International Journal of Multidisciplinary Engineering in Current Research - IJMEC
Volume 10, Issue 6, June-2025, http://ijmec.com/, ISSN: 2456-4265

Prediction of Heart Disease Using Machine Learning

Dr. K AshokKumar, Bobbilla Aparna, Govindolla Karthika, Munugala Kavyasree

[1]Assistant Professor,ECE Department Bhoj Reddy Engineering College for Women

[2,3,4]B. Tech Students, Department Of Ece, Bhoj Reddy Engineering College For Women, India.

ABSTRACT

Heart disease is one of the biggest causes of death around the world. In today's fast-paced life, it has become a major concern, with one person losing their life to heart-related issues every minute. Identifying heart disease early can save lives, but it's not always easy. This is where machine learning can make a big difference. In this project, we have developed a system that predicts the chances of heart disease at an early stage using machine learning. The system uses data from past patients, such as medical parameters and health records, to make predictions for new cases. We used a machine learning method called the Random Forest algorithm, which processes patient data stored in a CSV file. By analyzing this data, the system can calculate how likely someone is to have heart disease. This approach to provide accurate results quickly. It's also flexible and has a high success rate. With this system, healthcare providers can detect heart disease early, helping prevent severe outcomes and saving lives. The prediction of heart diseases using electrocardiogram (ECG) data, employing bio- inspired optimization algorithms such as Genetic Algorithm, Bat Algorithm, and Bee Algorithm. These techniques are utilized to perform effective feature selection, thereby enhancing the accuracy and efficiency of classification models. The system is developed using Python and incorporates a user-friendly interface to facilitate data input, algorithm execution, and result visualization.

1-INTRODUCTION

Heart disease is a major global health issue, affecting millions and remaining one of the top causes of death, particularly in countries like the United States. According to the European Society of Cardiology, around 26 million people suffer from heart disease, with 3.6 million new cases emerging each year. Traditional diagnostic methods rely on clinical tests, physical examination, and patient history, which are often time-consuming, costly, and require medical expertise. These limitations highlight the need for more efficient solutions. Machine learning (ML) offers a powerful, data-driven approach to predict heart disease early by analyzing large volumes of patient data. This study focuses on building an ML-based model that uses advanced classification techniques and feature selection algorithms to improve diagnostic accuracy and efficiency.

Existing System

Current heart disease prediction systems rely on machine learning techniques such as Decision Tree, K-Nearest Neighbour (KNN), Adaptive Boost, and K-Means. These models often use all available features without filtering irrelevant ones, which can reduce accuracy and increase computational time. Data preprocessing is typically done by replacing missing values with average values, followed by an 80-20 train-test split. While Decision Tree uses information gain and KNN relies on Euclidean distance, other methods like Vector Quantization often result in lower prediction accuracy. Manual analysis also increases the risk of error and lacks automation.

Proposed System

The proposed system employs the Random Forest Algorithm for heart disease prediction, which aggregates results from multiple decision trees to improve classification accuracy and reduce overfitting. Patient data stored in a CSV file is analyzed, and predictions are made based on averaged outcomes from the trees. Additionally, three bio-inspired feature optimization algorithms Genetic Algorithm, Bat Algorithm, and Bee Algorithm are used to select the most relevant features. This approach reduces computational load, improves model accuracy, and ensures better reliability. Although the Ant Colony Optimization technique was considered, it was not used as it is more suitable for path-finding problems like the Traveling Salesman Problem.

2-SYSTEM DESIGN

System Architecture

The heart disease prediction system includes several key components. First, medical datasets are collected from reliable sources like the UCI Repository or hospital records, containing essential patient health details. The data undergoes preprocessing to handle missing values, outliers, and inconsistencies this includes encoding categorical data and normalizing numerical features. Feature selection is then performed to identify the most impactful variables, such as age, blood pressure, cholesterol, and ECG results, using correlation analysis or domain knowledge. The data is split into training (80%) and testing (20%) sets. The Random Forest algorithm is used for model training, building multiple decision trees for improved prediction. The final model is evaluated using metrics like accuracy, precision, recall, F1-score, and ROC-AUC to ensure it performs reliably on new data.

Workflow

The system workflow for heart disease prediction begins with data preprocessing to ensure the dataset's quality and consistency. This involves handling missing values, removing outliers, encoding categorical variables, and normalizing feature values using techniques like standardization or min- max scaling. Once prepared, the Random Forest algorithm is applied. This ensemble method builds multiple decision trees and combines their outputs to enhance prediction accuracy and reduce overfitting, effectively capturing complex, nonlinear patterns in the data.

After training, the model's performance is evaluated using various metrics. Accuracy reflects overall correctness, precision shows how well false positives are avoided, and recall assesses the model's ability to identify actual positives crucial in medical contexts. The F1-score balances precision and recall, especially in imbalanced datasets, while the ROC-AUC score indicates how well the model distinguishes between classes. These steps together ensure a reliable and efficient heart disease prediction system. The model can assist healthcare professionals in early diagnosis and treatment planning. It also demonstrates how machine learning can support decision-making in critical health applications.

