Gender Classification Using nonstandard ECG Signals - A Conceptual Framework of Implementation

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Abstract. This paper presents a comparison of nine models for gender identification using nonstandard ECG signal. Methods: QRS features, QT interval, RR interval, HRV features and HR were extracted from three minutes of 40 ECG's (from 24 female and 16 males) available at ALLab dataset and 108 ECG's (from 52 female and 56 males) available at CYBHi dataset. Models were developed using Decision tree, SVM, kNN, Boosted tree, Bagged tree, Subspace kNN, Subspace Discriminant, two majority vote and verified by external validation. Results: The study presented achieved as best results an accuracy of 78% from Boosted tree and 85% from majority vote. Conclusion: The automatic detection of gender by ECG could be very important and improve the development of predictive systems for cardiovascular disease. These classifications are promising due to the use of nonstandard ECG and to the simplicity of extraction of features that potentiated the correct classification

Keywords: Gender classification · nonstandard ECG · Real data · Machine learning

1 Introduction

The use of Electrocardiogram (ECG) signal to establish a person identity is an approach of biometrics by using features of an ECG signal as the inputs to an

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identification or authentication system. The feature extraction process results in five major deflection points (labeled P, Q, R, S and T) that combined show the ECG waveform. Besides these features, other ECG features are also used such as time domain features and frequency domain features, e.g., wavelet transform and power spectral density.

There are different types of ECG, depending upon the number of electrodes, such as 1-lead, 2-Lead, 6-Lead, and 12-Lead. The 12-lead ECG has many benefits over other kinds, including a) properly recreating the QRS, ST, and T waveforms, b) giving evidence of P wave and QRS complex morphology that cannot be detected with a single-lead ECG, and c) observing the changes in the ST segment the best. Thus, the 12-lead ECG became the standard electrocardiography [6,25]. Despite these advantages, nonstandard ECG can be suitable as a screening device for pathological rhythms or as ECG-based biometric system.

Prevention, management and treatment of many diseases do not reflect one of the most important risk factor for the patients, the gender [27]. There are important physiological differences between the two genders which deserve the attention of the scientific community, as to allow more relevance to "gender medicine" based on risk profiles, and to support the development of new predictive algorithms. Some cardiovascular diseases (CVD) have more prevalence in women than men, e.g. angina pectoris and stroke, and inversely coronary heart disease and heart failure have more prevalence in men than women. Gender is an essential, although sometimes overlooked, factor in determining human health. Clinical results, as well as the efficacy and safety of regularly used medications, may be significantly impacted by both sex and gender-related characteristics [15]. Recently, the incorporation of sex and gender views in clinical research and other sectors of adult health has enhanced the understanding of several diseases and produced convincing evidence for a more customized healthcare strategy [19,28]. Increased awareness of gender-specific differences-in basic and applied research, clinical portrayal, design of treatment regimens and procedures, guidelines, preventive strategies, and public health policies-may improve individualized care, appropriately address the unique needs of genders and sub-populations, and thereby reduce inequities, as well as present and future disease burden at the individual, community, national, and global scales [19,20]. Despite this, the sex- and gender-informed approach to medicine is a relatively new field based on current research, and it should be incorporated into both preclinical and clinical investigations to comprehend both male and female variations and obtain a fully individualized therapy [20,26].

Gender classification is a task relatively easy for humans, usually done through visual contact while assessing body shape and size, hair patterns, posture, facial features, clothing, or voice, not in this particular order and subject to cultural and environmental setting. Yet, for an identification system, this task can be a major challenge. In [16] the human gender classification is categorized into appearance and non-appearance approaches. Among the appearance approaches, we found still features, dynamic body features and apparel features, while the non-appearance approaches include biometrics features, bio-signals features and social information. In the last decade, the development of small acquisition devices that allow the collection of bio-signals in different scenarios has gained the attention of the scientific community. Of particular interest to this research, some bio-signals are used for gender classification, such as encephalography (EEG), ECG and deoxyribonucleic acid (DNA) [16].

Gender classification has applications in different fields which stand out: mobile applications and video games, demographic research, commercial development, surveillance systems, Human-Computer Interaction, and healthcare [33].

Relatively to gender differences in ECG signal Kumar et al. [14] concluded that male athletes had significantly greater QRS duration, Q-wave duration, and T wave amplitude and female athletes had a significantly greater QT interval. Xue & Farrell [34] also concluded that QRS duration is higher in men and QT interval is higher in female.

