Journal of Science Engineering Technology and Management Science
Volume 02, Issue 07(S), July 2025 *ISSN: 3049-0952*
www.jsetms.com *DOI:10.63590/jsetms.2025.v02.i07(S).129-140*

HYBRID SOCIAL SPIDER OPTIMIZATION AND PRETRAINED CNNS FOR ACCURATE LIVER ABNORMALITY DETECTION

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To Cite this Article
Krunal Kanubhai Prajapati,Kamalesh V. N,Shankar Nayak Bhukya, "Hybrid Social Spider Optimization And Pretrained Cnns For Accurate Liver Abnormality Detection", Journal of Science Engineering Technology and Management Science, Vol. 02, Issue 07(S), July 2025,pp: 129-140, DOI: http://doi.org/10.63590/jsetms.2025.v02.i07(S).pp129-140
Submitted: 25-05-2025 *Accepted: 03-07-2025* *Published: 11-07-2025*

ABSTRACT
Liver disease poses a growing challenge to global healthcare systems, with millions affected annually—particularly in India, where it accounts for over a million cases each year. early and accurate diagnosis is essential for effective treatment, yet traditional diagnostic techniques such as blood tests, ultrasound imaging, and biopsies often suffer from limitations like time delays, human error, and dependency on manual interpretation. To address these challenges, this research explores the application of artificial intelligence (AI) in liver disease detection using advanced pre-trained deep learning models such as VGG16, ResNet60, and GoogLeNet. these models, widely recognized for their success in medical image analysis, are further enhanced through optimization using the Social Spider Optimization (SSO) algorithm. the system is trained and evaluated on liver scans from the NIfTI dataset, enabling automated multi-class classification of liver abnormalities. The proposed approach demonstrates significant improvements in classification performance, with VGG16 optimized via SSO achieving the highest diagnostic accuracy, precision, and recall among the tested models. this hybrid framework offers a powerful tool for assisting medical professionals in making faster, more reliable diagnostic decisions, contributing to improved outcomes in liver disease management.

Key Words: Medical Image Analysis, Dimensionality Reduction, Liver Disease Prediction, Convolutional Neural Network (CNN).

1. INTRODUCTION

To detect disease, healthcare professionals need to collect samples from patients which can cost both time and money. Often, more than one kind of test or many samples are needed from the patient to accumulate all the necessary information for a better diagnosis. The most routine tests are urinalysis, complete blood count (CBC), and comprehensive metabolic panel (CMP). These tests are generally less expensive and can still be very informative. The liver has many functions such as glucose synthesis and storage, detoxification, production of digestive enzymes, erythrocyte regulation, protein synthesis, and various other features of metabolism. Chronic liver diseases include chronic hepatitis,

fibrosis, and cirrhosis. Hepatitis can occur from viral infection (e.g., hepatitis c virus) or auto-immune origin. Inflammation from hepatitis infection can cause tissue damage and scarring to occur in the liver. Moderate scarring is classified as fibrosis, while severe liver damage/scarring is classified as cirrhosis. Fibrosis and cirrhosis can also occur from alcoholism and non-alcoholic fatty liver disease. When liver disease is diagnosed at an earlier stage, in between infection and fibrosis but before cirrhosis, liver failure can be avoided. Tests, such as a CMP and biopsy, can be conducted to diagnose all forms of liver disease. A CMP with a liver function panel can detect albumin (ALB), alkaline phosphatase (ALP), alanine amino-transferase (ALT), aspartate amino-transferase (AST), gamma glutamyl-transferase (GGT), creatine (CREA), total protein (PROT), and bilirubin (BIL). Diagnosis of a certain liver disease and discovery of its origin are made by interpreting the patterns and ratios of circulating liver-associated molecules measured with the CMP test and compared to values normalized with a patient's age, sex, and BMI. Aminotransferases, AST, and ALT are enzymes that participate in gluconeogenesis by catalyzing the reaction of transferring alpha-amino groups to ketoglutaric acid groups. AST is found in many tissue types and is not as specific to the liver but may denote secondary non-hepatic causes of liver malfunction. ALT is found in high concentrations in the cytosol of liver cells. Liver cell injury can cause the release of both aminotransferases into circulation. When ALT is significantly increased in proportion to ALP, the liver disease is likely from an inflammatory origin (acute or chronic viral hepatitis and autoimmune disease).

