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Novel genetic ensembles of classifiers applied to myocardium dysfunction recognition based on ECG signals

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ABSTRACT

This article presents an innovative genetic ensembles of classifiers applied to classification of cardiac disorders (17 classes) based on electrocardiography (ECG) signal analysis.
From a social point of view, it is extremely important to prevent heart diseases, which are the most common cause of death worldwide. According to statistical data, 50 million people are at risk for cardiac diseases worldwide.
This research collected 744 fragments of ECG signals from the MIT-BIH Arrhythmia database for one lead, MLII, from 29 patients. Novel methodology that consisted of the analysis of longer (10-s) fragments of the ECG signal was used (an average of 13 times less classifications). To enhance the characteristic features of the ECG signal, the power spectral density was estimated (using Welchs method and a discrete Fourier transform). In research designed two genetic ensembles of classifiers optimized: by classes and by sets, based on: SVM classifier, 10-fold cross-validation method, ensemble learning, layered learning, genetic selection of features (frequency components), genetic optimization of classifiers parameters and novel genetic training (selection of experts votes) used to combining classifiers.
The best genetic ensemble of classifiers optimized by sets, obtained a classification sensitivity of 17 heart disorders (classes) at a level of 91.40% (64 errors per 744 classifications, accuracy = 98.99%, specificity = 99.46%, time for classification of one sample = 0.0186 [s]). Against the background of the current scientific literature, these results represent some of the best results obtained.

1. Introduction

Diagnosing heart conditions by analyzing electrocardiography (ECG) signals has been popular for many years and is the basic method used in the prevention of cardiovascular diseases. The wide range of application of ECG signal analysis is due to the fact that it is a simple and non-invasive method that provides substantial valuable information about the function of the circulatory system.

Currently, we observe a very high incidence of cardiovascular disease and the very high mortality caused by them. Despite the preventive measures taken, cardiovascular diseases are the leading cause of death worldwide (17.3 million people per year, accounting for 37% of all deaths [1–3]) and the most serious and costly health problems facing the world today [4,5]. Circulatory system diseases are usually chronic diseases that require long-term and expensive treatment. The tendency for the incidence of cardiovascular diseases will increasingly intensify due to the progressive aging of the population (the number of deaths will increase from 17.3 million in 2016 to 23.6 million in 2030 [1–3,6]).

The classification of cardiac disorders based on existing methods based on the calculation of morphological and dynamic features of individual QRS complexes (heart evolution; combination of three of the graphical deflections seen on a typical electrocardiogram) is difficult and error prone due to the variability of these features in different patients [7]. For this reason, solutions currently described in the scientific literature do not achieve a satisfactory efficiency [8].

This is why it is very important to develop specialized software supporting medical diagnostics to more effectively identify myocardium dysfunctions earlier and monitor the conditions of patients in real time. The reduction in computational complexity is also an important aspect in the context of deploying the solution in mobile devices.

In the research was applied a novel methodology [9] characterized by: 1) analysis of longer, 10-s (time period corresponding to a standard clinical ECG examination performed by a cardiologist) ECG signal fragments (as opposed to QRS complex classification), which contain

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multiple heart evolutions, 2) applied feature extraction based on power spectral density estimation using Welchs method and a discrete Fourier transform, 3) applied genetic selection of features (frequency components), 4) not applying the QRS complex detection and segmentation of the ECG signal, and 5) not applying signal filtering.

By analyzing longer (10-s) fragments of ECG signals, the number of classifications has been reduced (an average of 13 times less classification, assuming that heart rate is 80 beats per minute), and eliminating the need for detection and segmentation of QRS complexes, which reduces the computational complexity and opens the possibility to use the solution in practice, in mobile devices. Also analyzing longer ECG signal fragments give better results for recognition some disorders (e.g. pre-excitation syndromes (e.g., Wolff-Parkinson-White syndrome - WPW), atrio-ventricular and atrial-sinus conduction blocks, and elongate PQ intervals) [9].

Ensembles of classifiers are a very popular tool recently [10–15], used to improve obtained results. Ensembles of classifiers are a hybrid that combines the advantages of all component classifiers and minimizing their disadvantages and the effect of over-fitting. With this approach, we can increase the efficiency of the entire ensemble compared to individual component classifiers. The increasing capabilities of computers also allow development of increasingly complex systems. The field of ensemble learning is developing very dynamically. In view of this fact, there are a huge number of methods described in the literature: [10,16–22].

The methods for creating ensemble of classifiers include: 1) applying different subsets with training data for the same classifier, 2) applying different parameters to create models for the same classifier, 3) applying different classifiers, and 4) introduction of randomness in learning process. The methods of combining ensemble of classifiers include: 1) classifiers fusion or mixture of experts, 2) classifier selection, and 3) cascade classifiers or multi-stage classifiers. All of the methodologies described above assume that the classifiers group achieve a better result than the single classifier [10,23–25]. In many cases single classifiers give results that are deterministic but also unstable (modification of the training set, generates significant different models). By combining different models generated from different training sets, we can get a significant increase in the correct classifications [26]. Ensembles can consist of the same classifiers (e.g. Bagging and Boosting methods) or ensembles can combine many different classifiers using the strengths of each. Ensembles are classifier packages that make decisions. Rules of classifiers fusion can be divided into: 1) algebraic, 2) voting, 3) probability of belonging, 4) classifier competence, 5) meta-classifiers. It is important to select component classifiers (ensemble members). It is worth paying attention to three basic assumptions: 1) statistical independence (diversity), 2) efficiency (speed), 3) quality. All of these assumptions are difficult to meet. In practice, the greatest attention should be paid to the statistical independence, and secondly to the quality [26]. In addition to the advantages offered by the ensembles of classifiers in terms of greater stability and greater recognition efficiency, their use is burdened with the disadvantage of a much higher computational complexity.

The most popular ensembles of classifiers can include: 1) Bagging (Bootstrap aggregation) [27,28], 2) Boosting/AdaBoost [29,30], 3) Random Forest [27], 4) Stacked Generalization (Stacking) [31] and 5) Mixtures of Experts [32]. In the field of heart disorders recognition, ensembles of classifiers are also popular and used with success: [33–37], Mixture of experts [38], Negatively Correlated Learning [38], Bagging [39]. An effective and popular tool for optimizing ensembles of classifiers is the genetic algorithm (GA) [40–42] belonging to the family of evolutionary algorithms [43].

The inspiration to undertake research on evolutionary computation (EC) [44] was the imitation of nature in its mechanism of natural selection, inheritance and functioning. Evolutionary computation are used to teach and solve complex tasks, mainly for optimization. It is taught based on species, not on an individuals, that goes through the life of many generations of individuals. As a result, generations of solutions are generated that increasingly meet the conditions of the task (they have better adaptation to the environment).

The Evolutionary Computation (EC) [44] include Evolutionary Algorithms (EA) [43], which include: 1) Genetic Algorithm (GA) [40], 2) Genetic Programming (GP) [45], 3) Evolutionary Programming (EP) [46], 4) Evolution Strategy (ES) [47], 5) Differential Evolution (DE) [48–51], and 6) Learning Classifier System (LCS) [52,53] etc. Related techniques, also belonging to EC, are: 7) Ant Colony Optimization (ACO) [54], 8) Artificial Bee Colony algorithm (ABC) [55], 9) Particle Swarm Optimization (PSO) [56], 10) Artificial Immune Systems (AIS) [57], 11) Self-organization (e.g. self-organizing maps [58]) and, 12) Swarm Intelligence (SI) [59].

It is also worth mentioning the combination of evolutionary computation with ensemble methods. Examples of such hybrid systems can be found in the literature: 1) DE algorithm with ensemble of parameters or mutation strategies [60–63], 2) data and model based ensemble [64], 3) micro genetic algorithm [65], 4) coevolution algorithms [66], 5) parallel genetic algorithms [67], 6) GA with ensemble method [68], 7) ABC with stacking ensemble [69].

Evolutionary computation are used with success in the field of heart disorders classification: Genetic Algorithm (GA) [70–76], Particle Swarm Optimization (PSO) [77–83], Artificial Immune Systems (AIS) [84], Artificial Bee Colony algorithm (ABC) [85], and Ant Colony Optimization (ACO) [86].

1.1. Aims

The main aims of the research were the following:

Aim 1 Develop new and effective ensembles of classifiers for the automatic recognition of myocardium dysfunctions based on ECG signals.

Aim 2 Design algorithms for use in tele-medicine and mobile devices for patient self-control and prevention applications (low computational complexity).

Aim 3 Design universal algorithms not for individuals but for the general population.

1.2. Novelty

Based on a literature review e.g. Refs. [8,87,88], it can be stated that the innovative elements of this research include the following:

Genetic ensembles of classifiers – based on: SVM classifier, 10-fold cross-validation method, ensemble learning, layered learning, genetic selection of features (frequency components), genetic optimization of classifiers parameters and novel genetic training (selection of experts votes) used to combining classifiers:

optimized by classes (GECC) – designed a two-layer ensemble of classifiers, consisting of: 17 SVM classifiers (nu-SVC, corresponding to 17 classes) + 1 SVM classifier (C-SVC), and

optimized by sets (GECS) – designed a two-layer ensemble of classifiers, consisting of: 10 SVM classifiers (nu-SVC, corresponding to 10 combinations of training and test sets) + 1 SVM classifier (C-SVC), modified *Bagging* method.

2. Materials and methods

2.1. Assumptions

The adopted research methodology consisted of the following assumptions:

Table 1
A description of the database with the selected ECG signals along with the allocation of signals to the training and test sets for 10-fold cross-validation method.