Research works on gender classification systems using ECG is still scarce, and we will briefly detail some of them (Table 1).

Different methods have been proposed previously for gender classification using ECG signals [1,4,7,9,10,12,13,17]. Some works used datasets with 12-lead ECG signals [4,9], but most of works used other configuration more suitable for a context of identification [1,7,10,12]. From ECG feature extraction, time domain (TD), frequency domain (FD), QRS features, heart rate variability (HRV), wavelets transform (WT), power spectral density (PSD) are commonly used, but some works proposed features based on Poincare section [10] or features based on Attractor Reconstruction (AR) [17]. Among the machine learning techniques highlights SVM, decision tree, kNN and CNN.

This paper is focused on the performance comparison of the nine models, three based on individual classifiers, four are ensembles and two models based on consensus decision using majority vote method, for gender identification using an ECG signal.

In the present study, 108 ECG signals (from 52 female and 56 male) are used to train the different models and 40 ECG's have been recorded (from 24 female and 16 male) to validate the models. For feature extraction the QRS features, QT interval, RR interval, heart rate (HR) and other HRV features were considered, and the following seven different classifiers have been trained and tested for gender classification: Decision tree (DT), Support vector machine (SVM), k-nearest neighbors (kNN), Boosted Tree, Bagged Tree, Subspace Bagged Discriminant, Subspace Bagged kNN. Also, we proposed two decision consensus using majority vote to balance out the individual models weaknesses. The remainder of this paper is organized as follows: this paragraph concludes section I, where the goal of the research was announced, and a brief but concise report of the most significant previous research was presented. Section II is limited to the presentation of the datasets used in this work. Section III describes the methodology and section IV presents the results. Discussion of the results follows in section V and section VI concludes this paper.

Table 1. Previous studies

Study(year)	Dataset	Features	Techniques	Results (Acc)
Tripathy et al. (2012) [13]	37 sets of input-output patterns	HRV	LS-SVM (RBF Kernel Function), 12 sets validation	92%
Ergin et al. (2014) [9]	MIT-BIH normal sinus rhythm (5M /13F)	QRS, TD, WT and PSD	C4.5 decision tree	f-score: 98.6%
Lyle et al. (2017) [17]	ecgrdvq database (11F/11 M)	AR and TD	SVM (Leave one-patients data-out validation)	93.1 (AR), 74% (TD)
Cabra et al. (2018) [7]	ECG-ID 308 templates (50%F)	TD	kNN (5-fold validation)	88.0%
Cabra et al. (2018) [7]	CYBHi. 1750 F F 469M Synthetic: 1281 M templates	TD	kNN (30% holdout validation)	95.1%
Attia et al. (2019) [4]	Train 499727 patients, 52%M Test 275056 patients	n/a	CNN (399750 training and 99977 in the internal validation)	90,4%
Goshvarpour & Goshvarpour (2019) [10]	ECG-ID 37 M 42 F	Poincare section-based	SVM (5-fold validation)	93.66%
Khan et al. (2020) [12]	ECG-ID 90 patients (153M and 159 F templates)	TD, FD	Fine decision tree (10-fold validation)	95.2%
Al Alkeem et al. (2021) [1]	ECG-ID: 44M 46F and PTB ECG: 209 M 81 F, 58 virtual patients	QRS	CNN (validation on virtual data)	90.04% (NA) 83.33% (MD) 82.18% (MD and NA) 100% (DA)

M- male; F- female;

2 Data

2.1 ALLAB Dataset

The experimental installation consists of a wireless physiological data acquisition system bioPlux [24] (1000 Hz sampling rate, 12 bits sample size), which is connected to an ECG sensor (Gain: 1000, band-pass: 0.05 Hz–30 Hz, common-mode rejection ratio: 110 dB). According to the ECG lead placement protocol, the three ECG leads were placed in the horizontal plane precordial position (V3, V4, V5). In this study we collected 40 ECGs at rest during 3–5 minutes from 16 male and 24 female, with ages between 18 and 72 years old, with a mean age of 33.09 ± 18.7 years. The collected data is transmitted from the device to a computer using a Bluetooth connection and an application that was provided by the manufacturer [24] recorded the data in a text file organized in a column-formatted manner. The 4th column corresponds to ECG signal (except for three files that the 2nd column corresponds to ECG). This data was collected as part of the research work for the BSc project in Bioengineering, subject "Caracterização de género através de um sinal ECG" (in English "Gender Classification through an ECG signal"). The data used in this research is publicly available at the ALLab MediaWiki [2].

