Detection of Cardiac Arrhythmias using ECG Signal

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Abstract

Cardiac arrhythmia is a condition in which the heart's electrical activity is irregular or faster or slower than normal. To detect a heart condition, we need to record the electrical activity in the heart as an electrical signal, which ultimately results in a cardiac signal. Then, the resulting signal must be detected by means of a Hadamard matrix transform using a neural network so that the system can detect whether the signal is out of its normal form. In this paper, we intend to obtain information using a number of medical records registered at the University of London site and analyze and train the system components in Python software using principal component analysis and random forest analysis. Our goal is to classify the patient into one of a variety of cardiac arrhythmias that, after selecting the appropriate features, are classified and evaluated using machine learning algorithms. These classifications were accurate using 64% common neighborhood k, 73% logistic regression, naïve Bayes with 52%, and vector support machine with 66% accuracy.

Keywords: Arrhythmia Detection, ECG, Algorithm Classification, Machine Learning.

1. Introduction

Today, many researchers and scientists in many parts of the world and in disciplines and trends Various academics are conducting research on increasing the level of prevention, health, and treatment They are human diseases. The seriousness and volume of this research are mainly proportional to the degree of risk-taking of the subject in question in destroying personal health, in other words, the amount of investment and commitment of universities and research institutes around the world are too sensitive and risky topics such as heart health. The brain,

blood, nervous system, spinal cord, etc. have been at a very high level. Today, increasing the level of public health in the developed countries of North America and Europe is one of the first priorities of the managers of these countries. According to official statistics World Health Organization (WHO), [1] in countries with moderate incomes, heart disease was the leading cause of death. The issue of diagnosing heart disease and predicting some risky events related to the cardiovascular system such as heart attack, sudden death, coronary artery stenosis, blood pressure shocks, and valvular and mechanical heart problems, is one of the important scientific aspirations of scientists, and researchers in the field over the past five decades. In general, researchers from major American and European universities over the past few decades, with the beginning of a coherent and coordinated movement, have tried to find a solution with acceptable accuracy and appropriate resistance, and significant research budgets to solve this great problem.

Among heart disease problems, researchers are paying more attention to atrial fibrillation, tachycardia, bradycardia, rapid atrial fibrillation, cardiac death, and syncope. This is because all of these diseases are treatable in the early stages, while over time, with acute stages, there may be a severe risk to normal heart function. Among all the different tissues and parts of the body, the part that is most active is mechanical, it is the heart. In order to check the function of a human heart, physicians routinely perform specific measurements and tests, and then, by putting together all the evidence and useful information obtained from the measurements, make an appropriate decision (diagnosis). In general, physicians' measurements of a person are divided into two categories invasive and non-invasive. In hospitals, the sections related to these measurements are subtitled, which they call non-invasive and offensive [2-6].

In non-internal measurements, the sensors are used to perform their measurements without entering the individual's body and provide it to the conversion and collection system. These include a stethoscope, thermometer, electrocardiogram (ECG), echocardiogram (ERI), MRI, Phonocardiogram-PCG, Forearm Pressure Cuff, Pulse Pressure, and Imaging. Nuclear such as SPECT CT and PET are mentioned. Due to the periodic function of the mammalian heart, measurements related to cardiac activity are generally seen periodically and periodically, so signals related to various cardiac activities, such as PCG, ECG, and ABP, include events that can be diagnosed. The initial stages of the disease can be done by machine according to these characteristics [7-11].

At a glance, it can be said to diagnose heart disease with the help of machines. The calculator first needs to make and record appropriate measurements that contain useful and effective information about heart activity. In the next step, the events of each type of measurement must be detected by a noise-resistant method, and the perturbations in the measurement, with acceptable and appropriate accuracy. After this stage, it is necessary to collect and compile a database with a suitable scope with the help of physicians and cardiologists so that it can be used to make appropriate inferences to diagnose heart disease and defects.

