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Article

Tree-Based Learning Algorithms to Classify ECG with Arrhythmias

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SUMMARY

An arrhythmia is an abnormality in heart rate or rhythm. Depending on which part of the heart is affected and its abnormality pattern (too fast, too slow or irregular), arrhythmia can be classified into around a dozen of classes. Accordingly, arrhythmia treatments vary depending on the type of arrhythmia. An electrocardiogram (ECG) records the electrical signals in the heart to profile the heart rate, rhythm, and patterns, which collectively allows the detection and diagnosis of different types of arrhythmias. Inconsistent and insufficient accuracy of ECG interpretation by medical professionals is a problem in clinics for which statistical algorithms can be a promising alternative. In this study, we explored four learning algorithms, gradient boosting, random forest, decision tree and extra trees, to classify arrhythmia on ECG signals from over 10,000 patients. Specifically, we extracted features from ECG signals, evaluated four tree-based learning on classification of arrhythmia and evaluated each learning algorithm's performance in terms of accuracy, precision, recall, and F1 based on 10-fold cross-validation. We hypothesized that gradient boosting would be able to classify arrhythmia with high accuracy when trained. Here we report that gradient boosting provided an accuracy of 95%, outperforming all other classification models in all the performance measures evaluated in this study. The findings here suggest that the statistical classification using the data science tools could greatly facilitate ECG detection and diagnostics.

INTRODUCTION

A heart arrhythmia is an irregular or abnormal heartbeat with respect to its timing or pattern (1). Arrhythmias have a significant impact on quality of life, and may incur massive medical expenditures. They are also relatively common, affecting 1.5% to 5% of the general population (2). For example, the heartbeat may be too quick or slow, or exhibit another irregular rhythm. Arrhythmia includes many different types of abnormalities, depending on what cardiac part is impacted and how those impacts heartbeat rhythms (2). Accurate diagnosis of types of arrhythmia is critical for selecting appropriate and relevant medication. Arrhythmias may derive from atria (upper compartment of the heart) or ventricles (lower compartment of the heart). Atrial fibrillation (AFIB), atrial tachycardia (AT), and atrial flutter (AFL) manifest rapid heartbeat involving the atria (3). The AFIB and AFL are typically closely associated since primary AFIB patients commonly manifest AFL, and vice versa (3). Patients with sinus bradycardia manifest slow heartbeat (2). AFIB is the most common type of arrhythmia, which is associated with sustained cardiac rhythm disorder, and confers substantial mortality and morbidity from stroke, thromboembolism, heart failure, and impaired quality of life (4).

Normally, the heartbeat is initiated by the specialized cells of the sinoatrial node, located on the top of the right atrium. These cells generate electrical pulses that spread throughout the heart along an electrical pathway consisting of atria, atrioventricular node, and ventricles. In this way, the contraction of the muscle in the atria and ventricles are coordinated for proper heart function. However, failure of the sinoatrial node to properly coordinate heartbeats or disruption along the heart electrical propagation pathway could lead to arrhythmia disorders (1).

The electrical signals in the heart can be readily monitored and recorded with electrocardiogram (ECG), which is applied to the skin surface of the limbs and chest (5, 6). The standard 12-lead ECG uses up to 10 electrodes to determine the heart's electrical potential profiles (magnitudes and durations) from 12 different angles ("leads") involving 12 specified sets of two electrodes. (6).

If the heart beats regularly and normally, it will produce the typical ECG profile (6) (**Figure 1**). The first peak, the P-wave, manifests as the electrical impulse, which originates from the sinoatrial node and propagates across the atria. The interval between the P-wave and Q-wave is due to the delay in transmission of the electrical signal as it reaches the sinoatrial node. The atria muscle contracts, ejecting blood into the ventricles, and is immediately followed by atria relaxation and its refilling with blood. The electrical impulses, upon reaching and spreading across ventricles, give rise to Q-, R-, and S- waves of the ECG (QRS complex) and trigger the ventricles contraction to pump blood to arteries. The T-wave at the end indicates the diminishing of the electrical impulse, and the relaxation of the ventricular compartments; so, the T-wave signifies the repolarization of the ventricles, which is the cardiomyocytes returning to the resting potential.

