

Optimization of Deep Learning Approach Using Chaotic Algorithm for Hepatitis Detection

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Abstract

Original Research

Hepatitis still remains one of the major health issues in the world and is responsible for a significant amount of morbidity and mortality due to diseases related to the liver. Traditional approaches for hepatitis detection are costly, laboratorial, time-consuming, and error-prone. While AI and DL have enhanced medical diagnosis significantly, current models are prone to problems such as overfitting, long convergence period, and lack of generalization, which are primarily associated with inefficiency of hyperparameter optimization. In this research, the authors propose the use of optimized deep learning model based on Chaotic Optimization Algorithm (COA) for hepatitis detection. This approach combines Multi-Layer Perceptron (MLP) and Deep Neural Network (DNN) models with the application of COA, which allows optimizing such parameters as learning rate, hidden neurons, momentum, and weights initialization. Two publicly available datasets (the Kaggle Hepatitis Dataset and the UCI Hepatitis Dataset) have been used in this research. Data preprocessing steps including handling missing values, encoding, normalization, and splitting data into train and test datasets were applied. The COA-DNN gave results of 85.11% for accuracy, 77.83% for precision, 83.24% for recall, 79.85% for F1 score, and 0.9054 for AUC on the Kaggle dataset compared to the conventional DNN which had an accuracy of 57.45%. For the UCI dataset, the highest accuracy rate was achieved by COA-DNN at 96.76%, precision of 95.86%, recall of 88.82%, F1 score of 91.94%, and AUC of 0.9793.

Keywords: Artificial Intelligence; Chaotic Optimization Algorithm; Deep Learning; Hepatitis Detection; Hyperparameter Optimization; Multi-Layer Perceptron; Neural.

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INTRODUCTION

Hepatitis, or inflammation of the liver due primarily to viral infection, is one of the globe's most pressing health concerns of the 21st century. According to the World Health Organization (WHO, 2023), over 28 million people worldwide are infected with hepatitis B or C viruses chronically, and millions of others have liver inflammation from alcohol toxicity, drug toxicity, autoimmune disorders, and metabolic disorders (Nguyen et al. 2024). The natural history of the disease will usually lead to

serious liver damage such as cirrhosis, fibrosis, and hepatocellular carcinoma, all of which are responsible for the morbidity and mortality worldwide.

Traditionally, the diagnosis of hepatitis has rested on biochemical investigations, histopathological analysis, and serology for the detection of viral antigens and antibodies (Kumar et al. 2023). Although these are reliable in the clinic, they have a few disadvantages like being costly to run, lab-intensive, and prone to

human errors in interpretation of results. These limitations have been the impetus for research into the use of Artificial Intelligence (AI) methods to automate and enhance the diagnostic process. AI has, in the last decade, revolutionized medicine by allowing machines to learn from medical data and predict with amazing accuracy (Saeed et al. 2023). Machine Learning (ML) and Deep Learning (DL) AI-based methods have been demonstrated to identify intricate and non-linear associations between biomedical data and effectively classify, cluster, and forecast diseases, such as hepatitis.

Several researchers have utilized different AI and heuristic optimization methods to improve the accuracy of diagnosis. For instance, (Assegie, 2021) applied Support Vector Machines (SVM) and K-Nearest Neighbor (KNN) classifiers which achieved great frequency in classifying hepatitis and liver disease, whereas studies have shown that these algorithms are better than traditional statistical algorithms in handling non-linear decision boundaries (Mostafa et al. 2021). Decision Trees (DT) and Random Forests (RF) have also been used due to their interpretability, robustness against missing values, and capacity for handling non-linear decision boundaries, and therefore their relevance in the prediction of early-stage liver disease (Mamun et al. 2025).

In advanced research, Deep Neural Networks (DNNs) and Artificial Neural Networks (ANNs) have been used to acquire intricate relationships in hepatitis datasets with higher diagnostic accuracy through the capacity for identifying linear and non-linear patterns (Chowdhury et al. 2025). However, despite their improved predictive performance, deep learning models are prone to face challenges such as overfitting, local minima trapping, biased data representation, and slow convergence (Kankal & Kasar, 2025).