No.	Class	Fragments number	Patients number	10-fold cross-validation			
				Groups 1–9		Group 10	
				Training set	Test set	Training set	Test set
1	Normal sinus rhythm	193	14	174	19	171	22
2	Atrial premature beat	58	8	53	5	45	13
3	Atrial flutter	17	2	16	1	9	8
4	Atrial fibrillation	93	3	84	9	81	12
5	Supraventricular tachyarrhythmia	11	3	10	1	9	2
6	Pre-excitation (WPW)	21	1	19	2	18	3
7	Premature ventricular contraction	78	9	71	7	63	15
8	Ventricular bigeminy	44	4	40	4	36	8
9	Ventricular trigeminy	13	4	12	1	9	4
10	Ventricular tachycardia	10	3	9	1	9	1
11	Idioventricular rhythm	10	1	9	1	9	1
12	Ventricular flutter	10	1	9	1	9	1
13	Fusion of ventricular and normal beat	11	3	10	1	9	2
14	Left bundle branch block beat	88	2	80	8	72	16
15	Right bundle branch block beat	47	2	43	4	36	11
16	Second-degree heart block	10	1	9	1	9	1
17	Pacemaker rhythm	30	1	27	3	27	3
	Sum	744	29	675	69	621	123

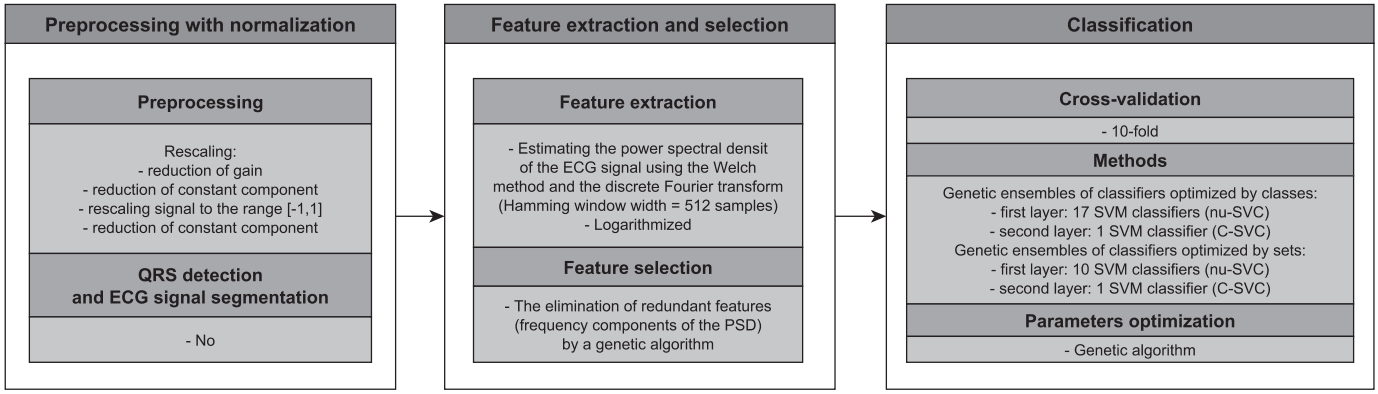

Fig. 1. Subsequent stages of processing and analysis of the ECG signals.

A1 Analysis of longer (10-s) ECG signal fragments, which contain multiple heart evolutions.
A2 Not applying signal filtering due to both the use of Welch's method and the genetic selection of features.
A3 Not applying the QRS complex detection and segmentation of the ECG signal.
A4 Analyzing ECG signal fragments that contain one class type (except of normal sinus rhythm).
A5 Applying a 10-fold cross-validation method that is more consistent with the subject-oriented validation scheme (inter-patient paradigm; the selection of elements for training and test sets based on signals from other patients) than class-oriented validation scheme (intra-patient paradigm) [8,89,90].
A6 The classification of the samples was based on the Winner-Takes-All (WTA) rule.

2.2. Materials

2.2.1. ECG database

For research purposes, the ECG signals were obtained from the PhysioNet [91] service from the MIT-BIH Arrhythmia [92] database. The created database with ECG signals is described below.

- The ECG signals were from 29 patients.
- The ECG signals contained 17 classes: normal sinus rhythm, pacemaker rhythm, and 15 types of cardiac dysfunctions (for each of which at least 10 signal fragments were collected).
- All ECG signals were recorded at a sampling frequency of 360 [Hz] and a gain of 200 [adu/mV].
- For the analysis, 744, 10-s (3600 samples) fragments of the ECG signal (not overlapping) were randomly selected.
- Only signals derived from one lead, the MLII, were used.

A description of the collected signals is given in Table 1, which presents the analyzed heart disorders, number of signal fragments collected for each disorder, number of patients from whom the ECG data were derived, and division of signal fragments into training and test sets for 10-fold cross-validation method.

An important aspect is the appropriate balance of data. In the research used a proportional number of ECG signal fragments for each class (from 1.34% to 25.94%, Table 1), which prevents the over-fitting effect and do not artificial increase the recognition efficiency.

Obtaining a greater number of suitable ECG signal fragments, from greater number of patients, for the rarest disorders (10 or 11 ECG signal fragments in Table 1) from the MIT-BIH Arrhythmia database for the MLII lead was not possible.

Table 2
Detailed information about genetic ensembles of classifiers optimized by classes or sets. All data are given in a sequence order: first, for GECC method, and then for GECS method.

Feature selection and classifier parameters optimization

The *genetic algorithm* coupled with the 10-fold cross-validation method was used for feature selection and classifier parameters optimization

GENETIC ALGORITHM

- Number of individuals in the population: 50 in first layer and 200 in second layer;
- Type of gene representation: floating-point vectors in first layer and string of bits in second layer;
- Chromosome construction of individual: In first layer: floating point vector of the form: $[g_1, g_2, f_1, \ldots, f_{4001}]$ for *SVM*, where g_1 – the first gene, which determines the value of the first parameter, γ $(-g)$, g_2 – the second gene, which determines the value of the second parameter, ν $(-n)$, and $f_1, \ldots, f_{4001}$ – 4001 genes, with values in the range of $[0, 1]$, which determine the feature selection, rounded to the values 1 – acceptance of a feature – or 0 – rejection of a feature; In second layer: bits vector of the form: $[f_1, \ldots, f_{289 \vee 170}]$, consisting of 289 or 170 genes, with values from the set: $\{0, 1\}$, where: 1 – acceptance of a feature – or 0 – rejection of a feature.
- Initial population: random, uniform;
- Range of the gene values for the initial population: In first layer: the local range of gene values for each classifier parameter, consistent with the information given in the line *Optimized parameters*, experimentally selected based on the global (broader) range. For feature selection, the range is $[0, 1]$; In second layer: from the set: $\{0, 1\}$;
- Target value of fitness function: 0;
- Maximum number of generations: 30 in first layer and 100 in second layer;
- Type of crossover: intermediate in first layer and scattered in second layer; Probability of crossover: 0.7 in first layer and 0.9 in second layer;
- Type of mutation: uniform; Probability of mutation: 0.3 in first layer and 0.1 in second layer;
- Number of individuals in the current generation that are guaranteed to survive to the next generation: 3 in first layer and 10 in second layer;
- Method of scaling the value of the fitness function: ranking;
- Method of parent selection: tournament;
- Fitness function of individuals calculated based on the following formulas:

  First layer:

  $$ERR_{1L} = w_l \cdot (w_z \cdot err_{LZsum} + err_{Lsum}) + w_t \cdot (w_z \cdot err_{TZsum} + err_{Tsum}) + w_f \cdot \frac{F_a}{F} \quad (1)$$

  Second layer:

  $$ERR_{2L} = w_l \cdot err_{Lsum} + w_t \cdot err_{Tsum} + w_f \cdot \frac{F_a}{F} \quad (2)$$

  where:
  $w_l = 1$ – weight for errors from the training set;
  $w_t = 1$ – weight for errors from the test sets;
  $w_f = 1$ – weight for acceptance feature coefficient;
  $w_z = 100$ – weight for priority class, for a given classifier, for GECC, or weight for the priority combination of sets, for GECS;
  err_{LZsum} – number of incorrect classifications only for priority class Z, for a given classifier, in 10 training sets, for GECC, or number of incorrect classifications only in priority training set Z, for a given classifier, for GECS;
  err_{Lsum} – total number of errors, for all classes, except for class Z, in 10 training sets, for GECC, or total number of errors, in 9 training sets, except training set Z, for GECS;
  err_{TZsum} – number of incorrect classifications only for priority class Z, for a given classifier, in 10 test sets, for GECC, or number of incorrect classifications only in priority test set Z, for a given classifier, for GECS;
  err_{Tsum} – total number of errors, for all classes, except for class Z, in 10 test sets, for GECC, or total number of errors, in 9 test sets, except test set Z, for GECS;
  $\frac{F_a}{F}$ – acceptance feature coefficient: the ratio of the number of acceptance features, F_a, to the total number of features, F;
- As a result of the feature selection, the length of the feature vector was on average reduced twice in first layer to approximately 2000 of 4001 features (frequency components of the ECG signal) and over 13-fold to value: 22 of 289 features, or over 4-fold to value: 38 of 170 features in second layer - Tables 4 and 5;

Classifiers

In first layer: 17 trained, tested and optimized classifiers:
In second layer: 1 trained, tested and optimized classifier:

Basic parameters

SVM

- Type: nu-SVC in first layer and C-SVC in second layer;
- Kernel function type: RBF (radial, Gaussian type) in first layer and linear in second layer;
- Number of outputs: 17, from the set: $\{0, 1\}$ in first layer and 1, from the set: $1, \ldots, 17$ in second layer;

Optimized parameters

Only for first layer, the final parameter ranges were selected experimentally based on a broader range

SVM

- The parameter γ $(-g)$ determines the spread of the radial basis function (RBF) of the kernel from the range $[2 \cdot 10^{-6}; 2 \cdot 10^{-4}]$, with resolution 10^{-14}, $50 \cdot 30 = 1500$ values;
- The parameter ν $(-n)$ determines the width of the margins from the range $[0.001; 0.05]$, with resolution 10^{-14}, $50 \cdot 30 = 1500$ values;

Table 3
A comparison of the obtained results. In all training sets, in all cases, the sum of the errors equals zero.

