International Journal for Innovative Engineering and Management Research
A Peer Revieved Open Access International Journal
www.ijiemr.org



IJIEMR Transactions, online available on 28th Apr 2023. Link :http://www.ijiemr.org/downloads.php?vol=Volume-12&issue=ISSUE-4

**DOI: 10.48047/IJIEMR/V12/ISSUE 04/173**

Title **Prediction of Heart Attacks Anticipation with Machine Acquisition Methods**

Volume 12, Issue 4, Pages: 1343-1352

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International Journal for Innovative Engineering and Management Research
PEER REVIEWED OPEN ACCESS INTERNATIONAL JOURNAL
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# Prediction of Heart Attacks Anticipation with Machine Acquisition Methods

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**Abstract:**
To predict and categorize the bosom disease patient, we utilized assorted machine acquisition algorithms like Random Forest, logistic regression, and SVM. Regulating how the model can be used to ameliorate the quality of bosom attack predictions for any individual was done in a very helpful way. Cardiovascular sicknesses are viewed as one of the most troublesome illnesses to treat and many individuals experience the ill effects of this illness on the planet including related demise because of bosom infections. The most difficult problem in studying medical checkup data are prognostic option bosom diseases. In the healthcare sector, machine acquisition has been utilized to analyze medical datasets and predict diseases, making it an intriguing technology. Bosom disease is acknowledged as one of the most common causes of causality worldwide. In hospitals, numerous medical specialty systems and instruments hold enormous amounts of clinical data. Therefore, improving prediction quality necessitates a thorough comprehension of bosom disease data. The execution of the framework created with a categorization algorithmic program and applicable attribute selected using assorted feature assortment approaches has been by experimentation measure in this article. With a performance value of 100%, the Random Forest algorithm outperforms the other four when using the MCDM technique, as demonstrated by the experimental results.

**Keywords:** Machine acquisition, SVM, Logistic Regression, Random Forest, Cardiovascular disease

## Introduction

One of the most important parts of the body, the bosom pumps bodily fluid throughout the body. In most cases, bosom failure can result in death. World Wellbeing Association (WHO) assessed that more than 17.3 million individuals pass on every year because of bosom-related infections which comprise 31% of all passings universally. Four out of every five people who die from cardiovascular disease (CVD) do so as a result of strokes or bosom attacks. Worldwide, millions of people are unable to control the hazardous element that contributes to cardiovascular malady, and another oblivious that they are at hazard. Increases in bodily fluid pressure and glucose levels, as well as obesity and overweightness, can indicate a person's hazard of cardiovascular disease. In healthcare facilities, these vital signs can be easily measured to identify patients most at hazard for cardiovascular disease. Data can now be collected and stored thanks to new technology in the healthcare sector. One of the most important aspects of the medical field is data analysis. Various machine acquisition algorithms are used to collect and analyze medical datasets to identify specific outlines and colligate. While the machine acquisition

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algorithm does not identify the underlying origin of diseases, it does make a significant contribution to disease prediction and acquisition from current data for future disease prevention. The model can study or train on its own and better on old findings when it draws finer predictions and conclusions, machine acquisition has gained popularity. Decision-making, classification, and prediction are just a few of the many uses for machine acquisition algorithms. As the MCDM performs for selecting the foremost ML method for CVD anticipation, performance analysis employing order orientation by sameness to the perfect result (TOPSIS) is presented. When it comes to analyzing captured datasets and spotting obscure discrete patterns, machine acquisition (ML) methods are an important part of the healthcare industry. During data imbalances, real model performance cannot be replicated by exploiting only ML model scrutiny and lone considering a few or no assessment criteria like preciseness, quality, sensitiveness, and AUC. A variety of ML algorithms have been utilized to predict CVDs in the past. In this paper, however, a different approach is taken by selecting ML algorithms. MCDM is utilized to choose the most reliable ML strategy. The criteria are ranked and evaluated using MCDM methods to select the best alternative.

Computer-aided systems boost the new center of power by producing massive amounts of raw data as the information age advances. Practitioners face a challenge when it comes to extracting significant information from this type of data. Using cutting-edge statistical methods, data production, AI, machine acquisition, and deep acquisition are comparatively recent and likely technologies for locating significant databases or establishing relationships. Many researchers are interested in the comparatively new and developing fields of medical data mining and knowledge exploration [1]. Physicians may be able to make more accurate diagnoses thanks to advances in medical data collection. Machine biomedical systems can also fastness the process and improve forecasting quality for a variety of diseases, including cancer, diabetes, skin diseases, kidney diseases, and bosom diseases. Cardiovascular sickness has been shown to have a swollen fatality rate among all of these conditions [1–4].

