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*Abstract* — **This Paper describes a clustering approach to be used for incoming data under computational constraints at an early stage of the signal processing chain. The algorithm is evaluated on the MIT-BIH Arrhythmia Database (MIT) and the European ST-T-Database (EDB) using a pseudo classification method to estimate the beat identification rates. The algorithm allows an extensive computational simplification, still providing reliable pattern recognition results for normal QRS beat types (Se=96.18 %; +P=99.61 % on MIT and Se=98.26 %; +P=99.95 % on EDB) as well as for ventricular ectopic QRS types (Se=97.61 %; +P=99.64 % on MIT and Se=99.07 %; +P=98.93 % on EDB). Besides its performance in terms of pseudo classification, the computational simplicity and few restrictions regarding its applicability render the proposed clustering method an interesting choice for online-clustering applications even apart from ECG processing.**

*Keywords—Electrocardiography, Pattern recognition, Clustering algorithms*

## I. INTRODUCTION

Holter recording systems are used in a wide range since their first practical introduction by N. J. Holter in 1961 [1], constantly being improved in terms of size, weight, recording quality and functionality. They even found their way into med- ical guidelines. Yet, they mainly aim at arrhythmia detection with focus on ventricular rhythm distortions. However, there are several devices available nowadays, not only providing the usual recoding task but also atrial arrhythmia detection, heart rate estimation, P- and T-wave annotation or ST-segment evaluation [2]–[5]. These developments show that ambulant long time recording tends towards new applications such as

- Identification of atrial fibrillation (AF) in terms of stroke risk stratification [6],

- Estimation of ST-T-Segment elevations as indicator for myocardial ischemia [7],

- Evaluation of QT-Interval prolongation and dynamics for drug effect studies [8], [9],

- Estimation of heart rate variability (HRV) to draw conclusions on the autonomous nervous system [10],

- Calculation of heart rate turbulence (HRT) as a powerful myocardial infarct (MI) risk predictor [11]

- or to provide post-surgery surveillance and therapy monitoring [6].

Also the Fraunhofer IPMS is developing an ambulant 24/7 monitoring system which includes automated electrocardio gram (ECG) analysis algorithms, focusing on ST-T-episode evaluation [12], [13].

The ST-T-episode algorithms as well as most of the above mentioned analysis methods need accurate identification of physiologically excited sinus rhythm heart beats to ensure a proper application of such further processing methods. Therefore, an accurate detection of clinical relevant arrhythmic events does not suffice the needs of those devices but a high accuracy normal beat detection is required additionally. Further development to reach this high accuracy is directed at the exploration of a full cardiac cycle. For now our work focuses on a morphological characterization of the most prominent part of the cardiac cycle, the QRS-complex.

Within this paper the task of morphological characterization is transferred to an online clustering problem, applied to a potentially infinite data input stream. Because the following evaluation algorithms in our mobile device are quite costly in terms of computational effort a simple and fast way to do this evaluation is desired.

The first section of this paper will give a brief outline on data clustering followed by a description of the used data material. In the next section the proposed algorithm will be elucidated. Thereafter its results are presented and discussed. Finally some conclusions will be drawn.

## II. METHODS AND MATERIALS

### A. Data Clustering

Data clustering describes a structure discovering multivariate analysis method, which assigns objects depending on their individual feature representation into a number of groups. These groups internally ought to be homogeneous, meaning objects of the same group should resemble to each other. Objects associated with different groups should have clearly heterogeneous characteristics to allow a good separation of the groups. [14]

In contrast to a classification task, clustering does not rely on predefined classes but objects are arranged based on the data immanent structures itself. [15], [16]

There are basically three components necessary to describe a clustering algorithm:

- A cluster method,

- A cluster representation approach,

- And a proximity measure.

The *cluster method* specifies the rules, if and how new clusters are created or old ones are deleted, how clusters fuse or how to split them and which connection rules may exist between clusters. Typically cluster methods are separated into so called hard- and soft-clustering methods, partitioning or hierarchically working approaches and disjunctive or overlapping object assignment. [14], [17] However, there may be methods not fitting in one of these categories.

