

Personating GA Neural Fuzzy Hybrid System for Computing HD Probability

Rahul Kumar Jha¹, Santosh Kumar Henge^{2*}, Sanjeev Kumar Mandla³, C Menaka⁴,
Deepak Mehta⁵, Aditya Upadhyay⁶, Ashok Kumar Saini⁷, Neha Mishra⁸

School of Computer Applications, Lovely Professional University, Punjab, India¹

Associate Professor, Department of Computer Applications-Directorate of Online Education,
Manipal University Jaipur, Jaipur, Rajasthan, India^{2*}

Assistant Professor, School of CS & IT, Jain (Deemed-to-be University) Bangalore, India^{3,5}

Associate Professor, School of CS & IT, Jain (Deemed-to-be University) Bangalore, India⁴

Assistant Professor, Directorate of Online Education, Manipal University Jaipur, Jaipur, Rajasthan, India⁶

Assistant Professor, Department of Computer Science & Engineering, Manipal University Jaipur, India⁷

JECRC University, Department of Computer Science & Engineering, Jaipur, 303905, India⁸

Abstract—The cardiovascular disease (CD) is a widespread, dangerous sickness involving an excessive rate of demise that necessitates quick pioussness for care and cure. There are numerous diagnostic methods, such as angiography, available to diagnose heart disease (HD). ML is an extremely leading option for scientists for discovering prediction-based explanations for heart disease, and several machine learning algorithms are discovered to find the leading key results in community assistance. Researchers are presented with numerous conventional approaches, and various supportive algorithmic sequences formulated through the artificial neural network (NN) family, such as adaptive, convolutional, and de-convolutional NN, and various extended versions of hybrid combinations, originate with suitable outcomes. This research integrated the design and computational analysis of a unified model through a genetic algorithm-based Neural Fuzzy Hybrid System, which is formulated for CD prediction. It included a dual hybrid model to forecast CD and measure the degree of a healthy heart, as well as more precise heart attack complications. Stage 1 of the study's implications integrates the two stages and plans HD prediction using patient data. The input was processed in stages. First, the data was delivered in pre-processing mode. Next, the mRMR algorithm was used to select features. Finally, the model was trained using a variety of ML algorithms, including SVM, KNN, NB, DT, RF, LR, and NN. The results were compared, and based on those findings, the model was tuned to produce the best results. In stage 2, HA possibilities and occurrences are determined by FuzIS intelligence using data from the first stage, which includes more than 13000 pre-generated rules of fuzzy implications. These rules cover both normal-level and dangerous-level cases, and the medical parameters are integrated and tuned to produce membership functions that are then sent to the model. It is composed with the comparison of a unified system, which consists of Genetic algorithms, Neural networks, and Fuzzy Inference systems. In the experiment, gaussian MF sketched the continuous series of data, enabling the inference system to generate a good accuracy of 94% in calculating the problem probability.

Keywords—*Dickey-Fuller test case (DF-TC); HA prediction (HAP); heart rate variability (HRV); artificial based neural network (AbNN); Fuzzy Inference System (FuzIS); genetic-based algorithm (GbA); multi-objective evolutionary Fuzzy classifier*

(MOEFC); heart attack (HA); fuzzification-mode (FuzM); defuzzification-mode (De-FuzM)

I. INTRODUCTION

Cardiovascular-based disease (CD) is a widespread, dangerous sickness involving a great level of disease that necessitates quick devoutness aimed at care, medication, and cure. Angiography is one of numerous treatments available to diagnose heart disease (HD), but it is a very expensive and time-consuming process and therefore out of reach for the masses. To conquer this crisis, the best medication, an auto-altered intelligent system, is necessary to reduce root-level causes, and individuals can inhale extreme difficulty. Many scientists are involved in integrating artificial intelligence techniques, which are used to build and execute technology-based medical experimental scenarios using data mining (DM) and machine learning (ML) procedures to discover the finest results for such challenges [1]. The expansion of the artificially based neural network (AbNN) into an intimated and unified system has carried it to a distinct range, and with the progress of the selection of features along with additional supporting procedures, it has carried it to human-like forecast control.

NN is mainly structured in three layers, which are the input, hidden, and output layers. Through every layer, a neuron will be associated with other neurons in succeeding layers, with their weights calculated with the activation function and a constant value called bias added to each layer as shown in Fig. 1 [19]. The bias is a persistent value injected in the network to adjust the activation function in AbNN and improves in deciding the participation of neurons in the network based on the threshold; otherwise, the output is ignored. ReLut is principally associated in the hidden layer along with their associated values, which represent 0 to x, with an identical outcome if input is positive (+); otherwise, it produces zero as the outcome, as shown in Fig. 1 [21].

$$h = \max(0, a), \text{ where } a = Wx + b \quad (1)$$

The sigmoid function with an output limited between 0 and 1 and an S-shaped graph is mostly used in classical calculus, where probability is to be predicted as an output. Logistic and

Softmax sigmoid functions are used for output related to binary and several levels of grade classification, respectively.

$$f(x) = \frac{1}{1+e^{-x}} \quad (2)$$

The Tanh is almost similar to the sigmoid, but the only difference is that its value lies between -1 and 1. Fig. 1 explains the difference between ReLU, sigmoid, and tanh functions [29–30].

A genetic-based Algorithm (GbA) returns a fitness value for each solution based on the phenomenon that the higher the fitness value, the better the solution [22–24]. There are mainly three operations in GA: selection, crossover, and mutation. Fuzzy inference system (FuzIS) primarily undergoes four stages after obtaining input: knowledge base, fuzzification mode (FuzM), inference engine, and defuzzification mode (De-FuzM) [24], which is the graphic symbol of the location of input-output neurons at each layer of AbNN. Below, in Fig.2, there is the pictorial representation of ANFuzIS, which is structured into five layers: input, membership, FuzM, normalization, and De-FuzM. The inference system is built mostly with the Sugeno method. Artificial Neural FuzIS (ANFuzIS) combines ANN and fuzzy systems, which use the capabilities of ANN to generate fuzzy inference rules with applicable membership function implications [25]. The x and y are inputs that are passed through ANFUZIS layers starting with the membership layer as the first layer, the second layer dealing with FuzM, normalization on the third layer, and De-FuzM on the fourth and last layer, i.e., the fifth layer is the output layer as shown in Fig. 2.