	Methods								
	Single Classifiers				Ensembles of Classifiers				
	kNN	RBFNN	PNN	SVM	RF	EP	CEC	GECC	GECS
Learner	*kNN*	*RBFNN*	*PNN*	*SVM nu – SVC*	*DT*	*SVM epsilon – SVR*	*SVM nu – SVC*	*SVM nu – SVC*	*SVM nu – SVC*
ERR_{sum}	**79**	**79**	**77**	**73**	**117**	**91**	**75**	**65**	**64**
ACC	98.75%	98.75%	98.78%	98.85%	98.15%	98.56%	98.81%	98.97%	98.99%
SEN	**89.38%**	**89.38%**	**89.65%**	**90.19%**	**84.27%**	**87.77%**	**89.92%**	**91.26%**	**91.40%**
SPE	99.34%	99.34%	99.35%	99.39%	99.02%	99.24%	99.37%	99.45%	99.46%
κ	**87.84%**	**87.84%**	**88.14%**	**88.70%**	**81.75%**	**85.94%**	**88.38%**	**89.95%**	**90.10%**
C_F	78.26%	47.86%	49.51%	49.09%	49.74%	–	48.84%	46.63%	46.44%
T_t [s]	0.1432	54.0503	0.3316	11.3537	43.1289	461.2191	115.8115	207.3403	115.8450
T_c [s]	**0.0853**	**0.0077**	**0.0055**	**0.0018**	**0.0016**	**0.0750**	**0.0186**	**0.0321**	**0.0186**

2.3. Methods

As part of the research, were tested many methods used for the subsequent stages of processing and analysis of ECG signals. Because of space limitation, they have not been described in detail. The most effective path (combination of methods) shown in Fig. 1 was selected based on obtained results for tested methods. The criteria for selecting the best methods were: 1) the sum of errors in all classifications, and 2) the sensitivity (SEN) coefficient 2.5. Based on them, the best methods (with the best obtained results) were selected.

The methods used in the subsequent steps of processing and analysis of the ECG signals:

Stage I – Preprocessing with normalization – Applied reduction of gain and reduction of constant component, and three normalization types were tested: 1) no normalization, 2) rescaling signal to the range [−1,1] and 3) signal standardization (mean signal value = 0 and signal standard deviation = 1). The best results was obtained for **rescaling.**

Stage II – Feature extraction – Based on the estimation of the power spectral density (PSD) [93] of the ECG signal was performed using the Welsh method [94] and the discrete Fourier transform (DFT) [93]. Then, to normalize the frequency components of the power spectral density, the transformed signal was logarithmized. This solution has strengthen the features (frequency components of the power spectral density of the ECG signal). To calculate the power spectral density, 4 Hamming window widths: 128, 256, 512 and 1024 samples were applied. The best results was obtained for **Hamming window with equal to 512 samples.** From a single fragment of ECG signal, a feature vector with a length of 4001 frequency components was obtained. To estimate the power spectral density, the following parameters were used: the number of common samples for 2 adjacent signal fragments equal to half of the width of the adopted Hamming window and a DFT vector length equal to 8000 as well as a sampling frequency equal to 360 [Hz].

Stage III – Feature selection – Were tested three methods: 1) no selection, 2) genetic selection and 3) particle swarm optimization (PSO [56]) selection. The best result was obtained for **genetic selection.** A genetic algorithm (GA) [44,95] was used for the feature selection (frequency components of the ECG signal). The genes in the population of individuals represented subsequent single features/attributes of the signal entered as input for the classifiers. Genes could take on the following values: 0 – reject a given feature or 1 – accept a given feature. GA parameters were presented in Table 2.

Stage IV – Cross-validation – Were tested two methods: 4-fold and 10-fold cross-validation (CV) [10]. The best results obtained for **10-fold CV method**: a total of 10 combinations of training and test sets. The test sets for the first nine groups were created by 9-fold selection of every tenth element, for each class (disorder), from the entire signal base. The test set for the tenth group was created from the remaining elements. The training sets consisted of elements that complemented the test sets for the entire signal base. Division of signal fragments into training and test sets is presented in Table 1.

Stage V – Machine learning algorithms – The following methods were tested: Probabilistic Neural Network (PNN [96]), Radial Basis Function Neural Network (RBFNN [97]), Support Vector Machine (SVM [98,99,119,120], type: nu-SVC, epsilon-SVR and nu-SVR with RBF kernel function), k-Nearest Neighbor (kNN [100]), Decision Trees (DT) [101], Discriminant Analysis [102], The Takagi-Sugeno Fuzzy System [103], Multi-Layer Perceptron and Recurrent Neural Networks [104]. The best result was obtained for **SVM classifier (nu-SVC).** The article presents the results for the best 4 classifiers, respectively: SVM (nu-SVC), PNN, RBFNN, and kNN (Table 3). SVM parameters were presented in Table 2.

Stage VI – Parameter optimization – Three methods were tested: 1) Grid search, 2) Genetic Algorithm and 3) Particle Swarm Optimization. The best result was obtained for **Genetic Algorithm.** GA parameters were presented in Table 2.

2.3.1. Evolutionary-neural system

In the research, for single classifiers, the best results were obtained for the evolutionary-neural system based on the SVM classifier. For this reason, the SVM classifier has been used in further research concerning ensemble of classifiers. An evolutionary-neural system consisted of a classifier (e.g., SVM) optimized by a genetic algorithm. The genetic algorithm coupled with a 10-fold cross-validation was used to select signal features and optimize the parameters of the classifier.

2.3.2. Classical ensembles of classifiers (CEC)

Two-layered ensemble of classifiers (*Bagging* type): the first layer contains 10 SVM classifiers (nu-SVC, RBF kernel function), each with optimized parameters under one of the 10 combination of sets: training and test (from 10-fold cross-validation). Connected, in the second layer, using the majority voting method. Parameters of component classifiers (SVMs) of the ensemble, were selected using a genetic algorithm.

2.3.3. Random Forest (RF)

The popular method of combining classifiers, proposed by Breiman [27]. In this method the component classifiers of the ensemble are decision trees, connected by bootstrap aggregating technique. Optimized by GA parameters were: 1) number of trees and 2) minimum number of observations per tree leaf.

2.3.4. Ensemble of predictors (EP)

Two-layered ensemble of predictors: the first layer contains 17 SVM classifiers (epsilon-SVC, RBF kernel function), each with optimized

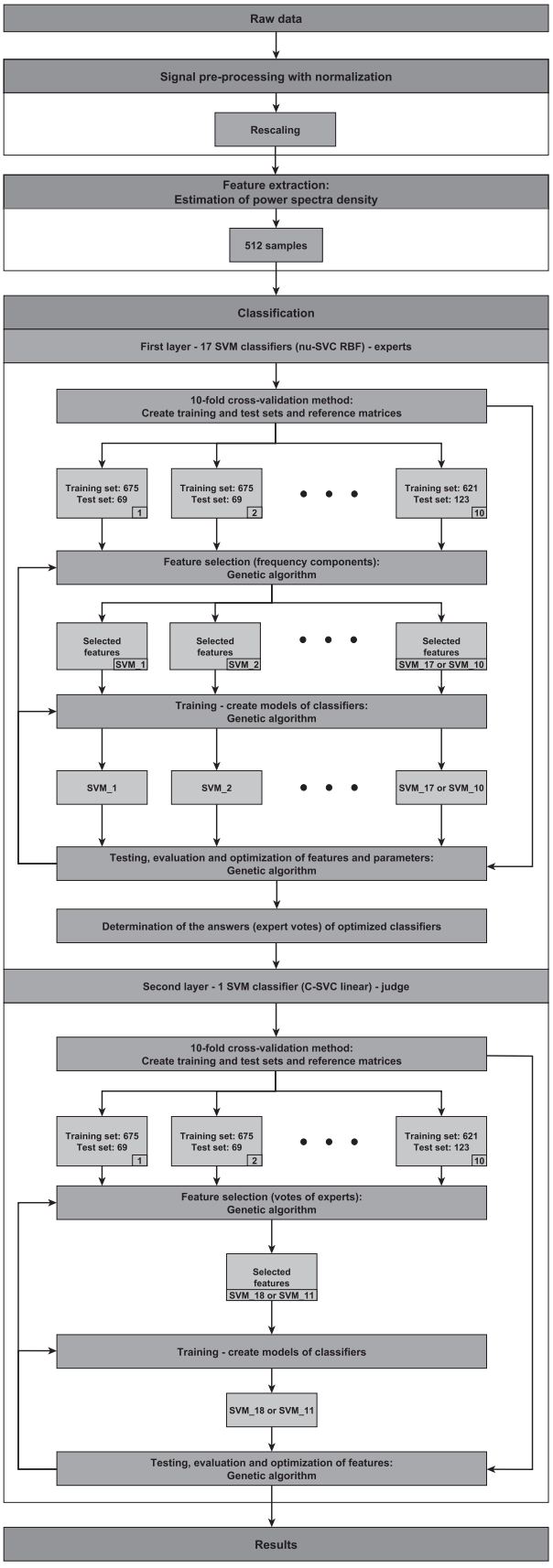

Fig. 2. Scheme of *Genetic ensemble of classifiers optimized by classes or sets*.

Algorithm 1: Procedure of Genetic ensembles of classifiers optimized by classes or sets.

Data:
X – matrix with raw data;
W – matrix with reference responses;
Result:
B – vector, with associated values of the fitness function; the determined optimal parameters; and the selected features;
CF – confusion matrix with the classifier responses of the SVM;
E – vector with the calculated evaluation coefficients of the SVM;

```
Perform signal pre-processing with normalization based on X
Perform feature extraction
Create training and test sets and reference matrices based on W and 10-fold CV method   /* First layer */
Set genetic algorithm parameters (Table No. 2)
for z ← 1 to 17 or 10 (number of classes or sets) do
    Create an initial population of individuals   /* Begin of GA */
    for i ← 1 to 30 (number of generations) do
        for j ← 1 to 50 (number of individuals) do
            Perform feature selection
            Save the value of the basic and optimized parameters of the SVM classifier.
            for k ← 1 to 10 (number of sets) do
                Create the model of the SVM classifier
                Determine the SVM classifier responses
                Determine the number of errors
            end
            Calculate the sum of the errors for the training and test sets
            Determine the value of the fitness function (f_p)
            Save the related values B_1L for the fitness function (f_p), classifier parameters and selected features as well as the matrices with classifier responses: R_L and R_T
        end
        if f_p == 0 then
            Lead out the "best" individual with the corresponding response matrices
            break
        else
            Perform the selection of individuals
            Apply the genetic operators: crossover and mutation
            Create a new population of individuals
        end
    end   /* End of GA */
    Lead out the "best" individual with the corresponding response matrices
    Create the confusion matrix CF_1L
    Calculate the evaluation coefficients E_1L for the SVM classifier
end
Transform 1-output responses: R_L and R_T (17 or 10 classifiers) on 17-output responses: R_17   /* Second layer */
Create training and test sets based on R_17 and 10-fold CV method
Set the value of the basic parameters of the SVM classifier.
Set genetic algorithm parameters (Table No. 2)
Create an initial population of individuals   /* Begin of GA */
for i ← 1 to 100 (number of generations) do
    for j ← 1 to 200 (number of individuals) do
        Perform feature selection
        for k ← 1 to 10 (number of sets) do
            Create the model of the SVM classifier
            Determine the SVM classifier responses
            Determine the number of errors
        end
        Calculate the sum of the errors for the training and test sets
        Determine the value of the fitness function (f_p)
        Save the related values B for the fitness function (f_p) and selected features as well as the matrices with classifier responses: R_L and R_T
    end
    if f_p == 0 then
        Lead out the "best" individual with the corresponding response matrices
        break
    else
        Perform the selection of individuals
        Apply the genetic operators: crossover and mutation
        Create a new population of individuals
    end
end   /* End of GA */
Lead out the "best" individual with the corresponding response matrices
Create the confusion matrix CF
Calculate the evaluation coefficients E for the SVM classifier
```