Architectural Diagram

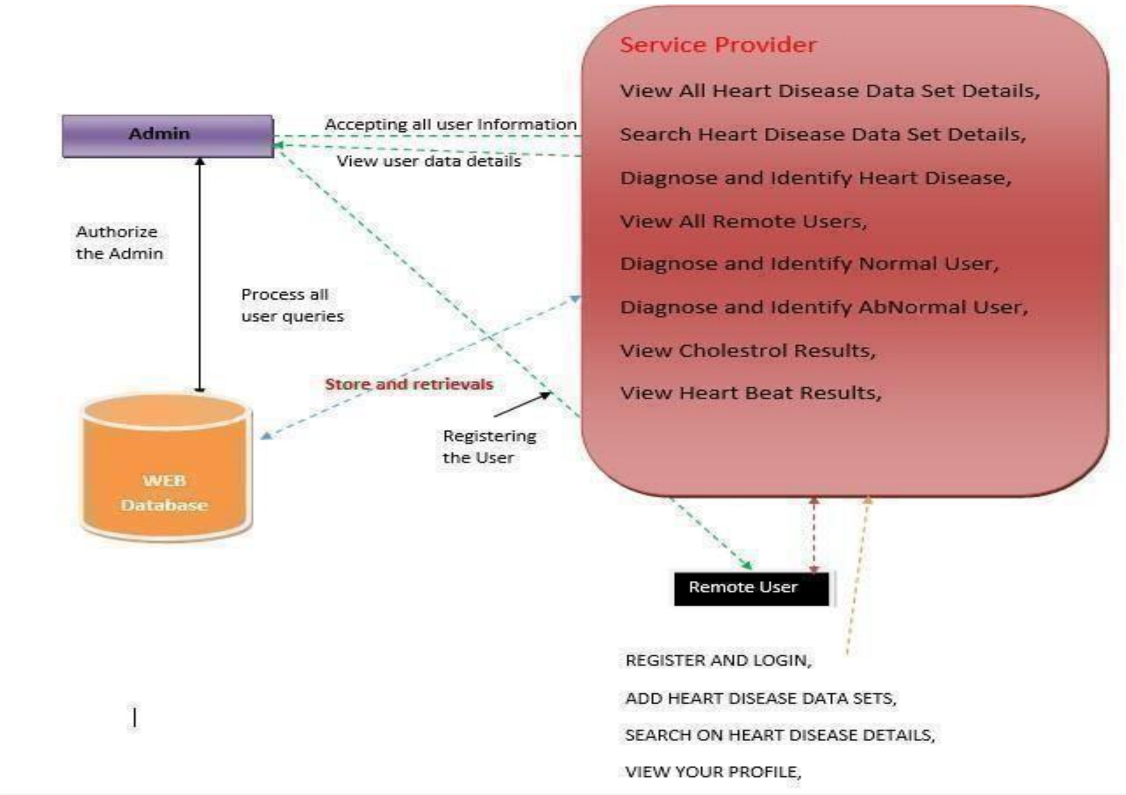


Fig2.1 Architectural Diagram

The architectural design of the system consists of several key components. The User Interface includes two modules: the Remote User Module, which allows users to log in, input patient data, and view results, and the Service Provider Module, which facilitates dataset management and system updates. The Database stores historical datasets in CSV format and maintains user credentials and logs to ensure secure access. It also supports scalability for integrating new patient records and features over time. The Processing Module employs the Random Forest algorithm for predictive analysis, extracting relevant features such as cholesterol, age, gender, and blood pressure to perform accurate and efficient analysis. This module ensures robustness and minimizes overfitting through ensemble learning techniques. the Output Module displays the risk levels of heart disease (low, medium, high) and presents the results in a user-friendly graphical interface. Additionally, the output interface supports data visualization tools like charts and graphs to enhance interpretability for end- users. This architecture ensures efficient data management& secure.

