Expert Systems With Applications 92 (2018) 334–349

Contents lists available at ScienceDirect

Expert Systems With Applications

journal homepage: www.elsevier.com/locate/eswa

Novel methodology of cardiac health recognition based on ECG signals and evolutionary-neural system

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ARTICLE INFO

Article history:
Received 14 June 2017
Revised 9 August 2017
Accepted 9 September 2017
Available online 13 September 2017

Keywords:
ECG
Biomedical signal processing and analysis
Classification
Machine learning algorithms
Neural networks
Support vector machine
K-nearest neighbor algorithm
Evolutionary-neural system
Genetic algorithm
Feature extraction and selection
Discrete Fourier transform

ABSTRACT

This article presents an innovative research methodology that enables the efficient classification of cardiac disorders (17 classes) based on ECG signal analysis and an evolutionary-neural system.

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. The subject of ECG signal analysis is very popular. However, due to the great difficulty of the task undertaken, and high computational complexity of existing methods, there remains substantial work to perform.

This research collected 1000 fragments of ECG signals from the MIH-BIH Arrhythmia database for one lead, MLII, from 45 patients. An original 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 spectral power density was estimated (using Welch's method and a discrete Fourier transform). Genetic optimization of parameters and genetic selection of features were tested. Pre-processing, normalization, feature extraction and selection, cross-validation and machine learning algorithms (SVM, kNN, PNN, and RBFNN) were used.

The best evolutionary-neural system, based on the SVM classifier, obtained a recognition sensitivity of 17 myocardium dysfunctions at a level of 90.20% (98 errors per 1000 classifications, accuracy = 98.85%, specificity = 99.39%, time for classification of one sample = 0.0023 [s]). Against the background of the current scientific literature, these results are some of the best results to date.

1. Introduction

Diagnosing heart conditions by analyzing 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.

The huge popularity of the ECG signal analysis is also reflected in research. In recent years, the most developed topics related to electrocardiography include: 1) ECG beat detection / classification: (Augustyniak, 2015; Martis, Acharya, & Adeli, 2014; Martis, Acharya, & Min, 2013; Song, Cho, Kim, & Lee, 2015; Yochum, Renaud, & Jacquir, 2016), 2) deep learning: (Acharya et al., 2017; Kiranyaz, Ince, & Gabbouj, 2016; Rahhal et al., 2016), 3) principal component analysis: (Castells, Laguna, Sörnmo, Bollmann, & Roig, 2007; Ceylan & Ozbay, 2007; Chawla, 2009; Elhaj, Salim, Harris, Swee, & Ahmed, 2016; Kallas, Francis, Honeine, Amoud, & Richard, 2012; Kanaan et al., 2011; Kim, Shin, Shin, & Lee, 2009; Martis, Acharya, Lim, & Suri, 2013; Martis, Acharya, Mandana, Ray, & Chakraborty, 2012; Martis, Acharya, & Min, 2013; Polat & Gunes, 2007; Rodriguez, Mexicano, Bila, Cervantes, & Ponce, 2015; Wang, Chiang, Hsu, & Yang, 2013), 4) higher order statistics: (Martis, Acharya, Mandana, Ray, & Chakraborty, 2013; Martis et al., 2013; Martis, Acharya, Ray, & Chakraborty, 2011), 5) feature selection / dimensionality reduction: (Bereta & Burczyński, 2007; Doquire, de Lannoy, Francois, & Verleysen, 2011; 2011; Kishore & Singh, 2015; Lin, Ying, Chen, & Lee, 2008b; Llamedo & Martinez, 2011; Mar, Zaunseder, Martineznez, Llamedo, & Poll, 2011; Martis et al., 2014; Nasiri, Naghibzadeh, Yazdi, & Naghibzadeh, 2009; Oh, Lee, & Moon, 2004; Wang, Yang, Teng, Xia, & Jensen, 2007; Yeh, Wang, & Chiou, 2010; Yu & Lee, 2012; Zhang, Dong, Luo, Choi, & Wu, 2014), 6) noise: (Li, Rajagopalan, & Clifford, 2014; Pasolli & Melgani, 2015; Roonizi & Sassi, 2016), 7) discrete wavelet transform: (Augustyniak, 2003; Daamouche, Hamami, Alajlan, & Melgani, 2012; Elhaj et al., 2016; Guler & Ubeyli, 2005; Islam, Haque, Tangim, Ahammad, & Khondokar, 2012; Kutlu & Kuntalp, 2012; Lin, Du, & Chen, 2008a;

