

Heart Disease Prediction Using Bi-GRU with GWO for Tuning Parameter

P.Chairmadurai, Research Scholar,
Department of Computer Science,
School of Computing Sciences

Vels Institute of Science, Technology & Advanced Studies
(VISTAS) Pallavaram,
Chennai, India
chairma17@gmail.com

P.Kavitha, Assistant Professor,
Department of Computer Applications,
School of Computing Sciences

Vels Institute of Science, Technology & Advanced Studies
(VISTAS) Pallavaram,
Chennai, India
pkavikamal@gmail.com

Abstract

Machine learning has improved its precision and accuracy in classifying clinical cardiac disease datasets in recent years. However, studies show that the quality of the heart disease feature used for training has a substantial effect on the prediction model's effectiveness. This work presents a reliable model for predicting cardiac disease using data from the UCI Machine Learning Repository. Class imbalance is addressed by increasing minority class representation with the Synthetic Minority Upper Model Technique (SMOTE). To pick the most relevant features and boost the model's efficiency, a hybrid feature engineering strategy combines forward feature selection with recursive feature elimination (RFE). Gray Wolf Optimization (GWO) is used to change hyperparameters for optimal model performance. A bidirectional recurrent unit (bi-GRU) is used for classification in order to identify biases and hierarchical patterns in the data. Accuracy, specificity, and sensitivity are used to evaluate the model, giving a thorough evaluation of its prediction power. A very accurate and dependable technique for predicting heart illness is produced by combining data imbalance, improved feature selection, optimization, and deep learning. This shows promise for useful clinical decision support in risk assessment and early diagnosis. The proposed approach produced the result as sensitivity, specificity and accuracy as 91%, 90% and 98%.

Keywords: heart disease, SMOTE, RFE, GWO, Bi-GRU, accuracy, sensitivity, specificity

1. Introduction

One important component of the human or animal body that is vital to animals' existence is the heart. By pumping blood throughout the body, the heart regulates blood pressure and provides oxygen to every region of the body. Together with the neurological and endocrine systems, the heart carries out its duties. The neurological system helps control heart rate, whereas the endocrine system produces hormones and controls blood pressure by making human blood vessels either relax or spasm. Nonetheless, the human brain sends messages instructing your heart to beat faster whether it is relaxed or under stress. Stress causes our hearts to beat more quickly than normal, which can result in major cardiac issues. In addition to stress, excessive alcohol consumption, smoking, and a high-fat diet exacerbate cardiac issues. Human health risks increase as a result of poor eating patterns, high levels of stress, inadequate sleep, and lifestyle modifications [1].

According to WHO estimates, heart disease is the leading cause of death worldwide, accounting for 31% of all deaths, or 17.9 million deaths annually. Predicting the severity of cardiac disease is one issue that can be resolved with

machine learning based on supervised learning approaches. By finding complex patterns and correlations in the enormous quantity of data pertaining to cardiac disease, such as patient demographics, medical histories, diagnostic tests, and lifestyle factors, supervised learning algorithms are able to forecast the severity of the issue. Predictive models that offer early identification of individuals at higher risk of developing serious heart disease can be created by combining expert algorithms like decision trees, support vector machines, or neural networks with strategies like SMOTE-based oversampling to address class imbalance [2–3]. In addition to helping healthcare providers make educated decisions about patient care and treatment regimens, these predictive models also provide the public with the knowledge they need to change to healthier lifestyles and take preventative measures to slow the progression of heart disease and reduce the rates of morbidity and mortality linked to it. By applying machine learning to cardiovascular care, we can save healthcare expenses, enhance patient outcomes, and eventually lessen the prevalence of heart disease worldwide.

Contribution of proposed heart disease prediction

- This study effectively handles class imbalance in a heart disease dataset using SMOTE, which improves model validity and predictive performance in minority classes.
- To ensure optimal and efficient selection of relevant features, a novel hybrid feature selection approach combining recursive feature elimination (RFE) and forward feature selection is introduced.
- Gray wolf optimization (GWO) algorithm is used for hyperparameter tuning, which demonstrates better performance in finding optimal model configurations compared to traditional grid or random search methods.
- The use of a Bi-GRU allows the application of temporal and continuous dependencies in the data, improving the model's ability to make accurate predictions.
- The proposed model is rigorously evaluated using several performance metrics – accuracy, specificity and sensitivity – to ensure its reliability and clinical relevance in cardiovascular disease prediction.