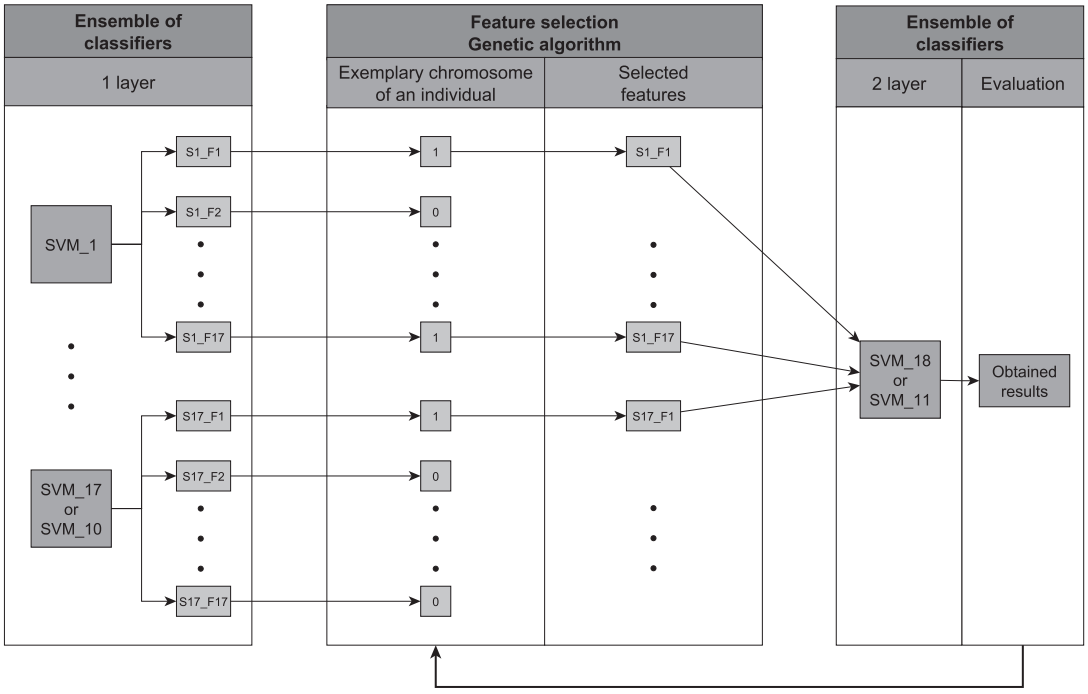

Fig. 3. Scheme of genetic training (feature selection by GA) used to combining classifiers for exemplary chromosome of individual and a single fragment of ECG signal.

parameters under one of the 17 disorders/classes. Connected, in the second layer, using one SVM (nu-SVC, RBF kernel function) classifier. The final decision is taken on the based of the responses of the input classifiers and the decision threshold. Parameters of component predictors (SVMs) of the ensemble, were selected using a genetic algorithm. Ensemble realizing the conversion: 1 output (with two values: priority class or the rest of the class) to 17 outputs. Only in this method not applied feature selection.

2.4. Genetic ensembles of classifiers

Genetic ensembles of classifiers are two-layered systems (modified *Stacking* method) based on: SVM classifier, 10-fold cross-validation method, ensemble learning, layered learning, genetic selection of features (frequency components), genetic optimization of classifiers parameters and genetic training (selection of experts votes) used to combining classifiers.

2.4.1. Philosophy

Name

- **Genetic** – because in this experiment an important role was played the **genetic algorithm**: applied in the first layer for feature **selection** (frequency components of ECG signals) and parameters **optimization** of 17 or 10 classifiers. In the second layer, the genetic algorithm was used for the innovative **genetic training** applied to tuning the ensemble of classifiers structure. Genetic training based on the feature selection, consisting in the elimination of incorrect responses of "experts" (classifiers of the first layer).
- **Ensemble of classifiers** – because the designed systems consisted of **18 or 11 classifiers** arranged in two layers. The ensemble of classifiers used **layered learning**, i.e., first applied supervised training for 17 or 10 classifiers from the first layer. Then, based on the responses obtained from 17 or 10 models of classifiers, created in the first layer, the supervised genetic training of one meta-classifier from the second layer was performed.

  Cross-validation – the genetic algorithm was coupled with 10-fold cross-validation (in the first and second layer of the ensemble of classifiers), which meant that each individual in the population (feature vector) was tested on all 10 training and test sets. This approach minimizes the effect of over-fitting.

First layer

- **Optimization** – was performed using a genetic algorithm (Table 2), which simultaneously selecting the input features and optimizing the parameters of the classifiers.
- **Votes** - each classifier (*expert*) have 17 outputs, where occur only one value "*1*" (according to the *WTA* rule), indicating the class recognized by the classifier (*expert*), and on the remaining 16 outputs, occur values "*0*" (indicating the classes not recognized).

Second layer

- **Genetic training** – was applied in second layer, consisting of the selection of features (*votes of experts*) from the first layer, based on reference responses. The task of the genetic algorithm was to reject the incorrect *votes* (responses) of classifiers from the first layer, based on the errors in all training and test sets, and accept only reliable *votes* (responses). Genetic training with conversion of 1 output to 17 outputs is a new method of combining classifiers (ensemble combination).

2.4.2. Optimized by classes (GECC)

Two-layer ensemble of classifiers, consisting of **17 SVM classifiers** (*nu-SVC, RBF*, corresponding to 17 classes) + **1 SVM classifier** (*C-SVC, linear*). In the ensemble of classifiers, each classifier of the input layer is optimized to maximize the efficacy of recognition of **particular heart disorders (classes)**. Classifier of output layer, based on the selected responses of input classifiers, makes the final decision.

The first layer of the system consists of 17 *experts*, specializing in the recognition of particular 17 classes (heart disorders). The aim of optimization (training) for the first layer was a suitable selection of features (frequency components of the ECG signals) in input vectors, and determining values of the parameters: γ (*-g*) and ν (*-n*) for 17 SVM

Table 4
The results for genetic ensemble of classifiers optimized by classes (GECC). Coefficient ERR_L - indicates the sum of the errors in all training sets, coefficient ERR_P - indicates the sum of the errors for the priority class, while coefficient $ERR_{P\%}$ - indicates the percentage error in the priority class.

Classifiers	Coefficients													
	$-g$	$-n$	ERR_L	ERR_P	$ERR_{P\%}$	ERR_{sum}	ACC	SEN	SPE	κ	C_F	T_t	T_c	T_o
The first layer of ensemble - 17 SVM classifiers (nu-SVC, RBF) corresponding to 17 classes - *experts*														
SVM_1	$1.37e-5$	0.0213	0	34/193	17.62%	75	98.81%	89.92%	99.37%	88.39%	49.64%	9.5704 [*s*]	0.0017 [*s*]	*about* 100 [*h*]
SVM_2	$4.97e-5$	0.0253	0	27/58	46.55%	75	98.81%	89.92%	99.37%	88.38%	48.81%	14.1858 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_3	$5.17e-5$	0.0250	0	1/17	5.88%	74	98.83%	90.05%	99.38%	88.54%	46.74%	13.2816 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_4	$4.32e-5$	0.0149	0	5/93	5.38%	74	98.83%	90.05%	99.38%	88.54%	48.19%	12.3993 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_5	$4.01e-5$	0.0200	0	5/11	45.45%	77	98.78%	89.65%	99.35%	88.07%	48.56%	12.2145 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_6	$4.38e-5$	0.0142	0	0/21	0.00%	78	98.77%	89.52%	99.35%	87.91%	49.61%	13.3080 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_7	$2.21e-5$	0.0240	1	26/78	33.33%	77	98.78%	89.65%	99.35%	88.08%	48.96%	10.2691 [*s*]	0.0017 [*s*]	*about* 100 [*h*]
SVM_8	$4.14e-5$	0.0242	0	15/44	34.09%	79	98.75%	89.38%	99.34%	87.76%	49.59%	12.8321 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_9	$1.46e-5$	0.0051	0	3/13	23.08%	78	98.77%	89.52%	99.35%	87.93%	50.04%	8.6842 [*s*]	0.0017 [*s*]	*about* 100 [*h*]
SVM_{10}	$5.54e-5$	0.0187	0	2/10	20.00%	79	98.75%	89.38%	99.34%	87.75%	49.44%	14.7380 [*s*]	0.0020 [*s*]	*about* 100 [*h*]
SVM_{11}	$9.29e-5$	0.0201	0	0/10	0.00%	77	98.78%	89.65%	99.35%	88.07%	49.36%	9.2320 [*s*]	0.0017 [*s*]	*about* 100 [*h*]
SVM_{12}	$5.40e-5$	0.0112	0	1/10	10.00%	77	98.78%	89.65%	99.35%	88.07%	48.04%	13.2559 [*s*]	0.0018 [*s*]	*about* 100 [*h*]
SVM_{13}	$2.64e-5$	0.0183	0	7/11	63.64%	73	98.85%	90.19%	99.39%	88.70%	49.09%	11.3613 [*s*]	0.0021 [*s*]	*about* 100 [*h*]
SVM_{14}	$1.35e-5$	0.0178	0	1/88	1.14%	78	98.77%	89.52%	99.35%	87.92%	49.54%	10.9933 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_{15}	$3.76e-5$	0.0255	0	2/47	4.26%	75	98.81%	89.92%	99.37%	88.39%	49.21%	13.4814 [*s*]	0.0021 [*s*]	*about* 100 [*h*]
SVM_{16}	$4.62e-5$	0.0254	0	0/10	0.00%	75	98.81%	89.92%	99.37%	88.38%	48.89%	15.0099 [*s*]	0.0020 [*s*]	*about* 100 [*h*]
SVM_{17}	$3.44e-5$	0.0163	0	0/30	0.00%	75	98.81%	89.92%	99.37%	88.39%	48.01%	12.4855 [*s*]	0.0020 [*s*]	*about* 100 [*h*]
The second layer of ensemble - 1 SVM classifier (C-SVC, linear) - *judge*														
SVM_{18}	–	–	0	–	–	65	98.97%	91.26%	99.45%	89.95%	7.61%	0.0380 [*s*]	$4.79e-6$ [*s*]	*about* 1 [*h*]
Summary														
Ensemble	–	–	0	–	–	**65**	98.97%	**91.26%**	99.45%	**89.95%**	46.63%	207.3403 [*s*]	**0.0321** [*s*]	*about* 70 [*days*]

classifiers. To minimize the number of errors for particular (priority) classes/disorders (for the first classifier from first class, etc.; 1 class on each of 17 classifiers; for the priority class, each error: FP and FN, was calculated with a weight equals to 100, and for remaining classes weights equal to 1, Table 2). For each of the 17 classifiers, selected an optimal and different set of parameters values: γ (*-g*) and ν (*-n*). At the inputs of each of the 17 classifiers, come selected fragments of ECG signals, containing the most characteristic features of the priority disorder - selected by the GA.

