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Review Article

Harnessing the Potential of Artificial Intelligence in Managing Viral Hepatitis

Guma Ali[1,3,*], Maad M. Mijwil[2], Ioannis Adamopoulos[4], Bosco Apparatus Buruga[5], Murat Gök[6], Malik Sallam[7,8]

[1] *Department of Computer and Information Science, Faculty of Technoscience, Muni University, Arua, 00256, Uganda*

[2] *Computer Techniques Engineering Department, Baghdad College of Economic Sciences University, Baghdad, Iraq*

[3] *Department of Computer Science, Faculty of Science, Islamic University in Uganda, Arua Campus, Arua, 00256, Uganda*

[4] *Hellenic Republic, Region of Attica, Department of Environmental Hygiene and Public Health and Sanitarian inspections, Greece*

[5] *Department of Library and Information Services, Muni University, Arua, Uganda*

[6] *Department of Computer Engineering, Yalova University, Yalova, Türkiye*

[7] *Department of Pathology, Microbiology and Forensic Medicine, School of Medicine, The University of Jordan, Amman, Jordan*

[8] *Department of Clinical Laboratories and Forensic Medicine, Jordan University Hospital, Amman, Jordan*

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ABSTRACT

Viral hepatitis continues to be a serious global health concern, impacting millions of people, putting a strain on healthcare systems across the world, and causing significant morbidity and mortality. Traditional diagnostic, prognostic, and therapeutic procedures to address viral hepatitis are successful but have limits in accuracy, speed, and accessibility. Artificial intelligence (AI) advancement provides substantial opportunities to overcome these challenges. This study investigates the role of AI in revolutionizing viral hepatitis care, from early detection to therapy optimization and epidemiological surveillance. A comprehensive literature review was conducted using predefined keywords in the Nature, PLOS ONE, PubMed, Frontiers, Wiley Online Library, BMC, Taylor & Francis, Springer, ScienceDirect, MDPI, IEEE Xplore Digital Library, and Google Scholar databases. Peer-reviewed publications written in English between January 2019 and August 2024 were examined. The data of the selected research papers were synthesized and analyzed using thematic and narrative analysis techniques. The use of AI-driven algorithms in viral hepatitis control involves many significant aspects. AI improves diagnostic accuracy by integrating machine learning (ML) models with serological, genomic, and imaging data. It enables tailored treatment plans by assessing patient-specific characteristics and predicting therapy responses. AI-powered technologies aid in epidemiological modeling, and AI-powered systems effectively track treatment adherence, identify medication resistance, and control complications associated with chronic hepatitis infections. It is vital in identifying new antiviral medicines and vaccines, speeding the development pipeline through high-throughput screening and predictive modeling. Despite its transformational promise, using AI in viral hepatitis care presents various challenges, including data privacy concerns, the necessity for extensive and varied datasets, and the possibility of algorithmic biases. Ethical considerations, legal frameworks, and multidisciplinary collaboration are required to resolve these issues and ensure AI technology's safe and successful use in clinical practice. Exploiting the full AI's potential for viral hepatitis management provides unparalleled prospects to improve patient outcomes, optimize public health policies, and, eventually, and alleviate the disease's negative impact worldwide. This study seeks to provide academics, medics, and policymakers with the fundamental knowledge they need to harness AI's potential in the fight against viral hepatitis.

1. INTRODUCTION

Viral hepatitis is a communicable disease that affects millions of people globally, causing chronic liver disease, cirrhosis, and hepatocellular carcinoma (HCC), necessitating early and comprehensive response [1]. Aditya and Neeraj [2] describe hepatitis as inflammation of the liver caused by viral infections, autoimmune illnesses, toxins, or excessive alcohol intake. Viral hepatitis can be acute or chronic, and it is a viral disease that can be transmitted from one infected person to another healthy person. This inflammation harms hepatocytes, compromising their function and jeopardizing the liver's capacity to absorb nutrients, filter toxins, and generate serum proteins [2]. Viral hepatitis is mainly caused by one of five different

*Corresponding author. Email: a.guma@muni.ac.ug

hepatotropic viruses: hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), hepatitis D virus (HDV, the delta agent), and hepatitis E virus (HEV), which cause liver inflammation and damage. Each virus is characterized by distinct epidemiology, structural biology, transmission routes, endemic patterns, risk of liver problems, and responsiveness to antiviral medications [3][4]. These five virus types significantly influence public health, resulting in disease, deaths, and the possibility of extensive epidemics [5-7]. Chronic hepatitis is sometimes referred to as a "silent killer" since most patients are asymptomatic and unaware of their sickness. They are detected accidentally or develop symptoms years after contracting the virus [8].

The World Health Organization (WHO) released its worldwide hepatitis report 2024 in April 2024, including the most recent estimates on disease burden and coverage of critical viral hepatitis services from 187 countries worldwide, emphasizing access action in low- and middle-income countries (LMICs). Globally, the expected number of fatalities from viral hepatitis grew from 1.1 million in 2019 to 1.3 million in 2022, with hepatitis B accounting for 83% and hepatitis C for 17% [9]. It causes around 1.4 million fatalities per year as a result of acute infection and associated liver cancer and cirrhosis [10]. Every day, 3,500 people die across the world from hepatitis B and C virus infections [9]. By 2040, it is expected to kill more people than HIV, malaria, and tuberculosis combined [11].

Fatigue, flu-like symptoms, jaundice, pale stool, stomach discomfort, itching, loss of appetite, swelling of the legs and abdomen, nausea and vomiting, weight loss, and dark urine are some of the symptoms of acute viral hepatitis [7][12]. These symptoms may arise rapidly in acute infections or build gradually over time in chronic instances. Fecal contamination of drinking water, unprotected sexual contact, use of unsterilized instruments in barber shops, being born into an infected family, fraudulent medical practices, reusing syringes, blood transfusions, tattoos and piercings, injection drug abuse, hemodialysis, or the use of non-sterile invasive medical devices are the main risk factors for viral hepatitis transmission [13-18]. If not appropriately managed, hepatitis can progress to severe liver cirrhosis, fibrosis, acute fulminant hepatitis, hepatic decompensation, HCC, liver cancer, vascular diseases, insulin resistance/diabetes, and even death [5][19-22]. Viral hepatitis is primarily preventable and treatable, but there are disparities in access to immunizations, diagnostics, and therapies, and most hepatitis patients are unaware that they have the disease.

Despite substantial breakthroughs in antiviral medications, managing viral hepatitis remains challenging due to delayed diagnosis, unpredictable treatment outcomes, and the need for continuing monitoring. The WHO has devised a global health plan for viral hepatitis that will be implemented between 2022 and 2030 to halt the spread of viral hepatitis infection at the public health level by 2030. The approach calls for a 90% decrease in incidence and 65% in death. This initiative intends to reduce the prevalence of chronic viral hepatitis infection and death rates among infected individuals by enhancing access to screening, universal vaccination, and medicines [5][23]. With advances in medical technology, AI provides intriguing possibilities for improving viral hepatitis diagnosis, treatment, and management. AI, machine learning (ML), deep learning (DL), and natural language processing (NLP) offer a variety of supervised or unsupervised algorithms and advanced neural networks that can more accurately predict hepatitis risk than traditional methods [24]. Linear regression, logistic regression (LR), support vector machines (SVM), random forests (RF), decision trees (DT), gradient boosting (GB), K-nearest neighbors (KNN), Artificial Neural Networks (ANNs), Adaptive boosting (AdaBoost), extreme gradient boosting (XGBoost), Gaussian Naive Bayes (GNB), Naive Bayes (NB), K-means, principal component analysis (PCA), hierarchical clustering, Gaussian mixture models (GMM), density-based spatial clustering of applications with noise (DBSCAN), and self-organizing maps (SOMs) are effective and cost-efficient methods for predicting hepatitis [18][25-27]. DL algorithms such as Neural Networks (NNs), Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), Generative Adversarial Networks (GANs), Autoencoders, Transformer Models, Neural Architecture Search (NAS), Q-learning, State-Action-Reward-State-Action (SARSA), and Deep Q-Networks (DQN), showed significant predictive performance for hepatitis early detection [28-30]. AI, ML, DL, and NLP play a significant role in early diagnosis and prediction of viral hepatitis, enhancing patient care, identifying patients at high risk of infection, controlling hepatitis disease spread, forecasting the progression of hepatitis, drug discovery, enhancing patient engagement and adherence to antiviral therapy, predict disease progression, reducing the disease burden, preventing future outbreaks, improving clinical decision-making, and addressing the evolving needs of patients for a more effective and patient-centric approach to managing chronic hepatitis [22][30-34].

This review explores how AI can help manage viral hepatitis. This technology allows healthcare practitioners to obtain more precise diagnoses, personalized therapies, and effective patient monitoring. Furthermore, using AI can improve public health monitoring by giving real-time information on hepatitis disease prevalence and environmental risk factors. However, to fully utilize the potential of AI, issues such as data privacy, regulatory and legal issues, public opposition to change, system integration, data collection and variable selection, data interoperability, data quality and integration, ethical concerns, and biases associated with the selection of the clinical research problem, and algorithm development and post-development usage must be addressed. In this review, we aim to (1) introduce hepatitis and AI technologies, (2) summarize AI applications in viral hepatitis management, and (3) discuss current limitations and future considerations for AI applications in hepatology.

The remainder of this paper is arranged as follows: Section 2 looks at the materials and methods utilized in the study. Section 3 describes hepatitis and AI technology. Section 4 discusses how AI may be used to manage viral hepatitis. Section 5

summarizes the limitations and potential implications of AI applications in hepatology. Finally, Section 6 covers the conclusions.

2. MATERIALS AND METHODS

The study aims to comprehensively examine the potential of AI technologies in managing viral hepatitis. The process includes a structured literature evaluation, data synthesis, and analysis of the selected literature. The review used a variety of databases, including Nature, PLOS ONE, PubMed, Frontiers, Wiley Online Library, BMC, Taylor & Francis, Springer, ScienceDirect, MDPI, IEEE Xplore Digital Library, and Google Scholar. The search keywords included "artificial intelligence," "machine learning," "deep learning," "natural language processing," "viral hepatitis," "hepatitis B," "hepatitis C," "hepatitis management," "disease prediction," "healthcare AI," and other relevant terms. The researchers considered studies published in English between January 2019 and August 2024, including peer-reviewed articles, conference presentations, and substantial technical reports. Non-English papers, preprints, and duplicate research were all excluded. Four authors independently retrieved relevant material from the selected research databases using predefined key information, including (1) title, authors, and publication year, (2) objectives and research questions, (3) study design, (4) methods of analysis, (5) results, (6) conclusions, (7) viral hepatitis, (8) AI techniques, (9) AI application in viral hepatitis management, and (10) limitations, and future considerations. The extracted data was structured in a consistent format to guarantee uniformity and correctness.

A total of 168 relevant research papers were reviewed, with 9 from Nature, 2 from PLOS ONE, 10 from PubMed, 5 from Frontiers, 3 from Wiley Online Library, 8 from BMC, 5 from Taylor & Francis, 6 from Springer, 10 from ScienceDirect, 31 from MDPI, 12 from IEEE Xplore Digital Library, and 67 from Google Scholar. These research papers were assessed, appraised, and classed based on their relevance to AI applications for viral hepatitis management. Fig. 1 shows the distribution of selected research papers among digital libraries.

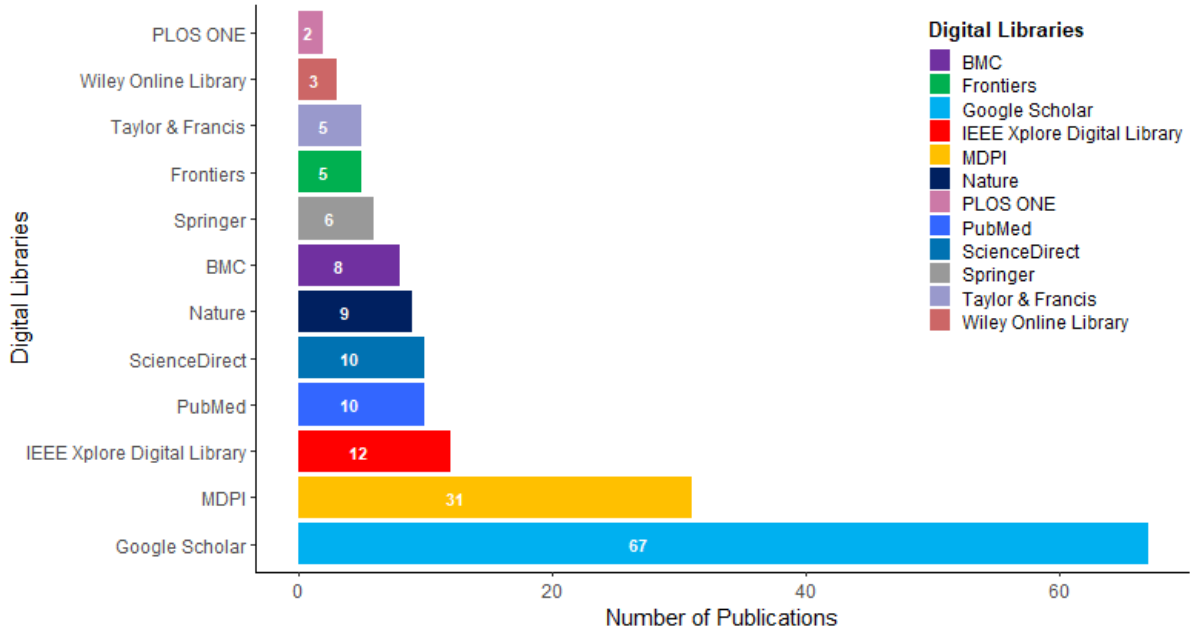

Fig. 1. Shows the distribution of the selected research papers according to the digital libraries.

Fig. 2 depicts the distribution of chosen research paper types among digital libraries.

Fig. 3 represents the distribution of chosen research from various digital libraries based on the year of publication.

The quality of the included research studies was evaluated using criteria such as study design, sample size, AI model validation, and applicability to hepatitis management. The studies were assessed based on their methodological rigor, data validity, and relevance to the research issues. A test-retest methodology, thorough search tactics, transparent reporting, peer review, critical appraisal, sensitivity analyses, conflict of interest disclosure, and meta-analysis were employed to reduce literature search biases. Maintaining patient privacy and data security in AI-powered hepatitis management systems was emphasized.

The data retrieved from the selected research studies were synthesized and analyzed using qualitative synthesis and theme analysis techniques. The study focuses on viral hepatitis, AI approaches, and using AI to manage viral hepatitis. The findings

were corroborated by cross-referencing them with prior literature research and critically evaluating the conclusions' quality. Each research paper was assessed for quality based on the robustness of the methodology, the validity and reliability of the findings, and their relevance to AI applications in viral hepatitis management. A scoring methodology was utilized to evaluate the studies, ensuring that only high-quality research publications were included in the final analysis. Because this study analyzed existing literature, no primary data was gathered; ethical approval was unnecessary. However, ethical norms were followed by adequately attributing all sources and avoiding plagiarism.

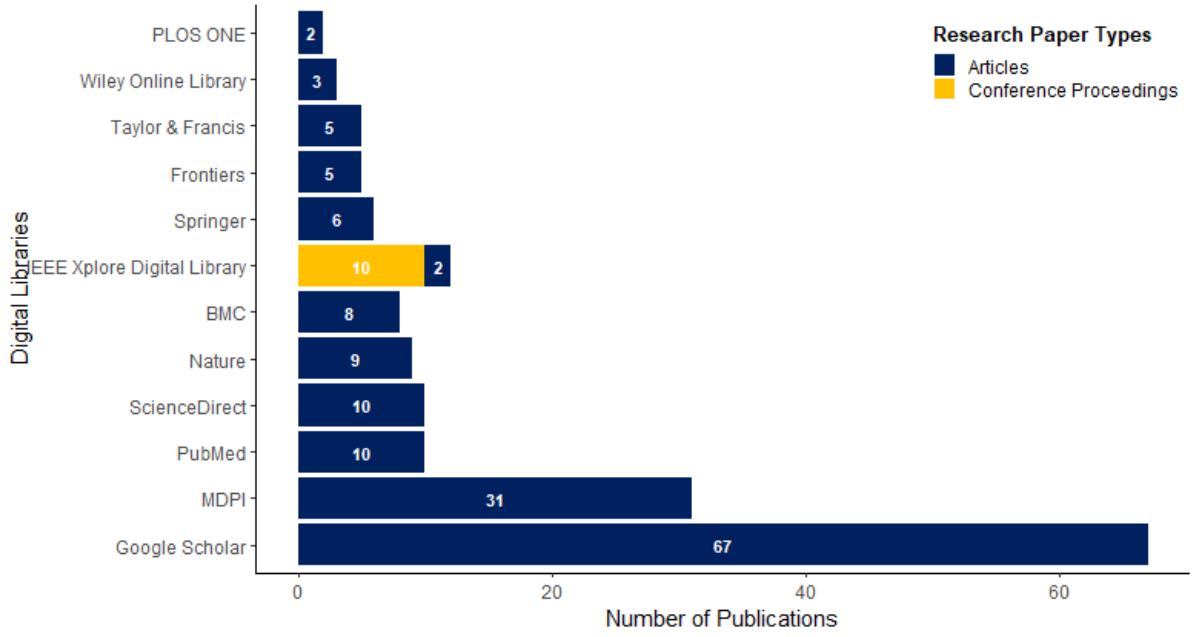

Fig. 2. Depicts the distribution of selected research paper types among digital libraries.