To overcome these issues, researchers have increasingly turned to heuristic and metaheuristic optimization techniques where computer programs derived from nature, biology, and physics that guide deep learning models to optimal solutions. These include Genetic Algorithms (GA), Particle Swarm Optimization (PSO), Ant Colony Optimization

(ACO), Grey Wolf Optimization (GWO), and Simulated Annealing (SA) (Saleh & Hussien, 2023; Shaban, 2024). All of these techniques have been applied to determine optimal values of parameters of neural networks such as learning rate, weight initialization, and feature selection.

Related Works

A study on the effectiveness of machine learning techniques to predict esophageal varices in Egyptian chronic hepatitis C patients. In their work, Abd El-Salam et al. (2019) explore new diagnostic tools for esophageal varices, which are very serious consequences of liver cirrhosis. The authors note that, although the current diagnosis approach of upper gastrointestinal endoscopy is very effective, it can be too costly and time-consuming due to the large amount of tests. They analyzed the data collected during 2006-2017 years on 4,962 patients with chronic hepatitis C at 15 hospitals in Egypt and identified 2,218 cases with esophageal varices and 2,744 patients without it.

The purpose of the research was to develop a predictive model using the data of the clinical characteristics of the patients via several machine learning techniques, such as Neural Networks, Naïve Bayes, Decision Trees, Support Vector Machines, Random Forest, and Bayesian Networks. Through feature selection techniques, the authors were able to identify nine vital predictors: Gender, Platelets, Albumin, Total Bilirubin, Base line PCR, Size of the Liver & Splenomegaly, Stiffness, and Prothrombin. In terms of effectiveness in the study, Bayesian network performed the best as it obtained the highest Area Under the Receiver Operating Characteristic curve (AUC), which was 74.8%, while the accuracy was 68.9%. The results reveal that machine learning has huge potential in the improvement of early diagnosis and management of esophageal varices.

Harabor et al. (2023) conducted research on the use of machine learning models in predicting the seropositivity of hepatitis B (HBV) and C (HCV) among people undergoing screening in Romania. Four different machine learning models were used: Support Vector Machine (SVM), Random Forest (RF), Naïve Bayes (NB), and K Nearest Neighbors (KNN). These machine learning

models were used to assess their ability to predict the patients' seropositivity according to clinical characteristics gathered through a structured survey. It was found that the machine learning models performed quite well in predicting HCV seropositivity, with the best accuracy being achieved using KNN model with 98.1%. SVM and RF models had equal accuracy of 97.6% in predicting HCV seropositivity. On the other hand, the machine learning models performed less accurately in predicting the seropositivity of HBV infection, where the accuracies ranged between 78.2% and 97.6%.

METHODOLOGY

This chapter gives an outline of the research methodology suggested to be used for conducting the research on the topic of the “Optimization of Deep Learning Techniques using Chaotic Algorithm for Hepatitis Diagnosis.” It highlights the aspects of the methodological approach, experimental setup, datasets used, preprocessing steps, modeling, and evaluation methods. The study focuses on creating an optimized deep model, i.e., Multi-Layer Perceptron (MLP) and Deep Neural Network (DNN), whose learning parameters will be tuned using a chaotic optimization algorithm to enhance prediction stability and accuracy for hepatitis detection.

Hepatitis C Prediction Dataset (UCI) (Dataset)

The first dataset proposed is the Hepatitis C Prediction Dataset sourced from the UCI Machine Learning Repository. The dataset includes laboratory values from blood donors and patients diagnosed with Hepatitis C, alongside demographic data. This dataset is crucial for developing predictive models to differentiate between healthy blood donors and individuals at various stages of Hepatitis C progression. The dataset has 615 records with 14 attributes.

Kaggle Hepatitis dataset (Kaggle) (Dataset)

The second dataset employed in this research work is the Kaggle Hepatitis dataset, extracted from Kaggle Hepatitis Dataset (<https://www.kaggle.com/datasets/codebreaker6>

[19/hepatitis-data](#)). This medical data is a structured data intended for predicting the outcome of hepatitis patients' based on their demographic information, treatment details, clinical findings, and symptoms using machine learning models. The dataset involves patients having different ages in the range of 7-78 years. While there are both males and females in the database, females dominate this particular dataset.