Organization of the paper

The literature on heart disease prediction is reviewed in Section 2, which also highlights the methods and conclusions of other researchers in this area. The suggested algorithms for predicting heart disease in this study are presented in Section 3, which also details each stage of the model

construction process. A thorough performance study of the suggested system is given in Section 4, which assesses its effectiveness using a number of measures. The study is finally concluded in Section 5, which highlights the significance of the suggested strategy in enhancing heart disease prediction and summarizes the key findings.

2. Related work

Chintan et al., (2023) to use predictive modeling methods to lower mortality from cardiovascular disease. Huang's initialization technique and K-means clustering are used across a number of classifiers, such as XGBoost (XGB), Random Forest (RF), Decision Tree (DT), and Multilayer Perceptron (MLP), to improve model performance. Both cross-validation and no cross-validation were used to evaluate the models. The accuracy ratings for XGB, RF, DT, and MLP were 86.37%, 86.53%, 86.87%, and 87.02%, respectively, in the absence of cross-validation. The Multilayer Perceptron obtained the maximum accuracy of 87.28% when cross-validation was used. Strong discriminative power was also shown by the Area Under the Curve (AUC) scores, which for all models was continuously high at 0.94 for XGB and 0.95 for RF, DT, and MLP.

Arumugam et al., (2023) The area of data mining for healthcare, which has its roots in database statistics, is used to assess the efficacy of medical treatments. Diabetics are susceptible to a chronic illness called diabetes-related heart disease. There is little information to predict heart disease in diabetics, despite current classification techniques. A decision tree model outperforms naive Diabetes prediction using Bayes and support vector machine models.

Arsalan Khan et al., (2023) uses machine learning techniques such as logistic regression, decision trees, random forests (RF), Naïve Bayes, and support vector machines (SVM) to predict and classify people with cardiovascular disease (CVD) in Pakistan. The RF algorithm showed the best accuracy in prediction, sensitivity, and recursive operative characteristic curves (85.01%, 92.11%, 87.73%), as well as the lowest specification and misclassification errors (43.48% and 8.70%). Since the RF approach is the most effective in categorizing and forecasting CVD, it is helpful in the field of global health.

Nadikatla Chandrasekhar and Samineni Peddakrishna., (2023) This work uses machine learning approaches to increase the accuracy of heart illness forecasts. Six methods—K-nearest neighbor, random forest, logistic regression, gradient boosting, AdaBoost classifier, and Naïve Bayes—are assessed using datasets from the IEEE Dataport and Cleveland. GridsearchCV and five-fold cross-validation are used for hyperparameter tweaking. The usage of GridSearchCV with five-fold cross-validation for hyperparameter adjustment is what makes this work unique. Compared to previous research, the soft voting ensemble classifier technique greatly increases accuracy.

Rubini et al., (2021) New software has been created that uses basic symptoms such as age, sex, heart rate, and others to predict a person's risk of heart disease. The system evaluates machine learning methods including RF, LR, SVM, and NB using 14 important criteria. The system also provides information on the relationship between diabetes

and heart disease. This makes it easier for healthcare professionals to diagnose and confirm patient problems.

Tsehay Admassu Assegie et al., (2022) the correlation between machine learning models' ability to accurately forecast heart disease using recursive feature elimination with cross-validation (RFECV) and the quality of heart disease features. Using data from the University of California, Irvine, the experiment uses SVM, logistic regression, decision trees, and random forest models. With RF surpassing other approaches and reaching a prediction accuracy of 99.7%, the results demonstrate that feature quality has a major influence on model performance.

Pooja Rani et al., (2021) For the early diagnosis of heart illness in developing nations, the authors recommend a hybrid decision support system. The system employs fundamental scalar techniques, multivariate computing with the chained equations algorithm, and the hybrid SMOTE feature selection strategy. The system uses logistic regression, SVM, Adaboost, random forest, and naive Bayes classifiers. Our strategy outperformed some of the current heart disease prediction techniques in the literature, with an accuracy of 86.6% when tested on the Cleveland Heart Disease dataset.

Manoj Diwakar et al., (2021) One of the deadliest illnesses in the world, heart disease is challenging for both doctors and patients to identify. This study examines machine learning and image fusion classification techniques, illustrating how they may be used to diagnose cardiac conditions and giving a general overview of operational algorithms.

Zeinab Noroozi et al., (2023) explored the implications of feature selection techniques on machine learning algorithms used to anticipate cardiac illness. To determine the best models, the Cleveland heart disease dataset was treated to seven different algorithms. The findings demonstrated that feature selection enhanced model performance in certain methods while impairing it in others. The maximum accuracy was attained using SVM-based filtering strategies, whereas wrapper-based and evolutionary algorithms enhanced model performance in terms of sensitivity and specificity.