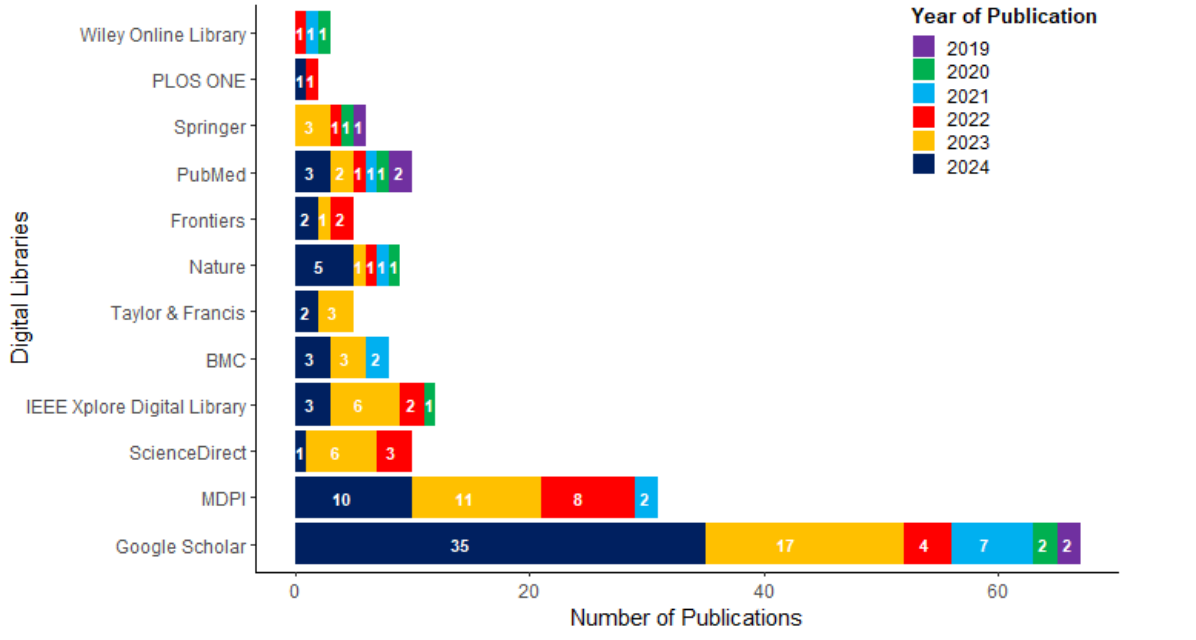

Fig. 3. Represents the distribution of selected research papers from various digital libraries based on the year of publication.

3. HEPATITIS AND ARTIFICIAL INTELLIGENCE

In hepatology, AI has proven critical for increasing medical care efficiency with limited human resources and assisting medical decision-making. Several AI techniques reported offer several tasks, such as prediction, diagnosis, prognosis, and recommendations for the best therapeutic method in viral hepatitis management [35].

3.1 Hepatitis

Hepatitis is a liver inflammation caused by several infectious viruses and non-infectious substances, which can result in various health issues. Both communicable and non-infectious sources can cause hepatitis. Hepatitis A, B, C, D, and E are the five primary types of viral hepatitis, and each type is caused by one of five hepatotropic virus strains, namely HAV, HBV, HCV, HDV, and HEV [12]. Individuals infected with HBV, HCV, or HDV (among those with HBV infection) can develop chronic hepatitis, cirrhosis, and HCC, with significant morbidity and death rates if no treatments are implemented [36]. Hepatitis viruses differ significantly in structure, epidemiology, modes of transmission, incubation time, clinical manifestations, natural history, diagnosis, and prevention and therapeutic options [1][12]. Below is a detailed description of the five primary types of viral hepatitis.

3.1.1 Hepatitis A

Hepatitis A is a primary worldwide health concern, particularly in areas of Africa, Asia, and Latin America with inadequate sanitation and hygiene standards. It is caused by the HAV, which belongs to the *Picornaviridae* family and the *Hepatovirus* genus [37]. It is often a transient infection that does not progress to chronic liver disease [12]. In 2020, 170 million new cases of HAV were recorded globally [37], and HAV is responsible for an estimated 1.4 million infections each year and around 7,134 deaths, accounting for 0.5% of viral hepatitis mortality [1]. Acute hepatitis A has a broad clinical spectrum, ranging from mild instances with no apparent symptoms often in young age, with most persons recovering completely and remaining resistant to future HAV infections, to sudden liver failure (fulminant hepatitis) leading to death in highly severe cases [2]. HAV infections are typically asymptomatic or have very moderate symptoms, and the illness usually has a benign course with spontaneous remission [5]. The most frequent symptoms are exhaustion, abrupt nausea and vomiting, stomach pain or discomfort near the liver, clay-colored feces, lack of appetite, low-grade fever, dark urine, joint pain, and jaundice. HAV is usually transmitted by food or drink contaminated with fecal matter carrying the virus, but it can also be transmitted from person to person through intimate contact and certain sex behaviors [5][38]. They may induce acute liver inflammation.

3.1.2 Hepatitis B

Chronic Hepatitis B infection is a substantial worldwide health hazard, affecting millions of individuals worldwide. Hepatitis B is caused by the HBV, a member of the *Hepadnaviridae* family and the *Orthohepadnavirus* genus [2][29]; it frequently progresses to chronic infection, resulting in severe consequences such cirrhosis, liver failure, and HCC [39]. About 400 million people are now infected with HBV, and approximately 2 billion people have antibody evidence of viral exposure [40]. Every year, around 30 million individuals worldwide become infected with HBV, and 296 million people today live with chronic HBV. Although an estimated 1 million individuals die from HBV each year, less than 10% of those infected are detected, and just around 1% receive treatment. It is the world's sixth leading cause of death, with rates most significant in East Asia and Sub-Saharan Africa [15]. More than 60 million individuals in Africa alone are infected with hepatitis B, resulting in approximately 60,000 fatalities per year [41]. HBV symptoms include fever, fatigue, weakness, joint pain, lack of appetite, stomach discomfort, dark urine, whiteness in the eyes, jaundice, vomiting, and nausea [42]. Hepatitis B is typically spread by contact with contaminated blood or other bodily fluids, sexual contact with an infected person, infected mother-to-child transmission during childbirth, transfusions of HBV-contaminated blood and blood products, contaminated injections during medical procedures, accidental needle stick injuries to healthcare workers, and sharing of drug-injection equipment [2][12]. It causes both acute and chronic liver illnesses, including liver cancer, cirrhosis, HCC, and liver failure [2][5][12][41][43-45].

3.1.3 Hepatitis C

Hepatitis C is a prominent cause of liver-related illness and mortality, accounting for an estimated 400,000 deaths yearly. Hepatitis C is caused by HCV, identified for the first time in 1989, and is a member of the *Flaviviridae* family and the *Hepacivirus* genus. It is the primary cause of cirrhosis and hepatocellular cancer. Because of its error-prone reproduction method via the RNA dependent RNA polymerase, seven genotypes and at least eighty viral subtypes have been identified [46]. Without therapy, around 25% of acutely infected people recover from the virus on their own within six months. Those who do not clear the virus progress to chronic infection; eventually, 15-20% will develop liver fibrosis, which can proceed to cirrhosis [46]. According to the WHO, around 50 million individuals worldwide have chronic hepatitis C by 2023, with 3.2 million being adolescents and children, resulting in 230,000-580,000 deaths each year, primarily from cirrhosis and liver cancer [47][48]. Furthermore, 1.5 million new infections are recorded yearly [1][41][49]. The annual worldwide economic cost of HCV surpasses US$10 billion, including the expense of screening, antivirals, managing hepatic and extrahepatic consequences, and lost productivity due to poor quality of life [46]. Hepatitis C symptoms include tiredness, fever, muscle

and joint pain, nausea, and jaundice. It is spread through blood transfusions, intravenous drug use with shared needles, mother-to-child transmission during childbirth, sexual transmission, unsafe medical procedures, and tattoo piercings with non-sterile equipment [2][5][12][33][49][50]. Hepatitis C can cause long-term health issues such as acute and chronic hepatitis, cirrhosis, fibrosis, liver cancer, and mortality from liver disease [12][41][51].

3.1.4 Hepatitis D

Hepatitis D, commonly known as hepatitis delta, is a rare and severe type of viral hepatitis caused by the HDV, a member of the *Kolmioviridae* family and the Delta virus genus. It arises in people infected with HBV, as HDV needs the HBV surface antigen to proliferate [2]. The HDV, identified in 1977 among HBV patients with severe liver damage, is a defective, obligatory satellite virus of HBV that requires hepatitis B surface antigen (HBsAg) proteins from its companion virus to create viral particles. The minor ribonucleic acid (RNA) virus infects humans, measuring 36-40 nm in diameter and containing around 1.7 kb of single-stranded negative-sense circular RNA. There are at least eight HDV genotypes, numbered 1 through 8. Genotype 1 has a global distribution and is most prevalent in Europe, North America, and parts of Asia, with a variable course of infection; genotype 2, which is widespread in Russia, Taiwan, and Japan, has a greater rate of remission than genotype 1; genotype 3, found in the Amazon Basin, is associated with early onset of HCC and acute liver failure; and genotype 4, found in Russia, Taiwan, and Japan, is associated with faster progression to cirrhosis. Genotypes 5, 6, 7, and 8 are found in Africa and among African migrants in Europe, but data is scarce, and the course of infection is poorly classified [41]. The incidence of hepatitis D varies significantly by area, with more excellent rates found in Central Asia, Eastern Europe, the Mediterranean, the Middle East, and Africa. Around 15-20 million individuals worldwide are infected with HDV, accounting for around 5% of those with chronic HBV. Sub-Saharan Africa has a high HDV prevalence, which leads to poor clinical outcomes for those who are HIV/HBV/HDV tri-infected [41][52]. Hepatitis D symptoms are comparable to those of other types of viral hepatitis. They might include nausea and vomiting, fatigue, stomach discomfort, jaundice, lack of appetite, loss of appetite, dark urine, and joint pain [53]. HDV, like HBV, is spread through contact with infected blood, saliva, semen, or other bodily fluids, unprotected sexual contact, sharing needles with an infected person, perinatal transmission, intravenous drug use, and exposure to infected blood [2][12]. Hepatitis D can cause more severe liver disease, including fibrosis, cirrhosis, HCC, hepatic decompensation, and HCC [5][12][54].

3.1.5 Hepatitis E

Hepatitis E is a zoonotic feco-oral virus caused by HEV, a member of the *Hepeviridae* family that includes *Orthohepevirus* and *Piscihepevirus* [17]. Orthohepatitis virus is classified into four species: A, B, C, and D. The Cutthroat trout virus is the sole member of the Piscihepevirus family. The Orthohepevirus A genome has eight HEV genotypes: genotypes 1 and 2 only infect humans, whereas genotypes 3, 4, and 7 are zoonotic. Pigs, rabbits, and cattle carry genotypes 3 and 4; genotypes 5 and 6 have only been detected in wild boars, whereas genotypes 7 and 8 have been reported in camels [55][56]. According to the WHO, there are approximately 20 million HEV infections globally each year, resulting in an estimated 3.3 million symptomatic cases of acute hepatitis and >44,000 deaths every year [57-59]. Hepatitis E symptoms are comparable to those of other kinds of viral hepatitis and might range from mild to severe. Fatigue, jaundice, fever, lack of appetite, nausea and vomiting, stomach discomfort, dark urine, clay-colored feces, joint pain, and itching are common symptoms that develop between 2 and 10 weeks after viral contact. While most instances of hepatitis E are mild and self-limiting, serious consequences can develop, particularly in high-risk populations. These consequences can include abrupt liver failure, chronic hepatitis E, severe illness in pregnant women, and neurological symptoms [38]. Hepatitis E spreads mainly through the fecal-oral pathway, consumption of contaminated water or food, zoonotic transmission through contact with infected animals and raw meat products from these animals, sexually transmissible in men who have sex with men, and through blood transfusions [2][5][12][17][60]. HEV also causes acute liver inflammation, increased mortality, and chronic infections, which may be associated with extrahepatic illnesses such as neurological abnormalities, kidney failure, and blood cell diseases [61].

3.2 Artificial Intelligence

AI is among the most disruptive technologies, promising to solve complicated issues and improve human skills. It is a field of computer science focusing on creating computer systems that employ data analysis and pre-programmed instructions to mimic and perform intelligent tasks, such as learning, pattern recognition, natural language understanding, problem-solving, perception, and decision-making that require human intelligence [32][62-64]. It consists of various intelligent processes and behaviors developed by computational models, algorithms, mathematical formulas, or rules that support computer systems and are inspired by how the human brain functions [64][65]. AI capabilities in hepatology became conceivable with the introduction of current, powerful computer technology and the capacity to record and store vast amounts of data [66]. It offers services to computer vision, pattern recognition, expert systems, language processing and translation, speech recognition, robotics, the Internet of Things, and others. It has extensive data analytics capabilities and can quickly, effectively, and precisely evaluate massive amounts of electronic healthcare data [63][64]. AI includes ML, DL, NLP, computer vision, robotics, and expert systems [63][67]. Fig. 4 depicts the relationships among AI, ML, and DL.

3.2.1 Machine Learning

ML is the primary engine driving the advancement of AI. Bal [32] and Ali et al. [63] define ML as a segment of AI that creates algorithms and statistical models capable of learning from essential datasets, identifying new patterns, and making data-driven predictions or performance related to a specific task without being explicitly programmed. ML approaches also incorporate rules and methods for recognizing or forecasting new data patterns or practices [64][68]. It creates a mathematical algorithm using a training dataset to predict outcomes or make autonomous decisions [32][69][70]. ML models in healthcare can be trained using medical images, electronic records, genomics, and other patient data to identify disease signatures. These models and algorithms extract patterns from data and associate them with compact classes of samples [62]. In most cases, enormous volumes of data must be fed into a machine-learning system. The algorithm analyzes and identifies data patterns, relationships, and trends before using these insights to create a mathematical model capable of making predictions, powering predictive analytics, or taking actions when presented with new, previously unseen data [71][72].

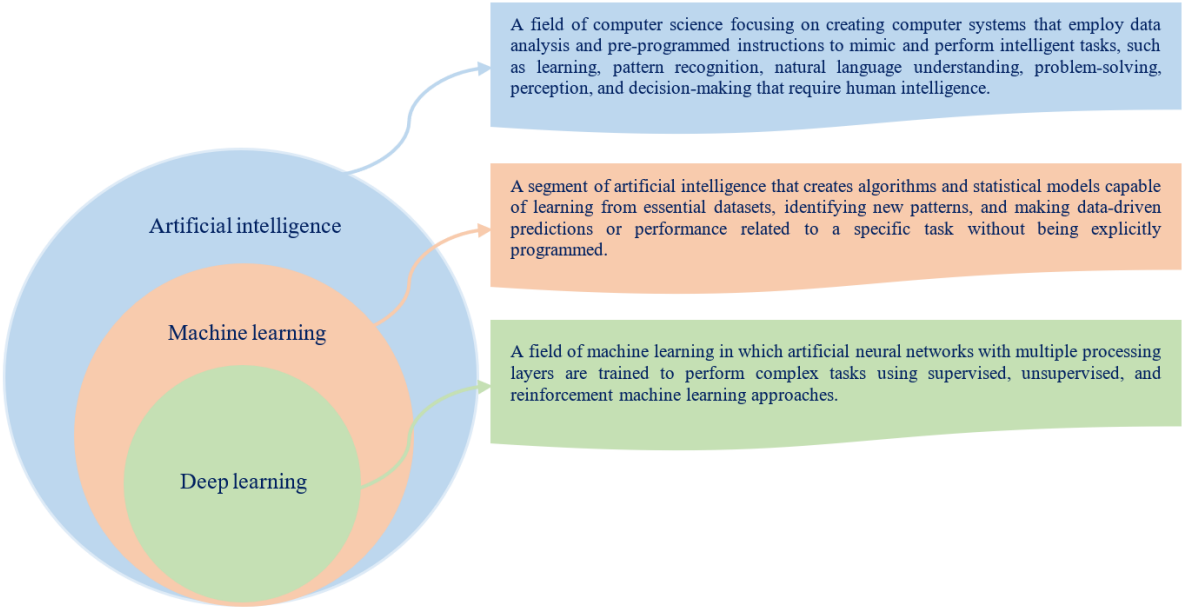

Fig. 4. Shows the associations between AI, ML, and DL.

ML approaches fall into four categories: supervised, unsupervised, semi-supervised, and reinforcement learning.

