

ST-segment and T-wave Anomalies Prediction in an ECG Data Using RUSBoost

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Abstract—Electrocardiogram (ECG) datasets are among the most challenging records that have been widely studied for early automatic prediction of cardiac anomalies. In order to achieve high performance automatic prediction, existing works make use of complex and time consuming techniques and/or show high rates of false positives. In this paper, we introduce a new method to analyze an ECG dataset and perform an efficient prediction of 7 ST-segment and T-wave anomalies related to Myocardial Infarction (MI) or Ischemia. Our method combines both Decision Trees Boosting and Random Under Sampling (RUS) techniques to respectively improve the prediction performance and solve the class imbalance problem. This method, named RUSBoost, has been validated using data of 7 leads, collected from a real ECG dataset [1], and the obtained results show a higher balance between true and false positives for all the 7 leads. Obtained average sensitivity and specificity are respectively 86% and 94.85%, which outperform the existing results of other related works.

Index terms— ECG, ST segment, T-wave, Decision Trees, Boosting, Random Under Sampling, RUSBoost.

I. INTRODUCTION

Electrocardiogram (ECG) is a graphical representation of the electrical activity of a heart. By using special electrodes, that are placed on particular places of a patient's body and connected to an electrocardiograph, it has been possible for decades to capture a representation of any heart activity. In an ambulatory conditions, these electrodes record at least 12-ECG signals known as leads. These leads include six in the frontal plane, named Limb Leads (I, II, III, aVR, aVL, aVF), and six in the horizontal plane, named Precordial Leads (V1, V2, V3, V4, V5, V6). Each lead is a succession of ECG heartbeats. An ECG heartbeat refers to a depolarization or re-polarization of the heart, and is electrically represented by five major waves, namely: *P*, *Q*, *R*, *S*, and *T*. Figure 1 illustrates a typical ECG heartbeat with its main waves and segments.

ECG is a very interesting signal to study as it is both non-invasive for heart function control and indicative of various anomalies. Among these anomalies, Ischemia and Myocardial Infarction (MI) are considered as very serious ones. These anomalies are typically characterized by changes in ST segment and/or T-wave of ECG heartbeats. Ischemia is generally the first stage and is characterized by Hyperacute or Inverted T-wave. MI is the next stage and is generally characterized by ST segment elevation (STEMI), which is normally iso-electric for healthy subjects. ST segment depression (NSTEMI) may also be a sign of MI. Figure 2 shows normal and MI ECG heartbeat.

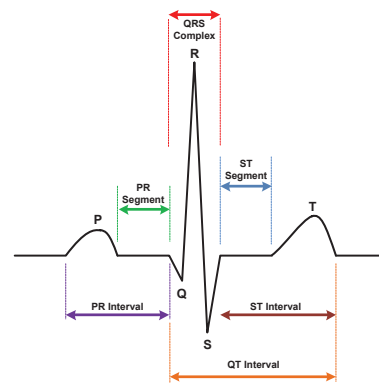
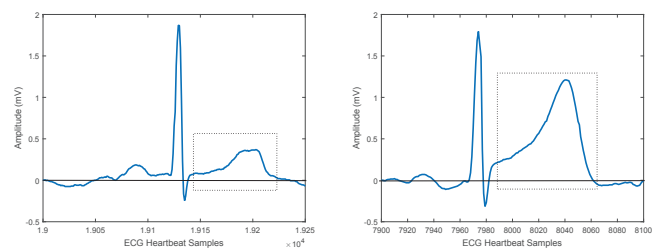


Fig. 1: An ECG Heartbeat with waves and segments



(a) Normal ST segment and T-wave (b) Elevated ST segment and T-wave

Fig. 2: Normal and Ischemic Heartbeat from Physionet [1]

In this paper, an automatic ECG analysis method is presented for relevant prediction of ST segment and T-wave anomalies. The goal is to achieve a high prediction performance using a lightweight method, compatible with a real-time application. The rest of this paper is organized as follows. Section II surveys some related works, section III describes our proposed approach, section IV discusses experimental results and finally, Section V concludes this paper.