The *cluster representation* describes the way how a cluster is referenced by other clusters or new input objects. Possible representations are nearest-neighbors-approaches (Single-Linkage, Complete-Linkage or K-Nearest-Neighbors), averaging models (Average-Linkage, Weighted-Average-Linkage), input objects as representatives or artificially constructed cluster centers. [14]

The *proximity measure* quantifies the relation between two elements, either the object-cluster-relation or the cluster1-cluster2-relation. Upon this calculation it is determined whether two objects are alike and therefore are assigned to the same cluster or not. An often used measure is the Euclidean Distance given by

$$d(\vec{x}, \vec{y}) = \sqrt{\sum_{n=1}^{N} (x_n - y_n)^2}, \tag{1}$$

where $N$ is the number of features in the elements $\vec{x}$ and $\vec{y}$.

### B. Databases

To evaluate the proposed algorithm the MIT-BIH Arrhythmia Database [18] (MIT) and the European ST-T Database [7] (EDB) by Physionet [19] are selected. Both provide complete reference annotations (beat times, beat types, rhythm annotations) over a record duration of 30 minutes (MIT) and 2 hours (EDB), respectively. This is a total of more than 850 000 beats to be evaluated with a wide variation of different QRS morphologies. For both databases all records have been evaluated without any exclusion.

### C. Quantitative performance assessment by Pseudo Classification

As described in the previous section data clustering discovers data structures and is capable of ordering the given data based on these structures. However, in the context of our work it is important to know if a proposed cluster algorithm is able to distinguish between diagnostically relevant morphologies. Therefore we apply a procedure which we call pseudo classification to allow an assessment, using the provided reference annotations.

If a new cluster is generated it receives a class identifier, based on the annotation of the respective beat in the reference annotation file. For each following beat assigned to this particular cluster, the annotated beat class is compared with the corresponding cluster class identifier. In this way it is possible to estimate if the discovered cluster structures are related to groups of diagnostic value and if the proposed clustering algorithm is capable of distinguishing between beat morphologies of medical relevance.

## III. ALGORITHM DESCRIPTION

### A. Boundary Conditions

The algorithm is intended to be used on an ambulatory device for continuous incoming data. This implies heavy computational constraints and requires a clustering approach capable of adapting to the input at the moment of its occurrence, not having the possibility to present the same input vector once again to the algorithm. Additionally the memory space available on a microcontroller is very limited. To define a maximum of iterations through existing clusters and to preliminary determine a memory heap the number of available clusters is limited to ten.

### B. Cluster Method

The proposed cluster method is based on a procedure described by Schwenker et al. [20] as *adaptive cluster analysis*. This algorithm is able to create a new cluster if the distance $d(\vec{x}, \vec{c}_{j*})$ between the presented object $\vec{x}$ and the nearest cluster $\vec{c}_{j*}$ is higher than the threshold $\theta_{new}$, or to merge two cluster if their distance $d(\vec{c}_i, \vec{c}_j)$ (where $i, j = 1 \ldots 10 \wedge i \neq j$) is smaller than the threshold $\theta_{merge}$. Additionally we added the possibility to delete a cluster if the maximum number of clusters available is reached and a reduction by merging two similar clusters is not possible. In such a case the cluster, not being activated for the longest time, is removed. This keeps the cluster representation adapted to the current input data stream, always having a good representation of the actual QRS complexes.

### C. Cluster Representation

Initially there are no clusters defined and the first QRS complex will be handled like having a higher threshold than $\theta_{new}$. A new cluster will be created from it. Following complexes, meeting the merge distance, will be assigned to this cluster and will adapt the cluster center using a similarity depended moving average approach as follows.

$$\vec{c}(n)_{j*} = (1 - a \cdot s) \cdot \vec{c}(n-1)_{j*} + a \cdot s \cdot \vec{x}(n) \tag{2}$$

In this equation $\vec{c}(n)_{j*}$ is the actual winning cluster, $\vec{x}(n)$ is the actual input object at time $n$, $a$ is a fix adaption constant ($a$=0.1) and $s$ is the similarity score of $\vec{x}(n)$ and $\vec{c}(n-1)_{j*}$, which is described in the next passage. This slight modification of the usual moving average adaption diminishes the influence of outliers, preventing the cluster centers from adapting too fast to input vectors, which are only being presented rarely.