Flowcharts of Remote User and Service Provider

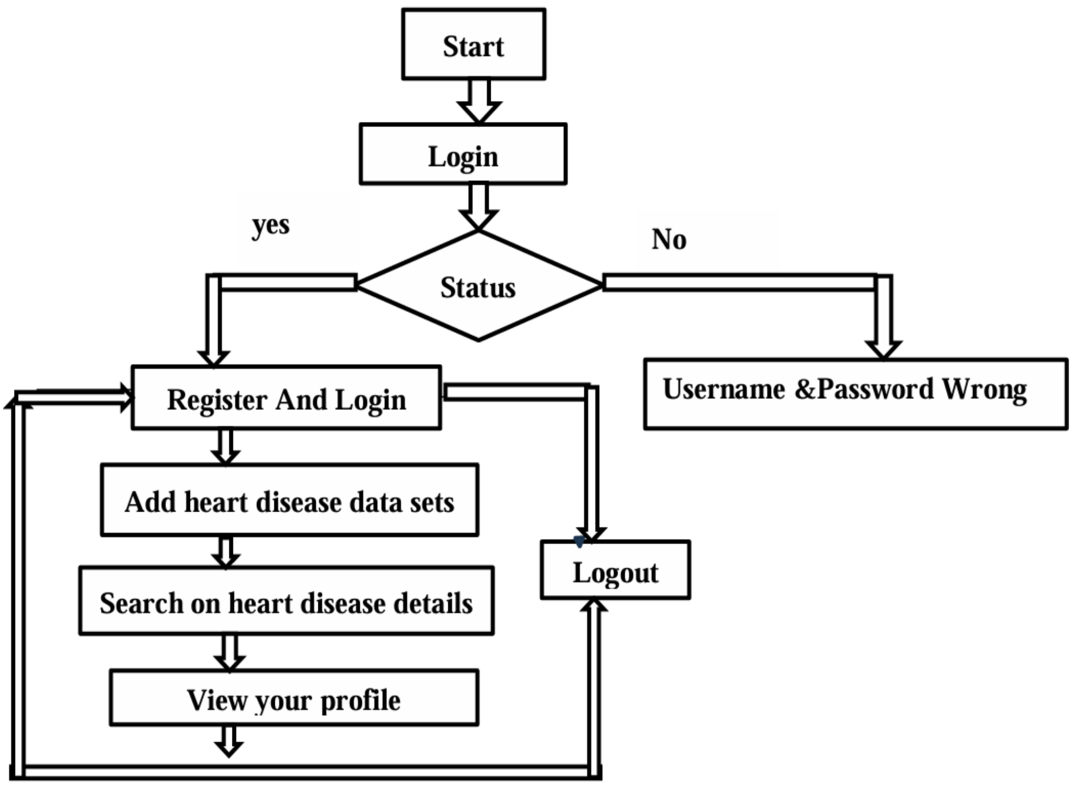


Fig 2.2 Remote User

2-FUNCTIONALDESIGN &OVERVIEW OF PYTHON

Functional Design

The functional design of the project focuses on how the system behaves when different user actions are performed. It describes the functions the system must perform to meet the project's goals namely, predicting the stage of heart disease using bio-inspired algorithms after selecting the most relevant features from a dataset. Each function plays a crucial role in the overall workflow of the application and contributes to the effectiveness of the system.

1. Uploading the Heart Disease Dataset: The first function is to allow users to upload the heart disease dataset from their system. This dataset is a CSV file containing 14 features such as age, sex, cholesterol level, chest pain type, ECG results, and others, along with class labels indicating disease stage. When the user clicks on the “Upload Heart Disease” button, the system loads the data and displays a preview for confirmation. This function ensures that the correct dataset is used before applying any algorithm.

2. Feature Optimization Using Genetic Algorithm: Once the dataset is loaded, the user can run the Genetic Algorithm (GA). This function performs feature selection by evaluating different combinations of features and selecting the set that gives the highest prediction accuracy. During execution, a black console is displayed showing the selection process, and empty windows may briefly

appear as the algorithm iterates. After completion, the function displays accuracy, precision, and recall values for the selected feature set using GA.

3. Feature Optimization Using Bat Algorithm: This function allows the user to run the Bat Algorithm, another bio-inspired optimization method. Like GA, it is applied to the dataset to select the most effective subset of features. Once the Bat Algorithm finishes processing, it displays the accuracy, helping the user evaluate its performance in comparison to the other algorithms. This function is useful for testing the efficiency of different optimization strategies on the same data.

Data Flow Diagram

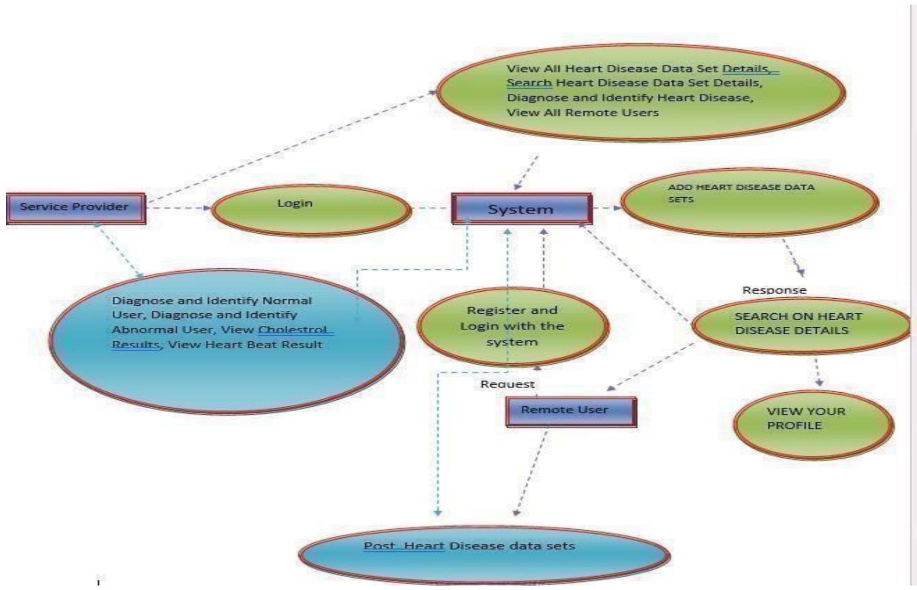


Fig 3.1 Data flow diagram

The diagram provided represents the process flow of a system designed to predict heart disease using machine learning. Below is an explanation of the elements and their relationships:

Implementation Details & Testing

Software Requirements

The following software is required to implement the heart disease prediction system:

1. Operating System: Windows 7 Ultimate or higher is recommended for running the software and ensuring compatibility with the development tools and libraries.

2. Programming Language: Python is chosen for its ease of use and extensive support for machine learning and data analysis tasks. Python provides access to powerful libraries and frameworks needed for data processing and machine learning model development.

