Optimizing Neural Networks Using a Group Learning Algorithm for Heart Disease Prediction with the Cleveland Dataset

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One of the major health issues that afflict human beings is heart disease which is regarded as a major cause of death in the world. Neural networks are just one of the ways used to forecast heart disease. When creating neural networks, one might employ the traditional optimization algorithms to explore more complicated search spaces and quickly locate global optima. This paper proposed an optimization strategy based on the Group Learning Algorithm (GLA) to adjust vital neural network parameters and feature selection was also implemented in the training. Cleveland dataset was used in the experiment. The strategy enhances the accuracy and generalization of the model, selecting the most useful parameters and a subset of features. The competitive advantages of the proposed method are shown through experimental results in comparison with the traditional neural networks. The suggested approach was repeated 30 times in a row and had the highest accuracy of 93.44 with the standard deviation of the result of 3.01 which is similar or even higher than other leading approaches. Our approach is more predictive of heart disease than multi-dataset. The research could contribute to making heart disease prediction more accurate so that more useful models can be used to benefit the medical industry.

Povzetek: Članek predlaga optimizacijo nevronskih mrež in izbiro značilk na naboru Cleveland, kar izboljša natančnost in posploševanje pri napovedi srčnih bolezni v primerjavi s klasičnimi pristopi.

1 Introduction

Heart disease is one of the most prevalent world-wide health crises, a multifactorial spectrum of disorders in the structure, operations, and vascular system of the heart. It has substantial morbidity, mortality, and socioeconomic costs, and the World Health Organization (WHO) has ascribed 31% of global mortality in the last 15 years to causes of cardiovascular disease [1, 2]. It is quite interesting to note that countries like Australia, India, Canada, the United Kingdom, and the United States have cardiovascular disease as one of the main causes of death therefore highlighting its widespread danger [2]. The multifactorial interaction of modifiable and non-modifiable risk factors such as genetic predisposition, age, lifestyle, hypertension, diabetes, and obesity has been determined to be the etiology of heart disease
[3-5]. As these factors accumulate over time, early intervention and prediction are necessary to prevent disease development and reduce healthcare costs.

Artificial Intelligence (AI) has transformed the sphere of medical diagnostics and offered creative tools to forecast the illnesses over the last decade. Machine learning techniques, especially neural networks (NNs), have demonstrated the potential to identify heart disease risk patterns on clinical data [6-10]. Even with these advances, long-lasting high accuracy in prediction is not attained. The deterministic methods are less flexible with respect to nonlinear relationships in healthcare data whilst the stochastic approaches, heuristic and metaheuristic strategies, are trying to balance their focus between exploration (diversification) and exploitation (intensification) to explore complex solution space [11, 12]. These methods, however, are still prone to premature convergence or intensive computing needs thereby restricting their clinical acceptability.

Other machine learning methods had their popularity; neural networks had the ability to represent non-linear relationships and generate complex and data driven representations of the relationships. Although the effectiveness of the neural networks depends largely on the technique of selecting the parameters and features to

be included in the model, these parameters and features may result in overfitting or under fitting, and hence the decrease of the generalizability of the model. Besides, the dimensionality of clinical data is so high that it requires some powerful feature selection methods that keep only the most informative variables in the training [13].

The development of the parameter selection and the feature selection technique requires an exploration of how these two methods can be combined to improve the performance of the neural networks to predict heart disease. This is to be achieved overcoming data problems and optimizing generalizability to real life situations. This research paper suggests a new model that combines the use of the Group Learning Algorithm (GLA) with traditional neural networks to enhance the predictability of heart disease, in terms of research results. The proposed method in this work aims to improve the trade-off between exploration and exploitation in stochastic optimization, thereby enhancing model efficacy. One of the significant contributions of this study is the formulation of a technique that leverages the complementary nature of neural networks to achieve more accurate predictive performance than traditional approaches. With this innovation, we aim to promote AI-driven tools for early diagnosis of heart disease, which will, in turn, enable timely clinical decision-making and improve patient outcomes.

