Neutrosophic Systems with Applications, Vol. 10, 2023
https://doi.org/10.61356/j.nswa.2023.75

Heart Disease Prediction under Machine Learning and Association Rules under Neutrosophic Environment

Ahmed A. El-Douh [1], SongFeng Lu [2], Ahmed Abdelhafeez [3], Ahmed M. Ali [4,*] and Alber S. Aziz [5]

[1] Faculty of Information, Systems and Computer Science, October 6th University, Cairo, 12585, Egypt; ahmed.eldouh.csis@o6u.edu.eg

[2] School of Cyber Science and Engineering, Huazhong University of Science and Technology, Wuhan 430074, China; lusongfeng@hust.edu.cn.

[3] Faculty of Information Systems and Computer Science, October 6th University, Cairo, 12585, Egypt; aahafeez.scis@o6u.edu.eg.

[4] Faculty of Computers and Informatics, Zagazig University, Zagazig 44519, Sharqiyah, Egypt; aabdelmonem@fci.zu.edu.eg.

[5] Faculty of Information, Systems and Computer Science, October 6th University, Cairo, 12585, Egypt; albershawky.csis@o6u.edu.eg.

* Correspondence: aabdelmonem@fci.zu.edu.eg.

Abstract: Early identification and precise prediction of heart disease have important implications for preventative measures and better patient outcomes since cardiovascular disease is a leading cause of death globally. By analyzing massive amounts of data and seeing patterns that might aid in risk stratification and individualized treatment planning, machine learning algorithms have emerged as valuable tools for heart disease prediction. Predictive modeling is considered for many forms of heart illness, such as coronary artery disease, myocardial infarction, heart failure, arrhythmias, and valvar heart disease. Resource allocation, preventative care planning, workflow optimization, patient involvement, quality improvement, risk-based contracting, and research progress are all discussed as management implications of heart disease prediction. The effective application of machine learning-based cardiac disease prediction models requires collaboration between healthcare organizations, providers, and data scientists. This paper used three tools such as the neutrosophic analytical hierarchy process (AHP) as a feature selection, association rules, and machine learning models to predict heart disease. The neutrosophic AHP method is used to compute the weights of features and select the highest features. The association rules are used to give rules between values in all datasets. Then, we used the neutrosophic AHP as feature selection to select the best feature to input in machine learning models. We used nine machine learning models to predict heart disease. We obtained the random forest (RF) and decision tree (DT) have the highest accuracy with 100%, followed by Bagging, k-nearest neighbors (KNN), and gradient boosting have 99%, 98%, and 97%, then AdaBoosting has 89%, then logistic regression and Naïve Bayes have 84%, then the least accuracy is support vector machine (SVM) has 68%.

Keywords: Machine Learning; Heart Disease Prediction; Association Rules; Neutrosophic AHP; Feature Selection; Accuracy.

1. Introduction

The worldwide burden of morbidity and death due to cardiovascular disease continues to be high. Preventative measures, optimal therapeutic approaches, and a decrease in adverse cardiovascular events may all benefit greatly from the early identification and precise prediction of

persons at risk for heart disease. The early identification of people at risk for cardiovascular disease has been the subject of a great deal of study over the years, leading to the development of prediction models and risk assessment approaches. This study examines the state of the art in predicting cardiovascular illness and discusses the obstacles, opportunities, and future paths that lie ahead [1, 2].

Heart disease, which includes coronary artery disease, myocardial infarction, and heart failure, is a complicated multifactorial ailment impacted by a wide range of hereditary, environmental, and behavioral variables. Understanding these characteristics and how they interact is crucial for accurately predicting an individual's risk of developing heart disease [3, 4]. The risk of cardiovascular disease may be estimated using conventional risk assessment models like the Framingham Risk Score, which takes into account variables including age, gender, blood pressure, cholesterol levels, and smoking status. Despite their usefulness, these models often employ a small number of variables and may fail to capture important interplays between potential dangers.

Novel methodologies using machine learning, artificial intelligence, and big data analytics have emerged as powerful instruments for cardiac disease prediction thanks to the development of technology and the availability of large-scale healthcare data. These methods may one day be able to analyze massive volumes of data, unearth previously unknown patterns, and provide unique risk assessments for each individual user. Predictive models for cardiovascular illness have been progressively developed using machine learning methods such as logistic regression (LR), decision trees, random forests, support vector machines (SVMs), and neural networks. Clinical, genetic, lifestyle, and imaging data may all be included in these algorithms to provide solid models for precise risk assessment [3, 5].

There has been a lot of interest in incorporating genetic data into heart disease prediction algorithms. Individual vulnerability to heart disease is heavily influenced by genetic variables, and the addition of genetic markers may improve the accuracy and precision of prediction algorithms.

Wearable technology, such as activity trackers and smartwatches, may provide new information for predicting cardiovascular disease. For risk assessment and early diagnosis of cardiac disorders, these devices can constantly monitor physiological indicators including heart rate, activity levels, and sleep patterns [6, 7].

Electronic health records (EHRs) are increasingly being used as a reliable tool for predicting cardiovascular issues. EHRs are an invaluable resource for building accurate risk assessment models because they include so much information about patients. Although there have been improvements in heart disease prediction, there are still certain issues that require fixing. There are a number of obstacles that must be removed before predictive models can be widely used in clinical settings. These include data quality and standardization, interpretability of machine learning models, privacy concerns, and bias and fairness in predictive algorithms [8, 9].

Predicting cardiovascular illness raises important ethical questions. To keep patients confident in their healthcare professionals, it is critical that they respect their privacy, get their agreement before using predictive models, and share their results openly. In order to enhance patient outcomes and lessen the burden of cardiovascular illness, heart disease prognosis is a fast-developing subject with enormous promise. This study aims to improve cardiovascular care by fostering the creation of more precise, accessible, and individually tailored risk assessment tools by critically examining existing predictive models, addressing challenges, and exploring emerging technologies [10, 11].

This paper used three tools to predict heart disease, first step we used the neutrosophic analytical hierarchy process (AHP) as a feature section to select the best feature [12]. Then in the second step, we used the association rules to fined rules between variables in the data set. In the third step, we used machine learning models to predict the disease. Figure 1 shows the overall three steps to predict heart disease.

The rest of this paper is organized as follows: Section 2 introduces the challenges in heart disease prediction. Section 3 introduces the methodology of this paper and has three layers including

neutrosophic AHP as a feature selection, association rules, and machine learning models. Section 4 presents the results and analysis of the dataset. Section 5 introduces the managerial implications of heart disease prediction. Finally, Section 6 presents the conclusion of this paper.