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http://dx.doi.org/10.1016/j.eswa.2017.09.022
0957-4174/

Martis, Acharya, & Min, 2013; Mishra, Thakkar, Modi, & Kher, 2012; Thomas, Das, & Ari, 2015; Yan & Lu, 2014), 8) independent component analysis: (Chawla, 2009; Elhaj et al., 2016; Martis, Acharya, & Min, 2013; Sarfraz, Khan, & Li, 2014; Yu & Chou, 2008; 2009), 9) ensemble learning: (Guler & Ubeyli, 2005; Huang, Liu, Zhu, Wang, & Hu, 2014; Javadi, Arani, Sajedin, & Ebrahimpour, 2013; Mert, Kılıç, & Akan, 2012; Osowski, Hoai, & Markiewicz, 2004; Osowski, Markiewicz, & Hoai, 2008; Sambhu & Umesh, 2013), 10) hybrid systems: (Engin, 2004; Meau, Ibrahim, Narainasamy, & Omar, 2006; Osowski & Linh, 2001; Osowski et al., 2008; Ozbay, Ceylan, & Karlik, 2006).

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 (AHA, 2004; 2016; WHO, 2014)) and the most serious and costly health problems facing the world today (Heron & Smith, 2003; National Center for Health Statistics, 2005). 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 (AHA, 2004; 2016; Healthsquare, 2007; WHO, 2014)).

The classification of cardiac disorders based on existing methods based on the calculation of morphological and dynamic features of individual QRS complexes (heart evolution) is difficult and error prone due to the variability of these features in different patients (Padmavathi & Ramakrishna, 2015). For this reason, solutions currently described in the scientific literature do not achieve a satisfactory efficiency (da S. Luz, Schwartz, Cmara-Chvez, & Menotti, 2016).

The existing approaches are also ineffective for certain cardiac disorders, characterized by complex dependencies between subsequent evolutions of heart, for which the most important are “prolapsed” evolutions of heart (time intervals between subsequent heartbeats) and not the QRS complexes that may be correct. The group of these dysfunctions can include pre-excitation syndromes (e.g., Wolff-Parkinson-White syndrome - WPW), atrio-ventricular and atrial-sinus conduction blocks, and elongate PQ intervals.

This is why it is very important to develop specialized software supporting medical diagnostics to more effectively identify heart pathologies 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.

For recent years, we can distinguish two main approaches in the literature on the automatic recognition of cardiac disorders based on the analysis of ECG signals:

- classification of QRS complexes (Alvarado, Lakshminarayan, & Principe, 2012; de Chazal, O'Dwyer, & Reilly, 2004; Mateo, Torres, Aparicio, & Santos, 2016; Oster et al., 2015; Ye, Kumar, & Coimbra, 2012a; Zhang & Luo, 2014),
- analysis of longer ECG signal fragments (Abawajy, Kelarev, & Chowdhury, 2013; Padmavathi & Ramakrishna, 2015; Romero & Serrano, 2001; Vafaie, Ataei, & Koofigar, 2014).

It should be noted that the first approach concerning the classification of QRS complexes is substantially more popular. A key element of this approach is the effective detection of QRS complexes. On this basis, it is possible to segment an entire signal into individual QRS complexes and then analyze them using morphological features (determining the shape of the heart evolutions) and dynamic features (determining dependencies between subsequent heart evolutions).

An alternative approach is the analysis of longer, from a single QRS complex (lasting approximately 1 s), signal fragments, usually lasting approximately 10 s; this is the time period corresponding to a standard ECG examination at a cardiologist. Such analysis is based on distinctive feature extraction, for a given disorder, for whole, longer fragments. The identification of heart pathology is based on the extracted features.