Hardware Requirements

To run the heart disease prediction system efficiently, the following hardware specifications are recommended:

- Processor: Pentium IV or higher ensures smooth processing for data analysis and model execution.
- RAM: 4 GB (minimum) is requiredto handle dataset manipulation, model training, and visualization without significant lag.
- Hard Disk: 20 GB of free space ensures there is enough room for storing datasets, model outputs,

logs, and other project files.

- Monitor: SVGA(Standard VGA) monitor for clear display of results, graphs, and logs. Higher resolution monitors will improve the user experience.

Dataset

The dataset used for training and testing the heart disease prediction system comes from the UCI Heart Disease dataset, which is publicly available. It consists of 303 records and 14 attributes that describe various health parameters related to heart disease.

Attributes:

- Age: Age of the patient.
- Sex: Gender of the patient (male or female).
- Chest pain type: Categorical variable indicating the type of chest pain.
- Resting blood pressure: Blood pressure measurement when the patient is at rest.
- Cholesterol levels: Serum cholesterolconcentration.

3-MODEL DEVELOPMENT AND TESTING

The following steps were taken in the development and testing of the heart disease prediction model:

- Dataset Splitting: The dataset was divided into two subsets: one for training the model (80% of the data) and another for testing its performance (20% of the data). This ensures that the model is evaluated on unseen data, preventing overfitting and providing an unbiased assessment of its accuracy.
- Random Forest Algorithm: The Random Forest algorithm was selected as the machine learning model for predicting heart disease. This algorithm is an ensemble method that builds multiple decision trees during training and outputs the class that is the mode of the classes from individual trees. Random Forest is preferred due to its ability to handle large datasets and its robustness to overfitting.
- Hyperparameter Tuning: To optimize the performance of the Random Forest model, hyperparameter tuning was conducted. This includes adjusting parameters like: Number of trees in the forest, Maximum depth of each tree to control complexity, Minimum samples split to avoid overfitting by limiting the number of samples required to split a node, Minimum samples leaf to ensure that each leaf node contains a sufficient number of samples.

SystemTesting

Testing aims to discover errors and ensure software meets requirements. Various testing types are used to validate components and the entire system. Testing is a crucial stage in the development lifecycle, serving as a quality control mechanism to identify and resolve software errors before deployment. Its primary goal is to ensure that the application functions as intended and aligns with the specified requirements. A robust testing process involves multiple testing levels, from verifying individual units to assessing the complete behavior of the application under various conditions. This chapter outlines different testing types, methodologies, data preparation strategies, and the comprehensive testing strategy adopted in the project.

Types of Tests Employed

To ensure comprehensive evaluation, several testing types are applied during different phases of development. These include:

1. Unit Testing: Unit testing involves verifying the smallest parts of the software—individual functions, methods, or classes. Each unit is tested in isolation to confirm that it performs correctly and returns the expected output for various inputs. This phase focuses on logical correctness, internal decision-making, and handling of edge cases or incorrect data entries. For instance, if there is a function to calculate the Body Mass Index (BMI) from height and weight, it should return accurate values for typical and

extreme cases alike .Key aspects tested during this phase: Field validations (e.g., age should not be negative). Component output for boundary inputs.

2. **Integration Testing**: Integration testing evaluates the interactions between combined modules or components. This process ensures that the individual units, when integrated, work together harmoniously without errors in data flow or control logic. Integration issues such as incorrect API calls, broken linkages between GUI and backend logic, or data misinterpretation are identified and fixed. Approaches used :Top-Down Integration: Begins with higher-level modules and tests downward using "stubs" (dummy modules).Bottom-Up Integration: Starts with low-level components and integrates upward using "drivers" (test harnesses).This testing validates real-world execution paths through the full workflow such as uploading a dataset, preprocessing, running prediction models, and visualizing the output.
3. **Functional Testing**: Functional testing is a black-box approach that ensures the software behaves according to specified functional requirements. It tests whether each feature performs its intended function. Inputs are given, and outputs are checked against expected results, without knowledge of internal code logic. Key test scenarios: Uploading CSV datasets and verifying format compatibility. Ensuring proper execution of selected bio-inspired algorithms (GA, BAT, BEE).Correct display of metrics such as accuracy, recall, and precision.

4-SYSTEM IMPLEMENTATION AND EVALUATION

Dataset Description

The heart disease dataset used in this project includes 14 input features and one output class, which represents the stage of heart disease. These features were carefully chosen based on widely recognized clinical indicators that significantly impact cardiovascular health. The input features are as follows: the patient's age in years, sex (male or female), and chest pain type, which can be categorized as typical angina, atypical angina, non-anginal pain, or asymptomatic. Resting blood pressure is measured in mm Hg, while cholesterol refers to the serum cholesterol level in mg/dl. The fasting blood sugar feature indicates whether the fasting blood sugar level is greater than 120 mg/dl and is represented as a binary value. Resting ECG captures the resting electrocardiographic results, and maximum heart rate achieved records the peak heart rate during exercise. The dataset also includes exercise-induced angina (yes or no), ST depression induced by exercise compared to rest, and the slope of the ST segment during peak exercise. Another important feature is the number of major vessels colored by fluoroscopy, ranging from 0 to 3. The thalassemia status is categorized as normal, fixed defect, or reversible defect. Additionally, the dataset may include other clinical indicators relevant to the patient's overall health.