The volunteers were informed of the nature and purpose of this research, an Ethics Committee approved the experimental protocol and the subjects signed an informed consent form. The volunteers declared to be healthy and to suffer from no cardiac disease.

2.2 CYBHi Dataset

The Check Your Biosignals Here initiative (CYBHi) dataset [32] is composed of short-term and long-term signals, the data acquisition was made using a bioplux device with a sampling rate of 1000 Hz Hz. The short-term signals were collected for an overall total of 65 participants, where 49 males and 16 females and the average age of 31.1 $\pm$ 9.46 years. ECG signals at the hand palms and fingers were recorded.

A set of 63 subjects, 14 males and 49 females, with an average age of 20.68 $\pm$ 2.83 years, were available for data acquisition of long-term signals. ECG signals at the fingers were recorded. In both cases, none of the participants reported any health problems.

3 Methodology

The proposed method is composed of a sequence of processing steps: data preparation, feature extraction and classification.

3.1 Data Preparation and Feature Extraction

The ECG signals extracted from the individual data file of each participant are carried out in MATLAB software. The 148 ECGs are analyzed and we opted to use only the first three minutes of each signal (180000 samples). As preprocessing the base line drift and drive direct current (DC) are removed and a Savitzky-Golay filter [30] is used to smooth out some of the noise from the ECGs, due to its ability to smooth ECG without much destroying its original properties [5,11].

The features used in this work can be listed as time domain (TD) features (RR interval, QT interval, QRS complex amplitude and duration), HRV features (SDNN, RMS, NN50 and PNN50) and heart rate.

From the TD feature extraction process results the detection of five deflection points, labeled P, Q, R, S and T waves. The P wave is an upward deflection and appears before the Q wave, depicting a downward deflection. The R wave follows as an upward deflection and the S wave is downward deflected following the R wave. The Q, R and S are successive waves and together create the QRS complex, with a duration 0,08–0,12 s [31], and a quite variable amplitude from lead to lead and from person to person. The T wave is an upward deflection and follows the S wave.

The RR interval (0,6–1 s [8]) is the duration between successive heart beats and the QT interval is the duration between the beginning of the Q wave and the end of the T wave (0,35–0,43 s [31]). The QT interval calculation is dependent of correct detection of the beginning of the Q wave and the end of the T wave. Statistical features have been extracted from the QT intervals, RR intervals, QRS amplitude and duration, and HR. Figure 1 shows an ECG waveform with the associated features labeled.

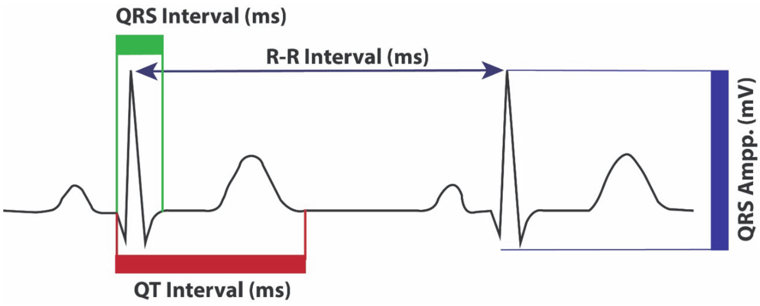

Fig. 1. ECG waveform with the associated features labeled.

Also, we extracted heart rate (HR), the standard deviation of the RR intervals (SDNN), the root mean square of successive differences between RR intervals (rMSSD), the number of times successive heartbeat intervals exceed 50ms (NN50) and the proportion of consecutive RR intervals that differ by more than 50ms (PNN50). Table 2 shows the 24 feature extracted from each subject ECG.

Table 2. Features Extraction.

