A method for context-based adaptive QRS clustering in real-time

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Abstract—Continuous follow-up of heart condition through long-term electrocardiogram monitoring is an invaluable tool for diagnosing some cardiac arrhythmias. In such context, providing tools for fast locating alterations of normal conduction patterns is mandatory and still remains an open issue. This work presents a real-time method for adaptive clustering QRS complexes from multilead ECG signals that provides the set of QRS morphologies that appear during an ECG recording. The method processes the QRS complexes sequentially, grouping them into a dynamic set of clusters based on the information content of the temporal context. The clusters are represented by templates which evolve over time and adapt to the QRS morphology changes. Rules to create, merge and remove clusters are defined along with techniques for noise detection in order to avoid their proliferation. To cope with beat misalignment, Derivative Dynamic Time Warping is used. The proposed method has been validated against the MIT-BIH Arrhythmia Database and the AHA ECG Database showing a global purity of 98.56% and 99.56%, respectively. Results show that our proposal not only provides better results than previous offline solutions but also fulfills real-time requirements.

Index Terms—Adaptive clustering, Electrocardiogram (ECG), Dominant Points, Dynamic Time Warping, QRS clustering.

I. INTRODUCTION

NOWADAYS the surface electrocardiogram (ECG) is recognized as an invaluable tool for monitoring heart condition, since its analysis provides decisive information that can reveal critical deviations from normal cardiac behavior. Recent developments in mobile sensors and mobile computing have enabled new scenarios for continuous ECG monitoring as an inexpensive tool for the early detection of some cardiac events [1], especially in those cases where symptoms appear intermittently.

As the monitoring period increases, the interpretation task becomes more time consuming and decision-support tools are needed to help cardiologists to reduce the time spent on it. If a continuous follow-up is required, these tools become imperative. Their main aim is to provide the cardiologists with a summary of all the acquired signals, enhanced with a fast locating of those anomalies detected.

Cardiac arrhythmias are the most relevant among the ECG findings. There are two main sources of arrhythmias: an automatism disorder, that is, a set of alterations in the beat activation point due to changes in its location or activation frequency; or a conduction disorder, that is, an abnormal propagation of the beat wavefront through the cardiac tissue. They both have an effect on the ECG, affecting the beat morphology and/or beat rhythm. In order to support their identification, a method for separating the beats by their activation point and conduction pattern should be provided.

Beat classification arises as the task of assigning each beat in an ECG a label identifying its physiological nature. Machine learning techniques have been applied to this task by estimating the underlying mechanisms that produce the data of a training set. The main drawback of this approach is its strong dependence on the pattern diversity present in the training set. Thus, inter-patient differences show that it cannot be assumed that a classifier trained on data of a large set of patients will yield valid results on a new patient [2]–[4], and intra-patient differences show that this cannot be assumed even for the same patient throughout time. In addition, class labels only provide gross information about the origin of the beats in the cardiac tissue, loosing all the information about their conduction pathways. This approach does not distinguish the multiple morphological families present in a given class, as occurs in multifocal arrhythmias.

In contrast, beat clustering aims at dividing the ECG recording in a set of beat clusters, each one of them preserving some similarity properties. Previous proposals have focused on an offline approach, from a priori maximum number of clusters [5]–[8] and they imply processing the ECG signal once the acquisition has been completed. This approach has given good noise robustness, but as a side effect a single morphology is usually replicated in several clusters and rare beat morphologies can be missed. It also omits the dynamic aspect of ECG and, in particular, ignores the temporal evolution of morphologies. Furthermore, the detection of critical events can be deferred too long to provide timely attention. For all these reasons, a dynamic online approach must be considered.

In this paper, we present a real-time method for adaptive beat clustering, with a potential application not only as a previous step for classification [9], but also as a summary about those beat morphologies present in a certain period, their temporal evolution and variability, or even to detect the presence of alternating morphologies. The proposed method emulates the experts behavior in exploiting the temporal context for assigning each new beat to the most appropriate cluster. To this end, clusters are continuously adapting to the temporal evolution of beat morphologies, and they can be dynamically created, merged or modified, resulting in a variable number of clusters.

Beat clustering requires extracting from the ECG a set of representative measurements for every beat. Bibliography
III. Pre-processing

IV. A Rhythm-based label

IV. B-D Cluster selection

IV. E Cluster set updating

The proposed method processes a real-time multilead ECG signal through a set of data-driven stages as shown in Fig. 1. In order to obtain comparable results, signals from two standard ECG signal databases are used as data source (section II). The pre-processing stage comprises real-time beat detection and baseline filtering (section III). Then, a fixed-length signal segment is selected for extracting and characterizing the QRS complex (subsection IV.A). QRS complexes are compared to obtain the best matching cluster (subsections IV.B–D). Afterwards, the current cluster set is updated in one of three ways: creating a new cluster, modifying the most similar one or merging two or more clusters (subsection IV.E). The next stage performs a noise analysis for each lead in order to detect noisy intervals and avoid the processing of noisy beats or discard the clusters created from them (section V). Finally, the beats are classified by their rhythm type and a set of groups with common morphology and rhythm is obtained (section VI).

The ECG databases have been processed and their beat class labels have been used to validate the purity of the final cluster and group sets (section VII). These results are discussed in section VIII along with the conclusions of the work.

II. ECG Signal Databases

The ECG databases recommended by the ANSI/AAMI EC57 [15] standard for reporting the performance of arrhythmia detectors were used for validation purposes: the MIT-BIH Arrhythmia Database and the AHA ECG database.

The MIT-BIH Arrhythmia Database [16] [17] can be referred to as the golden standard for beat clustering and classification tasks and it is the reference database for almost all the literature in this field. This database is composed of 48 recordings of ambulatory ECG, obtained from 47 different patients which comprise a very complete set of examples of common and rare arrhythmias. Each record has a duration of 30 min, and includes two channels with the same leads in almost all of them: a modified-lead II (MLII) in the first one and lead V1 in the second one. MLII was replaced by lead V5 in three records and V1 was replaced by MLII, V2, V4 or V5 on eight records. The signals were digitized at $f_s = 360$Hz and bandpass filtered with cutoff frequencies at 0.1 and 100Hz. All beats present in the database were annotated by at least two expert cardiologists, and assigned a class label using a 16 label set.

The AHA ECG database was compiled by the American Heart Association and it is composed of 155 recordings of ambulatory ECG digitized at $f_s = 250$Hz containing the most relevant types of ventricular arrhythmias. Each record is three
hours long with two channels but only the last 30 minutes have been manually annotated by experts.

III. PRE-PROCESSING

The major drawback of processing long-term ECG signals is the presence of a high level of noise with multiple manifestations—baseline wandering, power line interference or electromyographic activity—so an initial filtering stage needs to be performed. The efforts have been focused on filtering the baseline wandering, as this is the most relevant source affecting the reliability of the clustering algorithm because of the distortion it can cause on the QRS morphology.

