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ADDITIONAL DATA PREPROCESSING AND FEATURE EXTRACTION IN AUTOMATIC CLASSIFICATION OF HEARTBEATS

Abstract: The paper presents the classification performance of an automatic classifier of the electrocardiogram (ECG) for the detection abnormal beats with new concept of feature extraction stage. Feature sets were based on ECG morphology and RR-intervals. This paper compares two strategies for classification of annotated QRS complexes: based on original ECG morphology features and proposed new approach - based on preprocessed ECG morphology features. The mathematical morphology filtering and wavelet transform is used for the preprocessing of ECG signal. Within this framework, the problem of choosing an appropriate structuring element in mathematical morphology filtering in signal processing was studied. Configuration adopted a Kohonen self-organizing maps (SOM) and Support Vector Machine (SVM) for analysis of signal features and clustering. In this study, a classifiers was developed with LVQ and SVM algorithms using the data from the records recommended by ANSI/AAMI EC57 standard. The performance of the algorithm is evaluated on the MIT-BIH Arrhythmia Database following the AAMI recommendations. Using this method the results of identify beats either as normal or arrhythmias was improved.

Key words: ECG, preprocessing, mathematical morphology, ECG filtering, wavelet approximation, feature extraction, heartbeat classification

1. Introduction

The analysis of heart beat cycles in ECG signal is very important for long-term monitoring of heart patients. Automatic classification of cardiac rhythms remains a vital problem in clinical cardiology, especially when it is performed in real time. Several researchers have addressed the problem of automatic classification of cardiac arrhythmias [1-7]. Annotation of ECG recording requires the detection of various types of heartbeats. This is a pattern recognition task. Very often, a

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classifier is to be trained to recognize different types of beats. The training set of the classifier is usually a large database, which consists of the ECG beats from a large pool of patients. However, these classifiers suffer from the problem of poor generalization because there are usually some variations in the "normal" range among human beings. Even doctors may experience difficulty in assessing abnormal ECG beats if only considering the reference values based on the general patient population.

There are two general approaches to the training process: building general heartbeat classifier [3-7] and patient-adapting classifier [1,2]. However, most of the approaches proposed in the literature deal with a limited number of arrhythmic types and process the entire ECG signal extracting several features from it, such as the P wave, which is an extremely time-consuming process and sometimes difficult due to the presence of noise. Other researches suggested that there is a need to incorporate local information of a specific patient to improve the recognition of abnormal ECG beats and thus help to improve the generalization.

This work proposes a method for the unification of variations in ECG beats, based on mathematical morphology and resampling model, which can be easily applied to the ECG signal.

2. Mathematical morphology

By "morphological signal processing" we mean a broad and coherent collection of theoretical concepts, mathematical tools for signal analysis [12]. Originally mathematical morphology (MM) was applied to analyzing images from geological or biological specimens. However, its rich theoretical framework, algorithmic efficiency, easy implementability on special hardware, and suitability for many shape-oriented problems have propelled its widespread diffusion and adoption by many academic and industry groups in many countries as one among the dominant image analysis methodologies [8-11].

As a result, MM nowadays offers many theoretical and algorithmic tools to and inspires new directions in many research areas from the fields of signal processing, image processing and machine vision, and pattern recognition.

2.1. Mathematical morphology transformations

Morphological filters are nonlinear signal transformations that locally modify geometric features of signals. They stem from the basic operations of a set-theoretical method for signal analysis, called mathematical morphology, which was introduced by Serra [12].

156

In morphological filtering [8-11], each signal is viewed as a set, and its geometrical features are modified by morphologically convolving the signal with a structuring element (SE), which is another set of simple shape and size. By varying the structuring element we can extract different types of information from the signal.

A structuring element is characterized by its shape, width, and height. Its width, or length, is largely determined by the duration of the major waves and the sampling rate. The values of the structuring element determine the shape of the output waveform.