This study used a genetic algorithm-based neural fuzzy hybrid system to integrate the design and computational analysis of a single model that was developed for CD prediction. It is made up of a comparison of an integrated system that uses fuzzy inference, neural networks, and genetic algorithms. In the experiment, Gaussian MF sketches of continuous data series allowed the inference system to produce a good accuracy of 94% when estimating the likelihood of a problem.

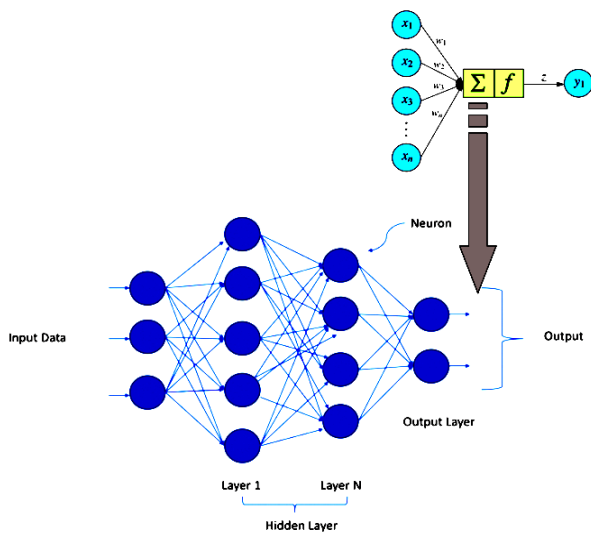


Fig. 1. AbNN with input, output, processed neurons along with activation function.

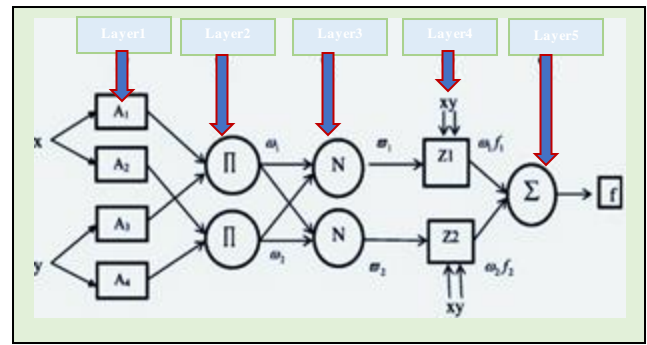


Fig. 2. ANFuzIS structure with 5-layered mode.

This article deals with the assessment and evaluation of the consequences of conventional processes and unified structures by employing distinct patterns like cross-validation with feature selection and discovering the choice of these accumulations in unified systems. Successive sections of this article have been composed with various supporting sections: Section II encompasses the related work of earlier developments of conventional AI, ML, and deep learning-based techniques. Section III contains the proposed methodology for genetic-based algorithm (GbA)-AbNN-based Fuzzy Inference System (FuzIS) Implications with Existing Dataset Parameters. It has described the methodological sequences in detail through Neural FuzIS (NFUZIS) and stage-wise execution of GbA-AbNN-based AbNN-FuzIS Implications. Section IV designated an experimental setup with System specification, Dataset, Relevance of medical parameters, and GANN algorithm with mRMR feature selection, along with experimental scenarios for determining the possibility of heart attack (HA) using Rule Creation Membership functions. Final: Section V contains details of inference.

II. RELATED WORK

Many scientists in earlier times did excellent exploration on discovering the finest possible answers for assessment of HD, benefiting from numerous conventional and progressing ML classification and regression algorithmic sequences. A few of them are Decision Trees (DT), Random Forest (RF), SVM (Support Vector), NB, LR, K-NN, ANN, DNN, GA, AGA, NFS, and many others. This list is regularly growing by generations and exhibits the attention of investigators from all spheres in the associated field. On the dataset, UCI Cleveland, Hungary, and Switzerland were favorites during liability trials and testing.

The authors, Shadman N. et al., offered a cloud-based ML scheme trained through WEKA, a Java-coded data mining tool for estimating HD [2]. The outcomes examined and the model (SVM) recorded SENS as 97.53, ACC as 97.53, and SPEC as 94.94 percentages. The authors, Amin Ul Haq et al., offered a model through DT, K-NN, RF, LR, SVM, ANN, and NB classification algorithms permitted with three selections of features such as LASSO, mRMR, and relief, which are validated by the K-Fold-concluded prevalent Cleveland HD dataset [3]. The authors, W. K. U. R. A. R.-S. T. V. M. P. P. Moloud Abdar, presented a N2Genetic-nuSVM algorithm for prediction of coronary artery disease (CAD) with better

performance compared to other classical ML techniques [4]. The Z-Alizadeh Sani HD dataset was pre-processed and applied to various traditional ML algorithms like SVM, DT, K-NN, and so on, and the model was trained. Later, GA-PSO techniques paired with 10-fold cross-validation were employed, and the results were showcased, explaining the benefit of the optimization approach in improving the model prediction. Algorithm recorded the best ACC among all experimented methods of 93.08%; greatest F1-score with 91.51%.

The authors RK. Jha et al. [5] stated an analysis to assess various categorization algorithmic sequences for estimation of HD where several conventional processes like SVM, KNN, DT-DNN, NB, and RF [17–18] were utilized to be valid selection of features over the Rapid Minor (RM) instrument to train-learn employing the Cleveland dataset from the UCI repository environment [28–33]. The authors, M. M. J. K. H. I. W. Mehrdad Agha Mohammadi [6], had proposed a unified system comprising ANFUZIS through GA and cross-validation of K-fold for estimation of HD and attained ACC as 84.43, SENS as 91.15, and SPEC as 79.16 percentage of results. The authors, M. P. K. at el., projected a hybrid adaptive genetic algorithm authorized by fuzzy logic with a rough set of features to predict HD [9] and attained ACC as 90, SENS as 91, and SPEC as 90 percent of results.