A. Baseline filtering

The baseline filtering is performed through the estimation of the baseline wandering and its posterior elimination from the original ECG. To achieve this goal, each signal is processed by two sequentially connected median filters of 200ms and 600ms, respectively, as described in [2]. A global delay of 400ms is added by this process, independently of the sampling rate.

B. Beat detection

In order to carry out an evaluation of the clustering method separately from beat detector and provide a fair comparison framework for future algorithms, we used the beat position provided by the ECG databases as fiducial points.

A beat detector is required for real scenarios, affecting the quality of results. However, it virtually does not increment the global computational complexity as QRS detection represents only a small fraction of it. The global delay would not be affected either, since the beat detection can be performed concurrently with baseline filtering with a shorter delay.

IV. CLUSTERING

In this paper the following notation is used. Bold face variables (e.g., \( x \)) to represent vectors and sequences, lower case alphabets with subscripts to represent their components (e.g., \( x_i \)) or superscripts when a temporal index is used as a subscript, case alphabets with subscripts to represent functions (e.g., \( f \)) or superscript will be used for calculating the curvature, and they are given by:

\[
K(q_j, q_n) = \max_{i \in I^-_j, k \in I^+_j} \cos \tilde{q}_i \tilde{q}_j \tilde{q}_k,
\]

where \( 2 \leq j \leq w-1 \). The terms \( I^-_j \) and \( I^+_j \) denote the intervals used for calculating the curvature, and they are given by:

\[
I^-_j = \{ i \mid (j-\theta) \leq i < j \wedge \forall a \in (i, j), (\max_{b \in [a, j)} \Delta q_{j,b} - \Delta q_{j,a}) < \rho_{\min} \}
\]

\[
I^+_j = \{ k \mid j < k \leq (j+\theta) \wedge \forall a \in (j, k), (\max_{b \in [j, k)} \Delta q_{j,b} - \Delta q_{j,a}) < \rho_{\min} \}
\]

where \( \Delta q_{j,x} = |q_j - q_x| \). The term \( \theta \) is the maximum physiologically meaningful width of a QRS wave between its peak location and its left or right end, so that it is the upper limit
of \( I_j^- \) and \( I_j^+ \). The term \( \rho_{\text{min}} \) is the minimum height for a signal deflection to be considered physiologically relevant and, therefore, to be excluded from the calculation of curvature.

We define the **dominance region** of a sample \( q_j \) as:

\[
\text{dominance}(q_j) = [-r^-, r^+],
\]

where \( r^- = \min(\arg\max_{i\in I_j^-} \cos \angle q_j q_k) \) for any fixed \( k \in I_j^+ \) and \( r^+ = \max(\arg\max_{k\in I_j^+} \cos \angle q_j q_k) \) for any fixed \( i \in I_j^- \).

We define the set of **dominant points** of \( q_n \) as:

\[
D_n = \{ p_j | p_j = q_j \land j = \arg\max_{a \in \text{dominance}(q_j)} K(q_a, q_n) \land \Delta q_j > \rho_{\text{min}} \},
\]

where \( \Delta q_j = \min(\Delta q_{j-r^-}, \Delta q_{j+r^+}) \).

We define the set of **relevant points** of \( q_n \) as:

\[
R_n = \{ p_j | p_j \in D_n \land \Delta q_j > \rho_{\text{QRS}} \}
\]

where \( \rho_{\text{QRS}} \) is the minimum height for a signal deflection to be considered a relevant QRS wave, with \( \rho_{\text{QRS}} > \rho_{\text{min}} \). If \( R_n = \emptyset \), then it is redefined as: \( R_n = \{ \arg\max_{p_j \in D_n} \Delta q_j \} \).

The limits of \( \text{dominance}(q_j) \) can be located at any point in the edge of a wave. Since we are interested in capturing its full extent, the **support region** of a relevant point \( p_j \in R_n \) is defined as:

\[
\text{support}(p_j) = [j^-, j^+]
\]

where \( j^- \leq r^- \) and \( j^+ \geq r^+ \) are the sample numbers nearest to \( r^- \) and \( r^+ \) where slope sign changes:

\[
j^- = \min(\{i | i \leq r^- \land \forall a \in [i, r^-], \Delta q_{j,a} > \Delta q_{j,a+1} \})
\]

\[
j^+ = \max(\{k | k \geq r^+ \land \forall a \in [r^+, k], \Delta q_{j,a} < \Delta q_{j,a+1} \})
\]

In consequence, adjacent support regions can now overlap.

A relevant point \( p_j \) is said to be in a concave wave if \( q_j > q_{j-} \) and \( q_j > q_{j+} \). Otherwise, it is said to be in a convex wave. The wave height is defined as \( \Delta p_j = \min(\Delta q_{j,j-}, \Delta q_{j,j+}) \).

Finally, the \( n \)th beat is represented by the QRS signal segment and the set of its relevant points and support regions \( P_n = \{ (p_j, \text{support}(p_j)) | p_j \in R_n \} \) and denoted by:

\[
B_n = \langle q_n, P_n \rangle.
\]

There is not a consensus in the literature about the limits for width and height of QRS complex or individual QRS waves. The AAMI standard [20] recommends a minimum amplitude of 50µV and duration of 10ms for a QRS wave to be detected, and 150µV for peak-to-peak QRS amplitude, with a minimum duration of 70ms. On the other hand, the AHA [21] and CSE [19] report lower amplitude for QRS waves (down to 20µV and 10ms), based on measures over averaged beats with increased Signal-to-Noise ratio. These limits were not established for physiological reasons, but for signal noise level or instrumentation limitations. Nothing is stated about maximum QRS width beyond a reference to case-based duration values (e.g. the CSE study [19] reports a maximum QRS width of 210ms). In our case, due to the Signal-to-Noise ratio present in the ambulatory signals, the value of \( \rho_{\text{QRS}} \) is set to 150µV in order to avoid the detection of small waves caused by noise and the value of \( \theta \) is set to 100ms to accept QRS waves with a maximum width of 200ms. The value of \( \rho_{\text{min}} \) is set to 50µV following the AAMI standard [20] and will be useful to detect noise contaminated QRS complexes.

In order to perform the comparison between a new beat \( B_n \) and the current set of clusters \( C_{n-1} \), each cluster \( C_{n-1} \) is represented by a template:

\[
T_{n-1}^e = \langle q_{n-1}^e, P_{n-1}^e \rangle,
\]

where \( q_{n-1}^e = \{ q_1^e, \ldots, q_E^e \} \) is derived from the QRS of the beats assigned to \( C_{n-1}^e \) as will be explained in section IV-E.

### B. QRS temporal alignment

In order to compare a beat \( B_n \) with a cluster template \( T_{n-1}^e \), a temporal alignment of \( q_n \) and \( q_{n-1}^e \) is performed using Dynamic Time Warping (DTW) [22]. The aim of this alignment process is twofold: First, to correct any temporal misalignment due to a misplaced fiducial mark. And second, to reduce the contribution of the height and width variability of the QRS waves to the dissimilarity measure.