2.2. Elementary mathematical morphology operators

In the sequel we use definitions of grey-level morphology basic operators in the same form as in [12]. Let us recall that *erosion* Θ of a function $f : R \to R$ by a structuring element $b : R \to R$ can be defined as

$$(f \Theta b)(s) = \min_x \{ f(s+x) - b(x) : (s+x) \in D_f \wedge x \in D_b \} \tag{2}$$

where $D_f = \operatorname{supp} f$, $D_b = \operatorname{supp} b$. In a similar way, *dilation* $\oplus$ is an operator given by

$$(f \oplus b)(s) = \max_x \{ f(s-x) + b(x) : (s-x) \in D_f \wedge x \in D_b \} \tag{3}$$

Two other operators: *closing* $\bullet$ and *opening* $\circ$ are defined with help of (2) and (3), i.e.

$$f \bullet b = (f \oplus b) \Theta b, \quad f \circ b = (f \Theta b) \oplus b \tag{4}$$

3. SOM and LVQ

3.1. Self-Organization Map

The Self-organizing Map (SOM) is an artificial neural network architecture based on unsupervised, competitive learning [14]. It provides a topology preserving, smooth mapping from a high-dimensional input space to the map units usually arranged as a two-dimensional lattice of neurons (nodes). Thus, the SOM can serve as a tool for cluster analysis of complex, high-dimensional data.

A parametric reference vector *m*, is associated with every node. A data vector *x* is compared to all reference vectors in any metric and the best matching node is defined, e.g., by the smallest Euclidean distance between the data vector and any of the reference vectors. During learning, those nodes that are topographically close

in the array up to a certain distance will activate each other to learn from the same input:

$$m_i(t+1) = m_i(t) + h_{ci}(t)[x(t) - m_i(t)] \tag{5}$$

where t is an integer representing time, and $h_{ci}(t)$ is the so-called neighbourhood kernel describing the neighbourhood that is updated around the best-matching node. Several suitable kernels can be used, e.g. a so-called bubble kernel or a gaussian kernel, relating to different ways of determining the activating cells. The kernel also includes the learning rate parameter $\alpha(t)$. With time, the size of the neighbourhood and the learning rate are diminished. The described learning process leads to a smoothing effect on the weight vectors in the neighbourhood and by continued learning to global ordering of the nodes [14,15].

The SOM consists of a two-dimensional lattice that contains a number of neurons. These neurons are usually arranged in a rectangular or hexagonal way. The position of the units in the grid, especially the distances between them and the neighborhood relations, are very important for the learning algorithm. A prototype vector (also "model" or "codebook" vector) is associated with each neuron, which is a vector of the same dimension as the input data set. This prototype vector approximates a subset of the sample vectors. The dimension of the sample is called input dimension, and is usually larger than 2, the dimension of the lattice, which is called output dimension. For training and visualization purposes, the sample vectors are assigned to the most similar prototype vector, or best-matching unit (BMU), formally

$$c(x) = \arg \min_i \{|x - m_i(t)|\} \tag{6}$$

The learning process itself gradually adapts the model vectors to match the samples and to reflect their internal properties as faithfully as possible, which means that input vectors which are relatively close in input space should be mapped to units that are relatively close on the lattice.

3.2. Learning Vector Quantization

Learning Vector Quantization (LVQ) [14, 22] is a supervised, clustering-based classification technique which classifies a feature vector according to the label of the cluster prototype (code word) into which is clustered. Classification error occurs when the feature vectors within the same cluster (hence, assigned to the same class label) are actually drawn from different classes. To minimize classification error, the LVQ algorithm fine tunes the clustering boundary between clusters of different class labels by modifying the position of the clustering center

158

(prototype or code word). This method is called "learning vector quantization" because this clustering based classification method is similar to the "vector quantization" method used for signal compression in the areas of communication and signal processing.

Assume that a number of 'codebook vectors' $m_i(t)$ (free parameter vectors) are placed into the input space to approximate various domains of the input vector x by their quantized values. Usually several codebook vectors are assigned to each class of x values, and x is then decided to belong to the same class to which the nearest mi belongs. According to (6) we defined the nearest $m_i(t)$ to x, denoted by mc. Values for the $m_i(t)$ that approximately minimize the misclassification errors in the above nearest-neighbor classification can be found as asymptotic values in the following learning process. Starting with properly defined initial values, the following equations define the basic LVQ1 process:

$$mc(t+1) = mc(t) + \alpha(t)[x(t) - mc(t)], \tag{7}$$

if x and mc belong to the same class,

$$mc(t+1) = mc(t) * \alpha(t)[x(t) - mc(t)], \tag{8}$$

if x and mc belong to different classes,

$$m_i(t+1) = m_i(t) \tag{9}$$

for i not in c,

Here $0 < \alpha(t) < 1$, and $\alpha(t)$ may be constant or decrease monotonically with time. In the above basic LVQ1 it is recommended that alpha should initially be smaller than 0.1

4. Support Vector Machine

Support Vector Machine is a method for finding a hyperplane in a high dimensional space that separates training samples of each class while maximizes the minimum distance between the hyperplane and any training samples [26]. SVM approach can apply any kind of network architecture and optimization function.

