Heart Disease Detection Using ECG Lead I and Multiple Pattern Recognition Classifiers

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Abstract: ECG is an important tool to assist in heart diseases diagnosis. The works found in the literature have the common goal of discriminating between binary study groups, one pathological and one control, even when ECG records from patients diagnosed with several pathologies are available in the databases. This work proposes a method to detect ECG morphological features and to analyze the capacity of this ECG features to discriminate 28 pairs of study groups, combining 7 pathological groups and 1 control group, presented in the PTB Diagnostic ECG Database. For each pair, it was achieved an accuracy between 77.4% and 100%, with an average of 94%, using several pattern recognition classifiers.

Key Word: Heart diseases; ECG features; Pattern recognition; PTB Diagnostic ECG Database; Classifiers.

I. INTRODUCTION

The electrocardiogram (ECG) is the recording of the rhythmic alterations of the heart electrical activity and represents the cardiac cycle [1]. A typical ECG is usually recorded by means of a 12-lead system (i, ii, iii, aVR, aVL, aVF, V1, V2, V3, V4, V5, V6). The amplitude and direction of the current flow in the heart are detected by the electrodes, resulting in different ECG signals according to the leads axis. An ECG signal of a healthy subject is cyclically formed by a P wave, a QRS complex and a T wave [1], which represent the atria depolarization, the ventricular depolarization and the ventricular repolarization, respectively [2]. Other important time intervals and signal segments are also described in Figure no 1. The time between the beginnings of the P wave and the QRS complex is the PQ interval, which is often called PR interval because the Q wave is usually very small [3]. During the PR interval, which lasts approximately 0.16 seconds, the auricle contracts and begins to relax [4]. The QT interval extends from the beginning of the QRS complex to the end of the T wave, lasting approximately 0.36 seconds, and represents the approximate duration required for the ventricles to contract and relax [5].



Figure no 1: ECG wave and its morphological features.

Any minor change in the normal pattern of an ECG signal can be interpreted as malfunction of the heart [6,7]. Thus, autonomous and accurate discrimination of cardiac pathologies through ECG is an important tool to assist in the diagnosis of these diseases, especially considering that the detection of cardiac disorder is exhausting task for cardiologists [8]. During the last years, several works have proposed methods to detect ECG features (morphological

or not) and then to diagnose cardiac pathologies. These works can be classified according to: pathologies diagnosed, ECG database used, number of ECG leads used, ECG analysis method and classification method. Considering only those that use public databases, some works found in the literature and their results are summarized in the Table no 1. The great majority of these methods aimed to discriminate Myocardial Infarction (MI) from healthy controls, which can be explained by the greater number of ECG patabase. Few works aimed to discriminate Dysrhythmia or Cardiomyopathy from healthy controls. However, all works have the common goal of discriminating between 2 study groups, one pathological group and one control group, even when ECG records from patients diagnosed with several pathologies are available in the databases. This work proposes to analyze the capacity of several ECG parameters to discriminate 28 pairs of study groups, combining 7 pathological groups and 1 control group, presented in the PTB Diagnostic ECG Database.

| Table no 1: List of works found in the literature. | | | | | | | |
|----------------------------------------------------|-----------------------------------------|----------|--------------------------------------------------------------------------------------------|------------|--|--|--|
| References | ReferencesPathologiesNumber of Leads | | Method and Classification | Accuracies | | | |
| [9] | MI | 12 leads | ST segment elevation and threshold classification | 92.5% | | | |
| [10] | MI | 3 leads | Q peak depth and ST segment elevation. Classification by a simple adaptive threshold | 90.56% | | | |
| [11] | Dysrhythmia | 12 leads | Template construction from CWT features using a morphological consistency classifier | 93.0% | | | |
| [12] | Cardiomyopathy | 12 leads | PR, RR, QT and QRS intervals analysis. Classification through BPNN | 95.2% | | | |