Computational complexities are normally performed by the computer while complexities Decisions are the responsibility of physicians and specialists. The role of computers in more accurate medical diagnoses of human heart conditions can be improved by increasing artificial intelligence and expanding and smartening the knowledge base. ECG signal events can be divided into Impulsive and Non-Impulsive. This paper reveals the Incident Location, Onset, and Offset points of each ECG signal event. For the reasons mentioned, identifying and revealing each of the above three points is complex. Which has been the subject of much research in the field of detection of heart disease in recent years [12-18]. This paper consists of 4 main sections: introduction, mathematical models, results of proposed algorithms, and conclusions.

2. Method and Algorithm

The total number of deaths due to cardiovascular disease with the justification of the causes of death. The World Health Organization is 17.3 million a year. Therefore, how to predict cardiac arrhythmias in real life is very important. In this paper, we intend to develop a machine-learning system that can classify a patient into different classes of cardiac arrhythmias. Detection of cardiac arrhythmia can be classified into different classes based on the study of electrocardiogram (ECG) and other characteristics. The first class is for the average patient, while the other classes should show different types of cardiac arrhythmias such as tachycardia, bradycardia, and coronary artery disease, which is a supervised learning issue. The standard data set used for the project is taken from UCI. There are 452 rows, each with a different patient's medical record. There are 279 characteristics such as age, weight, and ECG data related to the patient [19]. General characteristics such as age and weight have discrete integral values, while other ECG properties such as QRS duration have real value. The class variable is our target variable. There are a total of 13 classes [20]. The databases are used in Table 1.

Table 1. The databases.

Number	Class	Instances
1	Normal	245
2	Ischemic changes	44
3	Anterior Myocardial Infarction	15
4	Inferior Myocardial Infarction	15
5	Sinus tachycardia	13
6	Sinus bradycardia	25
7	Ventricular Premature Contraction	3
8	Supraventricular Contraction	2
9	Left bundle branch block	9
10	Right bundle branch block	50
11	Left ventricle hypertrophy	4
12	Atrial Fibrillation or Flutter	5
13	Others	22

The goal is to differentiate between the presence and absence of cardiac arrhythmia and its classification into one of the groups. Given that Python software, which is more efficient than other software, has a relatively good speed and accuracy, it has been used to implement this work, to train and evaluate the data. However, there are differences in the classification of cardiovascular programs. By considering the cardiologist as a benchmark standard, our goal is to minimize this difference by using machine learning tools.

In the first step, some definite features were removed, which 95% of the time represented 1 or 0. If each instruction example has a missing value for a given attribute, the mean value plus or minus the standard deviation for that class attribute to which Belongs is determined. If the majority of values for a specified attribute are missing, we remove that attribute and remove it from the tutorial. Properties can be grouped into 6 blocks, 1- Features related to biographies, such as age, sex, height, weight, and heart rate, 2- Features related to the average wavelength of each interval (PR distance, QRS complex, and ST time intervals), 3- Properties related to the vector angle of each wave, 4- Features related to the width of each wave.

Random forests or random decision forests are a combination learning method for classification, and regression, which is based on a structure consisting of a large number of decision trees, on the training time and output of classes (classification), or on the predictions of each tree. They work separately. Random forests are suitable for decision trees that are over-fitted in the training complex. The first algorithm for random decision forests was developed

by Tin Kam Ho using the random subspace method. Today, in many cases, we are faced with a large amount of data. The rapid advancement of technology in the last century has confronted us with a huge amount of information.

Analyzing this data is very challenging due to the many auxiliary variables that are usually available. The high dimension of the variables and their different effects along with the interaction of the variables has caused the modeling and analysis of such data to be different from the usual data. In this context, we can refer to data mining methods to facilitate the data analysis process. One way to model and analyze this data set is to categorize the data. In this regard, decision trees can be used. The decision tree is one of the best methods for clustering information. This method uses a tree pattern to make a decision. In this method, strategies are used to most likely achieve the desired goal. Another feature of decision trees is conditional probability calculation.