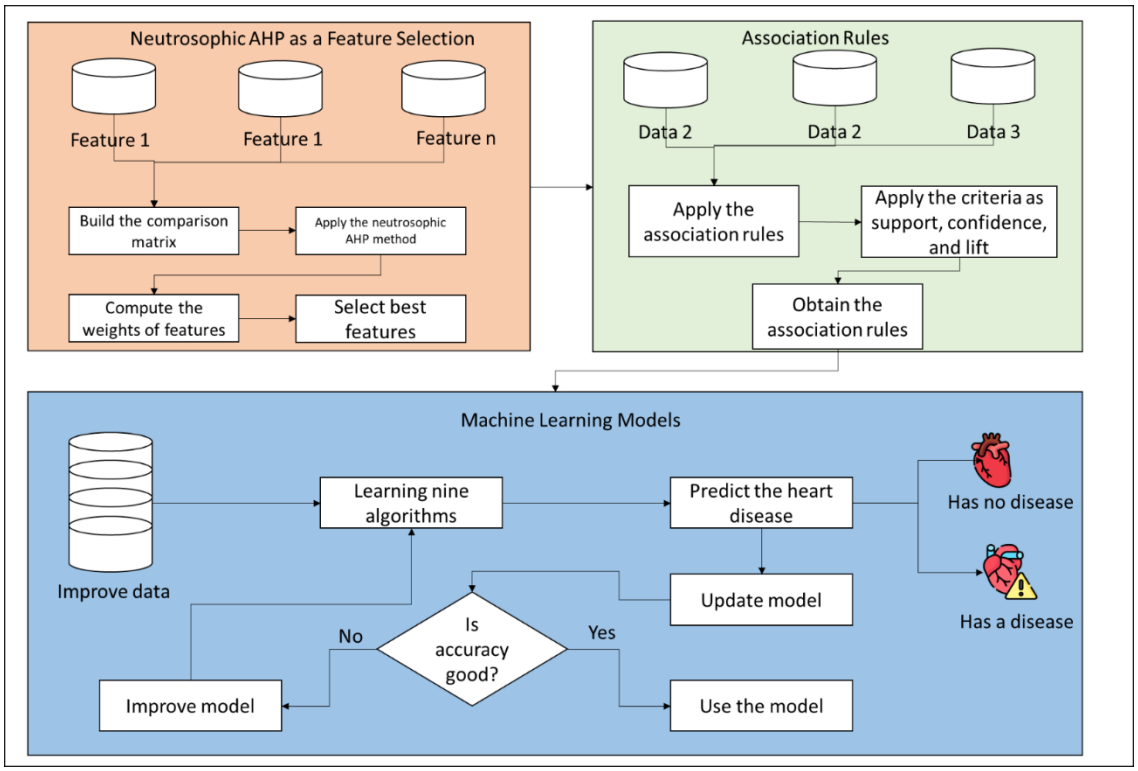

Figure 1. The overall steps of the proposed model to predict heart disease.

2. Heart Disease Prediction

Public health systems face substantial difficulties from cardiovascular disease, which remains a primary cause of morbidity and death globally. In order to adopt preventative measures, optimize treatment options, and reduce the burden of cardiovascular events, early identification and precise prediction of those at risk is critical. Predictive models and risk assessment approaches that help in the early detection of heart disease susceptibility have been the subject of intensive research and development in recent years. The purpose of this study is to present an in-depth analysis of the current status of cardiac disease prediction, including its successes, failures, and prospective future developments [13, 14].

Integration of demographics, medical history, lifestyle choices, and clinical biomarkers allows for more accurate prediction of cardiovascular disease. To calculate an individual's risk of cardiovascular disease, doctors have traditionally used risk assessment models like the Framingham Risk Score. The advent of technology and the availability of massive quantities of healthcare data, however, has led to the development of creative methodologies that use machine learning algorithms, artificial intelligence, and big data analytics to provide more precise and individual predictions.

Researchers and medical practitioners encounter a number of obstacles while attempting to foresee cases of heart disease. Among these difficulties are:

The accuracy and quality of the data used in heart disease prediction models are crucial. However, the accuracy, consistency, and completeness of data might vary widely depending on the source. To maintain the consistency and accuracy of prediction models, it is important to take data quality and standardization into account when integrating data from several sources, such as electronic health records, wearable devices, and genetic databases [15, 16].

While machine learning algorithms are useful for making predictions, they are not always easy to understand. Some models have a black box quality that makes it hard to decipher what is really driving forecasts. Gaining an understanding of the prediction process, fostering confidence among healthcare professionals, and aiding sound decision-making all depend on having access to interpretable models.

Prediction algorithms for cardiovascular disease depend on highly private medical information. It is critical that personal information about patients be kept private and that data be kept secure. Predicting cardiovascular illness is complicated by the need to protect individual privacy while yet providing researchers with access to necessary data [17, 18].

Fairness and Bias: Predictive methods may unwittingly amplify existing biases in the training data. Predicting cardiac disease may be difficult because of racial, ethnic, socioeconomic, and gender biases in healthcare. To guarantee fair and objective forecasts for everyone, it is essential to address and mitigate these biases.

External validation and generalizability Predictive models built for one population or healthcare system may not be applicable to another. To evaluate the efficacy and applicability of models, it is essential to conduct external validation in a variety of populations. The issue of designing models that work well for a wide range of users and contexts persists.

Dynamic variables that change over time have an impact on heart disease, as shown by longitudinal studies. Changes in risk variables, illness progression, and response to therapy are all important to account for in predictive models. Predicting the onset of cardiac disease is difficult since it requires taking into account both static and dynamic factors.

Including Genetic Data: Many people's predisposition to developing heart disease is determined by their genes. The precision and accuracy of prediction models may be improved by including genetic information in their construction. However, there are obstacles such as the difficulty in analyzing genetic data, the need for big genetic databases, and the ethical concerns with genetic testing and privacy [17, 19].

Fewer people from underrepresented groups have been included in heart disease research and data collection, for example, people of color. This underrepresentation may impair the development of specific risk assessment models for different groups and lead to discrepancies in forecast accuracy. Important steps towards a solution include filling up data gaps and ensuring research is inclusive [20, 21].

Improving the precision, fairness, and practicality of heart disease prediction algorithms depends on resolving these issues. We want to overcome these obstacles by creating highly accurate prognostic tools for the effective prevention and treatment of cardiovascular disease.

3. Methodology

This section has three layers. First, the neutrosophic AHP used as a feature selection is used to select the best feature in the dataset. Then, we used the association rules to find the rules between data. Finally, we applied nine machine learning models to predict heart disease.

3.1 Neutrosophic AHP as a Feature Selection

In order to choose which characteristics should be included in a model for predicting heart disease, neutrosophic AHP feature selection is used. The goal of neutrosophic feature selection is to deal with data uncertainty and imprecision by giving each feature a degree of membership [22]. This permits the characteristics most helpful to the model's prediction ability to be chosen, with their neutrosophic nature taken into account. By zeroing in on the most relevant characteristics, the accuracy and interpretability of heart disease prediction models may be increased by utilizing neutrosophic AHP feature selection approaches. We used the neutrosophic AHP method as a feature selection [23-25].

Each input layer is given due consideration using the AHP technique as a means of producing a well-informed choice. When employing the AHP, you may use both quantitative and qualitative data because of the hierarchical structure provided by comparing each criterion. The AHP technique allows for a rating scale from 1 to 9 for any given set of data.

