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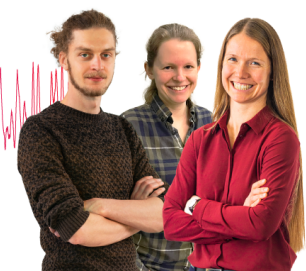
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A Novel Enhanced Prediction of Possibility for Cardiac Arrest in Cardiovascular Disease of Heart Patients by Comparing Support Vector Machine over Decision Tree

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Abstract. The goal is to anticipate cardiac arrest in heart disease patients. Machine learning methods like SVM and decision tree categorise photos (DT). To effectively and reliably analyse labelled pictures with G power of 80%, threshold 0.05 percent, CI 95 percent mean and standard deviation, SVM and Decision Tree sample sizes of $n = 5$ were iterated 10 times. The Support Vector Machine (SVM) outperformed the Decision Tree (DT) in predicting and categorising cardiac patients' data with a p-value of 0.05. Support Vector Machine predicts cardiomyopathy risk better than Decision Tree.

Keywords: Heart disease, Support Vector Machine, Decision Tree, Machine Learning, Novel Prediction method for Cardiac Arrest, Cardiovascular disease.

INTRODUCTION

When the heart or blood vessels malfunction, a cardiovascular illness ensues. Heart disease now kills more people worldwide than cancer. Heart disease is the biggest cause of mortality globally. Cardiovascular disease killed 17.9 million individuals worldwide in 2015, according to the WHO. This work uses a UCI Machine Repository heart disease patient data set to enhance cardiac sickness detection. [1]. Most algorithms diagnose (via feature categorization) or forecast atrial fibrillation (AF), the most common cardiovascular disease. AI-powered systems may now predict atrial fibrillation (AF) based on an ECG diagnostic. This study uses the MIT-BIH AF Database to incorporate healthy persons, patients with AF, and onset characteristics in the unique cardiac arrest prediction algorithm (AFDB). Paroxysmal atrial fibrillation (PAF), an irregular heartbeat, may lead to heart failure and stroke if ignored. [2]. Thus, early PAF detection prevents complications and death. Despite their limited computational capabilities, implanted defibrillators can diagnose and treat the condition. With this restriction in mind, the authors of this work provide a novel set of criteria that may accurately diagnose PAF. ECG signals from PhysioNet's atrial fibrillation prediction database (AFPDB) are used to test the method. [2], [3]

Google Scholars has 1200 articles and Elsevier 400. Here is key survey-based research. Heart disease kills almost 30% of all persons globally, or 1.5 crore, according to the WHO. [4] [5]. We use E-KNN, an extension of KNN, to predict cardiac events and compare them to KNN, SVM, and trees for classification and regression. The suggested approach prioritises attributes using the chi-square test. [6]. Data analysis tools were available to scientists. [7]. In recent years, system innovation in medicine, disease discovery, and patient engagement has increased. [8]. Investigations have had two stages. The first step is kNN classification of test data. In phase 2, the ACO seeds the population and finds the optimum solution. Our staff has extensive research expertise in several fields. [9]–[29]

Age, gender, BMI, heart rate, smoking status, glucose levels, daily cigar intake, blood pressure drugs, and others were utilised to distribute the heart disease dataset's complete features. Most major health issues need assessment include diabetes, hypertension, and stroke. This study compares the Support Vector Machine with the decision tree to suggest a better risk prediction method for cardiomyopathy in cardiovascular disease patients.

MATERIALS AND METHODS

The Image Processing Lab at SIMATS' Saveetha School of Engineering was the location where the research on the novel prediction approach for cardiac arrest was conducted. Two different sets of classifier algorithms are used to determine how serious a cardiac condition is likely to become in the future. The Support Vector Machine, abbreviated as SVM, and the K-Nearest Neighbor Decision Tree make up the first category (KNN). The number of samples taken from each group was determined to be five, for a total of ten samples. An first investigation was carried out with the help of Clinical.com utilising the following parameters: an 80 percent G power; a 5 percent threshold; a 95 percent confidence interval (CI); and a 95 percent standard deviation. The standard deviations for SVM= 0.8646 and Decision Tree= 0.7240 were used to establish the sample sizes for each group, which came out to be five individuals in each group.