Decision trees consist of three types of decision nodes, random node, and end node. A square typically represents the decision node. The random node is marked with a circle. The end node is marked with a triangle. But in practice, when faced with a vast amount of information, one has to use a vast set of decision trees, or in other words, "random forests". The following examines how to build a random forest decision algorithm. Random tree forest produces many decisions. To classify a new object, place the input vector at the end of each random forest tree. Each tree gives us a classification and we say that this tree "votes" for that class. The forest prefers the category with the most votes (among all forest trees).

If N is the number of modes in the train data set, the N modes are randomly sampled by placing the original data. This is a sample work set for this tree. If we have M variables and consider m smaller than M so that in each node, the m variables are randomly selected from M, and the best separation on m is used to separate the node. The value of m is considered constant during forest construction. Each tree grows as large as possible. There is no pruning. The forest error rate depends on the following two factors, the correlation between the two trees in the forest. Increasing the correlation increases the forest error rate. The power of each tree in the forest. A tree with a low error rate is a strong classifier. The increasing correlation increases the forest error rate. Decreasing m reduces both correlation and power. And increasing it increases both.

The number of trees refers to the number of times a data set is randomly sampled. In addition, in each sampling iteration, a random set of features is selected. In the decision trees, each node

points to one of the input variables. Each leaf corresponds to a class tag value, according to the values of the input variables that are displayed from the root node to the leaf node. The number of trees and the number of leaves is learned through cross-validation [21].

PCA is used to identify patterns in data and then express the data in a way that highlights similarities and differences. First, we use PCA to reduce the number of dimensions by identifying more important features, such as core components. The number of principal components is less than or equal to the number of principal variables. The first principal component has the largest possible variance, and each subsequent component has the highest possible variance under the constraint orthogonal to the previous components. From the Python software library to select a feature, first, the sklearn, SelectKBest, chi, and pca libraries are called, then using the convert_strarr_floatarr and explained_variance_ratio functions, feature extraction, and higher variances are found.

In the PCA algorithm, the first step is data selection. The second step is to subtract the average of the data. At this point, the average of each dimension is reduced by the values of that dimension so that the average of the data in each dimension is zero. As seen in Equation (1).

$$u[m] = \frac{1}{N}\sum_{i=1}^{N} X[m, i] \tag{1}$$

Which is specifically the experimental means applied to the rows of the matrix. Then the distance matrix to the mean is obtained as Equation (2).

$$B = X - uh \tag{2}$$

In the third step, the covariance matrix is calculated. We obtain the covariance matrix. For our example, this matrix is a 2×2 matrix.

$$C = E[B \otimes B] = E[B.B^{*}] = \frac{1}{N} B.B^{*} \tag{3}$$

In the fourth step, special vectors and special values are calculated. The covariance matrix is a symmetric positive semidefinite matrix. According to the theorems of linear algebra, a symmetric matrix n×n has n independent eigenvectors and n eigenvalues. A positive semi-definite matrix also has non-negative eigenvalues, such as equation (4).

$$V^{-1}CV = D \tag{4}$$

V is a matrix of special vectors and D is a diagonal matrix whose diameter values are eigenvalues. As it turns out, each eigenvalue corresponds to a particular vector. Special vectors are rearranged based on the size of their corresponding special values. That is, special vectors are rearranged in descending order of eigenvalues. As shown in equation (5).

$$p \le q \rightarrow \lambda_p \le \lambda_q \tag{5}$$

In this way, the data components are sorted from important to minor.

The fifth step is to select the components and create a Feature Vector. Here, if we want to reduce the data volume, we can delete the subcomponents. Of course, this involves a small amount of data loss. What needs to be done at this point is to create a Feature Vector. Which is actually a matrix of vectors. This matrix contains property vectors that hold them. If we put all the attribute vectors in this matrix, no information is lost and exactly the same original data is retrieved. In the sixth step, new data is obtained. In the last step of PCA, only the Feature Vector matrix metadata obtained in the previous step is multiplied by the normalized data metadata. A row Feature Vector is a matrix in which the eigenvectors are arranged in rows of eigenvalues from top to bottom, and Row Data Adjust is a matrix that contains data whose mean is subtracted after each dimension. In this matrix, the data is stored in its columns and each row corresponds to one dimension [22]. These machine-learning techniques can be deployed in hospitals where a large data set is available and can help physicians make more informed decisions and reduce the number of heart disease injuries in the future.