We are given a set of N data points $\{x_i, y_i\}_{i=1}^{N}$, where $x_i \in \mathbf{R}^n$ is the i-th input data, and $y_i \in \{-1, +1\}$ is the label of the data. The SVM approach aims at finding a classifier of form:

$$y(x) = sign\left[\sum_{i=1}^{N} \alpha_i y_i K(x_i, x) + b\right] \tag{10}$$

159

Where α_i are positive real constants and b is a real constant, in general, $K(x_i, x) = \langle \phi(x_i), \phi(x) \rangle$, $\langle \bullet, \bullet \rangle$ is inner product, and $\phi(x)$ is the nonlinear map from original space to the high dimensional space.

In the high dimensional space, we assume the data can be separated by a linear hyperplane, this will cause:

$$y_i \left[w^T \phi(x_i) + b \right] \geq 1, \quad i = 1, \ldots, N \tag{11}$$

In case of such separating hyperplane does not exist, we introduce a so called slack variable ξ_i such that

$$\begin{cases} y_i \left[w^T \phi(x_i) + b \right] \geq 1 - \xi_i, & i = 1, \ldots, N \\ \xi_i \geq 0, & i = 1, \ldots, N \end{cases} \tag{12}$$

According to the structural risk minimization principle, the risk bound is minimized by the following minimization problem:

$$\min_{w, \xi} J_1(w, \xi) = \frac{1}{2} w^T w + c \sum_{i=1}^{N} \xi_i \tag{13}$$

subject to (12). One constructs the Lagrangian function as

$$L_1(w, b, \xi, \alpha, \beta) = J_1(w, \xi) - \sum_{i=1}^{N} \alpha_i \left\{ y_i \left[w^T \phi(x_i) + b \right] - 1 + \xi_i \right\} - \sum_{i=1}^{N} \beta_i \xi_i \tag{14}$$

where $\alpha_i \geq 0$, $\beta_i \geq 0$ $(i = 1, \ldots, N)$ are the Lagrangian multipliers. The optimal point will in the saddle point of the Lagrangian function, i.e.

$$\max_{\alpha, \beta} \min_{w, b, \xi} L_1(w, b, \xi, \alpha, \beta) \tag{15}$$

Substitute (10), we will get the following quadratic programming problem:

$$\max_{\alpha} Q_1(\alpha) = -\frac{1}{2} \sum_{i, j=1}^{N} \alpha_i \alpha_j y_i y_j K(x_i, x_j) + \sum_{i=1}^{N} \alpha_i . \tag{16}$$

where $K(x_i, x_j) = \langle \phi(x_i), \phi(x_j) \rangle$ is called the kernel function. Solving this QP problem subject to constrains in (13), we will get the hyperplane in the high dimensional space and the classifier in the original space as in (10).

5. Evaluation method

The proposed method consists of four steps: (a) preprocessing (denoising, baseline drift removal and feature extraction), (b) additional data filtering and wave form transformation (feature extraction), (c) building feature vector (feature selection) (d) arrhythmic episode classification. The MIT-BIH arrhythmia database [17] is used for evaluation of the method.
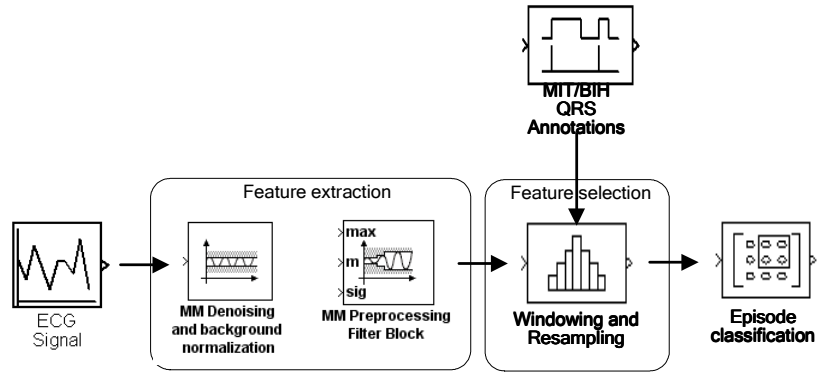

Fig. 1. Block diagram of the proposed morphological filtering based transformation.