Features	
QT interval (ms)	Mean, standard deviation, variance, maximum and minimum
RR interval (ms)	Mean, variance, maximum and minimum
Amplitude QRS (mV)	Mean, standard deviation, variance, maximum and minimum
Duration QRS (ms)	Mean, standard deviation, variance, maximum and minimum
HRV	SDNN, rMSSD, NN50, PNN50
HR	Mean

3.2 Classifiers

As the literature on gender classification with ECG is scarce, we have chosen to use several types of classifiers in order to verify which one presents better performances. The choices were made based on their features:

- Decision tree: provides an output easily interpreted by humans, it is fast, but the algorithm is greedy (there is a trade-off here); provides fast prediction but it depends always on the dataset [29].
- SVM: Provides fast predictions for binary classifications, the risk of over fitting is reduced, deliver a unique solution (no local minima), provides the maximum separating margin for a linearly separable dataset (approximation to bound on the test error rate), Kernel trick allows non-linearly separable dataset to may be linearly separable in a higher dimensional space [35].
- kNN: It is robust to noisy data and effective if the training data is large.
- Bagged tree and Boosted tree: more robust than a single decision tree [23].
- Subspace discriminant and Suspace kNN: good for binary classification, it can be used with many predictors [3].
- Majority vote: can be suitable for a set of well performing model in order to balance out their individual weaknesses [21].

Table 3 shows the chosen classifiers with the parameters used in this study. The classifiers are carried out using a machine learning module for Python, sklearn [22].

3.3 Train and Leave-One-Dataset-Out Validation

The dataset used to train the models contains 108 samples, from both short-term and long-term of CYBHi dataset, in which 52 samples are ECGs from females and 56 are ECGs from males. Thus, a 2-class dataset was obtained where each class had ECG features from male (class 1) and female (class 0) subjects. The validation method used is the leave-one-dataset-out using the ALLab dataset that contains 40 samples, in which 24 samples are ECGs from females and 16 are ECGs from males.

Table 3. Classifiers parametrization.

Classifiers	Classifier Type	Classifier Parameters
Decision tree	sklearn.tree.DecisionTreeClassifier	Maximum leaf nodes: 10 Split criterion: entropy Maximum features: auto
SVM	sklearn.svm.SVC	Kernel: rbf Regularization parameter: C=10
kNN	sklearn.neighbors.KNeighborsClassifier	Number of neighbours: 2
Boosted Tree	sklearn.ensemble.AdaBoostClassifier	number of estimators: 400 Learning rate: 0.5 Algorithm: SAMME
Bagged Tree	sklearn.ensemble.AdaBoostClassifier	number of estimators: 30 Maximum features:4 Random state: 4
Subspace Bagged kNN	sklearn.ensemble.BaggingClassifier	Base estimator: KNeighborsClassifier(2) number of estimators: 30 bootstrap=False Maximum features:4
Subspace Bagged Discriminant	sklearn.ensemble.BaggingClassifier	Base estimator: LinearDiscriminantAnalysis(solver='eigen', shrinkage='auto') number of estimators: 10 bootstrap=False Maximum features:4
Majority vote 1	sklearn.ensemble.VotingClassifier	Estimators: Boosted tree, Subspace kNN Voting: hard
Majority vote 2	sklearn.ensemble.VotingClassifier	Estimators: Boosted tree, Subspace kNN, Bagged tree Voting: hard

4 Results

Analysing the results presented in Table 4, it can be seen that different classifiers have different behaviours. In this study, overall, nine classifiers were applied (seven different and two majority votes based on the sevens) in order to detect person gender through ECG signal.

The accuracy and recall are calculated (see Eqs. 1 and 2) with the values extracted from the confusion matrix: True Positive (TP), True Negative (TN), False Positive (FP) and False Negative (FN).

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$Recall = \frac{TP}{TP + FN} \tag{2}$$

Table 4 summarises the results obtained when using the nine models.

Table 4. Classifiers Performances.

Classifiers	Best performance			
	%Accuracy (avg.)	%Accuracy	%Recall (class 0)	%Recall (class 1)
Decision tree	61.3	78.0	83.0	69.0
SVM	65.0	65.0	92.0	25.0
kNN	68.0	68.0	92.0	31.0
Boosted Tree	78.0	78.0	75.0	81.0
Bagged Tree	70.0	70.0	71.0	69.0
Subspace kNN	69.9	80.0	83.0	75.0
Subspace Discriminant	66.0	78.0	88.0	62.0
Majority vote 1	71.9	82.0	83.0	81.0
Majority vote 2	76.9	**85.0**	**88.0**	**81.0**

5 Discussion

The difference between the two genders is an important factor in determining human health. The medical knowledge about gender differences in anatomy, physiology, genetics support prognostic and diagnostic of diseases, e.g., cardiovascular diseases present different risk factors for men and women.