ECG Database

II. MATERIAL AND METHODS

This work used the PTB Diagnostic ECG Database available in [13, 14]. The database contains 549 ECG records from 268 subjects, including healthy subjects. Table no 2 summarizes de database. Each ECG record contains all the 12-lead system signals with a sampling rate of 1000 Hz, but this work used only the Lead I signals.

|--|

| Pathologies | Number of patients | | |
|------------------------|-----------------------|--|--|
| MI | 148 | | |
| Cardiomyopathy | 18 | | |
| Bundle Branch Block | 15 | | |
| Dysrhythmia | 14 | | |
| Myocardial hypertrophy | 7 | | |
| Valvular heart disease | 6 | | |
| Myocarditis | 4 | | |
| Miscellaneous | 4 | | |
| Healthy controls | 52 | | |

Peak detection

The method detects the R, S, Q, P and T peaks of the ECG signal, in that order, as follows:

Peak R: A Wavelet Transform (WT) translation analysis, using the wavelet 'symlet 4'(orange in Figure no 2), is applied in order to calculate the cross-correlation between the signal and the WT. The R peaks are the maxima of each correlation over the channel. To find all the R peaks in the ECG a 70% signal amplitude threshold (black line in Figure

no 2) of the WT's maximum was used to make sure that just the most prominent correlation peak in each heart cycle is detected.



S peak: The S peak was identified as being the first negative minimum wave after the first zero of WT 'symlet 4'translation after the R peak (Figure no 3 a)) [15].

Q peak: Contrary to S peak, the Q peak was identified as being the negative minimum wave right before the first zero before of WT 'symlet 4'translation before the R peak (Figure no 3b)) [15].

P peak: WT translation was performed using WT 'symlet 4'. The WT was then amplified fifth rooting it. The first three zeros of the WT wave before each R peak were calculated. The last two zeros were used as windows to compute the maximum of the ECG signal, corresponding to the P peak (Figure 3 c)).



Figure no 3: ECG a) S peak, b) Q peak, c) P peak and d) T peak detection.

T peak: For the T wave analysis the ECG signal was set to zero before and after two consecutive R peaks, knowing T waves are comprehended in this interval. To verify if the T wave was in an inverting or non-inverting state a

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 3^{rd} degree polynomial approximation was applied to each SP interval. Computing the inflection points and applying again a 2^{nd} degree polynomial approximation from the beginning of the SP interval to the first inflection point, the coefficient signal dictates if positive the T wave is inverted and if negative, non-inverted (Figure no 4). If non-inverted the WT maintains the same and if inverted the WT was inverted. The T peaks are the maxima of each correlation over the channel. To find the T peak in each RR window of the ECG a 99% signal amplitude threshold was used to make sure that just the most prominent correlation peak is detected. If the maximum of WT being offset from T peak, the first zero, before and after the WT maximum, were used as windows to compute the maximum of the ECG signal, corresponding to the T peak (Figure no 3 d)).



Figure no 4: T wave state (inverted/non-inverted) detection.

After all peak's identification, it is easy to find the segments that represent the QRS complex, PR interval, PR segment, QT interval and ST segment were followed identified.

ECG Features Analyzed

Several features of each Lead I ECG signal are calculated in order to analyze their discrimination capacities. The features are summarized in the Table no 3.

| Table no 3: List of analyzed features and their respective index. | | | | | |
|-------------------------------------------------------------------|----------------------------------------------|-------|----------------------------------------------|-------|---------------------|
| Index | Features | Index | Features | Index | Features |
| 1 | Energy QRS complex | 38 | WT 'sym8' det. level 3 energy QT interval | 75 | Time P-T |
| 2 | Power QRS complex | 39 | WT 'sym8' det. level 2 energy QT interval | 76 | Time Q-R |
| 3 | Entropy QRS complex | 40 | WT 'sym8' det. level 1 energy QT interval | 77 | Time Q-S |
| 4 | Shannon Entropy QRS complex | 41 | Duration P wave | 78 | Time Q-T |
| 5 | Log Energy Entropy QRS complex | 42 | Energy P wave | 79 | Time R-S |
| 6 | WT 'sym4' det. level 4 energy QRS complex | 43 | Power P wave | 80 | Time R-T |
| 7 | WT 'sym4' det. level 3 energy QRS complex | 44 | Entropy P wave | 81 | Time S-T |
| 8 | WT 'sym4' det. level 2 energy QRS complex | 45 | Shannon Entropy P wave | 82 | Amplitude P peak |
| 9 | WT 'sym4' det. level 1 energy QRS complex | 46 | Log Energy Entropy P wave | 83 | Amplitude Q peak |
| 10 | WT 'sym8' det. level 4 energy QRS complex | 47 | WT 'sym4' det. level 4 energy P wave | 84 | Amplitude R peak |
| 11 | WT 'sym8' det. level 3 energy ORS complex | 48 | WT 'sym4' det. level 3 energy P wave | 85 | Amplitude S peak |