The authors, Fatma Zahra Abdeldjouad et al., projected ML training through hybrid methods: LR, MOEFC, FURIA, GFSLB, and Vote to Expect HD using Keel through Weka software [11]. Outcomes stats were analyzed, and it was concluded that out of all the other classification models, Vote outperformed ACC, SENS, and SPEC by 80.20%, 84.76%, and 74.82%, respectively. Indu Yekkala et al. projected RF, XGBoost, and NN-based models to be tuned by GA (as feature selection) to optimize (high ACC, low rate of errors) the HD estimation solution [12]. The Z-Alizadeh Sani dataset was used for training purposes. Python language with Jupyter Notebook IDE was selected for experimentation as well as for data mining and attained ACC of 93.85, SENS of 97, and SPEC of 92 percent of results. The authors, Farman Ali et al., projected a healthcare system containing collaborative DL and feature fusion for estimation of HD [13] and attained good results. The model showed an ACC of 98.5%, which is better than many other models. The authors, L.A. Demidova et al., presented an algorithm for self-tuning multi-objective GA through flexible parameter selection [14].

In this study, heart illness is initially detected using an artificial neural network (ANN) using default parameters. Then, to increase classification accuracy, a hybrid strategy combining an artificial neural network (ANN) and a genetic algorithm (GA) is suggested. Finally, the Cleveland dataset from the UCI machine learning repository is used to demonstrate the success of the suggested approach [10]. Another study combined four supporting data sets—from the VA Long Beach, Cleveland, Hungary, and Switzerland—with Multivariate dataset features [15] in order to identify the existence of cardiac disease in the patient. The output of a neural network, such as yes or no, is determined by activation functions based on neural networks. The obtained values are mapped between 0 and 1 or -1 and 1 [20]. In a different study,

the author used membership functions to predict output type constant and linear value and used two sets that could predict all eight functions [26]. The membership functions were initially combined with an artificial neural fuzzy inference system. The researchers integrated multiple data mining algorithms used in health care analytics and also paid attention to how to systematically represent analytical data in order to produce results while employing diverse data mining algorithms [27]. This cutting-edge information can be protected via a variety of techniques, including embedding, concealing, and so forth [38].

The author suggested a technique for improving classification accuracy called k-modes clustering with Huang beginning. Models like the decision tree classifier (DT), multilayer perceptron (MP), random forest (RF), and XGBoost (XGB) are employed. To improve the outcome, GridSearchCV was used to fine-tune the model's parameters. A real-world dataset of 70,000 occurrences from Kaggle [39] is used to test the suggested approach. Another study used KNN and logistic regression, two machine learning algorithms, to predict and categorize patients with heart disease. The regulation of how the model can be utilized to increase the precision of heart attack prediction in any individual was done in a very helpful way. The proposed model's ability to predict signs of having a heart illness in a specific individual by utilizing KNN and Logistic Regression was quite gratifying, and it demonstrated a high degree of accuracy in contrast to previously employed classifiers such as naive bayes, etc. [40]. Another study found that the ML technique chosen and the attributes in the dataset used to train the model had a big impact on the model's performance. The Cleveland dataset was reduced to a lower-dimensional subspace using the Jellyfish optimization algorithm to prevent overfitting (caused by the curse of dimensionality) due to the excessive number of characteristics. The Jellyfish method is versatile in finding the best features and has a high convergence speed [41].

The author developed a potential machine learning model using a variety of feature selection strategies to uncover important features in the early stages of predicting heart disease. Chi-square, ANOVA, and mutual information were three separate methods used for feature selection, and the chosen feature subsets were designated as SF1, SF2, and SF3, respectively [42]. A soft voting ensemble classifier developed by another author that used all six algorithms improved accuracy even further, yielding 93.44% accuracy for the Cleveland dataset and 95% accuracy for the IEEE Dataport dataset. On both datasets, this outperformed the logistic regression and AdaBoost classifiers [43]. Another author has combined nine machine learning classifiers into the final dataset for the prediction of heart disease, including random forest (RF), XGBoost (XGB), decision trees (CART), support vector machine (SVM), multinomial Nave Bayes (MNB), logistic regression (LR), linear discriminant analysis (LDA), AdaBoost classifier (AB), and extra trees classifier (ET) [44]. This assumption is strengthened by the esteemed machine learning algorithms performances for both classification and regression complexity [45]. To detect the presence of cardiac anomalies, the author employed ML approaches [46]. In a different study, the author starts by providing succinct

summaries of the machine learning classification approaches that are most frequently employed to identify cardiac disorders [47].

III. PROPOSED METHODOLOGY: GENETIC-BASED ALGORITHM GBA-ABNN-BASED FUZIS IMPLICATIONS WITH EXISTING DATASET PARAMETERS

Various criteria were investigated to discover the greatest attempt, pick out the finest features, and train-learn the model to obtain the highest score of accuracy. The feature selection (FS) algorithmic sequences employed to stream features for data tuning, and apart from this, validation methods like cross-validation have been used to validate the model and pick the most advantageous set of features. In the testing process, the data was deployed to assess the level of prediction accuracy.

A. Neural Fuzzy Inference System (NFuzIS)

The AbNN with FuzIS operated separately. The unified NFUZIS utilize process to discover all factors from FIS [25]. NFUZIS can correspond to exercise data produced from n-measurements of functionalities. NFUZIS comprises the fault figuring segment to advance the learning-training directions while the faults been unhurried, primarily membership sequences demarcated, then membership arrangements constraints stimulated. and inexact inputs transformed into neuron-inputs as $A(i_1 \dots i_n)$ as shown in Fig. 3, then fuzzy-type

of inputs such as fuzzy sets are generated to form neuron-inputs translated for further process [16-18] [28-33]. The experimental scenario has been described in Fig. 3.