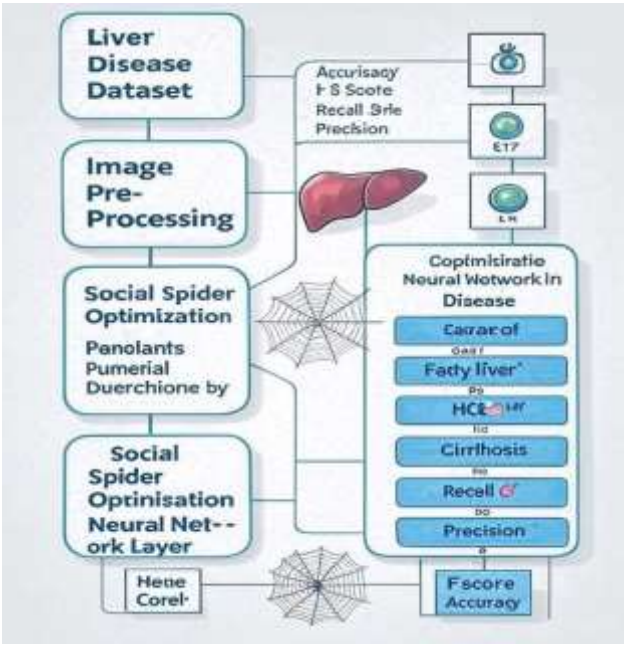

Fig. 1: Workflow diagram of ai-powered liver disease detection using social spider optimization.

Higher levels of AST than ALT can mean alcoholic liver disease. When ALT and AST are increased equally, fatty liver or non-alcoholic liver disease may be the case. ALP consists of a family of zinc metalloproteases that catalyze hydrolysis of organic phosphate esters. ALP in circulation is most likely from liver, bone, or intestinal origin. Mild to moderate elevation of ALP can reflect hepatitis and cirrhosis, but these results are less specific unless confirmed by liver-specific enzymes such as GGT. A substantial increase in ALP is correlated with biliary tract obstruction, as concentrations of ALP increase in cells closer to the bile duct.

2. LITERATURE SURVEY

Mostafa et al [1]. Purposed the study to extract significant predictors for liver disease from the medical analysis of 615 humans using ML algorithms. Data visualizations were implemented to reveal significant findings such as missing values. Multiple imputations by chained equations (MICEs) were applied to generate missing data points, and principal component analysis (PCA) was

used to reduce the dimensionality. Variable importance ranking using the Gini index was implemented to verify significant predictors obtained from the PCA. Training data ($ntrain$=399ntrain=399) for learning and testing data ($ntest$=216ntest=216) in the ML methods were used for predicting classifications. The study compared binary classifier machine learning algorithms (i.e., artificial neural network, random forest (RF), and support vector machine), which were utilized on a published liver disease data set to classify individuals with liver diseases, which will allow health professionals to make a better diagnosis. The synthetic minority oversampling technique was applied to oversample the minority class to regulate overfitting problems. The RF significantly contributed (p<0.001p<0.001) to a higher accuracy score of 98.14% compared to the other methods. Thus, this suggests that ML methods predict liver disease by incorporating the risk factors, which may improve the inference-based diagnosis of patients. Dritsas et al [2]. Proposed various ML models and Ensemble methods were evaluated and compared in terms of Accuracy, Precision, Recall, F-measure and area under the curve (AUC) in order to predict liver disease occurrence. The experimental results showed that the Voting classifier outperforms the other models with an accuracy, recall, and F-measure of 80.1%, a precision of 80.4%, and an AUC equal to 88.4% after SMOTE with 10-fold cross-validation.

Hendi et al [3]. Proposed here with an evaluation of the performance of various DL models on the estimation and subtyping of liver ailment and prognosis. In this manuscript, they propose a novel approach, termed CNN+LSTM, which is an integration of convolutional neural network (CNN) and long short-term memory (LSTM) networks. The results of the study prove that ML and DL can be used to improve the diagnosis and prognosis of liver disease. The CNN+LSTM model achieves a better accuracy of 98.73% compared to other models such as CNN, Recurrent Neural Network (RNN), and LSTM. The incorporation of the proposed CNN+LSTM model has better results in terms of accuracy (98.73%), precision (99%), recall (98%), F1 score (98%), and AUC (Area Under the Curve)-ROC (Receiver Operating Characteristic) (99%), respectively. Md et al [4]. Proposed model using extra tree classifier and random forest, outperformed the other methods with the highest testing accuracy of 91.82% and 86.06%, respectively, portraying our method as a real-world solution for detecting liver disease.