The dataset is stored in CSV format, which allows for easy handling and seamless integration with various Python libraries. To facilitate the training and evaluation of machine learning models, the dataset is divided into two subsets. The training set includes both the input features and their corresponding class labels, and it is used to train the predictive models. In contrast, the test set contains only the input features without the associated class labels, serving as a basis for assessing the model’s ability to make accurate predictions on previously unseen data. This structured approach ensures that the model learns effectively from known data while being tested on new, unlabelled data to evaluate its generalization performance.

Data Preprocessing

Raw medical data often contains noise, inconsistencies, or missing values, which can negatively impact the performance of machine learning models. To ensure the quality and reliability of the input data, several preprocessing steps were undertaken. Data cleaning was performed by handling missing values either by removing incomplete records or imputing them using methods such as mean or median substitution, or predictive imputation. Additionally, outliers were identified and treated to avoid skewed model outcomes. Normalization was applied to address the issue of varying feature scales, such as between age and cholesterol levels. This process scaled all features to a common range, typically between 0 and 1, which is especially beneficial for algorithms that rely on distance metrics. Categorical encoding was used to convert non-numeric features, such as chest pain type and thalassemia status, into numerical formats using techniques like one-hot encoding or label encoding, ensuring compatibility with machine learning algorithms. Finally, feature balancing was considered by analyzing the distribution of class labels. In cases where significant class imbalance was detected, strategies like oversampling minority classes or under sampling majority classes were explored to promote fairness and enhance predictive accuracy.

Genetic Algorithm:

The Genetic Algorithm (GA) is inspired by the principles of natural selection and genetics. It works by evolving a population of feature subsets through genetic operations such as selection, crossover, and mutation. A fitness function, typically based on classification accuracy, evaluates each subset, and the best-performing subsets are passed on to the next generation, gradually converging towards an optimal solution.

BAT Algorithm:

The BAT Algorithm, modeled after the echolocation behavior of bats, dynamically balances exploration and exploitation. By adjusting parameters such as pulse emission rate and loudness, the algorithm efficiently searches the solution space to converge on an optimal set of features.

BEE Algorithm:

The BEE Algorithm mimics the foraging behavior of honey bees. It involves scout bees exploring the feature space, while employed bees focus on refining promising feature subsets. This division of labor ensures a thorough search and optimization process. Each of these algorithms ultimately outputs a reduced and optimized set of features, eliminating redundant or irrelevant attributes. This refined feature set improves classifier performance, ensuring that the model is trained on the most informative data while avoiding confusion caused by unnecessary variables

5-WORKING OF BIO-INSPIRED ALGORITHMS

Bio-inspired algorithms are computational techniques inspired by natural biological processes such as evolution, the behavior of animals, and the principles of natural selection. These algorithms mimic how living organisms adapt and make decisions in complex environments. They are especially useful in solving optimization problems, where traditional methods may struggle due to the large size or complexity of the data. three bio-inspired algorithms Genetic Algorithm (GA), BAT Algorithm, and BEE Algorithm were implemented for two main purposes: feature selection and classification in predicting heart disease. Feature selection involves choosing the most important and relevant data points (features) from a large dataset. This step is crucial because using unnecessary or irrelevant features can reduce the performance and accuracy of prediction models. These bio-inspired algorithms help in efficiently scanning through vast amounts of medical data (such as ECG readings or patient parameters) to find patterns and relationships that are most indicative of heart disease. Once the best features are selected, the algorithms assist in classifying whether a patient is at risk of heart disease or not.

Genetic Algorithm (GA)

The Genetic Algorithm (GA) is inspired by the principles of natural selection and genetics, where the strongest individuals—those best adapted to their environment are more likely to survive and reproduce. Over successive generations, this process leads to improved populations. GA applies similar principles to problem-solving by evolving a population of possible solutions through operations like selection, crossover (recombination), and mutation. The Genetic Algorithm is employed to optimize feature selection from the heart disease dataset. Each individual in the population represents a unique combination of features (for example, age, blood pressure, cholesterol levels, etc.). These combinations are evaluated based on their classification performance, typically using a machine learning classifier like decision trees or SVMs. The better a feature combination performs in correctlypredicting heart disease, the higher its fitness score. Through iterative processes:

- Selectionpicks the best-performing combinations,
- Crossover mixes themto explore new possibilities,
- Mutation introduces slight randomchanges to maintain diversityand avoid localoptima.

By the end of multiple generations, GA converges on an optimal or near-optimal subset of features, which are then used to train a more accurate and efficient classification model. This not only improves prediction accuracy but also reduces the dimensionalityofthe data, speeding up computationand enhancing interpretability.

Working Procedure:

The process begins with a randomly generated population of feature sets, where each set represents a possible combination of features from the heart disease dataset. Each individual is then evaluated using a fitness function, which measures the classification accuracy achieved when that feature set is used to train a model. Based on these fitness scores, the algorithm applies genetic operations: selection chooses the best-performing feature sets, crossover combines pairs of these sets to create new offspring by mixing their features, and mutation introduces small random changes to maintain diversity and explore new possibilities. This cycle of evaluation and genetic operations is repeated over multiple generations, allowing the population to progressively improve. Eventually, the algorithm converges to an optimal or near-optimal feature set that maximizes classification accuracy while minimizing redundant or irrelevant features.