### D. Proximity Measure

The similarity score $s$ describes the alikeness of two compared objects and is based on the Euclidean Distance in (1). It is defined as

$$s = 1 - \frac{d(\vec{x}, \vec{y})}{d_{max}(\vec{x}, \vec{y})}, \tag{3}$$

with $d_{max}(\vec{x}, \vec{y})$ describing the maximum Euclidean Distance of $\vec{x}$ and $\vec{y}$, by summing the absolute values of their respective

feature components. This maximum distance results if each feature in $\vec{x} = \{x_1, x_2, \ldots, x_N\}$ has the opposing sign to the corresponding feature in $\vec{y} = \{y_1, y_2, \ldots, y_N\}$.

$$d_{max}(\vec{x}, \vec{y}) = \sqrt{\sum_{n=1}^{N} (|x_n| + |y_n|)^2} \qquad (4)$$

In that way distance normalization is attained, penalizing a certain difference between two large scale feature vectors less than between two low scale ones. Using this similarity score the merge and creation thresholds $\theta_{merge}$ and $\theta_{new}$ do not have to be adjusted to the input range but can be chosen as a value between 0 and 1, i.e. independent from signal gain or individual QRS morphologies.

### E. Feature Representation

As feature representation a well-known strategy is pursued, which has proven its worth in former applications [21]–[23]. For each QRS complex the feature vector $\vec{x}$ is extracted from a time window of $100\,\text{ms}$ before and after the corresponding fiducial point (FP). This generates 10 subsequent $20\,\text{ms}$ sum integral values of the area below the curve as shown in Fig. 1.

To allow a separation of normal beats and supraventricular ectopic beats the algorithm is using the beats preceding RR-interval as an additional feature with veto-characteristics. If the difference between the RR-interval of the current object and a cluster center is higher than $15\,\%$ the similarity score for this pairing is set to zero regardless of the morphological pattern. In any other case this $10 + 1^{\text{th}}$ feature is not contributing to any similarity estimations.
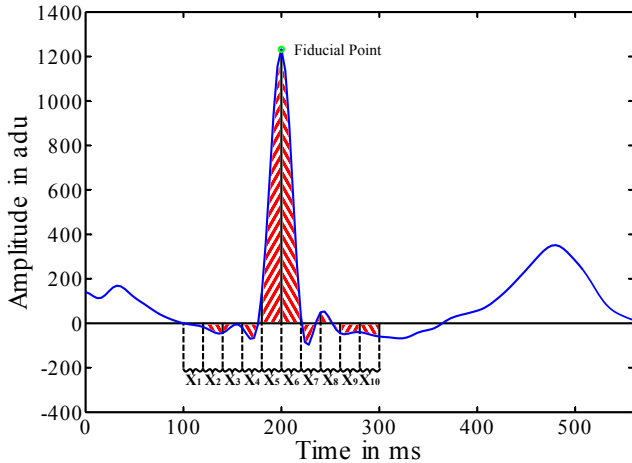


Fig. 1. Feature extraction starting $100\,\text{ms}$ before FP and ending $100\,\text{ms}$ after it. Each value of $\vec{x}$ is holding the sum integral of $20\,\text{ms}$.

## IV. RESULTS

Using the pseudo classification approach with the proposed algorithm a new annotation is created for each record of the database. To compare the new annotation with the provided reference the program `bxb` is used, which is included in the Physionet software package. As stated in [24] the annotations are distinguished into 5 class labels: normal beats (N), supraventricular ectopic beats (S), ventricular ectopic beats

TABLE I. PSEUDO CLASSIFICATION RESULTS OF MIT AND EDB

| Class | MIT | | EDB | |
| | Se [%] | +P [%] | Se [%] | +P [%] |
|---|---|---|---|---|
| N | 95.74g | 99.59g | 98.30g | 99.95g |
| | 96.18a | 99.61a | 98.26a | 99.95a |
| S | 92.23g | 42.01g | 77.00g | 6.36g |
| | 75.10a | 67.08a | 69.16a | 53.19a |
| V | 98.12g | 99.66g | 97.20g | 83.40g |
| | 97.61a | 99.64a | 99.07a | 98.93a |

Abbreviations: g...gross, a...average

TABLE II. BEAT TO CLUSTER RATIO IN MIT AND EDB

| Database | Gross [bpc] | Average [bpc] |
|---|---|---|
| MIT | 27.14 | 43.87 |
| EDB | 22.74 | 56.93 |

(V), fusion beats of a ventricular and a normal beat (F) and paced beats, fusion of a paced and a normal beat or beats that cannot be classified (Q).