II. RELATED WORKS

Various techniques and methods were proposed in the literature for automatic ECG anomalies detection, especially arrhythmia and more recently Ischemia and Myocardial Infarction. The majority of these methods are based on traditional

machine learning techniques in order to classify ECG into normal or abnormal. Considering Ischemia and Myocardial Infarction, several methods were explored over the last few years, the majority of which has 2 output classes (Normal or MI Anomaly). For example in [2], Pei-Chann Chang et al. proposed a classification method of MI based on a Hidden Markov Model (HMM) and a Gaussian Mixture Model (GMM). In [3], Muhammad Arif et al. proposed a detection and localization of MI based on K-Nearest Neighbor (KNN). Another work [4], done by Akshay Dhawan et al. used Multilayer Support Vector Machine (SVM) and Genetic Algorithm (GA) to detect MI. Old MI detection was studied by Zheng et al. [5] by testing SVM, Naïve Bayes (NB) and Random Forest (RF) methods. Artificial Neural Networks (ANN) algorithms were also widely explored for MI detection and classification, as in [6], where probabilistic neural networks classification was used by Keshtkar et al. to discriminate MI patients from healthy subjects. In the work of Bhaskar [7], ANN classification performance was compared to SVM in MI subjects diagnosis.

These proposed methods generally report a high prediction performance, however, a common problem with traditional classification techniques is the true positives (sensitivity) vs true negatives (specificity) balance. The classifiers with a very good detection rate have also a high false positives rate (low true negatives). The existing classification methods are often based on complex techniques which involve a big training time and memory consumption, this is generally not adapted to real-time applications context. Also, in existing methods, the kind of heartbeat anomalies related to MI is generally not classified. Recently, ensemble learning methods are widely used by scientists in many fields to improve the classification performance, these methods started to be used for general ECG analysis like [8], [9] and [10], but very few for MI or Ischemia prediction.

III. PROPOSED APPROACH

We describe here the main components of our approach shown in figure 3.

Below are the main parameters taken into account :

- *Multiple Leads* : we take into account a maximum number of leads. As we are limited by available databases, we could study 7 different leads : V1, V2, V3, V4, V5, I, III.
- *Multiple ECG extracted features* : our approach focuses on ST and T-wave anomalies prediction, but we use features related to all ECG waves and segments as input parameters. We also introduce ratios between specific waves and segments parameters that are more significant.
- *Multiple ST and T anomalies Classes* : we consider 7 different ST and T anomalies classes (see table III).
- *Learning Time* : as our approach is designed to be implemented in a real-time context with periodic update of the training set, the learning time is important to consider.

We consider a k -lead raw ECG received in real-time as shown in figure 3–(a). Our ECG analysis method includes 2 main steps detailed in next subsections.

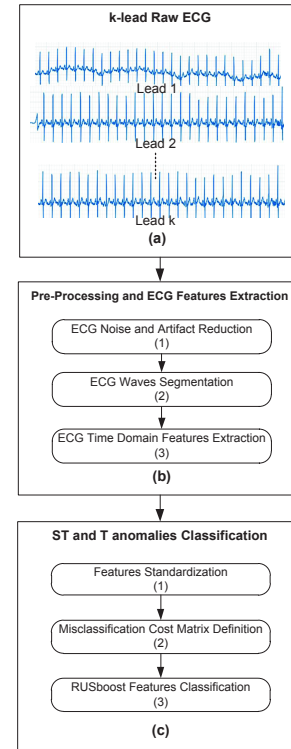


Fig. 3: Design Steps of our Method

A. ECG Pre-processing and Features Extraction

ECG pre-processing and features extraction (figure 3–(b)), are standard requirements to any ECG diagnosis system. We describe in what follows how these steps are done in this study.

1) *ECG Noise and Artifact Reduction*: ECG can be contaminated with various noises that can seriously affect the ECG records quality and distort the results of the analysis :

Power line noise around 50Hz or 60Hz comes from electronic circuits of ECG recorder. It is a narrow-band signal centered at a frequency of 50Hz or 60Hz with a bandwidth of less than 1Hz. Generally, this noise is filtered by ECG signal acquisition hardware.