DTW was previously used for this purpose in [6], providing a relation \( \mathbf{m} = (m_1, \ldots, m_K) \) between \( q_n \) and \( q_{n-1}^e \) called warping path, with \( m_k = (x_k, y_k) \in [1,w] \times [1,w], k \in [1,K] \) and \( K \geq w \). Each \( m_k \) represents the alignment of the index \( x_k \) of \( q_n \) with the index \( y_k \) of \( q_{n-1}^e \) under three conditions: first, \( m_1 = (1,1) \) and \( m_K = (w,w) \); second, \( x_1 \leq x_k \) and \( y_1 \leq y_k \) \( \forall i < k \); and third, \( m_{k+1} - m_k \in \{ (1,1), (1,0), (0,1) \} \). These conditions preserve the time-ordering of points and prevent some point being missed in the alignment.

Let \( G \) denote the cost function associated to a warping path defined by \( G(\mathbf{m}) = \sum_{k=1}^{K} G_l(x_k, y_k) \), where \( G_l(x, y) = |y_l - q_E^e| \) is the local cost function associated with each element of \( \mathbf{m} \). The optimal warping path is the one that minimizes \( G \).
Fig. 3. Example of the DDTW alignment process. For each subfigure, the
upper solid and dashed lines represent the beat and template data, respectively;
bottom solid lines represent their absolute difference. (a) Shows \(q_n\) and \(q^c_{n-1}\)
subsequences; (b) \(\hat{q}_n\) and \(\hat{q}^c_{n-1}\) derivative approximations; (c) optimally-
aligned derivatives of length \(K \geq w - 1\); (d) subsequences \(\hat{q}_n\) and \(\hat{q}^c_{n-1}\) of
length \(K\) obtained from the optimally-aligned derivatives. In (b) and (c), the
difference is equivalent to the local cost function \(\hat{q}_n(x,y) = |x_k - y_k|\). Notice
the temporal increment \(K\) in (c) and (d) as a result of the process. The
absolute difference may also be increased in (d) outside the support regions,
but this is irrelevant.

horizontal segment into the aligned signals. Since this can lead to
unacceptable distortion of the QRS, we adopt the Derivative
Dynamic Time Warping (DDTW) [23] which uses the estimation
of the derivative instead of the signal itself. The derivative
is approximated by the first difference: \(\hat{q}_n = (\hat{q}_1, ..., \hat{q}_{w-1})\) and
\(\hat{q}^c_{n-1} = (\hat{q}^c_1, ..., \hat{q}^c_{w-1})\) with \(\hat{q}_n = q_{n+1} - q_n\) and \(\hat{q}^c_n = q^c_{n+1} - q^c_n\).

We imposed some additional conditions on the selected
warping path so as to restrict the alterations of aligned signals.
A global restriction is set in the search process by defining a
warping window \(\delta\) (named Sakoe-Chiba band [22]) to limit the
temporal distance between aligned samples so \(|x_k - y_k| < \delta\).
We set \(\delta = 5\), which corresponds to a distance of 1.4ms
with \(f_s = 360\)Hz, and is long enough to deal with small
misalignments of beat marks. A local restriction is also used
to limit the number of times the same sample can be aligned,
setting a slope constraint: \(m_{k+u} - m_k \neq \{0, a\}, \forall u > \lambda\).
We set \(\lambda = 2\) to limit the variation in the amplitude of the
aligned signals. Both conditions together allow the DDTW
to cancel out wave differences up to three times in amplitude
and up to \(\delta\) samples in width.

Finally, after the optimal warping path \(m\) is found, the
aligned signals \(\hat{q}_n\) and \(\hat{q}^c_{n-1}\) are obtained with coordinates
\(\hat{q}_{k+1} = \hat{q}_k + \hat{q}_{k+1}\) and \(\hat{q}^c_{k+1} = \hat{q}^c_k + \hat{q}^c_{k+1}\) for \(k \in [1, K]\),
where \(\hat{q}_1 = q_1\) and \(\hat{q}^c_1 = q^c_1\). Fig. 3 shows the result of the alignment of
the current QRS complex and a template.

C. Template matching

In order to assign a beat \(B_n\) to an existent cluster \(C^c_{n-1}\),
we design a similarity calculation that only considers the
difference between signals over the support region of each
relevant point, thus limiting the comparison to the constituent
waves of the QRS. Given a pair \((p_j, [\hat{j}^-, \hat{j}^+])\) ∈ \(P_n\), we are
interested in verifying whether \(T_{n-1}\) contains a similar wave
in the same location of the QRS. In order to do so, the
interval \([\hat{j}^-, \hat{j}^+]\) of \(q^c_{n-1}\), aligned with the interval \([\hat{j}^-, \hat{j}^+]\)
of \(q_n\) must be obtained (see Fig. 4). To this end, the warping
path \(m\) is used to map \(j^+\) and \([\hat{j}^-, \hat{j}^+]\) from \(q_n\) into \(\hat{q}^c_n\)
attaining the equivalent index \(\hat{j}\) for the relevant point, and
\([\hat{j}^-, \hat{j}^+]\) for its support region where: \(\hat{j} = \max\{k | x_k = j\}, \hat{j}^- = \min\{k | x_k = j^-\}\) and \(\hat{j}^+ = \max\{k | x_k = j^+\}\),
bearing \((x_k, y_k) \in m\). Afterwards, since \(\hat{q}^c_{n-1}\) and \(\hat{q}_n\) are
already aligned by the application of DDTW, the same interval
\([\hat{j}^-, \hat{j}^+]\) from \(\hat{q}^c_{n-1}\) is selected and mapped into \(q^c_{n-1}\) using
the warping path. The interval \([\hat{j}^-, \hat{j}^+]\) is given by \(\hat{j}^- = y_j^-\)
and \(\hat{j}^+ = y_j^+\).

Once the aligned intervals are obtained we proceed to
evaluate the concordance of both vectors. The segment \(q^c_{n-1}\)
is said to concord with \(q_n\) at \(p_j\) and denoted by \(q^c_{n-1} \approx_p q_n\) if
\(q^c_{n-1}\) contains a deflection in \([\hat{j}^-; \hat{j}^+]\) with height \(\Delta \hat{p}_{j^c} > r_{min}\)
likely to be considered a significant waveform, where \(\Delta \hat{p}_j = \min\{\hat{p}_{\text{peak}} - \hat{q}^c_j, \hat{q}^c_j - \hat{p}_{\text{peak}}\}\) being \(\hat{p}_{\text{peak}} = \arg\min_{\hat{j}} |\hat{q}^c_j - \hat{q}^c_{\hat{j}-1}|\).

We define the concordance ratio of \(q^c_{n-1}\) with respect to
\(q_n\) at \(p_j\), denoted by \(C_{p_j}(q^c_{n-1}, q_n)\), as:

\[
C_{p_j}(q^c_{n-1}, q_n) = \frac{\min(\Delta \hat{p}_j, \Delta \hat{p}_{j^c})}{\max(\Delta \hat{p}_j, \Delta \hat{p}_{j^c})}
\]

if \(q^c_{n-1} \approx_p q_n\). Otherwise, \(C_{p_j}(q^c_{n-1}, q_n) = 0\).