Performance Metrics: Accuracy: 91.6%

BAT Algorithm

The BAT Algorithm is inspired by how bats use echolocation to locate prey and navigate. In this algorithm, each bat represents a potential solution to the problem. These bats "fly" through the solution space by adjusting their position, velocity, frequency, and loudness which control how they explore and exploit the search area. This balance allows the algorithm to perform both a global search (exploring new areas) and a local search (refining current solutions), helping it avoid getting stuck in

International Journal of Multidisciplinary Engineering in Current Research - IJMEC
Volume 10, Issue 6, June-2025, http://ijmec.com/, ISSN: 2456-4265

suboptimal solutions and improving the chances of finding the best overall answer.

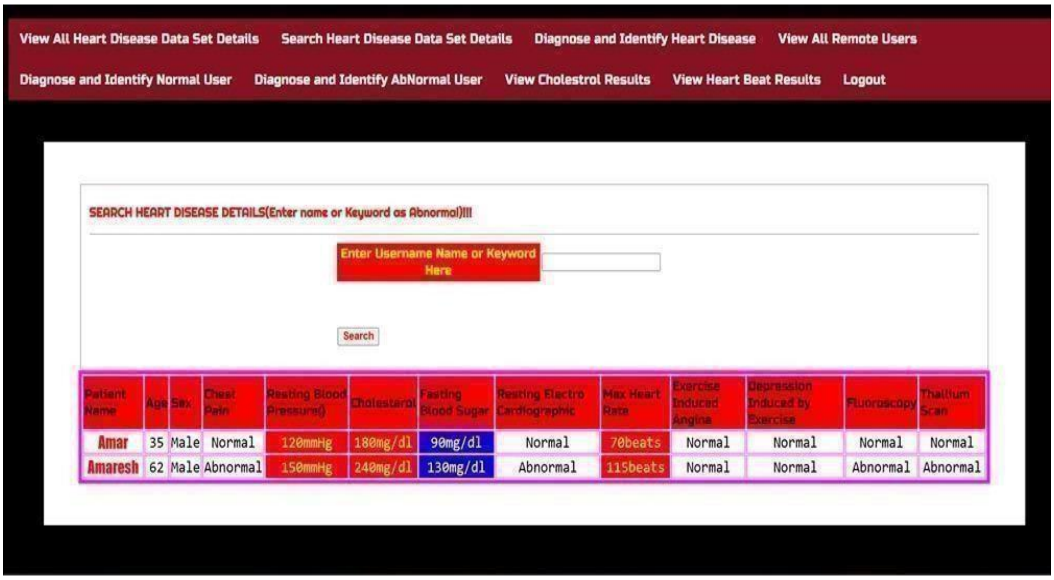
6-OUTPUT INTERPRETATION

The model classifies the output into two categories:

Normal: The prediction indicates that the patient is unlikely to have heart disease. This outcome suggests that the risk level for the individual is low, based on the input features.

Abnormal: The prediction indicates that the patient is at risk of having heart disease, meaning the model has detected patterns in the data that are typically associated with cardiovascular conditions.

Stage 1 output



Patient Name	Age	Sex	Chest Pain	Resting Blood Pressure()	Cholesterol	Fasting Blood Sugar	Resting Electro Cardiographic	Max Heart Rate	Exercise Induced Angina	Depression Induced by Exercise	Fluoroscopy	Thallium Scan
Amar	35	Male	Normal	120mmHg	180mg/dl	90mg/dl	Normal	70beats	Normal	Normal	Normal	Normal
Amaresh	62	Male	Abnormal	150mmHg	240mg/dl	130mg/dl	Abnormal	115beats	Normal	Normal	Abnormal	Abnormal

Fig 1 Heart Disease Diagnosis System Interface

Patient Name	Age	Sex	Chest Pain	Resting Blood Pressure(mmHg)	Cholesterol(mg/dl)	Fasting Blood Sugar(mg/dl)	Resting Electro Cardiographic	Max Heart Rate(beats)	Exercise Induced Angina	Depression Induced by Exercise	Fluoroscopy	Thallium Scan
Amar	35	Male	Normal	120	180	90	Normal	70	Normal	Normal	Normal	Normal
Ganesh	40	Male	Abnormal	180	220	120	Abnormal	110	Abnormal	Normal	Normal	Normal
Govind	45	Male	Normal	120	190	80	Normal	80	Normal	Normal	Normal	Normal
Raja	55	Male	Normal	120	170	90	Normal	76	Normal	Normal	Normal	Normal
Mala	34	Female	Normal	120	180	87	Normal	80	Normal	Normal	Normal	Normal
Roja	38	Female	Normal	125	230	125	Abnormal	115	Normal	Normal	Abnormal	Abnormal
Ramesh	61	Male	Abnormal	160	250	130	Abnormal	115	Normal	Normal	Abnormal	Abnormal
Ranga	65	Male	Abnormal	155	245	128	Abnormal	110	Normal	Normal	Abnormal	Abnormal
Sugumar	70	Male	Abnormal	165	250	135	Abnormal	115	Normal	Normal	Abnormal	Abnormal
Suresh	50	Male	Normal	120	185	91	Normal	85	Normal	Normal	Normal	Normal
Amala	55	Female	Normal	120	170	90	Normal	76	Normal	Normal	Normal	Normal
Rakshith	40	Male	Abnormal	180	220	120	Abnormal	110	Abnormal	Normal	Normal	Normal
Amaresh	62	Male	Abnormal	150	240	130	Abnormal	115	Normal	Normal	Abnormal	Abnormal
Kumari	78	Female	Normal	125	230	125	Abnormal	115	Normal	Normal	Abnormal	Abnormal