This medical dataset involves mainly categorical and binary features pertaining to symptoms and treatment condition among others. Examples of features include fatigue, malaise, anorexia, hepatomegaly (enlarged liver), liver firmness, splenomegaly (enlarged palpable spleen) and use of steroids and antivirals. The feature that shows the survival status of patients in the dataset has two categories, namely live or dies. Out of all the features in this dataset, only age is continuous whereas the rest of the features are Boolean variables.

Data Preprocessing

Real-world data are often partial, noisy, and inconsistent; hence, the data pre-processing procedures employed in this study encompass:

- i. The identification and management of missing values and extraneous characters using missing value imputation (e.g., mean, median, mode imputation) or removal of rows/columns with excessive missing data through the Simple Imputer from Sklearn library.
- ii. Converting category data into numerical values instead of characters. This will be achieved by encoding categorical variables using label encoding. The label encoder library will be used here.
- iii. Normalizing the chosen dataset to a range of 0 to 1 using the Min-Max-Scaler algorithm from the Sklearn library.
- iv. Dividing the dataset into training and testing subsets according to conventional machine learning training and testing ratio distributions of 70% for the training set and 30% for testing sets.

Multi-Layer Perceptron

The Multi-Layer Perceptron (MLP) proposed in this study is a feed-forward neural network with an input layer of dimension d , one or more hidden layers, and a softmax output layer for multi-class classification (Sachdeva et al. 2024). Let the network have L layers (index 1 to L), layer l containing $n^{(l)}$ neurons; the input is $x \in \mathbb{R}^d$. Each layer computes a pre-activation vector $z^{(l)}$ and activation $a^{(l)}$ by

$z^{(l)} = W^{(l)}a^{(l-1)} + b^{(l)}, a^{(l)} = \phi^{(l)}(z^{(l)})$	3.2
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Deep Neural Network (DNN)

Deep Neural Network (DNN) presented in this research is an evolved feed forward artificial neural network that has an input layer, multiple hidden layers, and an output layer. Contrary to Multi-Layer Perceptron (MLP), which has one or two hidden layers only, the DNN uses deep architecture that can learn complex and nonlinear relationships inherent in hepatitis data sets. DNN will enhance feature representation and classification performance by discovering hierarchical relationships in clinical and laboratory data related to hepatitis diagnosis. Let the DNN contain L hidden layers. Given an input feature vector $x \in \mathbb{R}^d$, the output of each hidden layer is computed. The DNN model captures complex interactions among hepatitis risk factors and provide improved predictive capability compared with shallow neural architectures.

Chaotic Optimization Algorithm (COA)

Chaotic optimization replaces or augments the pseudo-randomness used by many optimizers with deterministic chaotic sequences (Qi et al. 2024). A commonly used chaotic map is the Logistic Map:

Chaotically Optimized MLP/DNN

The Chaotically Optimized MLP and DNN is a deep learning hybrid model that uses the Multi-Layer Perceptron (MLP), DNN, and the Chaotic Optimization Algorithm (COA) for the purposes of hyperparameter optimization and general classification performance. The integration overcomes the shortcomings of typical gradient-

based optimization algorithms, which are prone to being trapped in local minima and converge slowly while optimizing neural networks.

Here, MLP and DNN are the primary predictive models which learns nonlinear interdependencies of the hepatitis characteristics and target variable (hepatitis diagnosis). Chaotic Optimization Algorithm, on the other hand, is a meta-optimizer that adaptively adjusts significant hyperparameters of the MLP and DNN during model training. These hyperparameters include the learning rate (η), momentum coefficient, number of neurons per hidden layer, and the regularization factor, all of which impact considerably the learning behavior and generalization performance of the MLP and DNN algorithm.