In order to run the Novel Prediction method for Cardiac Arrest on Jupyter Notebook, you will need a processor with an Intel i3 chip, a hard drive with 100 gigabytes of storage space, 8 gigabytes of random access memory, and a Windows operating system on which the Jupyter Python software package has been installed. The information on cardiac patients that is shown in Table 1 comes from Kaggle [30]. This data includes the patients' ages, genders, smoking status, blood pressures, heart rates, and other vitals.

The Support Vector Machine, sometimes known as SVM, is a method of supervised machine learning that may be used to problems involving classification and regression. It is often utilised as a solution to classification problems in this environment. The SVM performs regular updates to the database in order to locate the best possible border between the various outputs. Classification work may be done by a Support Vector Machine (SVM) by locating the hyperplane that achieves the best possible balance between the two classes. The "Support vectors" are what define the hyperplane in question. Next it moves to the next step, then it is to fit the model and the data to determine achieve accuracy. This step involves both training and testing data. The SVM Algorithm determines which hyperplane has a larger margin than the others. The classification process may be simplified by translating the data to a high-dimensional domain and employing linear decision surfaces. Regularization, Gamma, and Kernel analysis are the three types of data analysis that may be controlled by adjusting these parameters.

Pseudo Code for Support Vector Machine

1. Importing the Support Vector Machine (SVM) classifier from the scikit-learn library.
 - `'from sklearn.svm import SVC'`
2. Setting up a grid search for hyperparameter tuning. This step is crucial for finding the best combination of hyperparameters for the SVM model. You specify a range of values for the 'C' and 'gamma' hyperparameters.
 - Creating an SVM classifier ('SVC') with an RBF kernel and enabling probability estimation.
 - Using 'GridSearchCV' to perform a grid search over the specified hyperparameters with 10-fold cross-validation.
 - The result is stored in 'svm_clf', which is an optimized SVM model.
3. Fitting the SVM model to the training data and finding the best hyperparameters based on cross-validation results.
 - `'svm_clf.fit(X_train, y_train)'`
 - `'svm_clf.best_params_'` retrieves the best hyperparameters found during the grid search.
4. Initializing predictions on the test dataset using the optimized SVM model.
 - `'svm_predict = svm_clf.predict(X_test)'`
5. Printing the accuracy of the SVM model on the test dataset.
 - `'print(f"Using SVM we get an accuracy of {round(svm_accuracy*100,2)}%")'`
6. Printing a classification report. This report provides detailed information about precision, recall, F1-score, and support for each class, allowing you to assess the model's performance in more depth.
 - `'print(classification_report(y_test, svm_predict))'`
7. Calculate performance parameters and print the values

9. Ending the code sequence.

When paired with techniques for machine learning, a decision tree may provide a representation of the decision-making process and the many possible outcomes in the form of a tree. In this context, it covers the events that take place, the results of those events, the costs of resources, and the value of the possibilities. In the same way that algorithms and flowcharts can only use if/then statements to control what happens, decision trees can only control what happens in the same way. In an inverted decision tree, the root node of the decision tree might be placed at the very top of the tree. The nodes at the base, the leaves at the tips, and so on are the three primary elements that make up every decision tree. It's possible that a test or an event is represented by each internal node in this decision tree. To find out which comes up first, flip a coin and see what it lands on. After compiling all of the essential characteristics, the last nodes of the decision tree, known as the leaf nodes, provide the appropriate class labels for each test result. The categorization criteria may be deduced from the routes that lead from the root node to the leaf nodes. Applications of classification and regression analysis might benefit from the usage of decision trees as a machine learning tool. The target is assessed by the classification tree in order to establish whether or not it was the head or the tail. Similar representations may be seen in regression trees, which make predictions based on continuous variables rather than discrete ones.