Based on a current literature review (Augustyniak & Tadeusiewicz, 2009; da S. Luz, Nunes, de Albuquerque, Papa, & Menotti, 2013; da S. Luz et al., 2016), the typical research methodology in the field of ECG signal analysis consists of

1. obtaining data from public databases (MIT-BIH, EDB, AHA, CU, and NST),
2. pre-processing and signal normalization,
3. QRS detection and ECG signal segmentation,
4. extraction of characteristic signal features and rejection of redundant and erroneous information (extraction and selection of features),
5. classification of QRS complexes (recognition of heart disorders), e.g., data cross-validation, training, testing and optimization of classifier parameters, and
6. evaluation of the obtained results.

In the literature, the most popular method for creating training and test sets is cross-validation, where the two most popular validation schemes are Afkhami, Azarnia, and Tinati (2016) and da S. Luz et al. (2016)

- class-oriented validation schemes (intra-patient paradigm) - the selection of elements for training and test sets based on signals from the same patient, and
- subject-oriented validation schemes (inter-patient paradigm) (de Chazal et al., 2004) - the selection of elements for training and test sets based on signals from other patients.

Designing universal algorithms for the general population, not for an individual person, using a subject-oriented validation scheme is a better solution. This solution demonstrates lower effectiveness on the test set but is more reliable and stable and performs better in practice due to the smaller fit of the models to the training set and better knowledge generalization (Afkhami et al., 2016).

The evolutionary-neural system (Rutkowski, 2008) is a hybrid that combines the advantages of two computational intelligence methods: broadly defined Neural Networks (Prieto et al., 2016) and Evolutionary Computation (Back, Hammel, & Schwefel, 1997). With this synergy, we can achieve greater efficiency through better optimization of the classifier tuning by Genetic Algorithm (Holland, 1992) that are parts of the system. In the field of heart disorders recognition, evolutionary-neural systems are also popular and used with success: (Daamouche et al., 2012; Dilmac & Korurek, 2015; Ince, Kiranyaz, & Gabbouj, 2009; Khazaee & Ebrahimzadeh, 2010; Korurek & Dogan, 2010; Lessmann, Stahlbock, & Crone, 2006; Melgani & Bazi, 2008; Shadmand & Mashoufi, 2016).

The main aims of the research were the following:

Aim 1 Develop new and effective methods for the automatic recognition of myocardium dysfunctions based on ECG signals modeled on the work of cardiologists.

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.

Based on a literature review (da S. Luz et al., 2013; da S. Luz et al., 2016), it can be stated that the innovative elements of this research include the following:

Table 1
A description of the database with the selected 1000 ECG fragments along with the allocation of signals to the training and test sets for 10-fold cross-validation method.

				10-fold cross-validation			
				Groups 1–9		Group 10	
No.	Class	Fragments number	Patients number	Training set	Test set	Training set	Test set
1	Normal sinus rhythm	283	23	255	28	252	31
2	Atrial premature beat	66	9	60	6	54	12
3	Atrial flutter	20	3	18	2	18	2
4	Atrial fibrillation	135	6	122	13	117	18
5	Supraventricular tachyarrhythmia	13	4	12	1	9	4
6	Pre-excitation (WPW)	21	1	19	2	18	3
7	Premature ventricular contraction	133	14	120	13	117	16
8	Ventricular bigeminy	55	7	50	5	45	10
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	103	3	93	10	90	13
15	Right bundle branch block beat	62	3	56	6	54	8
16	Second-degree heart block	10	1	9	1	9	1
17	Pacemaker rhythm	45	2	41	4	36	9
	Sum	1000	45	904	96	864	136

Methodology - a new approach to ECG signal analysis. The designed system is modeled on the work of a cardiologist based on the analysis of longer (10-s) ECG signal fragments, which contain multiple heart evolutions.

17 recognized classes - normal sinus rhythm + pacemaker rhythm + 15 cardiac disorders.

Genetic training and optimization of classifiers - a genetic algorithm coupled with 10-fold cross-validation for signal feature selection and classifier parameter optimization.