The second layer of the system consists of one *judge* - (SVM classifier). This one classifier was designed to evaluate *the votes of experts* from the first layer. Each of the 17 classifiers (from the input layer) had 17 outputs (corresponding to 17 classes), so the vector of input features, to the second layer, had 289 *votes*.

In the research also tested the solution in which the classifiers from the first layer have two outputs (priority class or other classes) instead of 17 outputs. However, such a solution did not improve the results.

2.4.3. Optimized by sets (GECS)

Two-layer ensemble of classifiers, consisting of **10 SVM classifiers** (*nu-SVC, RBF*, corresponding to 10 combinations of training and test sets) + **1 SVM classifier** (*C-SVC, linear*), modified *Bagging* method. In the ensemble of classifiers, each classifier of the input layer is optimized to maximize the efficacy of recognition of heart disorders for **particular combinations of training and test sets**. Classifier of output layer, based on the selected responses of input classifiers, makes the final decision.

The first layer of the system consists of 10 *experts*, specializing in the recognition of classes (heart disorders) from particular 10 priority combinations of training and test sets, created by 10-fold CV method. The aim of optimization (training) for the first layer was a suitable selection of features (frequency components of the ECG signals) in input vectors, and determining values of the parameters: γ (*-g*) and ν (*-n*) for 10 SVM classifiers. To minimize the number of errors for particular (priority) combinations of sets (for the first classifier in first combination of sets: training set no. 1 and test set no. 1, etc., from Table 1; for the priority combination of sets, each error: FP and FN, was calculated with a weight equals to 100, and for remaining combination of sets weights equal to 1, Table 2). For each of the 10 classifiers, selected an optimal and different set of parameters values: γ (*-g*) and ν (*-n*). At the inputs of each of the 10 classifiers, come selected fragments of ECG signals, containing the most characteristic features - selected by the GA.

The second layer of the system consists of one *judge* - (SVM classifier). This one classifier was designed to evaluate *the votes of experts* from the first layer. Each of the 10 classifiers (from the input layer) had 17 outputs (corresponding to 17 classes), so the vector of input features, to the second layer, had 170 *votes*.

Fig. 2 shows the scheme of *Genetic ensemble of classifiers optimized by classes or sets*. Procedure No. 1 presented *Genetic ensemble of classifiers optimized by classes or sets* algorithm. In Fig. 3, scheme of genetic training (for exemplary chromosome of individual and a single fragment of ECG signal) is presented.

As part of the research, many parameters configurations of the genetic algorithm and SVM classifier have been tested. On this basis, optimum values of parameters were selected. Table 2 presents information about the genetic algorithm applied to the feature selection and classifier parameter optimization (basic and optimized classifier parameters) for classifiers in first and second layer of GECC or GECS. All data in Table 2 are given in a sequence order: first, for GECC method, and then for GECS method.

2.5. Evaluation criteria

To evaluate the designed methods, the following coefficients were determined [105,106]: 1) Accuracy *ACC*, 2) Sensitivity *SEN*, 3) Specificity *SPE*, 4) κ coefficient, and 5) Sum of errors ERR_{sum}. These coefficient were calculated based on the generated *confusion matrices* and calculated values (*TP – True Positive*, *TN – True Negative*, *FP – False Positive*, *FN – False Negative*) for all experiments, methods, and classifiers. The following coefficients were also determined: 6) Acceptance feature coefficient C_F, 7) Optimization time T_o, 8) Training time T_t, and 9)

Table 5
The results for genetic ensemble of classifiers optimized by sets (GECS). Coefficient ERR_L - indicates the sum of the errors in all training sets, coefficient ERR_P - indicates the sum of the errors for the priority class, while coefficient $ERR_{P\%}$ - indicates the percentage error in the priority test set.

Classifiers	Coefficient													
	$-g$	$-n$	ERR_L	ERR_P	$ERR_{P\%}$	ERR_{sum}	ACC	*SEN*	*SPE*	κ	C_F	T_t	T_c	T_o
The first layer of ensemble - 10 SVM classifiers (nu-SVC, RBF) corresponding to 10 combination of sets - expertsr														
SVM_1	$1.61e-5$	0.0078	0	6/69	8.70%	83	98.69%	88.84%	99.30%	87.14%	48.79%	9.5868 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_2	$9.03e-6$	0.0196	0	7/69	10.15%	79	98.75%	89.38%	99.34%	87.77%	48.94%	9.5183 [*s*]	0.0017 [*s*]	*about* 100 [*h*]
SVM_3	$2.81e-5$	0.0112	0	7/69	10.15%	73	98.85%	90.19%	99.39%	88.70%	49.64%	11.1354 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_4	$5.64e-5$	0.0118	0	2/69	2.06%	78	98.77%	89.52%	99.35%	87.91%	47.94%	14.1601 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_5	$8.53e-6$	0.0091	0	5/69	7.25%	80	98.74%	89.25%	99.33%	87.60%	48.24%	8.6126 [*s*]	0.0017 [*s*]	*about* 100 [*h*]
SVM_6	$3.09e-5$	0.0185	0	5/69	7.25%	76	98.80%	89.79%	99.36%	88.24%	50.21%	12.6103 [*s*]	0.0020 [*s*]	*about* 100 [*h*]
SVM_7	$3.43e-5$	0.0119	0	9/69	13.04%	78	98.77%	89.52%	99.35%	87.93%	48.14%	11.7691 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_8	$4.22e-5$	0.0096	0	4/69	5.80%	75	98.81%	89.92%	99.37%	88.38%	48.34%	12.9232 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_9	$4.60e-5$	0.0201	0	5/69	7.25%	74	98.83%	90.05%	99.38%	88.54%	49.31%	13.8194 [*s*]	0.0019 [*s*]	*about* 100 [*h*]
SVM_{10}	$3.33e-5$	0.0129	0	15/123	12.20%	74	98.83%	90.05%	99.38%	88.54%	48.89%	11.7098 [*s*]	0.0018 [*s*]	*about* 100 [*h*]
The second layer of ensemble - 1 SVM classifier (C-SVC, linear) - judge														
SVM_{18}	–	–	0	–	–	64	98.99%	91.40%	99.46%	90.10%	22.35%	0.0335 [*s*]	$4.52e-6$ [*s*]	*about* 1 [*h*]
Summary														
Ensemble	–	–	0	–	–	**64**	98.99%	**91.40%**	99.46%	**90.10%**	46.44%	115.8450 [*s*]	**0.0186** [*s*]	*about* 70 [*days*]

Table 6
Indicative comparison of the results under the methods based on the subject-oriented validation scheme and the same database - MIT-BIH Arrhythmia [8].

No.	Work	Year	# of classes	Feature set	Classifier	Acc = SEN
1.	Escalona-Moran et al. [107]	2008	5	Raw wave	RC	98%
2.	Huang et al. [34]	2014	5	Random projection, RR-intervals	Ensemble of SVM	94%
3.	Llamedo and Martinez [108]	2011	5	Wavelet, VCG + SFFS	Weighted LD	93%
4.	Lin and Yang [109]	2014	5	Normalized RR-interval	Weighted LD	93%
5.	Bazi et al. [110]	2013	5	Morphological, Wavelet	SVM, IWKLR, DTSVM	92%
6.	Soria and Martinez [111]	2009	5	RR-Intervals, VCG, morphological + FFS	Weighted LD	90%
7.	Mar et al. [112]	2011	5	Temporal Features, Morphological, statistical features + SFFS	Weighted LD, MLP	89%
8.	Zhang and Luo [113]	2014	5	RR-intervals, morph. features, ECG-inter. and segments, wavelet coeff.	Combined SVM	87%
9.	Zhang et al. [114]	2014	5	RR-intervals, morphological features, ECG-intervals and segments	Combined SVM	86%
10.	Ye et al. [115]	2012	5	Morphological, Wavelet, RR interval, ICA, PCA	SVM	86%
11.	Park et al. [116]	2008	5	HOS, HBF	Hierarchical SVM	85%
12.	de Lannoy et al. [117]	2012	5	RR-intervals, ECG-segments, morphological, HBF, HOS	Weighted CRF	85%
13.	de Chazal et al. [89]	2004	5	ECG-Intervals, Morphological	Weighted LD	83%
14.	de Lannoy et al. [118]	2010	5	ECG-Intervals, morphological, HOS, HBF coefficients	Weighted SVM	83%
	Pławiak		**15** **17**	**Frequency components of the power spectral density of the ECG signal**	**Genetic ensemble of SVM classifiers optimized by sets**	**93%** **91%**

Classification time T_c.

The definitions of the calculated coefficients are as follows:

- **Accuracy**

$$ACC = \left(\sum_{i=1}^{N} \frac{TP + TN}{TP + FP + TN + FN} \right) \cdot 100\% \Big/ N \tag{3}$$

- **Sensitivity**

$$SEN = \left(\sum_{i=1}^{N} \frac{TP}{TP + FN} \right) \cdot 100\% \Big/ N \tag{4}$$

- **Specificity**

$$SPE = \left(\sum_{i=1}^{N} \frac{TN}{FP + TN} \right) \cdot 100\% \Big/ N \tag{5}$$

where:

N – Number of sets used in the cross-validation variant: 4-fold or 10-fold validation,
TP – True Positive,
TN – True Negative,
FP – False Positive, and
FN – False Negative.