The primary objective of this study is to develop a predictive model of cardiovascular disease by enhancing the performance of artificial neural networks through the application of metaheuristic optimization algorithms. This effectively reduces the error rate, improves the accuracy rate of predictions, and expands the generalizability of the findings to new datasets.

The main objectives of this study are:

- To design and implement a hybrid predictive model that integrates neural networks with GLA to enhance the accuracy of heart disease prediction.
- To improve the model's performance not only in terms of accuracy, but also in terms of robustness to noisy or imbalanced data, and its ability to generalize across multiple heart disease datasets.
- To reduce the error rate through effective parameter tuning and selection of the most influential features.

To achieve the main objectives of this study, this research addresses the following questions: Does the proposed model outperform conventional models in terms of accuracy? Does the model maintain high robustness when exposed to noisy or imbalanced data? Can the proposed model generalize its performance well across multiple cardiac datasets, not just a single dataset?

The contributions of this research are as follows:

- Developing a hybrid framework: Introducing a predictive model based on neural networks with an optimization algorithm (GLA) integration, allowing for improved prediction accuracy for heart disease.
- Improving parameter and feature selection: Adopting advanced strategies to optimize parameter values and select essential features from the data reduces the error rate and increases the model's generalizability.
- Comparison with traditional methods: Conduct comparative experiments between the proposed and conventional models, highlighting the differences in performance and effectiveness in predicting heart disease.

The rest of the paper is organized as follows: Section 2 discusses previous studies, Section 3 explains the methodology employed in this work, Section 4presents the results and discussion, and finally, Section 5 contains conclusions and future work.

2 Literature review

AI applications, in particular Machine learning have been used in many applications as investigated by [14-20]. A large number of researchers have tried to formulate and enhance models of predicting heart disease by using different algorithms and approaches; the literature review history presented below underscores some of these endeavors.

A three-stage system proposed by [21] includes feature extraction through statistical dispersion analysis, dimensionality reduction through normalized mutual information-based PCA (NM-PCA), and ensemble of the RF, SVM and KNN classifiers. This was optimized by a hybrid Deer Updates Flame Optimization algorithm and gained competitive accuracy on the Cleveland, Switzerland, Hungarian and VA Long Beach datasets. On the same note, Patro et al. [2], used Bayesian optimization to optimize the SVM kernel functions and weights and combined KNN and Naive Bayes classifiers to reach 93.44 percent accuracy on Cleveland dataset.
[22] complemented the functioning of Random Forest by using a variety of training sets based on multi-objective particle swarm optimization (MOPSO). On six datasets (Cleveland, Statlog, SPECT, SPECTF, VA Long Beach and Eric) this method was tested with accuracies to 88.26 percent using classifiers like C4.5, LR and QDA. Cherian et al. [3] combined the LA and PSO algorithm with PCA to reduce features and were found to be effective on UCI datasets.

The recent works focus on metaheuristic-powered optimizations. Manikandan et al. [23] compared the logistic regression, decision tree and support vehicle machine (SVM) performance with Boruta feature selection on Cleveland dataset and with no feature selection. The research revealed that the six pertinent characteristics that Boruta chose enhanced the model performance with the logistic regression being the most effective with an accuracy of 88.52. Cenitta et al. [24] suggested a feature selection algorithm, squirrel search algorithm (IHDSSO), combined with Forest, to find ischemic heart disease risks. A privacy sensitive MABC-SVM framework proposed by Yaqoob et al. [25] enhanced the prediction accuracy by 1.5 percent and

reduced the computation load. [26] combined gravitational search optimization (GSOA) with DBN-CNNs to analyze IoMT data, predicting cardiac risks via SVM-based classification. An improved variant of the Grey Wolf Optimization algorithm was successfully applied to optimize neural network training, resulting in improved robustness and generalization performance on clinical datasets [27]. Hybrid models that combine classical neural networks with quantum elements, as represented by the Kolmogorov-Arnold Classical-Quantum Dual-Channel Neural Network, offer better interpretability and uncertainty estimation while maintaining competitive predictive performance [28].