Halaha. Al-Alshaikh et al., (2024) The study presents a model for predicting heart illness that includes evolutionary algorithms, recursive feature reduction approaches, and undersampling clustering oversampling techniques. With 94.8% accuracy and 95.5% precision, respectively, the machine learning-based technique (ML-HDPM) does fairly well. The system's sensitivity (recall) has a high accuracy rate of 96.2%, and its F-score is 91.5%. The findings suggest that ML-HDPM might transform heart disease prediction and improve patient outcomes.

Diaa Salama AbdElminaam et al., (2023) heart disease is one severe condition that can significantly impact a person's life. Despite the fact that early diagnosis can save lives, it is challenging to predict for several reasons. Predictions might become more straightforward and reliable using machine learning. Out of the three datasets used, Logistic Regression was the most accurate. Random Forest scored the highest with 98.6% accuracy.

Huating Sun and Jianan Pan., (2023) proposed five ML models to determine the predictive power of self-measured physical health indicators for heart disease in comparison to all indicators evaluated by health care providers. A database containing the results of 13 diagnostic tests and the risk factors for heart disease in 303 people was used in the study. The results showed that physical health indicators measured at home were less accurate than all physical indicators, and that all matrices in the five models had higher accuracy rates than the home matrices.

Debabrata Swain et al., (2022) Early identification and treatment help avoid cardiovascular illnesses, which cause over one-third of deaths worldwide. In order to forecast cardiac illnesses, this study suggests a model that takes into account heredity, stress, smoking, and poor eating habits. Using a dataset from the UCI repository, the model employs five algorithms: Bootstrap Aggregation using Random Forests, MultiLayer Perceptron Classifier with PCA, SVM, Logistic Regression, and Deep Neural Network. The model incorporates a number of variables from several datasets and is appropriate for real-world situations.

Rohit Bharti et al., (2021) In order to predict cardiac disease, this article contrasts deep learning and machine learning techniques. The UCI Machine Learning Heart Disease dataset, consisting of 14 characteristics, is evaluated using several techniques. The study manages irrelevant characteristics using Isolation Forest, normalizes data, and produces encouraging findings that are confirmed using accuracy and confusion matrices. The report also explores its possible integration with multimedia technologies like mobile devices. Deep learning was used to attain an accuracy of 94.2%.

Azam Mehmood Qadri et al., (2023) With an emphasis on patient health parameter data, the current study attempts to enhance heart failure identification using machine learning. Along with nine machine learning techniques, the researchers also suggested a unique Principal Component Heart Failure (PCHF) feature engineering strategy. By developing a new feature set and carrying out several trials, they improved the PCHF mechanism. With a 100% accuracy score, the suggested decision tree approach fared better than the used models and other cutting-edge research. Cross-validation approaches were used to effectively validate all implemented procedures. This study might save patients' lives in the treatment of heart failure and has made important scientific contributions to the medical community.

3. Proposed methodology

Machine Learning Repository and focuses on the prediction of heart disease. Synthetic Minority Over-sampling Technique (SMOTE) is used for data augmentation to overcome class imbalance. Recursive feature elimination (RFE) is used for better feature extraction, while forward feature selection is used to increase model efficiency as part of a hybrid feature engineering strategy. Hyperparameter tuning is performed using Gray Wolf Optimization (GWO) to improve model performance. The Bidirectional Gated Recurrent Unit (Bi-GRU) is used for classification, leveraging sequential dependencies in data. Model effectiveness is evaluated using accuracy, specificity, and

sensitivity, ensuring a reliable and accurate heart disease prediction system.