- **κ coefficient** (Fleiss' kappa) – a coefficient used to evaluate the efficiency of the designed classifier/algorithm. It is used for multi-class problems concerning the recognition of more than two classes. A higher value indicates a better result.

$$\kappa = \left(\sum_{i=1}^{N} \frac{M \sum_{j=1}^{n} m_{j,j} - \sum_{j=1}^{n} (G_j C_j)}{M^2 - \sum_{j=1}^{n} (G_j C_j)} \right) \cdot 100\% \Big/ N \tag{6}$$

where:

N – the number of sets used in the cross-validation variant: 4-fold or 10-fold validation,
j – the class index,
n – the number of classes = 17,
M – the total number of classified samples that are being compared to ground truth;
$m_{j,j}$ – the number of samples belonging to the ground truth class j that have also been classified with a class j (i.e., values found along the diagonal of the confusion matrix);
C_j – the total number of classified samples belonging to class j; and
G_j – the total number of ground truth samples belonging to class j.

- **Sum of errors** (ERR_{sum}) – calculated on the basis of the confusion matrix based on the number of erroneous classifications and is equal to the sum of the off-diagonal entries of the confusion matrix per 744 classifications.
- **Acceptance feature coefficient** (C_F) – the ratio of the number of accepted features F_a to the total number of features F expressed as a percentage. Determined through the use of genetic feature selection. This coefficient is calculated according to the following formula:

$$C_F = \frac{F_a}{F} \cdot 100\% \tag{7}$$

where:

F_a – the number of accepted features and
F – the total number of features.

- **Optimization time** (T_o) – calculated for a given classifier as the sum of all training and classification times for all training and test sets for a given variant of the cross-validation method (4-fold or 10-fold cross-validation). This time is the time required to find the optimal parameter configuration of the given classifier or the optimal vector of input features within the feature selection. This is used for ECG

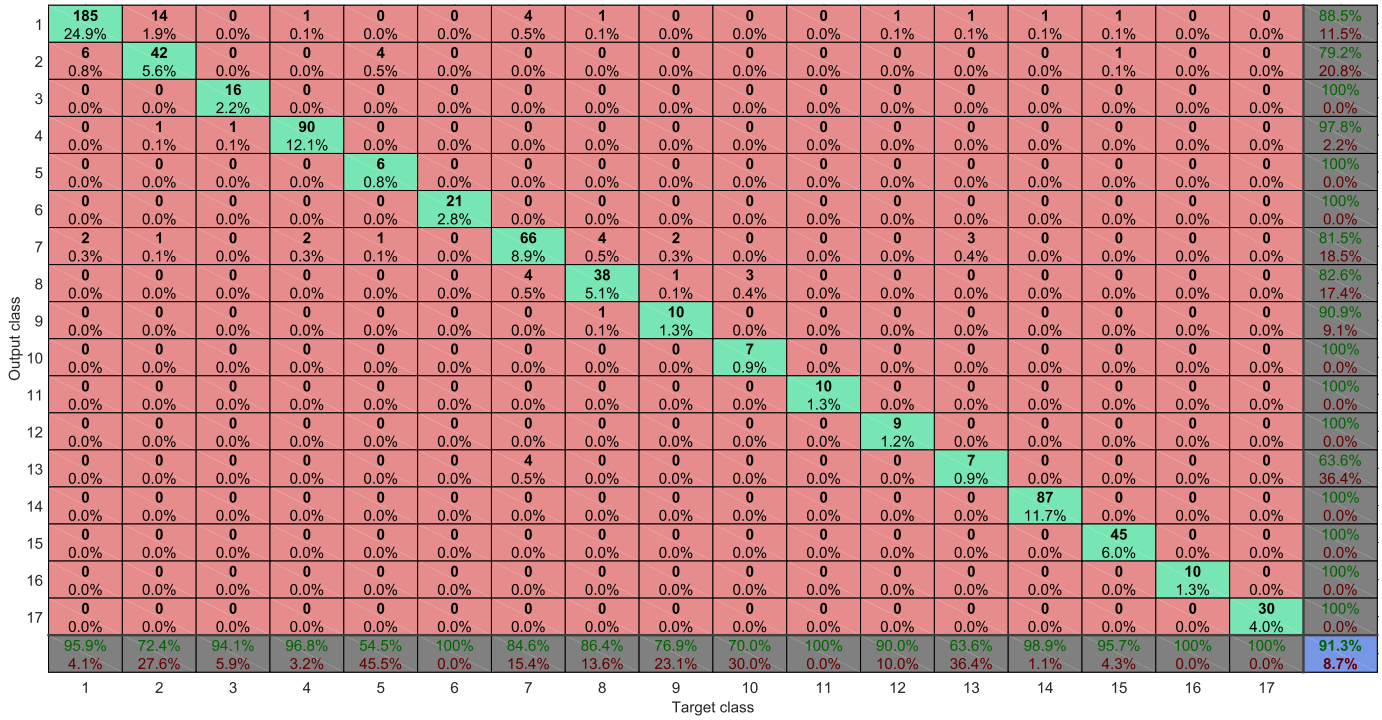

Fig. 4. Confusion matrix for GECC method.

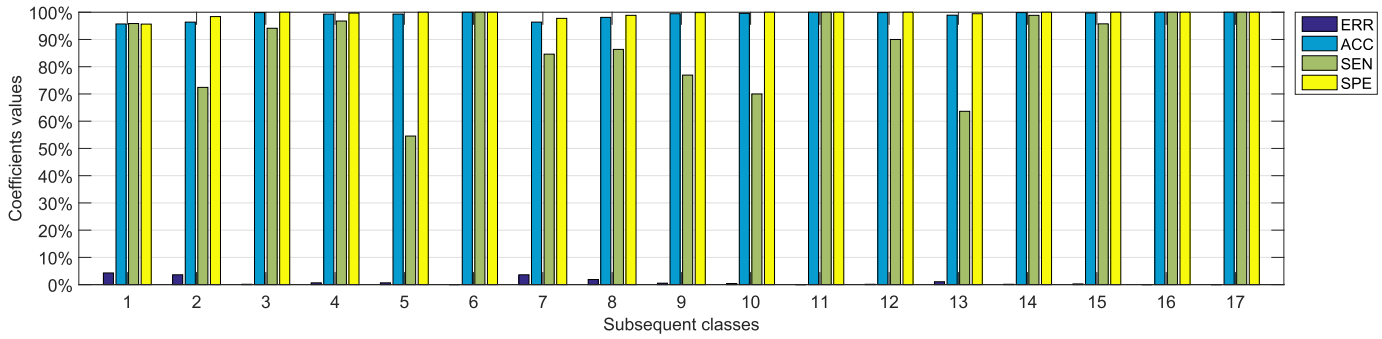

Fig. 5. Comparison of coefficient values, for GECC method, for each class.

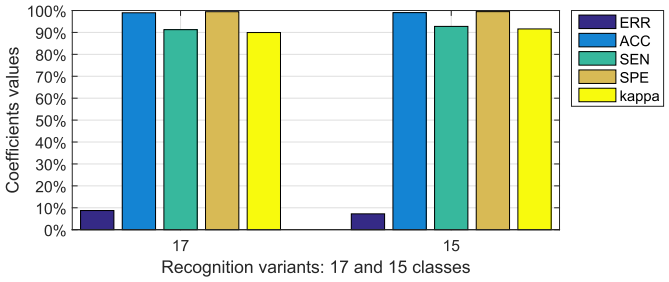

Fig. 6. Comparison of coefficient values, for GECC method, for the recognition variants of 17 and 15 classes.

signals after pre-processing and feature extraction.

- **Training time** (T_t) – calculated for a given classifier as the sum of the training times for all training sets for a given variant of cross-validation method (4-fold or 10-fold cross-validation). This is used for ECG signals after pre-processing and feature extraction and selection.
- **Classification time** (T_c) – calculated for a given classifier as the average time for a single classification of a 10-s fragment of an ECG signal after pre-processing and feature extraction and selection.

The above-mentioned coefficients are applied to estimate the overall performance of the machine learning methods used in this research with respect to the recognition of the different classes of ECG signal fragments. To verify the efficiency of the recognition of individual classes, the same coefficients were calculated but for class *S*. For this purpose, the values of *TP*(*S*), *TN*(*S*), *FP*(*S*), and *FN*(*S*) were calculated for each class. These values were calculated based on the confusion matrix using the traditional method. Then, based on these values, the values of the coefficients *ACC*(*S*), *SEN*(*S*), and *SPE*(*S*) were calculated.

In this article (Table 6), the sensitivity coefficient (SEN) is equal to the overall accuracy coefficient (Acc) from the literature [8,89]. This is because the WTA (Winner-Takes-All) method was used for the classifiers.

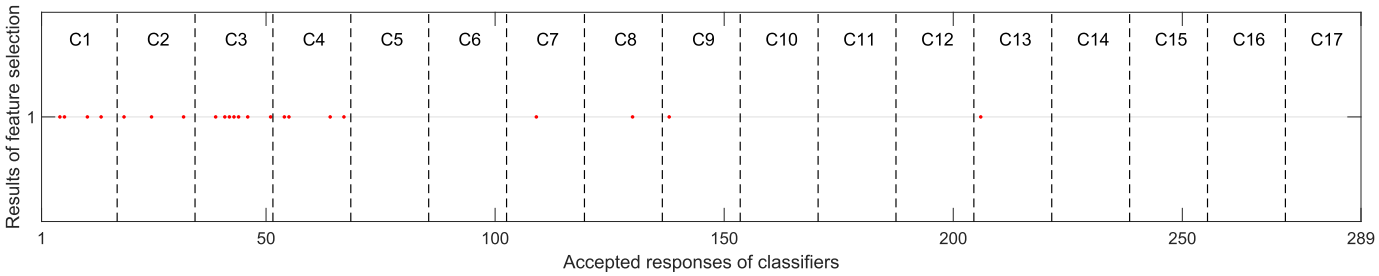

Fig. 7. Visualization of feature selection (*genetic training*) effects for the second layer of GECC system - accepted responses of classifiers (experts votes).