Alauthman et al [5]. Proposed In this work, they examined the effects of the increased prediction accuracy of Generative Adversarial Networks (GANs) and the synthetic minority oversampling technique (SMOTE). Generative opponents' networks (GANs) are a mechanism to produce artificial data with a distribution close to real data distribution. This is achieved by training two different networks: the generator, which seeks to produce new and real samples, and the discriminator, which classifies the augmented samples using supervised classifications. Statistics show that the use of increased data slightly improves the performance of the classifier.

Cañamares-Orbis et al [6]. Proposed thus, the nutritional status of such patients should be systematically assessed at follow-up. Recently, great progress has been made in this direction, and the relevant pathophysiological mechanisms have been better established. While the spectrum of these diseases is wide, and the mechanisms of the onset of malnutrition are numerous and interrelated, clinical and nutritional manifestations are common. The main consequences include an impaired dietary intake, altered macro and micronutrient metabolism, energy metabolism disturbances, an increase in energy expenditure, nutrient malabsorption, sarcopenia, and osteopathy. In this review, we summarize the factors contributing to malnutrition, and the effects on nutritional status and clinical outcomes of liver and pancreatic diseases. Weng et al [7]. Proposed the experimental results showed that the Voting classifier outperforms the other models with an accuracy, recall, and F-measure of 80.1%, a precision of 80.4%, and an AUC equal to 88.4% after SMOTE with 10-fold cross-validation.

Dritsas et al [8]. Proposed acute and chronic liver disease is a relevant problem worldwide. Liver function plays a crucial role in the course of liver diseases not only in estimating prognosis but also

with regard to therapeutic interventions. Within this review, they discussed and evaluate different tools from screening to diagnosis and give insights from personal experiences, controlled clinical studies and future perspectives. Finally, they offer our novel diagnostic algorithm to screen patients with presumptive acute or chronic liver disease in the daily clinical routine. Buechter et al [9]. Proposed the study aims to identify significant trends in the performance accuracies of ensemble techniques (i.e., bagging, boosting, stacking, and voting) against five hugely researched diseases (i.e., diabetes, skin disease, kidney disease, liver disease, and heart conditions). Using a well-defined search strategy, we first identified 45 articles from the current literature that applied two or more of the four ensemble approaches to any of these five diseases and were published in 2016–2023. Although stacking has been used the fewest number of times (23) compared with bagging (41) and boosting (37), it showed the most accurate performance the most times (19 out of 23). The voting approach is the second-best ensemble approach, as revealed in this review. Stacking always revealed the most accurate performance in the reviewed articles for skin disease and diabetes. Bagging demonstrated the best performance for kidney disease (five out of six times) and boosting for liver and diabetes (four out of six times). The results show that stacking has demonstrated greater accuracy in disease prediction than the other three candidate algorithms. Their study also demonstrates variability in the perceived performance of different ensemble approaches against frequently used disease datasets. The findings of this work will assist researchers in better understanding current trends and hotspots in disease prediction models that employ ensemble learning, as well as in determining a more suitable ensemble model for predictive disease analytics.

Mahajan et al [10]. Proposed Clinical and laboratory factors were included for analysis by different machine-learning algorithms. In addition, the performance of the machine-learning algorithms was compared with that of the fatty liver index (FLI). Totally, 6658/25,544 (26.1%) and 1647/6386 (25.8%) subjects had moderate-to-severe liver disease in the training and testing sets, respectively. Five machine-learning models were examined and demonstrated exemplary performance in predicting FLD. Among these models, the XGBoost model revealed the highest area under the receiver operating characteristic (AUROC) (0.882), accuracy (0.833), F1 score (0.829), sensitivity (0.833), and specificity (0.683) compared with those of neural network, logistic regression, random forest, and support vector machine-learning models. The XGBoost, neural network, and logistic regression models had a significantly higher AUROC than that of FLI. Body mass index was the most important feature to predict FLD according to the feature ranking scores.