- ***Supervised Learning***

Supervised learning algorithms train algorithms using labeled datasets with preset input and output. The goal is to train the data to create a prediction model that accurately anticipates reactions to previously unknown data. Supervised ML employs classification and regression methods [70]. Classification is a supervised learning activity that aims to predict the category label of a given input. The output variable, or goal, is discrete and frequently denotes groupings or classes. Regression is a supervised learning task that attempts to predict a continuous numerical value based on a given input. The output variable, or target, is continuous and reflects real-valued data. Linear regression, LR, SVM, RF, DT, GB, KNN, NN, and NB are examples of supervised learning algorithms [63][73-76].

- ***Unsupervised Learning***

Unsupervised learning includes training on a dataset with no class labels, resulting in output data clusters that require further interpretation. Such models are used for exploratory data analysis, data clustering, feature extraction, and dimensionality reduction, e.g., identifying patient subgroups from unlabeled clinical data [63][73][74][77]. Unsupervised learning is classified into clustering and association [70]. Clustering is the process of grouping things to be more similar than those in other groupings. Clustering is one of the most often used unsupervised learning algorithms. The objective is to find natural groups within the data. The association entails identifying relevant links or associations between variables in massive datasets. The idea is to find rules that describe the connections between objects or events. Unsupervised learning algorithms include K-means, PCA, hierarchical clustering, GMM, DBSCAN, autoencoders, GANs, and SOMs [71][75].

- ***Semi-supervised learning***

Semi-supervised learning is a type of ML that employs a small amount of labeled data and a massive amount of unlabeled data for training. It trains models using labeled and unlabeled data, which is particularly useful when labeled data is few but unlabeled data is abundant. Semi-supervised learning uses unlabeled data to increase learning accuracy and efficiency, spanning the gap between supervised and unsupervised learning. It effectively utilizes labeled and unlabeled data to generate more accurate and efficient models. Mixing the advantages of supervised and unsupervised learning can give a practical solution to many real-world problems in which labeled data is few, but unlabeled data abounds. Semi-supervised learning employs a wide range of techniques, including generative models, graph-based models, mixture models, entropy minimization, and semi-supervised SVM [63][73][74].

- ***Reinforcement learning***

Reinforcement learning is a ML technique that involves an agent interacting with its environment to gain knowledge via experience [74]. It entails learning by contact with the environment rather than training the model on a predetermined dataset. Agents learn through trial and error by interacting with their surroundings and receiving feedback through rewards or punishments. Reinforcement learning is often utilized in autonomous systems to make judgments. It is best exemplified by the chess game and a pet's training. Reinforcement learning techniques include Q-learning, SARSA, and DQN [63][73].

Fig. 5 summarizes the ML techniques for managing viral hepatitis.

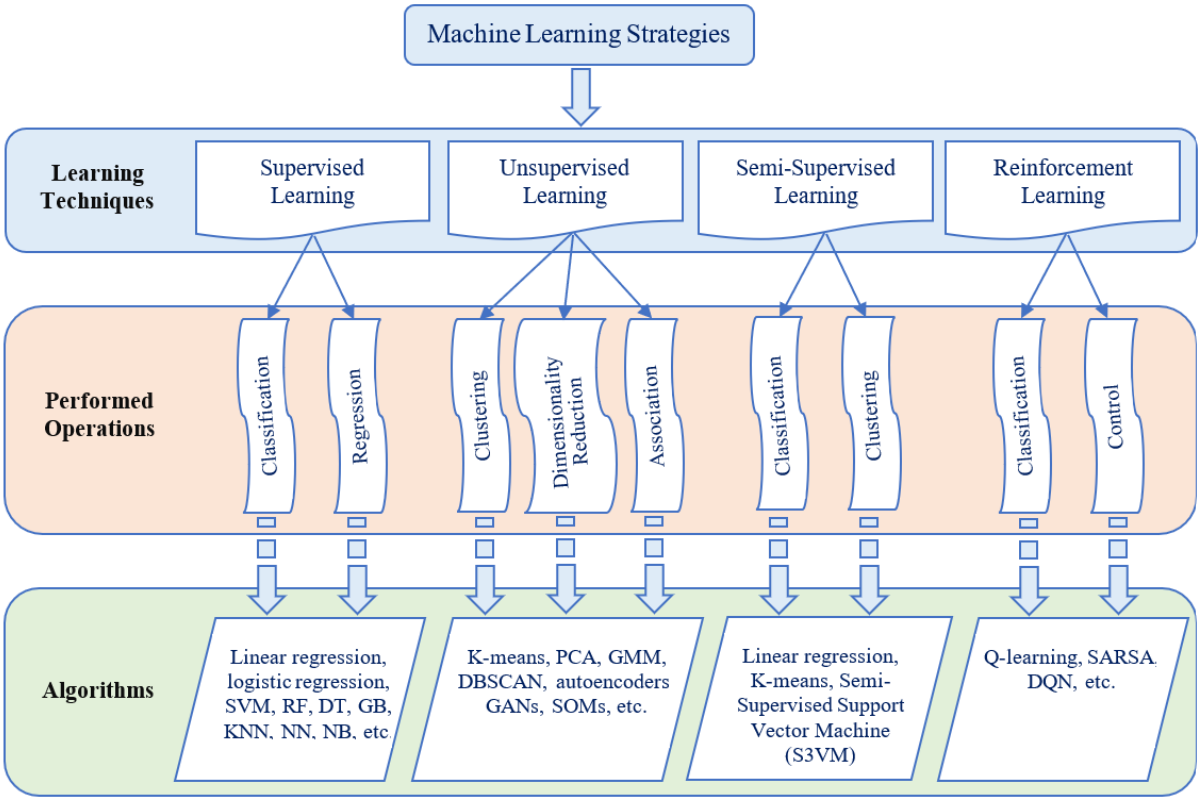

Fig. 5. Summary of the ML techniques in managing viral hepatitis.

3.2.2 Deep Learning

DL is a field of ML in which artificial neural networks with multiple processing layers are trained to perform complex tasks using supervised, unsupervised, and reinforcement ML approaches [32][63][69][77]. Artificial neural networks are the primary branch of DL, while convolutional neural networks are a subset of artificial neural network techniques. Neural networks draw inspiration from the structure and function of the human brain, with many layers of linked nodes that conduct analytical learning by assessing data such as text, images, and audio [32][62][63]. A neural network is organized into input, output, and hidden layers. The input layer is where external information enters the artificial neural network. Input nodes process data, evaluate or categorize it, and forward it to the next tier. Hidden layers receive information from the input layer or other hidden levels. Artificial neural networks can have a significant number of hidden layers. Each hidden layer examines the previous layer's output, processes it further, and forwards it to the next layer. The output layer displays the outcome of all data processing by the artificial neural network. It can have one or more nodes, as shown in Fig. 6 [78]. Many applications

train DL models on big datasets to improve their performance on higher-level tasks [63]. It is appropriate for supervised, semi-supervised, and unsupervised learning. It has shown great potential in improving the accuracy and efficiency of viral hepatitis management, particularly in image and voice recognition [74]. It has transformed fields including computer vision, medical diagnosis, image recognition, NLP, machine translation, and speech recognition by allowing models to learn hierarchical data representations [32]. DL has a significant advantage in processing large volumes of unstructured data. It applies to classification tasks and automatic feature extraction, where it may address the challenges of partial detectability and feature accessibility when extracting information from these crucial data sources [66]. DL models are classified as FNNs, CNNs, RNNs, GANs, Autoencoders, Transformer Models, and NAS [71][74].

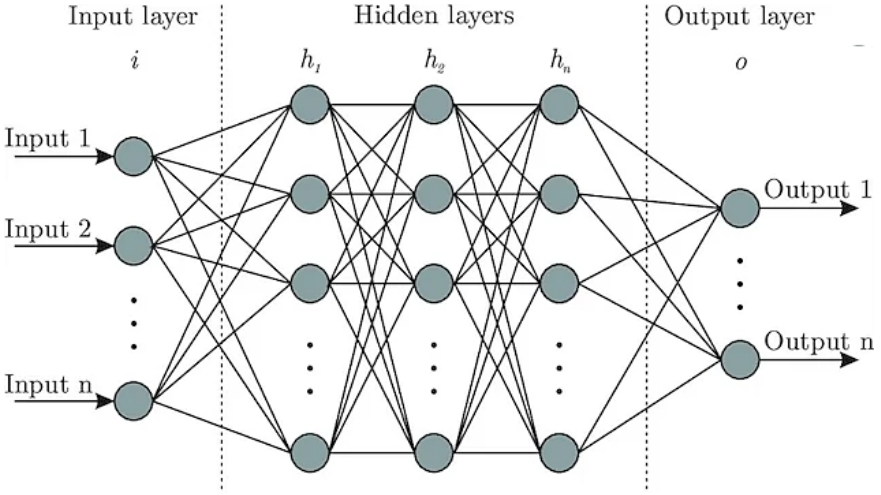

Fig. 6. Shows a simple neural network.

3.2.3 Natural Language Processing

NLP and AI have advanced significantly, enabling the development of various tasks, such as machine translation, text summarization, sentiment analysis, speech analysis, and medicine. As defined by Ali et al. [63] and Schneider et al. [79], NLP is a discipline within computer science and AI that employs ML to allow computers to perceive, understand, and synthesize human language, including voice and text. It allows computers to connect with people using natural language and accomplish tasks, including language translation, sentiment analysis, text summarization, speech recognition, and language creation [63][79][80]. Organizations now have massive amounts of speech and text data from various communication channels, including emails, text messages, social media newsfeeds, video, audio, and more. They employ NLP software to automatically interpret this data, analyze the message's purpose or sentiment, and reply quickly to human conversation. With the expanding usage of electronic health records (EHR), a growing corpus of text material in healthcare is suitable for NLP and ML [81]. NLP has two overlapping subfields: (1) natural language understanding - which focuses on semantic analysis or discerning text's intended meaning, and (2) natural language generation – which focuses on machine-generated writing. NLP encompasses a variety of algorithms and techniques designed to analyze, understand, and generate human language. Key NLP algorithms and methods include tokenization algorithms, text classification algorithms, sequence modeling algorithms, word embedding algorithms, contextual embeddings, machine translation algorithms, named entity recognition (NER) algorithms, text summarization algorithms, question-answering systems, and dialogue systems. AI is quickly altering the area of hepatology, providing new approaches to identifying and treating viral hepatitis. AI, which includes ML, DL, and NLP techniques, has emerged as a disruptive force in healthcare, particularly for hepatitis [32][79][82].

4. ARTIFICIAL INTELLIGENCE IN VIRAL HEPATITIS MANAGEMENT

AI improves viral hepatitis management by developing novel apps that improve diagnosis, therapy, and patient outcomes. ML algorithms, NLP, and predictive analytics are examples of AI techniques that improve the efficiency with which viral hepatitis is managed. This section looks at the primary uses of AI in viral hepatitis management.

4.1 Early hepatitis diagnosis and detection

Hepatitis diagnosis and therapy are difficult due to the wide variety of diagnostic indicators, which include viral, host, and liver disease variables. Beyond well-known diagnostic techniques, substantial progress has been made in discovering novel viral and host diagnostic variables with a high potential for supporting treatment decisions, predicting outcomes, or determining infection susceptibility. Such a large volume of data is challenging to analyze and can sometimes make or postpone decisions. AI may be used to streamline the diagnostic process and minimize misdiagnosis [83]. Large datasets of

medical records, imaging studies, and laboratory findings may be analyzed using AI algorithms to detect patterns suggestive of viral hepatitis. AI systems help analyze medical imaging, e.g., ultrasound (US) and magnetic resonance imaging (MRI), to detect liver abnormalities linked with hepatitis. Convolutional neural networks can improve imaging diagnostic accuracy by identifying key regions and giving quantitative estimates of liver damage. Early detection rates improved as AI algorithms discovered disease-related patterns that older approaches may have missed. By evaluating patient data and medical imaging, diagnostic technologies driven by AI made diagnosis faster and more accurate. Biomarkers related to viral hepatitis can be identified using AI-driven omics data analysis (genomics and proteomics). SVM and NN have demonstrated great accuracy in diagnosing hepatitis B and C by detecting subtle patterns in diagnostic data. They examine genomic and proteomic profiles to uncover novel biomarkers that might increase diagnostic accuracy and aid in early disease detection. Electronic health records and ML classifiers predict healthy control diagnoses for patients with hepatitis C and cirrhosis [84][85]. ML algorithms can efficiently build predictive models using longitudinal information while incorporating several predictor variables without compromising the accuracy of risk prediction, and many ML models have been used to find undiagnosed patients with hepatitis C infection [86]. ML algorithms can evaluate data trends to predict disease development [87]. They have been successfully employed as a classification approach to extract information from medical data and create accurate predictions for HBV diagnosis [88]. Electronic health data can be analyzed using NLP to identify individuals with viral hepatitis symptoms or risk factors. NLP can help with early detection and appropriate intervention by extracting pertinent information from clinical notes and medical histories. NLP algorithms can identify possible viral hepatitis cases by extracting symptom descriptions from patient narratives or clinical records.

Some notable studies that use AI in early hepatitis diagnosis and detection include the following. Bharathi et al. [33] used classification modeling techniques such as SVM, DT, LR, and RF, with and without feature selection, to create an accurate HCV prediction model. The dataset of hepatitis patients was analyzed using several approaches, such as SVM, DT, LR, and RF, to predict the results for each classifier effectively. The analysis considers the infection's natural course and evaluates the effects of numerous variables on disease progression. The results reveal that RF with feature selection outperformed RF without feature selection with an accuracy of 89% and 88.33%, respectively. Ara et al. [26] used numerous machine-learning approaches to predict hepatitis C disease based on readily available and cheap blood test data, allowing them to detect and treat patients earlier. The study used SVM, LR, and DT algorithms on a single dataset. The confusion matrix, precision, recall, F1 score, accuracy, receiver operating characteristics (ROC), and performance of several strategies were evaluated to choose an appropriate technique for disease prediction. The SVM model has the most outstanding overall accuracy of all three models, at 0.92. The findings showed that SVM and LR approaches accurately diagnose hepatitis C in its early stages. Yao et al. [10] combined LR with ML models to screen and identify high-risk variables for HBV infection in the community. Understanding the shifting environment of Hepatitis B epidemiology enables early detection and treatment of HBV infections. Ordouei and Moeini [89] used a combination of the DT algorithm and the Harris Hawks Optimization evolutionary method to identify hepatitis disease. The efficiency of the suggested Harris Hawks Optimization optimizer technique was evaluated on 29 functions, as well as numerous real-world engineering situations. The statistical results and comparisons reveal that the Harris Hawks Optimization method performs well, if not better, than other well-known meta-heuristic strategies. Using the Harris Hawks Optimization with the DT classification technique, an automated system was demonstrated on the dataset collected from the HCV dataset from the UCI reference, which diagnosed the HCV disease with 95.9112% accuracy. Harabor et al. [29] performed research in which patients' clinical features were gathered from a structured survey and used in four ML-based models, i.e., SVM, RF, NB, and KNN, and their predictive accuracy was evaluated. When predicting HCV status, all of the evaluated models performed better. The KNN algorithm produced the best prediction performance with an accuracy of 98.1%, followed by SVM and RF with identical accuracies of 97.6% and NB with an accuracy of 95.7%. The models' predictive ability for HBV status was low, with accuracies ranging from 78.2% to 97.6%. Therefore, ML-based models may be valuable tools for predicting HCV infection and risk stratification in adult patients undergoing a viral hepatitis screening program. Wang et al. [90] used machine-learning algorithms to predict hepatitis C disease based on blood test data, resulting in early diagnosis and treatment for patients. To predict hepatitis C, they combined characteristics from the literature with real data and used six machine-learning algorithms: LR, SVM, KNN, DT, RF, and AdaBoost. Various techniques were compared using criteria such as accuracy, precision, recall, F1-score, receiver operating parameters, and area under the curve to discover appropriate strategies for this disease. The UCI dataset results show that AdaBoost had the most fantastic accuracy of 97.8% and an area under the curve of 0.994, indicating that it is an effective and cost-efficient strategy for predicting hepatitis C. Moulaei et al. [91] conducted a thorough study and meta-analysis to investigate the effectiveness of ML algorithms in predicting viral hepatitis. Twenty-one original research studies were included, totaling 82 algorithms. Sixteen research studies used five methods to predict hepatitis B, and ten employed five methods to predict hepatitis C. For hepatitis B prediction, SVM algorithms had the most incredible sensitivity (90.0%; 95% confidence interval (CI): 77.0%-96.0%), specificity (94%; 95% CI: 90.0%-97.0%), and diagnostic odds ratio (DOR) of 145 (95% CI: 37.0-559.0). For hepatitis C prediction, KNN algorithms had the highest sensitivity (80%; 95% CI: 30.0%-97.0%), specificity (95%; 95% CI: 58.0%-99.0%), and DOR (72; 95% CI: 3.0-1644.0). The SVM algorithm performed better at predicting hepatitis B, whereas the KNN method performed best at predicting hepatitis C. Sachdeva et al. [92] created an accurate machine-learning model to improve predicting success rates for hepatitis disease. The medical information of 155