Baseline wandering is usually due to patient movements and respiration. It ranges between 0.15Hz and 0.5Hz and causes changes in ECG iso-electric line. This noise is generally removed by a highpass digital filter or by a standard Wavelet Transform (WT). In this study, we use a 0.5Hz FIR highpass filter without loss in the original ECG signal.

Electrodes Motion artifacts ranging from 1Hz to 10Hz and EMG noise from 25Hz to 100Hz are more difficult to remove because they may be complex stochastic processes within a wide-band, and traditional digital filters can't remove them. In this study, we use Undecimated Wavelet Transform (UWT), a form of Discrete Wavelet Transform (DWT) which has a better balance between smoothness and accuracy, and ensures no loss of signal features. More details on its use for ECG denoising

can be found in [11]. We use UWT with db6 wavelet and 4 decomposition levels.

2) **ECG Waves Segmentation:** ECG heartbeats segmentation must be performed to estimate the time positions of heartbeat waves (QRS complex, P-wave and T-wave). The method used for segmentation is based on UWT decomposition used with the bi-orthogonal wavelet at 8 levels. First, the waves pics are detected, then the onsets and offsets of wavelets are calculated. The pics correspond to zero-crossing points in details coefficients $D_i, i = 1, \dots, 8$ and onsets/offsets are calculated by finding zero-crossing points in a windows w around each pic.

As we consider k ECG leads, the process described above is applied on each lead. Table I synthesizes the 6 waves parameters extracted for each heartbeat i of lead k and represented by variables $p_{i,1}^k, p_{i,2}^k, p_{i,3}^k, p_{i,4}^k, p_{i,5}^k, p_{i,6}^k$.

TABLE I: Waves parameters for each heartbeat i of lead k

| Parameter | Variable | Description |
|----------------|-------------|--|
| P_{onset} | $p_{i,1}^k$ | Start time of P-wave of heartbeat i |
| P_{offset} | $p_{i,2}^k$ | End time of P-wave of heartbeat i |
| QRS_{onset} | $p_{i,3}^k$ | Start time of QRS complex of heartbeat i |
| QRS_{offset} | $p_{i,4}^k$ | End time of QRS complex of heartbeat i |
| T_{onset} | $p_{i,5}^k$ | Start time of T-wave of heartbeat i |
| T_{offset} | $p_{i,6}^k$ | End time of the T-wave of heartbeat i |

3) **ECG Features Extraction:** Based on the waves parameters variables $p_{i,l}^k, l = 1, \dots, 6$, we calculate the heartbeats features. The more data we have about heartbeats, the better the analysis will be. After collecting several medical information on MI and Ischemia anomalies [12], we choose to calculate standard temporal waves features, in addition to ratios of these temporal features as we think that ratios are more significant than values. For each heartbeat i of lead k , the $x_{i,j}^k, j = 1, \dots, 18$ features calculated based on $p_{i,l}^k$, are described in table II. Durations are in ms and amplitudes in milliVolts mV .

We assume that each lead k is composed of m heartbeats, then, each heartbeat i can be defined by its features vector $X_i^k = (x_{i,1}^k, x_{i,2}^k, \dots, x_{i,n}^k), n = 18$. We define for each lead k the vector $F_j^k = (x_{1,j}^k, x_{2,j}^k, \dots, x_{m,j}^k), j \in \{1, 2, \dots, n\}$, representing the values of feature j of all the m heartbeats received. Each lead k can then be represented by $m * n$ matrix ECG^k , where columns are features and lines are heartbeats :

$$ECG^k = \begin{matrix} & \mathbf{F}_1^k & \mathbf{F}_2^k & \dots & \mathbf{F}_n^k \\ \mathbf{X}_1^k & \begin{pmatrix} x_{1,1}^k & x_{1,2}^k & \dots & x_{1,n}^k \\ x_{2,1}^k & x_{2,2}^k & \dots & x_{2,n}^k \\ \vdots & \vdots & \ddots & \vdots \\ x_{m,1}^k & x_{m,2}^k & \dots & x_{m,n}^k \end{pmatrix} \\ \mathbf{X}_2^k & \\ \vdots & \\ \mathbf{X}_m^k & \end{matrix} \quad (1)$$

B. ST and T anomalies Classification

We describe here how we classify each heartbeat features vector X_i^k into one class $y_i^k \in \{c_1, c_2, c_3, c_4, c_5, c_6, c_7\}$ detailed in table III. We define for each lead k , the vector $Class^k$ corresponding to classes of all m heartbeats. The classes y_i^k are known for training set and unknown for test set.