When thinking about the first issue, the AHP method works well. This is due to the fact that AHP approaches may rank competing criteria in order of preference based on contextual factors. Indicators used in selecting choices may also be affected by the structure of the regional forwarding network [26]. The optimal size of a collection of cooperative candidates for a relay is the second open question. Cooperative candidate relay sets may include groups of nearby nodes with varying data redundancy rates, cooperative relay delays, and delivery ratios. One of the sets of a certain size is deemed the cooperative candidate relay set after being evaluated based on its characteristics, compatibility with the vehicular environment, and good trade-off among the necessary aspects.

Step 1. The hierarchical analysis between features in dataset is performed.
The hierarchal used to define the goal from the problem, and define the features.
Step 2. Build pairwise comparison matrix.
We used the triangular neutrosophic scale to evaluate the features [27].

$$A_{ij}^{t} = \begin{bmatrix} a_{11}^{t} & \cdots & a_{1n}^{t} \\ \vdots & \ddots & \vdots \\ a_{n1}^{t} & \cdots & a_{nn}^{t} \end{bmatrix} \quad (1)$$

Where a_{1n}^{t} refers to the triangular neutrosophic number, n refers to the number of criteria, t refers the decision makers.
Step 3. Obtain the crisp value.
We used the score function to obtain the crisp value [27].
Step 4. Combine the opinions of experts.
We used the average method to combine the different pairwise comparison matrix into one matrix.
Step 5. Compute the row average.

$$w_i = \frac{\sum_{j=1}^{n}\left(a_{ij}^{t}\right)}{n} \quad (2)$$

Step 6. Normalize the crisp values.

$$w_i^{m} = \frac{w_i}{\sum_{i=1}^{m} w_i} \quad (3)$$

Step 7. Compute the consistency ratio (CR).

$$CR = \frac{CI}{RI} \quad (4)$$

$$CI = \frac{\lambda\_max - n}{n-1} \quad (5)$$

Where λ_max refers to the weighted sum vector.

3.2 Association Rules

In order to model and uncover the interdependencies between database entries, association rules are used. Support, confidence, and lift are criteria to show the importance of associations [28-31].

3.2.1 Support

This metric provides insight into how often a certain collection of products appears in all trades. Let's pretend that Set1 is bread and Set2 is shampoo. There will be a lot more bread purchases than shampoo purchases. You correctly predicted that the support for set1 would be greater than that for set2. Let's say set1 is "bread and butter" and set2 is "bread and shampoo." Bread and butter are common cart items, but how often do you see bread and shampoo? Not really. In this situation, set1 is more likely to be preferred than set2 in terms of popularity. In mathematical terms, the amount of backing for an item set is the share of all transactions that include those objects.

$$\text{Support}\{\{x\} \rightarrow \{y\}\} = \frac{\text{Transactions containing both x and y}}{\text{total number of transactions}} \quad (6)$$

Using support value, we can determine which rules are worth investigating further. If there are 10,000 transactions, for instance, it may be useful to focus on the subset of item sets that appears at least 50 times, or has support = 0.005. Without further data, we cannot make any firm conclusions about the nature of the relationships among the items in a very poorly supported item set.

3.2.2 Confidence

This metric describes the probability that the consequent will be present on the cart, assuming that the antecedents are present. That is to say, of all the purchases that included the term "Captain Crunch," how many also included the word "Milk?" It's well known that the "Captain Crunch" vs. "Milk" guideline should be taken very seriously. Confidence, in technical terms, is the chance that the consequent will occur given the antecedent.

$$\text{Confidence } (\{x\} \rightarrow \{y\}) = \frac{\text{transactions containing both x and y}}{\text{transaction containing x}} \tag{7}$$

First, let's take a moment to think about a few additional situations. How sure are you that "Butter" and "Bread" are synonymous? To clarify, what percentage of purchases included both butter and bread? Extremely high, or very near to 1? Yeah, you nailed it. What about milk and yogurt? Back on top of the world. Milk for your toothbrush? Still unsure? Since "Milk" is such a common commodity, it is safe to assume that this rule will always hold true.

3.2.3 Lift

When determining the conditional probability of occurrence of Y given X, Lift accounts for the support (frequency) of consequent. The word "lift" is used to describe this metric rather literally. Imagine this as the *boost* to our self-assurance that comes from having Y in the shopping basket thanks to the presence of X. To restate, lift is the increase in the chance of Y being on the cart due to the knowledge of X's existence relative to the probability of Y being on the cart due to ignorance of X's presence.

$$\text{Lift } (\{x\} \rightarrow \{y\}) = \frac{\text{(transactions containing both x and y)/ (Transaction containing x)}}{\text{Fraction of transactions containing y}} \tag{8}$$

3.3 Machine Learning Algorithms

Classification is a supervised learning technique in machine learning; it also denotes a predictive modelling challenge in which a class label is predicted for an input sample. Specifically, it is a mathematical function (f) that maps input variables (X) to target variables (Y), where Y might be a label or category. It may be performed on either structured or unstructured data to make predictions about the class of provided data items. Examples of classification the heart disease.

Classification problems with just two possible answers (true or false) are known as "binary classification." For example, in a job requiring binary classification, "normal" may be one class and "abnormal" another. As an example, if the work at hand includes a medical test, and the result is "cancer not detected," then "cancer detected" may be seen as the aberrant condition. In the same way, the "spam" and "not spam" categories used by email service providers are also regarded to be binary [23, 33].

The machine learning and data science field is rife with suggested categorization methods. The most widely-used approaches to predicting heart disease are summed up here.

3.3.1 Naïve Bayes

By using Bayes' theorem under the premise of feature independence, the naïve Bayes (NB) algorithm is developed. In many practical applications, such as document or text categorization, spam filtering, etc., it performs admirably and may be used for both binary and multi-class categories. The NB classifier may be used to efficiently categorize the data's noisy examples and build a solid prediction model. The main advantage is that it just requires a minimal amount of training data to rapidly and accurately estimate the required parameters, in contrast to more complex methods.

However, it makes very strong assumptions about the independence of characteristics, which might reduce its performance. Common NB classifier versions include the Gaussian, Multinomial, Complement, Bernoulli, and Categorical distributions [34, 35].

3.3.2 Logistic Regression

LR is another popular probabilistic-based statistical model used to address classification problems in machine learning. A logistic function, often known as the sigmoid function from its mathematical definition, is commonly used in LR to assess probabilities. Overfitting is possible with high-dimensional data, and it performs best when the data can be linearly partitioned. In these cases, regularization (L1 and L2) methods may be employed to prevent over-fitting. The linearity assumption between the dependent and independent variables is seen as a fundamental limitation of LR. Although it is more typically employed for classification difficulties, it may also be used for regression issues [36].

$$\mathrm{LR}(r) = \frac{1}{1+\exp(-r)} \tag{9}$$

3.3.3 K-Nearest Neighbors

Known as a "lazy learning" method, k-nearest neighbors (KNN) is a kind of "instance-based learning" or non-generalizing learning. Rather than concentrating on building a single, overarching model, it maintains an n-dimensional database of all occurrences that correlate to training data. Similarity metrics (such as the Euclidean distance function) are used by KNN to classify fresh data points. Each point is assigned to a category based on a majority decision of its k closest neighbors. The accuracy is data-dependent, however, it is quite tolerant to noisy training data. Choosing the right number of neighbors to use might be challenging when using KNN. KNN is versatile, since it may be used for both classification and regression [37].