ECGs perform signal preprocessing, heartbeat segmentation, feature extraction and learning and prediction to detect and classify cardiac irregularities (6). ECG signal preprocessing and heartbeat segmentation has been widely explored. However, there is still room for improvement of arrhythmia classification (7). A decision tree is a is a tree-structured-based model which describes the classification process based on input features (8, 9). Extra trees classifier is an ensemble tree-based machine learning approach that relies on randomization of both attribute and cut-point choice to reduce the risk of overfitting (10). Random forests combine the output of multiple decision trees to reach a single result (8, 11). In contrast, gradient boosting is an additive ensemble learning approach using decision trees as

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weak learners. This method fits a new predictor to the residual error made by the previous predictor. Each new model tries to correct the previous model and combines weak learners into strong learners (8, 12, 13). In this study, we used 12-lead, 500 Hz, ECG signals from over 10,000 patients, extracted features from ECG signals and evaluated four tree-based learning algorithms on classification of arrhythmia including decision tree and three tree-based ensemble methods (gradient boosting, random forest, and extra trees classifiers) (14,15,16).

We hypothesized that gradient boosting could classify arrhythmia with high accuracy. Here we report the outcome from the 4 algorithms, among which gradient boosting provided the best accuracy for arrhythmia classification. This provides compelling evidence that appropriately optimized statistical algorithms, such as gradient boosting, could achieve high accuracy in classifying different types of clinical types of arrhythmia, thus relevant medical treatment could be provided accordingly.

RESULTS

In this study, we evaluated several tree-based learning algorithms on classification of arrhythmia based on ECG signals of over 1000 patients, including decision tree and three tree-based ensemble methods (gradient boosting, random forest, and extra trees classifiers) (**Figure 2**). First, we processed ECG signals from each patient to extract features related to variation of peak interval, heart rate, heart rate time interval and peak amplitude. We selected all features or a subset of features for model training. We split our dataset into training and testing datasets. We employed the different learning algorithms to develop arrhythmia classification models using the training dataset. We then applied the learned classifiers to testing dataset for prediction of arrhythmia in unseen instances.

We developed the arrhythmia classification models using a research database for 12-lead ECG signals with 500 Hz sampling rate. In this study, we used ECG signals from 10,525 patients, including 11 arrhythmia types: atrial flutter (AF), atrial fibrillation (AFIB), atrial tachycardia (AT), atrioventricular node reentrant tachycardia (AVNRT), atrioventricular reentrant tachycardia (AVRT), sinus atrium to atrial wandering rhythm (SAAWR), sinus

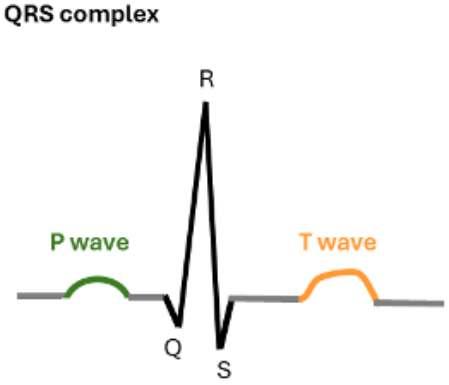

Figure 1: Typical ECG waveform showing P-wave, QRS complex and T-wave. The ECG that is produced when the lead I trace connects the left arm and the right arm. P-wave manifests as the electrical impulse propagates from the sinoatrial node across the atria. The electrical impulses, upon reaching and spreading across ventricles, give rise to Q-, R- and S-waves of the ECG (QRS complex). T-wave at the end indicates the diminishing of the electrical impulse, and the relaxation of the ventricles.