Pseudo Code for Decision Tree

1. Importing the DecisionTreeClassifier from scikit-learn.
 - `'from sklearn.tree import DecisionTreeClassifier'`
2. Creating a DecisionTreeClassifier instance with a specified random seed for reproducibility.
 - `'dtree = DecisionTreeClassifier(random_state=7)'`
3. Defining a dictionary of hyperparameters for the Decision Tree classifier and setting up a grid search for hyperparameter tuning.
 - `'params'` is a dictionary that contains different values for the maximum number of features to consider for splitting (`'max_features'`), the minimum number of samples required to split an internal node (`'min_samples_split'`), and the minimum number of samples required to be at a leaf node (`'Min_samples_leaf'`).
 - `'tree_clf'` is a GridSearchCV object that takes the DecisionTreeClassifier, the parameter grid (`'params'`), and the number of CPU cores to use in parallel (`'n_jobs=-1'`) for grid search.
4. Fitting the Decision Tree model to the training data and finding the best hyperparameters based on cross-validation results.
 - `'tree_clf.fit(X_train, y_train)'`
 - `'tree_clf.best_params_'` retrieves the best hyperparameters found during the grid search.
5. Initializing predictions on the test dataset using the optimized Decision Tree model.
 - `'tree_predict = tree_clf.predict(X_test)'`
6. Calculating the accuracy of the Decision Tree model on the test dataset using `'accuracy_score'`.
 - `'tree_accuracy = accuracy_score(y_test, tree_predict)'`
7. Printing the final accuracy of the Decision Tree model on the test dataset.
 - `'print(f"Using Decision Trees we get an accuracy of {round(tree_accuracy*100,2)}%")'`
8. Ending the code sequence.

Statistical Analysis

IBM SPSS version 21 was used for the research that was done on the Novel Prediction Technique for Cardiac Arrest. It is an application for the analysis of data that makes use of statistical methods. The anticipated accuracy was recorded for each of the five iterations using a maximum of ten samples, regardless of whether the approaches under consideration were new or already in use. An independent Sample T-test was performed on the iteration outcomes to see how they compared. Age, gender, body mass index (BMI), heart rate (HR), smoking status (NST), and glucose levels are examples of independent variables. Cigarettes smoked per day, blood pressure medications, stroke prevalence, hypertension prevalence, and diabetes prevalence, in addition to the dependent variables and data point hyperplanes that are related with each of these conditions. It is essential to investigate these characteristics and

use visualisation to carry out prediction and grouping operations on the data in order to reduce the risk of having a heart attack.

RESULTS

Displayed here to provide an example of the datasets utilised by the Novel Prediction method for determining the risk of cardiac arrest are characteristics such as age, gender, body mass index (BMI), heart rate, smoking status, daily cigar consumption, blood pressure medications, and the prevalence of cardiovascular disease, hypertension, and diabetes. All of these characteristics can be found in the patient's medical history (Table 1).

TABLE 1. Age, gender, body mass index, heart rate, cigarettes smoked per day, number of cigars smoked per day, blood pressure medications, prevalence of stroke, hypertension, and diabetes are all characteristics of the datasets describing heart patients.

S.No	Attribute	Data Type	Value	Description
1	Gender	Integer	Sex	Gender of a Patient
2	Age	Integer	PRIMARY KEY	Age of a Patient
4	CurrentSmoker, CigsPerDay	Double	Smoking	Present patient smoking status and Number of Cigars smoking on a single day.
5	BPMeds, sysBP, diaBP	Double	Blood Pressure	Readings of Blood Pressure and Patient Meds and Diabetes.
6	PrevalentStroke, PrevalentHyd,	Integer	Prevalent of HeartStoke and Hypertension	Patient's prevalent of heart stroke and prevalent of Hypertension.
7	Diabetes, Glucose	Integer	Readings of Diabetes and Glucose	Recordings of patient diabetes and glucose level in the blood.
8	Heart Rate	Integer	Readings of Patient Heart rate	Readings of patient's heart rate per minute.
9	totChol	Double	Total Cholesterol	Readings of patient's cholesterol.

The Specified Data Visualization Showing Viewing Representation of Data for Patients That Meets All Module Requirements. (Table 2).

TABLE 2. The Specified Data Visualization Showing Viewing Representation of Data for Patients That Meets All Module Requirements.

S.No.	Gender	Age	currentSmoker	cigsPerDay	BPMeds	PrevalentStroke	PrevalentHyp	Diabetes	totChol	sysBP	diaBP	BMI	heartRate	glucose	TenYearCHD
1	1	39	0	0.0	0.0	0	0	0	195.0	106.0	70.0	26.9	80.0	77.0	0
2	0	46	0	0.0	0.0	0	0	0	250.0	121.0	81.0	28.7	95.0	76.0	0
3	1	48	1	20.0	0.0	0	0	0	245.0	127.0	80.0	25.3	75.0	70.0	0
4	0	61	1	30.0	0.0	0	1	0	225.0	150.0	95.0	28.5	65.0	103.	1
5	0	46	1	23.0	0.0	0	0	0	285.0	130.0	84.4	23.1	85.0	85.0	0

Multiple iterations of SVM and Decision Tree with a sample size of 150 and accuracy calculations in (Table 3).