3.3.4 Support Vector Machine

SVMs are another prominent machine learning technology that may be used for classification, regression, and other applications. A SVM builds a hyper-plane or series of hyper-planes in high or infinite dimensional space. Since, in general, the larger the margin, the smaller the classifier's generalization error, it stands to reason that the hyper-plane, which has the largest distance from the closest training data points in each class, achieves a strong separation. It works well in high-dimensional spaces and exhibits varying behaviors depending on the kernel function used. Common kernel functions used in SVM classifiers include linear, polynomial, radial basis function (RBF), sigmoid, etc. SVM operates poorly, however, when there is more noise in the data set, such as when the target classes overlap [38, 39].

3.3.5 Decision Tree

One popular kind of supervised learning that does not rely on parameters is the decision tree (DT). Both the classification and regression jobs employ DT learning techniques. Popular DT algorithms include ID3, C4.5, and CART. And in the relevant application fields, such as user behavior analytics and Cybersecurity analytics, the newly suggested BehavDT and IntrudTree by Sarker et al. are successful. In order to categorize the instances, DT sorts the tree from its root node to a subset of its leaf nodes. Classifying instances involves traversing a tree from its root node to the leaf nodes along the branches that correspond to the attributes being checked. The Gini impurity and the entropy gain are two of the most often used metrics for partitioning [40].

We can define entropy and Gini as:

$$\mathrm{H}(x) = -\sum_{i=1}^{n} p(x_i) \log_2 p(x_i) \tag{10}$$

$$E = 1 - \sum_{i=1}^{c} p_i^2 \tag{11}$$

3.3.6 Random Forest

Well-known in the fields of machine learning and data science, random forest classifiers are employed as an ensemble classification approach. In this technique, "parallel ensemble" is used to simultaneously train several decision tree classifiers on independent subsamples of the data set, with

the final result being determined by a vote or an average of the results. As a result, it improves prediction accuracy and regulates the issue of over-fitting. That's why it's more common for the random forest (RF) learning model to outperform those using a single decision tree. It uses a hybrid of bootstrap aggregation (bagging) and random feature selection to construct several decision trees with intentional variety. It works well with both categorical and continuous data and may be used for classification and regression issues [41, 42].

3.3.7 AdaBoost

Adaptive Boosting (AdaBoost) is an iterative ensemble learning procedure that uses error feedback to improve underperforming classifiers. This concept, dubbed "meta-learning" after its creators Yoav Freund et al. AdaBoost employs a "sequential ensemble," in contrast to the random forest's parallel ensemble. In order to achieve a decent classifier with high accuracy, it combines multiple underperforming classifiers to produce a powerful classifier. AdaBoost is an adaptive classifier since it greatly improves the classifier's efficiency; yet, it might lead to overfits in certain situations. AdaBoost is sensitive to noisy data and outliers, making it best utilized to improve the performance of decision trees, the basis estimator, for binary classification tasks [43].

3.3.8 Gradient Boosting

Similar to the RFs example up top, Gradient Boosting is a kind of ensemble learning method that builds a final model from a collection of smaller models (usually decision trees). Like how neural networks employ gradient descent to optimize weights, we use the gradient to minimize the loss function [44].

3.3.9 Bagging

The model is comprised of homogenous weak learners, who acquire knowledge in isolation and in parallel, and then average their results. Bagging, or Bootstrap Aggregating, is a meta-algorithm for machine learning ensembles that increases the reliability and precision of statistical classification and regression models. The variance is reduced and overfitting is prevented. Typically, this is used in decision tree techniques. The method of bagging is a variant of the model-averaging strategy [45].

4. Results and analysis

This section summarizes the analysis of heart disease data and the obtained results from the various machine learning algorithms.

4.1 Description of Dataset

The information may be accessed by the general public on the Kaggle website. It was collected as part of an ongoing cardiovascular research on people living in the town of Framingham, which is located in the state of Massachusetts. The information about the patients may be found in the dataset. It consists of nearly 4,000 rows and fifteen different qualities. In furthermore, the different statistical results for the dataset's input parameters are displayed in Table 1, including the count, mean, standard deviation, minimum, 25%, 50%, 75%, and maximum values.

Table 1. The statistics values of the attributes in heart disease data.

Statistics	sex	cp	trestbps	chol	fbs	restecg	thalach
count	1025.000	1025.000	1025.000	1025.000	1025.000	1025.000	1025.000
mean	54.434	0.696	0.942	131.612	246.000	0.149	0.530
Std.	9.072	0.460	1.030	17.517	51.593	0.357	0.528
Min	29.000	0.000	0.000	94.000	126.000	0.000	0.000
25%	48.000	0.000	0.000	120.000	211.000	0.000	0.000
50%	56.000	1.000	1.000	130.000	240.000	0.000	1.000
75%	61.000	1.000	2.000	140.000	275.000	0.000	1.000
Max	77.000	1.000	3.000	200.000	564.000	1.000	2.000

Statistics	exang	oldpeak	slope	ca	thal	Target
count	1025.000	1025.000	1025.000	1025.000	1025.000	1025.000
mean	149.114	0.337	1.072	1.385	0.754	2.324
Std.	23.006	0.473	1.175	0.618	1.031	0.621
Min	71.000	0.000	0.000	0.000	0.000	0.000
25%	132.000	0.000	0.000	1.000	0.000	2.000
50%	152.000	0.000	0.800	1.000	0.000	2.000
75%	166.000	1.000	1.800	2.000	1.000	3.000
Max	202.000	1.000	6.200	2.000	4.000	3.000

Figure 2 shows the data of sex and target columns. Where red color refers to the female and blue color refers to male. 0 refer to the target class no disease and 1 refers to the target class 1 has a disease. The number persons of male greater than female in 0 class. Also in 1 class the number rows in male greater than female.

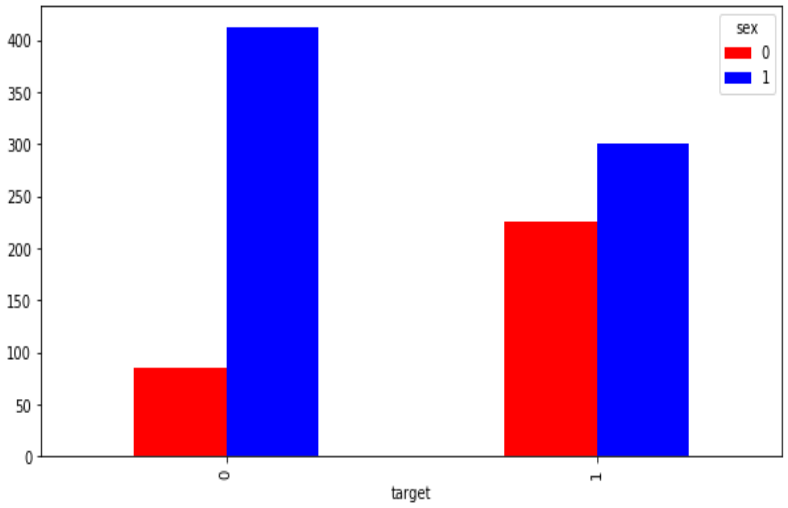

Figure 2. The sex and target columns.