We define the local dissimilarity of \(q^c_{n-1}\) with respect to \(q_n\)
at \(p_j\), and denoted by \(D_{p_j}(q^c_{n-1}, q_n)\), as a weighted relative
area difference between \(\hat{q}^c_{n-1}\) and \(\hat{q}_n\) at the interval \([\hat{j}^-, \hat{j}^+]\):

\[
D_{p_j}(q^c_{n-1}, q_n) = \left(\frac{(\Delta A_{j^-})^2}{A_{j^-}^2} + \frac{(\Delta A_{j^+})^2}{A_{j^+}^2}\right) \times \frac{1}{A_{j^-} + A_{j^+}}
\]

The terms \(\Delta A_{j^-}\) and \(\Delta A_{j^+}\) represent the areas under \(a = \hat{q}_n - \hat{q}^c_{n-1}\) over the intervals \([\hat{j}^-, j]\) and \([j, \hat{j}^+]\), respectively
(see Fig. 4b). Computing the area at each side of \(\hat{j}\) indepen
dently allows us to minimize the effect of vertical misalign
ment or amplitude variation on each interval by subtracting
their own median. Using the trapezoidal rule:

\[
\Delta A_{j^-} = \sum_{k \in [\hat{j}^-, j]} a_k + \frac{1}{2}(a_{\hat{j}^-} + a_j)(\hat{j} - j) M^-
\]

\[
\Delta A_{j^+} = \sum_{k \in [j, \hat{j}^+]} a_k + \frac{1}{2}(a_j + a_{\hat{j}^+})(j - \hat{j}^+) M^+
\]

where \(M^- = \text{median}_{k \in [\hat{j}^-, j]} a_k\) and \(M^+ = \text{median}_{k \in [j, \hat{j}^+]} a_k\).

The terms \(A_{j^-}\) and \(A_{j^+}\) represent the areas below \([\hat{j}^-, j]\)
and \([j, \hat{j}^+]\) intervals of \(\hat{q}_n\), respectively (see Fig. 4c). They
are estimated using the trapezoidal rule:

\[
A_j^\pm = \sum_{k \in \{j-j, j+j\}} \hat{q}_k \pm \frac{1}{2} (\hat{q}_{j-} + \hat{q}_{j+}) - (j-j^-)\hat{q}_j
\]

where \(\hat{q}_j = \max_{k \in \{j-j, j+j\}} q_k\) and \(\hat{q}^\pm = \max_{k \in \{j-j^\pm, j+j^\pm\}} q_k\) for \(p_j\) in a convex wave. Otherwise, \(\hat{q}_j\) is replaced by \(\min\).

We define the piecewise similarity of \(q_{n-1}\) with respect to \(q_n\), denoted \(\mathcal{PS}(q_{n-1}, q_n)\), as the sum of two bounded contributions from the set of concordant and non-concordant relevant points:

\[
\mathcal{PS}(q_{n-1}, q_n) = \sum_{p_j \in R_n} c_{p_j}(q_{n-1}, q_n) \cdot \text{sig}(D_{p_j}(q_{n-1}, q_n))
\]

where the sigmoid function \(\text{sig}(x) = 1 - \alpha x / \sqrt{1 + (\alpha x)^2}\) keeps the contribution of each point in the interval \([0, 1]\). The parameter \(\alpha\) determines the decrease rate of the contribution as the local dissimilarity increases and, as a consequence, the weight of a high dissimilarity value in the final piecewise dissimilarity. We limit the contributions of those points out of a range of admissible local dissimilarity. In order to set such range we consider the effect of amplitude and temporal variability of QRS waves. A temporal misalignment of one signal sample between the QRS waves of \(\tilde{q}_n\) and \(\tilde{q}_{n-1}\) can lead to local dissimilarities of around 20%. Then we set an interval of \([0, 25\%]\) with a slightly greater upper bound and \(\alpha = 4\) so the maximum contribution out of this interval is 0.30.

The previous measure is asymmetric since it depends on the relevant points and areas of one signal, so we define the similarity between \(B_n\) and \(T_{n-1}\) as:

\[
S(q_n, q_{n-1}) = \mathcal{PS}(q_{n-1}, q_n) + \mathcal{PS}(q_n, q_{n-1})
\]

thus obtaining a value which captures the concordance, similarity and morphological complexity of both signal segments.

This measure allows us to select the most similar template within a set, but we need a reference scale to evaluate the degree of matching. To this end, we define the normalized piecewise similarity as:

\[
\overline{\mathcal{PS}}(q_{n-1}, q_n) = \mathcal{PS}(q_{n-1}, q_n) / |R_n|
\]

and the normalized similarity as:

\[
\overline{S}(q_n, q_{n-1}) = S(q_n, q_{n-1}) / (|R_n| + |R_{n-1}|),
\]

where \(R_{n-1}\) is the set of relevant points of \(q_{n-1}\).

D. Cluster selection

The occurrence of different QRS morphologies in a segment of ECG signal is usually limited by a reduced set of activation points and conduction pathways. Thereby we expect that the majority of QRS complexes in an ECG recording share their morphology with some of the QRS complexes present in a short previous temporal interval. For that reason, the search for the cluster \(C_{\text{win}}^{n-1} \subset C_{\text{win}}^n\) that best matches a beat \(B_n\) is first performed in the set of clusters present in its temporal context \(C_{\text{ctx}}^{n-1} \subset C_{\text{win}}^{n-1}\) (see Fig. 5). We define the temporal context as the set of \(\tau\) beats previous to \(B_n\), \(\tau-\text{ctx}^{-}(B_n) = \{B_{n-i} | 1 \leq i \leq \tau\}\), and \(C_{\text{ctx}}^{n-1} = \{C_{\text{ctx}}^l \subset C_{\text{win}}^{n-1} | \exists B_i \in \tau-\text{ctx}^{-}(B_n) \wedge B_i \in C_{\text{ctx}}^l\}\). The context length is set to \(\tau = 15\) beats, the number of beats displayed in the typical 10s ECG strip used by cardiologists for a heart rate of 80 beats/min. This context is long enough to include every QRS morphology present in multifocal arrhythmias. Throughout this section, the \(l\) superscript is used to denote the lead.

The similarity measure is used to identify the most similar template for each lead as \(\text{sim}^l = \arg \max q_{n-1} \cdot \text{sim}(q_n, q_{n-1}^{(l)})\) and then the best matching cluster is obtained by majority vote as \(\text{sim} = \text{mode}\{\text{sim}^l | l \in [1, L]\}\). If multiple clusters are selected, a second vote is performed to obtain a single one using the normalized similarity.

Beat \(B_n\) is assigned to \(C_{\text{sim}}^{n-1}\) if the condition \(\overline{S}(q_n, q_{n-1}^{\text{sim}}) > \gamma\) is fulfilled in all leads. Then \(C_{\text{win}}^{n-1} = C_{\text{sim}}^{n-1}\). We set a value of \(\gamma = 0.30\) which corresponds to the maximum contribution of a point with local dissimilarity outside the admissible interval.