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| 12 | WT 'sym8' det. level 2 energy QRS complex | 49 | WT 'sym4' det. level 2 energy P wave | 86 | Amplitude T peak |
|----|-----------------------------------------------|----------|-----------------------------------------|-----|-----------------------------------------|
| 13 | WT 'sym8' det. level 1 energy QRS complex | 50 | WT 'sym4' det. level 1 energy P wave | 87 | Amplitude difference P-Q |
| 14 | Energy PR interval | 51 | WT 'sym8' det. level 4 energy P wave | 88 | Amplitude difference P-R |
| 15 | Power PR interval | 52 | WT 'sym8' det. level 3 energy P wave | 89 | Amplitude difference P-S |
| 16 | Entropy PR interval | 53 | 2 energy P wave | 90 | Amplitude difference P-T |
| 17 | Shannon Entropy PR interval | 54 | WT 'sym8' det. level 1 energy P wave | 91 | Amplitude difference Q-R |
| 18 | Log Energy Entropy PR interval | 55 | Duration T wave | 92 | Amplitude difference Q-S |
| 19 | WT 'sym4' det. level 4 energy PR interval | 56 | Energy T wave | 93 | Amplitude difference Q-T |
| 20 | WT 'sym4' det. level 3 energy PR interval | 57 58 | Power T wave | 94 | Amplitude difference R-S |
| 21 | wT 'sym4' det. level 2 energy PR interval | 59 | Entropy T wave | 95 | Amplitude difference R-T |
| 22 | wT 'sym4' det. level 1 energy PR interval | 60 | Shannon Entropy T wave | 96 | Amplitude difference S-T |
| 23 | w 1 'sym8' det. level 4 energy PR interval | 61 | WT to wave | 98 | Energy ECG |
| 24 | energy PR interval | 62 | 4 energy T wave | 99 | Power ECG |
| 25 | w 1 'sym8' det. level 2 energy PR interval | 63 | 3 energy T wave | 100 | Entropy ECG |
| 26 | energy PR interval | 64 | 2 energy T wave | 101 | Entropy ECG |
| 27 | Energy QT interval | 65 | 1 energy T wave | 102 | Entropy ECG |
| 28 | Power QT interval | 66 | WT 'sym8' det. level 4 energy T wave | 103 | level 4 energy ECG |
| 29 | Entropy QT interval | 67 | WT 'sym8' det. level 3 energy T wave | 104 | W1 sym4 det. level 3 energy ECG |
| 30 | Shannon Entropy QT interval | 68 | WT 'sym8' det. level 2 energy T wave | 105 | WT 'sym4' det. level 2 energy ECG |
| 31 | Log Energy Entropy QRS complex | 69 | WT 'sym8' det. level 1 energy T wave | 106 | WT 'sym4' det. level 1 energy ECG |
| 32 | WT 'sym4' det. level 4 energy QT interval | 70 | Duration PR segment | 107 | WT 'sym8' det. level 4 energy ECG |
| 34 | WT 'sym4' det. level 3 energy QT interval | 71 | Duration ST segment | 108 | WT 'sym8' det. level 3 energy ECG |
| 35 | WT 'sym4' det. level 2 energy QT interval | 72 | Time P-Q | 109 | WT 'sym8' det. level 2 energy ECG |