B. Stage Wise Execution of GbA-AbNN based AbNN- FuzIS Implications

Fig. 3 determines the architecture of the proposed examination exertion, which is further split into two stages: stage 1 and stage 2, wherein stage 1 clarifies HD estimation and stage 2 describes the method to find the HA possibilities. This research reveals the unified model, which comprises AbNN motorized by GA and integrates the intellect of FuzIS. It has been explained in detail in the below sub-sections.

Stage 1: In stage 1, HD prediction has been planned through the patient’s data. It processed the input through various stages: firstly, it was delivered through the data pre-processing mode; then, the mRMR algorithm was implicated for the selection of features; then, the model was trained using diverse ML algorithms such as SVM, KNN, NB, DT, RF, LR, and NN; results were compared; and based on that, the model was tuned to get the optimal result. In the subsequent stage, an AbNN designed for training persistence produces weights through GbA. The proposed method was trained, and on each cycle of occurrence, it generated new offspring using parental classes with the help of crossover and mutation logics. The outcome is forwarded as an input to the second stage.

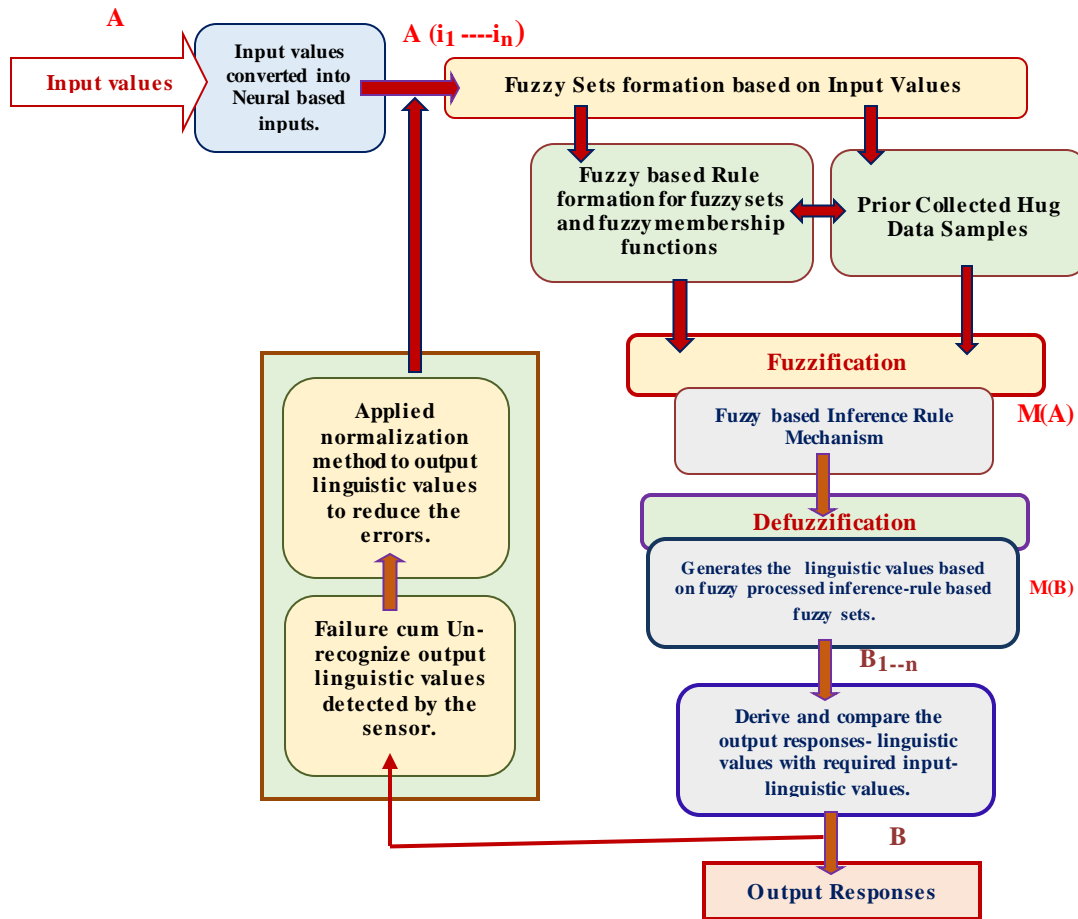


Fig. 3. Proposed NFuzIS-based methodology for HD detection.

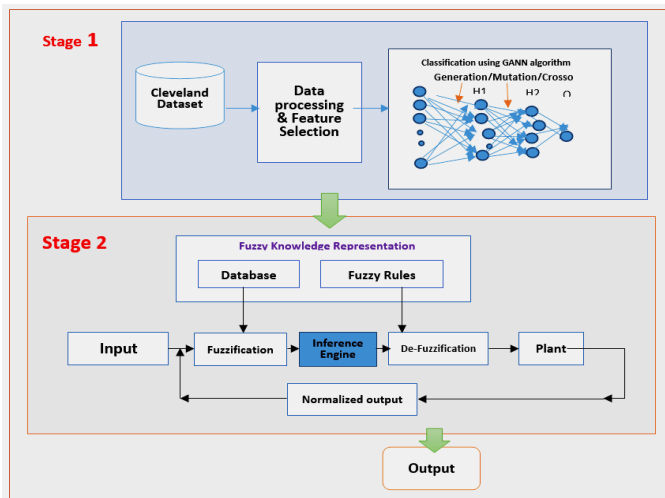


Fig. 4. Stage wise execution of GbA-AbNN based FuzIS Implications.

Stage 2: In this stage, HA possibilities and occurrences calculated through FuzIS intelligence take the input from the first stage, where more than 13000 pre-generated rules of fuzzy implications are fed into the system, which covers equally the cases such as normal-level and dangerous-level. The medical parameters are integrated and tuned to generate membership functions passed to the model as shown in Fig. 4.

