Risk Prediction Analysis of Ventricular Tachycardia Using QRS Complex Features

K Haripriya¹, G Laxmi Deepthi ², P. Bharath Kumar Chowdary³, Ravikanth Motupalli⁴, Bhagya Rekha Konkepudi⁵

^{1,2,3,4,5} Dept. of Computer Science and Engineering, VNR VJIET, Hyderabad – 500 090, TS, India Email: ¹haripriya_k@vnrvjiet.in, ²laxmideepthi_g@vnrvjiet.in, ³bharathkumar_p@ vnrvjiet.in, ⁴ravikanth m@vnrvjiet.in, ⁵konrekha@gmail.com

Abstract:

Early detection of Ventricular Tachycardia (VT) has the potential to save many patients' lives. VT is a 'Heart Rhythm' condition(arrhythmia) caused by abnormality in the sinus rhythm, which is initially generated in the lower chambers (ventricles) of the heart. A normal heart beats faster than usual in this condition. An ECG signal is crucial in the first identification and examination of cardiac abnormalities. This study proposes a noise filtering, distinct collection of ECG characteristics, and machine learning-based classifier model for the prediction of ventricular tachycardia arrhythmia. Before extracting the signal's features, the signal is detrended and denoised to remove the noise and improve feature detection. We will be using "QRS" complex shape features to improve VT prediction performance.

Keywords: Ventricles, QRS Complex Shape, Electrocardiography (ECG), ECG signals

1.Introduction

Ventricular tachycardia (VT) raises the risk of sudden cardiac death and is prevalent in patients with structural heart disease. If not properly diagnosed and treated, cardiomyopathy, hypertension, ST-segment abnormalities, or chronic obstructive pulmonary disease (COPD) are the leading causes of ventricular arrhythmias, which can lead to a quick death. More than 1/2 of all cardiac fatalities and up to fifteen% of usual mortality are because of unexpected demise. The electrocardiogram (ECG), which reflects the cyclic rhythm of cardiac muscle contraction and rest is an indicator of the coronary heart's bioelectrical activity. A rapid or slow heartbeat is called an arrhythmia. The diagnosis of heart illness is based on arrhythmia, which may be a sign of more serious cardiac issues. The problem with using an ECG to decide cardiac ailment is that anyone's normal ECG is unique reading and their particular arrhythmias are unique, making the process more difficult. It takes time and effort to diagnose certain arrhythmias by visual inspection

1731



Fig. 1.1: Cardiac action cycle

Several electrodes are used to get the ECG data. The amplitude of the beats differs across individuals, and the ECG records have noise in them. Beat detection and feature extraction hence need preprocessing of the signal. All significant components of the ECG signal are contained in the waves represented by P,Q,R,S,T. In fig.1. an example ECG waveform is displayed. Different forms of arrhythmia are categorized using the characteristics of these waves. The vital and plain portions of the ECG signals can be separated. The majority of the crucial data in the ECG signal is concentrated on the 'P-wave', 'QRS-complex', and 'T-wave'. The position and size of the PR interval and seg are typically used to identify diseases.



Fig. 1.2: QRS Complex Shape representing P-wave, QRS-complex, T-wave of a heart

2. Related Work

[1] The data of four hundred and twenty patients who effectively received Catheter Ablation (CA) procedure for treating Ventricular Tachycardia or percent have been included within the education, validation, and testing records units, which had 340 (81%), 38 (9%), and 42 (10%) people, respectively. They again and again learned a system gaining knowledge of a model with sixteen lakhs eight hundred characteristics received from '12-lead ECGs' of schooling group patients using our specialized method. The internal validation facts had been used to generate the vicinity underneath the 'AUC curve' of receiver running characteristic, that's used to choose quality discretization cutoff level for prediction.

[2] A total of 2302 patients' data was collected and used. The information included demographic data, genetic info, results from clinical studies, drug interactions, and instances of diseases. Four classification models were used and SHAP (SHapley Additive exPlanations) was used to explain the models' choices. 'Heart Failure', 'Sudden Cardiac Death', other

cardiac deaths, and all-causes of death are considered unwanted cardiac occurrences. The proposed machine learning approach has performed better than the comparable existing riskstratification models: it attained inflated Accuracies by 0.17, 0.9, and 0.1, respectively. The best performance accuracy of 82% was attained by the boosted trees. With accuracies of 90%, 88%, and 86%, the resulting model predicted VT, HF, and ICD with higher accuracy.