3. Results

The study utilized the MATLAB R2014b environment together with the LIBSVM library [99]. The computations were performed on an Intel Core i7-6700 K 4.0 GHz machine with 32 GB of RAM (only a single core was used). The total computation times, consisting of the training, testing, and optimization phases, are shown in Table 3 and in Tables 4 and 5.

This section presents the results of conducted experiments. On all the training sets, the obtained recognition sensitivity (*SEN*) of myocardium dysfunctions was 100% (zero errors). The ERR_{sum} coefficient equals the sum of the errors on all training and test sets per 744 classifications (in the training sets, in all cases, the sum of the errors equals zero).

Due to the use of the WTA method and the recognition of 17 classes, the most significant of the calculated coefficients are sensitivity (*SEN*) and sum of errors (ERR_{sum}), Table 3. The values of accuracy (*ACC*) and specificity (*SPE*) coefficients are very high for all methods (*ACC* > 98%, *SPE* > 99%, Table 3).

In Table 3, a comparison of the obtained results is presented for single classifiers: kNN, RBFNN, PNN, SVM and ensembles of classifiers: CEC, GECC, GECS.

3.1. Genetic ensembles of classifiers

3.1.1. Optimized by classes (GECC)

In Table 4, the detailed results with values of optimized parameters for the method GECC for 17 SVM classifiers (nu-SVC, RBF) from the first layer and 1 SVM classifier (C-SVC, linear) from the second layer are presented.

Coefficient ERR_L - indicates the sum of the errors in all training sets, coefficient ERR_P - indicates the sum of the errors for the priority class, while coefficient $ERR_{P\%}$ - indicates the percentage error in the priority class.

In Figs. 4–6, the results for entire GECC method (from Table 4) are presented. In Fig. 4, the confusion matrix is presented. In Fig. 5, the following coefficient values are presented: the sum of errors (*ERR*), accuracy (*ACC*), sensitivity (*SEN*), and specificity (*SPE*) for each class. In Fig. 6, a comparison of the coefficient values: sum of errors (*ERR*), accuracy (*ACC*), sensitivity (*SEN*), specificity (*SPE*), and κ coefficient, for the following recognition variants is presented: 17 and 15 classes.

In Fig. 7, a visualization of feature selection (*genetic training*) effects, for the second layer, is presented, by presenting the accepted features (classifiers responses) by red points. The dashed black line separated votes (responses) of particular 17 classifiers (experts) from the first layer.

3.1.2. Optimized by sets (GECS)

In Table 5, the detailed results with values of optimized parameters for the method GECS for 10 SVM classifiers (nu-SVC, RBF) from the first layer and 1 SVM classifier (C-SVC, liniowy) from the second layer are presented.

Coefficient ERR_L - indicates the sum of the errors in all training sets, coefficient ERR_P - indicates the sum of the errors for the priority class, while coefficient $ERR_{P\%}$ - indicates the percentage error in the priority test set.

In Figs. 8 and 9, and in Fig. 10, the results for entire GECS method (from Table 5) are presented. In Fig. 8, the confusion matrix is presented. In Fig. 9, the following coefficients values are presented: the sum of errors (*ERR*), accuracy (*ACC*), sensitivity (*SEN*), and specificity (*SPE*) for each class. In Fig. 10, a comparison of the coefficient values: sum of errors (*ERR*), accuracy (*ACC*), sensitivity (*SEN*), specificity (*SPE*), and κ coefficient, for the following recognition variants is presented: 17 and 15, classes.

In Fig. 11, a visualization of feature selection (*genetic training*) effects, for the second layer, is presented, by presenting the accepted features (classifiers responses) by red points. The dashed black line separated votes (responses) of particular 10 classifiers (experts) from the first layer.

In Table 6, a summary of the results (with the highest overall accuracy = sensitivity in the recognition of cardiac disorders) from the current scientific literature together with the results obtained by the author is presented. The summary is based on the same database - MIT-BIH Arrhythmia and the more objective subject-oriented validation scheme [8,90], includes information about the applied ECG signal analysis methods.

The comparison of results is indicative. It is not possible to completely objectively compare the obtained results because of the different research methodologies (proposed analysis of longer, 10-s, ECG signal fragments vs. QRS detection and classification). However, on the basis of the comparison, it can be stated that the obtained results are competitive and promising against the background of the current scientific literature.

4. Discussion

4.1. Hypothesis

The obtained results confirmed the hypothesis: the application of the proposed novel genetic ensembles of classifiers will enable the automatic, effective, universal, low computational complexity and fast recognition of heart pathologies based on ECG signal analysis.

The confirmation of this statement is given by the obtained results, summarized in Tables 3 and 6. The presented results show that the recognition **sensitivity** of the 17 classes for the best genetic ensemble of classifiers optimized by combination of sets (GECS) is ***SEN* = 91.40%** (*ACC* = 98.99%, *SPE* = 99.46%). The obtained result is one of the best in the scientific literature, where the three best results are ***Acc*/*SEN* = 98%** [107], **94%** [34] and **93%** [108,109] (Table 6). It should be noted that the results obtained by the author include the recognition of **17 classes** (a recognition sensitivity for 15 classes of 93%; Fig. 10). In contrast, the results presented in the scientific literature include the recognition of only 5 classes (for the subject-oriented

Output class \ Target class	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	
1	186 25.0%	13 1.7%	0 0.0%	1 0.1%	0 0.0%	0 0.0%	4 0.5%	1 0.1%	0 0.0%	0 0.0%	0 0.0%	1 0.1%	2 0.3%	1 0.1%	2 0.3%	0 0.0%	0 0.0%	88.2% 11.8%
2	5 0.7%	43 5.8%	0 0.0%	0 0.0%	4 0.5%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	82.7% 17.3%
3	0 0.0%	0 0.0%	16 2.2%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
4	0 0.0%	1 0.1%	1 0.1%	90 12.1%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	97.8% 2.2%
5	0 0.0%	0 0.0%	0 0.0%	0 0.0%	6 0.8%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
6	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	21 2.8%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
7	2 0.3%	1 0.1%	0 0.0%	2 0.3%	1 0.1%	0 0.0%	66 8.9%	4 0.5%	2 0.3%	0 0.0%	0 0.0%	0 0.0%	3 0.4%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	81.5% 18.5%
8	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	4 0.5%	38 5.1%	1 0.1%	3 0.4%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	82.6% 17.4%
9	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	1 0.1%	10 1.3%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	90.9% 9.1%
10	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	7 0.9%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
11	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	10 1.3%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
12	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	9 1.2%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
13	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	4 0.5%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	6 0.8%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	60.0% 40.0%
14	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	87 11.7%	0 0.0%	0 0.0%	0 0.0%	100% 0.0%
15	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	45 6.0%	0 0.0%	0 0.0%	100% 0.0%
16	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	10 1.3%	0 0.0%	100% 0.0%
17	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	0 0.0%	30 4.0%	100% 0.0%
	96.4% 3.6%	74.1% 25.9%	94.1% 5.9%	96.8% 3.2%	54.5% 45.5%	100% 0.0%	84.6% 15.4%	86.4% 13.6%	76.9% 23.1%	70.0% 30.0%	100% 0.0%	90.0% 10.0%	54.5% 45.5%	98.9% 1.1%	95.7% 4.3%	100% 0.0%	100% 0.0%	**91.4%** **8.6%**

Fig. 8. Confusion matrix for GECS method.

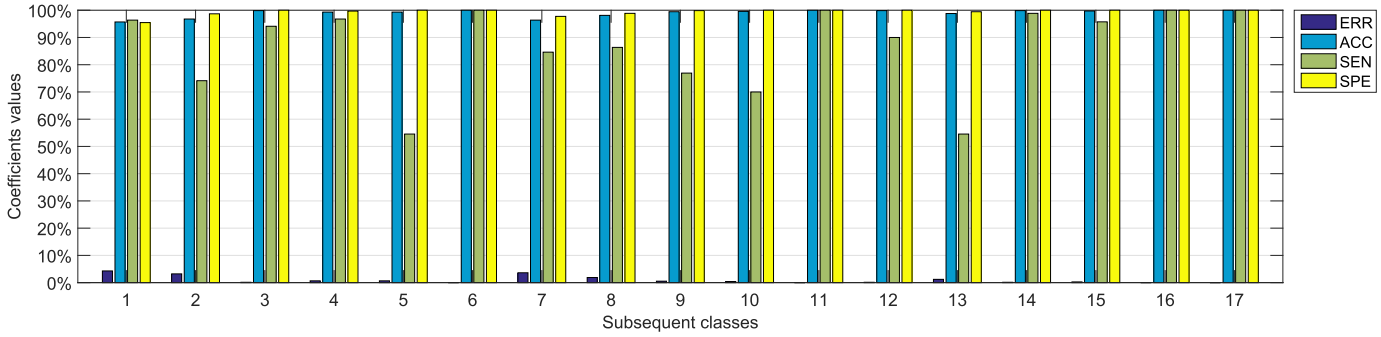

Fig. 9. Comparison of coefficient values, for GECS method, for each class.

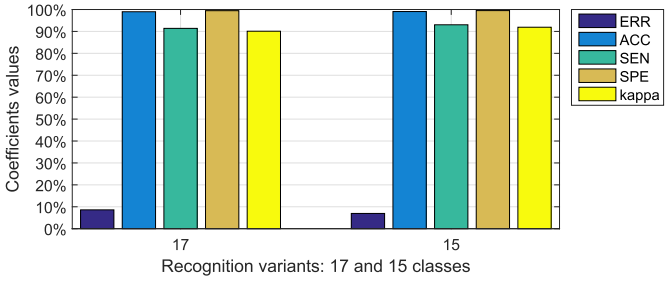

Fig. 10. Comparison of coefficient values, for GECS method, for the recognition variants of 17 and 15 classes.

validation scheme [8]).

The obtained classification time for the ECG signal fragments, $C_k = 0.0186$ [s], for the best GECS method is also very important.

4.2. Feature extraction

Analysis of longer ECG signal fragments results in increased efficiency. The use of the proposed feature extraction method, results in strengthening the characteristic features of the analyzed disorders due to the fact that the feature vector in frequency domain has more visible frequency band (characteristic of the particular disorder). It follows from the overlapping of the same heart evolutions (for particular class) occurring in the analyzed, longer, ECG signal fragments.