The integration begins by first randomly generating the MLP and DNN hyperparameters, which are then utilized as the optimization initial points. Subsequently, the chaotic sequences are generated through the Logistic Map, expressed

The Chaotically Optimized MLP/DNN algorithm, based on algorithm 3.3, is based on the idea of a two-level intelligent learning framework, where chaotic optimization will be used to configure the neural network, and the MLP and DNN will then be used to perform the actual learning. The Chaotically Optimized MLP and DNN algorithm is presented in detail step by step

RESULT AND DISCUSSION

In the experimental evaluation carried out in this research, the experiment was conducted by analyzing the performance between baseline neural networks such as MLP and DNN and the optimized versions using the COA to predict hepatitis disease. The conventional implementation of the baseline neural network models uses pre-set hyperparameter configurations, thus acting as benchmark models during performance evaluation. On the other hand, the use of optimization algorithms in the development of neural networks involves tuning hyperparameters such as learning rate, number of hidden neurons, batch sizes, and weight initialization techniques. The experimental evaluation involved a comparative study of the

impact of metaheuristic optimization on classification performance for medical applications. In this case, the experiments were conducted by training and validating the models using two different datasets, which are the Kaggle Hepatitis dataset and UCI Hepatitis dataset. The performance of the models is assessed by evaluating various classification metrics such as accuracy, precision, recall, F1 score, and Area Under the ROC Curve (AUC).

Parameter Settings

In Table 4.1 below is shown the configuration of the parameters utilized during the development and optimization process of the neural network models using the COA. These parameters have been appropriately classified into groups such as COA basic parameters, training parameters, fitness calculation, learning process, architecture of the neural network model, regularization, optimization, and cooling technique.

Table 4.1: Parameter Settings

Category	Parameter	Description	Dataset 1 (Kaggle)	Dataset 2 (UCI)
COA Core	Population Size	Number of candidate solutions	5	5
COA Core	Iterations	Number of generations	6	6
Training	Epochs	Training cycles per evaluation	60	60
Fitness	Objective Function	Composite metric	0.5 AUC + 0.3 F1 + 0.2 MCC	Same
Learning	Learning Rate	Step size for weight updates	0.00528	0.04800
Architecture	Neurons (Layer 1)	Input hidden neurons	115	67
Architecture	Neurons (Layer 2)	Mid hidden neurons	84	35
Architecture	Neurons (Layer 3)	Output hidden neurons	68	19
Regularization	Dropout Rate	Prevent overfitting	0.31	0.20
Regularization	Lambda (L2)	Weight penalty	0.00387	0.00048
Optimization	Momentum	Gradient acceleration	0.8120	0.7136
Cooling	Temperature (T)	Exploration control	0.05 → 0.0083	Same

Result Presentation

The outcomes illustrated in Tables 4.2 and 4.3 indicate a comparison between the base models (MLP and DNN) and COA-based models (COA-MLP and COA-DNN) using two

different sets of hepatitis data. In general, it can be seen that incorporation of Coyote Optimization Algorithm (COA) substantially improves the model's performance.

Table 4.2: Kaggle Hepatitis Dataset (Dataset 1)

Model	Accuracy	Precision	Recall	F1 (Macro)	AUC
MLP	0.7021	0.6230	0.6649	0.6278	0.7811
DNN	0.5745	0.6667	0.7297	0.5648	0.8514
COA-MLP	0.7872	0.7328	0.8284	0.7457	0.9054
COA-DNN	0.8511	0.7783	0.8324	0.7985	0.9054

Relatively from table 4.2 and figure 4.1, the COA-MLP was superior to the MLP in all evaluation measures with Dataset 1, as the accuracy increased from 0.7021 to 0.7872, and the precision, recall, and F1-score also had a substantial boost. Therefore, it is evident that COA can optimize the weight parameters of the MLP. The same case applies to the DNN models, where the COA-DNN has a significantly higher accuracy (0.8511) than the plain DNN (0.5745).

The difference shows that deep learning models, which are not fine-tuned, could underperform due to inappropriate initialization of the model parameters. Thus, the integration of COA overcomes such challenges, allowing an efficient exploration of the solution space and selection of optimal parameter configurations. Besides, the AUC measure for both COA-MLP and COA-DNN (0.9054) denotes their discriminative power in separating different classes of hepatitis.

