

Classification of Supraventricular and Ventricular Beats by QRS Template Matching and Decision Tree

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Abstract

This study presents a two-stage heartbeat classifier. The first stage makes initial assignment of beats towards continuously updated beat templates of the predominant rhythm, and calculates a set of features, tracking the morphology and RR-interval variation, and correlation to noise robust average beat templates. The second stage implements a decision tree for classification of supraventricular (SVB) and ventricular beats (VB). The training process on 3 large ECG databases (AHA, EDB, SVDB) applies splitting and pruning of the tree to different levels. A solution with 150 decision nodes and error cost <0.01 is selected for unbiased test-validation with MIT-BIH database, showing: specificity=99.7% for SVBs, sensitivity=95.9%, positive predictivity=95.1% for VBs. Decision trees combine high performance, rapid interpretation and easy configuration of the complexity.

1. Introduction

Automatic detection and classification of heartbeats is an important computerized diagnostic tool applied in monitoring applications and for assisting cardiologists in the task of long-term ECG inspection by marking the presence of sustained, transient or casual arrhythmias. The analysis of RR-intervals regularity and P-QRS-T waveform complexity by time-domain morphology delineation [1-5] and template matching [1,6] is commonly used for extraction of features which are then subjected to optimization in different decision support systems, aiming at the most reliable classification of normal or abnormal beats. The resource efficient classification methods are based on linear programming, including the K nearest neighbour clustering [2], linear discriminants [3], fuzzy analysis [1,7] and decision trees [4,5,7]. More complex classifiers implement support vector machines [6,8] and artificial neural networks [9,10], the last masking the features which are useful or worthless and how the net is making the decision.

The dimension of redundant feature vectors affects the

performance of the classifier if not appropriately optimized. Reduction of the feature space dimension by excluding irrelevant features which carry conflicting, duplicating or little information to the classifier has been applied by means of higher order statistics [11], perturbation method [8], fuzzy c-means clustering [9] or Hermite function decomposition [10].

This study aims at a reliable beat classification method based on correlation with noise robust average beat templates, morphology delineation features and a decision tree with easy configuration of the model complexity.

2. ECG databases

The study involves all full-length recordings in 4 ECG databases with reference heartbeat annotations:

- AHA – AHA database [12]: 80 ECG recordings, 2 leads with duration of 30 min per record ;
- EDB – European ST-T database [13]: 90 ECG recordings, 2 leads with duration of 2 hours;
- SVDB – MIT-BIH Supraventricular Arrhythmia Database [14]: 78 ECG recordings, 2 leads, 30 min;
- MIT-BIH – MIT-BIH Arrhythmia Database [15]: 48 ECG recordings, 2 leads with duration of 30 min.

All ECGs are processed with a common sampling rate of 250 Hz. EDB and AHA keep their original sampling frequency (250 Hz), while MIT-BIH (360 Hz) and SVDB (125 Hz) are linearly interpolated to 250 Hz. Filtering in a bandwidth 0.05–75 Hz is applied, although, signals could be already more band-limited within the databases. Two composite leads are next analysed:

- Magnitude: $mag = \sqrt{lead1^2 + lead2^2}$
- Velocity: $vel = \sqrt{(\Delta lead1)^2 + (\Delta lead2)^2}$

A QRS detector is run and any beat annotation label that can be paired with a valid QRS detection within a window of 150 ms is included in the study. The original beat annotation labels are interpreted according to the ANSI/AAMI EC57 standard [16], and two general heartbeat classes are defined:

- *SVB-class*: the class of beats with supraventricular origin, including sinus node beats (normal beat, left and

right bundle branch block beat) and supraventricular ectopic beats (an atrial or nodal (junctional) premature or escape beat, or an aberrant atrial premature beat);

- **VB-class:** the class of ventricular ectopic beats, including ventricular premature beat, R-on-T ventricular premature beat, or ventricular escape beat.

Independent datasets are used for training (AHA, EDB, SVDB) and test-validation (MIT-BIH).