Additionally, applying deep learning models supported by sophisticated feature augmentation methods has demonstrated a predictive accuracy enhancement of over 4%, indicating the significance of sophisticated data augmentation and optimization strategies [29]. Lastly, Begum et al. [30] confirmed the utility of integrating metaheuristic algorithms, such as HHO and PSO, with neural network frameworks, thereby facilitating the development of more precise and interpretable predictive solutions in cardiovascular diagnosis.

The previous works indicate the possibility of integrating metaheuristics with neural networks in order to deal with variability of medical data and improve the robustness of prediction. Nevertheless, there are still issues of weighting the exploration-exploitation trade-offs and extrapolating the models across heterogeneous data sets, hence our addition of a Group learning algorithm to neural network to improve heart disease forecasting performance.

3 Methodology

The research methodology suggested will optimize neural network configurations to predict heart disease by combining a Group learning algorithm (GLA) [31] to hyperparameter tuning and feature selection. The methodology can be broken down into four major steps:

3.1. Data preprocessing and chromosome encoding

The raw data are subjected to conventional preprocessing, such as removal of values of missing data, and normalization. In this work, missing values were handled by mode substitution per column. To avoid data leakage normalization using a Z-score was used with the parameter of the scale (mean and std) being learned only on the training set and then applied to the validation and test sets. Every indicator is then coded as 13 features and a binary target variable (0 or 1). The hyperparameters of the neural network, as well as choices of features are represented as a single chromosome, enabling an efficient search in high-dimensional parameter space. This chromosome is made out of two parts (Figure 1): a parameter section and a feature selection bit string. The parameter segment represents hyperparameters, including the number of hidden layers, neurons each layer, activation function, dropout rate, learning rate, the batch size, number of epochs, and optimizer. All numeric hyperparameters are rescaled to [0,1], and categorical values are coded as integer indices. The feature picking step includes a series of 13 bits, and each bit denotes the presence or absence of the respective feature in the training.

Hidden layer	neurons	activation	dropout	Learning rate	Batch size	epochs	optimizer	Feature 1	...	Feature 13
Number	Number	List	Rate	Rate	Number	Number	List	(0/1)	...	(0/1)

Figure 1: Solution representation

3.2 Fitness evaluation through neural network training

The encoded hyperparameters and feature subsets are then decoded in every candidate solution (chromosome). Then a feed-forward neural network is constructed through these settings and the training data is trimmed down to include only the features chosen by the chromosome. A sample of the preprocessed data is fed into the neural network which is then trained and the neural network performance is determined using the accuracy as the fitness measure on a dataset. This fitness test is used as the objective function to be used in optimization.

3.3. Optimization using the group learning algorithm (GLA)

To explore the intricate search space, there is the use of GLA. The algorithm starts with an initial random population of chromosomes. The most efficient solution is the so-called manager. This group is then further subdivided into groups and within a given group a group leader is then identified depending on fitness. The algorithm repeatedly refines the group leaders and individual solutions with the help of a set of operations:

- Leader Update: All group leaders are tuned depending on the variations between the world manager and a random scaling value.
- Group Member Update: Group members are updated by moving to the updated group leader.
- Global Influence: The optimum solution (manager) makes the rest of the people work toward converging. Also, mutation operator is introduced randomly to bring variations to make sure that the search space is explored and premature convergence is avoided The optimal chromosome is chosen after a specified number of steps which is the optimal combination of the neural network parameters as well as the most informative set of features.

3.4. Enhanced neural network for prediction of heart disease

The final neural network model is then configured by using the optimized chromosome. This more refined model, which benefits by optimized hyperparameters and a more fined feature subset, will have improved accuracy and generalization performance in predicting

heart disease risk. The last model is implemented experimentally and compared to the conventional optimization methods. Figure 2 presents the general structure of the proposed approach.