individuals is included in the publicly available hepatitis dataset, which can be obtained on the UCI ML repository. ML classifiers such as SVM, RF, KNN, LR, and GNB were used to predict the disease. Random forest has the best accuracy (100%) of any ML classification technique examined and 100% sensitivity, precision, and F-measure. Clinicians can use this model to predict hepatitis. Dutta et al. [93] investigated the categorization of hepatitis disease using six machine-learning approaches: LR, RF, DT, KNN, SVM, and NB. The results show that LR achieved the highest accuracy of 87.17% in predicting the presence of hepatitis. Koçak et al. [25] studied the application of AI technologies to detect the HCV disease status of patients based on blood samples. The study comprised a total of 615 people. The blood data was preprocessed, filtered, feature-selected, and classified. The correlation approach was used to pick characteristics, and the features with the highest correlation values were fed into five separate classification algorithms. The study results indicated that the KNN algorithm had the highest classification success rate for detecting HCV patients, at 99.1%. This result shows that AI technology is vital for early diagnosis of HCV-related diseases, and the KNN algorithm can extract transparent information regarding hepatitis infection from various blood parameters. Muneer and Khan [94] conducted research using AI to predict chronic hepatitis C. Five AI algorithms, including NB, DT, Bayesian Nets (BNs), SVM, and RF, were used to forecast changes in chronic hepatitis C patients. The forecasts' accuracy is increased by applying filter and wrapper feature selection approaches to reduce unnecessary components. Accuracy, sensitivity, and specificity are the metrics used to measure the performance of the suggested algorithms. The findings suggest that AI algorithms can deliver accurate forecasts and better outcomes when treating hepatitis C. Obaido et al. [88] employed SHapley Additive exPlanations (SHAP), a game-based theoretical technique, to explain and visualize ML models' predictions for hepatitis B diagnosis. They used demographic and clinical data from the UC Irvine ML Repository. Among other models, the AdaBoost model got an accuracy score of 92%, with bilirubin levels recognized as the primary factor leading to a greater death risk, followed by ascites. The algorithms used to create the models were DT, LR, SVM, RF, AdaBoost, and XGBoost, which produced balanced accuracies of 75%, 82%, 75%, 86%, 92%, and 90%, respectively. Meanwhile, the SHAP values revealed that bilirubin is the most crucial factor contributing to an increased death risk. The findings of this study can help health practitioners and policymakers understand the outcomes of ML models for health-related challenges. Vijayakumar [95] introduced a unique end-to-end framework for identifying the Hepatitis C Virus based on Transfer Learning and Hybrid Quantum Neural Networks (QNNs). Transfer Learning dramatically decreases the time necessary to train DL models for image analysis tasks by leveraging pre-trained models and transferring information to new functions while boosting the accuracy and precision of the results. Integrating hybrid QNNs into the training process speeds and improves model accuracy. Integration hardware and software accelerators onto AI edge devices onboard computed tomography (CT) scanners is presented, allowing for quicker inference and a viable way to produce an efficient early HCV diagnostic solution to aid radiologists. The technique allows for quick examination and categorization of HCV-related liver lesions, possibly lowering the burden of HCV-related liver disease. By changing the area of medical imaging, this technology can significantly increase the speed and accuracy of HCV detection and diagnosis, redefining the landscape of liver disease diagnosis and treatment. Using a Transfer Learning architecture with hybrid QNN layers, the model was trained faster and with improved accuracy in detecting indicators of liver disease. Harabor et al. [29] employed three neural networks to predict HBV and HCV incidence in a Chinese population using surveillance data spanning 13 years. The LSTM prediction model, the RNN model, and the BPNN model all performed well in predicting disease incidents early on. Oftadeh and Manthouri [96] introduced an intelligent system that evolved beyond the deep neural network. It can diagnose and distinguish between Hepatitis B and C by performing standard liver health tests. The Deep Boltzmann Machine (DBM) is the deep network employed in this study. The Restricted Boltzmann Machine (RBM) learning components produce the anticipated outcomes. RBMs extract features for use in an effective classification process. An RBM is a powerful computer tool ideal for extracting high-level characteristics and diagnosing hepatitis B and C. The technique was tested on common materials in laboratory testing to assess the liver's health. The DBM predicted hepatitis B and C with an accuracy of 90.1% to 92.04%. The predictive accuracy was acquired using 10-fold cross-validation. Compared to existing approaches, simulation results on DBM architecture show that the suggested method is more efficient in diagnosing Hepatitis B and C. Bagi and Mihuandayani [97] used the Learning Vector Quantization (LVQ) 3 method to categorize the different forms of hepatitis and to assess its accuracy. The LVQ3 algorithm can classify hepatitis types with an 88% accuracy utilizing 80 training and 25 test data. Xia et al. [28] used three DL algorithms: the LSTM prediction model, the RNN prediction model, and BPNN. The DL time series predictive models demonstrate their importance in forecasting hepatitis incidence and have the potential to assist decision-makers in making efficient decisions for the early detection of disease incidents, thereby significantly promoting Hepatitis control and management. Fong et al. [81] identified patients at high risk of HCV infection using NLP and ML. Models were created and validated to predict patients with newly discovered HCV infection (detectable RNA or reported HCV diagnosis). The models were assessed using three types of variables: structured (structured-based model), semi-structured and free-text notes (text-based model), and all variables (full-set model). Each model was applied to three data sets: patients with no history of HCV before 2020, patients with HCV before 2020, and all patients. XGBoost and ten-fold C-statistic cross-validation were employed to assess the models' generalizability. There were 3,564 distinct patients, 487 with HCV infection. The average C-statistics for all patients on the structured-based, text-based, and full-set models were 0.777 (95% CI: 0.744-0.810), 0.677 (95% CI: 0.631-0.723), and 0.774 (95% CI: 0.735-0.813). For patients with no history of HCV before 2020, the full-set model outperformed the structured-based model and was comparable to the text-based models, with average C-statistics of 0.780, 0.774, and 0.759, respectively. NLP identified six

additional risk variables that were inconsistently recorded in structured elements: imprisonment, needlestick injuries, substance use or misuse, sexually transmitted diseases, piercings, and tattoos. When data is scarce, having a variety of model alternatives (structured-based or text-based models) with comparable performance might give deployment flexibility.

4.2 Detection of liver fibrosis in chronic liver disease

Fibrosis is scar tissue formation in the liver due to chronic hepatitis C inflammation [98]. Liver fibrosis is the slow formation of scar tissue in the liver due to prolonged injury or inflammation. It is a reaction to recurrent liver injury in which fibrous connective tissue replaces normal liver tissue. This scarring can impair the liver's capacity to operate normally by interfering with the natural architecture and blood flow inside it. Chronic hepatitis B and C, alcoholic liver disease, non-alcoholic fatty liver disease (NAFLD), and inherited abnormalities are the leading causes of liver fibrosis. Monitoring the level of fibrosis is crucial for determining the severity of liver damage and making therapy options [98]. AI has great promise for improving the identification and management of hepatic fibrosis in chronic liver disease. It improves elastography picture interpretation, such as FibroScan, by increasing the accuracy and consistency of liver stiffness readings, which correspond with fibrosis levels. AI systems examine MRI and CT data for patterns and subtle alterations that indicate fibrosis. Radiomics is a technique that extracts quantitative information from medical pictures to help with fibrosis staging. AI helps to analyze liver biopsy slides by automating the detection and quantification of fibrotic tissue [99]. ML models may be trained to distinguish fibrotic patterns with great accuracy, decreasing the diversity in human interpretation. AI algorithms use combinations of blood indicators to predict the existence and severity of liver fibrosis. This method minimizes the need for invasive treatments such as biopsies. By analyzing patient data, AI can forecast the evolution of liver fibrosis and the likelihood of acquiring more serious liver illnesses. ML models consider a variety of characteristics, including genetic predisposition, lifestyle, and clinical history. AI helps to personalize treatment approaches based on fibrosis stage and patient-specific characteristics, which improves results and reduces side effects.

Some prominent research that applies AI to identify liver fibrosis in chronic liver disease includes the following. Zhang et al. [100] created a machine-learning algorithm that can accurately predict the fibrosis stage in chronic hepatitis B patients. Six ML models were built using LR, SVM, KNN, DT, NB, and RF, with maximum relevance, minimum redundancy, and gradient-boosting decision tree dimensionality reduction chosen characteristics from the training cohort. The DT model was built using five serological biomarkers: HBV-DNA, platelets, thrombin time, international normalized ratio, and albumin. The area under the DT model curve (AUC) values for assessing the training cohort had liver fibrosis stages (F0-1, F2, F3, and F4) of 0.898, 0.891, 0.907, and 0.944. The DT model's AUC values for assessing liver fibrosis stages (F0-1, F2, F3, and F4) in the external validation cohort were 0.906, 0.876, 0.931, and 0.933, respectively. Based on the cutoff value, the simulated risk classification demonstrated that the DT model's classification performance in identifying hepatic fibrosis stages accurately matched pathological diagnostic results. This study found that the ML model outperformed standard serological mixed indicators in identifying all four liver fibrosis phases in chronic hepatitis B patients. Gheorghe et al. [101] used a variety of ML classifiers, including SVM, NB, RF, and KNN, to stage liver fibrosis in chronic B hepatitis, exceeding the original Liver Fibrosis Index produced using regression studies on RTE pictures. Another stiffness value clustering and ML approach showed that the SVM model classified healthy vs chronic liver disease patients with 87.3% accuracy, 93.5% sensitivity, and 81.2% specificity. Still, DL was applied to measure liver fibrosis in a recent prospective multicentric experiment, with high area values under the receiver curve of 0.97 for F4, 0.98 for >=F3, and 0.85 for >=F2. This type of automated AI and DL/ML analysis based on CNNs will undoubtedly assist doctors in classifying and staging inflammation, steatosis, and fibrosis using noninvasive US techniques that are highly accurate, inexpensive, and widely available in the primary setting or at the point of care. Decharatanachart et al. [102] created ML algorithms to predict the risk and outcomes of liver diseases based on a variety of clinical parameters, including assessing liver fibrosis and steatosis, predicting liver decompensation in primary sclerosing cholangitis, screening and selecting liver transplant recipients, and predicting post-transplant survival and complications. This meta-analysis indicates that AI systems have great potential for diagnosing and staging liver fibrosis and NAFLD. Integrating AI with traditional noninvasive procedures results in excellent diagnostic tools with the best combination of sensitivity and specificity. Christou and Tsoulfas [103] created a gradient-boosting model that uses serum indicators to predict fibrosis and identify the fibrosis stage in two cohorts of HBV and HCV patients. Emu et al. [104] combine machine-learning techniques to create a noninvasive solution for predicting the severity of liver fibrosis. Random forests scored around 97.432% for the complete features set and 97.228% for the reduced set. The multilayer perceptron performance was between 96% and 98% for both feature sets. Logistic regression's accuracy is between 96% and 97%. According to this study, serum indicators can help predict the stage of liver fibrosis or the state of a patient's liver. Random forests were also applied to the whole dataset, and a smaller selection of 20 characteristics was identified based on their relevance. A decision tree was then built using the reduced feature set and the relative pathways discovered in the RF. With only 28 rules, the prediction accuracy is 97.45%. Bal [32] created a one-of-a-kind prediction CNN model based on multiple abnormalities discovered in ECG recordings of 5,212 patients who received liver transplants at three Mayo Clinic transplant facilities between 1988 and 2019. Using only ECG scans, the DL-based algorithm correctly distinguished patients with cirrhosis from control participants with an accuracy of 90% (84.9% sensitivity and 83.2% specificity). Wang et al. [105] assessed the performance of the recently developed deep-learning Radiomics of Elastography (DLRE) for determining liver

fibrosis stages. DLRE uses a radiomic method to quantify heterogeneity in two-dimensional shear wave elastography (2D-SWE) pictures. Prospective multicenter research was done to examine its accuracy in patients with chronic hepatitis B, compared with 2D-SWE, aspartate transaminase-to-platelet ratio index, and fibrosis index based on four parameters, with liver biopsy as the reference standard. Its accuracy and robustness were further evaluated using varied acquisition numbers and training cohorts. Six hundred fifty-four potentially eligible patients were prospectively enrolled from 12 hospitals, and 398 patients with 1,990 pictures were included. ROC curves were analyzed to determine the appropriate AUC for cirrhosis (F4), advanced fibrosis (≥F3), and significant fibrosis (≥F2). DLRE performed much better than other approaches, with AUCs of 0.97 for F4 (95% CI 0.94 to 0.99), 0.98 for ≥F3 (95% CI 0.96 to 1.00), and 0.85 (95% CI 0.81 to 0.89) for ≥F2. The only exception was 2D-SWE in ≥F2. Acquiring ≥3 pictures from each subject enhanced diagnosis accuracy. There was no significant performance variance when different training cohorts were used. DL Radiomics of Elastography outperforms 2D-SWE and biomarkers to predict liver fibrosis stages. It is valuable and practical for noninvasive, reliable identification of liver fibrosis stages in HBV-infected individuals. ML algorithms can consistently predict the fibrosis stage, with CNN-based classifiers, SVM, and RF classifiers doing exceptionally well. Although these AI-assisted tools cannot replace liver biopsy, they outperform noninvasive options, such as biomarkers and imaging technologies. AI-assisted noninvasive approaches offer enormous promise for reliably identifying liver fibrosis, enabling early risk factor adjustment, and suitable therapy [106]. Lee et al. [107] investigated the accuracy of artificial neural networks in predicting substantial fibrosis in chronic hepatitis C patients. ANN accurately predicted the presence or absence of severe fibrosis based on clinical factors, avoiding an unnecessary liver biopsy. Radiomics and DL algorithms may be utilized to evaluate liver fibrosis quantitatively using medical imaging. In prospective multicenter research, deep-learning radiomics of elastography predicted liver fibrosis more accurately than shear wave elastography or blood biomarkers in individuals with chronic hepatitis B. A radiomics model, the radiomics fibrosis index, was created using godoxetic acid-enhanced MRI. This approach is more accurate in staging liver fibrosis than normalized liver enhancement, aspartate aminotransferase-to-platelet ratio index, and fibrosis-4 index.

4.3 The prognosis of chronic liver disease

Chronic liver disease has a complex prognosis, which is determined by the underlying etiology, disease stage, existence of comorbidities, and patient-specific variables. Early diagnosis, adequate therapy, and lifestyle modifications are essential in enhancing the prognosis and quality of life for patients with chronic liver disease. Ma et al. [108] describe the prognosis of chronic liver disease as the illness's expected course and outcome, including the possibility of recovery, progression, and the risk of complications or death. Chronic liver disease refers to a variety of liver disorders, including chronic hepatitis, liver cirrhosis, NAFLD, and alcoholic liver disease. The prognosis varies depending on (1) underlying causes like hepatitis B and C, alcoholic liver disease, and NAFLD/Non-Alcoholic Steatohepatitis (NASH); (2) disease stages such as fibrosis and cirrhosis and compensated/decompensated cirrhosis; (3) the presence of complications due to portal hypertension, ascites, and hepatic encephalopathy; and (4) patient factors such as age and gender, comorbid conditions, and genetics. AI has demonstrated significant potential in identifying chronic liver disease in various applications, including early detection, disease progression prediction, and therapy response tracking [109]. DL models can analyze medical images such as US, CT scans, and MRI to detect early indicators of liver disease. These programs can detect slight changes that human radiologists might overlook. AI can assess complicated datasets, such as genomic, proteomic, and metabolomic data, to detect indicators of liver disease early. ML algorithms can predict the evolution of chronic liver disease by assessing patient data such as demographics, clinical history, laboratory results, and imaging findings. These models can assist physicians in predicting problems such as liver fibrosis, cirrhosis, and cancer. AI-driven NLP techniques can extract valuable information from unstructured clinical notes, allowing researchers to follow illness development and identify risk factors. AI can help adapt treatment strategies based on specific patient features and projected therapeutic outcomes. This strategy can improve therapy efficacy while minimizing side effects. Wearable gadgets and mobile health applications that use AI can continually monitor patients' health indicators, providing real-time input to physicians and allowing for prompt treatments. AI-powered clinical decision support systems can stratify patients based on their likelihood of developing problems, assisting physicians in prioritizing high-risk patients for more intense monitoring and treatment. These systems can offer evidence-based therapy suggestions by assessing patient data and existing clinical guidelines. AI can combine and analyze massive volumes of data from various sources, including clinical trials, EHR, and research databases, to discover novel therapeutic targets and speed drug development. It can generate illness models to test the efficacy of possible medicines, assisting in selecting the most promising candidates for clinical trials.