4.3. Genetic ensembles of classifiers

Obtained results from Table 6, have confirmed rightness of use the new methods: GECC i GECS. The calculated coefficients for the GECC and GECS methods are respectively: $ERR_{sum} = 65, 64$; $SEN = 91,26\%, 91,40\%$; $\kappa = 89,95\%, 90,10\%$, are better than the coefficients obtained for the classical ensemble of classifiers (CEC): $ERR_{sum} = 75$; $SEN = 89,92\%$; $\kappa = 88,38\%$, and are better than the coefficients obtained for the best single classifier - SVM: $ERR_{sum} = 73$; $SEN = 90,19\%$; $\kappa = 88,70\%$

4.3.1. Optimized by classes

Based on the results presented in Table 4, we find that the entire GECC ensemble obtained better result ($EER_{sum} = 65$, $SEN = 91.26\%$) then the best component classifier from the first layer of ensemble:

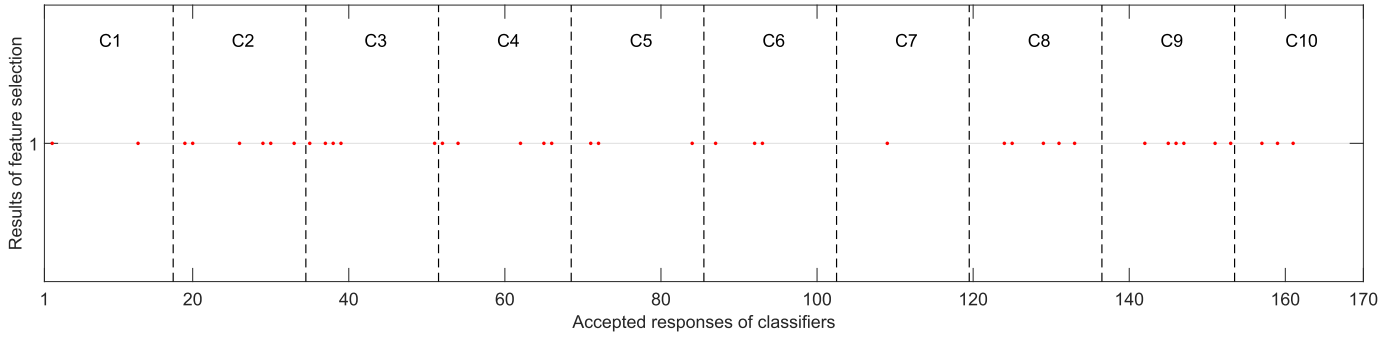

Fig. 11. Visualization of feature selection (*genetic training*) effects for the second layer of GECS system - accepted responses of classifiers (experts votes).

EER_{sum} = 73, *SEN* = 90.19%. The average result for all component classifiers from first layer was: EER_{sum} = 76, *SEN* = 89.75%.

It should also be mentioned that, despite the fact, that the entire ensemble consists of 18 classifiers, the classification time of a single fragment of ECG signal is only: **0.0321**[*s*].

4.3.2. Optimized by sets

Based on the results presented in Table 5, we find that the entire GECS ensemble obtained better result (EER_{sum} = 64, *SEN* = 91.40%) then the best component classifier from the first layer of ensemble: EER_{sum} = 73, *SEN* = 90.19%. The average result for all component classifiers from first layer was: EER_{sum} = 77, *SEN* = 89.65%.

It should also be mentioned that, despite the fact, that the entire ensemble consists of 11 classifiers, the classification time of a single fragment of ECG signal is only: **0.0186**[*s*].

4.4. Component classifiers of the ensemble

Obtained results (Tables 3–5, and Figs. 4 and 8) have confirmed the high efficiency of the GECC and GECS methods. This was achieved by: 1) diversity of component classifiers (other classifiers make other errors), 2) quality of the component classifiers of the ensembles and 3) applying genetic training in the second layer of ensembles (genetic selection of votes/features from experts/classifiers of first layer of ensemble). Worth emphasizing is the fact that the high efficiency of genetic selection of votes was due to the conversion of 1 output to 17 outputs of each of the component classifiers.

Combining classifiers using genetic selection of features has enabled the use of the advantages of all component classifiers, while minimizing their disadvantages (by eliminating incorrect votes/responses of classifiers from first layer). The success of designed ensembles of classifiers has also been achieved through the use of: 1) layered learning (which facilitated and accelerated the training), 2) genetic selection of features (frequency components) in the first layer of ensembles, and 3) genetic optimization of parameters (appropriate balance between exploration and exploitation) coupled with 10-fold cross-validation, which significantly reduced the over-fitting effect and consequently increased the efficiency of the ensembles of classifiers.

4.4.1. GECC

Based on Table 4, we can see a large diversity between the component classifiers of the ensemble (ERR_{sum} between 73 and 79 errors). Noteworthy is also the fact that each of the component classifiers was optimized to recognize another (priority) class, which increased the diversity of the component classifiers of the ensemble.

Based on Fig. 7, it can be seen that, as a result of the selection of votes, component classifiers corresponding to classes Nos. 5, 6, 10, 11, 12, 14, 15, 16 and 17 were completely eliminated (lack of accepted outputs/responses/votes; no impact on the final decision), while in component classifiers Nos. 7, 8 and 9 only one output (one class) is taken into account. This situation is due to the fact that the greatest diversity and quality is brought to the ensemble by component classifiers corresponding to classes Nos. 1, 2, 3 and 4. These are classes, most visually similar to each other: normal sinus rhythm and atrial type disorders. Other classes are more separated or difficult to recognize.

4.4.2. GECS

Based on Table 5, we can see a large diversity between the component classifiers of the ensemble (ERR_{sum} between 73 and 83 errors). Noteworthy is also the fact that each of the component classifiers was optimized to recognize another (priority) combination of training and test sets from 10-fold cross validation, which increased the diversity of the component classifiers of the ensemble.

Based on Fig. 11, it can be seen that no component classifiers were eliminated as a result of the selection of votes. Only incorrect outputs/responses/votes from each component classifier were rejected. We may conclude that this situation is due to the fact that in each combination of sets (corresponding to particular component classifiers) there are important and valuable (for final decision) fragments of the ECG signal. Therefore, all component classifiers provide important information.

4.5. Dysfunctions/classes

In Figs. 5 and 9, the recognition efficiency for each class is presented with the GECC and GECS methods. Based on this, we can observe a high recognition efficiency for practically all classes: ***SEN* over 70%**. The worst results were obtained for *supraventricular tachyarrhythmia* (*SEN* over 50%) and *fusion of ventricular and normal beat* (*SEN* over 60% and 50%).

Worse results are due to the facts that: 1) classes Nos. 5 i 13 are among the most difficult to recognize classes (visually similar to other classes), and 2) a small number of ECG signal fragments (11 - Table 1), collected for these classes, which is one of the work limits.

Supraventricular tachyarrhythmia (class No. 5) has similar dynamic features to *atrial premature beat* (class No. 2), which is confirmed by the obtained results (confusion matrices) in Fig. 4 class No. 5 confused with class No. 2 (4 times) and in Fig. 8 class No. 5 confused with class No. 2 (4 times).

Fusion of ventricular and normal beat (class No. 13) has similar morphological features to *normal sinus rhythm* (class No. 1) and *premature ventricular contraction* (class No. 7), which is confirmed by the obtained results (confusion matrices), in Fig. 4 class No. 13 confused with class No. 7 (3 + 4 times) and class No. 1 (1 time) and in Fig. 8 class No. 13 confused with class No. 7 (3 + 4 times) and class No. 1 (2 times).

Based on the obtained results presented in Figs. 5 and 9, we removed dysfunctions with the smallest value of the *SEN* coefficient (below 65%). As a result, one other recognition case was considered: **15 classes** (Figs. 6 and 10) (after removing the *supraventricular tachyarrhythmia* and *fusion of ventricular and normal beat* classes). The indicated classes are similar to others and are included in larger groups of disorders

(atrial and ventricular type). The number of ECG signal fragments (11 - Table 1) for these classes is also low, and for this reason they are difficult to recognize. Therefore, the analysis of this case is justified. The best method, GECS, obtained the following sensitivity for heart dysfunction recognition for **17 and 15 classes**, respectively: ***SEN*** **= 91.40%, 93.04%**, and κ **= 90.10%, 91.92%**.

5. Conclusion

The aim of the conducted research was to develop a new ensembles of classifiers that enables the efficient recognition of heart disorders (17 classes: normal sinus rhythm + pacemaker rhythm + 15 heart disorders), based on analysis of 10-s fragments of ECG signals. In this research, 744 fragments of ECG signals were analyzed from the MIH-BIH Arrhythmia database for one lead, MLII, from 29 patients. In research designed two innovative genetic ensembles of classifiers optimized: by classes and by sets, based on: support vector machines classifier, 10-fold cross-validation method, ensemble learning, layered learning, genetic selection of features (frequency components), genetic optimization of classifiers parameters and novel genetic training (selection of experts votes) used to combining classifiers.

The best **genetic ensemble of classifiers optimized by sets (GECS)**, obtained a recognition sensitivity of **17 myocardium dysfunctions** at a level of **91.40%** (**64 errors** per 744 classifications, accuracy = 98.99%, specificity = 99.46%, time for classification of one sample = **0.0186 [s]**). Against the background of the current scientific literature, these results are some of the best results to date.

The following should be emphasized: the recognition of **17 classes**, application of **10-fold cross-validation** (analogous to **subject-oriented validation scheme**) and **correct balance of data** for all classes. This raises the level of the conducted research and strengthens the value of the obtained results.

The obtained results confirm the validity of the conducted research and prove that the aims (Section No. 1.1) was realized - we developed a novel ensembles of classifiers for the automatic, efficient (Table 6), universal (Table 1), low computational complexity (Section No. 1) and fast (Table 3) recognition of myocardium dysfunctions.

To the advantages of the proposed solution we can include: 1) recognition of 17 classes, 2) high efficiency/sensitivity, 3) possibility to implement on mobile devices: lower computational complexity (an average of 13 times less classifications) and only one lead, 4) elaboration of new machine learning method - Genetic Ensemble of Classifiers and 5) elaboration of new genetic training used to combining classifiers.

This research is worth continuing in order to: increase the recognition sensitivity for heart disorders and overcome the limitations (small number of ECG signal fragments for the most rare classes - Table 1). Therefore, further research will focus on: 1) testing and modifying deep learning methods, and 2) collecting more number of appropriate ECG signal fragments, especially for the most rare classes.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at https://doi.org/10.1016/j.swevo.2017.10.002.

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