Using the comparison statistics of `bxb` we calculated the sensitivity (Se) and the positive predictive value (+P) for N, S and V beat types. Table I gives a summary for both databases. Note that the calculations for normal beats and ventricular ectopic beats do not include beats which have been annotated as fusion, since the algorithm shall not be penalized nor rewarded for treatment of this beat type, as stated in [24].

Additionally the number of created cluster centers during a complete evaluation of one record is logged. Combined with the total number of beats present in this record it is now possible to estimate the beat to cluster ratio (BCR) for each data file. This value is showing the average number of beats being represented by one cluster center, and hence, being classified by only one full feature classification if no pseudo classification would have been used. A BCR of 10 is therefore equal to a reduction of the full classification effort by $90\,\%$ $(1/10 = 0.1)$. Table II is showing the average number of beats per cluster (bpc) for MIT and EDB.

## V. DISCUSSION

It has been demonstrated that the proposed clustering approach allows to separate normal beats from ectopic beat forms with a sensitivity of at least $95\,\%$ and a positive predictive value above of $99,5\,\%$. This is a quite valuable result considering the vast mass of applications which rely on a secure identification of normal beats to be working correctly.

ST-T-segment analysis for example, is only possible if applied to normal beat signal morphologies, since it is necessary to estimate an isoelectric reference level within the PQ-intervall to calculate a reasonable ST-T-level deviation. Moreover, repolarization behavior will of course alternate depending on the focus of the myocardial excitation spot. [13], [29]

Heart rate variability estimations in are also heavily relying on accurate identification of sinus excited beats. Any ectopic beat will disturb the assessed beat interval series, possibly leading to wrong conclusions about the vegetative nervous system.

TABLE III.     COMPARISON OF THE PROPOSED APPROACH TO METHODS DESCRIBED IN LITERATURE

| Reference | Used Methods | | N | S | V |
|---|---|---|---|---|---|
| this algorithm | 10 sum values across QRS, dynamic clustering | Se [%] | 96.18 | 75.10 | 97.61 |
| | | +P [%] | 99.61 | 67.08 | 99.64 |
| Yeh et al. [25] | 9 features across PQRST-Segment, fuzzy C-neans | Se [%] | 98.28 | 94.86 | 92.19 |
| | | +P [%] | 97.38 | 93.87 | 86.82 |
| Jekova et al. [26] | 26 features across 2 channels | | | | |
| | K-Nearest-Neighbors | Se [%] | 99.91 | - | 97.76 |
| | | +P [%] | 99.82 | - | 99.92 |
| | fuzzy fogic | Se [%] | 99.85 | - | 97.40 |
| | | +P [%] | 99.75 | - | 99.47 |
| | linear discriminant analysis | Se [%] | 96.64 | - | 96.94 |
| | | +P [%] | 99.37 | - | 72.29 |
| | neural networks | Se [%] | 99.88 | - | 97.99 |
| | | +P [%] | 99.83 | - | 98.65 |
| Korürek et al. [27] | 2 RR-intervalls and QRS-amplitude, ACO | Se [%] | 95.49 | 86.78 | 93.33 |
| | | +P [%] | - | - | - |
| Kamath [28] | TEO in time and frequency domain, NN | Se [%] | 100 | - | 100 |
| | | +P [%] | - | - | - |

Abbreviations: ACO...ant colony optimization, TEO...Teager energy operator, NN... neural networks

There are smart algorithms available dealing with those disturbances [30], but they are not usable for every case as far as they are relying on RR-intervals only. A morphological estimation would introduce additional physiological information, which may help to avoid drawing wrong conclusions.