The following are some noteworthy studies that use AI to predict chronic liver disease. Hossain et al. [27] intend to enhance liver disease diagnoses using machine-learning approaches such as preprocessing, model selection, and validation. Using ML algorithms to detect liver disease and cancer early is a significant advancement in medical research. The paper dives into the improvements and uses of numerous ML algorithms, such as XGBoost, RF, and SVM, emphasizing their contributions to early detection and better patient care. XGBoost has emerged as a reliable algorithm for detecting fatty liver disease in individuals in general. A hybrid XGBoost model, fine-tuned by hyperparameter optimization, can accurately predict liver disease. Random Forest is another widely used method for its precision and accuracy in liver disease diagnosis. SVM

approaches have also shown potential for detecting liver illness. When combined with LR, SVM provides a strong foundation for disease prediction by resolving the issues of overfitting and underfitting. The adaptability of SVM makes them an excellent tool for the early identification of liver illness, adding considerably to the arsenal of machine-learning approaches in medical diagnostics. The literature also investigates the effect of ensemble learning and sophisticated optimization strategies in increasing predictive model performance. Ensemble learning models, such as RF, GB, XGB, and light gradient boosting machines (LGBM), outperform other methods in predicting liver disease in the early stages. The Bayesian optimization of Extra Trees for liver disease prediction demonstrates the power of optimization approaches in refining prediction models to improve outcomes. The Bayesian Optimized ExtraTrees model stood out for its excellent accuracy in predicting liver disease. Lee et al. [107] used non-contrast-enhanced computed CT scans to create two radiomics signatures that predict hepatitis disease progression, guiding therapy decisions and determining the best way to manage patients with chronic liver disease. They accurately diagnosed gastroesophageal varices and predicted high-risk varices in compensated advanced chronic liver disease. Using RF analysis, the DL-based model performance for HCC development alone at 1 and 3 years was less robust (AUROC 0.65-0.70), but it performed well for transplant-free survival at 1 and 3 years (AUROC 0.80-0.85). According to Parisi et al. [110], AI-based decision-making support tools, such as ML and ANN-based algorithms, can recognize patterns in input variables that can impact the disease's progression. ML can detect such subtle disease patterns and deal with highly nonlinear, highly dimensional, and ill-behaved solution spaces, indicating that it has the potential to help in prognostic assessments in clinical settings. Unsupervised ANN-based learning classifiers, such as self-organizing maps (SOM) and KNN, can classify input patient data without knowing its classes. Supervised AI-based learning classifiers, such as the ANN-based Multi-Layer Perceptron (MLP) and the ML-based Lagrangian SVM (LSVM), assume that the patient input data's actual classes are known beforehand. An ANN is trained iteratively to detect underlying patterns in input data to enhance classification performance. Transfer functions aid learning in ANN, where weights are iteratively altered in the training procedure depending on the goal outputs. This repeated learning procedure causes the ANN to reduce its training error while increasing its classification performance. Finally, the moduli of the weights establish the proportional relevance of the desired categorization. In the field of hepatology, the potential for using ANN to learn to predict the prognosis of patients with hepatitis has been demonstrated. After an extensive evaluation of the classification accuracy of the hybrid model LSVM-MLP against the MLP, the LSVM-MLP has been demonstrated to be the most accurate, reliable, and computationally fastest AI-based classifier for predicting the survival of patients with chronic hepatitis.

4.4 Detection of non-alcoholic fatty liver disease (NAFLD)

In recent years, fatty liver disease has gradually evolved into a hidden pandemic, mainly owing to increased obesity, type 2 diabetes, dyslipidemia, and hypertension rates, with a global incidence of roughly 25%. However, the burden of NAFLD is far more significant, and its prevalence is steadily growing at an alarming rate [111]. This is a prime concern because it can progress to a more severe form known as NASH, causing cirrhosis, fibrosis, liver cancer, and HCC [79][111][112]. As a result, NAFLD is now recognized as a principal public health problem since it causes the most common chronic liver illnesses and is a risk factor for increased morbidity [79][101][111][112]. NAFLD is a disorder characterized by the buildup of extra fat in the liver cells of people who drink little or no alcohol. AI is becoming more significant in detecting, treating, and controlling NAFLD. Many ML techniques estimate the risk factors for NAFLD. It has been demonstrated that the LR, KNN, SVM, NB, BN, DT, and K2 algorithms help diagnose NAFLD [111]. DL algorithms examine medical imaging data such as US, MRI, and CT scans. These AI algorithms can detect indications of NAFLD with great accuracy, sometimes outperforming human specialists. AI aids in identifying new biomarkers from big datasets, enhancing NAFLD diagnosis without invasive procedures, and involves the examination of blood tests, genetic information, and other clinical characteristics. Predictive models are created utilizing ML approaches to predict clinical outcomes using a significant profile dataset with numerous characteristics, such as clinical data and microbiota-based multi-omics, to forecast the outcome or severity of disorders like NAFLD and NASH [113]. These models can consider several factors to forecast illness development, including genetics, lifestyle, and metabolic characteristics. AI can examine long-term health information to follow illness development and detect early indicators of deterioration. It facilitates the creation of individualized treatment regimens based on unique patient data such as genetics, lifestyle, and reactions to previous therapies. AI-powered smartphone applications and wearable devices monitor patients' adherence to treatment regimens and lifestyle changes, offering real-time feedback and assistance. AI speeds up the drug development process by evaluating large datasets to find possible therapeutic targets and forecast the efficacy of novel drugs. AI enhances clinical trial design and execution by improving patient selection, monitoring, and data analysis. AI models can forecast long-term outcomes for NAFLD patients, such as the chance of acquiring cirrhosis, liver cancer, or other problems. AI-powered decision support systems let doctors make educated decisions regarding patient care based on a thorough study of available data.

Some prominent research that applies AI in NAFLD include the following. Lee et al. [107] used ML to identify and stage NAFLD and liver fibrosis. They trained supervised ML classifiers on digital pictures of pathology slides from 47 liver biopsies taken from individuals with normal livers and those with NAFLD. Automatic categorization of white areas yielded an 89% accuracy and identified microscopic markers such as steatosis, bile ducts, portal veins, and sinusoids. Detecting microscopic liver anatomical landmarks can help locate additional histological abnormalities based on the liver's

microscopic architecture. Sherman et al. [114] developed a NLP algorithm that automatically scores metabolic dysfunction-associated steatotic liver disease (MASLD) histological characteristics using field-standard criteria. After ruling out heavy alcohol consumption and other causes of liver disease, all individuals (1987-2021) with steatosis on index liver biopsy were identified from the Mass General Brigham health care system computerized medical record. A Python-based NLP method was developed to detect steatosis, lobular inflammation, ballooning, and fibrosis phases from free-text pathology reports, and it was manually validated in over 1,200 reports. Patients were tracked from the index biopsy until the occurrence of decompensated liver disease, accounting for confounders. The NLP algorithm produced positive and negative prediction values ranging from 93.5% to 100% for all histologic concepts. Among 3,134 patients with biopsy-confirmed MASLD monitored for 20,604 person-years, the composite endpoint rate increased monotonically with worsening index fibrosis stage (p for linear trend <0.005). In comparison to simple steatosis (incidence rate, 15.06/1000 person-years), the multivariable-adjusted HRs for cirrhosis were 1.04 (0.72-1.5) for MASH/F0, 1.19 (0.92-1.54) for MASH/F1, 1.89 (1.41-2.52) for MASH/F2 and 4.21 (3.26-5.43) for MASH/F3. The NLP system correctly evaluates histological aspects of MASLD from pathological free text. This method allows the creation of a large and high-quality MASLD cohort across a multihospital healthcare system, revealing an increasing risk of cirrhosis depending on the index MASLD fibrosis stage. Based on pathology and imaging reports, Schneider et al. [79] investigated whether NLP data in EHR might detect undiagnosed individuals with hepatic steatosis. A rule-based NLP algorithm was developed using a Linguamatics literature text mining tool to search 2.15 million pathology reports and 2.7 million imaging reports in the Penn Medicine EHR from November 2014 to December 2020 for evidence of hepatic steatosis. For quality control, two independent doctors manually evaluated randomly selected biopsy and imaging reports (n = 353, PPV 99.7%). After removing people with other types of hepatic steatosis, 3,007 patients with biopsy-proven NAFLD and 42,083 patients with imaging-proven NAFLD were discovered. Surprisingly, increased alanine aminotransferase (ALT) was not a reliable predictor of the presence of steatosis, and only half of the biopsied patients with steatosis got an international classification of diseases (ICD) diagnostic code for NAFLD/NASH. NLP found a strong link between the PNPLA3 and TM6SF2 risk alleles and steatosis. Two hundred thirty-four illnesses were substantially over- or underrepresented in all participants with steatosis, and alterations in serum markers (e.g., GGT) were related to steatosis. The work illustrates the viability of using NLP-based algorithms to detect individuals with steatosis in imaging and pathology reports throughout an extensive healthcare system, revealing NAFLD undercoding in the general population. Identifying patients at risk might lead to better care and results. Finally, NLP-based techniques can identify huge groups of steatosis patients diagnosed by biopsy or imaging. It is more accurate in recognizing biopsy-proven NAFLD and NASH in the EHR than ICD codes and ALT serum levels within one year of the biopsy/imaging. Van Vleck et al. [115] investigated the efficacy of NLP for identifying patients with NAFLD, analyzing disease progression trends, and identifying treatment gaps caused by breakdowns in communication among clinicians. All clinical notes on the 38,575 Mount Sinai BioMe cohort patients were entered into the NLP system. Structured and unstructured EHR data were analyzed using NLP, free-text search, and diagnostic codes, validated against expert adjudication. The NLP findings were used to assess physicians' perceptions of progression from early-stage NAFLD to NASH or cirrhosis. The same NLP results were utilized to discover NAFLD references in radiological reports that did not appear in clinical notes. It found 2,281 cases of NAFLD among 38,575 individuals. The remaining 10,653 patients with equivalent data density were chosen as a control group. NLP fared better than ICD and text search regarding sensitivity (NLP: 0.93, ICD: 0.28, text search: 0.81) and F2 score (NLP: 0.92, ICD: 0.34, text search: 0.81). Of the 2281 NAFLD patients, 673 (29.5%) were thought to have advanced to NASH or cirrhosis. The average progression time among 176 patients with NAFLD before NASH was 410 days. 619 (27.1%) NAFLD patients had their condition documented solely in radiological reports, not other clinical documentation forms. Following a median of 1057.3 days, 170 (28.4%) were found to have likely developed NASH or cirrhosis. NLP-based techniques were more accurate in detecting NAFLD in the EHR than ICD/text search-based methods. In summary, NLP-based techniques outperform ICD/text search-based approaches in detecting NAFLD inside the EHR.

4.5 Prediction of hepatitis relapse and HBsAg sero-clearance

One of the most challenging aspects of managing chronic hepatitis B is anticipating disease recurrence and tracking the path toward HBsAg sero-clearance, a significant indicator of recovery and long-term prognosis. HBsAg sero-clearance occurs seldom in the ordinary course of chronic hepatitis B infection and is linked with better clinical outcomes. It is a functional cure and the best treatment outcome for chronic hepatitis B [116]. Fang et al. [116] define HBsAg sero-clearance as the continuous elimination of HBsAg from serum. Chronic hepatitis B patients with cleared HBsAg have an excellent clinical outcome with a low chance of acquiring hepatocellular cancer or cirrhotic complications [117]. Many variables influence HBsAg seroconversion, including immunological and viral factors. However, understanding the immunological mechanisms underlying HBsAg sero-clearance remains a challenge. HBsAg sero-clearance is the ultimate goal of HBV therapy [118]. Traditional approaches for predicting recurrence and sero-clearance are sometimes constrained by their dependence on clinical criteria and biochemical markers, which may fail to represent HBV infection's complexity and multifaceted nature. AI and ML have intriguing opportunities for improving the prediction of hepatitis recurrence and HBsAg sero-clearance.

AI-driven approaches can integrate and analyze large datasets with diverse data types, such as clinical data (e.g., patient histories, treatment responses, lab results, and disease progression), genomic data (e.g., genetic variants affecting hepatitis

B virus infection and treatment response), imaging data (e.g., liver US, MRI, or CT scans for assessing liver damage), and lifestyle factors (e.g., data on alcohol consumption, diet, and other lifestyle factors that could impact disease progression), to identify patterns and predictors that conventional methods may miss. Predictive models may be developed using AI to deliver more accurate, tailored, and timely forecasts, improving patient care and treatment results. This introduction emphasizes the potential of AI in changing the landscape of hepatitis B management by allowing for early detection of disease recurrence and promoting HBsAg sero-clearance. Integrating AI-based technologies into clinical practice allows healthcare practitioners to adapt treatment methods better, evaluate patient progress, and enhance long-term outcomes for people with chronic hepatitis B. AI transforms the prediction of hepatitis recurrence and HBsAg sero-clearance by identifying trends and making accurate forecasts using advanced algorithms and vast datasets.

AI can create prediction models to assess the chance of relapse or sero-clearance using ML techniques such as RF, Gradient Boosting Machines, and SVM, which can be taught to predict outcomes based on past data. Recurrent neural networks and CNNs can process complicated, multidimensional data, such as consecutive health records or imaging data. AI models can classify patients into risk groups, such as high-risk identification (i.e., identifying patients more likely to relapse or fail to achieve sero-clearance, allowing for targeted interventions) and personalized risk scores (i.e., generating individual risk scores based on clinical, genetic, and lifestyle factors). It assists in early detection by evaluating longitudinal data to discover early warning indications of relapse or non-sero-clearance and predictive warnings by notifying doctors of high-risk patients, allowing for appropriate revisions to treatment programs. AI can help tailor treatment strategies by recommending personalized treatment regimens based on predicted outcomes and individual patient profiles, as well as by tracking patient adherence to treatment and predicting potential issues that could lead to relapse. AI can help clinicians make better decisions by providing AI-driven insights and recommendations to supplement clinical judgment, data visualization, and intuitive visualizations of complex data and predictions. It makes research easier by using data mining to unearth new insights from current information, perhaps identifying novel biomarkers or therapy targets, and modeling multiple treatment scenarios to predict results and enhance therapeutic methods.

Some prominent research that employed AI to predict hepatitis relapse and HBsAg sero-clearance include the following. Huang et al. [119] developed a Bayesian network model based on accessible medical records to predict HBsAg sero-clearance in chronic hepatitis B patients and evaluated its efficacy. The study included 1,966 chronic hepatitis B patients between January 2006 and June 2015, with an average age of 39.04 ± 11.23 years. The demographic and clinical variables, laboratory data, and imaging parameters were used to develop a Bayesian network model and assess the likelihood of HBsAg sero-clearance. Baseline serum HBsAg and HBeAg levels, virological response, and HBeAg sero-clearance were the strongest predictors of HBsAg sero-clearance. Patients with baseline HBsAg values ≤2000 IU/mL, negative baseline HBeAg, first virological response, and no HBeAg sero-clearance were more likely to have HBsAg sero-clearance (post-test probability table). The Bayesian network model had an area under the receiver operating characteristic curves of 0.896 (95% confidence interval [CI]: 0.892, 0.899), a sensitivity of 0.840 (95% CI: 0.833, 0.846), a specificity of 0.880 (95% CI: 0.876, 0.884), and an accuracy of 0.878 (95% CI: 0.874, 0.882) for predicting HBsAg sero-clearance. The constructed Bayesian network model correctly predicted the likelihood of HBsAg sero-clearance and is a viable tool for clinical decision-making. Tian et al. [120] investigated the optimum model for predicting HBsAg seroclearance. Laboratory and demographic data for 2,235 chronic hepatitis B patients were gathered from the South China Hepatitis Monitoring and Administration (SCHEMA) study. HBsAg sero-clearance was seen in 106 individuals in total. Models were created using four algorithms: XGBoost, RF, DT, and LR. The area under the AUC was used to identify the optimum model. The AUCs for the XGBoost, RF, DCT, and LR models were 0.891, 0.829, 0.619, and 0.680, respectively, with XGBoost providing the most significant predictive performance. The XGBoost model's variable significance plot showed that the level of HBsAg was the most important factor, followed by age and HBV DNA levels. ML techniques, particularly XGBoost, successfully predict HBsAg sero-clearance from available clinical data.

4.6 Identification of viral hepatitis serology markers

Identifying and interpreting viral hepatitis serological markers is crucial for diagnosing, monitoring, and treating hepatitis infections. As hepatitis B and C infections continue to pose considerable worldwide health risks, reliable and fast diagnoses are critical. While successful, traditional techniques of assessing serology markers need manual interpretation, which can be time-consuming and prone to human error. AI in this procedure has transformed the industry, improving accuracy, speed, and consistency in detecting viral hepatitis. ML algorithms can detect trends in serological test results. These algorithms may identify complicated antibody and antigen level patterns that suggest distinct phases of viral hepatitis infections, i.e., acute, chronic, or resolved. AI systems may automatically measure levels of numerous serology markers such as HBsAg, anti-HBc, and anti-HCV and interpret the data, minimizing the possibility of human mistakes and speeding up the diagnosis procedure [121].

AI can distinguish between hepatitis kinds, i.e., A, B, C, D, and E, by examining the mix of serology markers present. For example, in hepatitis B, AI may differentiate between acute and chronic infection based on HBsAg, anti-HBc IgM, and HBeAg levels. Based on trends in serology markers over time, AI may assess whether a hepatitis B virus is dormant,

chronically active, or has resolved [122]. AI algorithms can predict disease progression in hepatitis patients by examining patterns in serology markers and other clinical data. For example, AI can identify individuals who are more likely to advance from chronic hepatitis B to cirrhosis or hepatocellular cancer. It can anticipate how a patient will react to antiviral medication by examining baseline serology markers and their changes throughout treatment, allowing for more tailored treatment approaches.