[3] This examination introduces and confirms the primary hybrid model for short "pc-guided tempo-mapping" that blends populace and patient-particular device gaining knowledge so that you can separate among-issue variations and regionalize the region of VT starting place, a "population-primarily based deep learning model" changed into first constructed offline. After initialized, via the population-based totally prediction for a brand new affected person with a goal VT, an online patient-specific version was then developed in real time, actively signaling where to research next and consistently improving the prediction with each new piece of pacing data supplied., steadily guiding tempo-mapping toward the web page of VT starting place. The hybrid methodology that has been proposed ought to assist with the short tempo-mapping of interventional targets in VT.

[4] Simulations are performed to predict the effects of 'Lopinavir', 'Ritonavir', 'Chloroquine', and 'Azithromycin' on ventricular action potentials (APs) in humans.primarily premised on a completely observed ways of many capsules influence cardiac ion channels, they have predicted that every drug considered as a remedies for COVID-19 will affect the intermediary complement of ionic currents. The changes done to ionic currents had been carried out on a mathematical version of the HVEM and are being watched for drugprecipitated modifications to cardiac APs. Simulations with each medication at ten times the indicated EFTPC reveal that all tablets can cause full-size AP prolongation at those high concentrations, with lopinavir causing the most harm.

[5] They employed "QRS" complex shape characteristics to increase the accuracy of forecasting VF. Traditional HRV characteristics were also compared. To forecast the beginning of VF 30 seconds before it occurred, these characteristics were derived from HRV and ECG data for 2 minutes, ORS Complex Signed region and R-peak Amplitude, ANN classifiers were built and illustrated the utilization of function units gathered from heart rate variability and the "QRS" complex form utilizing ten-fold go-validation. The prediction accuracy calculated the usage of eleven HRV traits turned into 72%, while that anticipated use of 4 "QRS" complicated shape capabilities became 98.6%.

[6] This study included data of 113 critical COVID-19 patients. Out of all 50 patients who passed away, 63 patients made a full recovery. The percentage of patients who had ventricular arrhythmia was higher among those who died than those who recovered, and it was also higher among those who had acute heart injury than among those who had not. Old age people around 70 years, initial neutrophil count more than

6.5, Lactate Dehydrogenase greater than 300 U/L and C-reactive protein greater than 100 mg/L were verified as independent predictors of death from COVID The risk of mortality can be decreased with immunoglobulin therapy.

[7] The principal novelty of this research is the picture representation based on the usage of time-frequency(t-f) as the classifier's input avoids the conventional feature selection and extraction stage, as well as the associated information loss. The databases from American Hospital Association and Massachusetts Institute of Technology-Beth Israel were used for appraisal and author comparison with other writers. To assess the validity of the technique without regard to a specific classifier, 4 different machine learning classifiers were used like "Logistic Regression with L2 Regularization", "Adaptive Neural Network Classifier", "Support Vector Machine", and "Bagging classifier".

[8] In this paper, it was proposed to implement a frequency area approach to the use of Discrete Cosine rework (DCT) for feature extraction. Exceptional arrhythmia conditions were investigated at the side of ordinary ECG. ECG facts for this research were obtained from the Physio bank website. The average class accuracy received through the proposed approach is over 90%. Future directions have to pay attention to data reduction to improve the category time. The ECG information for the arrhythmia category is obtained from MIT-BIH Physio Bank arrhythmia database. The facts are preprocessed to find RR c programming language, DCT is carried out to convert the RR durations and Random tree is used for classification.

[9] This paper developed a technique for classifying ECG beats based on RR interval and waveform similarity. The suggested classifier is a classifier that is patient-specific. The classifier builds a beats database from the patient's ECG. The ECG signal was denoised using the suggested method's wavelet transform-based approaches. A java implementation is also utilized to lessen noise brought on by baseline wander cancellation and high oscillation noise. The collected RR intervals are used as characteristics. Fuzzy logic or a neural network may be used for classification. High accuracy was attained in the experimental results for the beat classification.

[10] This article offered a useful method for identifying and classifying arrhythmic episodes and arrhythmia beats based on the application of knowledge-based systems. The RR interval that was removed from the ECG signal served as the foundation for the recommended method. A set of guidelines and a deterministic automaton based on the behavior of the RR interval during arrhythmic events are used to categorize beats and arrhythmic episodes. A database maintained by MIT-arrhythmia BIH was utilized to assess the suggested strategy. The final results show, suggested approach accurately categorized episodes and beats.

3. Materials And Methods

3.1 Datasets

The fundamental goal of our suggested strategy is to create a machine learning model that can detect the onset of Ventricular Tachycardia (VT) from the data collected by Bilkent University, Department of Computer Engineering and InformationScience and Baskent University, School of Medicine.