Figure 3 shows the scatter diagram of data in age and cholesterol columns. Where the red color refers to the disease and blue color refers to no disease. The age between 30 and 40 years old have disease more than no disease.

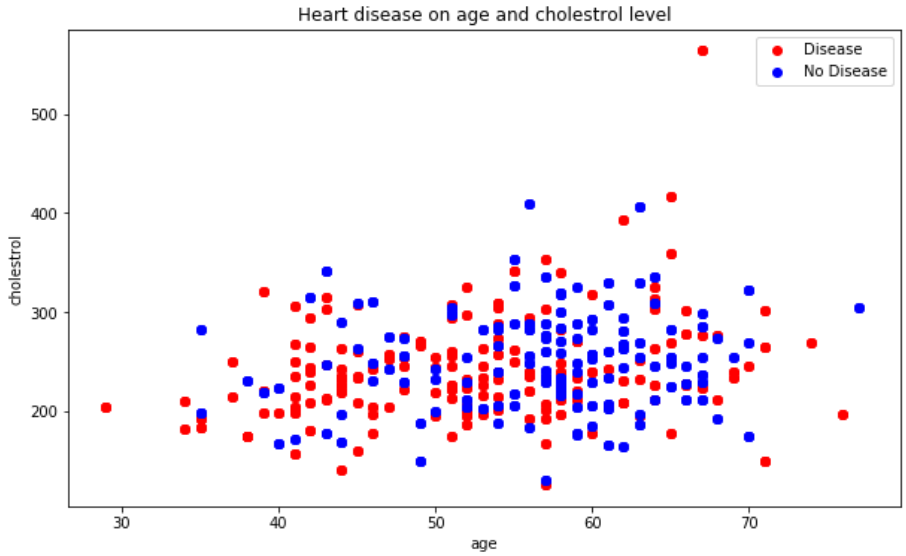

Figure 3. The scatter diagram of age and cholesterol.

Figure 4 shows the heatmap and correlation in dataset. In the age row, there are six criteria are negative correlation and other are positive correlation. The ca criterion is the highly positive correlated with the age criterion. The age criterion has a negative correlation with the target variable. In the sex criterion, there are 8 negative correlation criteria and 5 positive correlation criteria. The sex criterion has a negative correlation with the target variable. The thal is the highly correlated with the sex variable. In cp variable, there are six variables positive correlated and other are negative correlated. The cp has a positive correlation with the target variable. The cp variable is the most correlated variable with the target variable. In the trestbps, there are 7 positive correlated variables and other are negative correlated variable. Trestbps has a negative correlation with the target variable. In the chol, there are 7 positive correlated variables and other are negative correlated variable. Chol has a negative correlation with the target variable. In the fbs, there are 8 positive correlated variables and other are negative correlated variable. fbs has a negative correlation with the target variable. In the restecg, there are 4 positive correlated variables and other are negative correlated variable. restecg has a positive correlation with the target variable. In the thalach, there are 4 positive correlated variables and other are p correlated variable. thalach has a positive correlation with the target variable. In the exang, there are 8 positive correlated variables and other are negative correlated variable. exang has a negative correlation with the target variable in the oldpeak, there are 8 positive correlated variables and other are negative correlated variable. oldpeak has a negative correlation with the target variable. In the slope, there are 4 positive correlated variables and other are negative correlated variable. Slope has a positive correlation with the target variable. In the ca, there are 8 positive correlated variables and other are negative correlated variable. ca has a negative correlation with the target variable. In the thal, there are 7 positive correlated variables and other are negative correlated variable. thal has a negative correlation with the target variable.

In all variables there are four variables are positive correlated with the target variable and all other variables are negative correlated. The variables have positive correlation with the target variable are (cp, restecg, thalach, and slope). Between four variables, the cp is the largest positive correlated with the target variable. So, the cp, restecg, thalach, and slope have an association correlation with the target variable.

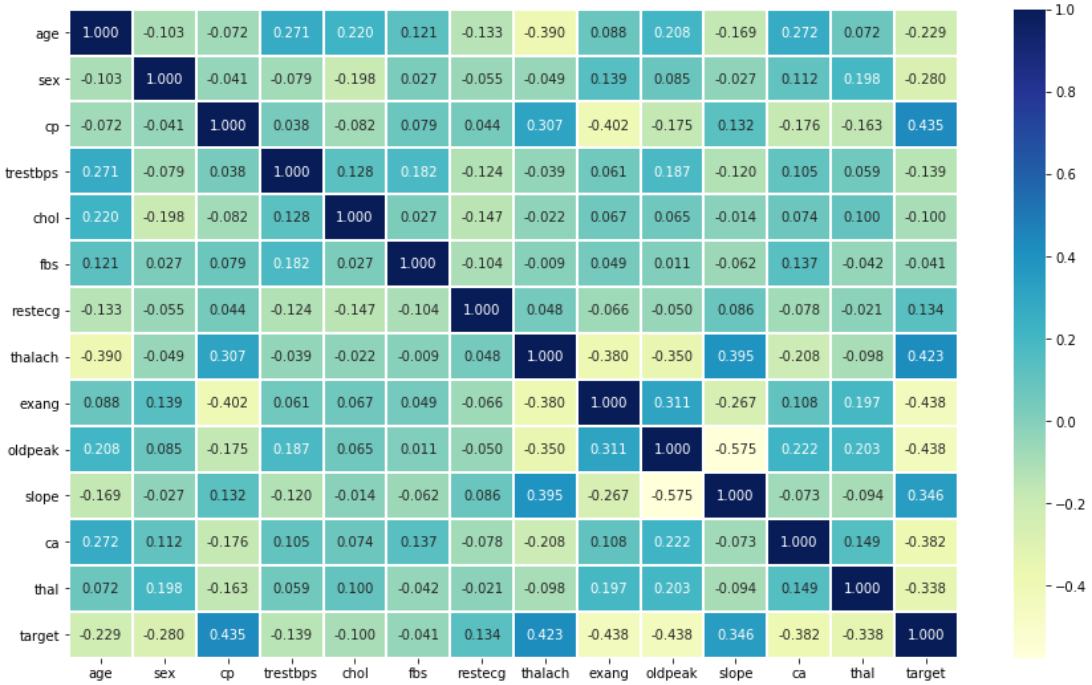

Figure 4. The heatmap in the dataset.

4.2 Neutrosophic AHP as a Feature Selection

We build the comparison matrix between 13 features. This matrix contains the triangular neutrosophic number. Table 2 shows the triangular neutrosophic numbers for 13 features. Then replace these numbers with the crisp values [27]. Then compute the normalization matrix. Then compute the weights of features as shown in Figure 5.

Table 2. Comparison matrix between 13 features.