Fig 2 Heart Disease Patient Data Upload & Overview

Stage 2 output

To runthis project double click on ‘run.bat’ file to get below screen

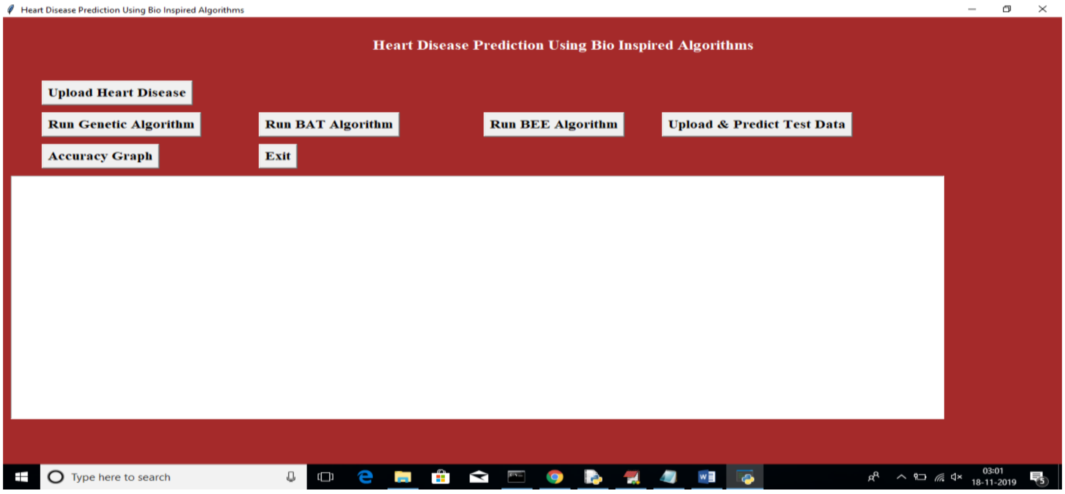


Fig 3 Heart Disease Prediction – Algorithm Execution Interface

In above screen click on 'Upload Heart Disease' button and upload heart disease dataset. See below screen

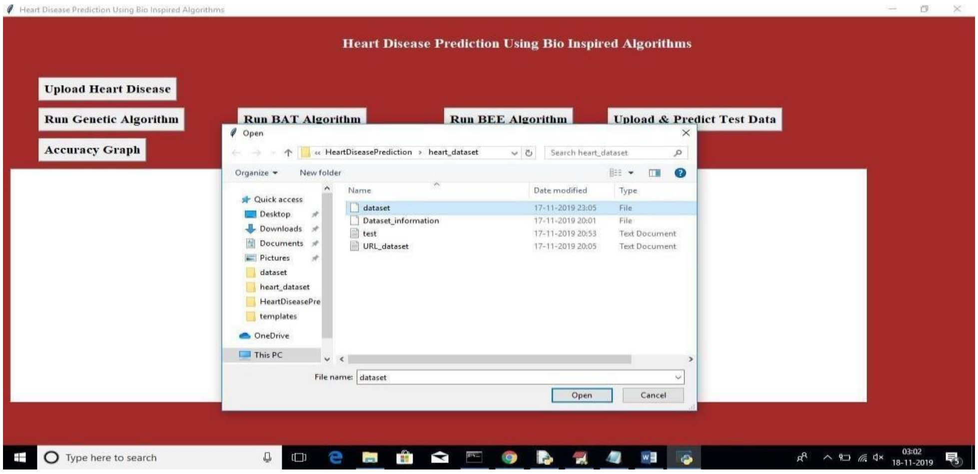


Fig 4 Heart Disease Prediction -Dataset Upload Interface In above screen uploading dataset file, after uploading will get below screen