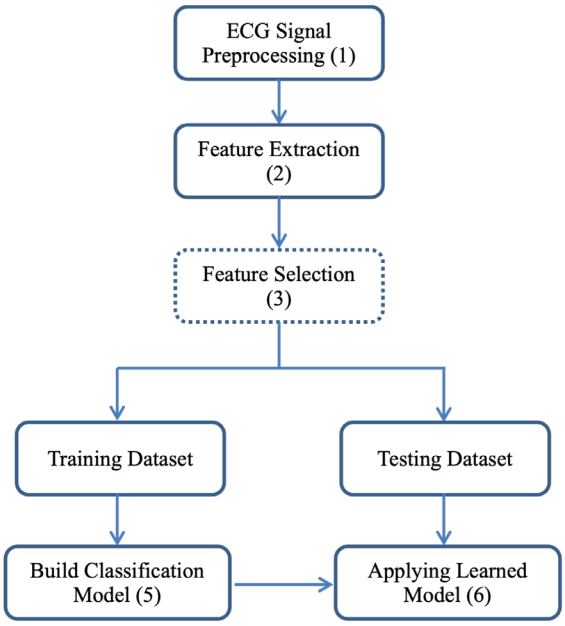

Figure 2: Workflow of arrhythmia classification. The diagram shows the workflow for the development of arrhythmia classification model and evaluation of model performance. This workflow involves: 1) ECG signals processing for heartbeat segmentation; 2) extraction of features from ECG signals; 3) Optional subselection of features based on feature importance; 4) splitting of datasets into training and testing datasets; 5) development of classification models using training dataset; 6) and prediction of arrhythmia in the testing dataset. Dotted rectangle step is not needed if all features are used to building a model.

tachycardia (ST), supraventricular tachycardia (SVT), sinus bradycardia (SB), sinus irregularity (SI) and sinus rhythm (SR). Because some types such as AVRT, SAAWR, etc. have a very small number of cases to be reliably classified, we regrouped these 11 arrhythmia types into 4 broader groups (AFIB, GSVT, SB and SR). Among the arrhythmia patient population, there were 2,205 AFIB cases, 2,216 GSVT cases, 3,882 SB cases and 2,222 SR cases, respectively (**Table 1**).

Patient age ranged from 4–98 years old. Over 70% of patients were 50 years or older. GSVT group had the highest mean ventricular rate (125.0), whereas SB group had the lowest mean ventricular rate (55.5). AFIB group had the highest mean atrial rate (143.2) and SB group had lowest mean atrial rate (55.3) (**Table 2**).

We implemented 4 supervised machine learning algorithms to develop classifiers, by selecting either all features or subsets of features based on the importance of the features as input. We trained classification models with 75% of the dataset, and then tested with the remaining 25% of the dataset. We compared the proportion of various rhythms and gender (male) between the training and test datasets using z-test for proportions and the distribution of age, ventricular rate and atrial rate distribution using t-test for each arrhythmia type between the training and testing dataset. There is no significant difference in the distribution of these features in the training and testing datasets ($p > 0.1$), except mean atrial rate in AFIB is higher in the training dataset than in the testing dataset ($p=0.01$), as displayed in **Figure 3**. We employed a10-fold cross validation to optimize the model parameters based on unweighted mean F1-score across 4 groups. **Figure 4** shows the performance measurement

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Arrhythmia group	Arrhythmias included	Count	Total
AFIB	Atrial Flutter	431	2205
	Atrial Fibrillation	1774	
GSVT	Atrial Tachycardia	121	2216
	Atrioventricular Node Reentrant Tachycardia	15	
	Atrioventricular Reentrant Tachycardia	6	
	Sinus Atrium to Atrial Wandering Rhythm	7	
	Sinus Tachycardia	1559	
	Supraventricular Tachycardia	508	
SB	Sinus Bradycardia	3882	3882
SR	Sinus Irregularity	397	2222
	Sinus Rhythm	1825	

Table 1: Arrhythmia information and number of patients in each arrhythmia group

including accuracy, F1-score, precision, and recall of 10-fold cross validation for each learning algorithm utilizing either all features or selected features. Based on the feature importance, we selected 18, 66, 7, and 81 features for gradient boosting, random forest, decision tree and extra trees, respectively. Patient age, ventricular rate, and atrial rate were selected for all these learning algorithms. Decision tree algorithm appeared to perform better when models were trained with selected features. For the other three algorithms, models with all features included performed slightly better. The best performance based on 10-fold cross-validation is observed with gradient boosting. Among these 4 arrhythmia groups, prediction of SB achieved the highest F1-score, accuracy, precision, and recall, followed by SR, GSVT and AFIB. In the testing dataset, the weighted accuracy of gradient boosting, random forest, decision tree and extra trees algorithms is 95%, 94%, 94% and 94%, respectively (**Figure 5**).