The innovative elements of this research in the analysis of long (10-s) fragments of ECG signals include the following:

Feature extraction - strengthen the characteristic features of signals by estimating the power spectral density using the Welch method and the discrete Fourier transform (data analysis in the frequency domain for several Hamming window widths).

Genetic selection of features – the elimination of redundant features (frequency components of the power spectral density of the ECG signal) by a genetic algorithm.

2. Materials and methods

2.1. Materials

2.1.1. ECG database

For research purposes, the ECG signals were obtained from the http://www.physionet.org PhysioNet (Goldberger et al., 2000) service from the MIT-BIH Arrhythmia (Moody & Mark, 2001) database. The created database with ECG signals is described below.

- The ECG signals were from 45 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, 1000, 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.

An important aspect is the appropriate balance of data. The number of signal fragments corresponding to physiological heart evolutions should not be significantly greater than the number of ECG signals for the other classes. This may cause an artificial increase in the recognition efficiency for cardiac disorders. Therefore, the research used a proportional number of ECG signal fragments for each class, (from 1.00% to 38.04%, Table 1), which prevents the over-fitting effect.

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. In addition, keeping in mind the correct balance of data: 1) between classes and 2) between patients, the maximum number of ECG signals should not exceed 1000 fragments. Because increasing the number of fragments may cause incorrect training of classifiers. Not all classes / patients will have an impact on creation of models.

Collected data from all 48 records is not possible because records no. 102 and 104 do not have signals from MLII lead. In record no. 232, the entire signal containing rhythm “Sinus bradycardia” (not recognized in the article).

2.2. Methods

This section presents the subsequent stages of processing and analysis of the ECG signals along with the methods utilized.

2.2.1. Step I - Preprocessing with normalization

The aim of this stage was to unify the data from various ECG devices (gain reduction, frequency uniformity, and constant component reduction) and from different patients (normalization of signal amplitude).

In the research, the data were properly organized, and three preprocessing (normalization) paths were tested:

- **no normalization**:
  - reduction of gain
  - reduction of constant component (mean signal value)
- **rescaling**:
  - reduction of gain

- reduction of constant component
- rescaling signal to the range $[-1, 1]$
- reduction of constant component

- **standardization**:
  - reduction of gain
  - reduction of constant component
  - signal standardization (mean signal value = 0 and signal standard deviation = 1)

Rescaling was performed on all the ECG signal fragments for a given disorder for a given patient.

In order to achieve the desired effects, the following methods were used:

reduction of gain:

$$S = \frac{S_g}{g} \tag{1}$$

where:

S – ECG value after gain reduction,
S_g – ECG value before gain reduction,
g – value of gain of device on which ECG signal was recorded.

- **reduction of constant component:**

$$\mu = \frac{1}{n} \cdot \sum_{i=1}^{n} x_j(i) \tag{2}$$

where:

n – number of signal samples j,
i – index of consecutive signal samples,
j – index of consecutive signals.

- **rescaling:**

$$\bar{x}_j(i) = \frac{x_j(i) - min(x_j)}{max(x_j) - min(x_j)} \tag{3}$$

where:

i – index of consecutive signal samples,
j – index of consecutive signals,
$min(x_j)$ – minimum signal amplitude value $j = -1$,
$max(x_j)$ – maximum signal amplitude value $j = 1$.

- **standardization:**

$$\hat{x}_j(i) = \frac{x_j(i) - \mu}{\sigma} \tag{4}$$

where:

i – index of consecutive signal samples,
j – index of consecutive signals,
μ – mean signal value j, calculated from the formula 2,
σ – standard deviation of the signal j, calculated from the formula:

$$\sigma = \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (x_j(i) - \mu)^2} \tag{5}$$

2.2.2. Step II - Feature extraction

The aim of this stage was to extract and strengthen the characteristic features of the signal and thereby increase the recognition efficiency for the dysfunctions.