In the next step, Sugeno FuzIS integrated for singleton production membership sequences with linear or constant functionalities of inputs incorporated, then the input undertaken through the FuzM process wherein data has been converted into fuzzy values with the help of fuzzy sets which then in the next step, with function $z_i = a_i x + b_i y + c_i$. Below pseudo code explains the workflow for the proposed system.

NFuzIS based Algorithm

1. Add Input for experiment
2. Apply data-processing, project the model, and add inputs, hidden along with output neurons.
3. Selection of features ← mRMR
4. Load primary population set with indiscriminate homogeneous chromosomes input samples.
5. Calculate matrix weight for population utilizing GbA and initiated model training steps
7. Replication 4 and 5 steps, record the scores.
8. Accomplish model testing with test data → {decision HD-patient / non-HD-patient}
9. Produce inference rules through precedence and medical complication based on dataset.
10. medical parameter → membership functions → fuzzy set.
11. Pass input through the FuzM process.
12. Process the fuzzy production to De-FuzM progression to acquire output crisps.
13. Test model to measure efficiency.

IV. EXPERIMENTAL SCENARIOS

The experimental setup is divided into two parts: in the first stage, the dataset has been instructed in a unified environment with GbA and ANN; the same steps were applied here as well; mRMR algorithmic sequences are simulated for the selection of accurate features; and in the second stage, FIS has been used for predicting HD.

A. System Specification

In this research, the experimental scenarios were formulated using Python libraries with the integration of more than 13000 inference rules.

B. Dataset

Cleveland, Hungarian, and VA-Long Beach datasets from the UCI container, which hold 76 features, are used in the experiment. Out of which, Cleveland's having 303 records is very popular [24]. 16 features are designated as inputs and 1 is a goal feature out of the 76 available features. Based on this input, we created one more feature named "HasHeartDisease" and filled in data 0 and 1, depending on "num" feature values.

The considered key parameters: patient (P) age, P-Gender, Level of Heart rate (LHR), balanced cholesterol, Patient Family Heart Disease History, chest pain type (CPT), Resting Blood Pressure (RBP), Level of ECG result (RestECG), Heart Status (HS), Fluoroscopy vessels count based on coloured (CA), Cigarette per day, Blood sugar level at fasting (FBS), Stress or Depression (OldPeak), Diagnosed HD (Num), Exercise induced Angina (Exang), Resting Heart Rate, and Slope for Peak-Exercise (Slope). The patients' health indicators demonstrating trial delivery between nutritious and risk levels of patients, such as patients deprived of heart disease (healthy) are 53.87% and patients with heart disease are 46.13%. The dataset is characterized into 0–4 states, where 0 represents healthy and 1-4 represents risk levels of patients, considering 1 is the least risky and 4 is the most. Fig. 5 shows the ratio of healthy patients to patients at risk. Statistics states that the dataset is normalized and has the same ratio between both; it also indicates that the dataset is ideal for experimentation.

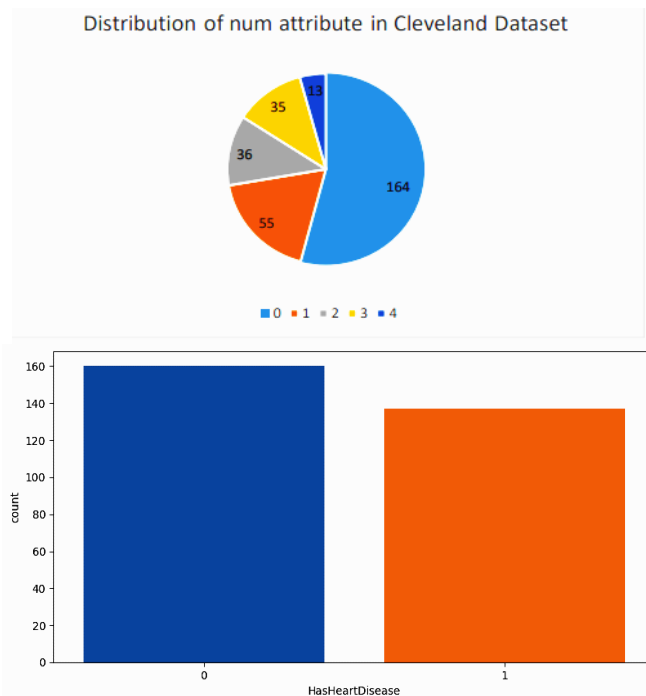


Fig. 5. Data representation of healthy and risky patients and graph showing statistics of healthy (137) and risky (160) patients.

C. Relevance of Medical Parameters

In the above sections, we have already listed the parameters that are being used in the experiments; now let’s discuss the relevance of a few of the parameters, like why they are important in predicting HD or in determining HD-affecting possibilities. The medical parameters with description and threshold to be used to calculate HD-probability are shown in Table I.

- Age: People of old age (above 65) or adults older than 40 are more likely to suffer from HA as compared to younger people or to develop coronary artery disease.
- Gender: According to available resources, the incidence of CVD in women is usually lower than that of men.
- Heart rate: An increase or decrease in heart rate should be alarming, and preventive measures should be taken.
- Blood pressure: This reflects problems in the heart and can damage the heart if the number is high for a long time.
- Blood sugar: A diabetic person is more likely to have HA. If a person has a high level of sugar, he can damage his heart too.
- ECG result: The spike created in the ECG can tell a lot about heart health, whether a person is healthy or not.
- Cholesterol: If a patient has high cholesterol, he can invite fat to deposit in the arteries and cause HA due to less delivery of blood oxygen to the heart and other parts.