TABLE 3. SVM and KNN iterations are grouped for statistical analysis by Mean (3.93), Standard Deviation (1.38), and Standard Error Mean (3.11). (4.23). The SPSS dataset is put through a descriptive Independent Sample Test of Accuracy and Precision.

	Group	N	Mean	Std.Deviation	Std. Error Mean
Accuracy	SVM	5	85.2380	1.06882	.47799
	Decision Tree	5	71.3380	1.11636	.49925
Precision	SVM	5	20.5540	.68664	.30708
	Decision Tree	5	17.2200	.65211	.29163

The average accuracy of SVM was found to be 86.46 percent, whereas the average accuracy of Decision Tree was found to be 72.40 percent. Calculated P-value = 0.001 and Significant value = .625, Mean Difference = 13.85, and Confidence Interval = (12.25614) - 15.44386 from Independent Sample Test of Accuracy and Precision (Table 4).

TABLE 4. Accuracy and Precision Assessed Through Random Sample Testing: T-Test scores are assumed to be equal with and without the use of this assumption. The result of an independent samples t test conducted by the Group Statistics department was .491, which is statistically significant above the .05 threshold. Therefore, this demonstrates that SVM and Decision Tree are distinctive from one another. The margin of error is then shown in the form of a bar chart with groupid on the X-axis and the mean purity on the Y-axis.

		Levene's test for equality of variances		T-Test for equality of means					95% confidence interval of the difference	
		F	Sig.	t	df	Sig. (2-tailed)	Mean difference	Std. error difference	Lower	Upper
Accuracy	Equal Variance assumed	.258	.625	20.0	8	<.001	13.85	.6911	12.25	15.44
	Equal Variance not assumed			20.0	7.985	<.001	13.85	.6911	12.25	15.44
Precision	Equal Variance assumed	.012	.916	7.87	8	<.001	3.334	.4234	2.357	4.310
	Equal Variance not assumed			7.87	7.979	<.001	3.334	.4234	2.356	4.311

SVM reformulates the problem so that data is mapped implicitly into this space as shown in (Fig 1).

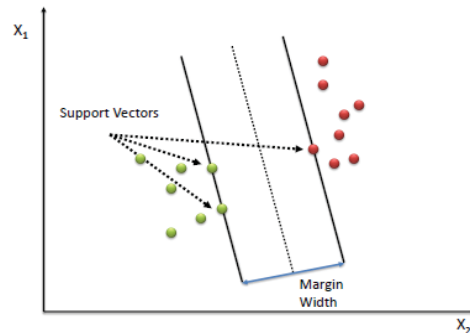


FIGURE 1. Maximum-margin Support Vector Machine optimum hyperplane (SVM). It obtains the support vectors by categorising the hyperplane to display the distance between the hyperplane in the support vectors' nodes.

Those between the ages of 51 and 63 (shown by the blue bars) have the greatest chance of having CHD (Fig 2).

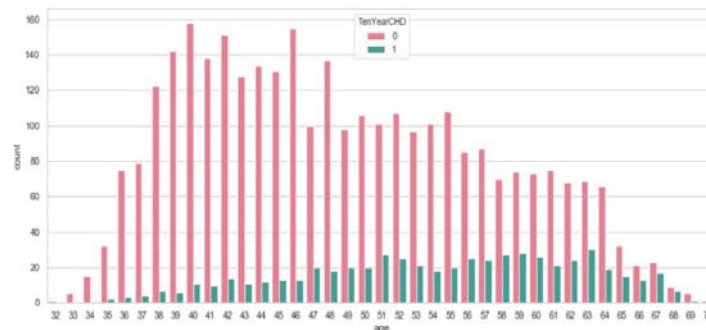


FIGURE 2. The people with the highest risk of developing CHD are between the ages of 51 and 63 i.e. the blue bars.