3. Results and discussion

Cardiac arrhythmia is a group of conditions in which the heart's electrical activity is irregular, either faster or slower than normal, and is one of the leading causes of death in both men and women worldwide. Our goal is to classify the patient into one of the arrhythmia classes such as tachycardia and bradycardia based on its electrocardiographic measurements and to help us understand the application of machine learning in medicine. After selecting the appropriate features, we intend to classify Naïve Bayes logical regression and SVM using machine learning algorithms, ie K nearest neighbor. In the next step, by modifying the kNN algorithm, by increasing the accuracy of the query points, we achieve the improvement of the percentage of classification of a new sample in one of the arrhythmia categories, in the evaluation stage.

3.1. KNN Results (K Nearest Neighbor)

First, we call the K neighbors Classifier function for KNN in Python from the sklearn.neighbors library. The reason for using KNN is its simplicity. Here, an object is classified by a majority vote of its neighbors, which is the most common class among its nearest neighbors [23]. This is done by measuring the distance between the object and its neighbors.

$$D(a,b) = \sqrt{\sum_{i}^{n} (Bi - Ai)^2} \tag{5}$$

Equation (6) shows the simple Euclidean distance in which "a" and "b" are the corresponding positions of the object and one of its neighbors. KNN is very sensitive to irrelevant or additional features, as all features contribute to similarity as well as classification. This is improved by selecting the precise features described earlier. The classification of KNN with PCA and KNN with RF are shown in Table 2 and Table 3, respectively.

Table 2. Classification of KNN with PCA.

Training-Testing Size	K-Neighbors	Training Accuracy	Test Accuracy
20%-80%	6	67%	61%
30%-70%	6	65%	62%

Table 3. Classification of KNN with RF.

Training-Testing Size	K-Neighbors	Training Accuracy	Test Accuracy
20%-80%	6	65%	64%
30%-70%	6	67%	62%

Figure (1) also shows the accuracy of KNN training and testing.

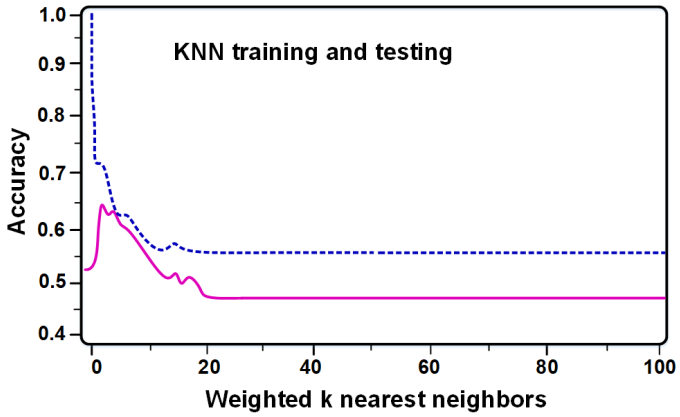

Fig. 1. Accuracy of KNN training and testing.

3.2. Logistic Regression Results

Since logistic regression is used to binary classify set data with dependent properties, in Python we must first convert it to a logarithm between zero and one using the sigmoid function, then the gradient_descent and we call lr_cost_function. In order to use logistic regression to multi-class data sets, we first classify the samples into two original categories. Class 1 (which includes all items labeled 01), And the Not-1class (which contains examples for all other classes) [24].

$$J(\theta) = -\frac{1}{m}\left[\sum_{i=1}^{m}(1-y^{(i)})\log(1-he(x^{(i)})) + y^{(i)}\log he(x^{(i)})\right]$$
$$= -\frac{1}{m}\left[\sum_{i=1}^{m}\sum_{j=0}^{1}1\{y^{(i)}=j\}\log p(y^{(i)}=j\,|x^{(i)};\theta)\right] \quad (6)$$

We have categorized and plotted our data using the lr and plot commands, about half of our samples are labeled as class 01. Figure 2 shows the logistic classification of regression graphically.