3. Methods

The presented heartbeat classifier is based on a two-stage decision system (Fig. 1), applying initial assignment of beats to SVB-class, close matching the reference beat template of the patient's predominant rhythm (Stage 1), and subsequent classification of the non-matched beats to SVB or VB-class by a decision tree (Stage 2).

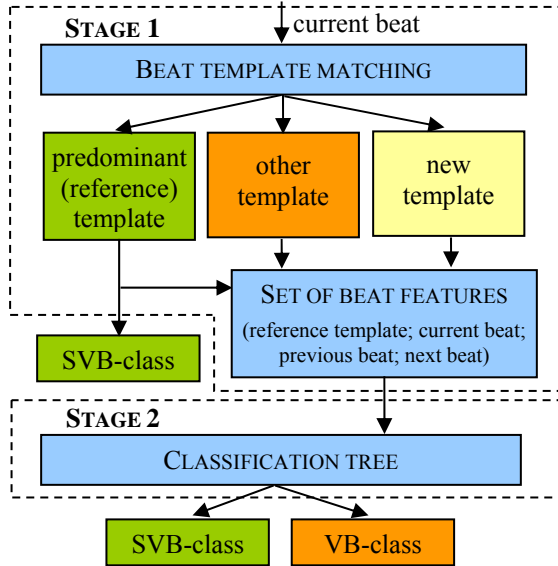


Figure 1. Block diagram of the two-stage beat classifier.

3.1. Stage 1: Beat template matching

Stage 1 is a kind of PQRST waveform preprocessor, which accumulates average beat templates, makes template matching and calculates a set of beat features. During a learning period (10s), the predominant normal (reference) beat template is created and any further beat is compared to it. If matching conditions are fulfilled:

- correlation >97.5% in non-noisy segments;
- correlation > 95% in noisy segments;
- adaptive correlation in strong noisy segments,

then the current beat is assigned to SVB-class and the reference template is continuously updated. If the current beat does not match the reference template, then matching to other beat templates is verified and the matched one is updated. Otherwise a new template is created. A limited number of templates is supported (e.g. up to 8 templates)

in order to save computation time, therefore, non-matched beats create a new template only if the limit of templates is not exceeded or replace an existing template if it hasn't been updated for a long time.

For each beat, Stage 1 calculates a set of 20 basic features, considering the behavior of the current beat but also the neighboring beats (previous, next), as well as the robust to noise average reference beat template:

- 3 features for the type of the current, previous and next beats, indicating if each of them is: matching the predominant beat template, matching another beat template or not matching any beat template;
- 2 features, indicating if the current beat and the reference beat template have a P-wave;
- 3 correlation coefficients, showing the waveform similarity between current beat, previous beat and next beat against the reference template (N=180ms), where the correlation (*corr*) between the waveforms (*a*, *b*) is:

$$corr = 100 \cdot \frac{\sum_{i=1}^N (a_i \cdot b_i)}{\sqrt{\sum_{i=1}^N a_i^2 \sum_{i=1}^N b_i^2}}, (\%)$$

- 3 QRS durations (*QRSdur*) of the current beat, the reference template and the difference between both, where *QRSdur* is defined between the QRS boundaries:

$$QRSdur = QRSoff - QRSon, (ms)$$

- 3 features for the relative QRS activity (*QRSact*) of the current beat, the reference template and the difference between both, where *QRSact* is the mean QRS magnitude (*mag*) within 180 ms window after the QRS onset normalized to the maximal QRS magnitude:

$$QRSact = 100 \cdot \frac{\sum_{i=QRSon}^{QRSon+180ms} (mag_i) / N}{\text{Max}(mag_i)}, (\%)$$