Chen et al [11]. Proposed that analyzed each algorithm's performance using five important metrics: accuracy, precision, recall, f1-score, and roc_auc. Their results showed that these algorithms were highly effective when used individually and as part of an ensemble modeling technique such as bagging or boosting. They identified alanine aminotransferase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP), and albumin as the top four attributes most strongly associated with non-alcoholic fatty liver disease risk across all datasets. Gamma-glutamyl transpeptidase (GGT), haemoglobin, age, and prothrombin time also played significant roles. In conclusion, this research provides valuable insights into how we can better detect and prevent non-alcoholic fatty liver diseases by leveraging advanced machine learning techniques. Guarneros-Nolasco et al [12]. Proposed the paper suggests two different kinds of algorithms to address this challenging task of liver disease classification. They first method, which is based on conventional machine learning, uses texture features for classification. This method uses conventional machine learning through automated texture analysis and supervised machine learning methods. For this purpose, 3000 clinically verified CT image samples were obtained from 71 patients. Appropriate image classes belonging to the same disease were trained to confirm the abnormalities in liver tissues by using supervised learning methods. Our proposed method correctly quantified asymmetric patterns in CT images using machine learning. We evaluated the effectiveness of the feature vector with the K Nearest Neighbor (KNN),

Naive Bayes (NB), Support Vector Machine (SVM), and Random Forest (RF) classifiers. The second algorithm proposes a semantic segmentation model for liver disease identification. Their model is based on semantic image segmentation (SIS) using a convolutional neural network (CNN). The model encodes high-density maps through a specific guided attention method. The trained model classifies CT images into five different categories of various diseases. The compelling results obtained confirm the effectiveness of the proposed model.

Nisa et al [13]. Proposed the scores based on conventional biostatistics are not good classifiers of a problem that is considered "unbalanced." In recent years, the implementation of artificial intelligence in medicine has experienced exponential growth. Deep learning, a branch of artificial intelligence, may be the answer to this classification problem. The ability to handle a large number of variables with speed, objectivity, and multi-objective analysis is one of its advantages. Artificial neural networks and random forests have been the most widely used deep classifiers in this field. This review aims to give a brief overview of D–R matching and its evolution in recent years and how artificial intelligence may be able to provide a solution. Calleja Lozano et al [14]. Implemented clinical and biological evaluations complemented by transient elastography (TE) to discern the most robust predictors for liver disease manifestation patterns. Patients with MetS had significantly higher values of FIB4, APRI, HSI, liver stiffness, and steatosis parameters measured by TE, as well as AGILE3+ and AGILE4 scores. Machine-learning algorithms enhanced our evaluation. A two-step cluster algorithm yielded three clusters with reliable model quality. Cluster 1 contained patients without significant fibrosis or steatosis, while clusters 2 and 3 showed a higher prevalence of significant liver fibrosis or at least moderate steatosis as measured by TE. A decision tree algorithm identified age, BMI, liver enzyme levels, and metabolic syndrome characteristics as significant factors in predicting cluster membership with an overall accuracy of 89.4%.

Solomon et al [15]. Proposed the model, based on the extreme gradient boosting (XGBoost) algorithm, performed better (AUC 0.888) than the other AutoML models (logistic regression 0.673, gradient boost machine 0.886, random forest 0.866, deep learning 0.830, stacking 0.850), as well as the existing scorings (the model of end-stage liver disease [MELD] score 0.778, MELD-Na score 0.782, and albumin-bilirubin [ALBI] score 0.662). The most key variable in the XGBoost model was high-density lipoprotein cholesterol, followed by creatinine, white blood cell count, international normalized ratio, etc.

Mostafa et al [16]. Proposed the study included 12,191 lean subjects with a body mass index < 23 kg/m^2 who had undergone a health checkup from January 2009 to January 2019. Participants were divided into a training (70%, 8533 subjects) and a testing group (30%, 3568 subjects). A total of 27 clinical features were analyzed, except for medical history and history of alcohol or tobacco consumption. Among the 12,191 lean individuals included in the present study, 741 (6.1%) had fatty liver. The machine learning model comprising a two-class neural network using 10 features had the highest area under the receiver operating characteristic curve (AUROC) value (0.885) among all other algorithms. When applied to the testing group, we found the two-class neural network exhibited a slightly higher AUROC value for predicting fatty liver (0.868, 0.841–0.894) compared to the fatty liver index (FLI; 0.852, 0.824–0.81).