**Related Work**

Before Various ML algorithms have been used by researchers to foretell bosom diseases, and various per centum of quality has been achieved through a variety of approaches. The primary objective is to categorize and anticipate bosom disease diagnoses. Golande and others analyzed several bosom disease prediction machine-acquisition algorithms. KNN, K-Means, and DT methods that can be used for categorization were used to assess with greater precision. After some investigation, it was determined that DT produced the most accurate results. The writer projected improving predictive quality using assorted algorithms and parametric quantity adjustments. G. D. Kumar and others implemented GB, SVM, NB, LR, and RF-supervised machine acquisition algorithms using a dataset from the UCI directory to propose a method for predicting cardiovascular disease. The LR algorithm was taken into consideration for CVD prediction after comparing the quality of all algorithms. It produced the best results when compared to the other algorithms. Khennou and coKNN were present to dimension missing data values from the UCI Repository. For classification, SVM and naive Bayes machine acquisition algorithms are utilized. According to the author's findings, NB outperforms SVM with a

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quality of 87%. D. Shah utilized the Cleveland dataset to make a prediction of cardiovascular disease. By the instrumentality of the DT, KKN, RF, and NB algorithms, he made use of 14 attributes. By using data pre-processing, null and noisy data can be altered and filtered. With a k value of 7, KNN achieves the highest quality of 90.79 percent. Toom and co. demonstrated a machine acquisition (ML) system for coronary artery bosom disease data analysis and prediction. UCI provided Cleveland bosom with data consisting of 304 diligent cases and 76 characteristics.13 attributes out of 77 properties are used. The writer used three ML methods in two experiments. Utilizing the WEKA data analysis tool to predict using SVM, FT, and Bayes Naive ML techniques achieved a quality of 88.3 percent in the Holdout test, 88.5 percent in the cross-validation test, and 83.8 percent in the SVM and Bayes Naive tests, respectively. Using the Best First selection method, the author chooses and applies the seven best attributes for cross-validation tests. The outcomes are: Bayes naive and FT both have a quality of 83.99%, while SVM has a quality of 85.1%. Parthiban and others utilized SVM ML and Naive Bayes methods to anticipate cardiovascular disease in diabetic patients. 500 patient cases from a Chennai-based Research Institute dataset are used.142 patients have the bosom disease, while 358 patients have no disease at all. The Naive Bayes algorithm with the WEKA tool had a quality of 74%, while the SVM algorithm had the highest quality of 94.6%. Based on the quality score, scientists chose the finest ML algorithmic rule from the papers. When choosing the best machine acquisition algorithm, the most parametric quantity. The utilization of model blend strategies, for example, MCDM is prescribed as the most ideal decision to decide in favor of the best forecast ML calculation [7].

Gao and others [5] suggested a model for predicting bosom disease that combined LDA and PCA feature extraction algorithms with ensemble approaches (boosting and bagging). For the purpose of predicting bosom attacks, Takci [6] utilized four feature selection techniques and 12 compartmentalization algorithms from assorted families. The quality of the exemplary, processing time, and ROC analysis results were used to evaluate them. That is what the outcome shows, without including determination, the greatest precision esteem was 82.59%; it rose to 84.81% when feature selection was used. By exploitation of linear SVM and naive Bayes, the model was accurate to 84.95 percent. Moreover, the handling time was lessened from 360 to 188 milliseconds. Based on the average quality value, the ReliefF algorithm has the highest model quality of the four different characteristic selection methods. As a result, the author stated that bosom attack prediction research benefits from feature selection when the right combinations are taken into consideration.

**Methodology**

The dataset includes several properties used for cardiovascular illness investigation and is used in our proposed method. The detailed flow drawing of the proposed procedure is shown in Figure 1. The dataset contained 14 features that were imported. Reprocessing, normalization, and the division of the data into portions for the training and testing datasets occur immediately. We utilized the ML algorithms LR, SVM, FR, NB, and KNN, which were chosen for their widespread use. We use the TOPSIS method to evaluate the proposed MCDM model in terms of its F1 score, quality, recall, precision, and AUC values in order to

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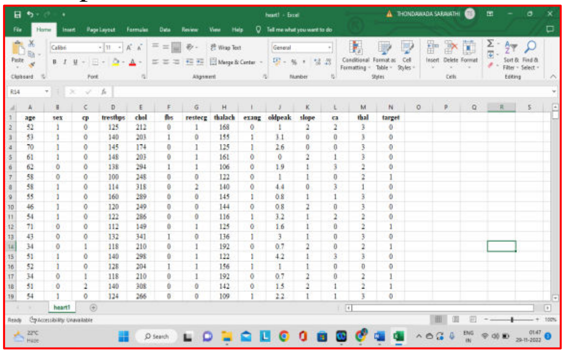
select the best ML algorithm from the five that were chosen.