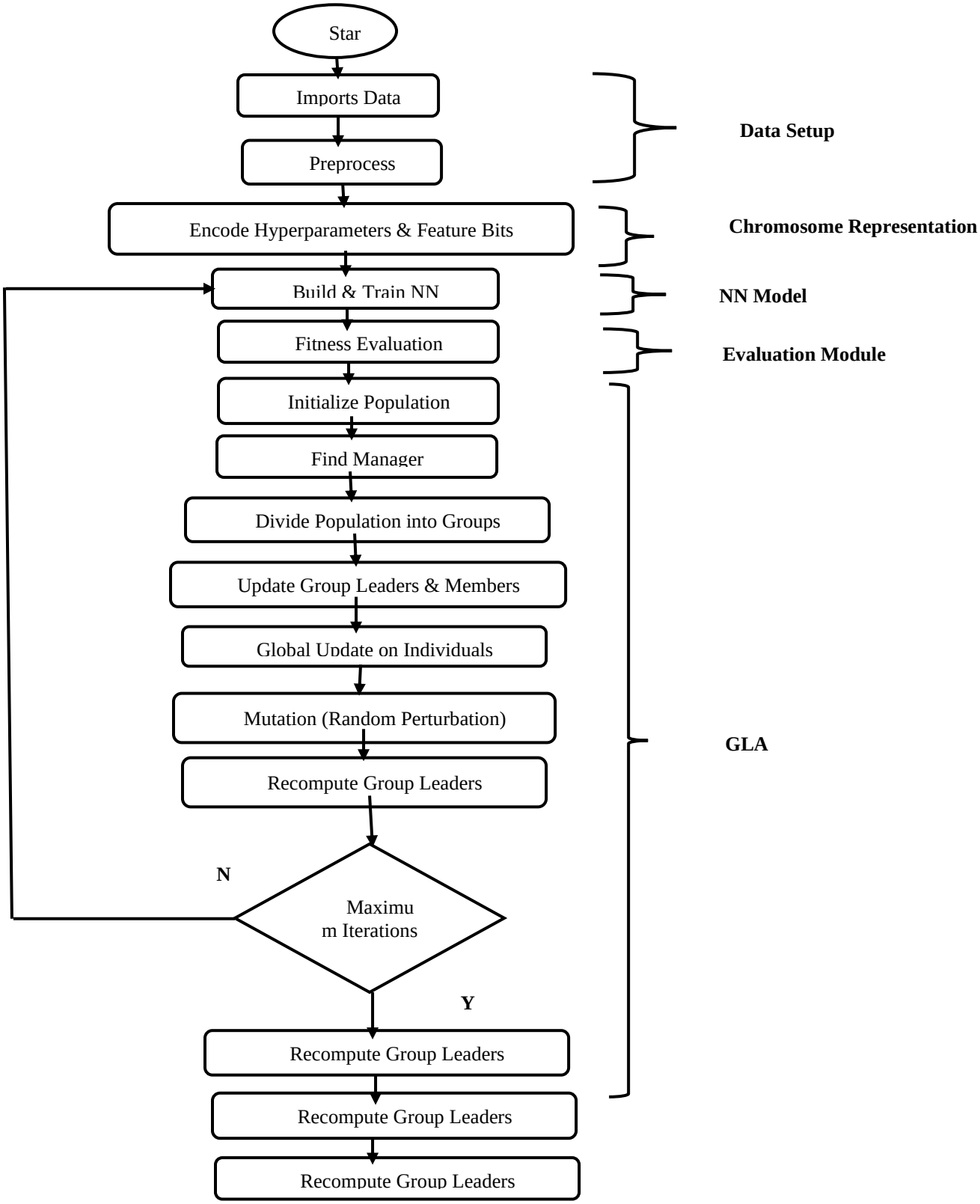

Figure 2: General structure of the proposed approach

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Algorithm 1 represents the proposed method in general.