When \(B_n\) and \(C_{\text{sim}}^{n-1}\) are not similar enough, a new comparison is performed within the subset \(C_{\text{win}}^{n-1} \setminus C_{\text{ctx}}^{n-1}\), obtaining the most similar cluster \(C_{\text{sim}}^{n-1}\). If \(B_n\) and \(C_{\text{sim}}^{n-1}\) are similar enough, the beat is assigned and \(C_{\text{win}}^{n-1} = C_{\text{sim}}^{n-1}\). Otherwise, the beat is not assigned to any existing cluster and its most similar cluster \(C_{\text{win}}^{n-1}^{\text{sim}}\) is selected between \(C_{\text{sim}}^{n-1}\) and \(C_{\text{win}}^{n-1}\) using the same voting criteria previously seen.
QRS complexes suffer from transient distortions in their morphology due to intrinsic variability, which makes them fall below the similarity threshold for their proper clusters. In this case, a new cluster is created which is subjected to an initial transient period during which the template for each lead can evolve getting closer to its most similar cluster.

In order to detect this situation, we define a relation \( closest \) which links each cluster with its most similar one among previous clusters. The relation is set for each new cluster as \( C_{n}^{\text{win}} = closest(C_{n}^{\text{new}}) \). As templates evolve with new assigned QRS complexes, the relation could have to be updated.

When \( B_{n} \) is assigned to \( C_{n}^{\text{win}} \), the cluster is updated to \( C_{n}^{\text{win}} \) and its most similar cluster may change. The \( closest \) relation is updated when multiple clusters in the same set than \( C_{n}^{\text{win}} \) 1, be it either \( C_{n}^{\text{ctx}} \) or \( C_{n}^{\text{ctx}} \), fulfill the assignment condition \( S(q_{n}^{l}, q_{n-1}^{l}) > \gamma \) in all leads (see subsection IV-D).

Afterwards, the special case of clusters within its transient period is considered. We establish the duration of this transitory state in terms of the number of assigned beats. Hence, if \( B_{n} \) is assigned to \( C_{n}^{\text{win}} \) and \( |C_{n}^{\text{win}}| < \mu \), the cluster is checked for merging with its closest one \( C_{n} = closest(C_{n}^{\text{win}}) \) (see Fig. 5). We set \( \mu \) as the minimum number of beats assigned to the cluster to confirm it represents an independent morphology and we consider \( \mu = 10 \) enough for this purpose.

When two clusters \( C_{n}^{\text{win}} \) and \( C_{n}^{c} \) are merged, the cluster set, cluster template and \( closest \) relation are updated accordingly (we suppose that \( C_{c}^{c} = closest(C_{c}^{c}) \));

1) \( C_{c}^{c} \) is updated to \( C_{c}^{c} = C_{c}^{c} \cap C_{n}^{\text{win}} \);
2) \( q_{n}^{c,l} \) is calculated by merging \( q_{n-1}^{l} \) and \( q_{n}^{l} \):
   \[
   q_{n}^{c,l} = (1-\beta)q_{n-1}^{l} + \beta \left( \{q_{x}^{l} \} \right)
   \]
   \[
   q_{n}^{c,l} = q_{n}^{c,l} + \beta \sum_{x,y} \{q_{x,y}^{l} \}
   \]
   where \( q_{1,n}^{c,l} = q_{1,n}^{l} \). The term \( \beta \) is the coefficient of the exponential update. Setting a value for \( \beta \) implies a trade-off between plasticity and stability of the cluster template. We set \( \beta = 1/8 \) so the last 16 beats assigned to the cluster provide 90% of the contributions to the current template. This allows the template to adapt to the evolution of the QRS morphology. Afterwards, the set of relevant points and support regions \( P_{n}^{c,l} \) is obtained from \( q_{n}^{c,l} \) and assigned to the template: \( T_{n}^{c,l} = \{q_{x,y}^{l} \}, P_{n}^{c,l} \}

3) Cluster merging: During the clustering process, different clusters can evolve to represent the same QRS morphology, so they should be merged. This situation is common when
V. Noise-cluster proliferation control

The dynamic creation of clusters entails the problem of identifying those QRS complexes contaminated by noise that could cause the proliferation of clusters. When noise appears in an ECG lead, the QRS can show different changes. In some cases, ECG segments with low Signal-to-Noise ratio present a high number of waves, and these can be detected by an abnormal number of dominant points. In other cases, domain knowledge is needed to discern if changes respond to a new QRS morphology or to a noisy version of a previous one. Some alterations are well known and described in literature, but others can be challenging even for an expert cardiologist, who compares every beat with those present in its temporal context in order to identify if it is related to a repetitive morphology change, a noisy interval or an isolated noisy beat. We follow a twofold, beat-based and context-based, approach to detect noisy QRS complexes. Noise can be present in one or more leads, and the influence of each lead in the clustering of a given beat will be analyzed in the following.

A state variable lead_noise<sub>¡</sub> is defined to denote the existence of a noisy interval in lead <em;l</em> containing the <em>k</em>th beat. Such noisy interval begins when the first noisy beat is detected in that lead just after a sequence of previous noise-free beats. The beats contained within this interval can be either noisy or noise-free in <em;l</em> and such condition will be represented as an attribute of the beat denoted by beat_noise<sub>¡</sub>. During the noisy interval, the characterization of any new beat <em>B</em><sub>n</sub> can represent not only QRS waves but also noise artifacts, so the cluster selection and assignment rules (subsection IV-D) are modified in lead <em;l</em>: the dominant points of the beat are ignored, replacing <em>S</em>(<em>q</em><sub>n</sub>, <em>q</em><sub>n-l</sub>) by <em>PS</em>(<em>q</em><sub>n</sub>, <em>q</em><sub>n-l</sub>) and <em>S</em>(<em>q</em><sub>n</sub>, <em>q</em><sub>n-l</sub>) by <sup>p</sup><em>PS</em>(<em>q</em><sub>n</sub>, <em>q</em><sub>n-l</sub>). Therefore, the condition for beat assignment is: <sup>p</sup><em>PS</em>(<em>q</em><sub>n</sub>, <em>q</em><sub>n-l</sub>) > <em>γ</em>.

The ending of a noisy interval in lead <em;l</em> is set just before <em>κ</em> = 3 contiguous beats are considered noise-free in that lead. A beat <em>B</em><sub>n</sub> is considered noise-free if beat_noise<sub>¡</sub> = false and it is assigned either to its winner cluster with <sup>p</sup><em>PS</em>(<em>q</em><sub>n</sub>, <em>q</em><sub>n-l</sub>) > <em>γ</em> or to a new cluster.

