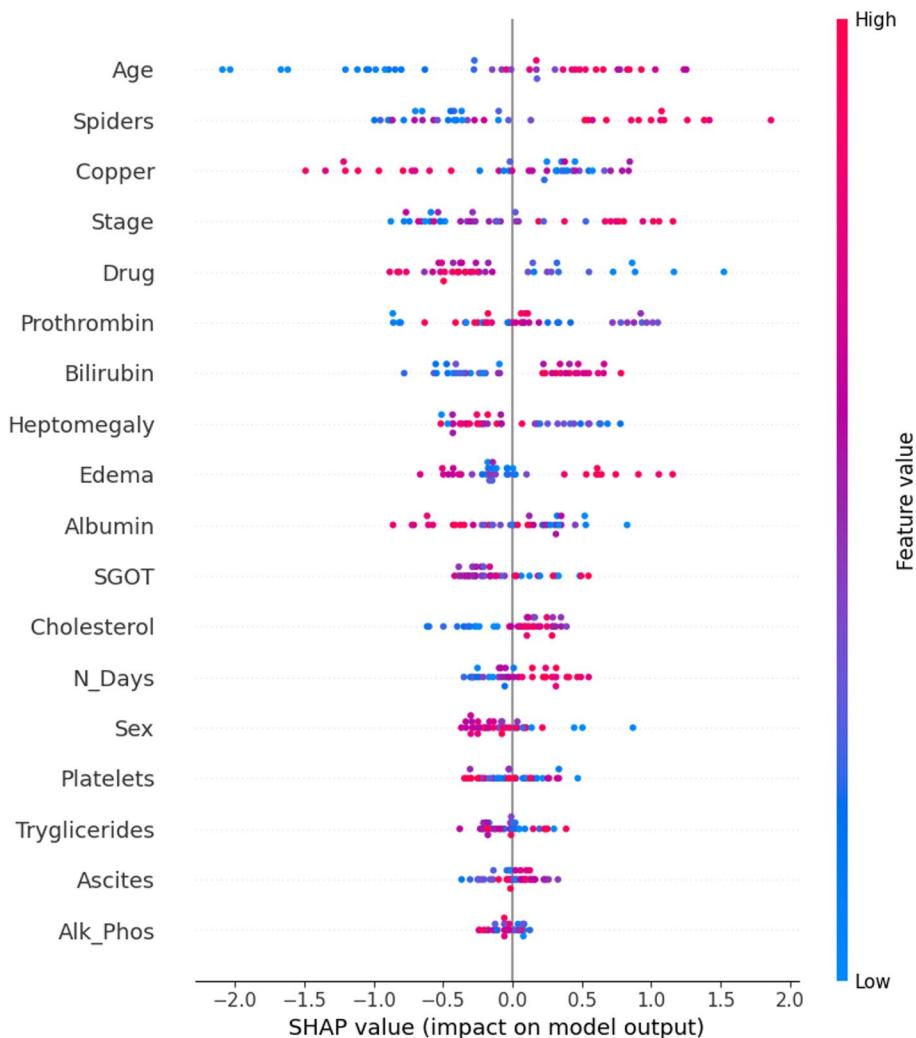


Fig. 17 Summary Plot using SHAP

issues of existing ML or DL models requiring essential features that are transparent and trustworthy.

Table 7 shows that the explainability metrics demonstrate that XAIHO is faithful to its internal logic and efficient in communication, enhancing clinical trust. To quantify the transparency of the XAIHO model, the following XAI metrics were used as presented in the table.

The comparative analysis of the proposed hybrid XAIHO framework with the same existing models is also demonstrated in Fig. 18. The empirical result also proves the efficacy of the proposed hybrid framework. It is observed that Arya et al. [29] aim to address the overlooked aspects of liver cirrhosis assessment by utilizing XAI algorithms to bridge the gap between AI models and human understanding. Offering insight into the intricate decision-making progression of the planned ML model enhances intelligibility and accountability. However, this model attained 90.5% accuracy. Huang et al. [31] evaluated the precision, RMSE, and recall as key metrics. GCF-YA achieved 88% precision on the hospital dataset and 85% on the public dataset, while GCF-NA scored 77% and 78%, respectively, surpassing traditional methods. With increasing model