	HDF$_1$	**HDF$_2$**	**HDF$_3$**
HDF$_1$	1	((1,1,1) ;0.50,0.50,0.50)	((6,7,8) ;0.90,0.10,0.10)
HDF$_2$	1/((1,1,1) ;0.50,0.50,0.50)	1	((4,5,6) ;0.80,0.15,0.20)
HDF$_3$	1/((6,7,8) ;0.90,0.10,0.10)	1/((4,5,6) ;0.80,0.15,0.20)	1
HDF$_4$	1/((1,2,3) ;0.40,0.65,0.60)	1/((6,7,8) ;0.90,0.10,0.10)	1((2,3,4) ;0.30,0.75,0.70)
HDF$_5$	1/((2,3,4) ;0.30,0.75,0.70)	1/((9,9,9) ;0.100,0.00,0.00)	1/((4,5,6) ;0.80,0.15,0.20)
HDF$_6$	1/((2,3,4) ;0.30,0.75,0.70)	1/((3,4,5) ;0.60,0.35,0.40)	1/((1,1,1) ;0.50,0.50,0.50)
HDF$_7$	1/((1,2,3) ;0.40,0.65,0.60)	1/((3,4,5) ;0.60,0.35,0.40)	1/((1,2,3) ;0.40,0.65,0.60)
HDF$_8$	1/((9,9,9) ;0.100,0.00,0.00)	1/((9,9,9) ;0.100,0.00,0.00)	1/((5,6,7) ;0.70,0.25,0.30)
HDF$_9$	1/((7,8,9) ;0.85,0.10,0.15)	1/((6,7,8) ;0.90,0.10,0.10)	1/((7,8,9) ;0.85,0.10,0.15)
HDF$_{10}$	1/((3,4,5) ;0.60,0.35,0.40)	1/((4,5,6) ;0.80,0.15,0.20)	1/((3,4,5) ;0.60,0.35,0.40)
HDF$_{11}$	1/((5,6,7) ;0.70,0.25,0.30)	1/((2,3,4) ;0.30,0.75,0.70)	1/((9,9,9) ;0.100,0.00,0.00)
HDF$_{12}$	1/((4,5,6) ;0.80,0.15,0.20)	1/((4,5,6) ;0.80,0.15,0.20)	1/((1,2,3) ;0.40,0.65,0.60)
HDF$_{13}$	1/((4,5,6) ;0.80,0.15,0.20)	1/((1,1,1) ;0.50,0.50,0.50)	1/((1,1,1) ;0.50,0.50,0.50)
	HDF$_4$	**HDF$_5$**	**HDF$_6$**
HDF$_1$	((1,2,3) ;0.40,0.65,0.60)	((2,3,4) ;0.30,0.75,0.70)	((2,3,4) ;0.30,0.75,0.70)
HDF$_2$	((6,7,8) ;0.90,0.10,0.10)	((9,9,9) ;0.100,0.00,0.00)	((3,4,5) ;0.60,0.35,0.40)
HDF$_3$	((2,3,4) ;0.30,0.75,0.70)	((4,5,6) ;0.80,0.15,0.20)	((1,1,1) ;0.50,0.50,0.50)
HDF$_4$	1	((5,6,7) ;0.70,0.25,0.30)	((3,4,5) ;0.60,0.35,0.40)
HDF$_5$	1/((5,6,7) ;0.70,0.25,0.30)	1	((3,4,5) ;0.60,0.35,0.40)
HDF$_6$	1/((3,4,5) ;0.60,0.35,0.40)	1/((3,4,5) ;0.60,0.35,0.40)	1
HDF$_7$	1/((1,2,3) ;0.40,0.65,0.60)	1/((5,6,7) ;0.70,0.25,0.30)	1/((7,8,9) ;0.85,0.10,0.15)
HDF$_8$	1/((1,2,3) ;0.40,0.65,0.60)	1/((7,8,9) ;0.85,0.10,0.15)	1/((5,6,7) ;0.70,0.25,0.30)
HDF$_9$	1/((1,1,1) ;0.50,0.50,0.50)	1/((6,7,8) ;0.90,0.10,0.10)	1/((6,7,8) ;0.90,0.10,0.10)
HDF$_{10}$	1/((1,2,3) ;0.40,0.65,0.60)	1/((1,1,1) ;0.50,0.50,0.50)	1/((4,5,6) ;0.80,0.15,0.20)
HDF$_{11}$	1/((5,6,7) ;0.70,0.25,0.30)	1/((3,4,5) ;0.60,0.35,0.40)	1/((9,9,9) ;0.100,0.00,0.00)
HDF$_{12}$	1/((1,1,1) ;0.50,0.50,0.50)	1/((7,8,9) ;0.85,0.10,0.15)	1/((5,6,7) ;0.70,0.25,0.30)
HDF$_{13}$	1/((1,2,3) ;0.40,0.65,0.60)	1/((2,3,4) ;0.30,0.75,0.70)	1/((3,4,5) ;0.60,0.35,0.40)
	HDF$_7$	**HDF$_8$**	**HDF$_9$**
HDF$_1$	((1,2,3) ;0.40,0.65,0.60)	((9,9,9) ;0.100,0.00,0.00)	((7,8,9) ;0.85,0.10,0.15)
HDF$_2$	((3,4,5) ;0.60,0.35,0.40)	((9,9,9) ;0.100,0.00,0.00)	((6,7,8) ;0.90,0.10,0.10)
HDF$_3$	((1,2,3) ;0.40,0.65,0.60)	((5,6,7) ;0.70,0.25,0.30)	((7,8,9) ;0.85,0.10,0.15)
HDF$_4$	((1,2,3) ;0.40,0.65,0.60)	((1,2,3) ;0.40,0.65,0.60)	((1,1,1) ;0.50,0.50,0.50)
HDF$_5$	((5,6,7) ;0.70,0.25,0.30)	((7,8,9) ;0.85,0.10,0.15)	((6,7,8) ;0.90,0.10,0.10)
HDF$_6$	((7,8,9) ;0.85,0.10,0.15)	((5,6,7) ;0.70,0.25,0.30)	((6,7,8) ;0.90,0.10,0.10)

HDF7	1	((3,4,5) ;0.60,0.35,0.40)	((5,6,7) ;0.70,0.25,0.30)
HDF8	1/((3,4,5) ;0.60,0.35,0.40)	1	((3,4,5) ;0.60,0.35,0.40)
HDF9	1/((5,6,7) ;0.70,0.25,0.30)	1/((3,4,5) ;0.60,0.35,0.40)	1
HDF10	1/((2,3,4) ;0.30,0.75,0.70)	1/((6,7,8) ;0.90,0.10,0.10)	1/((9,9,9) ;0.100,0.00,0.00)
HDF11	1/((6,7,8) ;0.90,0.10,0.10)	1/((1,1,1) ;0.50,0.50,0.50)	1/((1,2,3) ;0.40,0.65,0.60)
HDF12	1/((3,4,5) ;0.60,0.35,0.40)	1/((9,9,9) ;0.100,0.00,0.00)	1/((6,7,8) ;0.90,0.10,0.10)
HDF13	1/((5,6,7) ;0.70,0.25,0.30)	1/((7,8,9) ;0.85,0.10,0.15)	1/((3,4,5) ;0.60,0.35,0.40)