Due to the periodic nature of the ECG signal, the extraction of features based on the estimation of the power spectral density (PSD) (Smith, 2002) of the ECG signal was performed using the Welsh method (Welch, 1967) and the discrete Fourier transform (DFT) (Smith, 2002). Then, to normalize the frequency components of the power spectral density, the transformed signal was logarithmized.

For feature extraction applied the following methods:

Power spectral density - it represents the signal in the frequency or pulsation domain, it is obtained by Fourier transform, has dimensions: [*power*] per [*Hz*]. Spectral density describes how much signal (in terms of value) occurs per unit bandwidth.

Welch's method - it is used to estimate the power spectral density function of the signals. Welch's method amounts to averaging of several modified periodograms.

Periodogram - is a diagram that shows the most important periodic regularities in the signal. Peaks in the diagram correspond to periods (cycles) which closest correlate with the data. The periodogram method is one of the nonparametric methods used for estimation of power spectral density.

Fourier discrete transform - Fourier transform is used for signal distribution into sinusoidal and cosine waveforms, and thus transform the signal from the time domain to the frequency domain. The counterpart of the Fourier transform for the discrete (digital) and periodic signals is a discrete Fourier transform. It is calculated from the formula:

$$X(k) = \sum_{n=0}^{N-1} x(n) \cdot e^{-j \cdot \frac{2 \cdot \pi \cdot n \cdot k}{N}} \tag{6}$$

where:

$x(n)$ – is the nth sample of the discrete signal,
k – is the line number (frequency component number); $k = 0, \ldots, N-1$,
N – number of signal samples.

- **Hamming window** - is one of the functions describing the time window, which determines the way of sampling from the signal.
- **Series of logarithms of signals** - is a form of normalization of the features / attributes of the signals entering the inputs of the classifiers, calculated according to the formula:

$$x(n) = 10 \cdot log_{10}(P_{xx}(n)) \tag{7}$$

where:

n – index of consecutive signal samples,
$x(n)$ – series of logarithms of signal,
$P_{xx}(n)$ – power spectral density.

To calculate the power spectral density, 4 Hamming window widths: 128, 256, 512 and 1024 samples, were applied. The subsequent values of the tested Hamming window widths were determined using a geometric string (multiples of 2).

In all experiments, as a result of the feature extraction, 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 (in all experiments), 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].

2.2.3. Step III - Feature selection

The aim of this stage was to reduce the data (and thus accelerate the computations) and both extract and strengthen the characteristic features of the signal by reducing the features that carry redundant and erroneous information.

Genetic algorithms (GAs) (Holland, 1992; Rutkowski, 2008) are a method of problem solving based on natural evolution, mainly optimization problems. GAs are search procedures based on the mechanisms of natural selection and inheritance. They benefit from the evolutionary principle of survival of the best adapted individuals. GA belongs to a group of evolutionary algorithms.

In the research, a genetic algorithm (GA) was used for the feature selection. 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.

The genetic algorithm creates subsequent populations of individuals based on the fitness function and optimizes the efficiency of the classifiers through the selection of the most valuable features of the ECG signal.

2.2.4. Step IV - Cross-validation

The aim of this stage was to eliminate the effect of over-fitting the designed classifiers, thereby increasing the effect of generalizing knowledge and increasing the reliability of the obtained results.

The methods of selecting elements for training and test sets can be divided into the following types (Kuncheva, 2004): 1) resubstitution, 2) hold-out, 3) k-fold cross-validation, 4) leave-one-out cross-validation and 5) bootstrap.

We applied the method of k-fold cross-validation (CV) (Kuncheva, 2004) to the selection of elements for the training and test sets. Two types of cross-validation were used to create the training and test sets:

- **4-fold cross-validation**: A total of 4 combinations of training and test sets. The test sets for the first three groups were created by randomly selection elements, for each class (disorder), from the entire signal base. The test set for the fourth group was created from the remaining elements. The training sets consisted of elements that complemented to test sets for the entire signal base.
- **10-fold cross-validation**: A total of 10 combinations of training and test sets. The test sets for the first nine groups were created by randomly selection elements, 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.