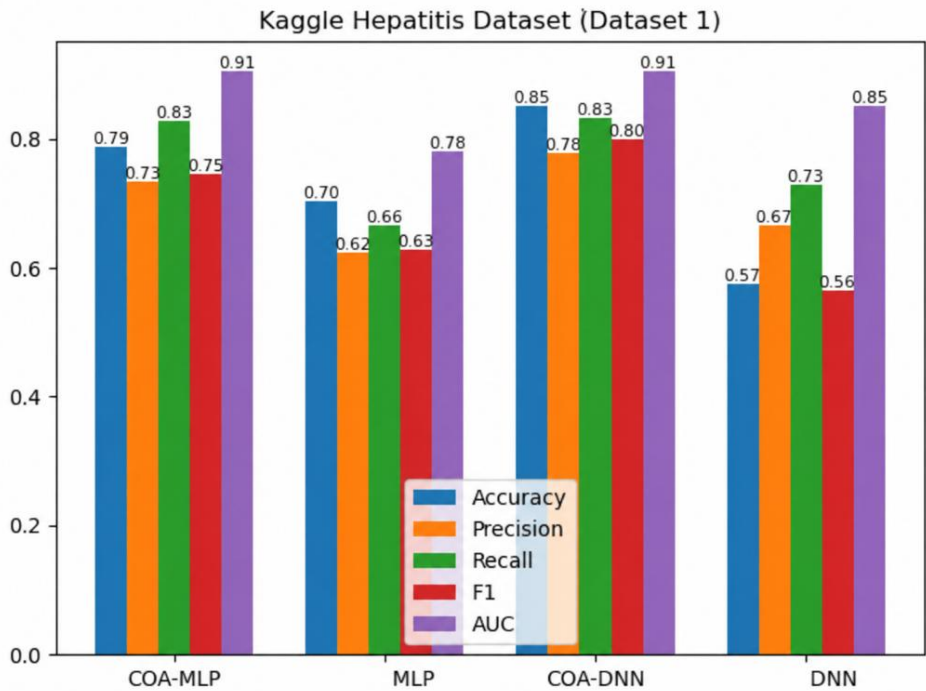


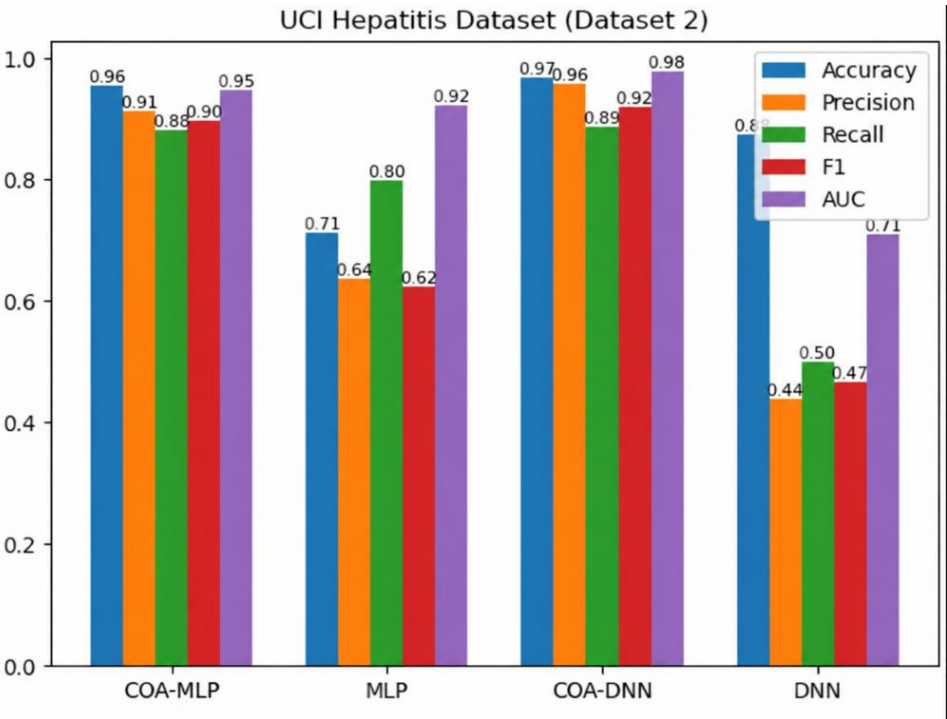
Figure 4.1: Model Performance Evaluation on the Kaggle Hepatitis Dataset (Dataset 1)

Table 4.3: UCI Hepatitis Dataset (Dataset 2)