	HDF10	**HDF11**	**HDF12**
HDF1	((3,4,5) ;0.60,0.35,0.40)	((5,6,7) ;0.70,0.25,0.30)	((4,5,6) ;0.80,0.15,0.20)
HDF2	((4,5,6) ;0.80,0.15,0.20)	((2,3,4) ;0.30,0.75,0.70)	((4,5,6) ;0.80,0.15,0.20)
HDF3	((3,4,5) ;0.60,0.35,0.40)	((9,9,9) ;0.100,0.00,0.00)	((1,2,3) ;0.40,0.65,0.60)
HDF4	((1,2,3) ;0.40,0.65,0.60)	((5,6,7) ;0.70,0.25,0.30)	((1,1,1) ;0.50,0.50,0.50)
HDF5	((1,1,1) ;0.50,0.50,0.50)	((3,4,5) ;0.60,0.35,0.40)	((7,8,9) ;0.85,0.10,0.15)
HDF6	((4,5,6) ;0.80,0.15,0.20)	((9,9,9) ;0.100,0.00,0.00)	((5,6,7) ;0.70,0.25,0.30)
HDF7	((2,3,4) ;0.30,0.75,0.70)	((6,7,8) ;0.90,0.10,0.10)	((3,4,5) ;0.60,0.35,0.40)
HDF8	((6,7,8) ;0.90,0.10,0.10)	((1,1,1) ;0.50,0.50,0.50)	((9,9,9) ;0.100,0.00,0.00)
HDF9	((9,9,9) ;0.100,0.00,0.00)	((1,2,3) ;0.40,0.65,0.60)	((6,7,8) ;0.90,0.10,0.10)
HDF10	1	((1,1,1) ;0.50,0.50,0.50)	((4,5,6) ;0.80,0.15,0.20)
HDF11	1/((1,1,1) ;0.50,0.50,0.50)	1	((2,3,4) ;0.30,0.75,0.70)
HDF12	1/((4,5,6) ;0.80,0.15,0.20)	1/((2,3,4) ;0.30,0.75,0.70)	1
HDF13	1/((3,4,5) ;0.60,0.35,0.40)	1/((1,1,1) ;0.50,0.50,0.50)	1/((1,2,3) ;0.40,0.65,0.60)

	HDF13
HDF1	((4,5,6) ;0.80,0.15,0.20)
HDF2	((1,1,1) ;0.50,0.50,0.50)
HDF3	((1,1,1) ;0.50,0.50,0.50)
HDF4	((1,2,3) ;0.40,0.65,0.60)
HDF5	((2,3,4) ;0.30,0.75,0.70)
HDF6	((3,4,5) ;0.60,0.35,0.40)
HDF7	((5,6,7) ;0.70,0.25,0.30)
HDF8	((7,8,9) ;0.85,0.10,0.15)
HDF9	((3,4,5) ;0.60,0.35,0.40)
HDF10	((3,4,5) ;0.60,0.35,0.40)
HDF11	((1,1,1) ;0.50,0.50,0.50)
HDF12	((1,2,3) ;0.40,0.65,0.60)
HDF13	1

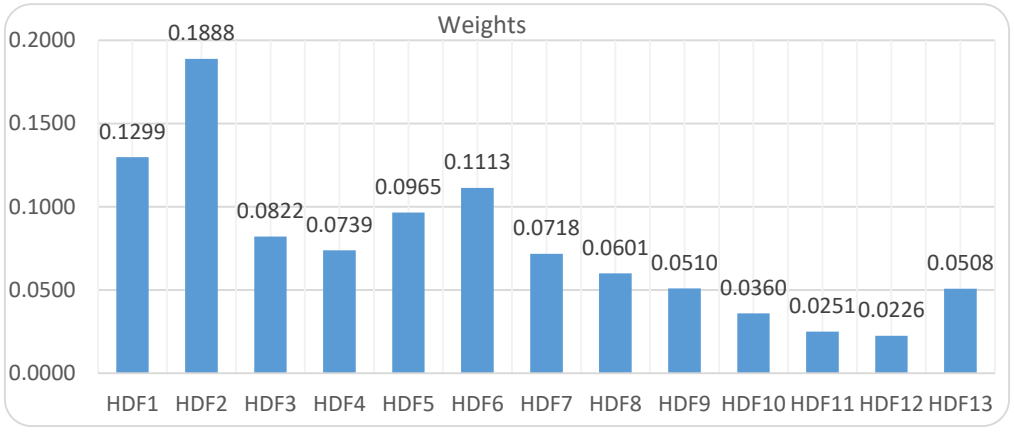

Figure 5. Weights of 13 features.

4.3 Association Rules

Table 3 shows the association rules between the target and other variables. Table 3 presents the support, confidence, and lift values.

Table 3. Comparison matrix between 13 features.

Column name in dataset	Target class	antecedent support	consequent support	Support	confidence	lift	leverage	Conviction
Age	0	0.8537	0.9756	0.8293	0.9714	0.9957	-0.0036	0.8537
	1	0.9756	0.8537	0.8293	0.8500	0.9957	-0.0036	0.9756
Sex	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
CP	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
trestbps	0	0.7755	0.7959	0.5714	0.7368	0.9258	-0.0458	0.7755
	1	0.7959	0.7755	0.5714	0.7179	0.9258	-0.0458	0.7959
fbs	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
restecg	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
thalach	0	0.7363	0.7802	0.5165	0.7015	0.8991	-0.058	0.7363
	1	0.7802	0.7363	0.5165	0.6620	0.8991	-0.058	0.7802
exang	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
oldpeak	0	0.650	0.875	0.525	0.8077	0.9231	-0.0437	0.650
	1	0.875	0.650	0.525	0.6000	0.9231	-0.0437	0.875
slope	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
ca	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf
thal	0	1.0	1.0	1.0	1.0	1.0	0.0	Inf
	1	1.0	1.0	1.0	1.0	1.0	0.0	Inf

4.4 Performance Measurements

Every confusion matrix provides a description of the operation of a classification algorithm on a set of test data for which the measured values are completely understood. The confusion matrix was used in the computation of the parameters stated in Table 4, which may be seen below. From Table 4 the random forest and decision tree have the best accuracy with 100% accuracy. We divide the dataset into train and test, the train set has 80% and the test set has 20% data. Figure 6 shows the confusion matrices.

Table 4. The results of machine learning algorithms.

	Logistic Regression	Random Forest	KNN	SVM	AdaBoosting	Bagging	Gradient Boosting	NB	Decision Tree
Accuracy	0.8439	1.0000	0.9805	0.6780	0.8927	0.9902	0.9756	0.8390	1.0000
Precision	0.8155	1.0000	0.9604	0.6165	0.9121	1.0000	0.9894	0.8333	1.0000
Recall	0.8660	1.0000	1.0000	0.8454	0.8557	0.9794	0.9588	0.8247	1.0000
F1-score	0.8400	1.0000	0.9798	0.7130	0.8830	0.9896	0.9738	0.8290	1.0000