Applying a k-fold cross-validation method that is more consistent with the subject-oriented validation scheme (inter-patient paradigm) than class-oriented validation scheme (intra-patient paradigm) (Afkhami et al., 2016; de Chazal et al., 2004; da S. Luz et al., 2016)

Table 1 shows the allocation of ECG signal fragments (divided into disorders) to training and test sets for 10-fold-cross-validation.

The reference matrices with the expected responses were created to enable a comparison of the final results. They contained the required outputs of the classifiers. The reference matrices for both variants of the cross-validation are not shown in this article because of their known form.

2.2.5. Step V - Machine learning algorithms

This research's aim was the recognition of heart disorders based on samples (ECG signal fragments). This analysis was based on the design and selection of appropriate parameters and subsequently retraining and testing the systems using machine learning algorithms (Alpaydin, 2014; Bishop, 2006; Engelbrecht, 2007).

The following methods were applied:

1. **Probabilistic Neural Network** (PNN) - an artificial neural network (Prieto et al., 2016; Tadeusiewicz, 2015) developed by Specht (1990). Used to solve classification problems, uses the kernel approximation technique to estimate the probability density function for classes. In the PNN network are at least three layers: input, radial and output. Radial neurons have parameters copied directly from the training data, each of them corresponds to one case. Output neurons sum up the values appearing on radial neurons outputs belonging to the class corresponding to the given output neuron. Output values are proportional to kernel estimators, probability density functions for different classes, and directly estimate the probability of belonging to each classes. The only parameter that influences the learning process of the PNN is the smoothing factor. This coefficient, representing the radial deviation of the appropriate Gaussian functions, is a measure of the range of impact of knowledge contained in the elements of the learning sequence on the surrounding areas of the input signals space.
2. **Radial Basis Function Neural Network** (RBFNN) - an artificial neural network developed by Broomhead and Lowe (1988). It usually has one hidden layer, containing radial neurons. Divides the space of the input signals using hyperspheres (defined by their centers and radii). The response surface of a single radial neuron is a Gaussian function, with a vertex located above the center and a decreasing value of the function along with distance from this point. You can change the slope of the Gaussian function. Radial neuron is defined by its center and a parameter called "radius". A point in an N-dimensional space is defined using N numbers, which exactly corresponds to the number of neuron weights.
3. **Support Vector Machine** (SVM, nu-SVC) - the classifier developed by Cortes and Vapnik (1995). The libsvm library for MATLAB (Chang & Lin, 2011) was utilized. It was originally used for binary classification. The principle of operation of the SVM algorithm, for the simplest problem of recognizing two classes, is to find a hyperplane that separates elements belonging to both classes. The hyperplanes fulfilling this condition are infinitely many, however, should be found optimal. For this purpose, the algorithm first finds the support vectors located at the periphery of the considered classes, and then determines the optimal hyperplane spaced from the elements of both classes (extreme vectors) with the maximum (the widest) margin. The effectiveness of the SVM algorithm depends on its type: C-SVC, nu-SVC, epsilon-SVR, nu-SVR and the type of the kernel function (Cristianini & Schölkopf, 2002; Scholkopf & Smola, 2001):
   - linear: $K(x_i, x) = X^T X_i$
   - polynomial: $K(x_i, x) = (yx^T x + c^d)$
   - radial (Radial Basis Function - RBF): $K(x_i, x) = -\gamma \|x - x_i\|^2, \quad \gamma > 0$
   - Gaussian RBF: $K(x_i, x) = exp(-\|x - x_i\|)^2/2\sigma^2$
   - sigmoid: $K(x_i, x) = tanh(yx^T x_i + c)$
4. **k-Nearest Neighbor** (kNN) - a non-parametric method used for classification and regression (Altman, 1992). The most famous minimum-distance classifier. This method consists in assigning a classified sample to the most common class among its neighbors, in the sense of a determined distance measure. The most commonly used distance measures are: *Euclideandistance* or *Manhattandistance*. Less frequently used, due to the higher computational cost, are metrics: *Chebyshev* or *Mahalonobis*. The *k*-NN classifier learning process consists in selecting parameter *k*. Many different methods of selecting this parameter have been proposed in the literature. However, the simplest and most commonly used method is cross-validation.