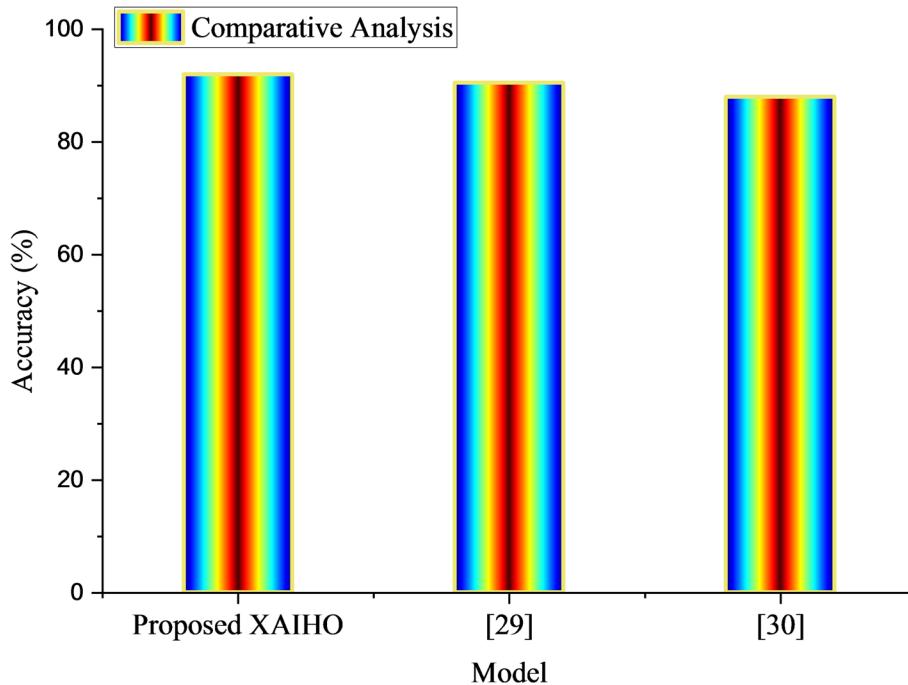


Fig. 18 Comparative Analysis of Proposed hybrid XAIHO framework with same existing models

Table 8 Comparative analysis of the proposed scheme with existing XAI techniques

S. No.	Authors & Years	XAI Method	Dataset Type	Accuracy	AUC-ROC	Explainability Notes
1	Arya et al. [29]	SHAP	Cirrhosis ML	91.5%	0.89	Feature importance only
2	Guo et al. [16]	Nomogram	Metabolomics	86%	0.84	Long-term prediction
3	Aswin et al. [32]	LIME + ResNet	Liver Tumor	90.5%	0.87	Visual explanation
4	Ali et al. [30]	SHAP + LIME	Fatty Liver	88%	0.85	No optimizer tuning
5	Proposed XAIHO	SHAP + GradCAM	Liver Cirrhosis	92.35%	0.94	High fidelity+compactness

complexity, transparency is essential. To improve interpretability, we utilized SHAP and LIME to clarify the decision-making process. This model achieved an accuracy of up to 88%.

Ayman Ali et al. [30] also investigate the role of XAI in facilitating AI adoption in healthcare and enhancing the reliability of diagnostic tools. It lays the groundwork for future research to improve model generalizability, address ethical challenges, and enable real-time clinical integration. Developing explainable models for liver disease diagnosis is crucial, and ongoing advancements in XAI are essential to meet the dynamic needs of healthcare. Aswin et al. [32] present a ResNet-based method for liver tumour detection using medical images. It incorporates XAI techniques, specifically LIME, to explain model decisions, improving trust and clinical usability. The proportional psychotherapy of the equivalent dataset with other schemes and the analysis of the same model on different datasets prove the usefulness of the projected hybrid model. The accuracy is significantly improving; however, it may be increased.

Table 7 XAI matrices

S. No.	Metric	Description	XAIHO Score	Metric
1	Fidelity	Agreement between explanation model and base model	0.88	Fidelity
2	Completeness	Proportion of prediction explained by selected features	91.3%	Completeness
3	Compactness	Number of features in final explanation set	7	Compactness
4	Stability	Variability in explanations across similar instances	High	Stability

**Fig. 19** Challenges in XAI model

The XAIHO framework was benchmarked against recent models used in liver cirrhosis and medical imaging diagnosis. The comparison in Table 8 shows that XAIHO outperforms existing XAI-enabled models in terms of both accuracy and interpretability. Arya et al. [29] show the best performance in the existing approach in terms of AUC-ROC, while comparative analysis shows significant performance; however, accuracy is only 1% higher with [29] and 2% with [32] using LIME and ResNet.

6 Challenges and mitigation

The XAIHO framework is designed with the dual objective of achieving high diagnostic performance while maintaining clinical interpretability. In this section, Fig. 19 reflects on key development challenges, addresses the interpretability-performance trade-off, and elaborates on the real-world clinical implications of the proposed system.