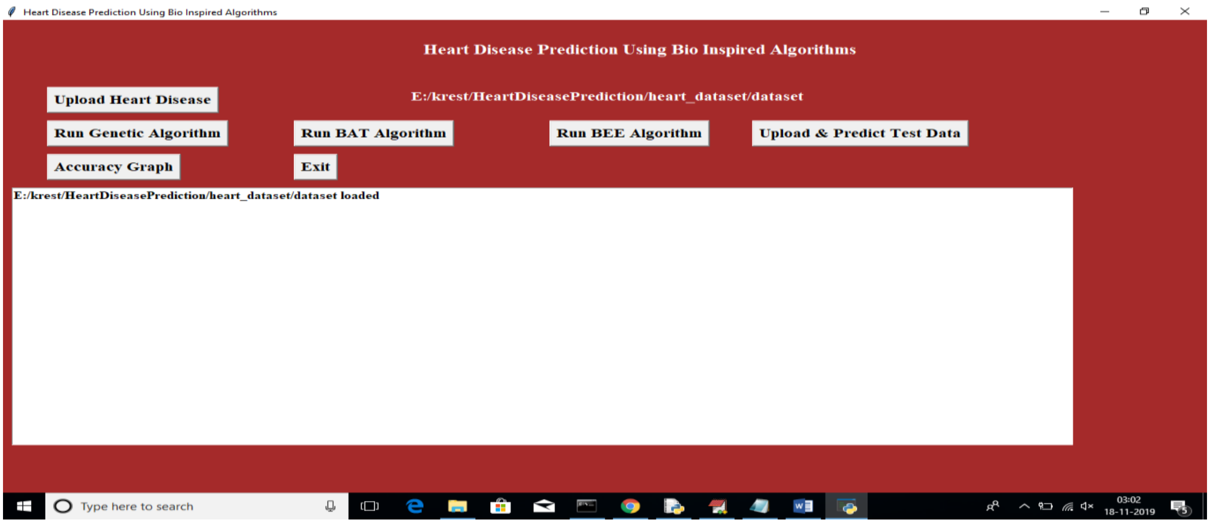


Fig 5 Dataset Successfully Uploaded for Heart Disease Prediction

Now click on 'Run Genetic Algorithm' button to run genetic algorithm on dataset and to get its accuracy details.

While running this algorithm u can see black console to see feature selection process, while running it will open empty windows, u just close all those empty windows except current window

Fig 6 Genetic Algorithm Results for Heart Disease Prediction

In above screen for GA accuracy, precision and recall we got 100% result. Now click on 'Run Bat' algorithm button to get its accuracy

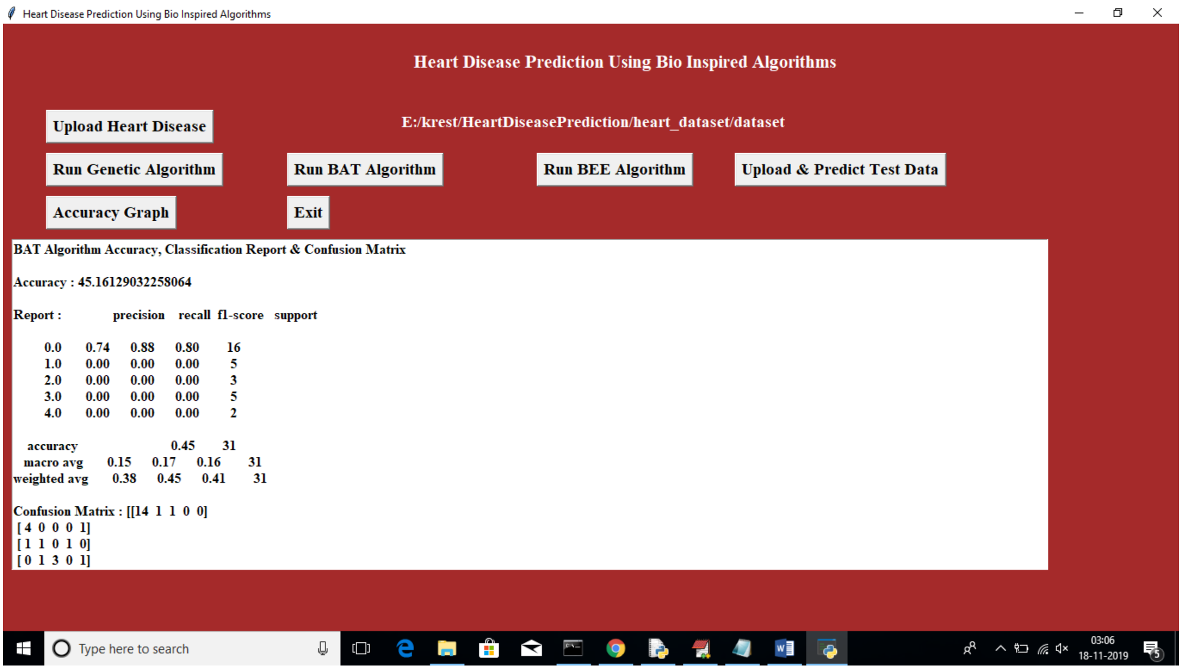


Fig 7 BAT Algorithm Results for Heart Disease Prediction

7-CONCLUSION

In Conclusion, this project effectively demonstrates the integration of bio-inspired algorithms Genetic, Bat, and Bee and machine learning techniques, particularly the Random Forest model, for accurate heart disease prediction. Among the bio-inspired methods, the Genetic Algorithm proved to be the most effective, enhancing prediction accuracy through optimized feature selection and reducing unnecessary data. Meanwhile, the Random Forest model provided reliable results based on key medical indicators such as cholesterol, blood pressure, and age, supporting early diagnosis and aiding healthcare professionals in identifying high-risk patients.

The use of advanced data processing techniques ensures scalability, automation, and efficiency, making the system a valuable tool in modern healthcare workflows. This approach not only accelerates diagnosis but also highlights how nature-inspired computing can contribute meaningfully to medical decision-making. However, for wider adoption, challenges such as data dependency, model interpretability, and privacy concerns must be addressed. Future enhancements, including the integration of IoT devices, adoption of deep learning methods, and inclusion of more diverse datasets, could further strengthen the system. With continuous improvement, this predictive model holds significant potential to combat heart disease, improve clinical outcomes, and ultimately save lives.

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