TABLE II: Features extracted for each heartbeat i of lead k

| Feature | Variable | Description |
|-------------|--------------|--|
| RR | $x_{i,1}^k$ | Interval duration between previous and current R peak of heartbeat i , lead k |
| HR | $x_{i,2}^k$ | Heart Rate calculated based on RR Interval of heartbeat i , lead k |
| P_{amp} | $x_{i,3}^k$ | P-wave amplitude of heartbeat i , lead k |
| P_{dur} | $x_{i,4}^k$ | P-wave duration of heartbeat i , lead k |
| QRS_{amp} | $x_{i,5}^k$ | R-wave amplitude of heartbeat i , lead k |
| QRS_{dur} | $x_{i,6}^k$ | Duration from Q-wave beginning to S-wave end of heartbeat i , lead k |
| T_{amp} | $x_{i,7}^k$ | T-wave amplitude of heartbeat i , lead k |
| T_{dur} | $x_{i,8}^k$ | T-wave duration of heartbeat i , lead k |
| PR_{dur} | $x_{i,9}^k$ | Duration from P-wave beginning to R-wave end of heartbeat i , lead k |
| QT_{dur} | $x_{i,10}^k$ | Duration from Q-wave beginning to T-wave end of heartbeat i , lead k . Specialists take into account the corrected QT interval QT_c calculated based on HR |
| ST_{amp} | $x_{i,11}^k$ | Level of ST segment from iso-electric line, of heartbeat i , lead k . It is calculated $80ms$ after the J point (end of QRS complex) if the HR $< 120bpm$, and $60ms$ otherwise |
| T/R | $x_{i,12}^k$ | Ratio of T-wave amplitude to R-wave amplitude for heartbeat i , lead k |
| ST/R | $x_{i,13}^k$ | Ratio of ST segment amplitude to R-wave amplitude for heartbeat i , lead k |
| QT/RR | $x_{i,14}^k$ | Ratio of QT interval duration to RR interval duration for heartbeat i , lead k |
| P/RR | $x_{i,15}^k$ | Ratio of P-wave duration to RR Interval duration for heartbeat i , lead k |
| PR/RR | $x_{i,16}^k$ | Ratio of PR segment duration to RR Interval duration for heartbeat i , lead k |
| QRS/RR | $x_{i,17}^k$ | Ratio of QRS complex duration to RR Interval duration for heartbeat i , lead k |
| T/RR | $x_{i,18}^k$ | Ratio of T-wave duration to RR Interval duration for heartbeat i , lead k |

$$Class^k = (y_1^k, y_2^k, \dots, y_m^k) \quad (2)$$

TABLE III: ST and T anomalies classes predicted

| Anomaly | Class | Description |
|---------|-------|--|
| N | c_1 | Normal heartbeat regarding studied anomalies |
| T+ | c_2 | Positive deviation of T-wave relative to a reference heartbeat point |
| T- | c_3 | Negative deviation of T-wave relative to a reference heartbeat point |
| ST+ | c_4 | Positive deviation of ST-segment relative to a reference heartbeat point |
| ST- | c_5 | Negative deviation of ST-segment relative to a reference heartbeat point |
| ST+T+ | c_6 | Combination of ST+ and T+ in the same heartbeat |
| ST-T- | c_7 | Combination of ST- and T- in the same heartbeat |

Figure 3-(c) shows the classification steps detailed below.

1) **Features Standardization:** We first standardize each F_j^k vector to rescale the features so that they will have the properties of a standard normal distribution with $\mu = 0$ and $\sigma = 1$. This step is not only necessary if we are comparing features that have different units, but is also a requirement for many machine learning techniques.