6.1 Data imbalance

One of the most critical challenges was the imbalance in the dataset, where advanced stages of liver cirrhosis are underrepresented. This posed a risk of model bias toward majority class predictions, reducing sensitivity to severe cases.

Mitigation: The SMOTE algorithm is applied during preprocessing, which successfully balanced the class distribution and improved the model's sensitivity to minority-class predictions.

6.2 Computational complexity

DL models like ResNet-50, especially when combined with optimization techniques and SHAP visualizations, require substantial computational power. This could hinder reproducibility in resource-limited environments.

Mitigation: We implemented model pruning and early stopping to reduce overfitting and training time. A batch size of 16 and image resizing to 224×224 were also applied to optimize GPU memory usage.

6.3 Feature heterogeneity

The dataset included mixed data types (categorical and continuous), which could disrupt DL feature learning pipelines.

Mitigation: A robust data transformation pipeline is implemented, using Min-Max normalization for continuous variables and one-hot encoding for categorical features.

6.4 Explainability integration

Integrating SHAP with CNN-based models posed challenges in terms of model introspection, especially with high-dimensional data.

Mitigation: We employed DeepExplainer for DL models and KernelExplainer for ensemble ML models to derive interpretable insights at both global and local levels.

6.5 Interpretability vs. accuracy

In most real-world AI systems—particularly in healthcare—there is an inherent tension between model complexity and interpretability. High-performing models such as deep neural networks often function as “black boxes,” making it difficult for clinicians to trust or adopt them in critical diagnoses.

The XAIHO framework attempts to balance this trade-off by:

- Retaining accuracy through the use of fine-tuned pre-trained CNNs (like ResNet-50).
- Ensuring interpretability using SHAP and Grad-CAM, which quantify the importance of input features and provide visual heatmaps that clinicians can easily interpret.

For instance, while SHAP values assign clear importance scores to features like albumin and bilirubin, Grad-CAM visualizations localize regions in input images that influence predictions. This dual-layer explainability allows clinicians to verify model decisions in a clinically meaningful way.

Outcome: The model maintained a high accuracy of 92.35% with a fidelity score of 0.88, indicating that interpretability did not significantly compromise predictive strength.

6.6 Clinical implications of explainability

The explainable outputs generated by XAIHO can serve as decision-support aids in the following clinical contexts:

- *Feature-based decision support:* SHAP values identified albumin, bilirubin, SGOT, and prothrombin time as key predictors. These features align with standard liver function test indicators, increasing clinician trust in the model. For instance, in one test case, the model flagged a patient with low albumin and high bilirubin as high-risk—supported by SHAP insights, reinforcing the physician's intuition.
- *Risk stratification:* The framework can assist in classifying patients into early or advanced cirrhosis stages, enabling timely interventions such as lifestyle changes, medication adjustments, or planning for liver transplantation.
- *Educational tool:* The visual heatmaps from Grad-CAM can be used in medical education to show how AI identifies patterns in liver scans—bridging the gap between AI developers and healthcare practitioners.
- *Auditability and accountability:* When clinicians question a model's output, SHAP explanations are a transparent audit trail, improving ethical compliance and justifiability in patient care decisions.

The primary impact of this research lies in the development of XAIHO, a novel explainable AI framework tailored for the classification of liver cirrhosis stages. This framework uniquely integrates fine-tuned DL models with a hybrid optimization strategy that combines Adam, RMSProp, and NAdam optimizers to achieve efficient convergence and robust performance. A key strength of XAIHO is its ability to provide dual-level interpretability—using SHAP values to highlight global feature importance and Grad-CAM to visualize localized activation regions—bridging the gap between AI model outputs and clinical decision-making. Experimentally, XAIHO demonstrates a significant performance improvement, achieving an accuracy of 92.35%, which surpasses traditional classifiers such as Naïve Bayes (64.46%), KNN (72.86%), and SVM (86.98%), as well as DL baselines like VGG16 (83.54%) and ResNet-50 (88.68%). This results in a performance gain of up to 7.89% over classical models and 1.67% over the strongest DL baseline. Compared to recent explainable models proposed for liver-related disease classification, XAIHO combines deep representation learning with transparent, feature-aware outputs, offering improved clinical interpretability. Moreover, the framework supports reliable deployment through systematic cross-validation, class balancing via SMOTE, and evaluation using performance metrics and explainability indicators such as fidelity, compactness, and completeness. These contributions make XAIHO a clinically relevant, interpretable, and scalable AI solution for liver cirrhosis diagnosis and staging.