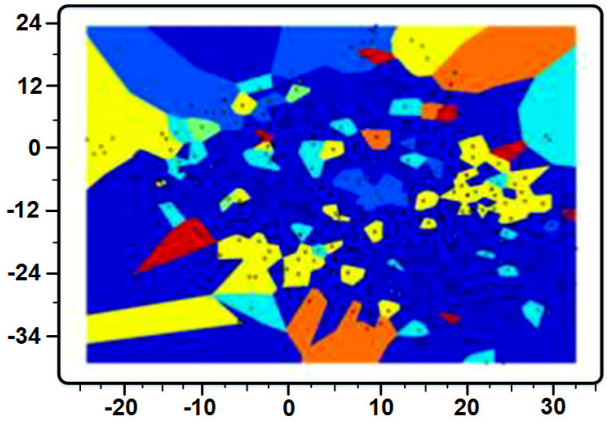

Fig. 2. Regression logistics classification.

The classification of regression logistics with PCA and regression logistics with RF are shown in Table 4 and Table 5, respectively.

Table 3. Classification of regression logistics with PCA.

Training-Testing Size	Training Accuracy	Test Accuracy
20%-80%	90%	69%
30%-70%	89%	67%

Table 4. Classification of regression logistics with RF.

Training-Testing Size	Training Accuracy	Test Accuracy
20%-80%	96%	69%
30%-70%	98%	68%

Figure (3) also shows the accuracy of regression logistics training and testing.

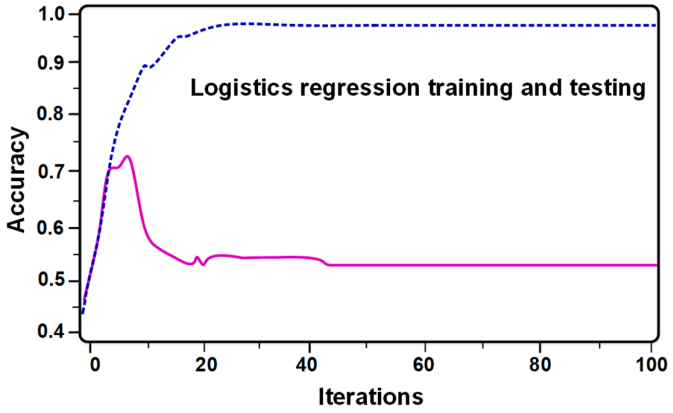

Fig. 3. Logistics regression training and testing.

3.3. SVM Results (Backup Vector Machine)

In SVM, a cloud screen is selected to separate the best points in the input variable space based on its class, either class 0 or class 1. In two dimensions this can be visualized as a line, which can be classified using these lines. By connecting the input values to the line equation, we calculate whether a new point is at the top or bottom of the line. Both linear and polynomial kernels were used, which worked better than polynomial kernels [22]. Initially, svm was called

from sklearn. Then in svm.SVC using kernel function mapping and linearization is done. Figure 4 shows a graphical representation of the SVM classification.

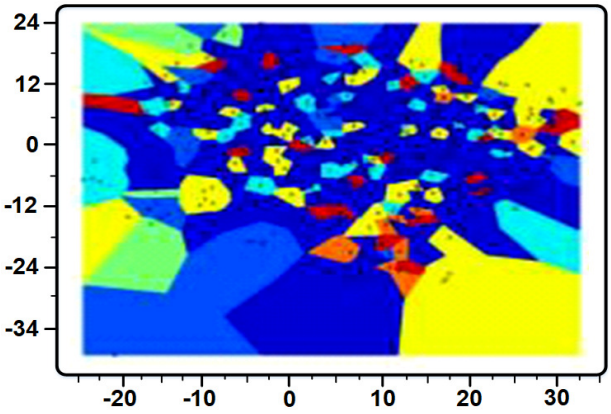

Fig. 4. The SVM classification.