**A. Dataset:** The dataset provided by the Cleveland Clinic Foundation is used in this paper. The UCI ML repository contains disease datasets and includes a vast array of datasets from various institutions. There are 1026 records and 14 properties in the UCI dataset, but 14 dimensions are used in our experiment, as shown below.



| age | sex | cp | trestbps | chol | fbs | restecg | thalach | exang | oldpeak | slope | ca | thal | target |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 52 | 1 | 0 | 125 | 212 | 0 | 1 | 168 | 0 | 1 | 2 | 2 | 3 | 0 |
| 53 | 1 | 0 | 140 | 203 | 1 | 0 | 155 | 1 | 3.1 | 0 | 0 | 3 | 0 |
| 70 | 1 | 0 | 145 | 174 | 0 | 1 | 125 | 1 | 2.6 | 0 | 0 | 3 | 0 |
| 61 | 1 | 0 | 148 | 203 | 0 | 1 | 161 | 0 | 0 | 2 | 1 | 3 | 0 |
| 62 | 0 | 0 | 138 | 294 | 1 | 1 | 106 | 0 | 1.9 | 1 | 3 | 2 | 0 |
| 58 | 0 | 0 | 100 | 248 | 0 | 0 | 122 | 0 | 1 | 1 | 0 | 2 | 1 |
| 58 | 1 | 0 | 114 | 318 | 0 | 2 | 140 | 0 | 4.4 | 0 | 3 | 1 | 0 |
| 55 | 1 | 0 | 160 | 289 | 0 | 0 | 145 | 1 | 0.8 | 1 | 1 | 3 | 0 |
| 46 | 1 | 0 | 120 | 249 | 0 | 0 | 144 | 0 | 0.8 | 2 | 0 | 3 | 0 |
| 54 | 1 | 0 | 122 | 286 | 0 | 0 | 116 | 1 | 3.2 | 1 | 2 | 2 | 0 |
| 71 | 0 | 0 | 112 | 149 | 0 | 1 | 125 | 0 | 1.6 | 1 | 0 | 2 | 1 |
| 43 | 0 | 0 | 132 | 341 | 1 | 0 | 136 | 1 | 3 | 1 | 0 | 3 | 0 |
| 34 | 0 | 1 | 118 | 210 | 0 | 1 | 192 | 0 | 0.7 | 2 | 0 | 2 | 1 |
| 51 | 1 | 0 | 140 | 298 | 0 | 1 | 122 | 1 | 4.2 | 1 | 3 | 3 | 0 |
| 52 | 1 | 0 | 128 | 204 | 1 | 1 | 156 | 1 | 1 | 1 | 0 | 0 | 0 |
| 34 | 0 | 1 | 118 | 210 | 0 | 1 | 192 | 0 | 0.7 | 2 | 0 | 2 | 1 |
| 51 | 0 | 2 | 140 | 308 | 0 | 0 | 142 | 0 | 1.5 | 2 | 1 | 2 | 1 |
| 54 | 1 | 0 | 124 | 266 | 0 | 0 | 109 | 1 | 2.2 | 1 | 1 | 3 | 0 |

**Fig: Bosom Disease Dataset**

**B. Trained classifiers:** In the proposed method for classification, we have considered five machine acquisition algorithms: Naive Bayes (NB), Logistic Regression (LR), Random Forest (RF), Support Vector Machine (SVM) and K-Nearest Neighbour (KNN). Each of the various classifiers that were evaluated as part of our projected system will be briefly represented in the sections that follow.

**C. Logistic Regression:** The well-known supervised machine acquisition algorithm known as logistic regression is primarily utilized in binary classification tasks. The categorical dependency class defines the variables in logistic regression, and the results must be a category or distinct feature. The logistic function is used in LR instead of proper a hyperplane or consecutive line to produce a range of values from 0 to 1 for the solution to a linear equation. If the more of attributes in the signaling dataset is less than the few of observations, the LR algorithm may overfit.