To accurately identify a patient's viral hepatitis status, AI may combine serology marker data with other clinical biomarkers, imaging findings, and medical history. This comprehensive technique increases diagnostic accuracy. AI systems can continually monitor changes in serology markers in patients undergoing therapy or monitoring, alerting doctors in real time to potential problems or treatment effectiveness [123]. In clinical laboratories, AI can automate the processing and first interpretation of enormous numbers of serology tests to improve productivity, shorten response times, and allow human specialists to focus on more complicated issues. It may monitor the quality of serology tests, detecting anomalies or flaws in the testing process that may impair the results' accuracy. AI is used to identify novel serological markers that indicate viral hepatitis infection or disease development. ML algorithms can use vast datasets to find novel, undetected biomarkers. In clinical trials for novel hepatitis treatments, AI can assist in monitoring serology markers to assess the efficiency and safety of experimental medications, resulting in more efficient and accurate studies. Healthcare AI can analyze the findings of various blood tests used to diagnose hepatitis, such as liver function tests and viral hepatitis serology testing.

4.7 Early detection of pre-cancerous lesions

The early diagnosis of pre-cancerous lesions in hepatitis patients is critical for successful treatment and better patient outcomes. Traditional diagnostic procedures, such as imaging and biopsy, can be intrusive and may fail to detect lesions early. Recent advances in AI have great opportunities for improving the early diagnosis of pre-cancerous lesions in hepatitis patients. AI technologies, particularly those based on ML and DL, have shown a fantastic ability to analyze complicated medical data with great precision and speed. AI systems can detect subtle patterns and anomalies that traditional diagnostic procedures may miss. They can accurately assess extensive imaging modalities, including fluorescence, hyperspectral, cytological, histological, radiological, endoscopic, clinical, and infrared thermal modalities. AI aids professionals in diagnostic procedures and reduces unintended mistakes. Neural networks improve the early identification accuracy of pre-cancerous lesions in hepatitis patients [124].

DL models analyze medical images such as US, CT scans, and MRIs to detect minute patterns or abnormalities that may signal pre-cancerous lesions, generally with greater accuracy and speed than previous approaches. Biomarkers in blood tests or tissue samples can be identified using AI. ML algorithms examine vast datasets to identify specific patterns or indicators linked with the early stages of cancer, sometimes before obvious symptoms or changes appear. AI may create prediction models to evaluate the risk of pre-cancerous lesions by combining diverse data sources such as patient history, genetic information, and environmental variables. These models assist in identifying high-risk people who might benefit from more regular monitoring or preventative actions [125].

NLP techniques may extract pertinent information from EHR and find patterns suggesting an increased risk of pre-cancerous lesions, allowing for earlier identification by highlighting individuals who require further study. AI can help healthcare practitioners make better decisions by analyzing data and making recommendations. These systems use a patient's clinical data and history to assess the possibility of pre-cancerous lesions [126]. AI can help adapt treatment and monitoring regimens based on individual risk profiles. This tailored strategy can enhance outcomes by ensuring high-risk patients receive timely therapies. It can directly aid in cancer detection by initiating investigations or referrals in screened patients based on clinical indicators and automating clinical operations in areas with limited capacity. AI may examine complicated data from various sources, including clinical text, genomic, metabolomic, and radiomic data [127]. AI in early cancer screening and detection has helped overcome the issue of limited human resources while improving diagnostic precision. It might help physicians reduce their workload and the number of misdiagnoses [126].

Notable research using AI to detect pre-cancerous lesions early includes the following. Bal [32] compared pathologists' performance with varying degrees of expertise to a DL network (trained using histopathological H&E images and the CNN method) in predicting malignant-benign differentiation and gene alterations impacting prognosis in localized liver lesions. The model performed similarly to a 5-year pathologist, with 96% accuracy in discriminating between malignant and benign lesions and 86.9% in categorizing HCC as excellent, intermediate, or poor prognosis. These findings show CNN's potential to assist pathologists in detecting gene alterations in HCC, improving diagnosis accuracy, and contributing to precision medicine. HCC-SurvNet is an AI-assisted pathology program that analyzes digital histopathology pictures to estimate disease recurrence risk following primary surgical resection for HCC. Risk scoring divides patients into low- and high-risk groupings, with significant disparities in survival rates, establishing HCC-SurvNet as a viable tool for improving the clinical care of HCC patients, exceeding the traditional Tumor-Node-Metastasis categorization system in prediction accuracy.

4.8 Identifying high-risk individuals

AI quickly transforms healthcare by providing revolutionary illness prevention, diagnostic, and management technologies. One of the crucial areas where AI has a substantial influence is detecting high-risk persons for hepatitis, a group of viral illnesses that pose severe global health threats. Hepatitis, particularly B and C, can cause chronic liver damage, liver cancer, and even death if not discovered and treated promptly. Traditional high-risk identification techniques sometimes use broad population-based approaches, which may ignore small but crucial risk markers. With its capacity to evaluate large and complicated information, AI provides a more accurate and tailored approach to risk detection. By combining data from EHR, genetic information, lifestyle characteristics, and social determinants of health, AI may identify individuals who will benefit the most from preventative measures, early detection, and treatment. This transition toward AI-driven risk stratification can improve public health initiatives, lower healthcare costs, and, ultimately, better results for patients at risk of hepatitis.

AI algorithms can be used to evaluate EHR data to identify those who are at a greater risk of developing viral hepatitis, such as those who have a history of intravenous drug use, blood transfusions, or sexual contact with someone infected with the virus. This data can help drive focused screening and preventative initiatives. HCV remains a severe infectious disease-related public health concern despite the availability of very effective treatments. AI models can be trained to detect individuals with risk factors such as previous blood transfusions, intravenous drug use, or hazardous sexual behaviors, highlighting those who should be tested first [32]. AI algorithms may be trained on using large datasets to forecast who is most likely to get hepatitis based on age, gender, medical history, geographic location, and behavioral risk factors such as drug use and sexual activity. It can evaluate genetic data to identify those who have a genetic propensity to hepatitis, especially for hepatitis B and C, where persistent infections can cause liver damage [69].

NLP technologies can process unstructured data from medical records, extracting essential information such as past diagnoses, test findings, and physician comments suggesting an increased risk of hepatitis. AI can monitor clinical notes for hepatitis-related symptoms and indications for early identification. It can classify people into risk categories, allowing healthcare practitioners to focus on those most likely to benefit from preventative interventions like immunizations or frequent screenings. AI can create individualized screening programs for high-risk groups, making better use of medical resources [128]. AI algorithms can forecast possible hepatitis epidemics by examining trends in population health data, travel patterns, and social variables. They can detect groups of high-risk individuals, allowing public health professionals to target treatments better. AI may scan data from social media, polls, and other sources to identify people who engage in high-risk activities, increasing their chances of developing hepatitis. It can track patient adherence to hepatitis therapy and identify individuals at risk of noncompliance problems.

Wearables driven by AI can measure health metrics like liver function indicators, delivering early warnings to people at risk of hepatitis. It can work with telehealth systems to remotely monitor at-risk patients, ensuring prompt action if risk factors deteriorate. AI may help lead public health campaigns by identifying demographic groups or places with a greater hepatitis prevalence, ensuring that resources are focused on where they are most needed. It can improve vaccination tactics by identifying unvaccinated high-risk individuals and forecasting the effects of various immunization situations. AI may minimize the number of false positives or persons who are checked but do not have the illness, thereby lowering the cost of the screening program and alleviating unneeded stress on HCV-negative patients. Finally, moving from a rules-based to a flexible AI approach may be more suited to identifying a diverse population [128].

Some significant research using AI to identify high-risk individuals includes the following. Dagan et al. [129] presented the creation of machine-learning models to meet the pressing requirement to detect unknown HCV carriers and assess the real-world effectiveness of this strategy when implemented statewide. Retrospective data on 18- to 79-year-old members of Israel's largest healthcare organization who tested positive for HCV from 2013 to 2021 were used to build and evaluate prediction models for detecting active carriers. In August 2021, the top-performing model based on XGBoost prospectively analyzed approximately 1.5 million members eligible for screening per the US Preventive Services Task Force (USPSTF) recommendations, and a tiered outreach process began with the members who were most in danger. The XGBoost-based screening yield in November 2022 was assessed and compared to contemporaneous testing of USPSTF screening-eligible participants. The retrospective cohort utilized for model development contained 492,290 people, with 0.1% verified as active HCV carriers. Based on XGBoost, the best-performing model has a region beneath the receiver operating characteristic curve of 0.95. Screening the top 0.1%, 1%, and 5% of high-risk adults yielded positive predictive values of 18.2%, 6.2%, and 1.9% and sensitivity values of 13.0%, 44.4%, and 67.6%, respectively. During the prospective outreach, 477 members were tested for HCV antibodies, and 38 were discovered to be active HCV carriers, resulting in an estimated number required to screen (NNS) 10. Among the 53,403 USPSTF screening-eligible participants tested over the same period, 38 were discovered to be active HCV carriers, providing an NNS of 1029. A nationwide application of machine-learning-based HCV screening found the same number of HCV carriers as the classic screening technique while increasing efficiency by more than 100 times. Butaru et al. [130] created two ANN models to identify at-risk people chosen using a targeted questionnaire. The research comprised 14,042 screened subjects from the southwestern area of Oltenia in Romania. Each participant filled out a 12-item questionnaire and underwent fast anti-HCV antibody testing. Subjects who tested positive for Hepatitis C were sent to care

and, if they had detectable viremia, might eventually get antiviral therapy. They created two ANNs, trained and tested them on the questionnaire dataset, and then used them to identify patients in an existing dataset. They discovered 114 HCV-positive individuals (81 females), with an overall frequency of 0.81%. They found significant risk factors, including sharing personal hygiene products, obtaining blood transfusions, undergoing dental or surgical procedures, and reusing hypodermic needles. When applied to an existing dataset of 15,140 people (119 HCV cases), the first ANN model accurately identified 97 (81.51%) HCV-positive individuals using 13,401 tests, but the second ANN model identified 81 (68.06%) patients using just 5192 tests. Using ANNs to choose screening candidates may enhance resource allocation and prioritize cases with a higher risk of serious illness. Using data from an easy-to-administer questionnaire, they reported two alternative ANN models to detect people at risk of contracting HCV. At the lowest confidence level, the first model found 13.5% more instances at the expense of 61.5% more tests needed. Thus, the first ANN model may be employed when more resources are available for testing, but the second can successfully prioritize at-risk groups when testing resources are scarce. Doyle et al. [128] created a prediction model to detect undiagnosed HCV patients by analyzing longitudinal medical claims and prescription data from about ten million individuals in the United States between 2010 and 2016. Patients' medical histories were analyzed to derive features containing information on demographics, risk factors, symptoms, therapies, and procedures related to HCV. Predictive algorithms were built using LR, RF, GBT, and a stacked ensemble. According to a descriptive study, patients had recognized HCV symptoms for an average of 2-3 years before being diagnosed. All algorithms had at least 95% accuracy at low recall levels (10%). The stacked ensemble scored best for recall levels greater than 50%, with an accuracy of 97%, compared to 87% for the GBT and 31% for the LR. For comparison, the CDC recommends screening in an at-risk subpopulation with an estimated HCV prevalence of 2.23%. The provided AI algorithm has much greater precision than the screening rates associated with suggested clinical recommendations, implying that AI algorithms can significantly improve the effectiveness of HCV screening.

4.9 Liver transplantation

Liver transplantation is an important therapy option for people suffering from severe liver damage caused by Hepatitis B and C. It is recommended for individuals with chronic hepatitis B or C, cirrhosis, liver cancer, or abrupt liver failure. Bhat et al. [69] and Pomohaci et al. [131] describe liver transplantation as a life-saving therapy for those with end-stage liver disease. Liver transplantation is a complicated operation that includes the examination of several donor and recipient characteristics and expert judgments to ensure long-term graft and patient survival. The numerous factors can make decision-making challenging [111]. Managing liver transplant patients is difficult since demographic, clinical, laboratory, pathology, imaging, and omics data must all be examined to build an effective treatment strategy. Current approaches for gathering clinical data are vulnerable to subjectivity [69].

AI is increasingly significant in liver transplantation for hepatitis patients, improving everything from donor matching to postoperative care. It can transform transplantation by enhancing organ allocation, donor selection, rejection prediction, and immunosuppressive precision medicine. AI systems can better match donors and recipients by analyzing massive databases. It can better predict transplant outcomes than traditional approaches by considering a wide variety of data, such as genetic markers, liver size, and overall health. AI techniques can help evaluate contributions and receivers. ML algorithms, for example, may determine imaging data to measure liver health, fibrosis, and other problems, resulting in a more thorough assessment than a manual review. AI can aid in surgery planning by producing precise 3D models of the liver and adjacent tissues, which helps surgeons visualize the organ and determine the optimal strategy for transplantation, perhaps decreasing problems and increasing results. AI-powered monitoring gadgets can immediately track patients' vital signs and other health indicators. These technologies can identify early indicators of problems, such as rejection or infection, allowing quicker treatments and better patient outcomes. AI can use past data to discover patterns and forecast transplant results, which involves forecasting graft and patient survival rates and the risk of postoperative complications. AI can help to create tailored treatment programs for hepatitis patients following liver transplantation. It can assist in customizing immunosuppressive medicines and other treatments to the requirements of individual patients, reducing adverse effects and increasing efficacy. AI can speed up research by uncovering novel biomarkers, therapy routes, and prospective therapeutic targets. This might lead to the developing of more effective hepatitis medicines and improved management techniques for liver transplant patients. ML applications in liver transplant medicine are divided into pre-transplant, donor-recipient matching, and post-transplant. ML technologies are ideally suited for capturing and analyzing the dynamics, patterns, and interrelationships between these factors to produce optimum result predictions. Some pretransplant AI applications include enhancing transplant candidacy decision-making and matching donors and recipients to decrease queue mortality and enhance post-transplant outcomes. AI might aid in treating liver transplant patients, particularly in forecasting patient and graft survival and detecting risk factors for disease recurrence and other problems. Increased usage of EHR and the storage of massive quantities of longitudinal health data have inspired a renewed interest in constructing predictive ML models in medicine and excellent organ transplantation.

ML algorithms may evaluate several variables or features from big datasets, possibly establishing complicated correlations between donor and recipient characteristics to aid clinical decision-making in liver transplantation. AI-enabled models are anticipated to help speed up future assessments of liver organ quality. Another significant gap in the transplant industry that

AI-enabled systems may fill in the future is donor-recipient matching. In the post-transplant setting, ML technologies may examine a similarly diverse range of data types, dynamics, and interrelationships to give diagnostic and prognostic value. Over time, ML methods have used trends and changes in clinical parameters, laboratory, radiomic, and histologic data to personalize post-transplant therapy. The results of ML algorithms for predicting transplant problems show promise and may enhance patient outcomes [69][132][133]. An AI detection tool would be critical in monitoring patients on the transplant list. An integrated AI method for lesion identification may increase diagnostic accuracy and transplant patient stratification [131].

Some vital research studies using AI in liver transplantation include the following. Many studies looked at pre-liver transplant cardiovascular risk assessment, using LR and k-means clustering algorithms to predict cardiometabolic risks based on health data and vascular age. Others used AI-enabled electrocardiograms and DL models to predict cardiovascular problems and dysfunction in liver transplant candidates, with encouraging AUC values that demonstrate the predictive ability of AI. Random forest, SVM, and GBM were used to predict significant adverse cardiovascular events following transplantation, often surpassing established clinical models' accuracy and predictive capabilities [133]. Zabara et al. [132] developed a machine-learning model to predict postoperative problems after liver transplantation. The model performed admirably and has potential for future clinical applications and research into accurately predicting post-transplant short-term evolution. As a result, the study lays the groundwork for the thorough and noninvasive identification of high-risk patients who may benefit from a more rigorous postoperative surveillance protocol. Nonetheless, the findings must be verified in extensive prospective studies to permit ML risk assessment in liver transplant patients.

4.10 Predicting the risk of complications from viral hepatitis

Regarding developing standard regression models to forecast hepatitis risk, the variability of viral hepatitis risk over time makes accurate prediction difficult for these models. AI is increasingly being utilized to forecast viral hepatitis problems. This application includes evaluating massive datasets of patient records, test findings, and other pertinent health information to uncover patterns and characteristics that may suggest a higher risk of problems such as liver cirrhosis, hepatocellular cancer, or liver failure. ML algorithms may analyze massive volumes of data to discover potential complication risks. These models are trained using historical patient data, which may include variables such as viral load, liver enzyme levels, genetic markers, and demographic information. It can help identify which individuals are most likely to move from chronic hepatitis to more severe liver disorders, allowing for early intervention and more tailored treatment programs. AI-powered image recognition systems can analyze liver imaging, such as US, CT, and MRI, to detect early signs of liver damage, fibrosis, or tumors that are invisible to the human eye, which is critical for the early detection of HCC. AI can help to find and analyze biomarkers that signal liver damage or cancer. By reviewing test data over time, AI can detect slight changes that indicate a higher risk of issues. Personalization of treatment strategies based on individual risk profiles is possible with AI. Patients who are more prone to develop liver cancer, for example, may be examined more closely or given more aggressive treatment options sooner. AI can help choose the best antiviral medication for individuals with viral hepatitis, considering parameters such as virus genotype, patient genetics, and past treatment responses. AI models can predict long-term results for viral hepatitis patients, such as survival rates and the need for a liver transplant. These forecasts can help healthcare practitioners and patients make informed decisions. It can classify patients based on their likelihood of developing issues, allowing for more targeted monitoring and management options. Predictive analytics can anticipate illness development, allowing doctors to make more educated treatment decisions. AI may be linked to EHR to monitor patients' health data continually. This real-time analysis can warn healthcare practitioners of emergent dangers, allowing faster reactions to problems. On a larger scale, AI can anticipate the burden of viral hepatitis complications in specific communities, allowing public health officials to allocate resources better and devise tailored preventative programs.