DISCUSSION

Detection of arrhythmia is very important for proper treatment. In this study, arrhythmia classification based on four machine learning algorithms, including gradient boosting, random forest, decision tree and extra trees, was conducted using 12-lead ECG signals from 10,525 patients representing four rhythm groups (SB, SR, GSVT and AFIB). 192 features including minimum, mean, maximum and variance describing the variation of R peak intervals, instantaneous heart rate, heart rate time interval, and peak amplitude were extracted from the 12-leads ECG signal data. A subset of features was selected based on the feature importance for each learning algorithm. Learning algorithms were trained with all features or selected features.

Compared to models with inclusion of subset of features, gradient boosting, random forest, and extra trees classification models had slightly better performance with all 206 features (192 ECG data features and 14 diagnostic file features) included. Decision tree classification model performed slightly better with a subset of features, including patient age, ventricular and rates, variance of heart rate time interval. Gradient boosting classification model outperforms all other classification models in terms of all performance measurements evaluated in this study. Various learning algorithms have been employed for arrhythmia classification including K-Nearest Neighbors, decision tree, random forest, gradient boosting (16), support vector machines (17, 18), artificial neural networks (19), and linear discriminant (20). With given features, one algorithm may perform better than the others (16). Zheng et al reported that gradient boosting and extreme gradient boosting produced the highest accuracy with rescaled features extracted from lead II ECGs (16). Aligning with prior studies, utilizing features extracted from 12 lead ECG signals, we found gradient boosting provided better prediction accuracy than other learning algorithms.

A 94% to 95% of accuracy for arrhythmia classification was achieved using these four learning algorithms, suggesting that the features related to the variation of R peak intervals, peak amplitude, heart rate and heart rate time intervals have a great capability to discriminate arrhythmia types. These features can reveal variation in heartbeat waves and time duration related to arrhythmia. Features related to the variation of interval between R peaks such as count, mean and variance of R peak intervals, have been used to classify rhythm types (7, 16). Arrhythmias often provoke the variations in the morphology of the heartbeat wave, which are correlated with the variations observed in the width of the R peak intervals (16, 19). Other features extracted from heartbeat intervals such as QRS intervals have also been widely utilized. QRS intervals have a great capacity to distinguish the types of arrhythmias that provoke variations in the QRS interval (7, 21). Features extracted from different leads may have different capacity to discriminate different arrhythmia classes. Lead II favors the identification of arrhythmias provoking the change of P, QRS and T-waves (Figure 1). On the other hand, lead V and its correlated leads (V1, V2) are more capable of classifying ventricular related arrhythmias (7). A combination of different leads has been reported to present better results (21). This study utilized 12 lead ECG signals and achieved good performance for arrhythmia classification. In the future, we could explore whether reduced number of leads could still provide similar effectiveness for arrhythmia classification. In this study, several arrhythmia types were grouped into broader groups due to small number of cases. Thus classification of these rare arrhythmia types was not evaluated. However, further investigation could be done with a large dataset with various arrhythmia classes.

Meta-analysis by Cook DA et al revealed that accuracy of ECG interpretation by medical professionals was low (42.0% - 74.9%) depending on their training levels from medical students to cardiologists (22), despite some improvement consequent

	AFIB	GSVT	SB	SR	Total
Number of Subjects	2205	2216	3882	2222	10525
Gender, n (%)					
Female	918 (41.6)	1120 (50.5)	1406 (36.2)	1199 (54.0)	4643 (44.1)
Male	1287 (58.4)	1096 (49.5)	2476 (63.8)	1023 (46.4)	5882 (55.9)
Age					
mean (sd)	72.9 (11.7)	55.7 (20.5)	58.3 (14.0)	50.9 (19.2)	59.3 (18.0)
(min, max)	(21, 98)	(4, 96)	(10, 98)	(4, 95)	(4, 98)
AgeGroup, n (%)					
<50	102 (4.6)	812 (36.6)	1002 (25.8)	988 (44.5)	2904 (27.6)
50-59	210 (9.5)	387 (17.5)	1039 (26.8)	457 (20.6)	2093 (19.9)
60-69	534 (24.2)	447 (20.2)	1156 (29.8)	435 (19.6)	2572 (24.4)
>=70	1359 (61.6)	570 (25.7)	685 (17.6)	342 (15.4)	2956 (28.1)
Other Cardiovascular Condition, n (%)					
No	496 (22.5)	1002 (445.2)	2196 (56.6)	1654 (74.4)	5348 (50.8)
Yes	1709 (77.5)	1214 (54.8)	1686 (43.4)	568 (25.6)	5177 (49.2)
Ventricular Rate					
mean (sd)	99.1 (29.4)	125.0 (27.6)	55.5 (3.9)	75.2 (10.0)	83.3 (33.1)
(min, max)	(39, 225)	(42, 222)	(39, 103)	(42, 108)	(39, 225)
Atrial Rate					
mean (sd)	143.2 (94.8)	121.4 (38.5)	55.3 (10.1)	75.5 (12.5)	91.9 (59.6)
(min, max)	(22, 535)	(0, 500)	(0, 468)	(44, 315)	(0, 535)