**D. SVM:** It is another categorization algorithmic rule that can handle bilinear and nonlinear data. SVM classifies the instance using kernel functions and then selects the best solution based on these modifications A discrimination classifier, or SVM in order to reduce the likelihood of misclassification.

**E. Random Forest:** Regression and classification problems can both benefit from the supervised machine acquisition technique known as Random Forest (RF). Bagging or bootstrap aggregation is used to gather decision trees, which are less likely to be over fitted in this approach. The fact that RF works well with large datasets and high dimensionality is its greatest advantage. RF uses a majority vote system in classification problems, whereas it uses the mean of all the outputs from every of the judgment trees in regression difficulty.

**Implementation**

Data mining methods like SVM, Decision Tree, Random Forest, Logistic Regression, and Naive Bayes are put-upon in the planned work to foretell the likelihood of bosom disease and categorize the hazard levels of patients. The following are the implementation of three algorithmic programs Random Forest, Support Vector Machine, and Logistic Regression. The results of selecting the best MCDM model for the bosom disease are presented in this section. The experimentation is carried out by preparation of 79% of the dataset, which consists of 241 instances and has 15 distinct constants. The remaining 21% of the dataset, which consists of 62 positions, is used for the test. The results of calculating various evaluation criteria are summarized in Table 2. Because the quality results for LR and SVM are

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comparable at 83.72 percent and NB has a quality of 83.3%, it will be hard to choose between them based on a rating criterion. Using only one performance criterion, such as quality, may result in conclusions that are incorrect and will make it more difficult to select the best algorithm.

### A. Support Vector Machine:

The following are the Support Vector Machine algorithm steps:

1. Include essential collection.
2. Attach the dataset and separately find the X and Y axis variables.
3. Separate the dataset into two parts: test and train.
4. Setting up the SVM classifier hypothesis
5. The SVM classifier model's adaptation

```
Command Prompt

C:\Users\SARAVATHI>notepad HeartSVM.py

C:\Users\SARAVATHI>python HeartSVM.py
Accuracy= 0.8731707317073171

C:\Users\SARAVATHI>
```

**Fig: quality of SVM on bosom Disease Dataset**

The figure explains the quality of the SVM is 87.31%.

### B. Logistic Regression:

The following are the Logistic Regression algorithm steps.

1. Import the necessary libraries.
2. Explore, visualize, and load the data.
3. Purify the data.
4. Take care of any anomalies.
5. Create a testing set and a training set from the data.
6. Using SKLearn, create a logistic regression model.
7. Make a prediction based on the test data and the model

```
Command Prompt

C:\Users\SARAVATHI>notepad HeartLogic.py

C:\Users\SARAVATHI>python HeartLogic.py
Accuracy= 0.8195121951219512

C:\Users\SARAVATHI>
```

**Fig: quality of LR on bosom Disease Dataset**

The figure explains the quality of the Logistic Regression (LR) is 81.95%.

### C. Random Forest:

The following are the Logistic Regression algorithm steps:

1. Pick some samples at random from a given dataset.
2. Every sample will make over a decision tree and use each group decision tree to get a prediction.
3. Give each predicted result a vote.
4. Select the reasoning that received the most votes.

```
Command Prompt

C:\Users\SARAVATHI>notepad HeartRF.py

C:\Users\SARAVATHI>python HeartRF.py
Accuracy= 1.0

C:\Users\SARAVATHI>
```

**Fig: quality of RF on bosom Disease Dataset**

The figure explains the quality of the Random Forest (RF) is 81.95%.

### D. Comparison Table:

The following is the comparison table with valid metrics.

| S. No | Name of the Parameter | SVM | LR | RF |
|---|---|---|---|---|
| 1 | Size of the Dataset | 37.2KB | 37.2KB | 37.2KB |
| 2 | No of instances | 1026 | 1026 | 1026 |
| 3 | quality | 87.31 | 81.95 | 100 |

**Table 1: Comparison between algorithms**

## Results

The fundamental thought of the execution is to guarantee that the Monkeypox sickness severer impacted job gathered measurements worked in a manner that can propel readiness, and development from their most memorable standpoint.