We use z-score normalization where μ_j^k and σ_j^k are respectively the mean and standard deviation of F_j^k , so the standardized features vector \bar{F}_j^k is calculated as follows :

$$\bar{F}_j^k = \frac{F_j^k - \mu_j^k}{\sigma_j^k} \quad (3)$$

and the standardized heartbeat vector $\bar{X}_i^k = (\bar{x}_{i,1}^k, \bar{x}_{i,2}^k, \dots, \bar{x}_{i,n}^k)$ is derived from X_i^k where :

$$\bar{x}_{i,j}^k = \frac{x_{i,j}^k - \mu_j^k}{\sigma_j^k} \quad (4)$$

2) **Misclassification Cost Matrix:** As ECG analysis is a medical application, we choose to treat classes asymmetrically. This means that we consider that mis-classifying observations of one class has more severe consequences than for another class. Failure to identify ST or T anomaly in a heartbeat (False Negative), has more impact than misidentifying normal heartbeat as anomalous (False Positive). So we assign high cost to misidentifying anomalies as normals and lower cost to misidentifying normals as anomalies. This is done using a mis-classification costs matrix C_{err} , which is a $nb_{class} * nb_{class}$ ($7*7$) square matrix with non-negative elements $c_{i,j} \in \{v_0, v_1, v_2, v_3\}$ representing the cost of classifying a heartbeat into class j if the true class is i . The cost matrix C_{err} is represented below.

$$C_{err} = \begin{matrix} & \begin{matrix} N & ST+ & ST- & T+ & T- & ST+T+ & ST-T- \end{matrix} \\ \begin{matrix} N \\ ST+ \\ ST- \\ T+ \\ T- \\ ST+T+ \\ ST-T- \end{matrix} & \begin{pmatrix} v_0 & v_2 & v_2 & v_2 & v_2 & v_2 & v_2 \\ v_3 & v_0 & v_1 & v_1 & v_1 & v_1 & v_1 \\ v_3 & v_1 & v_0 & v_1 & v_1 & v_1 & v_1 \\ v_3 & v_1 & v_1 & v_0 & v_1 & v_1 & v_1 \\ v_3 & v_1 & v_1 & v_1 & v_0 & v_1 & v_1 \\ v_3 & v_1 & v_1 & v_1 & v_1 & v_0 & v_1 \\ v_3 & v_1 & v_1 & v_1 & v_1 & v_1 & v_0 \end{pmatrix} \end{matrix} \quad (5)$$

Where:

$$v_0 = 0, v_1 = 1, v_2 = \alpha * v_1, v_3 = \beta * v_1, \beta > \alpha > 0$$

α and β values are chosen in experimentation.

3) **RUSboost classification:** In order to deal with drawbacks of traditional supervised learning classifiers and take into account specificities of ECG data analysis, we use the RUSboost classification concept [13] on our ECG data, by combining a Boosted Decision Trees, as our ensemble learning technique, and Random Under Sampling (RUS) to deal with ECG class imbalance problem. Both techniques are presented below.

– Boosted Decision Trees : Boosting consists in aggregating the results of T instances of a chosen classifier $h(x)$, named “weak classifier”, where each instance $h_t(x)$ is adapted on a specific part of the training data. This method builds a “strong” classifier as linear combination of the weak classifiers $h_t(x)$.

$$f(x) = \sum_{t=1}^T \alpha_t h_t(x) \quad (6)$$

Boosting technique produces the final prediction from all the weak learners through a weighted majority vote, this is a good balance between classification performance and cost (time and memory). The most common boosting algorithm is AdaBoost [14], that was also extended to the case of multi-classes [14], commonly known as AdaboostM2.

Boosting can be applied on various weak learners. The choice of the weak learner generally involves balancing cost and

accuracy. In this study, we choose Decision Trees (DT) as a weak learner as it offers very good performances and processing time when the number of classification features is low (18 features in our case).

– Random Under Sampling (RUS) : as class imbalance problem is inherent to ECG data, we introduce in our method a data undersampling technique to alleviate this problem. Several techniques for performing undersampling have been proposed, the simplest method is random under sampling (RUS), that removes examples randomly from the majority class until the desired balance is achieved.

RUSBoost [13] is the combination of RUS and boosting, it is especially effective for improving classification performance of imbalanced data. Algorithm 1 shows the adaptation of RUSboost to our k -lead ECG classification problem.