TABLE I. MEDICAL PARAMETERS WITH DESCRIPTION AND THRESHOLD TO BE USED TO CALCULATE PROBABILITY

Feature Name	Description	Threshold
RestingBP_RBP	BP measured when admitted at the hospital	Systolic/diastolic (in mm Hg) Normal: < 120/80 Abnormal: 120-140/80-120 Critical: 140/120 > [33, 34]
SerumCholesterol_SCH	In mg/dl	Total Cholesterol: Normal: <200, Moderate: 200 – 239, High: 239> HDL level: Normal: 40 – 60 Low: < 40, High: 60 > LDL level: Normal: <130, Moderate: 130 – 189, Critical: 189 >
FastingBloodSugar_FBS	Blood sugar level at fasting	0 for Normal, 1 for High
RestingECGResult_RES	ECG result	0 for Normal, 1 and 2 are other types
RestingHeartRate_RHR	Heart rate at resting	0-65 – Normal, 65-85 – Average, Above 85 high,
MaxHeartRate_MHR	Max heart rate	Till 100 – Normal, 100-140 – Moderate, 100-180 – High, Above 180 - Critical
CigratePerDay_CPD	Cigrate intake per day	Higher is the intake, more is the failure risk
HeartDiseaseFamilyHistory	Heart disease history in family	0 for No, 1 for Yes
IsHeartPatient	Is patient a heart patient	0 for No, 1 for Yes

V. RESULTS AND DISCUSSION

This section included the experimental test cases and results and discussed the integration of the trained model into a web service to expose it to the public domain. In this chapter, techniques for API exposure are discussed along with the deployment process so that it can be made available for public use.

Preliminary phase: First generation prepared with an arbitrarily produced population with supporting parameters set. The network chromosome was structured as 416 neurons, 2 hidden layers, and 1 output layer with ReLU and Sigmoid activation methods and gradient descent optimization. Evaluation phase: Here, each chromosome generated in the preliminary stage is trained, and accuracy is evaluated to find a fitness score. Selection phase: The system will sort according to the fitness values, and the one with the finest fitness is selected and others are rejected. Cross-over phase: Selected parents, chromosomes A and B, undergo mating to produce new offspring. Mutation phase: After cross-over, a few of the genes are mutated on a random basis to maintain diversity in the population.

A. Experimental Scenarios for Finding the Probability of HA

To cover up the second stage, an experiment has been carried out using FuzIS, wherein input from the neural system has undergone the FuzM and De-FuzM processes via the inference engine along with the fuzzy rules and membership function to get the desired output. The very first step after injecting input into the experiment is to create rules that should be used for the rest of the experiment. For creating rules, all the included features have been analyzed, and based on that, we set the priority of the features based on the impact they can have on the heart, like sleeping heart rate, cigarette per day, blood sugar, and HD history of the family. Later, once we had everything on our plate, we followed a few approaches to create rules, keeping in mind that they should be powerful enough to support the system and should be able to provide capability to the system for finding HA possibilities in person.

$$f(x; \sigma, C) = e^{-\frac{(x-C)^2}{2\sigma^2}} \tag{3}$$

A function of membership enables the presentation of sets of fuzzy values and groups with the help of graphs. In the experiments, triangular, trapezoidal, and Gaussian MFs were used. A function of membership has been formed for a separately fuzzy set created based on all supportive, reliable, and non-dependable medical parameters. The Gaussian function: MF parameters → vector [σ c], σ → standard deviation and c → mean. The 13824 total rules have been produced and integrated to identify the HA levels and their consequences from normal levels to risk levels, and gaussian MF sketched the continuous series of data, enabling the inference system to generate a good accuracy of 94% in calculating problem probability. Below, Table II shows the parameter setup applied for GANN model training. Different combinations have been experimented with, and based on the optimal result, we noted down the parameters for the model shown.

TABLE III. HYPERPARAMETER DETAILS FOR GANN

Hyperparameter	Values
Hidden layer used	2
Neurons in each hidden layer	8, 4
Activation method for Hidden Layer	ReLu
Activation Layer for Output Layer	Sigmoid
Learning-rate	0.001
Loss Function	Binary Cross-Entropy
Epoch	2000
Batch size	100
Mutation	3%

The very first step after injecting input into the experiment is to create rules that should be used for the rest of the experiment. For creating rules, all the included features have been analyzed, and based on that feature's priority, it is set based on the impact it can have on the heart, like "resting heart rate, cigarette per day, blood sugar, heart disease history of family," and later, once we had everything on our plate, we followed a few approaches to create rules, keeping in mind that they should be powerful enough to support the system and should be able to provide capability to the system for finding the probability of a heart attack in person. The number of antecedents could be more than one based on the if-else condition, but the consequent is always one. Rule creation for the experiment is composed of two approaches:

The Cleveland dataset has been based, and after data processing, we found 282 good and 21 bad data points out of 303. A total of 126 rules were generated based on the "num" feature, which defines the risk level as 1, 2, 3, or 4. An initial study has been done and defined the level of contribution of different features, like max heart rate, which can be proved to be top-risky with the reason that if the number goes higher, it will impact the heart a lot. Therefore, the contribution of the maximum heart rate was classified into four levels: normal, medium, high, and critical. Similarly, blood sugar was also found to be a contributing factor, but its level did not have an immediate impact on health. Hence, its threshold was set to normal or medium. Other features were also evaluated, and their contribution levels were determined to assess whether a person is at risk of a heart attack or not.

A set of 13824 rules has been generated to cover both normal and risky cases. A few of the inferences are listed in Table II for reference. GANN-based performance analyzed with the 2000 epoch. It can be noticed that at the initial stage, the model was in the learning phase, and the result was not so effective, but as it underwent the epoch again and again, new offspring were generated, which helped in the learning process. This also reflects in the curve plotted in the below graph. The GNFIS-based training inferences and fitness information are included in Table II. It can be clearly seen that the learning rate was very slow and the model accuracy was also very low, but gradually, after 600 epochs, the model started giving better results.

B. Test Case Analysis through API

Once the model has been trained properly and is available for prediction, the next step, which is more important, is to find a way to package the model so that it can be available for further use in applications. And the best way is to build a web service, integrate a trained model into it, and expose it via an end point. We have moved one step ahead in the research work and utilized a very popular Python library called FastAPI for this purpose. The whole process has been divided into several stages, like creating a packaged model, unpacking the packaged model, creating a web service, exposing an end point, and starting the web service for establishing the final connection. Let's discuss all these stages one by one.