## ERNN Algorithm

The most widely used method for Artificial Neural Network (ANN) systems is RNNs. It is a form of brain system organization in which input associations are represented by circles. Like the Multi-Layer Perceptron (MLP) design, the establishment yield is compared to the goal result, and a mistake is used to refresh the company hundreds using the Backpropagation error calculation, with the unique circumstance that the advantages of affiliation hundreds of neurons to enhance the accuracy and performance rate of the proposed model. The prototypical of the Elman network-based technique is evaluated and considered accurate by the following equation 1.

$$'S_{ij} = '(L * K)'_{ij} = \sum_{a=\left[-\frac{m}{2}\right]}^{\left[\frac{m}{2}\right]} \sum_{b=\left[-\frac{n}{2}\right]}^{\left[\frac{n}{2}\right]} 'L_{i-a,j-b}\, 'K_{\frac{m}{2}+a,\frac{n}{2}+b} \#(1)$$

## Algorithm Steps

ERNN [12] is one of the most utilized classes of networks of neurons. Its Arrangement and Labeling: The part of the conversation called "element acknowledgment" and "labeling" are very helpful and works well to get the desired results. We made positive improvements to traditional RNN and obtained ERNN in order to deduce the benefits by making a group of changes [13, 14] to existing prototype.

Our experiment involved the following related processes:

| |
|---|
| Step 1: Import required libraries |
| Step 2: Pre-processing of the dataset |
| Step 3: Combined RNN with Extended Neurons |
| Step 4: Perform 10-folded cross-validation with 2 classes |
| Step 5: Import Keras deep learning library with all supported libraries |
| Step 6: Reset all parameters of ERNN |
| Step 7: Enhance the ECNN part and about regulation of loss calculation function |
| Step 8: Enhancement of yield part of 10-folded with 2 classes |
| Step 9: Accumulate the ERNN parameters |
| Step 10: Adjusting the ERNN in the preparation of model |
| Step 11: Load the Monkeypox disease infection image dataset |
| Step 12: Predicting the infection severity through classifying the dataset into 2 classes |
| Step 13: Outcome of the trained model and stop the model |

**Table 1: The proposed ERNN model algorithm steps**

## Input Dataset

The research dataset collected from various open-source resources such as Kaggle had 871 instances

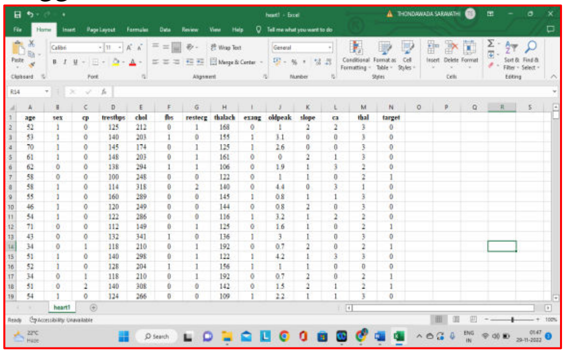

**Fig. 3: Input dataset of the proposed prototype**

## Conclusion

Here we use 14 medical characteristics of a patient to predict this and classify him as likely to have bosom disease. Three algorithms are used to train these medical attributes: logistic regression, random forest classifier, and SVM. The proposed exemplary is utilized in the Multi-Criteria Decision-Making (MCDM) approach that we propose and present in this paper to select the most suitable categorization algorithmic rule for the investigation of bosom disease reasoning. Different characterization methods are unmistakable that has emerged lately for adequacy and effectiveness in the determination of coronary illness. For improved bosom disease prediction analysis in the future, much than five antithetical machine acquisition methods would be utilized, and data from multiple medical institutions can be gathered to formalize the strengths and weaknesses of machine acquisition algorithms for improved MCDM evaluation.

This article's primary objective is to investigate the striking of characteristic option methods on bosom disease prediction quality. Using a variety of feature selection algorithms. To see how feature selection affected the results, experiments were carried out with and without feature assortment. Using the KNN classifier, the advanced result supply a model quality of 63.92% without feature selection. After that, feature selection was used to carry out the experiment. All the feature selection algorithms' models have seen an increase in prediction quality. The maximum quality was 100% without feature selection; Using backswept feature assortment and a decision tree morpheme, this measure was raised to 89.22 percent. Based on the results of the experiments, it appears that using feature selection algorithms can effectively classify the disease using only a small number of features.

Depending on the lineament selection method and acquisition algorithm used, there is a significant variation in the improvements made by overusing the original dataset; Consequently, in order to obtain the most effective model, it is essential to measure different combinations of characteristic selection plan of action and acquisition algorithms. However, it is not possible to foretell that will be salutary without conducting numerous experiments and analyses. The methods for aggregate feature action could be combined with methods for assembling (hybrid) to find the best feature subsets for modeling. Additionally, international real-time medical datasets can be utilized for model development. For bosom disease prediction, this could improve performance and quality.

**Acknowledgment**
Thanks to BlueCrest University for providing all facilities in the Department in order to execute these experiments.

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