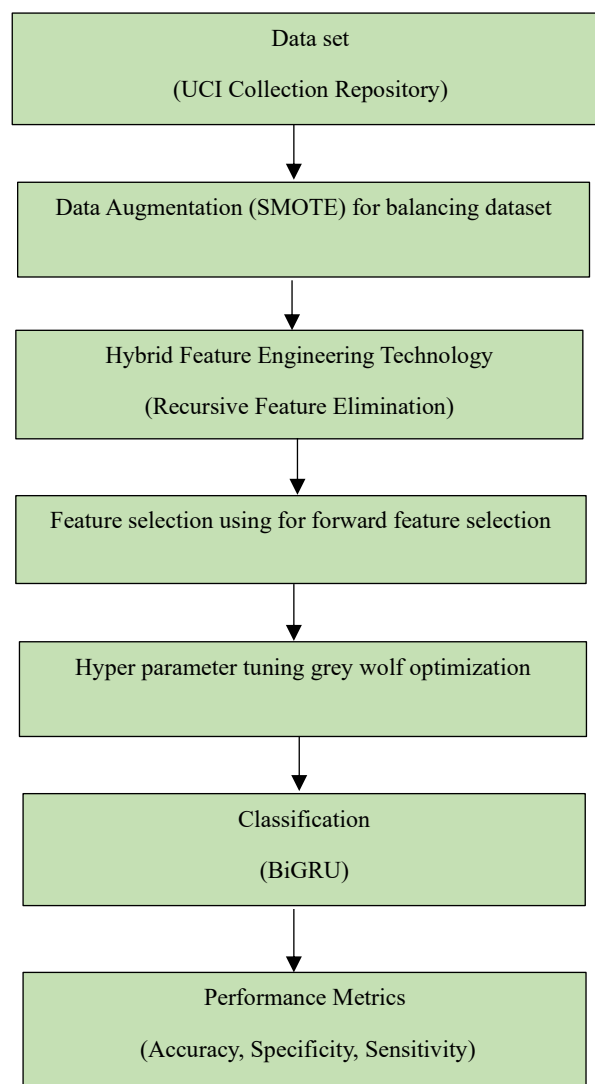


Figure 1. Flow diagram of proposed heart disease prediction

Dataset

Only 14 of the 76 traits in this database are utilized in all published research. In particular, machine learning researchers have only used the Cleveland database thus far. If the patient has heart disease, it is indicated in the "goal" column. Its integer value falls between 0 (no presence) and 4. Basic attempts to differentiate between presence (values 1, 2, 3, 4) and absence (value 0) have been the main focus of experiments using the Cleveland database.

Preprocessing: SMOTE (Synthetic minority oversampling techniques)

In a dataset, when the represents the minority class then it is called an imbalanced dataset. A biased and inaccurate forecast is produced in this instance by the machine learning algorithms, which attempt to fit the dominant majority class. Additionally, it provides an accurate intelligence. Even if we classified every record as alive in this case, we will still

achieve high accuracy, but that is not our goal. How we can handle such a situation is the question now. One method is to reduce the majority class while maintaining the minority class in order to make the data set more like the original. It certainly aids in dataset balance, however excluding observations might yield some important information, and this method may cause bias. Comparability When random oversampling occurs, we replicate part or all of the data several times in order to add extra observations at random. For this reason, the SMOTE methodology is employed both as a sampling method and to address these issues. SMOTE generates fresh data points or synthetic observations. Synthetic dataset creation using the SMOTE technique.

- Plotting each data point is the first step, after which the feature vector and its closest neighbors are found, and the difference between the two is calculated.
- Then just use a random integer gap between 0 and 1 to multiply the difference.
- The random integer is then added to the feature vector in order to identify a new data point on the line segment.
- Lastly, perform the same procedure for the feature vectors that were found. Every j -th characteristic of the artificial datasets,

$$X_{synthetic} = [X_{synthetic}^{(1)} + X_{synthetic}^{(2)} \dots X_{synthetic}^{(p)}] \quad (1)$$

Above the expressed as,

$$X_{synthetic}^{(fj)} = X^{(j)} + gap^{(j)} * [X_{neighbour}^{(j)} - X^{(j)}] \quad (2)$$

$X^{(j)}$ j – th feature of a chosen instance X

$X_{neighbour}^{(j)}$ j – th feature of a randomly chosen neighbour data point of instance $X_{gap}^{(j)}$ is uniformly distributed random variable from (0,1) for the j -th feature.

Recursive Feature Elimination (RFE)

In medical applications such as the prediction of heart disease, feature engineering is essential for improving the performance of machine learning models. In order to find and preserve the most important characteristics from the dataset, this study presents a hybrid feature engineering strategy that heavily relies on Recursive Feature Elimination (RFE).

RFE works by iteratively eliminating the least important features based on a machine learning evaluation's weight or importance score. At each iteration, the model is trained, features are ranked, and less contributing features are removed. This procedure keeps going until the ideal subset of characteristics is found, which lowers noise and overfitting and greatly improves prediction accuracy.

RFE is followed in the hybrid setup by Forward Feature Selection, which refines the feature space by gradually adding features that enhance model performance. This two-step approach ensures effective and precise cardiac disease

prediction by striking a compromise between dimensionality reduction and information preservation.

Feature selection

Building precise and effective machine learning models requires feature selection, especially in healthcare applications where datasets may contain duplicate or unnecessary information. To improve the efficacy of heart disease prediction, this work uses Forward Feature Selection (FFS) as a component of a hybrid feature engineering method.