Table 2: Patient baseline characteristics, cardiovascular conditions, and ventricular and atrial rates in different rhythm types. mean: average values of non-missing data; SD: standard deviation; min: minimum; max: maximum.

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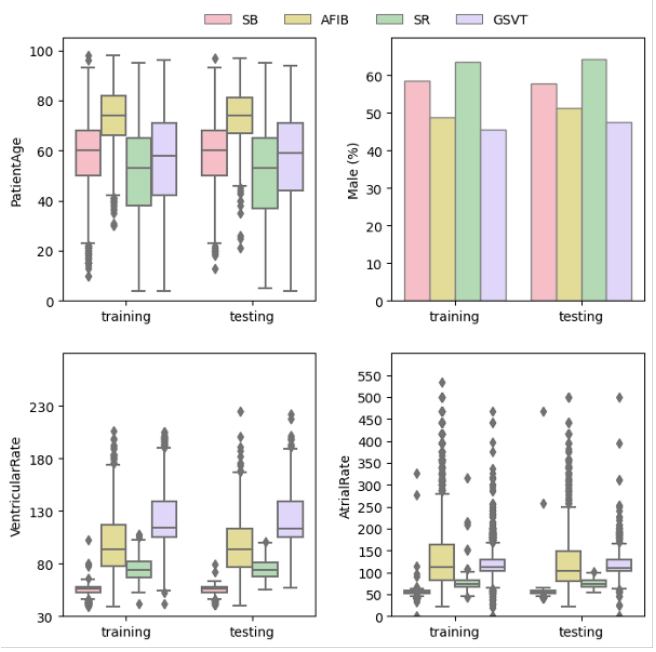

Figure 3: Distribution of age, gender, and ventricular and atrial rates in the training and testing datasets. Box plots display the distribution of numeric values in the training and testing datasets for (A) patient age (PatientAge), (B) proportion of male patients (Male (%)) in the training datasets, (C) ventricular rate (VentricularRate) and (D) atrial rate (AtrialRate).

to training or specification. Apparently, the 95% arrhythmia detection accuracy achieved by the Gradient boost algorithm could help significantly improve ECG interpretation accuracy in clinic; meanwhile it saves physicians practitioners' time and efforts from interpretation of ECG profiles, which provides critical information for diagnosis of different types of arrhythmias. The treatment of arrhythmia differs depending on their types. So, reliable classification of ECG with appropriate statistical algorithms could inform and improve the control or cure of irregular heartbeats, arrhythmias.

MATERIALS AND METHODS

Datasets

A research database for ECG signals was used for development and evaluation of arrhythmia classification in this study. The database was created under the auspices of Chapman University and Shapxing People's Hospital (Shaoxing Hospital Zhejiang University School of Medicine). Data was retrieved from ChapmanECG Figshare Collection (https://figshare.com/collections/ChapmanECG/4560497/1) (14). This dataset contains 12-lead ECGs with 500 Hz sampling rate from 10,646 patients, including 11 common rhythms and 67 heart conditions, which were labeled by experts. In this study, we used the ECG data processed from raw ECG data and denoised by removing the signal with a frequency above 50, followed by clearing of baseline wandering effect (16, 23). In addition, a diagnostics file containing patient demographic data (age and gender), rhythm information (rhythm label, beat rate Ventricular Rate, Atrial Rate, QRS duration, QT Interval, QT corrected, RAxis, TAxis, QRS Count, Q onset, Q offset, T offset) and heart conditions were acquired. The eleven rhythms included were Atrial Flutter (AF), Atrial Fibrillation (AFIB), Atrial Tachycardia (AT), Atrioventricular Node Reentrant Tachycardia (AVNRT),