Algorithm 1: Neural network optimization based on group learning algorithm
Input: Dataset, Population size (pop_size), Maximum iterations (max_iter), Number of groups (groups_count)
Output: Best solution, NN Model.
1. Initialize a population randomly.
2. Building an NN according to each solution.
2. Training NN models and evaluating the fitness of each solution in the population.
3. Identify the global manager as the solution with the highest fitness.
4. Divide the population into groups randomly.
5. Select the group leader (best solution) for each group.
6. For iteration = 1 to max_iter do:
For each group, update the group leader:
· Compute LA = (group_leader - manager) * r, where r ∈ [0,1]. (LA is the new group leader after it is affected by the manager.)
• Evaluate the fitness of the new leader and update if it improves
For each group member (excluding the leader): Update the individual:
• Compute New individual = (group_leader - individual) * r
• Evaluate fitness and update the manager if necessary.
• For each individual (excluding the manager): Update using global influence:
• Compute New individual = (individual - manager) * r
• Evaluate fitness and update the manager if necessary.
• Apply mutation: For each chromosome, with a probability equal to the mutation rate, randomly perturb one or more genes.
• Recompute group leaders for the next iteration based on updated fitness.
7. End For.
8. Return the best solution (manager) and NN Model.

We use an initial mutation rate of 0.1, which is gradually reduced by 0.95 with each iteration, applied to each member with a probability equal to the rate value. When a mutation occurs, one variable is randomly selected to be changed. The generation method depends on the type of variable. This mechanism aims to balance exploration with exploitation, with the mutation probability gradually decreasing to allow for finer tuning in the later stages.
After several iterations, the best chromosome (manager) is identified. This chromosome contains the optimal neural network hyperparameters and the best subset of features for predicting heart disease.

The optimized configuration is then used to build the final neural network model, which is expected to perform better in terms of accuracy and generalization. The final model is deployed to predict heart disease, providing a more accurate risk assessment to support clinical decision-making.
The computational complexity of the proposed algorithm is examined from two distinct viewpoints (the optimization phase and the model training/prediction phase). GLA is meticulously crafted to conduct an efficient search for optimal hyperparameters, with its complexity principally influenced by the population size (pop_size), the number of iterations (max_iter), and the computational cost associated with evaluating each individual. Given that each evaluation necessitates the training of a neural network for a maximum of (E) epochs, the time complexity of the optimization procedure can be approximated as O(pop_size * max_iter * E).
For the final trained model, the complexity associated with executing a singular prediction is predominantly governed by the feedforward propagation through the network. This operation is remarkably efficient and is contingent upon the number of hidden layers (L), the quantity of neurons per layer (K), and the total number of input features (F). Consequently, the complexity for a single prediction can be expressed as O (L * K * F). The cumulative complexity of the algorithm is primarily dictated by the hyperparameter optimization phase, which, although more computationally demanding than a singular training execution, is imperative for attaining the high performance corroborated in this work.

4 Results and discussion

Some heart disease datasets are available in the UCI repository, including those from Switzerland, Hungary, and Cleveland. This dataset contains 303 instances and 75 attributes. However, a subset of 14 of them was used in all reported tests. The target column in the presented dataset has two classes: 1 for heart disease and 0 for other conditions. The description for this dataset is given in Table 1. The reason for selecting a set of 14 features from the available features in the dataset is as follows:
First, we relied on a literature review and used the most common features in previous studies as a primary reference. Second, we analyzed the proportions of missing values for each feature and excluded variables that exceeded a specified percentage threshold for missingness. Finally, we conducted univariate analyses (Correlation tests and mutual information calculation) to assess the strength of the relationship between each feature and the target variable, and we used the results of these tests to select the final set.
The percentage of training data in the current work is 64%, the percentage of testing is 20%, and the percentage of validation is 16%.

Table 1:Cleveland dataset description

Attribute	Description
Age	Patient's Age
Gender	Patient's Gender
Cp	Type of Chest Pain

Thestbps	Resting Blood Pressure
Chol	Serum Cholesterol Level
Restecg	Resting Electrocardiographic Results
Fbs	Fasting Blood Sugar
Thalach	Maximum Heart Rate Achieved
exang	Exercise-Induced Angina
Oldpeak	ST Depression Induced by Exercise Relative to Rest
Slope	Slope of the Peak Exercise ST Segment
Ca	Number of Major Vessels Visualized
Thal	Type of Defect
Num	Diagnosis of Heart Disease (Angiographic Status)

For the preprocessing in this study, several steps were implemented to replace missing values, convert columns to numeric type, and convert target formats to binary. We used direct validation with Early Stopping to prevent overfitting and obtain the best validation weight. After preprocessing the dataset for heart disease prediction, we applied the proposed method, which integrates the Group learning algorithm (GLA) to enhance the neural network's structure and feature selection process. The optimization focused on determining the optimal number of hidden layers and selecting the appropriate number of neurons in each layer, thereby ensuring a thorough exploration of the solution space while leveraging local solutions. Table 2 shows the important parameters in the work and their values.