We evaluate various combinations of morphological filters and conduct experiments for different structuring elements [18,19] in feature extraction steps. It turns out that in results are strong depends on shape and size of structuring element. Since the opening and closing operations are intended to remove impulses, the structuring element must be designed so that the waves in the ECG signal are not removed by the process.

5.1. Datasets

To evaluate the performance of our approaches, we used the 48 tapes of the MIT-BIH arrhythmia database, which comes along with a very detailed annotation for each beat. The Association for the Advancement of Medical Instrumentation (AAMI) has summarized those detailed classes to four classes of clinical relevance, as shown in table 1 [20]. Four records (102, 104, 107, and 217), including paced beats, are excluded from the study in compliance with the standards recommended for reporting performance results of cardiac rhythms by the AAMI.

The original signals in the MIT-BIH arrhythmia database are two-leads, sampled at 360 Hz. The ECG signal of Lead 1 is used in this study. Accompanying

each record in the database is an annotation file in which each ECG beat has been identified by expert cardiologists. These labels are referred to as 'truth' annotations and are used in developing the classifiers and also to evaluate the performance of the classifiers in the testing phase.

Table 1

Beat classes according to MIT-BIH arrhythmia database and AAMI recommended practice

| MIT-BIH heartbeat types	AAMI heartbeat class	Notation used in this work
normal beat (NOR),	NORMAL (N) Any heartbeat not in the other classes	NL
left bundle branch błock beat (LBBB),		LB
rignt bundle branch block beat (RBBB),		RB
atrial escape beats (AE),		AE
nodal (junctional) escape beat (NE)		NE
atrial premature beat (AP),	SVEB (S) Supraventricular ectopic beat	AP
aberrated atrial premature beat (aAP),		AA
nodal (junctional) premature beat (NP),		NP
supraventricular premature beat (SP)		SP
premature ventricular contraction (PVC),	VEB (V) Ventricular ectopic beat	PV
ventricular escape beat (VE)		VE
fusion of ventricular and normal beat (fVN)	FUSION (F) Fusion beat	FS
paced beat (P),	NOTQRS (Q) Unknown beat	PB
fusion of paced and normal beat (fPN),		PF
unclassified beat (U)		NQ

5.2. Feature extractions

Many experiments have been done to test the performance of morphological filters used in ECG signal preprocessing [18,19]. The experiments show that nonstandard filter block construction, especially combination of elementary morphology operators (as sequence operations), has very big impact for characteristic of output signal. The morphological filter preprocessing stage was implemented using the MATLAB programming languages.

We propose a feature-preserved transformation for signal processing of ECG data, based on mathematical morphology (MM) filtering. Despite the fact that MIT-BIH [17] database consist of wide spectrum of ECG signals we obtained similar results for all data. For extraction and unification of the ECG features, the