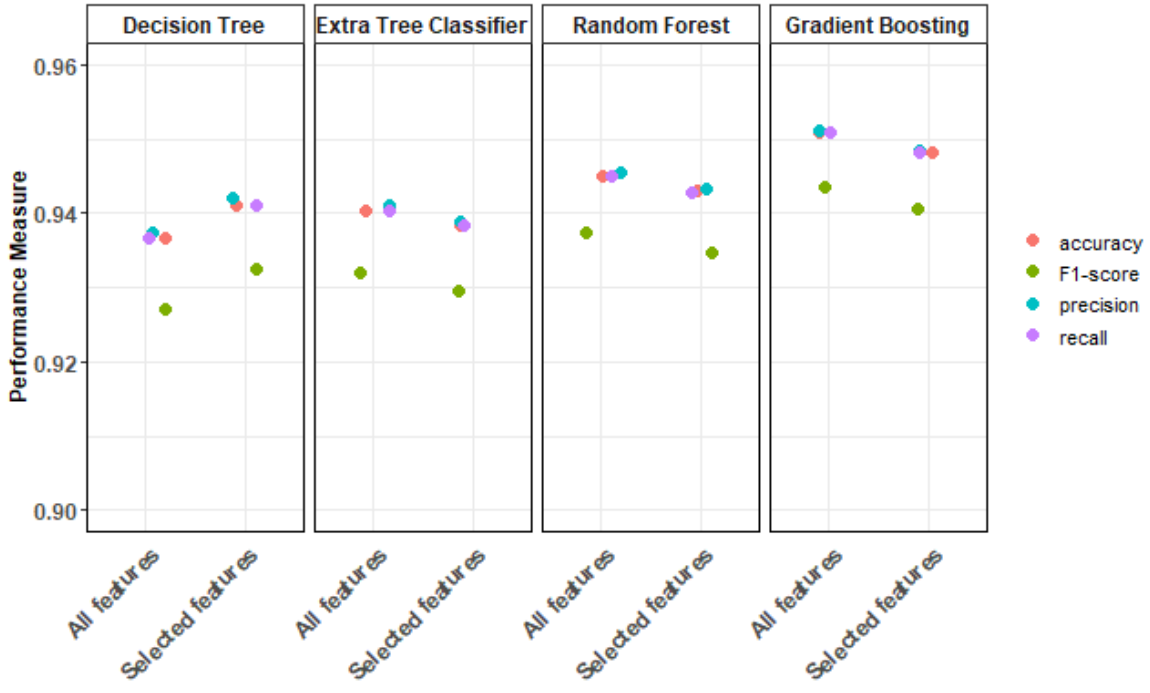

Figure 4: Performance measures of various learning algorithms based on 10-fold cross-validation. accuracy, F1-score, precision and recall are the average results from 10-fold cross-validation with 75% training data.