Table 2: Setting parameters

Parameter	Value
Population size	20
Number of groups	4
Initial mutation rate	0.15
Maximum iterations	50

The application of the proposed approach in rigorous experiments established an accuracy rate of 93.44, which is significant as compared to the conventional use of neural networks. The experiment was replicated 30 times in order to make sure that the proposed model performance is assessed thoroughly. The findings indicated an average accuracy of 88.99 with low standard deviation of 3.01. This low standard deviation means the performance of this model is not only due to a chance, but also is very stable and reliable in all runs. Table 3 presents the hyperparameters obtained via the application of our proposed method that also enhanced the performance of the neural network model.

Table 3: Hyperparameters chosen using our proposed approach

Hyperparameters	Value
hidden_layers	2
neurons	42
activation	elu
dropout	0.1847
learning_rate	0.00175
batch_size	38
epochs	75
optimizer	Adam

It should be mentioned that the dropout rate is rather small (0.1847), and this effect can be explained by the presence of the hyperparameter optimization algorithm designed to locate the best equilibrium between the model complexity and the generalization.

The Confusion Matrix of the evaluation process of the classification model is described in figure 3. The table shows how effective the model was to classify both classes appropriately. There are more values on the central diagonal (27 and 30) than those on the off-the-diagonal (2 and 2) that illustrate a better model performance and fewer prediction errors. In this figure, the model properly categorized the majority of samples with few errors (2 false positives and 2 false negatives) in this figure. This shows that the model has the capability of reducing classification errors in the negative (0) and positive (1) classes, an encouraging fact on its usefulness in similar prediction tasks.

The Training and Validation Accuracy curves are shown in figure 4 throughout the training epochs. The training accuracy (blue line) in the figure rises sharply during the first epochs, then tends to vary at a high level, which means that the model is successfully learning the trends in training data. The validation accuracy (the orange line) also shows a generally increasing trend, staying relatively close to the training accuracy, which suggests that the model is generalizing well to unseen data and is not overfitting. The minimal gap and similar behavior between the two curves are a promising sign of the model's effectiveness in prediction tasks.

Figure 5 is the Receiver Operating Characteristic (ROC) curve, with an area under the curve (AUC) of 0.96. This highly significant value indicates the model's excellent capacity to classify samples correctly and, hence, its effectiveness in striking an optimal trade-off between the False Positive Rate (False Alarm Rate) and the True Positive Rate (actual detection rate)