- 3 features for the QRS mobility (*QRSmob*) of the current beat, the reference template and the difference between both, where *QRSmob* represents a ratio of high-frequency to low-frequency QRS components, calculated from the area of the velocity (*vel*) divided by the area of the QRS magnitude within 180 ms window after the QRS onset:

$$QRSmob = 100 \cdot \frac{\sum_{i=QRSon}^{QRSon+180ms} (vel_i)}{\sum_{i=QRSon}^{QRSon+180ms} (mag_i)}, (\%)$$

- 2 features for the current/next RR-interval durations normalized to the mean RR-interval:

$$curRR = 100 \cdot \frac{\text{Current RR interval}}{\text{Mean RR interval}}; \text{nextRR} = 100 \cdot \frac{\text{Next RR interval}}{\text{Mean RR interval}}, (\%)$$

- 1 feature for the relative RR-interval variability within the last segment of 10 seconds:

$$relRRv = 100 \cdot \frac{\text{Reference RR variability}}{\text{Mean RR interval}}, (\%)$$

During the learning period (initial 10s of the recording) when there is no reference template, default values are taken for the reference template features: reference P-wave is present, *corr*=80%, reference *QRSdur*=100ms, reference *QRSact*=100%, reference *QRSmob*=100%.

Stage 1 extends the 20 basic features to a vector of 210 features created by full factorial design to degree 2. These features are next supplied to Stage 2.

3.2. Stage 2: classification tree (CT)

The second stage implements a CT for categorizing the beats in SVB/VB-class. CT resembles a graph with nodes (attributed to a class description) and branches (referring to a set of ‘if-then’ logical rules) that enable different features to be linked into a common class. Tree design approaches are aimed at finding ‘optimal’ solutions: minimum sized trees with high classification accuracy. Since a search on the whole set of possible trees for a given problem is impractical, this study follows the most common tree building strategy with two steps [17]:

- Step 1: Splitting of nodes – growing a tree, in a top-down way, until all possible leaf nodes are reached (i.e. purity), based on specific splitting criteria. The most popular concept is based on splitting of independent features at several split points taking into account the homogeneity of data at each node. Rigorous measures of impurity, based on computing the proportion of the data that belong to a class, such as entropy (maximum deviance reduction), Gini index, twoing rule are among the most commonly used splitting criteria to quantify the homogeneity in classification trees.
- Step 2: Pruning the tree by backward removing of branches based on specific pruning criteria, remedying the usual over-fitting of the final solution reached by Step 1. Complex trees usually exhibit meaningless extra nodes, i.e. with decision rules that do not make sense in terms of medical knowledge, and therefore, the accuracy, efficiency and generalization capability of the final solution relies on using an optimal scheme for tree pruning. To guide the tree pruning, the misclassification rate is typically measured so that branches giving less improvement in error cost are first pruned.

4. Results

The performance of the beat classifier is evaluated by three statistical indices – sensitivity (Se), specificity (Sp) and positive predictivity (P+):

$$Se = \frac{TP}{TP + FN}, Sp = \frac{TN}{TN + FP}, P+ = \frac{TP}{TP + FP},$$

where TP and FN are true positives and false negatives for VB-class; TN and FP are true negatives and false positives for SVB-class.

The CT model is generated and pruned by means of the statistical toolbox in Matlab 7.5 (Mathworks Inc.) The splitting criterion is set to ‘maximum deviance reduction’, beneficial in our case of large sample size. The training process builds a tree by iterative selection of the optimal feature space, minimizing the number of errors – both false positives in SVB-class and false negatives in VB-class are considered at equal weight, so that Mean(Se, P+) is progressively increasing at each splitting step, until a stop condition of minimum size of impure node to be split

is reached (setting of 10). The final step for the CT model is 221 decision nodes (Fig. 2-4). The training process scans the whole range of pruning levels, i.e. CT model with 1 to 221 final nodes is studied in terms of accuracy (Fig. 2), complexity (Fig. 3) and misclassification rate (Fig. 4). Considering an acceptable pruning level with error cost <0.01, our final CT solution is selected to include 150 decision nodes (see accuracy in Table 1).