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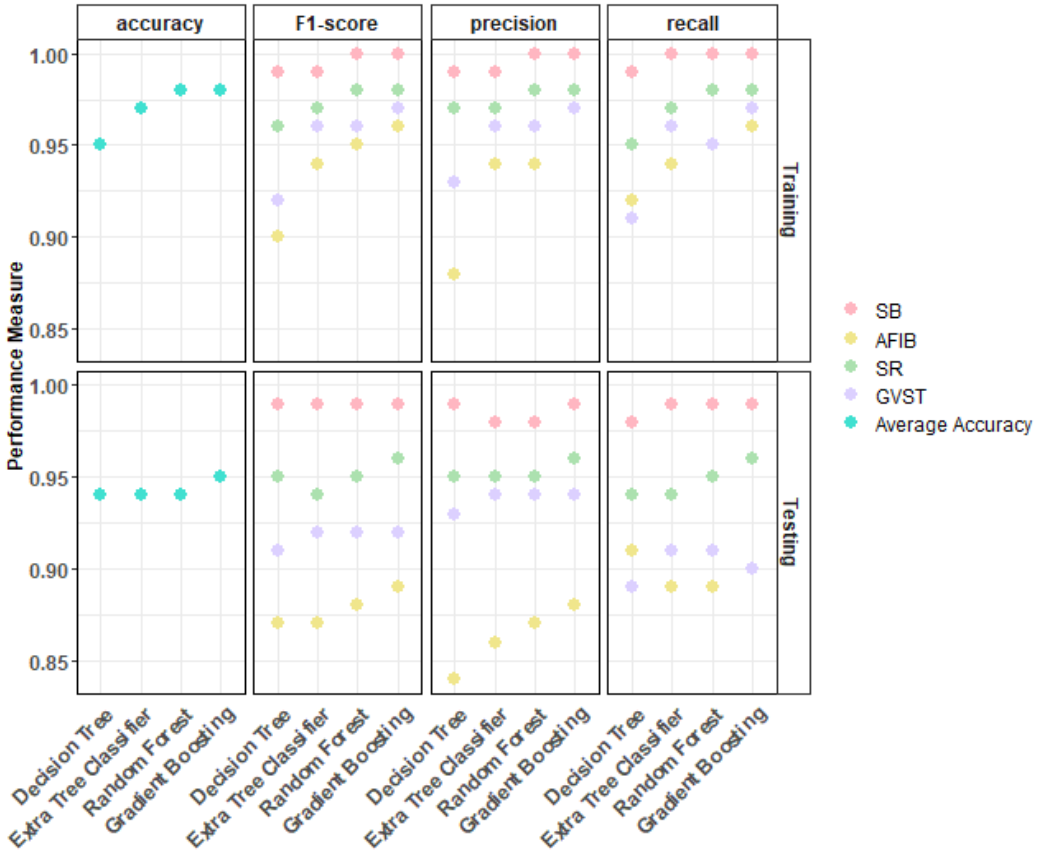

Figure 5: Performance measures of four classification models for prediction of training and testing datasets. Four arrhythmia types were predicted using each of the 4 learning models. Accuracy, precision, F1-score and recall were used to measure the performance of each model. accuracy: average accuracy of proportion of correctly predicted arrhythmias instances across all 4 groups; precision: proportion of patients with specific arrhythmias among all the instances predicted to have this condition. recall: proportion of actual arrhythmia type correctly identified by the classifier used. F1-score is the weighted average of precision and recall.

Atrioventricular Reentrant Tachycardia (AVRT), Sinus Atrium to Atrial Wandering Rhythm (SAAWR), Sinus Tachycardia (ST), Supraventricular Tachycardia (SVT), Sinus Bradycardia (SB), Sinus Irregularity (SI) and Sinus Rhythm (SR). Some rhythms were very rare, such as AVNRT, AVRT and SAAWR, with less than 20 cases in this dataset. Rhythms were grouped based on the type of arrhythmia: AFIB group included AF and SFIB; GSVT group included AT, AVNRT, AVRT, SAAWR, ST and SVT; SR group included SI and SR; and SB group included SB (16, 22).

Feature extraction

BioSPPy (https://github.com/PIA-Group/BioSPPy/) (23) was used to extract general ECG summary features for each of the 12 leads including R peak location, instantaneous heart rate (bpm), heartbeat templates and heart rate time axis reference (seconds). Based on these ECG summary features, additional features were derived including: 1) RR interval: interval between R peaks, 2) Heart rate time interval: interval between adjacent heart rate time axis references, and 3) Maximum amplitude of each segment in the templates. A total of 10,525 patients completed information

Classification Algorithms	Features	# estimators	learning rate	max depth	min samples per leaf	min samples to split	criterion
gradient boosting	all	100	0.1	3	1	2	NA
random forest	all	1200	NA	30	2	5	NA
decision tree	selected	NA	NA	7	8	1	gini
extra trees	all	200	NA	25	4	4	gini

Table 3: Specific parameters used to train each classification model. n_estimators: number of trees in the forest; learning_rate: learning rate shrinks the contribution of each tree by learning rate; max_depth: maximum depth of the tree; min_samples_leaf: minimum number of samples required to be at a leaf node; min_samples_split: minimum number of samples required to split an internal node; criterion: function to measure the quality of a split.