Many research have employed AI to forecast the likelihood of complications from viral hepatitis. Wong et al. [134] created a ML-based model, the HCC ridge score (HCC-RS), to diagnose HCC in chronic hepatitis patients. Compared to conventional risk assessment scores, the new approach predicts HCC more accurately in individuals with chronic viral hepatitis. Integrating HCC-RS into electronic health systems allows for real-time information on HCC risk. Ioannou et al. [135] investigated whether DL RNN models using raw longitudinal electronic health information might improve performance in predicting HCC risk. They analyzed data from 48,151 individuals with hepatitis C virus-related cirrhosis and followed them for at least three years after the diagnosis. The study revealed that RNN models outperformed classical logistic regression models (ACC: 75% vs. 68%, $p<0.001$). This accomplishment implies that DL models such as RNNs have tremendous promise for collecting temporal dynamics and long-term information, opening the door for more accurate forecasts of HCC risk. DL RNN models in the study outperformed conventional logistic regression models, implying that RNN models could be used to identify patients with hepatitis C virus-related cirrhosis at high risk of developing HCC for risk-based HCC outreach and surveillance.

4.11 Hepatitis drug discovery

AI is transforming drug research, opening new paths for treating complicated illnesses like hepatitis C. Traditional drug discovery approaches are time-consuming and expensive, with significant attrition rates during development. With its ability to examine big datasets, forecast molecular interactions, and improve clinical trial designs, AI is a vital tool in the search for

novel hepatitis therapies. ML and NLP enable and speed drug development by performing extraordinarily accurate and efficient analyses of large databases. DL is a powerful way to anticipate the efficiency of pharmaceutical compounds. The drug development process is divided into four stages: (i) target identification and validation, (ii) compound screening and refining for lead optimization, (iii) preclinical research, and (iv) clinical trials. AI-driven approaches are actively used throughout the process to improve efficiency in terms of time and cost [136]. Integrating AI into hepatitis medication research promises to reduce the time it takes to get new therapies to patients while paving the path for more tailored and effective therapy tactics [136]. AI systems can evaluate massive genomic datasets to find possible hepatitis medication targets, such as viral proteins or host components on which the hepatitis virus relies and can be suppressed to prevent infection. AI can anticipate how effectively a possible medicine molecule interacts with a target protein, which helps to identify viable options faster. DL can produce novel drug-like compounds with favorable features. These algorithms are trained on large chemical datasets and can recommend new hepatitis treatments. AI can forecast drug candidates' pharmacokinetic and pharmacodynamic features, including absorption, distribution, metabolism, and excretion profiles, which aid in optimizing molecules early in the medication development process [137].

AI and ML help discover viral infection treatments by accelerating and simplifying the process of repurposing and suggesting new essential molecules that inhibit viral replication. They can also use networks to anticipate drug-target interactions or gene expression connections with HAV infection. This data must be fed into AI and ML algorithms to build effective anti-HAV medicines. Although new drug development typically takes over ten years, this strategy may aid medication repositioning and rescue, allowing the creation of anti-HAV therapies more quickly. AI, ML, and DL techniques may also help avoid pharmacological adverse effects [138]. AI can scan existing medications to uncover ones that may be beneficial against hepatitis, which is especially useful because repurposed medications have already passed several safety tests, potentially reducing the time to clinical usage. It can improve clinical trial design by predicting which patient demographics would respond best to a new hepatitis medication, which boosts trial efficiency and success rates. AI can assist in finding biomarkers that indicate therapy response or disease progression, resulting in more tailored therapeutics for hepatitis patients.

Quantum machine learning (QML) technologies are frequently used to find prospective medication candidates because they can adequately anticipate a molecule's affinity for a target protein. This makes it easier to identify potential drug candidates, which may then be developed and refined further down the drug development pipeline [137]. QML approaches may use quantum computers' massive processing capability to undertake complicated simulations and analysis, which speeds up the target identification and validation process [137]. By merging quantum computing with ML algorithms, researchers may effectively browse massive databases and anticipate probable targets' therapeutic ability and efficacy and can produce more precise and efficient binding affinity predictions [137]. They may create models that depict the intricate interactions between molecular characteristics and binding affinities. QML provides a transformational method to this essential component of drug discovery by improving prediction accuracy, expediting drug screening, minimizing animal testing, and advancing precision medicine [137].

ML is the driving force behind the growth of accurate medicine, and it is widely recognized as a critical step toward improving patient outcomes and enhancing physician abilities [139]. AI algorithms can assess real-time patient data, such as liver function tests, to track hepatitis development and therapy success, allowing for dynamic treatment strategy adjustments. AI can forecast hepatitis development in individuals, allowing for early therapies and improved disease management. A NLP system can extract critical information about optimal antibiotic usage, such as clinical indications, antimicrobial selection, dose, and therapy duration [136]. AI can combine data from genomes, proteomics, metabolomics, and other omics technologies to offer a comprehensive knowledge of hepatitis at the molecular level, which helps to identify novel drug targets and understand resistance mechanisms. For example, DeepMind's AI system AlphaFold can accurately predict protein shapes, which is critical for creating medications targeting hepatitis-related proteins. IBM Watson was utilized to examine enormous scientific literature and molecular data to propose novel hepatitis medication candidates [77].

AI-based algorithms can help find novel drug development targets, such as specific biochemical or genetic processes implicated in illnesses. ML can predict tiny molecules' physical and chemical characteristics with precision comparable to quantum physics. AI can detect links between molecular representations and biological or toxicological activity. The synthesis routes of potential drug candidates are efficiently investigated utilizing AI-based systems. Combined with AI, robotics explores the chemical space for new reactions by automating the feasibility analysis. AI allows quick screening of a virtual compound library comprising billions of molecules in a few days. Identifying preclinical candidates using an AI-based computational workflow may be completed promptly.

Furthermore, DL techniques are utilized to anticipate natural protein folding and rapidly examine protein structures. It also contributes to innovative drug creation using current medicinal chemical databases [136]. ML techniques can be used to examine medications and vaccine behavior and create them in collaboration with pharmaceutical industry specialists [140]. One of the most potential applications of AI and ML algorithms is forecasting vaccination efficiency and effectiveness by selecting the most protective antigens [31].

4.12 Diagnostic imaging tests

Diagnostic imaging is an essential component of contemporary medicine, giving crucial insights into the human body that influence diagnosis, treatment planning, and patient care. AI-powered image identification and analysis techniques are increasingly used in liver imaging methods such as radiography, US, CT, MRI, and nuclear medicine. As imaging technologies like X-rays, CT, MRI, and the US advance, so does the complexity of the data they provide. The sheer complexity of imaging data creates enormous problems for radiologists and clinicians, who must interpret these pictures precisely and promptly to make correct diagnoses. AI quickly alters diagnostic imaging by providing solid tools for improving the accuracy, efficiency, and accessibility of medical imaging interpretation. AI systems can accurately evaluate image data using sophisticated algorithms, ML, and DL approaches. These algorithms can detect minor anomalies, assess disease development, and even forecast patient outcomes, exceeding human specialists in some tasks [141].

AI helps detect and characterize liver abnormalities linked with hepatitis, allowing for early identification and intervention. It has become more critical in identifying and diagnosing HCC through imaging modalities such as the US, CT scans, and MRI. AI systems have shown potential in detecting early-stage HCC in CT images, frequently before cancer becomes detectable to human radiologists, which is accomplished by examining minor textural patterns and contrast enhancement phases associated with hepatocellular cancer [32]. AI can calculate tumor size, volume, and growth over time, which is helpful for staging and treatment planning. It can also identify vascular invasion and metastasis, two essential elements in the evolution of HCC. AI-based radiomics includes collecting several variables from CT scans and analyzing them to predict the existence of HCC, its aggressiveness, and prospective treatment outcomes. This is significant because HCC is a severe consequence of chronic viral hepatitis, and early identification is critical for better patient outcomes [32]. DL algorithms can detect tiny variations in liver tissue that may signal an early or unusual presentation of HCC. When combined with AI, MRI's capacity to give multi-phase imaging, such as arterial, venous, and delayed phases, aids in precisely characterizing liver abnormalities. AI can use dynamic contrast-enhanced sequences to distinguish between HCC and other liver diseases. AI models are also utilized to evaluate functional MRI sequences, such as diffusion-weighted and perfusion imaging, to characterize tumor biology and forecast treatment effects.

DL evaluates US pictures to identify liver abnormalities that may signal HCC. These models accurately categorize lesions as benign or malignant. In addition to traditional ultrasonography, AI-enhanced elastography is utilized to detect liver stiffness. It improves the interpretation of elastography data by distinguishing between fibrotic and malignant tissues. Noise and operator reliance can impact US imaging, posing issues for AI models. However, sophisticated models are taught to overcome these constraints, resulting in more consistent detection. AI systems can analyze pictures like X-rays, CT scans, and MRIs to identify and categorize anomalies more accurately than human specialists. Furthermore, AI systems may identify patterns and traits that human specialists cannot see, making autonomous diagnosis faster and more accurate [106].

Thanks to recent AI and medical imaging technology breakthroughs, biomedical image analysis has improved clinical practice by giving better insights into human anatomy and disease processes. US is a widely utilized imaging technique for diagnosing chronic liver illnesses such as fibrosis, cirrhosis, and portal hypertension [142]. MRI, US, and CT are now the most often utilized diagnostic modalities in medical imaging for fatty liver. In terms of AI in medical imaging, sophisticated image processing techniques can extract many quantitative features from radiological images, which traditional biostatistical or AI models then analyze to diagnose or assess therapeutic responses. Several AI-assisted diagnosis models for fatty liver have been created [143]. Convolutional neural networks have demonstrated great accuracy in diagnosing hepatic steatosis using ultrasonography B-mode pictures. Automated liver segmentation was possible using a generalized CNN, even spanning CT and MRI, for automated liver biometry. As a result, one clinical application where AI may run in the backend of an imaging server is to emphasize the presence of increasing surface nodularity, prompting the radiologist to include the suspicions of cirrhosis in the structured reports [72].

4.13 Adherence monitoring in the treatment of hepatitis virus

Adherence monitoring is critical in treating hepatitis B and C to ensure patients follow their treatment regimens. Nonadherence can result in treatment failure, virus resistance, and higher healthcare expenses. AI has the potential to improve adherence monitoring significantly. It can examine patient data to anticipate individuals at a higher risk of nonadherence, allowing healthcare personnel to focus on patients who require further assistance. AI algorithms can utilize past data to anticipate when patients will likely skip medications or depart their treatment plan. AI can provide individualized patient reminders based on their habits and routines, improving their probability of sticking to their drug regimen. AI-powered chatbots or messaging systems can offer real-time assistance, answer queries, and promote adherence, particularly during essential treatment periods. Wearable gadgets or smart pill dispensers can instantly use AI to track medicine intake. These gadgets can notify healthcare practitioners if a dosage is missed. Apps powered by AI may track patient behavior, provide instructional information, and inform physicians about adherence statistics. AI can evaluate EHR data to detect noncompliance patterns across populations, resulting in a better understanding and treatment of adherence problems. These can be used to evaluate big datasets, identify risk factors for nonadherence, and design innovative tactics to address them. It can aid in developing individualized instructional materials that convey the necessity of adherence in a meaningful way to

particular patients. Virtual assistants and AI-based programs can engage patients in interactive sessions, helping them comprehend the repercussions of treatment noncompliance. Using AI to monitor patient adherence poses privacy and security problems, which must be addressed to maintain patient confidence. NLP can aid in analyzing and synthesizing treatment guidelines from medical literature and clinical procedures, providing healthcare practitioners with up-to-date, evidence-based advice for viral hepatitis management. It can track and evaluate patient medication adherence and side effects as reported in clinical notes or feedback, allowing treatment regimens to be adjusted and patient outcomes to be improved.

AI can help monitor adherence to antiviral medication, which is frequently long-term and necessitates regular patient compliance to avoid disease progression and resistance. AI-powered applications like mobile health platforms may give patients individualized reminders, educational materials, and support systems to help them stick to their treatment regimens. This comprehensive strategy may lead to better treatment results and a higher overall quality of life for those with chronic hepatitis B. AI can assist patients in completing the whole course of medication for Direct-Acting Antivirals, which is critical for obtaining a sustained virological response [30]. AI systems, such as AiCure®, are revolutionary technology-based adherence monitoring methods that use facial recognition to manage real-time doses. They are designed to enable synchronized audio-visual confirmation of medication use by monitoring patients' identities, drug kinds, and ingestion trends via a smartphone or camera tablet. AI systems can also remind patients when and how to take their medications, providing timely reminders for inappropriate medication administration and late or missing prescriptions. Encrypted dose data is stored on users' tablets/smartphones and wirelessly sent to web-based dashboards. Two pilot studies on the AiCure platform employed AI algorithms to measure HCV drug adherence [144].

4.14 Improving hepatitis patient education and communication

Traditional hepatitis patient education techniques frequently use static materials and one-size-fits-all approaches, which can be ineffective in meeting individual requirements and preferences. AI overcomes these limits by allowing more customized, interactive, and responsive educational experiences. AI can assess medical data and customize instructional materials to meet individual requirements. For example, it can suggest specific articles, videos, or interactive modules depending on a patient's health, treatment plan, and learning preferences [145]. NLP can create patient-friendly instructional materials based on complicated medical information, allowing patients to comprehend their diseases and treatment alternatives better. AI offers appropriate and practical techniques for medical data interpretation in hepatology, aiming to assist in diagnosis and customized therapy [109]. AI-powered chatbots or virtual assistants can give patients rapid, 24-hour access to information and answer common queries regarding their health, treatments, or prescriptions. AI can analyze and interpret human language, allowing it to create simple, intelligible explanations of complicated medical jargon and concepts, assisting patients in comprehending their health information. It can aid decision-making by evaluating medical data and giving recommendations that patients can use to make informed health decisions. AI can forecast prospective health difficulties and provide preventative actions or interventions that may be conveyed to patients to encourage proactive health management.

AI-powered translation technologies can assist in breaking down language barriers by offering educational materials and communication in different languages, ensuring that non-native speakers have access to the information they require. AI can monitor patient engagement with instructional materials and send reminders or follow-ups to help patients stay educated and stick to their treatment programs. AI systems can make instructional information more accessible to patients with disabilities, such as text-to-speech for those with visual impairments or simplified language for those with cognitive challenges. These AI-driven solutions may result in more effective patient education, enhanced communication, and better health outcomes. NLP-powered chatbots can give patients rapid answers to typical inquiries concerning viral hepatitis, treatment procedures, and lifestyle adjustments, increasing engagement and support. The health condition of hepatitis patients in various geographical locations might be tracked and monitored via social media. Using smartphone applications and social media for viral hepatitis eradication generates large amounts of data. Analyzing these data using AI platforms like ML might help health authorities. These analyses assist policymakers in surveillance by tracking the movement of viral hepatitis reservoirs [146].

Generative AI can alter patient education in resource-constrained places. Employing ML algorithms and other modern technologies can open new possibilities for tailored, accessible, and engaging patient education content. Generative AI can generate exciting and instructive patient multimedia material, including movies, animations, and infographics. It can increase education accessibility and quality by providing multimedia content production, customization, simulations, predictive analytics, and other capabilities, allowing for earlier illness identification and treatment [147].

4.15 Hepatitis data integration and analysis

AI transforms healthcare by providing novel answers to challenging issues like hepatitis management. Hepatitis needs extensive data analysis for successful prevention, diagnosis, treatment, and monitoring. However, the sheer number and diversity of data from clinical records, laboratory findings, imaging tests, and public health databases pose a difficult task. AI can handle and analyze enormous amounts of data rapidly and effectively, and it is positioned to address these difficulties by improving data integration, predicting models, and enabling individualized treatment. DL has enabled the extraction of

therapeutically helpful information from large and heterogeneous clinical datasets. Specifically, histopathology and radiological imaging data provide diagnostic, prognostic, and predictive information that AI can extract. DL algorithms often have many more free parameters than traditional ML approaches, which makes them more versatile and better suited to processing and categorizing complicated data sets such as language or imaging data [148].