The beat-based noise detection is trigged when a new beat <em>B</em><sub>n</sub> is detected. Then the number of waves in the QRS is estimated as |<em>D</em><sub>n</sub>| for each lead <em;l</em>. If |<em>D</em><sub>n</sub>| > <em>η</em>, <em>B</em><sub>n</sub> is considered noisy in lead <em;l</em> and beat_noise<sub>¡</sub> is set to true. The term <em>η</em> is the maximum number of waves that could be present in a noise-free QRS. We set <em>η</em> = 6 to admit complexes with Q, R and S waves, mixed with R′, S′ or spikes as occurs in paced, fusion or bundle branch block beats. Additionally, if |<em>R</em><sub>n</sub>| > <em>η</em>, the QRS complex is considered distorted with relevant waves caused by noise. If this happens in some but not all leads, such leads are ignored for cluster assignment and updating, but if it happens in all leads, the beat is considered failed and it is assigned to its most similar cluster.

The context-based noise detection is activated when a new cluster is created for <em>B</em><sub>n</sub>. Then two possible explanations are explored. A first explanation represents a hypothesis of noise, and every noisy beat will be assigned to its most similar cluster. A second explanation simply represents a change in morphology, so creation of new clusters is allowed. The evaluation of these hypotheses is performed over a temporal context of <em>τ</em> beats defined as <em>τ</em>-<em>ctx</em>+(<em>B</em><sub>n</sub>) = {<em>B</em><sub>n+i</sub> | 0 ≤ i < <em>τ</em>} which is long enough to check the evolution of cluster diversity.

A hypothesis of noise, denoted by hyp_noise<sub>n+i</sub>, is set over each lead for every beat <em>B</em><sub>n+i</sub> ∈ <em>τ</em>-<em>ctx</em>+(<em>B</em><sub>n</sub>)). The hypothesis is initialized using the current noise state for the first beat, hyp_noise<sub>n+i</sub> = lead_noise<sub>¡</sub>, and the value of the previous beat for each new one, hyp_noise<sub>n+i</sub> = hyp_noise<sub>n+i-1</sub>. This value can be further modified for a beat <em>B</em><sub>n+i</sub> under three circumstances:

- If <em>B</em><sub>n+i</sub> is considered noisy in lead <em;l</em> by the beat-based noise detection, beat_noise<sub>¡</sub> = true, then the hypothesis is set to hyp_noise<sub>n+i</sub> = true.
- If a new cluster is created for <em>B</em><sub>n+i</sub>, we define <em>L</em><sub>n+i</sub> as the set of leads with <sup>p</sup><em>PS</em>(<em>q</em><sub>n+i</sub>, <em>q</em><sub>n+i-l</sub>) ≤ <em>γ</em>, which are responsible for its creation and candidates to be set as noisy. For these leads, we check the assignment under noise interval conditions, <sup>p</sup><em>PS</em>(<em>q</em><sub>n+i</sub>, <em>q</em><sub>n+i-l</sub>) > <em>γ</em>. If the assignment condition is now fulfilled in all leads, the signal still resembles a previous QRS morphology and we set hyp_noise<sub>n+i</sub> = true, ∀<em;l</em> ∈ <em>L</em><sub>n+i</sub>.
- If <em>B</em><sub>n+i</sub> is the last of <em>k</em>th consecutive noise-free beat, we set hyp_noise<sub>n+i+j</sub> = true, ∀<em;j</em> ∈ [0, <em>κ</em>−1].

V. Rhythm analysis

The absence of an analysis of the P wave leads to the inability to discriminate premature, normal or ectopic beats which share a common QRS morphology. All previous clustering proposals include rhythm information within their beat characterization and claim its separation capabilities for this kind of arrhythmias. In order to make our results comparable, we include a rhythm processing stage that allows us to separate those beats into different groups.

A. RR-Interval characterization

The beat to beat interval (RR) between normal beats, commonly known as NN interval, is the result of a non-stationary stochastic process regulated by the sympathetic and
parasympathetic nervous systems. This implies that the RR value for beat $B_n$, denoted by $RR_n$, should be put in context using the rhythm of the surrounding beats to analyze its normality. To this end, we model the NN series as a stochastic process with marginal distribution $N(\bar{NN}_n, \sigma^2_n)$ at the $n$th beat. The mean is estimated as $\bar{NN}_n = \theta RR_{n-1} + (1-\theta)\bar{NN}_{n-1}$, with $\theta = 0.2$ for $RR_{n-1}$ values labeled as normal (as explained in next section). Otherwise, $\bar{NN}_n = \bar{NN}_{n-1}$. The standard deviation is estimated as $\sigma^2_n = \sum NN_i - \bar{NN}_n$ using the last $\tau$ beats with normal rhythm. Fig. 6 shows the evolution of the RR in an excerpt with a premature beat from the record 117 of the MIT-BIH database.

The first complete context, $\tau-cxtx^-(B_{+1})$, is used to initialize $\bar{NN}_n$ and $\hat{\sigma}_n$. Let TC denote the set of the first $\tau$ values of RR and let $K_i$ denote any subset of $\tau$ values from consecutive beats. A value $RR_{i_j} \in TC$ is said to be normal if $3K_i$ such that $RR_{i_j} \in K_i \land \sigma_{K_i} < 0.1$, where $\sigma_{K_i}$ is the normalized standard deviation of the $K_i$ set. Let $TC_N^+ = \{RR_{i_j} \mid RR_{i_j} \text{ is normal}\}$. If $TC_N^+ = \emptyset$, then $TC_N^- = \{RR_{i_j} \mid \sigma_{TC} < 0.1\}$. If $TC_N^- = \emptyset$, then the context in $TC$ is repeatedly moved forward one beat until $TC_N^- \neq \emptyset$ for a context $\tau-cxtx^-(B_{\tau+1})$. Finally we set $\bar{NN}_n = \bar{TC}_N$ and $\hat{\sigma}_n = \sigma_{TC_N}$, $\forall n \in \{1, \tau + 1 + i\}$.

### B. Rhythm labeling

The aim of rhythm processing is the discrimination of those abnormal RR values associated with arrhythmic beats from the normal ones. To this end, the rhythm of the $B_n$ beat is characterized through a vector $\mathbf{rr}_n = (\bar{RR}_n, \bar{RR}_n^+, \bar{RR}_n^-, \bar{NN}_n, \hat{\sigma}_n)$ where $\bar{RR}_n$ and $\bar{RR}_n^+$ are the RR values for the previous and next beat, respectively. Then, the model described in the previous section is used to establish a range of validity for the $\bar{RR}_n$ value which allows us to detect any alteration in the normal rhythm.

| $\Delta RR_n$ | GP | P | N | N | N | C | D |
|---------------|----|---|----|----|----|---|---|
| $\in (3 \sigma_n, \infty]$ | $D^6$ | $D^4$ | $C$ | $C$ | $N_+$ | $N_+$ | $C$ | $D$ |
| $\in (2 \sigma_n, 3 \sigma_n)$ | $C$ | $C$ | $N_+$ | $N_+$ | $N_+$ | $D^4$ | $D^4$ | $G^9$ |
| $\in [-2 \sigma_n, 2 \sigma_n)$ | $N_-$ | $N_-$ | $N_-$ | $N_-$ | $N_-$ | $N_-$ | $N_+$ | $N_+$ |
| $\in [-3 \sigma_n, -2 \sigma_n)$ | $G^{P^8}$ | $G^{P^3}$ | $G^{P^3}$ | $G^{P^3}$ | $G^{P^3}$ | $G^{P^3}$ | $G^{P^3}$ | $G^{P^3}$ |
| $\in [-\infty, -3 \sigma_n)$ | $G^{P^6}$ | $G^{P^6}$ | $G^{P^6}$ | $G^{P^6}$ | $G^{P^6}$ | $G^{P^6}$ | $G^{P^6}$ | $G^{P^6}$ |

We use seven rhythm labels to discern between four beat rhythm types: normal, (C) or without ($N, N^-, N^+$) compensatory pause, premature (P), group of premature (GP) and delayed (D). The explicit domain knowledge contained in Table I models, for each rhythm type, the relation of an $RR$ value with the normal rhythm from its temporal context. It also reflects the dependence of the rhythm type for an $RR$ value on the rhythm type of its adjacent beats. This model allows us to assign a rhythm label to the beat $B_n$ based on the $rr_n$ values and the rhythm label of the previous beat.