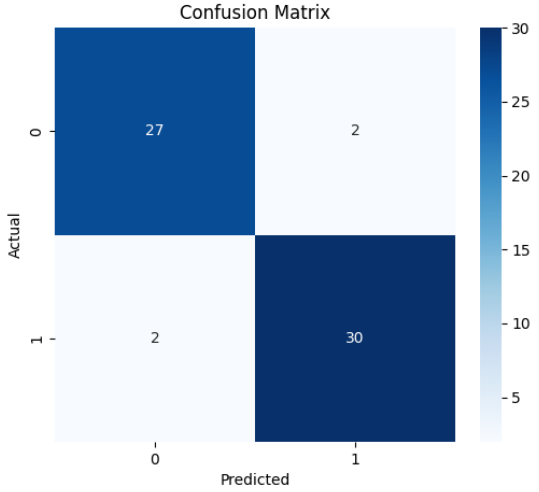

Figure :3 Confusion matrix of the model

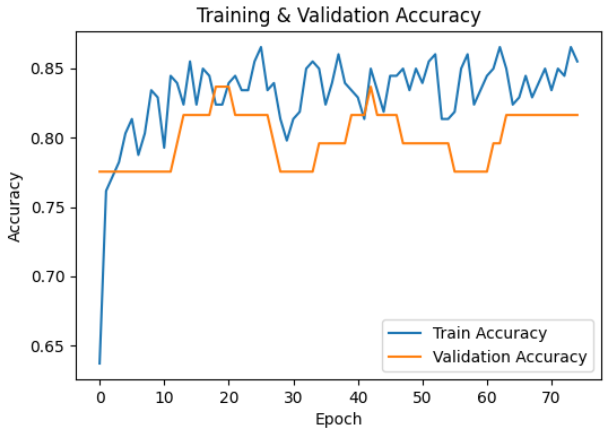

Figure :4 Training and validation accuracy and loss curves

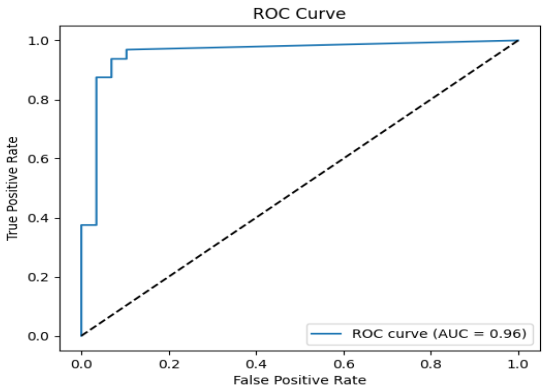

Figure: 5 Receiver operating characteristic

The application of the GLA algorithm in order to optimize the architecture of the neural network and the most relevant features selection has played a critical role in enhancing the accuracy of prediction. These attractive results suggest the prospects of using GLA to other research areas, where it can boost the work of traditional neural networks.

One of the main weaknesses of this study is that it has high computational complexity especially with deep models and large datasets. Nevertheless, this complexity

does not pose a serious barrier, because it is restricted to the model training stage alone.

Moreover, as it is indicated in Table 4, the outcomes of our proposed model are better than those of the existing literature, which proves the necessity to consider it as a more efficient instrument in predicting heart diseases. This shows how strong GLA is in improving the neural network structure. The findings reaffirm the ability of GLA to optimize the neural network morphology and feature selection to achieve more accurate heart disease prediction.

Table 4: Comparison between the proposed work and related studies.

Previous Study	Dataset	Method	Accuracy
Sheeba, et al. [14]	Cleveland, Hungarian Switzerland, and VA Long Beach	NM-PCA	91%
Patro, et al. [2]	Cleveland	BO-SVM	93.3%
Asadi, et al. [15]	Cleveland Statlog, SPECT SPECTF VA Long Beach Eric	MOPSO	Cleveland, 85.21% Statlog, 88.26 % SPECTF, 87.65 % SPECTF, 86.70% VA Long Beach, 87.50 Eric, 80.95 %
Proposed method	Cleveland	GLA Algorithm	93.44%

The proposed GLA Algorithm attained an accuracy rate of 93.44%, surpassing the efficacy of prior methodologies including NM-PCA (91.0%) and MOPSO (85.21%), while marginally exceeding the performance of BO-SVM (93.3%). The discerned disparities, especially in comparison to MOPSO and NM-PCA, suggest a significant enhancement in performance.

5 Conclusion

The study demonstrates that applying the Group Learning Algorithm (GLA) in a neural network architecture can significantly enhance heart prediction. Through skillful navigation of complex and large search spaces, the GLA-based optimization method effectively identifies the most critical parameters and feature subsets, resulting in improved accuracy and generalization compared to traditional optimization techniques. The experimental findings validate the competitive benefits of this solution, emphasizing its potential to reinforce predictive models and facilitate earlier and more accurate diagnoses of heart disease in clinical practice. Innovation underpins the viability of sustaining research activities and offers a model that can be applied to other health issues. Future research will enhance the GLA framework by incorporating adaptive hyperparameter tuning tailored to more complex datasets, evaluating its performance on larger, multi-modal datasets, and investigating its compatibility with advanced neural network architectures to achieve further improvements, and try to apply the model interpretability to future work.

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