The classification of the samples with the machine learning methods used in the present research was based on the Winner-Takes-All (WTA) rule. This means that the classification algorithm, depending on the value of certain algorithm-dependent response parameters, always assigns exactly one class identifier to a test sample, independent of the number of classes.

2.2.6. Step VI - Parameter optimization

The aim of this stage was to increase the efficiency of the designed algorithms.

Two methods for the parameter optimization were applied and compared:

- **Grid search** (Bergstra & Bengio, 2012) - this is a traditional method of hyperparameter optimization group, which consists in a complete search of a hand-specific subset of the space, the optimized parameter of the classifier, and
- **Genetic Algorithm**, Section 2.2.3 (Holland, 1992; Rutkowski, 2008).

2.3. Assumptions

The adopted research methodology consisted of the following assumptions, not described in Sections 2.1 and 2.2:

A1 Not applying signal filtering due to both the use of Welch's method and the genetic selection of features and
A2 Not applying the QRS complex detection and segmentation of the ECG signal.
A3 Analyzing ECG signals fragments that contain one class type (except of normal sinus rhythm).

2.4. Experiments

Four experiments were conducted based on the analysis of the ECG signal according to the assumptions from Sections 2.1–2.3: 1) basic analysis of ECG signals, 2) genetic optimization of parameters, 3) genetic selection of features and 4) enlarged database (from 744 ECG fragments and 29 patients to 1000 ECG fragments and 45 patients). 3 types of normalization, 4 widths of Hamming window, 2 types of cross-validation, 4 types of classifiers and 2 methods of parameter optimization were tested.

Fig. 1 shows the scheme of one of the conducted experiments.

2.5. Evolutionary-neural system

In research designed an evolutionary-neural system that consisted of a classifier (e.g., SVM) trained 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.

Table 2 contains detailed information about the genetic algorithm and optimum values of parameters for evolutionary-neural systems. Procedure No. 1 presented the evolutionary-neural system algorithm.

2.6. Evaluation criteria

To evaluate the designed classifiers, the following coefficients were determined (Fawcett, 2006; Sokolova & Lapalme, 2009): 1) the 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 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) Classification time T_c.

The definitions of the calculated coefficients are as follows:

- **Accuracy**

$$ACC = \left(\sum_{i=1}^{N} \frac{TP + TN}{TP + FP + TN + FN} \right) \cdot 100\%/N \tag{9}$$