### VII. Results

We have applied our clustering method to all the records of the MIT-BIH database. The parameters and threshold values of this method have been neither trained nor adjusted to fit this database. These values have been justified by physiological reasons, or by the expertise or intuition of experienced cardiologists. The method shows low sensitivity to small changes in parameter values; the results either improve or worsen slightly. Although better results could be obtained by a fine tuning of these parameters for each specific database, this is not the aim of this work but proving the validity of the present approach for continuous ECG monitoring.

For each record, a set of clusters is obtained reflecting the QRS morphologies present in them. Afterwards, the rhythm labels are used to split each cluster into groups of beats with the same rhythm type. In order to compare our results with the proposal in [5] under equivalent conditions, we adopted a fixed number of clusters (25) as the maximum number of groups. Thus, if that limit is exceeded for a record, a merging process is applied to obtain a reduced set of groups with the most prevalent rhythm and morphologies. If necessary, we
keep merging the groups with the lowest number of assigned beats until the maximum is reached. Table II shows the results before and after the merging process.

Each group is labeled with the majority class label of the beats assigned to this group from the database. An assigned beat is considered as correctly grouped if the class label in the database match the label of the group. A confusion matrix is obtained for each record comparing both labels for every beat. These matrices are summed to obtain the global confusion matrix for the whole validation set shown in Table III. Table IV shows the results using the AAMI class labels obtained from MIT-BIH labels as described in [15]. Table V shows the results on AHA database.

| Rec. | N  | N_{f1} | N_{f2} | N_{f3} | Rec. | N  | N_{f1} | N_{f2} | N_{f3} |
|------|----|--------|--------|--------|------|----|--------|--------|--------|
| 100  | 4  | 7      | 7      | 201    | 15  | 32     | 10     |
| 101  | 4  | 6      | 6      | 202    | 9   | 18     | 18     |
| 102  | 10 | 13     | 13     | 203    | 33  | 87     | 25     |
| 103  | 10 | 12     | 12     | 205    | 14  | 20     | 20     |
| 104  | 16 | 25     | 25     | 207    | 61  | 96     | 25     |
| 105  | 10 | 16     | 16     | 208    | 28  | 63     | 22     |
| 106  | 27 | 49     | 18     | 209    | 10  | 26     | 9      |
| 107  | 11 | 21     | 21     | 210    | 27  | 65     | 13     |
| 108  | 22 | 35     | 7      | 212    | 5   | 8      | 8      |
| 119  | 13 | 18     | 18     | 213    | 17  | 29     | 11     |
| 121  | 8  | 10     | 10     | 214    | 21  | 36     | 11     |
| 112  | 4  | 7      | 7      | 215    | 16  | 32     | 8      |
| 113  | 5  | 9      | 9      | 217    | 28  | 50     | 19     |
| 114  | 8  | 13     | 13     | 219    | 14  | 24     | 24     |
| 10   | 11 | 11     | 11     | 220    | 2   | 5      | 5      |
| 116  | 10 | 15     | 15     | 221    | 24  | 24     | 24     |
| 117  | 5  | 5      | 5      | 222    | 8   | 19     | 19     |
| 118  | 3  | 8      | 8      | 223    | 23  | 43     | 17     |
| 119  | 6  | 13     | 13     | 228    | 14  | 25     | 25     |
| 121  | 5  | 7      | 7      | 230    | 3   | 5      | 5      |
| 122  | 1  | 1      | 1      | 231    | 5   | 6      | 6      |
| 123  | 3  | 5      | 5      | 232    | 4   | 9      | 9      |
| 124  | 1  | 18     | 18     | 233    | 24  | 48     | 15     |
| 200  | 20 | 46     | 16     | 234    | 5   | 7      | 7      |

A. Real-time considerations

The proposed method processes an ECG recording with a bounded time delay comprising the intrinsic latency and computation time for the different stages. Only the baseline filtering and rhythm labeling stages present an intrinsic latency due to non-causality: 400ms and one beat, respectively. Since they both are executed concurrently, their contribution to the delay is given by the maximum of both. The computation time can be evaluated through the time complexity which is a bounded time delay comprising the intrinsic latency and processing method. Nevertheless, in a multiclass problem like this one, after characterizing the clusters, the values of sensitivity (Se), positive predictivity (+P), and false positive rate (FPR) should also be provided for each class, in order to obtain a multidimensional measure of the quality of the results from the perspective of each class involved. A global purity of 98.56% is obtained for MIT-BIH Arrhythmia database (98.84% with AAMI class labels) and a 99.56% for the AHA ECG database. The other values are shown in the last row of Tables III–V.

VIII. Discussion and Conclusion

We propose a new clustering method to dynamically separate QRS morphologies as they appear in a multichannel ECG signal, representing them with a dynamic number of clusters. This objective has not been previously addressed in the literature and only some partial solutions can be found, all of them restricted to offline processing [5]–[7] and some of them even limited to single channel signals and to a fixed subset of beat classes [6], [7].

The performance of the QRS clustering technique without using rhythm data shows a global purity of 97.15% and 99.43% for MIT-BIH and AHA databases, respectively. This confirms the validity of our approach, since no method, as far as we know, neither offline nor online, achieve this performance without using RR derived information. As expected, the main source of error is the group of supraventricular classes A, N, J, j, and e, that can only be separated using P wave and rhythm information. This is the reason for the difference between both results since AHA database does not contain this type of beats.