Using a wrapper-based approach, Forward Feature Selection adds features repeatedly, starting with an empty feature set. The algorithm chooses the feature that offers the most increase in prediction accuracy after assessing the model's performance with each of the remaining features at each stage. This method keeps on until a certain number of features is attained or no further progress is shown.

Forward Feature Selection enhances Recursive Feature Elimination in the context of heart disease prediction by honing the original feature set and retaining just the most predictive and instructive characteristics.

GWO

The fact that deep learning models like GRU are extremely sensitive to hyperparameters and that manual tuning or grid/random search is ineffective for complicated models is a compelling argument for combining Grey Wolf Optimizer (GWO) with Gated Recurrent Unit (GRU), or more precisely, Bi-GRU. With fewer evaluations, GWO provides a strong, effective, and naturally inspired optimization approach that can identify high-performing hyperparameter sets. Improved accuracy and generalization are frequently the results of optimization. GWO-tuned in the very precise field of heart disease prediction, Bi-GRU can perform better than manually adjusted or default models. A novel metaheuristic method for resolving optimization issues is called Grey Wolf Optimization (GWO). The program mimics how grey wolves hunt and exercise social leadership. The grey wolf population is divided into four groups: alpha (α), beta (β), delta (δ), and omega (ω). The alpha is responsible for deciding when to get up, where to hunt, and where to sleep, among other things. When making decisions, the alpha is assisted by the beta. In the event that one of the alpha wolves is too old to rule, the beta wolf is most likely to take over. The Delta Wolf, also known as the subordinate, is made up of scouts, sentinels, hunters, elders, and caregivers. Scouts keep an eye on the region's borders and alert the pack to any potential danger.

The lowest-ranked grey wolf, the omega wolf, is being exploited as a scapegoat. Alpha, beta, and delta are considered the best search agents for guiding omega wolves to favorable regions of the search space. During the hunt, the grey wolves encircle their victim and optimize their positions around α , β , and δ in the following manner:

$$E = |C \cdot y_p(t) - y(t)| \quad (3)$$

$$Y(t + 1) = Y_p(t) - A \cdot E \quad (4)$$

Throughout the iterations, the random vectors in $[0, 1]$ representing the prey location, the grey wolf position, and the current iteration are linearly lowered from 2 to 0.

Alpha is the most appropriate response for grey wolf hunting, even if beta and delta are believed to possess additional information on the possible location of prey. The remaining search agents have so far been forced to shift their positions to match those of the top three answers. To update grey wolf positions, the following mathematical model is proposed.

$$E_\alpha = |C_1 Y_\alpha - Y| \quad (5)$$

$$E_\beta = |C_2 Y_\beta - Y| \quad (6)$$

$$E_\delta = |C_3 Y_\delta - Y| \quad (7)$$

$$Y_1 = Y_\alpha - A_1 \cdot (E_\alpha) \quad (8)$$

$$Y_2 = Y_\beta - A_2 \cdot (E_\beta) \quad (9)$$

$$Y_3 = Y_\delta - A_3 \cdot (E_\delta) \quad (10)$$

$$Y(t + 1) = \frac{(Y_1 + Y_2 + Y_3)}{3} \quad (11)$$

where the alpha, beta, and delta are located, respectively. The present solution's location is defined by random vectors, and its final position is determined by the distances to alpha, beta, and delta, correspondingly.

Classification: Bi-GRU (Bidirectional-gated recurrent unit)

GRUs (gated recurrent units) make the LSTM model simpler. In particular, they create an update gate by combining the LSTM forgetting and inputting gates. Relationship categorization problems may be handled more effectively using GRU architecture.

More stable gradients and quicker convergence during training are the results of properly adjusted hyperparameters (such as learning rate, batch size, and number of units). GWO assists in avoiding poor configurations that could otherwise need too many epochs, delay learning, or result in disappearing gradients. For real-time or time-sensitive applications, the model achieves optimal performance more quickly, which is essential. The batch size of Bi-GRU 64 and balanced the gradient noise including training speed.

The update gate, z_t , determines how much of the previous state's information is forgotten and what information from the new material should be added. The reset gate, called r_t for short, controls how much of the current input and the previous hidden state are ignored. This is how the cell state, reset gate, and t -th update gate are identified.

$$z_t = \sigma(W_z \cdot [h_{t-1}, x_t]) \quad (12)$$

$$r_t = \sigma(W_r \cdot [h_{t-1}, x_t]) \quad (13)$$

$$\tilde{h}_t = \tanh(w \cdot [r_{t-1} \times h_{t-1}, x_t]) \quad (14)$$

$$h_t = (1 - z_t) \times h_{t-1} + z_t \times \tilde{h}_t \quad (15)$$

where x is the current input, h_t is the new cell state, and h_{t-1} is the new memory content, which is derived from h_{t-1} .