1) *Packaging trained model*: This is the first stage at which we usually package the model. Our final model is already prepared and is able to predict the disease as well as find the probability of a heart attack, so the next step is to pass this model for packaging into a system-readable bundle. For this, a very popular Python library named "joblib" has been used, which should package the model by storing all the required details in it. Once the model is packaged properly, it has been saved as a ".pkl" file.

2) *Loading/Unpackaging packaged model*: Once the model is packaged, before integrating it into a web service, it is required to load this model again in the system. For this, we have used the same Joblib Python library.

3) *Creating a web service*: Now that the model is loaded successfully into the system, it is time to create a web service, or API, and expose the endpoints. For this purpose, we used the "FastAPI" library, which is capable of performing this task.

4) *Starting the environment*: Now that there is a packaged model that can be reloaded into the system, an endpoint is also created for exposure purposes, so the last point is to start the environment and expose the API to the public. As the research work is local, the library that we are using will start the environment locally on the localhost 4000 port, and there the endpoints can be tested. The Python library that has been used is "uvicorn".

Now that the API is ready and up on localhost, the system is ready for testing (see below Fig. 6 and Fig. 7 show the request details for this endpoint).

```
{
  "Age": 60,
  "Sex": 1,
  "ChestPainType": 1,
  "RestingBP": 145,
  "SerumCholesterol": 233,
  "FastingBloodSugar": 1,
  "RestingECGResult": 2,
  "MaxHeartRate": 150,
  "ExerciseIncludedAngina": 0,
  "OldPeak": 2.3,
  "PeakExerciseSegment": 3,
  "VCA": 0,
  "ThalliumScan": 6,
  "RestingHeartRate": 70,
  "CPD": 5,
  "HDFH": 0
}
```

Fig. 6. Screen showing the API definition loaded on interface.

```

Curl
curl -X 'POST' \
  'http://127.0.0.1:4000/predictheart' \
  -H 'accept: application/json' \
  -H 'Content-Type: application/json' \
  -d '{
    "Age": 60,
    "Sex": 1,
    "ChestPainType": 1,
    "RestingBP": 145,
    "SerumCholesterol": 233,
    "FastingBloodSugar": 1,
    "RestingECGResult": 2,
    "MaxHeartRate": 150,
    "ExerciseIncludedAngina": 0,
    "OldPeak": 2.3,
    "PeakExerciseSegment": 3,
    "VCA": 0,
    "ThalliumScan": 6,
    "RestingHeartRate": 70,
    "CPD": 5,
    "HDFH": 0
  }'
Request URL
http://127.0.0.1:4000/predictheart

```

Fig. 7. Endpoint request in curl format with URL.

Total of 16 medical parameters have been passed as request to the endpoint as shown in figure.8. Below is the response for the same. In Fig. 7 and Fig. 8, response can be noticed for the given request wherein it is printed in two parts 1) predict, which predict the heart disease in patient and 2) risk percentage, which shows the probability percentage of heart attack. Here person is predicted as having heart disease and probability percentage is 57.81 which means that person has 57% chances of heart attack with current health condition which is based on give medical parameters.

```

Server response
Code    Details
200
Response body
{
  "data": {
    "Age": 60,
    "Sex": 1,
    "ChestPainType_CPT": 1,
    "RestingBP_RBP": 145,
    "SerumCholesterol_SCH": 233,
    "FastingBloodSugar_FBS": 1,
    "RestingECGResult_RES": 2,
    "MaxHeartRate_MHR": 150,
    "ExerciseIncludedAngina_EIA": 0,
    "OldPeak_OPK": 2.3,
    "PeakExerciseSegment_PES": 3,
    "VCA": 0,
    "ThalliumScan_THA": 6
  },
  "predict": "1",
  "risk_percentage": "57.81226836834753"
}
Response headers
content-length: 329
content-type: application/json
date: Wed, 04 May 2022 16:33:39 GMT
server: uvicorn

```

Fig. 8. Endpoint response for the request.

C. Test Cases

Below Table III shows few test cases along with the response using created API. It shows the request and response tested over API.

TABLE IV. API TEST CASES SHOWING REQUEST AND RESPONSE

Request	Response
<pre>{ "Age": 60, "Sex": 1, "ChestPainType": 1, "RestingBP": 145, "SerumCholesterol": 233, "FastingBloodSugar": 1, "RestingECGResult": 2, "MaxHeartRate": 150, "ExerciseIncludedAngina": 0, "OldPeak": 2.3, "PeakExerciseSegment": 3, "VCA": 0, "ThalliumScan": 6, "RestingHeartRate": 70, "CPD": 5, "HDFH": 0 }</pre>	<pre>"predict": "1", "risk_percentage": "57.81226836834753"</pre>
<pre>{ "Age": 45, "Sex": 1, "ChestPainType": 1, "RestingBP": 90, "SerumCholesterol": 200, "FastingBloodSugar": 0, "RestingECGResult": 2, "MaxHeartRate": 120, "ExerciseIncludedAngina": 0, "OldPeak": 2, "PeakExerciseSegment": 3, "VCA": 0, "ThalliumScan": 6, "RestingHeartRate": 70, "CPD": 5, "HDFH": 0 }</pre>	<pre>"predict": "1", "risk_percentage": "34.90275702665084"</pre>
<pre>{ "Age": 25, "Sex": 1, "ChestPainType": 1, "RestingBP": 90, "SerumCholesterol": 200, "FastingBloodSugar": 0, "RestingECGResult": 1, "MaxHeartRate": 120, "ExerciseIncludedAngina": 0, "OldPeak": 1, "PeakExerciseSegment": 1, "VCA": 0, "ThalliumScan": 4, "RestingHeartRate": 70, "CPD": 2, "HDFH": 0 }</pre>	<pre>"predict": "0", "risk_percentage": "34.90275702665084"</pre>

Below, Table IV and Fig. 9 show the result from GANFIS along with the comparison with similar work proposed in the past by other researchers. The result clearly shows that the proposed system outperforms with 94% accuracy.