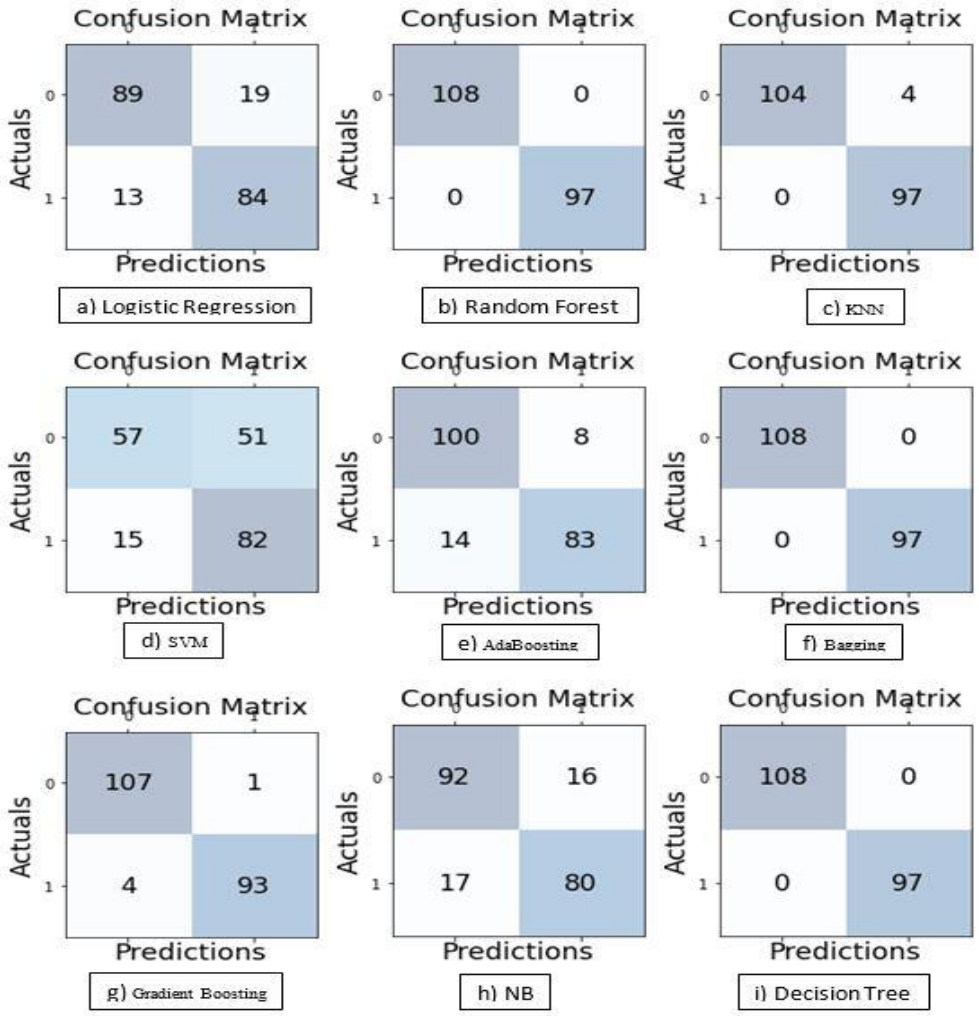

Figure 6. The confusion matrices.

5. Managerial Implications

The administrative implications of heart disease prediction for healthcare organizations and providers are many. Among the repercussions of this are:

Effective resource allocation is possible with the use of heart disease prediction models. Healthcare expenses may be reduced and resource utilization improved by targeting people at the highest risk via preventative measures like screens and treatments.

Healthcare administrators are able to create more effective preventative care programs because of heart disease prediction. High-risk patients might be targeted for preventative measures such as lifestyle changes, medication management, and routine monitoring by healthcare administrators. By taking preventative measures, healthcare outcomes for patients and costs for healthcare systems may both improve.

Workflow and Care Coordination: Prediction models for cardiovascular disease may help with both. Managers can pinpoint those patients most at risk and swiftly arrange them for the necessary preventative measures. Better patient care and results are the results of this effort to standardize care pathways and guarantee timely interventions.

Patient Engagement and Education: Prediction models for cardiovascular disease may help with both goals. Managers may utilize prognostic data to teach patients about their unique risk factors, the value of sticking to their treatment regimens, and the advantages of adopting healthier habits. Patients' desire and ability to make educated choices about their own heart disease prevention and treatment may both be improved by patient engagement.

The efficiency of preventative measures and the quality of treatment as a whole may be tracked using performance metrics such as heart disease prediction models. Managers may monitor the progress of high-risk people to see whether the interventions they've put in place are having the intended effect. With this information, we can make more educated choices about how to best treat cardiac disease.

Insurance firms and other payers may use heart disease prediction algorithms in risk-based contracts and insurance policies. Insurers may adjust customers' premiums, levels of coverage, and methods of payment to account for each person's unique estimated risk of cardiovascular disease by integrating predictive information. This method encourages individualized and economically viable medical protection.

Data generated by heart disease prediction models may be utilized for scientific inquiry and technological advancement. Data produced by prediction models may be analyzed by managers and researchers together to discover new risk factors, verify current models, and improve predictive algorithms. Working together, we can better understand how to anticipate and treat cardiac disease.

Predicting cardiovascular disease has broad administrative implications, including but not limited to budgeting, planning for preventative treatment, streamlining operations, increasing patient participation, enhancing product quality, reducing risk, and facilitating new studies. In the context of heart disease prevention and management, predictive models may help healthcare administrators make better choices, enhance the quality of treatment provided, and improve patient outcomes.

6. Conclusions

Predicting heart disease is important for several reasons, including bettering patient outcomes, maximizing resources, and permitting individualized treatment. By drawing from several data sets to build disease-specific prognostic models, machine learning algorithms have already shown their worth in this area. Better heart disease management and prevention are possible because of these models' ability to stratify risk, diagnose it early, and direct treatment accordingly.

Several administrative considerations arise from using machine learning to the problem of predicting cardiac disease. By focusing on those most at risk and implementing preventative

measures first, healthcare systems may make better use of their limited resources. Predictive models are used in personalized care plans to increase patient involvement and treatment compliance. Care coordination and optimization of workflow allow for prompt screenings and treatments for those at high risk. Additionally, cardiovascular disease prediction models allow for better performance tracking, quality enhancement, and groundbreaking new research.

The use of machine learning algorithms for the prediction of heart disease has enormous potential to improve cardiovascular treatment. Risk stratification, individualized care planning, and early identification of cardiac disease are all made possible by these models, which make use of massive datasets and sophisticated computational approaches. We used the neutrosophic AHP as a feature selection to select the best feature, then we applied the association rules to get importance from the rules between datasets. Finally, we used the nine machine learning algorithms to predict heart disease. From our data, we know that the highest accuracy is achieved by random forests and decision trees (100%), then by bagging, k-nearest neighbors, and gradient boosting (98%, 97%, and 89%, respectively), then by AdaBoosting (89%), then by logistic regression and Naive Bayes (84%), and finally by support vector machines (68%).

Acknowledgments

The author is grateful to the editorial and reviewers, as well as the correspondent author, who offered assistance in the form of advice, assessment, and checking during the study period.

Data availability

The datasets generated during and/or analyzed during the current study are not publicly available due to the privacy-preserving nature of the data but are available from the corresponding author upon reasonable request.

Conflict of interest

The authors declare that there is no conflict of interest in the research.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

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Received: 31 Mar 2023, **Revised:** 06 Sep 2023,
Accepted: 18 Sep 2023, **Available online**: 01 Oct 2023.