We would be using "QRS" complex features recorded in the above mentioned dataset. Feature extraction to get the necessary features from the dataset. Then, by applying various machine learning algorithms, we would detect the onset of the VT stroke and its location (right outflow tract or left outflow tract). By Training and testing different models, comparing their accuracy, precision, recall and other performance metrics using various machine learning algorithms, one definite algorithm is decided as the best algorithm to predict the VT disease and its location

3.2 Hybrid Machine learning model

A Voting Classifier is one of the categories of the overall machine learning model, trained on an ensemble of different models, which provides a prediction by choosing the class with the maximum probability as its output. It simply combines all the results of each classifier involved with the Voting Classifier and classifies the output based on the maximum number of votes for the class. The concept is the creation of a single model that makes use of the outputs of different dedicated models, thus making predictions based on the collective majority vote for each output class, rather than creating different models and then finding out how accurate each of them is. The Voting Classifier accepts two different kinds of voting.

Hard Voting: In hard voting, the output class predicted is the class that has the majority of

the votes i.e. the class which was highly predicted to be the output class by each of the classifiers. Assume three classifiers have predicted the output class(A, A, B), then here the majority of them predicted A as output.

Soft Voting: The prediction is done in soft voting considering the average of probability that was given to the specific class for output class. Assuming the given input to three models had prediction probabilities as for class A = (0.30, 0.47, 0.53) and for class B = (0.20, 0.32, 0.40). It will indicate that the average probability in Class A is 0.4333, whereas for Class B it shows 0.3067. Therefore, Class A stands as the winner because there is the highest average that calculated by each classifier.



Fig. 3.2: Steps in implementation

4 Results

We calculated whether the Ventricular Tachycardia originated from the left or right side of the heart by calculating the values of QRS_I and QRS_aVF values from the q_wave, r_wave and s_wave values that we have derived from the column fields in data set. Now we have calculated the axis deviation value using QRS_I and QRS_aVF values which are calculated as shown below. If the calculated axis deviation is greater than 45 then we conclude that the origin of Ventricular Tachycardia disease is from the right part of the heart(ventricles) else it has originated from the left part of the heart(ventricles). QRS_I=abs(q_wave)+abs(r_wave) QRS_aVF=abs(r_wave)+abs(s_wave)

Axis deviation=90-(math.atan(QRS_I/QRS_aVF)*(180/math.pi))

If the value is greater than 45 then the origin of VT is from the right else from the left. We have predicted that the origin of Ventricular Tachycardia is from the left part or right part of the heart using the axis deviation value.

LOCATION OF VENTRICULAR TACHYCARDIA	LOCATION OF VENTRICULAR TACHYCARDIA		
	Q Wave:		
Wave:	0		
1	R Wave:		
R Wave:	0		
0	C Minus		
5 Wave:	a wave.		
1			
Find Origin D/ VT	Find Origin Of VT		
Result: Originating from left	Result: Originating from right		

Fig. 4.1: Location of VT

The classification report showed high precision and recall values for hybrid model, indicating good performance in correctly identifying positive instances and avoiding false positives. The AUROC score provided a comprehensive assessment of the model's ability to distinguish between positive and negative cases. The high AUROC values for all classes, as well as the mean AUROC score, suggested that the hybrid model had high discriminative ability and was well-suited for pathology classification

Ensemble Algorithm 95.597%				
Algorithm	Accuracy	Precision	Recall	AUROC
Gaussian NB	94.7%	98.2%	78.5%	85.3%
KNN	92.3%	46.1%	50%	94.2%
Decision Tree	92.3%	73.1%	76.9%	77.9%
Random Forest	94.7%	90.4%	85.1%	94.6%

<Axes: >

Table 1: Classification Report

K-Nearest Neighbors : <Axes: >



Decision Tree Classifier

<Axes: >



100 100 80 80 5 60 60 40 40 1e+02 1 20 20 0 1 Gausian NB <Axes: >



Fig. 4.2: Confusion matrix

The confusion matrix showed high accuracy, with most of the diagonal values being high, indicating correct predictions

Conclusion:

In conclusion, the development of a reliable and accurate system for predicting VT disease using machine learning algorithms has the potential to greatly benefit patients by allowing for earlier diagnosis and more effective treatment. Our proposed system, which utilizes an ensemble algorithm to predict VT and identify the origin of the arrhythmia, has demonstrated promising results, and could be further refined and validated through additional research.

Furthermore, the incorporation of axial deviations in the heart into our models could provide important information about the origin of VT and guide treatment decisions. By continuing to refine and develop our system, we hope to improve our understanding of VT disease and ultimately improve patient outcomes.

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