TABLE V. COMPARING EXPERIMENTAL RESULTS WITH EXISTING STATE-OF-THE-ART RESULTS IN LITERATURE

Author and Ref	Integrated model	Method	Dataset	Result
Negar Ziasabounchi, 2014 [34]	ANFIS Based Classification Model for Heart Disease Prediction	ANFIS, GA	Cleveland dataset	92.30%
Oluwarotimi Williams Samuel et al. 2017 [7]	An integrated decision support system based on ANN and Fuzzy_AHP for heart failure risk prediction	ANN, Fuzzy_AHP	Cleveland dataset	91.10%
A.V. Senthil Kumar 2012 [35]	Diagnosis of Heart Disease using Fuzzy Resolution Mechanism	ANFIS, MATLAB	Cleveland dataset	91.83%
Zeinab Arabasadi et al. 2017 [8]	Computer aided decision making for heart disease detection using hybrid neural network-Genetic algorithm	ANN, GA	Z-Alizadeh Sani	93.85%
Kaan and Ahmet 2017 [36]	Diagnosis of heart disease using genetic algorithm based trained recurrent fuzzy neural networks	ANN-Fuzzy_AHP, GARFNN	Cleveland dataset	91.10%
G. S. G. Thippa Reddy et al. 2020 [9]	Hybrid genetic algorithm and a fuzzy logic classifier for heart disease diagnosis	GA, FL	Cleveland dataset	90%
MABushariah et al. 2014 [37]	Automatic Heart Disease Diagnosis System Based on Artificial Neural Network (ANN) and Adaptive Neuro-Fuzzy Inference Systems (ANFIS) Approaches	MLP, ANN, ANFIS, MATLAB	Cleveland dataset	87%
Proposed work, 2022	Dual Hybrid System (GANN-NFHS)	Cleveland dataset	Cleveland dataset	94%

The results in Section V demonstrated the scores based on different variance comparable model exercises with and without selection of features through mRMR on GANN. Results clearly demonstrate variance between various variances applied during model training, and they verify that performance prediction is enhanced by applying dissimilar methods according to dataset size and number of features. It has been observed that good results have been achieved with classical as well as hybrid approaches, and near 90% accuracy was recorded with the test set. There is more opportunity to record a higher score with hybrid as well as classical

approaches. An integrated system that makes use of fuzzy inference, neural networks, and genetic algorithms is compared. In the experiment, the inference system produced a good accuracy of 94% when assessing the likelihood of a problem using Gaussian MF sketches of continuous data series.

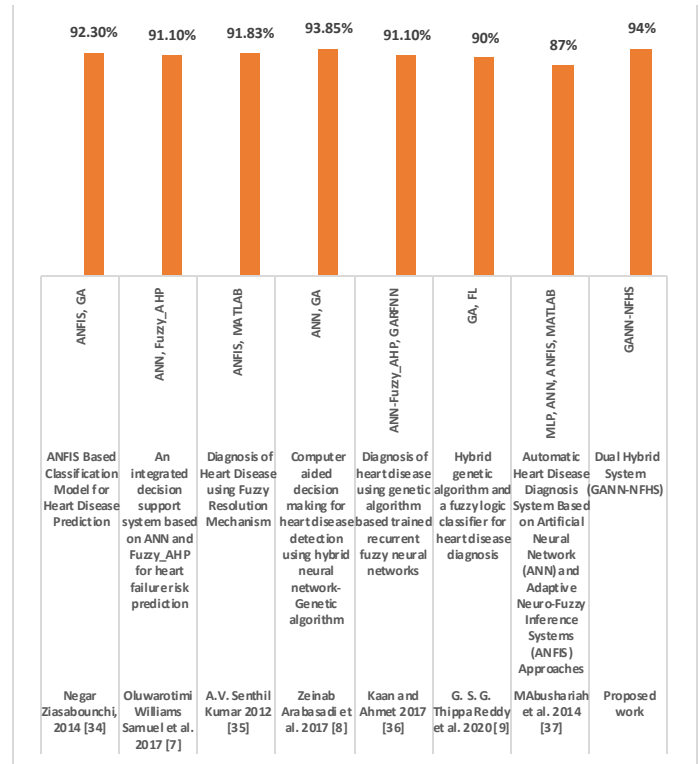


Fig. 9. Comparative analysis of experimental results with existing hybrid models.

VI. CONCLUSION

ML is an extremely leading option for scientists for discovering prediction-based explanations for heart disease, and several machine learning algorithms are discovered to find the leading key results in community assistance. Researchers are presented with numerous conventional approaches, and various supportive algorithmic sequences formulated through the artificial neural network (NN) family, such as adaptive, convolutional, and de-convolutional NN, and various extended versions of hybrid combinations, originate with suitable outcomes. This research integrated the design and computational analysis of a unified model through a genetic algorithm-based Neural Fuzzy Hybrid System, which is formulated for CD prediction. It is composed with the comparison of a unified system, which consists of Genetic algorithms, Neural networks, and Fuzzy Inference systems. In the experiment, Gaussian MF sketched the continuous series of data, enabling the inference system to generate a good accuracy of 94% in calculating the problem probability.

AUTHORS' CONTRIBUTION

Conceptualization: R.K., Jha., S.K. Henge; Methodology: R.K., Jha., S.K. Henge; Software: R.K., Jha., S.K. Henge., S.K. Mandal.; Validation: S.K. Henge., R.K., Jha.; Formal analysis: S.K. Henge, A.K. Saini., C. Menaka.; Investigation: S.K.

Henge., N. Mishra., C. Menaka.; Resources: S.K. Henge, D. Mehta.; Data curation: R.K., Jha, S.K. Mandal., A. Upadhyay.; Writing—original draft preparation, S.K. Henge, R.K., Jha; Writing—review and editing: S.K. Henge., A. Upadhyay., D. Mehta; Visualization: S.K. Henge., R.K., Jha., N. Mishra.; Supervision: S.K. Henge.

CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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