The validation results after using rhythm labels show a high sensitivity and positive predictivity for almost all classes while the purity increases. We observe in accordance with [5], that the largest number of errors in Table III are caused by beats with similar morphology. Fusion (F) of ventricular (V) and normal (N) beats are included with N or V clusters and vice versa. The same occurs with N, paced (f) and fusion of N and / beats (f). Finally, beats with supraventricular or nodal activation points (A, N, J, j, and e) with similar QRS are wrongly clustered when the rhythm information does not
TABLE III
CONFUSION MATRIX RESULTING FROM CLUSTERING MIT-BIH ARRHYTHMIA DATABASE. THE FIRST ROW CORRESPONDS TO THE ANNOTATION LABELS OF THE DATABASE, AND THE FIRST COLUMN, TO THE DOMINANT ANNOTATION LABEL IN THE CLUSTERS. Se, +P AND FPR DENOTE THE SENSITIVITY, POSITIVE PREDICTIVITY AND FALSE POSITIVE RATE FOR EACH BEAT CLASS RESPECTIVELY.

|   | N  | L  | R  | A  | V  | F  | J  | A  | S  | E  | j  | e  | f  | Q  |
|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| N | 74618 | 0  | 3  | 15 | 167 | 108 | 11  | 196 | 2  | 1   | 60 | 1  | 15  | 38  | 9  |
| L | 0  | 8059 | 0  | 0  | 1  | 2  | 0   | 0   | 0  | 0   | 0  | 0  | 0   | 2   | 0  |
| R | 32 | 0   | 7245 | 0  | 1  | 3  | 29  | 8   | 0   | 6   | 6  | 0  | 0   | 0   | 4  |
| a | 7  | 0   | 0   | 120 | 1   | 1   | 2   | 0   | 0   | 5   | 0  | 0  | 0   | 0   | 0  |
| V | 131| 1   | 0   | 11  | 6848| 83  | 0   | 20  | 0   | 0   | 0  | 0  | 1   | 4   | 6  |
| F | 26 | 0   | 0   | 2   | 56  | 606 | 0   | 2   | 0   | 0   | 0  | 0  | 0   | 0   | 0  |
| J | 1  | 0   | 0   | 0   | 0   | 42  | 0   | 0   | 0   | 0   | 0  | 0  | 0   | 0   | 0  |
| A | 44 | 4   | 3   | 2   | 25  | 0   | 0   | 2317| 0   | 0   | 0  | 0  | 0   | 1   | 0  |
| S | 0  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0  | 0  | 0   | 0   | 0  |
| E | 0  | 0   | 2   | 0   | 10  | 0   | 0   | 0   | 0   | 93  | 0  | 0  | 0   | 0   | 0  |
| j | 145| 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 158 | 0  | 0  | 0   | 0   | 0  |
| / | 9  | 0   | 0   | 0   | 1   | 0   | 0   | 0   | 0   | 7010| 0  | 127| 0   | 0   | 0  |
| e | 0  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0  | 0  | 0   | 0   | 0  |
| f | 9  | 0   | 0   | 0   | 5   | 0   | 0   | 0   | 0   | 13  | 0  | 816| 15  | 0   | 0  |
| Q | 0  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0  | 0  | 0   | 3   | 0  |
| ! | 0  | 0   | 0   | 0   | 0   | 12  | 0   | 0   | 0   | 6   | 0  | 0  | 0   | 0   | 403|

TABLE IV
CONFUSION MATRIX FOR MIT-BIH DB USING AAMI CLASS LABELS.

|   | N  | S  | F  | Q  |
|---|----|----|----|----|
| N | 89957| 342| 176| 113| 50 |
| S | 204 | 2648| 26  | 0  | 0  |
| F | 134 | 31  | 6951| 83  | 5  |
| Q | 26  | 4   | 56  | 606 | 0  |

TABLE V
CONFUSION MATRIX FOR AHA ECG DATABASE. CLASSES FROM THE MIT-BIH LABEL SET WITHOUT ASSIGNED BEATS ARE OMITTED.

|   | N  | F  | E  | /  | Q  |
|---|----|----|----|----|----|
| N | 318739| 472| 138| 7   | 150|
| V | 229 | 32090| 217| 0   | 9   | 66 |
| F | 33  | 115 | 885| 0   | 16  | 1  |
| E | 0   | 0   | 0   | 5   | 0   | 0  |
| / | 5   | 23  | 26  | 0   | 3128| 1  |
| Q | 11  | 32  | 0   | 0   | 0   | 354|

Se 99.46 99.84 99.89 80.00 96.09 75.56 50.60 91.04 0.00 87.74 69.00 99.80 0.00 83.10 9.09 85.38
+P 99.17 99.94 98.79 88.24 96.38 87.57 97.67 94.38 - 88.57 52.15 98.08 - 95.10 100.00 93.94
FPR 1.79 0.00 0.09 0.01 0.25 0.08 0.00 0.13 0.00 0.01 0.13 0.13 0.00 0.04 0.00 0.02

result determinant for their discrimination. This kind of errors represent 66% of the total.

Besides the clustering performance, the analysis of the number of clusters (N) generated for each record shows that it remains reduced: 34 records (71%) have 15 or less clusters; 12 records (25%) have between 16 and 30 clusters, both included and only two records (4%) has more than 30 clusters. The high number of clusters for record 207 is caused by the presence of an episode of ventricular flutter with QRS complexes replaced by irregular waves. The clustering results would be improved if an specific detection method were used for these kind of arrhythmias with absent QRS complex.

The N_BR column of Table II shows a general increase in the number of groups in all records with a mean of 24 groups per record. This increment reflects the presence of different rhythm labels in the beats assigned to the clusters although they do not always belong to different beat classes. Records with irregular rhythm like those with auricular fibrillation, or sudden rhythm change will render the RR information useless to discriminate premature or delayed beats. In such cases, the RR does not provide information about the beat activation point and the discrimination cannot be performed without an analysis of the P wave.

Since no other method for online clustering has been reported, we compare our clustering performance with existing offline proposals. Only the work of Lagerholm et al. [5] provides comparable results since others [6], [7] are designed to deal with a concrete subset of beat types and perform the evaluation over a single channel (usually the one with lower noise). Compared to [5] our method provides a slightly better purity (98.56% vs 98.49%). The sensitivity is improved in our work for 11 out of the 16 beat classes and slightly worsened for 3. Special mention should be made for classes a, A, R, j and E where the improvement is remarkable. Let us remember that [5] rely on a SOM with 25 clusters to represent the different beat classes. This approach has two main drawbacks, first the
clusters get saturated with dominant morphologies present in the learning stage, while rare morphologies are ignored as well as new morphologies that appear afterwards. Second, the generated clusters are redundant in those records with a low number of morphologies. In contrast, our method dynamically adapts the number of clusters to the number of morphologies detected.

The results of our proposal confirms the relevance of the temporal context for beat clustering. It allows us to switch from an offline to an online analysis achieving the same or even better results, and to address the temporal evolution of a beat morphology that otherwise would be projected into multiple clusters. The results of the experiments on ECG standard databases also show the adequacy of the present method for real-time ECG monitoring.

Our proposal provides the cardiologists with the information about the morphological diversity within a desired time frame and its temporal evolution. This information allows them to promptly detect the different conduction patterns and evaluate its relevance. It also can be useful for arrhythmia detection and classification which can be later addressed either automatically by classification algorithms or manually by the cardiologists.

In conclusion, we have presented an adaptive, multichannel context-based method for clustering beat morphologies in real-time that has been validated over the whole MIT-BIH Arrhythmia and AHA ECG databases with performance results that outperform its offline counterparts in the field.

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