According to the results of Seaborn's Correlation Heat Map, there is not a single feature that has a correlation of 0.5 or higher with the ten-year risk of CHD. This suggests that these factors are not accurate predictors of the outcome. This offers a rating system ranging from 0 to 1, inclusive (Fig 3).



FIGURE 3. Seaborn's Correlation Heat Map confirms that there are no characteristics that have a correlation of 0.5 or higher with the ten-year risk of CHD, indicating that these variables are not reliable predictors. As a result, we may create a hierarchy based on the ratio of (0.0 to 1.0).

The variables of age, total cholesterol, blood pressure (both systolic and diastolic), body mass index (BMI), heart rate (HR), and glucose levels (glucose) were plotted from birthdates using normal scaling (0, 50 to 140 Readings). Data has been made available for testing and training, and a classification analysis has been carried out to provide predictions about the result and accuracy. (Fig 4).

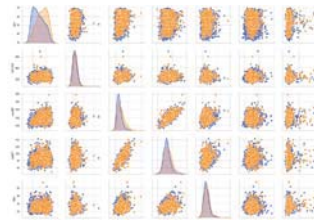


FIGURE 4. Age, total cholesterol, blood pressure (systolic and diastolic), body mass index (BMI), heart rate (HR), and glucose levels (glucose) plotted from birthdates using normal scaling (0, 50 to 140 Readings). Data has been provided for testing and training with the Classification analysis done to forecast the outcome and accuracy.

Therein lies the last point of convergence between SVM and Decision Tree. After that, we build a bar graph to examine the outcomes of our SVM-based Decision Tree for predicting cardiac illness. The groupid is plotted along the X-axis, and the mean purity is shown along the Y-axis. Numbers Contained Within a Group The significance level of the independent samples t test was 0.625, which is more than 0.05, which is the minimum acceptable value. (Fig 5).

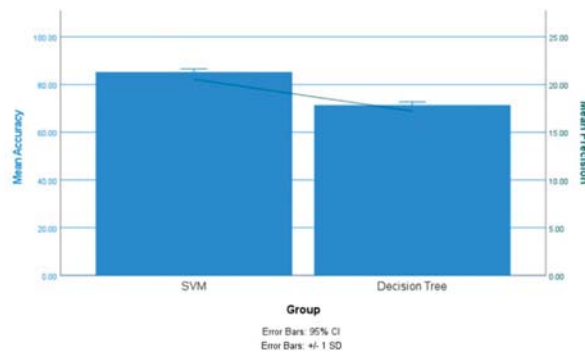


FIGURE 5. The mean accuracy of SVM and Decision Tree are compared. The results reveal that both the mean accuracy and the standard deviation are higher than those of Decision Tree. Results from an independent samples t test showed a significance of .491, over the threshold for statistical significance set at .05. The Y-axis shows the standard deviation of the mean detection accuracy, while the X-axis contrasts SVM with Decision Tree.

Fig. 5 shows a comparison of SVM's (86.46 percent) accuracy to that of Decision Tree's (72.40 percent), with a confidence interval level of 75% and an error bar of 95%.

DISCUSSION

According to the findings of the t-test conducted on independent samples, Decision Tree performs better than SVM in terms of accuracy ($p < 0.005$).

According to the Most Recent Discoveries [31], it has a more efficient value structure and surpasses SVM by a margin of 34%. The SVM and Decision Tree models, both of which have different capacities when confronted with a problem, are compared and contrasted in this study. In contrast to this prediction, which makes use of structural data for the purpose of forecasting strategies into the generation of relevant data, the analysis that is carried out using fundamental approaches has a lesser degree of acquiring accuracy.

As a consequence of this, the results of the study lead to an improvement in performance in both experimental and statistical analysis; nonetheless, the recommended work has some restrictions, such as threshold and accuracy, which limit its use. Validating the data visually has been accomplished using a number of different implementations of the confidence heart rate interval. As a direct result of this, strategies for geographical data training and the execution of packages in testing scenarios may be used in order to create the processed data. There has not been any evidence found that contradicts the conclusions of the present research as of yet.

CONCLUSION

In this research study, Support Vector Machine over K-Nearest Neighbour for higher classification on Heart Disease predictions. The outcome of the study shows the SVM provides 86.46% higher accuracy than Decision Tree 72.40%.

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