Algorithm 1 RUSBoost Algorithm applied to ECG lead k

- 1: $TS^k = \{(X_1^k, y_1^k), \dots, (X_m^k, y_m^k)\}$ with minority class $\bar{y}^k \in Y^k, |Y^k| = 7$
 - 2: Weak Learner = Decision Trees (DT)
 - 3: Number of iterations (Trees) = T
 - 4: Initial Weight $W_1(i) = \frac{1}{m}$ for all samples i
 - 5: **for** $t = 1, 2, \dots, T$ **do**
 - 6: Create temporary training set $T\bar{S}_t^k$ with weights \bar{W}_t using Random Under Sampling
 - 7: Apply DT on $T\bar{S}_t^k$ with weights \bar{W}_t
 - 8: Get a DT hypothesis h_t
 - 9: Calculate the weighted error ε_t when applying h_t on TS_t^k with weights W_t
 - 10: Calculate the weight update parameter $\alpha_t = \frac{\varepsilon_t}{1-\varepsilon_t}$
 - 11: Update the weights $W_t(i)$ for all samples i
 - 12: $W_{t+1}(i) = W_t(i) * e^{\alpha_t * I(y_i^k \neq h_t(X_i^k))}$
 - 13: **end for**
 - 14: Output the final hypothesis H
 - 15: $H(X^k) = \underset{y^k \in Y^k}{\operatorname{argmax}} \sum_{t=1}^T h_t(X^k, y^k) \log \frac{1}{\alpha_t}$
-

IV. EXPERIMENTAL RESULTS

In order to validate our proposed system, we use the European ECG ST-T Database (EDB) from Physionet [1]. It contains 90 annotated ambulatory ECG recordings from real patients (79 men and women of different ages) to whom Myocardial ischemia was diagnosed or suspected. This DB is specifically intended for evaluation of ST and T-wave changes methods as it contains a representative selection of 367 ST segment change episodes and 401 T-wave change episodes, with durations ranging from 30 seconds to several minutes. Each recording is 2 hours in duration (7200 heartbeats) and contains 2 ECG leads, each sampled at 250 samples per second, the leads are not the same in all recording, so that there are 7 distinct leads in the entire DB. Two cardiologists annotated each record beat-by-beat for changes in ST segment, T-wave morphology, rhythm, and signal quality. An anomaly code is associated to each beat as follows: (N) if the beat is normal, (T) for a T-wave change and (s) for a ST segment change. The type of the change (T+, ST+ for an elevation and T-, ST- for a depression) and the episodes boundaries (Onsets (“(”, Extrema “A” and Offsets”)”) are also indicated in annotations.

A. ECG Data Corpus Building

Several steps were necessary in order to build the data corpus for classification. First, all EDB records were pre-

processed for waves parameters extraction, this was performed by implementing our pre-processing method using Labview for signal processing [15]. Figure 4 shows an example of the extracted waves parameters from the lead V4 of the the EDB record e0104.

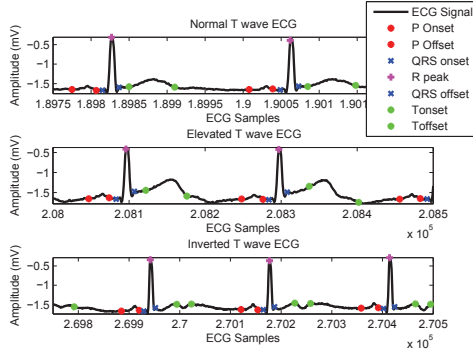


Fig. 4: Waves parameters for lead V4 of e0104 EDB record

Based on these waves parameters, the 18 ECG features were calculated for each heartbeat i of a given lead k to build the matrix ECG^k , we applied z-score standardization on matrix ECG^k . We also built the annotation vector $Class^k$ by converting normal, ST and T medical annotations into the 7 classes defined above.

All the EDB data was used to build our classification method corpus. The features were grouped by lead from all records. Table IV shows the data corpus obtained. For each lead, classes with less than 1% data were eliminated.