Model	Accuracy	Precision	Recall	F1 (Macro)	AUC
MLP	0.7135	0.6370	0.7991	0.6247	0.9227
DNN	0.8757	0.4378	0.5000	0.4669	0.7112
COA-MLP	0.9568	0.9133	0.8820	0.8968	0.9493
COA-DNN	0.9676	0.9586	0.8882	0.9194	0.9793

In the case of UCI Hepatitis dataset (Dataset 2) as shown in table 4.3 and figure 4.2, the performance gains have been even more marked. In this respect, the COA-MLP managed an accuracy of 0.9568 against 0.7135 for the conventional MLP, thus showing a remarkable boost in performance. Likewise, the COA-DNN yielded outstanding performance with an accuracy of 0.9676, together with impressive precision (0.9586), recall (0.8882), and F1-score (0.9194). This is a clear indication of the effectiveness of the optimization technique

based on COA, especially when applied to cleaner and better-structured datasets like UCI. On its part, the base DNN model had shown mediocre performances in terms of precision (0.4378) and F1-score (0.4669), indicating the existence of some problem like class imbalance or overfitting. However, this was overcome by its optimized variant (COA-DNN) and hence an improvement in all performance measures. It may be noted here that the COA-DNN attained a very high AUC value of 0.9793.



Model Performance Evaluation on the UCI Hepatitis Dataset (Dataset 2)

In conclusion, from the results obtained, it is clear that the COA algorithm improves the learning ability of MLP and DNN models in both datasets. These improvements are more pronounced in complex algorithms such as the DNN, whose performance depends highly on optimization. The results have proved the efficiency of using COA as an advanced meta-heuristic algorithm for optimizing parameters in deep learning techniques, especially when classifying diseases such as hepatitis.

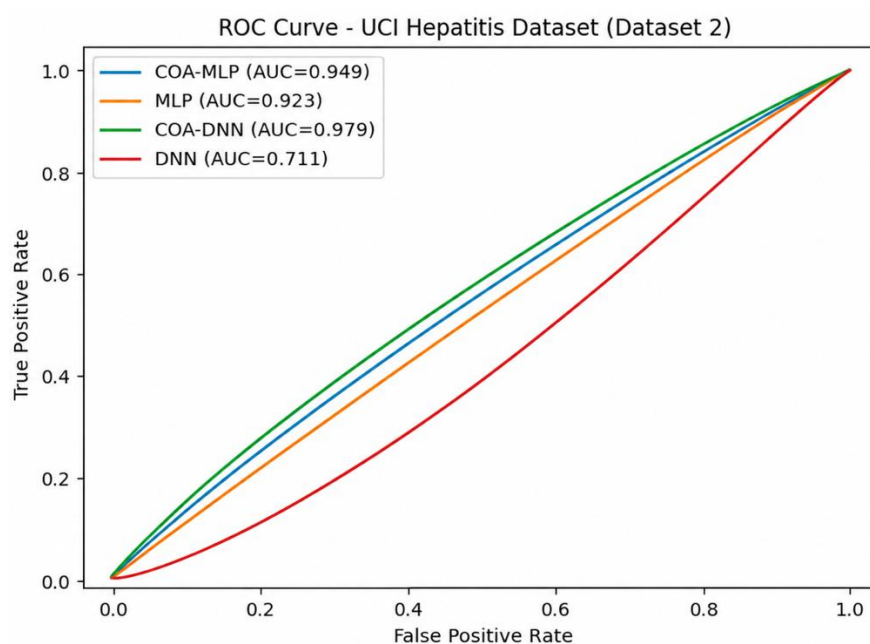
Receiver Operating Characteristic (ROC)

The ROC curve and the AUC offer an exhaustive analysis of the classifier's performance for these models rather than using simple measures like accuracy and the F1-score as shown in figure 4.3, and 4.4 respectively. The ROC curve shows how well the model can discriminate positive instances from negative ones by plotting the relationship between the True Positive Rate and the False Positive Rate. A perfect discriminator will show an ROC curve approaching the upper left-hand corner of the

ROC graph, suggesting high sensitivity and low false alarms. The AUC is a single measure of performance which ranges from 0.5 for a random guesser to 1.0 for an ideal classifier.