length of the SE should be less than QRS interval. Therefore, we chose 70 ms as the length of the SE. Here, we take the flat SE to illustrate preprocessing effect.
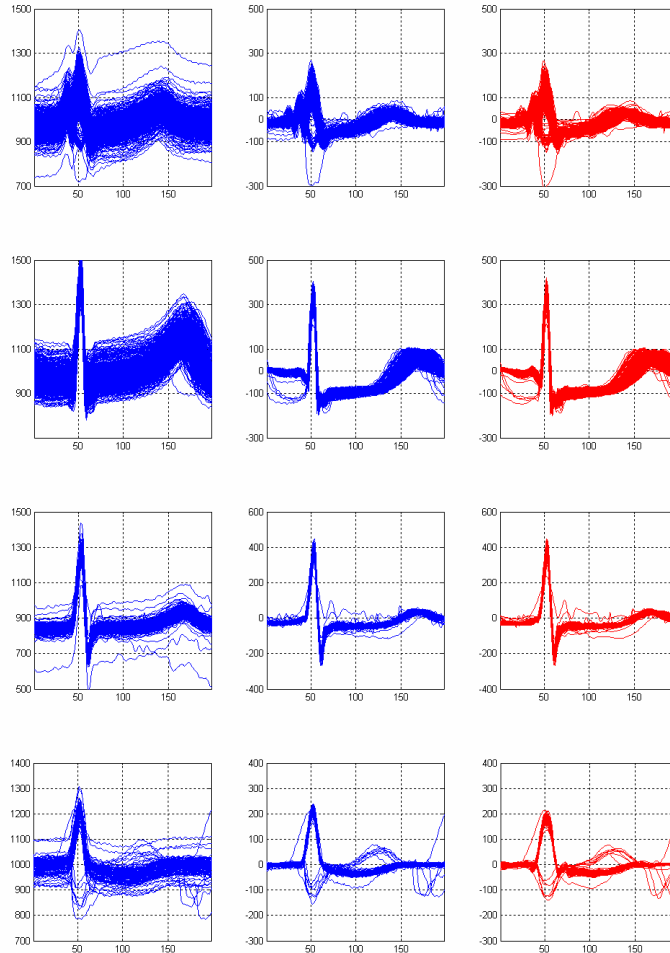
Fig. 2. Feature extraction stages combination: A – column 1) without preprocessing, B – column 2) only with MM denoising, baseline drift removal, C – column 3) MM denoising, baseline drift removal (1-st stage) and additional MM filtering block (2-nd stage). Record e.g. 111, 113, 123, 210 (top-down) from MIT-BIH Arrhythmia Database.

Also we evaluate various wavelets (WT) in feature extraction steps. Wavelets are well suited to approximate such signals when nonlinear approximation is allowed [25]. The compression features of a given wavelet basis are primarily linked to the relative scarceness of the wavelet domain representation for the signal. The notion behind compression is based on the concept that the regular

signal component can be accurately approximated using the following elements: a small number of approximation coefficients (at a suitably chosen level) and some of the detail coefficients.

To study compression behavior we done many experiments to test the performance of wavelet approximation used in ECG signal preprocessing. Here, we take the two wavelets: daubechies and symlet to illustrate preprocessing effect. For our experiments, we choose the decomposition of the signals at level n (where $n=5..7$) and forced to zero detail coefficients for level *1..n-2*.

5.3. Feature selection

Here we investigate the use of raw amplitude of the time domain ECG signals after noise suppression, baseline drift removal and additional preprocessing as feature vectors to represent the ECG beats. After the R-peak is found (using MIT-BIT database annotations), the ECG signal in a window of 550 ms is taken as an ECG beat. The lengths of the signal before and after the R-peak in each beat are 140 ms and 410 ms, respectively, such that the window covers most of the characterization of the ECG beat. The signal in each window is then resampled to form a feature vector of 20-dimensions. The R-R interval (the interval between two consecutive R-peaks) is also used in this study by appending it to the 20-dimensional feature vector.

5.4. Feature classification

In this study, a classifiers was developed with SOM/LVQ and SVM algorithms.

5.4.1. Clustering by SOM

The issue of SOM quality is a complicated one [16]. Typically two evaluation criterias are used: resolution and topology preservation. There are many ways to measure them. The ones used here were chosen for their simplicity:
- qe (quantization error) - Average distance between each data vector and its BMUs (best matching units). Measures map resolution,

The average quantization error is measure used for this purpose. In order to study the behaviour of these factors we chose hexagonal topology map with automatic determine map size.

We used the method to allocate manually detected heartbeats to one of the five or fifteen beat classes (Table 1) recommended by ANSI/AAMI EC57:1998 standard, i.e., normal beat (NORMAL), ventricular ectopic beat (VEB),

supraventricular ectopic beat (SVEB), fusion of a normal and a VEB (FUSION), or unknown beat type (NOTQRS) and second group with notation used in this work.
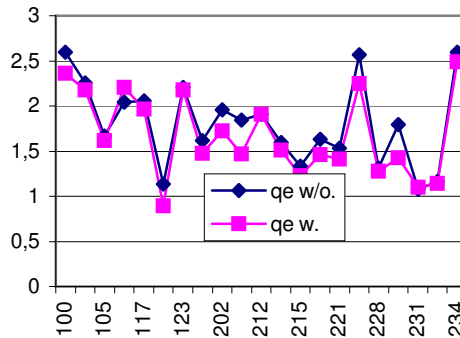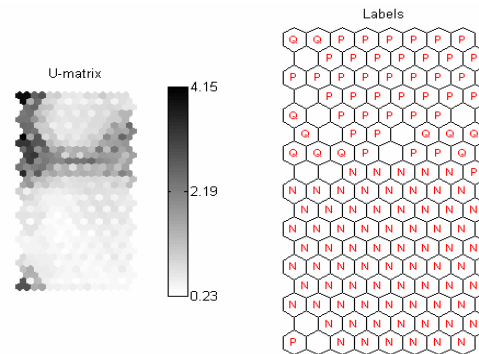