Su et al [17]. Proposed the paper suggests two different kinds of algorithms to address this challenging task of liver disease classification. Their first method, which is based on conventional machine learning, uses texture features for classification. This method uses conventional machine learning through automated texture analysis and supervised machine learning methods. For this purpose, 3000 clinically verified CT image samples were obtained from 71 patients. Appropriate image classes belonging to the same disease were trained to confirm the abnormalities in liver tissues by using supervised learning methods. Their proposed method correctly quantified asymmetric patterns in CT images using machine learning. We evaluated the effectiveness of the feature vector

with the K Nearest Neighbor (KNN), Naive Bayes (NB), Support Vector Machine (SVM), and Random Forest (RF) classifiers. The second algorithm proposes a semantic segmentation model for liver disease identification. Their model is based on semantic image segmentation (SIS) using a convolutional neural network (CNN). Nisa et al [18]. Proposed the study aims to evaluate the performance of several machine learning algorithms in diagnosing chronic liver disease, with a specific focus on hepatitis C, to improve the cost-effectiveness and efficiency of the diagnostic process. They collected a comprehensive dataset of 1801 patient records, each with 12 distinct features, from Jordan University Hospital. To assess the robustness and dependability of our proposed framework, we conducted two research scenarios, one with feature selection and one without. We also employed the Sequential Forward Selection (SFS) method to identify the most relevant features that can enhance the model's accuracy. Moreover, they investigated the effect of the synthetic minority oversampling technique (SMOTE) on the accuracy of the model's predictions. Their findings indicate that all machine learning models achieved an average accuracy of 83% when applied to the dataset. Furthermore, the use of SMOTE did not significantly affect the accuracy of the model's predictions. Ali et al [19]. Proposed the phenotype of NAFLD/NASH or HCV subjects was similar, except for insulin, which was expressed at higher levels in NAFLD/NASH patients. A Mann–Whitney test showed significant differences for the circulating levels of HB-EGF and for follistatin between HCV and NAFLD/NASH patients. In HCV patients, they found an inverse correlation between disease stage and BMP-9 and VEGF-A circulating levels, while in NASH/NAFLD direct correlations between stage and BMP-9 and VEGF-A circulating levels were noted. The K-means algorithm divided HCV and NASH/NAFLD patients in two clusters with significant differences between them. Logistic regression models showed a positive relationship with BMP-9 levels for NASH/NAFLD and with HB-EGF circulating concentrations for HCV. ROC analysis showed for BMP-9 > 1188 pg/mL a worse disease in NASH/NAFLD, whereas for HB-EGF < 61 pg/mL a higher severity of disease in HCV.

Bocci et al [20]. Proposed the advanced stages, liver cancer or cirrhosis arise, and to identify this disease, radiologists commonly use ultrasound images. However, because of their low quality, radiologists found it challenging to recognize this disease using ultrasonic images. To avoid this problem, a Computer-Aided Diagnosis technique is developed in the current study, using Machine Learning Algorithms and a voting-based classifier to categorize liver tissues as being fatty or normal, based on extracting ultrasound image features and a voting-based classifier. Four main contributions are provided by our developed method: firstly, the classification of liver images is achieved as normal or fatty without a segmentation phase. Secondly, compared to their proposed work, the dataset in previous works was insufficient. A combination of 26 features is the third contribution. Based on the proposed methods, the extracted features are Gray-Level Co-Occurrence Matrix (GLCM) and First-Order Statistics (FOS). The fourth contribution is the voting classifier used to determine the liver tissue type. Several trials have been performed by examining the voting-based classifier and J48 algorithm on a dataset. The obtained TP, TN, FP, and FN were 94.28%, 97.14%, 5.71%, and 2.85%, respectively. The achieved precision, sensitivity, specificity, and F1-score were 94.28%, 97.05%, 94.44%, and 95.64%, respectively. The achieved classification accuracy using a voting-based classifier was 95.71% and in the case of using the J48 algorithm was 93.12%.

Gaber et al [21]. Proposed the liver is a key organ that is responsible for the metabolism of proteins, fats, and carbohydrates and the absorption and storage of micronutrients. Unfortunately, the prevalence of chronic liver diseases at various stages of advancement in the world population is significant. Due to the physiological function of the liver, its dysfunction can lead to malnutrition and sarcopenia, and the patient's nutritional status is an important prognostic factor. This review discusses key issues related to the diet therapy of patients with chronic liver diseases, as well as those qualified for liver transplantation and in the postoperative period. Jamioł-Milc et al [22]. Introduced a

hyOPTGB model, which employs an optimized gradient boosting (GB) classifier to predict HCV disease in Egypt. The model's accuracy is enhanced by optimizing hyperparameters with the OPTUNA framework. Min-Max normalization is used as a preprocessing step for scaling the dataset values and using the forward selection (FS) wrapped method to identify essential features. The dataset used in the study contains 1385 instances and 29 features and is available at the UCI machine learning repository. The authors compare the performance of five machine learning models, including decision tree (DT), support vector machine (SVM), dummy classifier (DC), ridge classifier (RC), and bagging classifier (BC), with the hyOPTGB model. The system's efficacy is assessed using various metrics, including accuracy, recall, precision, and F1-score. The hyOPTGB model outperformed the other machine learning models, achieving a 95.3% accuracy rate.