AI can incorporate data from various sources, including EHR, laboratory findings, imaging studies, public health databases, and even socioeconomic determinants of health, resulting in a comprehensive dataset for hepatitis research. It can standardize and harmonize data across systems and formats, ensuring that various data sources are interoperable and can be studied concurrently. ML algorithms can predict the course of hepatitis, allowing doctors to identify patients who are more likely to develop problems such as liver cirrhosis or HCC. AI can examine patient data to anticipate how individuals respond to treatments, allowing for more customized health methods. AI systems can examine patterns in test findings, imaging, and clinical data to detect early indicators of hepatitis infection or liver damage, perhaps leading to an earlier diagnosis. NLP can extract useful information from clinical notes and unstructured data to diagnose and monitor hepatitis. The fast growth of biotechnology has resulted in the collection of massive volumes of multi-omics data, necessitating the improvement of bioinformatics and AI to allow computer modeling to diagnose and predict therapeutic outcomes [149]. Traditional ML and new DL algorithms impartially filter current data to find patterns and generate models that might influence healthcare choices [150]. AI can detect and predict hepatitis outbreaks by monitoring public health trends and finding odd patterns. It can use geographical data to identify hepatitis transmission hotspots and analyze the effectiveness of therapies.

AI can help physicians make real-time decisions based on clinical guidelines, ensuring patients receive evidence-based care. ML can utilize many data streams, including laboratory data, and overcome human constraints to provide clinicians with predicted and actionable outcomes [151]. It can offer the best treatment regimens based on particular patient data and the most recent research. AI-powered technologies can remotely monitor patients, tracking symptoms and test findings to give prompt treatments. It can assist patients in sticking to their treatment plans by evaluating drug use habits and giving reminders or interventions as needed. AI can examine vast datasets to discover novel hepatitis biomarkers, perhaps leading to the creation of new diagnostic tests or therapies. It can improve the design and execution of clinical trials for hepatitis therapies by enhancing patient selection and predicting trial outcomes.

Healthcare professionals and researchers may use AI to acquire more profound insights into illness patterns, optimize treatment options, and improve surveillance efforts. Integrating AI into hepatitis data analysis can enhance individual patient outcomes while advancing our understanding of hepatitis at the population level, resulting in more effective public health initiatives and treatments.

4.16 Streamlining workflow and reducing pathologist workload

In recent years, the incorporation of AI into pathology has emerged as a transformational force, providing new prospects to improve procedures and reduce pathologists' workloads. Traditional pathology depends mainly on personally inspecting tissue samples, which is time-consuming and prone to unpredictability. As the number of patients increases and diagnoses get complicated, the demand for more efficient solutions grows. AI technologies, notably ML and computer vision, are stepping in to help solve these problems by automating mundane processes and improving diagnosis accuracy. With the help of these sophisticated algorithms, pathologists may make better decisions by analyzing pathology slides with fantastic accuracy, seeing trends, and emphasizing problem regions. AI frees pathologists to concentrate more on diagnosis's intricate and subtle features by managing labor-intensive and repetitive duties [145].

AI algorithms can examine pathology pictures, such as tissue slides, to find and categorize anomalies, reducing the time pathologists spend manually inspecting and increasing diagnosis accuracy. It may detect patterns and abnormalities in pathology data that the human eye may overlook, allowing for earlier identification of illnesses and more accurate and prompt diagnosis. AI systems can assist in managing and organizing enormous amounts of pathology data, such as patient records and history data, allowing pathologists to more easily access and adequately interpret relevant and extensive volumes of data. This capability has resulted in various applications that have improved patient outcomes and reduced the workload for healthcare workers [152]. AI may use historical data to anticipate disease development and patient outcomes, allowing pathologists to make more educated therapy and follow-up care decisions. Many repetitive tasks in histopathological image analysis can be automated using AI, such as image pre-processing, feature extraction, and quantitative analysis, freeing pathologists' time to focus on complex cases and decision-making, thereby improving overall workflow efficiency [32][153].

AI may automate administrative activities like scheduling, reporting, and communication, allowing pathologists to focus on clinical work rather than paperwork. NLP and ambient clinical intelligence automate administrative tasks such as entering patient visits into EHR, improving clinical workflow, and allowing clinicians to spend more time with patients [154]. It can help maintain high standards by giving regular and objective evaluations, improving quality assurance, and reducing human error. AI can assist pathologists in making better decisions by offering evidence-based suggestions and allowing them to compare their results to an extensive database of cases. ML has the potential to dramatically increase the repeatability, speed, and ease of workload for doctors [155]. AI-powered chatbots assist healthcare practitioners in minimizing their burden,

letting them focus on more complex situations that demand their knowledge [156]. AI can change and simplify diagnostic processes [157][158].

Laboratory managers believe AI may improve operations but prefer maintaining control [159]. Convolutional neural networks have exciting solutions for streamlining healthcare workflows ([160]). AI can potentially alter physician workflow and patient care through its uses, which range from supporting physicians and replacing administrative activities to boosting medical expertise. AI can replace several duties typically performed by healthcare workers [161]. With the rising digitalization of cellular pathology services, AI becomes feasible, and the potential for boosting service efficiency via various AI tools becomes more critical than ever [145]. AI can potentially automate and streamline many pathology and radiology operations elements, including image processing, report preparation, and communication with other healthcare professionals. Incorporating AI approaches into clinical procedures, such as giving real-time feedback and decision support, can improve the interpretability of AI results. The frequent application of AI in radiology and pathology will yield significant advantages, from workload reduction to instrument quality control [162]. Large volumes of data may be translated and transferred in only minutes. DL may be used to reliably target regions of interest and diagnose patients using pictures obtained by imaging modalities such as X-ray, MRI, CT, US, and mammography. DL using CNNs has significantly improved image identification and is now widely used in diagnostic imaging [163].

AI in a digital pathology process can potentially lessen histopathologists' workloads by reducing tedious activities such as cell counting and tumor parameter measurement and standardizing immunohistochemical staining for companion diagnostic testing [164]. AI techniques can improve pathology reports and dramatically automate diagnostic operations. One of the first things to consider when using AI in the laboratory is how to incorporate it into clinical or operational procedures. These generally include operational algorithms that aid in data gathering, case triage, screening, quality control, and assistive algorithms that benefit from human-AI interaction [165].

Table 1 summarizes the latest state-of-the-art studies implementing AI techniques in managing viral hepatitis.

TABLE I. SUMMARY OF THE LATEST STATE-OF-THE-ART STUDIES IMPLEMENTING AI TECHNIQUES IN MANAGING VIRAL HEPATITIS.

S/No	Reference	AI Role	AI Techniques	Algorithms	Best Performing Algorithm(s)	Best Results
1	[33]	Early hepatitis diagnosis and detection	ML	SVM, DT, LR, and RF	RF	Accuracy = 89%, 88.33%
2	[26]	Early hepatitis diagnosis and detection	ML	SVM, LR, and DT	SVM	Accuracy = 0.92
3	[89]	Early hepatitis diagnosis and detection	ML	DT	DT	Accuracy = 95.9112%
4	[29]	Early hepatitis diagnosis and detection	ML	SVM, RF, NB, and KNN	KNN	Accuracy = 98.1%
5	[90]	Early hepatitis diagnosis and detection	ML	LR, SVM, KNN, DT, RF, and AdaBoost	AdaBoost	Accuracy = 97.8%
6	[91]	Early hepatitis diagnosis and detection	ML	SVM, KNN	SVM KNN	Sensitivity = 90.0% Sensitivity = 80%
7	[92]	Early hepatitis diagnosis and detection	ML	SVM, RF, KNN, LR, and GNB	RF	Accuracy = 100%
8	[93]	Early hepatitis diagnosis and detection	ML	LR, RF, DT, KNN, SVM, and NB	LR	Accuracy = 87.17%
9	[25]	Early hepatitis diagnosis and detection	ML	DT, KNN, SVM, ANN, and Ensemble classification	KNN	Accuracy = 99.1%
10	[88]	Early hepatitis diagnosis and detection	ML	DT, LR, SVM, RF, AdaBoost, and XGBoost	AdaBoost	Accuracy = 92%
11	[96]	Early hepatitis diagnosis and detection	DL	DBM, RBM	DBM	Accuracy = 90.1%-92.04%
12	[95]	Early hepatitis diagnosis and detection	DL	QNN	QNN	
13	[29]	Early hepatitis diagnosis and detection	DL	LSTM prediction model, the RNN model, and the BPNN model		
14	[81]	Early hepatitis diagnosis and detection	NLP and ML	XGBoost and ten-fold C-statistic cross-validation		

S/No	Reference	AI Role	AI Techniques	Algorithms	Best Performing Algorithm(s)	Best Results
15	[100]	Detection of liver fibrosis in chronic liver disease	ML	LR, SVM, KNN, DT, NB, and RF	DT	AUC = 0.906, 0.876, 0.931, 0.933
16	[101]	Detection of liver fibrosis in chronic liver disease	ML	SVM, NB, RF, and KNN	SVM	Accuracy = 87.3% Sensitivity = 93.5% Specificity = 81.2%
17	[104]	Detection of liver fibrosis in chronic liver disease	ML	RF, LR, and DT	RF	Accuracy = 97.45%
18	[32]	Detection of liver fibrosis in chronic liver disease	DL	CNN	CNN	Accuracy = 90% Sensitivity = 84.9% Specificity = 83.2%
19	[107]	Detection of liver fibrosis in chronic liver disease	DL	ANN	ANN	
20	[27]	Prognosis of chronic liver disease	ML	XGBoost, RF, and SVM	SVM	
21	[110]	Prognosis of chronic liver disease	ML and DL	ML and ANN-based algorithms	LSVM-MLP	
22	[114]	Identification of NAFLD	NLP	NLP algorithm	NLP algorithm	
23	[79]	Identification of NAFLD	NLP	A rule-based NLP algorithm	A rule-based NLP algorithm	
24	[115]	Identification of NAFLD	NLP	NLP-based techniques	NLP-based techniques	Sensitivity = 0.93 F2 score = 0.92
25	[120]	Prediction of hepatitis relapse and HBsAg seroclearance	ML	XGBoost, RF, DT, and LR	XGBoost	AUC = 891
26	[32]	Early detection of pre-cancerous lesions	DL	CNN	CNN	Accuracy = 96%
27	[129]	Identifying high-risk individuals	ML	XGBoost	XGBoost	Sensitivity = 13.0%, 44.4%, and 67.6%
28	[128]	Identifying high-risk individuals	ML	LR, RF, GBT, and a stacked ensemble	LR, RF, GBT, and stacked ensemble	Accuracy = 95%
29	[130]	Identifying high-risk individuals	DL	ANN	ANN	Accuracy: 81.51%
30	[135]	Predicting the risk of complications from viral hepatitis	DL	RNN models	RNN models	Accuracy = 75%

5. LIMITATIONS AND FUTURE CONSIDERATIONS

AI has enormous potential for controlling viral hepatitis, including advances in diagnosis, therapy, and monitoring. However, there are significant limits and future issues to consider when incorporating AI into hepatology, which include the following.

- Lack of data quality and quantity: There are few high-quality databases for viral hepatitis, especially those that include varied populations and uncommon subtypes. AI systems require massive volumes of data to train efficiently, and inadequate data might result in biased or erroneous models. Maintaining strong data quality, accuracy, and integrity requirements is critical for the effectiveness and dependability of AI-powered healthcare systems [32].
- Data integration and interoperability: Wearables, EHR, and lab findings are examples of data sources used by AI systems. Ensuring seamless integration and interoperability across these diverse data sources is difficult. A lack of defined procedures for data formats and communication among healthcare systems might stymie integration attempts.
- Algorithmic bias: AI algorithms trained on data from specific populations may underperform when applied to other demographic groups, resulting in discrepancies in diagnosis and treatment, particularly in underrepresented areas. If the training data is skewed, the AI models will inherit and perhaps magnify these biases, resulting in uneven healthcare outcomes [72][166][167].
- Privacy problems: Handling sensitive patient information, particularly in viral hepatitis instances, creates privacy problems [32]. Ensuring patient confidentiality when employing AI is a problem that must be met with solid data anonymization algorithms and safe data handling policies [166][167].
- Integration with current systems: Integrating AI technologies with existing healthcare infrastructure, such as EHR, may be complex. The lack of standards and interoperability between AI technologies and existing systems may impede seamless implementation. Healthcare practitioners may be hesitant to implement AI technology owing to

worries about dependability, a lack of knowledge, or a fear of job loss. Overcoming this reluctance involves education and demonstration of the real benefits of AI.

- Regulatory and legal aspects: AI-powered systems must undergo extensive testing and approval processes, which can be time-consuming. The legal landscape is still changing, and ambiguity in this area might cause delays in adopting AI solutions [166][168]. Adherence to healthcare service rules and acquiring relevant permits, such as Food and Drug Administration authorization for medical equipment linked with AI, are critical. Ensuring compliance while developing AI systems is critical for ethical and legal deployment [32].
- Ethical problems are fundamental to data privacy, confidentiality, and security. They guarantee that sensitive patient data is preserved and handled responsibly inside AI frameworks. Addressing biases and inequities in AI systems to avoid discriminatory consequences is an ethical obligation ([32]). To ensure trust and justice in AI-powered healthcare, ethical problems such as informed consent, accountability, and transparency must be adequately controlled [166][168].
- Cost and resource allocation: Creating and deploying AI systems may be costly, especially in low- and middle-income nations. The expense of AI technology may limit their availability and worsen the disparity in healthcare quality. DL techniques necessitate ample computational resources, which can be a bottleneck in resource-constrained environments.
- Resistance to change within established healthcare systems is a serious barrier. Implementing AI technology faces resistance due to changes in old practices, demanding comprehensive acceptance and adaptation techniques within healthcare frameworks [32].

To completely utilize AI in controlling viral hepatitis in the future, the following critical issues must be considered.

- Improve data collecting and sharing: Encouraging global cooperation to build significant, varied viral hepatitis datasets would increase the accuracy and generalizability of AI models. Efforts should be focused on developing standardized data formats and secure data-sharing mechanisms. Incorporating real-time data from diverse sources, including wearable devices and mobile health applications, can improve the timeliness and precision of AI-powered hepatitis management solutions.
- Addressing bias and equity: Identifying and minimizing biases in AI models is critical for achieving equal healthcare results. The ongoing monitoring and upgrading of AI systems to maintain fairness should be prioritized. Engaging a wide variety of stakeholders, particularly underrepresented communities, in developing AI tools will assist in guaranteeing that these technologies meet the requirements of all groups.
- Improving AI interpretability: Creating transparent AI models that adequately explain their judgments will increase confidence between healthcare practitioners and patients. Explainability is especially crucial in medical decision-making when understanding the rationale for a diagnosis or treatment suggestion is critical. Creating simple, user-friendly interfaces for AI tools will help healthcare practitioners accept new technologies and integrate them into everyday clinical practice.
- Regulatory framework development: Regulators must create adaptable frameworks that can keep up with the fast advances in AI technology. These frameworks should compromise between the necessity for rigorous evaluation and the ability to embrace new solutions. Harmonizing legislation across nations will make it easier to use AI technology on a global scale, ensuring that patients all around the world benefit.
- Sustainability and scalability: Research should focus on building low-cost AI systems that may be used in various healthcare settings, particularly in resource-constrained regions. Open-source AI models and cloud-based solutions might help cut costs and increase accessibility. Long-term research to analyze the effects of AI on viral hepatitis management will give vital insights into the technology's durability and efficacy.
- Advancements in AI algorithms: Developing more accurate and resilient AI algorithms capable of handling varied and noisy inputs will improve prediction model dependability. Investing in explainable AI research to help doctors understand and trust AI decision-making processes.
- Enhanced cybersecurity measures: Implementing sophisticated encryption and security techniques to safeguard data handled by AI systems. Setting up continuous monitoring and threat detection systems to protect against data breaches and cyberattacks.
- Create ethical principles and frameworks to guarantee AI and IoT's fair and appropriate application in healthcare. Ensure that new technologies adhere to changing legislation and standards for data protection and patient privacy.

By overcoming these constraints and taking into account future breakthroughs, AI has the potential to improve the battle against viral hepatitis, improving patient outcomes throughout the world.

6. CONCLUSIONS

AI represents a breakthrough possibility in viral hepatitis management, with advances throughout the disease prevention, diagnostic, treatment, and monitoring spectrum. Integrating AI technology into clinical practice can improve early detection by using powerful algorithms capable of processing large datasets, such as imaging and genetic data, leading to faster and more accurate diagnoses and better patient outcomes.

Predictive models based on AI can also help identify at-risk groups, allowing for targeted interventions and individualized treatment techniques. These talents are essential in resource-constrained situations where healthcare resources are scarce and the prevalence of viral hepatitis remains high. Furthermore, AI's real-time ability to evaluate massive amounts of information enables continuous patient monitoring and management and adaptive treatment regimens that respond dynamically to patient state changes.

However, successfully implementing AI in viral hepatitis management requires overcoming several problems. It is vital to ensure data quality and diversity, protect patient privacy, and overcome challenges to incorporating AI systems into healthcare infrastructures. Furthermore, continual collaboration among AI developers, healthcare practitioners, and politicians is required to guarantee that AI products are practical and ethical.

In conclusion, while challenges exist, AI has the potential to improve viral hepatitis management significantly. Continued research and innovation in this sector are required to leverage AI's potential fully, ultimately contributing to the worldwide effort to manage and eliminate viral hepatitis as an enormous public health issue.

Conflicts Of Interest

No competing relationships or interests that could be perceived as influencing the research are reported in the paper.

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