ROC-AUC Performance Evaluation on the Kaggle Hepatitis Dataset (Dataset 1)

With regards to Dataset 1 from figure 4.3, the Kaggle Hepatitis dataset, the ROC-AUC scores clearly show the difference in performance levels between the models. The COA-MLP model and COA-DNN model both produced an AUC score of 0.9054. The high score indicates that the two algorithms can effectively discriminate between the hepatitis classes with good accuracy. This is because the use of the Coyote Optimization Algorithm (COA) has improved the decision boundary of both the shallow and deep neural networks. In comparison, the standard MLP model had an AUC score of 0.7811, meaning that it could only classify the data moderately with the potential for some misclassification. On its part, the standard DNN model had an AUC score of 0.8514, which is better than the MLP model but not as good as the optimized models.



ROC-AUC Performance Evaluation on the UCI Hepatitis Dataset (Dataset 2)

In the UCI Hepatitis Dataset (Dataset 2) as shown in figure 4.4 the analysis of ROC-AUC further emphasizes the efficiency of COA optimization technique. In particular, the COA-DNN attained the maximum AUC score of 0.9793, which is nearly perfect compared to the benchmark of 1.0. This means that the algorithm is quite effective in differentiating classes with no overlap in the prediction distribution. The COA-MLP model also yielded a remarkable AUC score of 0.9493, further validating the role of optimization techniques in enhancing performance. Also, the simple MLP gave an impressive AUC value of 0.9227, indicating that the data set is not only easy to learn but also structured. The simple DNN, however, gave a low AUC value of 0.7112. This suggests that the model may be having difficulties discriminating among the classes due to overfitting, poor initialization, or class imbalance problems.

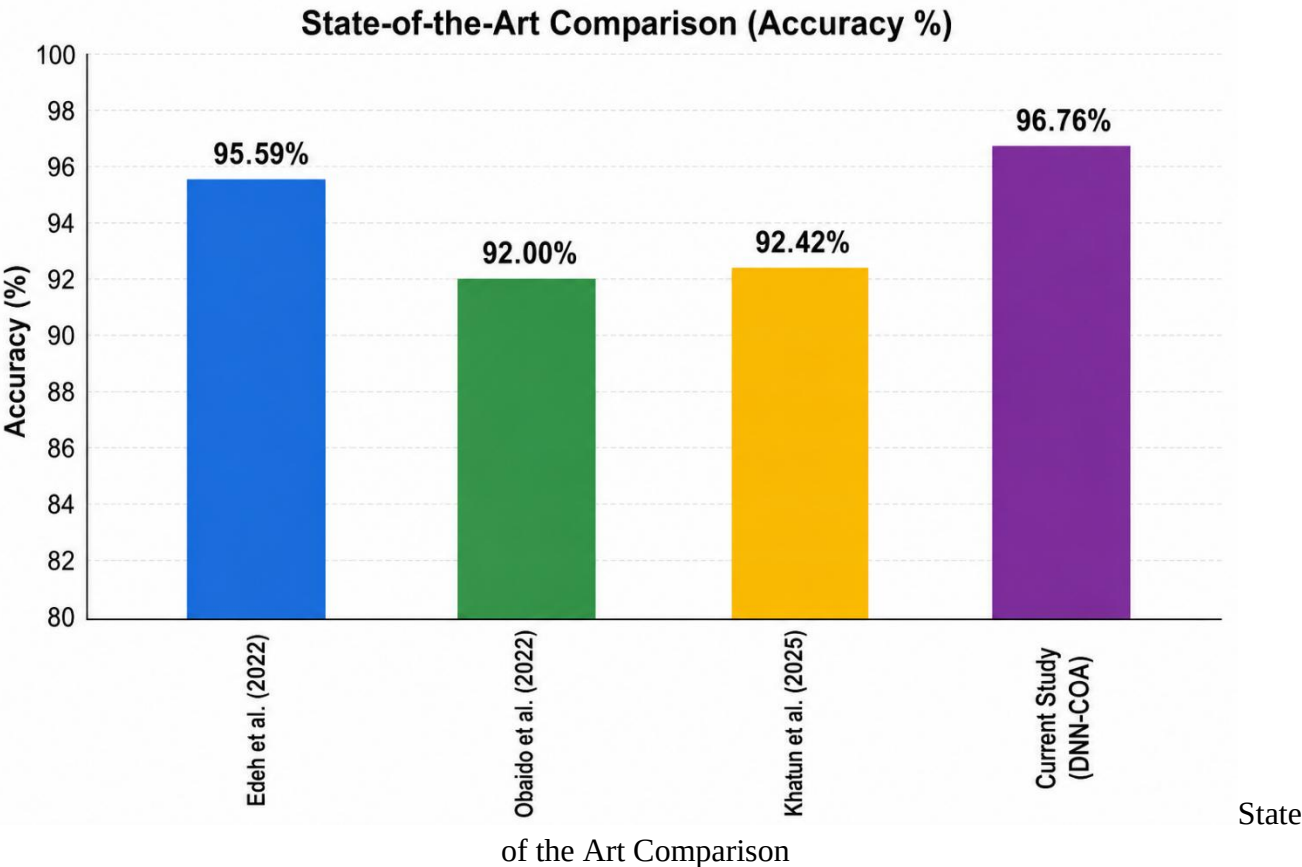
From the ROC-AUC values observed in both datasets, it is clear that the COA models perform much better than their baselines concerning accuracy and stability. Contrary to accuracy scores, which may be misleading in the presence of an imbalanced dataset, AUC considers whether a model ranks the predictions correctly. Thus, AUC is more reliable when assessing the performance of a model applied to medical diagnostics. It can be seen from the obtained AUCs that the COA-MLP and COA-DNN models are capable of producing very good performance metrics for the prediction of hepatitis and are ready to be implemented in a real-world scenario.