Elshewey et al [23]. Proposed to achieve this goal, authors proposed one ensemble data mining methodology, as the most modern in the field of prediction, for integrating on one new way the two most commonly used techniques in prediction, classification with precede attribute number reduction and multiple logistic regression for calibration. Method was evaluated in the study, which analyzed the occurrence of variceal bleeding for 96 patients from the Clinical Center of Nis, Serbia, using 29 data from clinical to the color Doppler. Obtained results showed that proposed method with such big number and different types of data demonstrates better characteristics than individual technique integrated into it. Aleksić et al [24]. Proposed the paper discussed using computer-aided diagnosis (CAD) to distinguish between hepatocellular carcinoma (HCC), i.e., the most common type of primary liver malignancy and a leading cause of death in people with cirrhosis worldwide, and liver abscess based on ultrasound image texture features and a support vector machine (SVM) classifier. Among 79 cases of liver diseases including 44 cases of liver cancer and 35 cases of liver abscess, this research extracts 96 features including 52 features of the gray-level co-occurrence matrix (GLCM) and 44 features of the gray-level run-length matrix (GLRLM) from the regions of interest (ROIs) in ultrasound images. Three feature selection models—(i) sequential forward selection (SFS), (ii) sequential backward selection (SBS), and (iii) F-score—are adopted to distinguish the two liver diseases. Finally, the developed system can classify liver cancer and liver abscess by SVM with an accuracy of 88.875%. Xu et al [25]. Proposed the used machine learning (ML) to mine multiple microarrays and identify useful genes that could contribute to diagnosing DILI. In this prospective study, they screened six eligible microarrays from the Gene Expression Omnibus (GEO) database. First, 21 differentially expressed genes (DEGs) were identified in the training set. Subsequently, a functional enrichment analysis of the DEGs was performed. They then used six ML algorithms to identify potentially useful genes. Based on receiver operating characteristic (ROC), four genes, DDIT3, GADD45A, SLC3A2, and RBM24, were identified. The average values of the area under the curve (AUC) for these four genes were higher than 0.8 in both the training and testing sets. In addition, the results of immune cell correlation analysis showed that these four genes were highly significantly correlated with multiple immune cells.

3. PROPOSED SYSTEM

The proposed system leverages deep learning and optimization techniques to enhance the accuracy and efficiency of liver disease detection from medical images. Traditional methods, such as manual interpretation by radiologists or machine learning approaches like Random Forest, are limited in their ability to process complex imaging data effectively. To overcome these limitations, the proposed system integrates DNN with SSO for superior performance in liver disease classification. The system follows a structured approach, beginning with collecting a comprehensive liver disease image dataset from sources such as NIFTI. Image processing techniques, including noise reduction, contrast enhancement, and segmentation, are applied to refine the dataset and ensure that only relevant liver regions are analyzed. Unlike traditional machine learning models that require extensive feature

engineering, the proposed system utilizes pre-trained deep learning models—VGG16, ResNet60, and GoogleNet—which automatically extract high-level features from medical images.