Fig. 3. Quantization error for each recording of the test set.

Figure 2 shows the quantization error for all MIT/BIH datasets. Average distance between each data vector and its BMUs is smaller for almost all records.
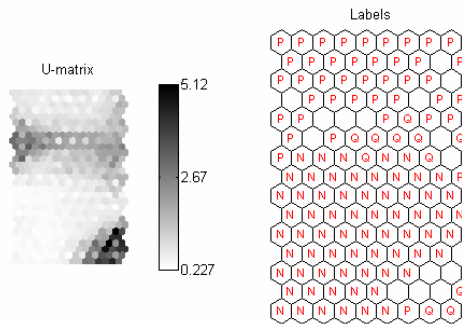
Fig. 4. Distance matrix U-matrix and labes for clustering of record 200 (MIT/BIH) without preprocessing; i.e. NORMAL (N), VEB (V), SVEB (S), FUSION (F), NOTQRS (Q)

Fig. 5. Distance matrix U-matrix and labes for clustering of record 200 (MIT/BIH) with preprocessing; i.e. NORMAL (N), VEB (V), SVEB (S), FUSION (F), NOTQRS (Q)

Clusters on the map are typically visualized using the unified distance matrix (U-Mmatrix) method. The U-matrix of the example system is shown in Fig. 3 (without preprocessing) and Fig 4 (with additional preprocessing). The lighter the color of a unit, the, the closer it is to its neighbors.

It is demonstrated that the map direction is changing smoothly on the SOM. Moreover, the fully trained SOM did not include any meaningless or random maps. Of all teaching runs, the SOM that resulted in the lowest quantization error of the test set was chosen for further classification.

5.4.1. LVQ training and classification

According to Kohonen, there are three different LVQ algorithms, called LVQ1, LVQ2, and LVQ3 developed at subsequent stages to handle classification problems with different natures. In this study, the learning-rate LVQ1 algorithm was used for the training and fine-tuning of the code book respectively. This stage is based on applying the training and accuracy classification using the MATLAB SOM Toolbox [21] and LVQ_PAK [22].

5.4.2. Support Vector Machine (SVM)

We have performed many experiments to determine best classification performance. We have used Gaussian radial kernels with $\gamma = 1$. The parameter C used in experiments was set to *1000*. Our experiments confirmed that classification ratio strongly depends on this parameters.

Waikato Environment for Knowledge Analysis (WEKA) [29] workbench was used for the experiments. We ran experiments with SVM algorithm that is

available as Weka's implementation with SMO approach. Sequential Minimal Optimization (SMO) is a fast method to train SVM. SMO breaks this large QP problem into a series of smallest possible QP problems. These small QP problems are solved analytically, which avoids using a time-consuming numerical QP optimization as an inner loop. The amount of memory required for SMO is linear in the training set size, which allows SMO to handle very large training sets.

6. Results and discussion

The method allocates manually detected heartbeats (using MIT/BIT database annotations) to one of the classes showed in Table 1 (MIT-BIH heartbeat types). The labels in the annotation files of MIT-BIH database made by cardiologists are used as the ground truth in evaluating the classifier.

Classifier performance has been estimated using MIT-BIH heartbeat types showed in Table 1. Because SMO algorithm and memory limitations all recordings were divided into two datasets with each dataset containing ECG data from 22 recordings with the same approximate proportion of beat types. Both datasets contain a mixture of the routine and complex arrhythmia.

Dataset in this study comprises data from recordings 100, 103, 105, 111, 113, 117, 121, 123, 200, 202, 210, 212, 213, 214, 219, 221, 222, 228, 231, 232, 233, 234. The available data was used as training and testing data. Training stage containing the data from 22 records and then we test classifier for each record. To determine the classification performance of our method, on next step each record (LVQ) and ten test sets (SVM) was processed as testing data.