When training a Bi-GRU model, 64 is usually the ideal batch size since it provides a realistic trade-off between model generalization and efficient processing. For the majority of real-time and resource-conscious applications, batch size 64 is the best choice since it consistently produces steady convergence, manageable training times, and strong predictive performance.

4. Result and discussion

Heart disease continues to be the leading cause of mortality in many middle-class and industrialized nations. The explanations are attributed to a variety of predispositions, including hereditary vulnerability to certain personal and professional life practices. Death prevention is significantly impacted by medical accuracy, efficiency, and early detection of heart disease. These are the feature extraction datasets that include things like treetops, cholesterol, age, and gender. Large data sets from several sources, like age, gender, cholesterol, treetops, etc., are helpful in predicting heart disease, as necessary by the medical sector. One of the fastest-growing techniques is artificial learning, which is useful in the medical area and enables the analysis of vast volumes of data from many different domains. These may be accomplished by decreasing the discrepancy between the actual and projected outcomes, which takes the role of traditional computer-based prediction modelling techniques for comprehending the intricate non-linear interactions between many variables.

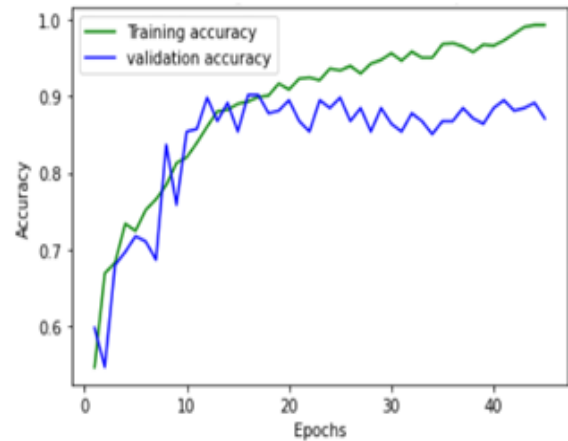


Figure 2. Accuracy of proposed heart disease

Figure 3. Losses of heart disease prediction

The loss function, which is the binary cross entropy loss function, determines the loss or inaccuracy of the model's prediction. Another purpose of early halting is to avoid the model from overfitting during training. It accomplishes this by stopping training when there is a noticeable discrepancy between the accuracy of the training and validation. Figures 2 and 3 show the model's accuracy as well as the loss curve analysis that supports the early halting. The accuracy of the proposed design initially increases linearly with the training accuracy on the validation set, as shown in Figures 2 and 3. Even with precautions, overfitting of the model always results in a gap. In order to maintain the model's generalization on the validation set and stop it from learning the noise from the training set, we have implemented early stopping. The loss curve is supported by the same reasoning as the accuracy curve. The model overfits and begins to memorize the training data and undesired noise in the training data in an attempt to perform better on the training set, which increases the loss in the validation set. Error increases as its generalization capabilities on the validations are reduced since there is less opportunity for improvement. This justifies the early halt to prevent overfitting and unnecessary computational expenses for additional model training.

Because the optimization procedure is done offline and has no effect on runtime performance, deploying a Bi-GRU model with GWO-optimized parameters in a real-time clinical decision support system takes just a small amount of processing power. A common CPU configuration with 2–4 cores, 4–8 GB of RAM, and 100 MB of storage is usually adequate for real-time inference, allowing for prediction latency of less than 100 ms. The model, which is trained to maximize accuracy and efficiency, can be used on-site or in the cloud and doesn't need a GPU unless it's doing batch or high-throughput processing.

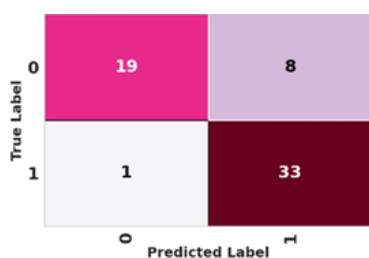
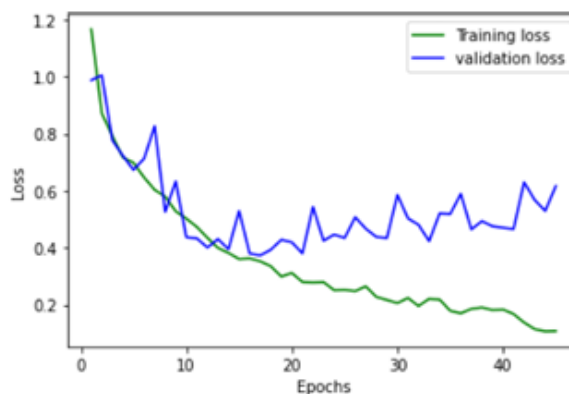