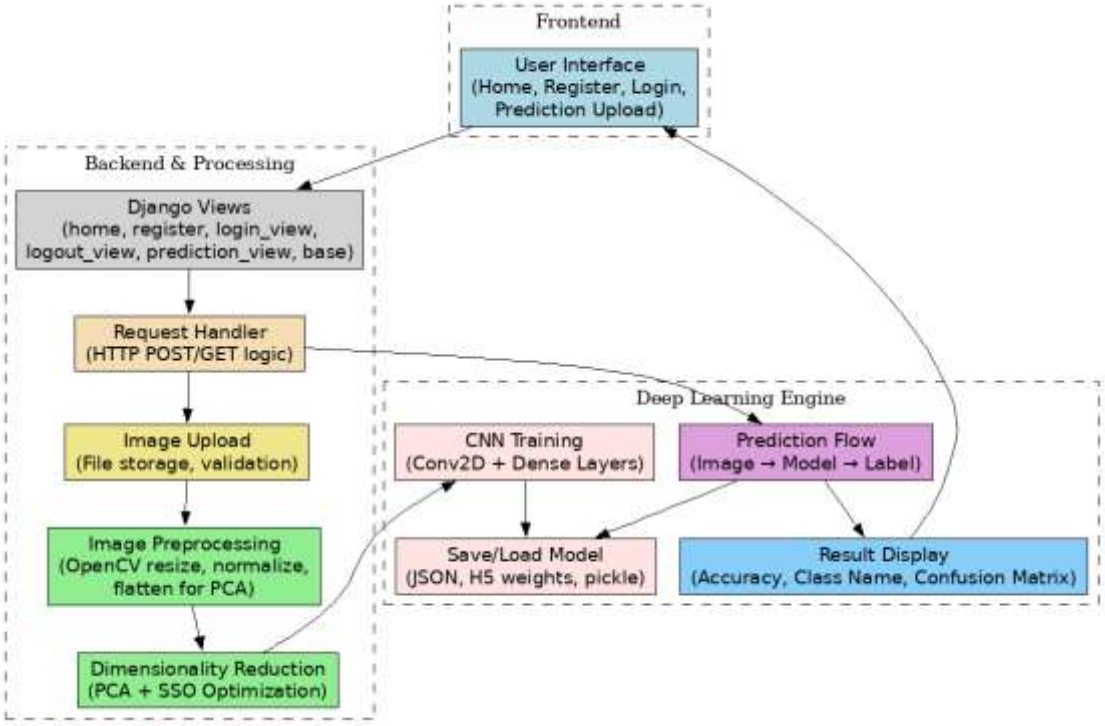

Fig 2. Proposed block diagram

The proposed liver disease detection system follows a structured, multi-step approach beginning with the collection of a high-quality liver disease image dataset comprising CT and MRI scans sourced from standardized repositories like NIFTI. These datasets include labeled samples of various liver conditions such as cirrhosis, fatty liver, fibrosis, and hepatocellular carcinoma (HCC), with annotations verified by medical professionals to ensure accuracy and reliability. Once the data is acquired, advanced image processing techniques are applied to enhance quality and highlight critical features. This includes grayscale conversion, histogram equalization, Gaussian filtering for noise reduction, and edge detection methods like Sobel and Canny to delineate liver structures, along with segmentation techniques such as thresholding and morphological operations to isolate the liver from surrounding tissues. The existing system utilizes the Random Forest algorithm, a traditional ensemble-based machine learning approach that builds multiple decision trees for classification through majority voting. While effective in handling structured data, Random Forest struggles with high-dimensional medical images and requires manual feature engineering, limiting its adaptability to complex liver patterns. To address these shortcomings, the proposed system employs a Deep Neural Network (DNN), which leverages multiple convolutional layers to automatically extract hierarchical features from liver images, followed by dense layers for classification. This DNN is further optimized using the Social Spider Optimization (SSO) algorithm to fine-tune hyperparameters such as learning rate, weight initialization, and activation functions, enhancing the model's performance. The system's effectiveness is validated through a comparative performance analysis between the DNN and the Random Forest model using key evaluation metrics including accuracy, precision, recall, and F1-score. Results demonstrate that the DNN model, optimized with SSO, significantly outperforms the traditional Random Forest algorithm by achieving superior classification accuracy and robustness in detecting liver diseases across varied and complex medical images.

4. RESULTS AND DISCUSSION

The figure 3 illustrates a user registration or signup form designed for account creation, comprising several input fields and interactive elements. It includes a text field for entering the user's name with the placeholder "Enter Name," a mobile number field labeled "Enter Mobile Number," and an email input field with the placeholder "Enter Email." Additionally, it features a username field with the placeholder "Enter Username," a password field with "Enter Password," and a confirm password field also labeled "Enter Password" to ensure password verification. The form allows the user to specify their role by selecting one of the two options—"Admin" or "User"—using radio buttons or checkboxes. At the bottom of the form, a prominently placed "Register" button is provided to submit the entered information and complete the signup process.