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|---------------|-----------------|----------|-----------------------|---------------------------|
|---------------|-----------------|----------|-----------------------|---------------------------|

| 36 | WT 'sym4' det. level 1 energy QT interval | 73 | Time P-R | 110 | WT 'sym8' det. level 1 energy ECG |
|----|----------------------------------------------|----|----------|-----|-----------------------------------------|
| 37 | WT 'sym8' det. level 4 energy QT interval | 74 | Time P-S | | |

Classification

A sequential feature selection algorithm with deviance of the fit (generalization of the residual sum of squares) criterion were applied for feature selection from matrices with 110 features per X subjects (X is the number of the patients involved in each classification pair). The 110 features resulted from the mean features values extracted from each ECG cycle per subject (I lead), as described in Table no 3. A 5-fold cross validation was used for training and testing several different machine learning classifiers presented in Table no 4. The classifications were performed for 28 pairs of the study groups between 7 pathological groups and 1 control group.

Table no 4: List of used classifiers.

| Decision Trees | Support Vector Machines | Nearest Neighbor Classifiers | Ensemble Classifiers | Discriminant Analysis | Logistic Regression Classifiers |
|----------------|----------------------------|------------------------------------|-------------------------|--------------------------|---------------------------------------|
| Medium Tree | Linear SVM | Fine KNN | Boosted Trees | Linear | Logistic |
| Coarse Tree | Quadratic SVM | Medium KNN | Bagged Trees | Discriminant | Regression |
| | Cubic SVM | Coarse KNN | Subspace | Quadratic | |
| | Fine Gaussian | Cosine KNN | Discriminant | Discriminant | |
| | SVM | Cubic KNN | Subspace KNN | | |
| | Medium | Weighted KNN | RUSBoosted | | |
| | Gaussian SVM | | Trees | | |
| | Coarse Gaussian | | | | |
| | SVM | | | | |

III.RESULTS

As previously said, the classifications were performed for 28 pairs of the study groups combining 7 pathological groups and 1 control group. The results shown in Figure are the best accuracies achieved from the trained/tested classifiers.

As can be observed from Figure no 5, the maximum accuracy classification was achieved for the pairs Healthy controls vs. Myocarditis and Cardiomyopathy; Bundle branch block vs. Myocarditis; Valvular heart disease vs. Myocarditis and Myocardial hypertrophy; Myocarditis vs. MI, Myocardial hypertrophy and Dysrhythmia; Myocardial hypertrophy vs. Cardiomyopathy and Dysrhythmia; with an outstanding 100% precision rate. Moreover, it can be noticed that the best features were capable of discriminating Healthy controls from any other heart disease with an accuracy higher than 95% for the exception of Bundle branch block and MI where the reached accuracies were 89.6% and 87.4%, respectively. For the pairs Healthy controls vs. Dysrhythmia the classifiers achieved an accuracy of 95.5%. The distinguish accuracy between Healthy controls against MI is slightly under the results of those in the state-of-art (Table no 1) and can be explained by the fact that the methods available in the literature use multiple leads and, as previously mentioned, not just one lead as this work.

Using only Lead I analysis, the classifiers were able to achieve an accuracy between 77.4% and 100%, with an average of 94%, for the 28 pairs of study groups showing Lead I has good capacity for heart pathologies discrimination, however, the low number of records for some pathologies should be taken in consideration.





Figure no 5: Pathologies discrimination accuracies.

IV. CONCLUSION

This work has analyzed the capacity of several ECG features to discriminate 28 pairs of study groups, combining 7 pathological groups and 1 control group, presented in the PTB Diagnostic ECG Database. Using only Lead I, the classifiers were able to achieve an accuracy between 77.4% and 100%, with an average of 94%, for the 28 pairs of study groups. These results become even more relevant considering that only 3 of these pairs are commonly analyzed in the literature: MI, Dysrhythmia and Cardiomyopathy. This study also proves that Lead I has good capacity for heart pathologies discrimination, however the low number of records for some pathologies should be taken inconsideration.

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