Figure 4. Confusion matrix

As seen in Figure 4, a confusion matrix is used to assess the effectiveness of the suggested heart disease prediction system, which is based on the Bi-GRU model. Patients with and without cardiac disease are distinguished by this binary classification approach. True positives (rightly predicted cases of heart disease), true negatives (rightly predicted cases of non-disease), false positives (non-disease cases wrongly predicted as disease), and false negatives (disease cases wrongly predicted as non-disease) are the four main outcomes shown in the confusion matrix. Critical assessment

criteria including accuracy, sensitivity (recall), specificity,



may be considered to these findings. The model's excellent prediction accuracy, as shown in Figure 4, validates its efficacy and dependability in detecting heart disease patients with little misclassification.

Table 1 performance analysis

Model	Sensitivity	specificity	Accuracy
LSTM	82%	87%	82%
GRU	84%	88%	85%
Bi-GRU	91%	90%	98%

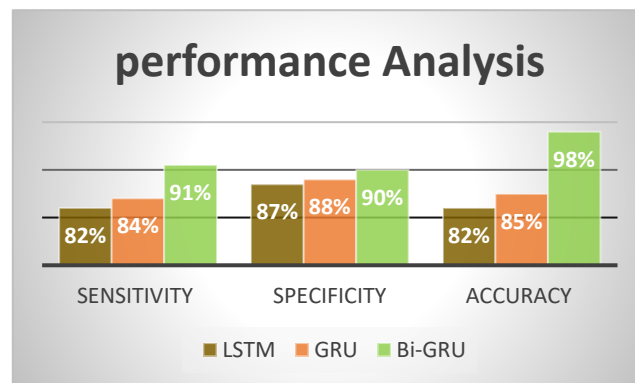


Figure 5. Performance analysis of heart disease prediction

Figure 5 shows the performance study results for the proposed Bi-GRU-based cardiovascular disease prediction model. This figure compares the key evaluation metrics necessary to determine how useful a classification model is, including accuracy, sensitivity, specificity, and accuracy. By achieving consistently high values in all performance metrics, the Bi-GRU model is shown to be robust in accurately recognizing both positive (heart disease) and negative (no disease) cases. The high specificity of this model shows that it performs well in accurately identifying cases of noncardiac disease, while its high sensitivity shows that it can successfully identify those with cardiac disease. The overall accuracy of the model demonstrates its balanced prognostic potential, making it a reliable tool for early diagnosis and clinical decision support. Figure 5 provides a clear illustration of the applicability of the Bi-GRU model to real-world heart disease prediction tasks.

5. Conclusion

This work integrates cutting-edge methods in data preparation, feature selection, hyperparameter optimization, and classification to create an efficient and trustworthy heart disease prediction model. The use of SMOTE successfully addresses data imbalance, while the hybrid feature engineering approach significantly improves feature matching and model performance. The parameters of the model can be efficiently adjusted using Gray Wolf Optimization (GWO), and the Bi-GRU classifier uses the temporal patterns of the dataset to produce exceptional predictive performance. High accuracy, specificity, and sensitivity are highlighted in the assessment findings, which confirm the resiliency of the proposed system. This integrated framework not only improves prediction accuracy, but also has potential for use in clinical decision support systems aimed at early detection of heart disease.