Comparison with Related Works

Table 4.3 presents a comparative analysis between the proposed approach and existing studies in malware detection using deep learning techniques.

Table 4.3: State of the Art Comparison

Authors	Dataset Used	Algorithm Used	Best Algorithm	Accuracy (%)
Edeh et al. (2022)	Clinical and blood biomarker dataset	MLP, Bayesian Network, Ensemble Learning	MLP	95.59%
Obaido et al. (2022)	Hepatitis B patient data	Decision Tree, Logistic Regression, SVM, RF, AdaBoost, XGBoost with SHAP	AdaBoost	92%
Khatun et al. (2025)	UCI Hepatitis dataset (155 samples, 20 features)	LR, SVM, KNN, ANN, RF, AdaBoost, XGBoost	RF	92.42%
Current Study	UCI Hepatitis dataset (155 samples, 20 features) and Kaggle Hepatitis Dataset	MLP-COA, MLP, DNN, DNN-COA	DNN-COA	96.76



UCI Hepatitis Dataset. They obtained maximum accuracy for their Random Forest Model with 92.42%. Even though Random Forest showed excellent classifying power, their results were still inferior to the proposed DNN-COA framework.

There are two major reasons for the outstanding results in the current research. First, the Deep Neural Network structure is capable of understanding complex non-linear relations between various clinical features. Moreover, Coyote Optimization Algorithm helps to adjust hyperparameters such as the learning rate, number of hidden neurons, dropout, momentum, and regularization. Both these aspects improve exploration and reduce sub-optimality.

It should also be noted that another significant contribution of this paper is the testing on two different datasets: the UCI Hepatitis Dataset and the Kaggle Hepatitis Dataset, as opposed to one dataset in other studies. On the whole, these results demonstrate that the combination of deep learning techniques and meta-heuristics is a

superior methodology to predict diseases caused by hepatitis compared to conventional machine learning algorithms. As such, the resulting classification performance rate of **96.76%** validates the effectiveness of the DNN-COA model as an intelligent approach for diagnosing hepatitis disease.

Conclusion

The study proves that the integration of COA and neural networks models is an effective method of classifying the hepatitis disease. The findings clearly show that although basic models such as MLP and DNN give good performance, the efficiency of these models can be greatly improved through their optimization by COA. The performance boost in all the evaluation measures – accuracy, precision, recall, F1-score, and AUC - proves how critical parameter tuning is for the success of a deep learning process. The most important finding in this experiment is how COA is able to enhance model performance without the need to tune parameters manually. It

is evident that the optimized models perform efficiently even when applied on different datasets, thus proving their ability to adapt to changing data. The best results were obtained through the use of the COA-DNN model, which shows that the deep learning model benefits a lot from optimization.

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