The gender identification using ECG signals can be useful in home-care systems, remote screening device for pathological rhythms or as ECG-based biometric system.

The 12-lead ECG configuration presents several advantages in terms of signal quality and interpretability, but nonstandard ECGs configurations allow data collection outside of a clinical context.

In this study, gender classification was conducted using nonstandard ECGs, resorting to CYBHi and ALLab datasets. CYBHi dataset comprises short-term and long-term signals, we used both signals to train our models. Allab dataset comprises short-term signals, and it was used for evaluating the models. The experimental settings of these two datasets were different, but the signals were collected with the same sampling rate (1000 Hz). The differences in experimental settings can compromise the good classification of genders, but nowadays it is possible to collect ECG using wearable devices in chest, wrist, or hands. We are aware that the orientation of the leads affects the morphology and amplitude of the measured ECG but in other side increase usability and allow more versatile solutions.

Another concern we had was to present a real and balanced training dataset without resorting to synthetic data.

Different classifiers are implemented, the results presented in Table 4 show that the better models are Boosted tree, Bagged tree and Subspace kNN with average accuracy from 78.0%; 70.0% and 69.9%. How we can verify the difference in the results is related to the behavior of each classifier, so, we also proposed resort to the majority vote to obtain two consensus decisions: 1. Boosted tree and Subspace kNN and 2. Boosted tree, Bagged tree and Subspace kNN. Both achieved a better recall balance.

The heart changes as we get older, and this is reflected in the features visible on the ECG. As a result, we may conclude that the difference in class results is directly influenced by this component [18].

These consensus decision results suggest the importance of feature selection. Table 5 shows the more important features for the method based on the majority vote using Boosted Tree, Bagged tree and Susbspace kNN. Generally, RR interval (mean and variability), duration of QRS (mean, variability, maximum), amplitude of QRS (mean, variability, maximum and minimum), QT interval (variability, maximum and minimum) and mean HR are the most important features.

Table 5. Feature importance.

Features	Models		
	Boosted Tree	Bagged tree	Subspace k-NN
mean RR		X	
Mean duration QRS	X		
Mean amplitude QRS	X		X
QT variability			X
RR variability	X		
QRS duration variability		X	
QRS amplitude variability			X
Maximum QT		X	
Minimum QT	X		
Maximum QRS duration	X		
Maximum QRS amplitude			X
Minimum QRS amplitude	X		
Mean HR		X	X

Automatic gender identification was tried by Tripathy et al. [13], Ergin et al. [9], Lyle et al. [17], Cabra et al. [7], Attia et al. [4], Goshvarpour & Goshvarpour [10], Khan et al. [12], and Al Alkeem et al. [1] with results above 90%. However, we tried and only got 85.0. We think that the previous papers may have had better results because length of the test dataset [9,13], unbalanced datasets [9], additional features [10,17], synthetic data [1,7] or data augmentation [1], noise addition [1] and internal validation [4,10,12].

In our view, what is needed is the proposal of a versatile framework for gender identification that allows realistic classifications. Our current approach uses real ECG signals to train the models and external validation. Besides, the ECG signals are collected using nonstandard configuration and settings, allowing usability in different context. So, in future work, we intend to propose a framework that can be incorporated as a gender identification module.

6 Conclusion

Many cardiovascular diseases (CVD) have more prevalence in women than men (angina pectoris, stroke) and inversely (coronary heart disease "CHD", heart failure), so the automatic detection of gender by ECG could be very important and improve the development of predictive systems for CVD and also in mobile or remote healthcare.

Considering the type of used ECG signals which can be collected from IoT devices, the proposed method can have several applications such as: reducing the data in face recognition research; improving CVD and other diseases with computer-aied diagnosis. in telemonitoring of where patient information is limited or in a monitoring center with cross information.

The main findings of this work are summarised as follows:

- Our method offers a realistic gender classification based on a simple feature extraction using nonstandard ECG signal;
- Bossted tree model provides good balance between each gender classification using a balanced dataset to train;
- The results from Bossted tree, Bagged tree and Subspace kNN suggest that feature selection improve the classification;
- A consensus decision can be used to improve and balance the classifications.

This work presents some limitations as a small dataset to train the models and the non-distinction between patients age, which can vary HRV features and QRS amplitude. So, in future work we are considering use ECG-ID dataset to apply our framework and added a new module for analysis of age similarities.

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