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for general ECG summary features and derived features, which was used in this study. Because inter-person ECG waves vary, the number of these features varies among different patients. For example, one patient had 19 R peaks from lead I, another person may have 16 R peaks. The direct use of these features in the learning algorithms is not feasible. To represent the distribution of these features across different patients and conditions, minimum (min), mean, maximum (max) and variance (var) of these derived features as well as heart rate from each of 12 ECG leads were calculated. There were 192 features derived from ECG data, including RR interval, heart rate time interval, heart rate, maximum amplitude of each segment in templates, with each feature having 4 statistics (min, mean, max, and var) and 12 leads. Together with an additional 14 features from diagnostics file, there are a total of 206 features.

Data splitting

The dataset was randomly divided with a ratio of 3:1, called training dataset and testing dataset, respectively. The training dataset, consisting of 7,893 samples, was used for developing classification models. The testing dataset, consisting of 2,632 samples, was used to evaluate the performance of classification models.

Learning algorithms

Four supervised learning algorithms were employed to develop classification models for arrhythmia classification, including decision tree, random forest, extra trees, and gradient boosting. For each learning algorithm, classifiers were built based on all 206 features as well as a subset of features. The subset of features was selected using SelectFromModel function from sklearn's feature selection class. The threshold was set as the means of the feature importance of pre-trained model's feature importance score. Only those features with an importance greater than the threshold were used for model development.

For each model, hyperparameters were tuned by grid searching hyperparameter space for optimum values to optimize the model. Model parameters are learned to optimize a loss function during model training. Ten-fold cross validation was used to evaluate various models. Specifically, the training data is randomly split into 10 folds. The model is trained on the 9 folds, while one fold is left to test a model. The classification error is computed in the held-out fold. This procedure is repeated 10 times. A different group of observations is treated as a validation set.

The decision tree was constructed using sklearn's DecisionTreeClassifier class. The random forest classifiers were built and optimized using sklearn's RandomForestClassifier class. Extra trees classifier was developed using ExtraTreeClassifer class from sklearn library. Gradient boosting was created and optimized using GradietBoostingClassifier class of sklearn library. **Table 3**. listed the hyperparameters tuned for each algorithm. The decision tree was tuned with respect to the maximum depth, the number of features considered when looking for the best split, the minimum number of samples required to split at an internal node and the criterion used to determine the impurity of a split (24). Random forest was tuned with respect to the number of decision tress, the maximum depth, the number of features considered when looking for the best split, the minimum number of samples required to split an internal node, and the minimum number of samples (or observations) required in a terminal node or leaf (24). The hyperparameters for Extra trees classifier were tuned including the number of decision tress, the maximum depth, the number of features considered when looking for the best split, the minimum number of samples required to split an internal node, the minimum number of samples (or observations) required in a terminal node or leaf and the criterion used to determine the impurity of a split. Gradient boosting was tuned for the maximum depth of a tree, the number of features considered when looking for the best split, the minimum number of samples required to split an internal node, the minimum number of samples (or observations) required in a terminal node or leaf and learning rate (24).

Performance evaluations

Performance of all six models for predicting arrhythmias was evaluated using metrics including accuracy, precision, recall and f1-score. The formulas used to calculate these performance metrics were shown below:

		Predicted	
		Negative	Positive
Actual	Negative	a	b
	Positive	c	d

$$\text{Accuracy} = \frac{(a + d)}{(a + b + c + d)}$$

$$\text{Precision} = \frac{d}{(d + b)}$$

$$\text{Recall} = \frac{d}{(d + c)}$$

$$F1 = 2 \times \frac{(\text{Precision} \times \text{Recall})}{(\text{Precision} + \text{Recall})}$$

Accuracy determines the accuracy of the algorithm in predicting arrhythmias instances. Precision determines the classifier's ability to provide correct positive predictions of arrhythmias. Recall is the proportion of actual positive cases of arrhythmias correctly identified by the classifier used. F1-score is the weighted average of precision and recall.

Statistical analysis

z-test was used to compare the proportion between the training and test datasets. T-test was used to compare the distribution of continuous values such as age, ventricular rate and atrial rate between training and testing datasets.

Software and packages

Data preprocessing, plotting, model fitting, model selection and model evaluation were performed using python (version 3.9.13) in jupyter notebook with the following versions of packages: numpy (version 1.21.5), panda (version 1.4.4), matplotlib (version 3.5.2), seaborn (version 0.11.2) and scikit-learn (version 1.0.2) libraries.

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