TABLE IV: Data Corpus built from EDB

| Lead | N | T+ | T- | ST+ | ST- | ST+T+ | ST-T- |
|------|--------|------|------|------|-------|-------|-------|
| I | 74361 | 906 | 1248 | 3143 | 6818 | < 1% | 1373 |
| III | 194591 | 8630 | 3715 | 2664 | 7744 | 6787 | < 1% |
| V1 | 50210 | 2516 | 1851 | < 1% | 6548 | < 1% | 2514 |
| V2 | 35162 | 634 | 7992 | < 1% | 2528 | 878 | 6603 |
| V3 | 39726 | 3178 | 1252 | < 1% | 1674 | < 1% | 620 |
| V4 | 163041 | 7029 | 6807 | < 1% | 16024 | < 1% | 5808 |
| V5 | 261681 | 8096 | 5689 | < 1% | 38486 | < 1% | 3812 |

Table V indicates experimentation parameters of our method.

TABLE V: Experimentation Parameters of our Method

| Parameter | Description |
|----------------------|--|
| Weak Learner | Decision Tree (C4.5) |
| Ensemble Learner | Random Under Sampling (RUS) + Boosting |
| Number of iterations | 200 |
| Cost Matrix | we set $\alpha = 2$ and $\beta = 10$ so that $C_{i,j} \in \{0, 1, 2, 10\}$ |
| Train/test Method | 10-fold cross validation |

B. ST and T anomalies classification performance

In order to evaluate the performance of our method, we measured various parameters presented in the following figures and tables. Figure 5 shows the variation of cumulative classification error for each lead depending on the number of learners used

by the ensemble learning. As we can see, the classification error can reach 0% for ECG lead V1, 20% to 25% for leads I, III, V3,V4 and 25% to 30% for leads V2 and V5. For the majority of leads, the classification error decreases as the number of learners increases, which is expected. However, the minimum number of learners differs by ECG lead : 40 trees are enough for lead V2, around 60 for leads I and V3, 80 for lead III, 100 for lead V5, 140 for lead V1 and until 200 for lead V4.

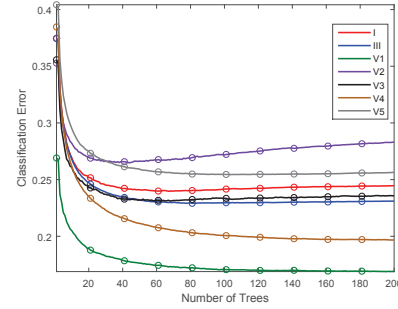


Fig. 5: Cumulative classification error per lead

Table VII shows average classification performance, per lead, obtained from 10-fold cross validation. We calculated the global accuracy and the confusion matrix (CM) performance parameters of each class, as indicated in the formula of table VI. The parameters per class were averaged to obtain results per lead presented in table VII. We globally obtain very interesting performance, the global Accuracy obtained per lead varies between 73% and 83%, an average sensitivity of 86% and average specificity of 94.85%, these indicate true positives rate and true negatives rate respectively. The difference between leads performance is not very significant, V1 presents a slightly better performance in general, where lead V2 and V5 presents a slightly lower accuracy (73% and 74% respectively), but similar sensitivity and specificity. We also estimated the models building time by applying the models on all available data. The obtained times are reported in last column of table VII. We can see that building time is clearly dependent on training set size, but even for the worst case (V5 with 317764 samples), it is around 20min, which is acceptable for a real application as the models are built at the beginning and depending on application (once a day, a week, etc.), they are updated with new data at a non real-time manner by self-learning. Table VIII compares our proposed method with some existing works.

We calculated the ROC curves (Receiver Operating Characteristic) for each class c_i per lead. ROC curve represents the true positive rate ($Sensitivity_{c_i}$) against the false positive rate ($1 - Specificity_{c_i}$) at various threshold settings. We obtained in most cases, a $Sensitivity_{c_i} \geq 90\%$ with $1 - Specificity_{c_i} \leq 10\%$.