6.1. Evaluation of results

Table 2 shows classification performance using LVQ and SVM classifier respectively. Some interesting trends emerge from these results. The results shows that the classification performance for PV (premature ventricular contraction - PVC) preprocessed by hybrid wavelet-MM filter are notably higher than the same resulting without wavelet compression stage. Specifically, accurate detection of premature ventricular contractions (PVCs) is imperative to prepare for the possible onset of lifethreatening arrhythmias.

According to AAMI recommendations classes, we see that also aggregate classification performance for normal beats (NL, LB, RB, AE, NE) from any others heartbeat may be very high performance with this method for both classifier (LVQ and SVM).

Classification performance of MIT-BIH heartbeat type each recording using the LVQ and SVM algorithms on MM preprocessed and MM+WT preprocessed ECG data, (better results in gray).

Performance [%]	MIT-BIH Arrhythmia Database heartbeat types												
	NL	AP	NQ	PV	PB	LB	AA	FS	VE	RB	AE	NE	NP
total beats	9175	432	306	788	3	1021	8	106	1	881	35	43	12
w/o preproc.	95,99	86,34	92,81	80,71	0,00	49,56	0,00	56,60	0,00	87,63	97,14	58,14	16,67
only 1st MM (LVQ)	96,70	85,90	97,70	92,80	0,00	97,40	0,00	78,30	0,00	95,00	94,30	44,20	16,70
and 2nd MM (LVQ)	93,65	82,87	90,85	81,47	0,00	51,32	0,00	70,75	0,00	94,10	97,14	39,53	0,00
and 2nd WT[1] (LVQ)	97.20	79.86	42.16	85.41	0,00	92,65	0,00	69.81	0,00	87.74	91.43	41.86	0,00
and 2nd WT[2] (LVQ)	94.87	85.88	93.46	88.32	0,00	51.03	0,00	70.75	0,00	85.81	97,14	69.77	0,00
only 1st MM (SVM)	96,70	85,90	97,70	92,80	0,00	97,40	0,00	78,30	0,00	95,00	94,30	44,20	16,70
and 2nd MM (SVM)	94.87	85.88	93.46	88.32	0,00	51.03	0,00	70.75	0,00	85.81	97,14	69.77	0,00
and 2nd WT (SVM)	89.17	85.65	90.20	82.11	0,00	51,22	12.50	66.04	0,00	86.04	97,14	37.21	0,00

For our experiments, we choose Deubechies wavelets (Table 2, db2 as WT[1] and db6 as WT[2]). The meaning of the labels in Table 2 are as follow:

- w/o preproc - without preprocessing,
- only 1st (MM) - only with MM denoising, baseline drift removal,
- and 2nd (MM) - MM denoising, baseline drift removal (1st stage) and additional MM filtering block (2nd stage),
- and 2nd (WT) - MM denoising, baseline drift removal (1st stage) and additional wavelet transformation (2nd stage).

6.2. Comparison with other works

Reporting performance results of cardiac rhythm algorithms has been standardized by the Association for the Advancement of Medical Instrumentation (AAMI) [20]. However, despite the existence of this standard very few studies have reported performance results in own format.

Due to memory limitation of SMO implementation of SVM algorithm we have used dataset containing 12811 ECG beats from MIT-BIH Arrhythmia Database for learning and testing. In the numerical experiments we have used ECG data of 13 heart rhythm types corresponding to the normal sinus rhythm (N) and 12 types of arrhythmias.

Chazal *et al.* [2] achieved a 97.4% accuracy in separating VEBs from non-VEBs (Table I) and 94.6% accuracy in separating SVEBs from non-SVEBs, used the same 22 records but the heartbeat P-QRS-T points times (e.g. QRS onset and offset and T-wave offset times; a boolean value indicating the presence/absence of

a P-wave and, if present, the P-wave onset and offset) provided with the MIT-BIH were manually verified.

Lagerholm *et al.* [23] described a method for clustering ECG heartbeats from a recording into 25 clusters and determined that on average 98.5% of the heartbeats in any one cluster were from the same heartbeat class. However Lagerholm's system used 25 clusters, and need annotating of the dominant beat of a cluster by an expert before the classification of a cluster can be made to one of 16 types of MIT-BIH beat types.