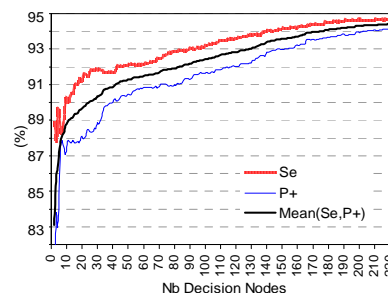


Figure 2. Training process: Accuracy of CT model.

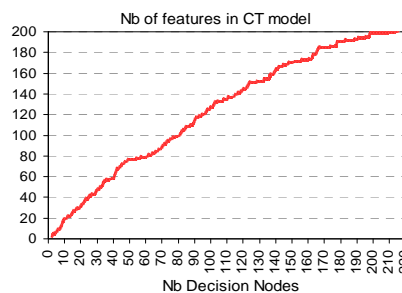


Figure 3. Training process: Complexity of CT model.

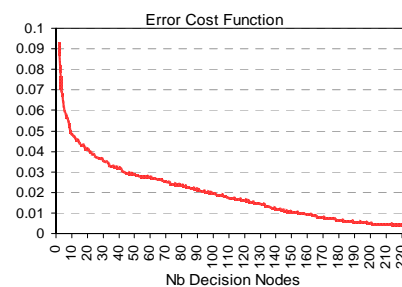


Figure 4. Training process: Error cost function.

Table 1. Training and test-validation performance of the two-stage beat classifier with CT model, including 150 decision nodes, 170 features.

ECG database	Sample size		Accuracy (%)		
	SVB class	VB class	Sp	Se	P+
AHA - training	164992	16488	99.8	94.7	98.0
EDB - training	785992	4467	99.9	97.0	86.6
SVDB - training	174553	9934	99.7	90.5	95.2
MIT-BIH - test	102205	7235	99.7	95.9	95.1

5. Discussion and conclusions

This study presents a low resource-cost beat classifier, which can be applied in real-time, without a need for local expert intervention in any of the 2 processing stages.

The most important design considerations for Stage 1 as a PQRST waveform preprocessor are:

- Template matching conditions – correlation coefficient adapted to signal-to-noise levels is preferred as a common and fast-computation estimator of the PQRST waveform similarity to the reference template and initial assignment of beats to SVB-class. We also consider the false positive errors, which influence the reported total accuracy of the two-stage classifier in Table 1.
- Set of heartbeat features – a set of 20 basic features with a physiological meaning are extracted following three main concepts: (i) morphological and RR-interval features are calculated for the current PQRST waveform; (ii) morphological and RR-variability features are calculated for the neighboring beats, thus giving information about the ongoing patient's rhythm; (iii) noise robust morphological features are extracted from continuously averaged reference beat templates. The feature space is extended to a 210-sized vector by full-factorial design to degree 2 of the basic 20 features. The implementation of a decision tree classifier of SVB and VB beats in Stage 2 has the following benefits:
 - Easy configuration of the performance by setting different complexity of the model (i.e. by pruning the tree to different levels).
 - Fast interpretation of results as a set of 'if-then' rules.
 - Clearly defined ranges of features pertinent to the given class of beats.
 - Derivation of results without a need for deep knowledge on the tested beat features, which significantly increases the practical applications of the CT model for solving heartbeat classification problems, suggested also for more than two classes.
 - High accuracy ($Sp=99.7\%$, $Se=95.9\%$, $P+=95.1\%$), outperforming or similar to other more complex classifiers. The general concepts followed during the development, training and test process are:
 - Multidatabase training approach for feature selection to ensure better generalization properties of the optimal feature set. Due to the large sample size and great variety of arrhythmias represented in the databases, the reported performance can be considered very similar to the one expected in clinical environment.
 - Unbiased performance evaluation on independent test ECG database (MIT-BIH Arrhythmia database) which is a common standard for inter- and intra-study comparisons.
 - Iterative training for selection of the optimal feature space, aiming to minimize the number of false positive and false negative errors at each step.

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