Correct estimation of normal and ventricular escape beats is crucial for calculations of the heart rate turbulence (HRT) as well. According to the International Society for Holter and Noninvasive Electrophysiology [11] the calculation of the HRT needs certain recognition of a single ventricular ectopic beat (VES) preceded by at least 2 and succeeded by at least 15 sinus rhythm beats to be used correctly. Moreover, this estimation has to be made for at least 5 isolated VES, since the HRT has to be calculated on averaged tachograms.

With an average sensitivity of 96.18 % and a positive predictive value of 99.61 % for normal beats and a Se of 97.61 % with a +P of 99.64 % for ventricular ectopic beat morphologies, the estimated results on the MIT for the proposed clustering algorithm are reaching similar values as several approaches described in literature. Of course, one has to keep mind, that the presented results are obtained using pseudo classification as a verification method. They are therefore not directly comparable to results of usual classification methods. However, the results of the pseudo classification are well suited to document the usability of the proposed algorithm. Here, a high performance is obtained with a comparatively simple approach. The above mentioned classification methods which include fuzzy hybrid neural networks [25], [26], third order cumulants [31], wavelet entropy [31], autoregressive coefficients [31], linear discriminant analysis [26] or Teager energy functions [28] usually imply a higher computational complexity of the preliminary feature extraction procedure and their evaluation algorithms. The higher calculation effort in comparison to the proposed method becomes even more evident if the used features are extracted form the whole PQRST-sequence. Jenkova et al. [26] for example, is using a total of 26 features including several slopes, amplitudes, durations, ratios and energy-/area- estimations collected from two channels. This will most likely not be reconcilable with the needs to be implemented on a microcontroller and parallel processing requirements. Table III summarizes some of the mentioned methods and their statistics.

Though its simplicity, the proposed morphological clustering approach reaches considerable identification results with a comparably low computational effort. Particularly the high positive predictive value has to be pointed out, meaning a normal beat labeling is true with an average error of less than 1 %, providing a very good basis for the above explained subsequent estimations.

Identification of SVES though, is not reaching this high level of quality (Se=75.10 %; +P=67.08 % on MIT and Se=69.16 %; +P=53.19 % on EDB). These results are not surprising. Since supraventricular beats are normally following the same electrical excitation path through the heart as normal beats do, their morphologies are typically quite similar. However, the aim of introducing the RR-interval-veto was not to achieve an ideal identification of SVES, but to provide a tool preventing SVES to be considered as normal beats. In this way the positive predictive value of normal beat identification is raised significantly.

As the presented algorithm is only identifying similar signal morphologies on an early stage of the signal processing chain a diagnostic classification step has to follow, if necessary. The idea is to prelocate the proposed approach to a high level classification method, which will speed up classification procedures, only needing to do a full classification on every $50^{th}$ beat on average. This reduces the full feature classification effort by 98 %. In one case it was even possible to describe more than 2400 beats with only 6 cluster centers, resulting in a BCR of more than 400 bpc, which equals a reduction of 99.75 %. Several other records reached at least values of more than 100 bpc. But there is also the same number of records having a lower ratio than 10 bpc. Considering the cluster center limit of maximum 10 clusters, such low beat per cluster ratios had to be expected in some cases. In records yielding more than 10 different reoccurring beat morphologies this may result in recreation of former known cluster centers, which is of course raising the cluster creation count.

Note, that we did not use any filtering at this early processing stage. Thus, of course more clusters will appear in disturbed signal periods than in such without noise.

## VI. Conclusion

Using pseudo classification the capability to separate diagnostically relevant signal morphologies was estimated for the proposed cluster algorithm as individual processing step. By only using a simple morphologic representation of the QRS complex the reliability of the approach was demonstrated. Beat identification quality for normal beats and ventricular ectopic morphologies exhibit similar results as existing methods described in literature. However, the computational effort in terms of algorithmic complexity and preliminary feature extraction procedures is considerably lower in the proposed approach.

The described cluster algorithm is introduced as a preceding evaluation step in an early stage of the signal processing chain. Used in this manner the method proved to be utilized to estimate signal quality and to even reduce the need for a full feature beat classification to 2 % on average.

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