The classification of SVM with PCA and regression logistics with RF are shown in Table 6 and Table 7, respectively.

Table 6. Classification of SVM with PCA.

Training-Testing Size	Training Accuracy	Test Accuracy
20%-80%	99%	65%
30%-70%	99%	61%

Table 7. Classification of SVM with RF.

Training-Testing Size	Training Accuracy	Test Accuracy
20%-80%	100%	67%
30%-70%	99%	66%

3.4. Modification of KNN Algorithm

One way to modify the KNN classification algorithm is to bring the weight of each of K neighbors to the nearest neighbors according to their distance to the query point [25]. Figure 5 shows the accuracy of KNN training and testing in the weighted state.

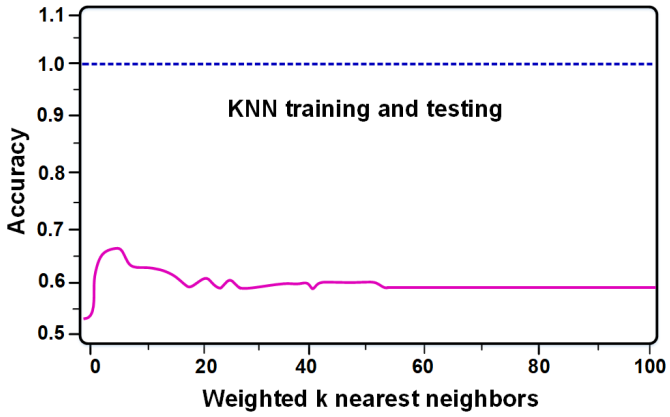

Fig. 5. Accuracy of KNN weighted training and testing.

The classification of KNN with PCA and KNN with RF are shown in Table 8 and Table 9, respectively.

Table 8. Classification of KNN with PCA.

Training-Testing Size	K-Neighbors	Training Accuracy	Test Accuracy
20%-80%	6	99%	65%
30%-70%	6	99%	64%

Table 9. Classification of KNN with RF.

Training-Testing Size	K-Neighbors	Training Accuracy	Test Accuracy
20%-80%	6	100%	67%
30%-70%	6	99%	66%

After applying the weighted KNN, it improves the percentage of accuracy in all classification steps, the results of which are shown in Table 10.

Table 10. Comparison of weighted kNN modification.

Algorithm	Accuracy Before Modifying the Algorithm	Accuracy After Modifying the Algorithm
KNN	64%	72%
Regression	73%	79%
Naïve Bayes	52%	55%

SVM	66%	71%

As shown in Table 10, the algorithms are calculated as a percentage in the pre-correction and post-correction state and have significant improvements. The highest improvement is in Algorithm kNN with an increase of 8%, and the lowest improvement is in Algorithm naïve Bayes with an increase of 3%.

4. Conclusion

In this article, the main goal is to create a system that can seriously detect arrhythmia. The second objective of this study was to develop a method for robustly classifying ECG tracking into one of 13 widespread arrhythmia classes. Performance was reported for each of the five methods using both PCA and RFT methods. It is clear from the data that the SVM algorithm and logical regression are able to automatically detect arrhythmias with reliable accuracy. Training data is 98%, and test data is 73%. In addition, random forests consistently perform better than PCA in terms of feature selection. The general approach in this study is to start with KNN, and try to apply maximum accuracy to different values of K, which are from 3 to 13. Then logistic regression is used which uses the sigmoid function, and it was implemented using the gradient method and the Newton method. Logistic regression showed much better results with an average accuracy of about 73%. The New Biz classification yielded poor results due to the problem of lack of training samples (452) and a myriad of features. Using linear cores, SVM provided the best results with a classification accuracy of approximately 99% for the training suite and 73% for the test suite.

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