References

1. M. G. Tektonidou, "Cardiovascular disease risk in antiphospholipid syndrome: thrombo-inflammation and atherothrombosis," *Journal of Autoimmunity*, vol. 128, Article ID 102813, 2022.
2. I. P. Kamila, C. A. Sari, E. H. Rachmawanto, and N. R. D. Cahyo, "A Good Evaluation Based on Confusion Matrix for Lung Diseases Classification using Convolutional Neural Networks," *Advance Sustainable Science, Engineering and Technology*, vol. 6, no. 1, p. 0240102, Dec. 2023.
3. N. R. D. Cahyo, C. A. Sari, E. H. Rachmawanto, C. Jatmoko, R. R. A. Al-Jawry, and M. A. Alkhafaji, "A Comparison of Multi Class Support Vector Machine vs Deep Convolutional Neural Network for Brain Tumor Classification," in *2023 International Seminar on Application for Technology of Information and Communication (iSemantic)*, IEEE, Sep. 2023, pp. 358–363.
4. Chintan M. Bhatt, Parth Patel, Tarang Ghetia and Pier Luigi Mazzeo, "Effective Heart Disease Prediction Using Machine Learning Techniques", *Algorithms*, 16, pp. 1-13, 2023.
5. K. Arumugam, Mohd Naved, Priyanka P. Shinde, Orlando Leiva-Chauca, Antonio Huaman-Osorio, Tatiana Gonzales-Yanac, "Multiple disease prediction using Machine learning algorithms", *Materials Today: Proceedings*, Vol. 80, pp. 3682-3685, 2023.
6. Arsalan Khan, Moiz Qureshi, Muhammad Daniyal and Kassim Tawiah, "A Novel Study on Machine Learning Algorithm-Based Cardiovascular Disease Prediction", *Health & Social Care in the Community*, Vol. 2023, 2023.
7. Nadikatla Chandrasekhar and Samineni Peddakrishna, "Enhancing Heart Disease Prediction Accuracy through Machine Learning Techniques and Optimization", *Processes*, Vol. 11, pp. 1-31, 2023.
8. Rubini PE, Dr. C. A. Subasini, Dr. A. Vanitha Katharine, V. Kumaresan, S. Gowdham Kumar, T.M. Nithya, "A Cardiovascular Disease Prediction using Machine Learning Algorithms", *Annals of the Romanian Society for Cell Biology*, Vol. 25, Issue. 2, pp. 904-912, 2021.
9. Tsehay Admassu Assegie, Prasanna Kumar Rangarajan, Napa Komal Kumar, Dhamodaran Vigneswari, "An empirical study on machine learning algorithms for heart disease prediction", *IAES International Journal of Artificial Intelligence (IJ-AI)*, Vol. 11, No. 3, pp. 1066~1073, 2022.
10. Pooja Rani, Rajneesh Kumar, Nada M. O. Sid Ahmed, Anurag Jain, "A decision support system for heart disease prediction based upon machine learning", *Journal of Reliable Intelligent Environments*, Vol. 7, Issue. 3, pp.263-275, 2021.
11. Manoj Diwakar, Amrendra Tripathi, Kapil Joshi, Minakshi Memoria, Prabhishkek Singh, Neeraj kumar, "Latest trends on heart disease prediction using machine learning and image fusion", *Materials today: proceedings*, Vol. 37, pp.3213-3218, 2021.
12. Zeinab Noroozi, Azam Orooji and Leila Erfannia, "Analysing the impact of feature selection methods on machine learning algorithms for heart disease prediction", *Scientific Reports*, Vol. 13, 2023.
13. HalahA. Al-Alshaikh, Prabu P, Ramesh Chandra Poonia, Abdul Khader Jilani Saudagar, ManojYadav, Hatoon S. AlSagri & AbeerA. AlSanad, "Comprehensive evaluation and performance analysis of machine learning in heart disease prediction", *Scientific Reports*, Vol. 14, 2024.
14. Daa Salama Abdelminaam, Nada Mohamed a, Hady Wael, Abdelrahman Khaled, Adham Moataz, "MLHeartDisPrediction: Heart Disease Prediction using Machine Learning", *Journal of Computing and Communication* Vol.2, No.1, PP. 50-65, 2023.
15. Huating Sun and Jianan Pan, "Heart Disease Prediction Using Machine Learning Algorithms with Self-Measurable Physical Condition Indicators", *Journal of Data Analysis and Information Processing*, Vol. 11, pp. 1-10, 2023.
16. Debabrata Swain, Badal Parmar, Hansal Shah, Aditya Gandhi, Manas Ranjan Pradhan, Harprith Kaur and Biswaranjan Acharya, "Cardiovascular Disease Prediction using Various Machine Learning Algorithms", *Journal of Computer Science* 2022, Vol. 18, Issue. 10, 2022.
17. Rohit Bharti, Aditya Khamparia, Mohammad Shabaz, Gaurav Dhiman, Sagar Pande, Parneet Singh, "Prediction of Heart Disease Using a Combination of Machine Learning and Deep Learning", *Computational Intelligence and Neuroscience*, Vol. 2021, Issue. 1, 2021.
18. Azam Mehmood Qadri, Ali Raza, Kashif Munir, and Mubarak S. Almutairi, "Effective Feature Engineering Technique for Heart Disease Prediction with Machine Learning", *IEEE Access*, Vol. 11, pp. 56214- 56224, 2023.