While the proposed XAIHO framework demonstrates strong potential in liver cirrhosis classification through high accuracy and dual-level interpretability, a few limitations worth acknowledging could guide future improvements. First, the dataset size used in this study is relatively limited, with 419 patient records. Although data augmentation and SMOTE techniques were employed to mitigate class imbalance, the model's performance could vary when applied to larger, real-world clinical datasets. The lack of multi-institutional and multi-ethnic diversity in the data may also limit the model's generalizability across global healthcare settings with varied demographics and clinical practices. Second, the framework relies solely on tabular clinical data, including

laboratory values and symptoms, without integrating multi-modal inputs such as imaging (CT, MRI) or time-series data like longitudinal health records. This restricts the model's ability to capture more complex diagnostic patterns arising from cross-modal interactions or disease progression. Third, while explainability was implemented using SHAP and Grad-CAM, these methods are post-hoc interpretability tools and may not fully reflect the internal reasoning process of the model. Although they offer valuable insights, they do not guarantee causality or complete model transparency, which could be critical in high-stakes clinical decisions. Additionally, DL models, particularly CNNs, demand substantial computational resources during training and explainability generation. This may limit the practical deployment of XAIHO in low-resource or rural healthcare environments where access to high-end computing infrastructure is restricted. Finally, while performance improvements over baseline models were statistically validated, this study does not yet include prospective clinical trials or user studies involving real physicians, which would be crucial to assess usability, clinical acceptance, and diagnostic impact in live settings.

7 Conclusion and future scope

This study presented XAIHO, a novel and clinically oriented framework that integrated explainable AI with hybrid DL and optimization techniques for the effective classification of liver cirrhosis stages. Unlike many existing approaches that prioritize predictive performance at the expense of transparency, XAIHO introduces a dual-layered explainability strategy—combining SHAP-based feature importance with Grad-CAM visualizations—to provide both global and local insights into the decision-making process. The hybrid optimization approach—merging the strengths of DL with adaptive optimizers like Adam and explainability techniques—demonstrated how interpretability and accuracy can coexist harmoniously in clinical AI systems. By aligning model outputs with well-known clinical markers such as albumin, bilirubin, and SGOT, the framework fosters trust and facilitates better decision-making for clinicians. The explainable outputs were not only valuable for diagnosis but also served as educational and audit tools, addressing concerns of fairness, transparency, and accountability in AI-assisted medicine. XAIHO, therefore, serves as a step forward in developing deployable AI systems for liver disease detection, offering an interpretable, optimized, and generalizable tool for medical professionals and institutions.

To further enhance the robustness and applicability of the XAIHO framework, several future research directions are:

Privacy-Preservation: To address data-sharing restrictions across hospitals and geographies, federated learning can be integrated into XAIHO, allowing multiple institutions to collaboratively train models without exposing sensitive patient data.

Multi-Modal Data Integration: Future versions of XAIHO could combine imaging data (e.g., CT/MRI scans) with laboratory test reports, patient demographics, and clinical history to build a more comprehensive and context-aware diagnostic model.

Cross-Population Generalizability: The current dataset has geographic and ethnic limitations. Evaluating and retraining XAIHO on diverse, multi-ethnic, and multi-institutional datasets will be crucial for improving its generalizability and global adoption in different healthcare settings.

Temporal and Longitudinal Analysis: Incorporating temporal data such as patient progress over time could help the model forecast cirrhosis progression and assist in treatment planning and monitoring.

Clinician-AI Collaboration Tools: Future extensions may include the development of interactive interfaces where clinicians can adjust thresholds, visualize decision paths, and contribute to semi-supervised learning loops, increasing engagement and reliability.

By focusing on these directions, XAIHO can evolve into a scalable, privacy-aware, and globally usable AI platform for liver disease prediction and beyond.

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Author contributions

The idea and predicament formulation along with planned resolution, result analysis, and by Prashant & . Prof. Chaurasia, and verifies by Mr. Prashant, . Prof. Chaurasia and Prof. Shukla.

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Data availability

The data set generated and/or analyzed during the in progress learning is available upon realistic request from the corresponding author. However, data sets are accessible as open source. Dataset: Online available at: <https://www.kaggle.com/datasets/shawnxian/cirrhosis>.

Declarations

Ethics approval and consent to participate

No.

Competing interests

The authors declare no competing interests.

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The work is not submitted in any other journal. There is no divergence of significance.

Consent to publish

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