Osowski *et al.* [28] achieved a 95.9% sensitivity in separating the same 13 heart rhythm types like ours. Despite that beats come from 52 patients of the database as a result of such strategy for data selection, we don't know how the records were subdivide. The total number of data used in learning neural networks was equal 6690 and 6095 data points have been left for testing. According to [28] 12785 beats used in learning and testing.

Table 3

Classification performance of MIT-BIH heartbeat type each recording using the LVQ and SVM algorithms on MM preprocessed and MM+WT preprocessed ECG data, (better results in gray).

Method	Perf. [%]	No. of classes	Descriptions
Present work (only MM)	95,53	13	used the same 22 from MIT-BIH, 12811 ECG beats for
Present work (MM / WT)	97,82	13	training and cross-testing
Chazal *et al.* [1] V-nV	97,40	2	used the same 22 records but the heartbeat P-QRS-T
Chazal *et al.* [1] SV-nSV	94,60	2	points times provided with the MIT-BIH were manually verified
Lagerholm *et al.* [2]	98,50	25	used 25 clusters, but need annotating of the dominant beat of a cluster by an expert before the classification of a cluster can be made to one of 16 types of MIT-BIH beat types
Osowski *et al.* [3]	95,90	13	12785 beats used in learning and testing, come from 52 patients – but don't know strategy for data selection

Additionally feature vectors for all these approaches was totally different: characteristic P-QRS-T points times, Hermite functions coefficients and resampled P-QRS-T ECG morphology window.

7. Conclusions

Results showed that the proposed hybrid algorithm leads to an improvement in the heartbeat classification using MIT-BIH arrhythmia database, especially good recognition rates have been achieved for those beats, for which the large number of cases were available in the database. The efforts to improve the performance of the algorithm and to investigate its effects on the subject are currently continuing.

The experiment results show that using mathematical morphology and wavelet model together can result in high accuracy of classification. This confirms that a highly reliable classifier can be obtained by combining a number of classifiers.
A more comprehensive study is necessary to assess the utility of this method. This is our preliminary work for applying hybrid wavelet-MM filtering to ECG data for normalization patient-specific features.

The future research will be oriented on the improvement of the performance of the presented algorithm, e.g. build more suitable feature vector containing RR-interval features, heartbeat interval features and ECG morphology features and training and testing on all records from MIT-BIH database.

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DODATKOWE PRZETWARZANIE WSTĘPNE I EKSTRAKCJA CECH W PROCESIE AUTOMATYCZNEJ KLASYFIKACJI RYTMU SERCA

Streszczenie: Artykuł prezentuje nowe podejście do problemu klasyfikacji zapisów ECG w celu detekcji zachowań chorobowych. Podstawą koncepcji fazy ekstrakcji cech jest proces przetwarzania wstępnego sygnału ECG z wykorzystaniem morfologii matema-

tycznej oraz innych transformacji. Morfologia matematyczna bazując na teorii zbiorów, pozwala zmienić charakterystyczne elementy sygnału. Dwie podstawowe operacje: dylatacja i erozja pozwalają na uwydatnienie lub redukcję wielkości i kształtu określonych elementów w danych. Parametry charakterystyki zapisów ECG stanowią bazę dla wektora cech. Do klasyfikacji przebiegów ECG w pracy wykorzystano samoorganizujące się mapy (SOM) Kohonena z klasyfikatorem LVQ oraz algorytm Support Vector Machines (SVM). Eksperymenty przeprowadzono klasyfikując sygnały pomiędzy trzynaście kategorii rekomendowanych przez standard ANSI/AAMI EC57, to jest: prawidłowy rytm serca i 12 arytmii. Zaproponowany w artykule algorytm opiera się na wykorzystaniu elementarnych operacji morfologii matematycznej i ich kombinacji. Ocenę wyników eksperymentów przeprowadzono na sygnałach z bazy MIT/BIH. Na tej podstawie zaproponowano wyjściową architekturę bloku filtrów morfologicznych dla celów ekstrakcji cech oraz unifikacji wejściowego sygnału ECG jako danych wejściowych do budowy wektora cech.

Słowa kluczowe: ECG, przetwarzanie wstępne, morfologia matematyczna, filtrowanie ECG, ekstrakcja cech, klasyfikacja rytmu serca