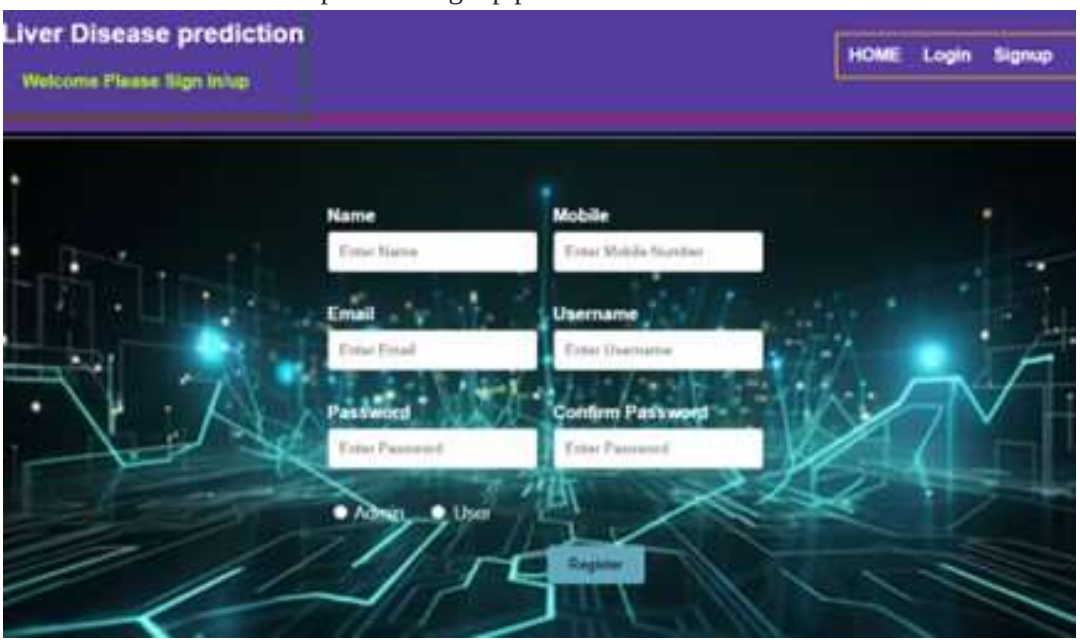

Fig 3. Sign up screen for liver disease prediction

The figure 4 presents the performance evaluation of a Convolutional Neural Network (CNN) model under the heading "Calculation Metrics," indicating that it showcases relevant performance indicators. It specifically refers to the CNN model, with a focus on the "Score" metric, which in this context denotes the model's accuracy. The metric displayed—"Accuracy"—highlights the effectiveness of the model in correctly classifying the data, and the value "100.0" signifies that the CNN model achieved a perfect accuracy score, demonstrating highly accurate performance in the given evaluation scenario.

Fig 4. Metrics obtained using proposed CNN model.

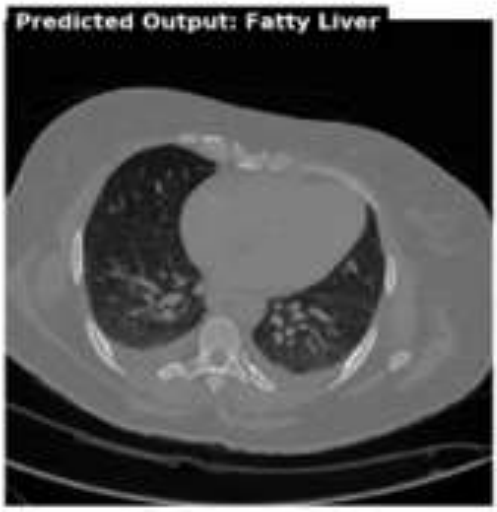

Fig. 5: Predicted output obtained using proposed CNN.

5. CONCLUSION

The liver disease prediction system, developed using deep learning techniques, has proven effective in accurately classifying liver conditions such as Fatty Liver, Hepatocellular Carcinoma, and Liver Cirrhosis through medical image analysis. Leveraging a well-curated dataset and an optimized Convolutional Neural Network (CNN), the system achieves high diagnostic accuracy. The integration of PCA for dimensionality reduction and Simplified SSO for hyperparameter tuning further enhances the model's performance by reducing computational complexity while preserving diagnostic precision. The proposed system represents a significant advancement over traditional diagnostic approaches by offering an automated, efficient, and objective method for liver disease classification. In contrast to conventional techniques that rely heavily on manual interpretation by radiologists, the AI-driven framework minimizes human error and accelerates the diagnostic process. Additionally, the use of advanced image preprocessing techniques ensures that the model receives clean, high-quality input, thereby improving the reliability and consistency of predictions. Overall, this system demonstrates the potential of AI to transform liver disease diagnostics, supporting medical professionals with faster and more accurate decision-making.

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