V. CONCLUSION

In this paper, we proposed a new method for predicting 7 ST segment and T-wave ECG anomalies that are highly indicative of MI or Ischemia occurrences. Our approach extracts

TABLE VI: Confusion matrix (CM) parameters per class

| Parameter | Significance | Formula |
|---|---|--|
| Global Accuracy | Correctly Classified Instances Rate | $\frac{\sum_{i=1}^{nbclass} CM_{ii}}{\sum_{i=1}^{nbclass} \sum_{j=1}^{nbclass} CM_{ij}}$ |
| Sensitivity_{c_i} (Recall_{c_i}) | True Positive Rate (completeness indicator) | $\frac{CM_{ii}}{\sum_{j=1}^{nbclass} CM_{ij}}$ |
| Specificity_{c_i} | True Negative Rate | $\frac{\sum_{k=1, k \neq i}^{nbclass} \sum_{j=1, j \neq i}^{nbclass} CM_{kj}}{\sum_{k=1, k \neq i}^{nbclass} \sum_{j=1, j \neq i}^{nbclass} CM_{kj} + \sum_{j=1, j \neq i}^{nbclass} CM_{ji}}$ |
| Precision_{c_i} | Exactness Indicator | $\frac{CM_{ii}}{\sum_{j=1}^{nbclass} CM_{ji}}$ |
| F-score_{c_i} | Precision/Recall Balance Indicator | $2 * \frac{\text{Precision}_{c_i} * \text{Recall}_{c_i}}{\text{Precision}_{c_i} + \text{Recall}_{c_i}}$ |

TABLE VII: Average classification performance per lead

| Lead | Acc. | Se. | Sp. | Precision | F-score | Training Time(s) |
|---------------|------|------|------|-----------|---------|------------------|
| I | 0.76 | 0.87 | 0.95 | 0.44 | 0.53 | 87.56 |
| III | 0.77 | 0.84 | 0.95 | 0.45 | 0.54 | 394.77 |
| V1 | 0.83 | 0.87 | 0.96 | 0.56 | 0.68 | 114.83 |
| V2 | 0.73 | 0.86 | 0.94 | 0.60 | 0.66 | 93.1 |
| V3 | 0.76 | 0.87 | 0.95 | 0.51 | 0.60 | 70.89 |
| V4 | 0.80 | 0.85 | 0.95 | 0.58 | 0.66 | 578.91 |
| V5 | 0.74 | 0.84 | 0.94 | 0.47 | 0.55 | 1225.26 |
| Global | 0.77 | 0.86 | 0.95 | 0.52 | 0.60 | 366 |

TABLE VIII: Comparison with existing works

| Reference | ECG Parameters | Leads | Method | Data Corpus | Performances |
|------------------------|--------------------------|----------------|-----------------------|-------------------|-------------------------|
| Chang et al. [2] | 4 HMM parameters | 4 Leads | GMM | 1129 clinical ECG | Se.=85.71%, Sp.=79.82% |
| Dhawan et al. [4] | 60 ECG parameters | 12 Leads | GA + SVM | 210 clinical ECG | Se.=86.61%, Sp.=91.01% |
| Keshkar et al. [6] | 6 WTS/ECG parameters | 3 Leads | PNN | PTBDB | Se.=93.0%, Sp.=86.0% |
| Park et al. [16] | 3 ECG parameters | 2 Leads | KDE | EDB | Se.=93.9%, Sp.=91.2% |
| Spilka et al. [17] | 8 ECG parameters | 3 Leads | Ripper, C4.5, and SVM | 2596 ECG | Se.=82%, Sp.=93% |
| Proposed Method | 18 ECG parameters | 7 Leads | RUSBoost | EDB | Se.=86%, Sp.=95% |

18 temporal ECG features per heartbeat that are obtained after a pre-processing that combines filtering and Undecimated Wavelet Transform (UWT). These features are used as inputs of the proposed classification method, which is based on a combination of the Random Under Sampling (RUS) technique, to deal with class imbalance problem of ECG data, and the decision trees boosting, to improve the classification performance. We validated our method using 7 different leads, from a real ECG database [1], by applying a 10-fold cross validation to calculate confusion matrix performances and model building time.

The results obtained indicate a satisfactory balance between true and false positives for all leads (ROC curves), with an average global sensitivity and specificity of 86% and 94.85% respectively.

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