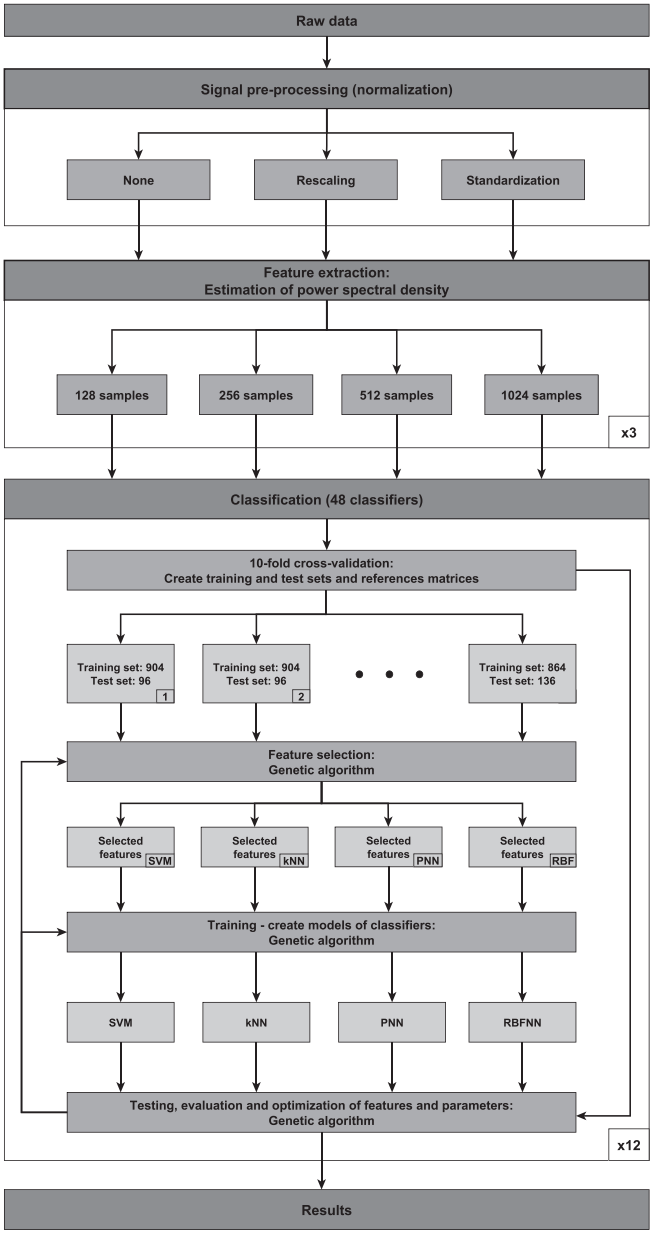

Fig. 1. Scheme of Experiment.

- **Sensitivity**

$$SEN = \left(\sum_{i=1}^{N} \frac{TP}{TP + FN} \right) \cdot 100\%/N \tag{10}$$

- **Specificity**

$$SPE = \left(\sum_{i=1}^{N} \frac{TN}{FP + TN} \right) \cdot 100\%/N \tag{11}$$

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

Table 2
Detailed information about designed evolutionary-neural systems.

Feature selection and classifier parameter optimization	
The *genetic algorithm* coupled with the 10-fold cross-validation method was used for feature selection and classifier parameter optimization	
GENETIC ALGORITHM	• Number of individuals in the population: 50; • Type of gene representation: floating-point vectors; • Chromosome construction of individual: Floating point vector of the form $[g_1, g_2, c_1, \ldots, f_{4001}]$ for *SVM*, where g_1 – the first gene, which determines the value of the first parameter, γ, g_2 – the second gene, which determines the value of the second parameter, ν, 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. For the other classifiers (*kNN*,*PNN*, and *RBFNN*), the chromosome consists of one gene, *g*, which determines the value of one optimized parameter; • Initial population: random, uniform; • Range of the gene values for the initial population: 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]; • Target value of fitness function: 0; • Maximum number of generations: 30; • Type of crossover: intermediate; Probability of crossover: 0.7; • Type of mutation: uniform; Probability of mutation: 0.3; • Number of individuals in current generation that are guaranteed to survive to the next generation: 3; • Method of scaling the value of the fitness function: ranking; • Method of parent selection: tournament; • Fitness function of individuals calculated based on the following formula: $ERR = w_l \cdot err_{Lsum} + w_t \cdot err_{Tsum} + w_f \cdot \frac{F_a}{F}$ (8) 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; err_{Lsum} – total number of errors in the 10 training sets; err_{Tsum} – total number of errors in the 10 test sets; $\frac{F_a}{F}$ – acceptance feature coefficient: the ratio of the number of accepted 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 to approximately 2000 features (frequency components of the ECG signal) - Table 3;
CLASSIFIERS	
Basic parameters	
SVM	• Type: nu-SVC; • Kernel function type: RBF (radial, Gaussian type); • Number of outputs = 1, from the set: {1, ..., 17};
KNN	• Number of nearest neighbors = 1; • Metric of distance calculation: *Minkowski*; • Number of outputs = 1, from the set: {1, ..., 17};
PNN	• Activation function: radial (Gaussian type) - competition; • Training algorithm: mapping of training set based on distance; • Method of calculating the objective function: sse; • Topology (neurons): length of the feature vector – 904∨864 – 17; Biases: 1 – 0; • Number of outputs = 17, from the set: {0, 1};
RBFNN	• Activation function: radial (Gaussian type) - linear; • Training algorithm: mapping of training set based on distance; • Method of calculating the objective function: sse; • Topology (neurons): length of the feature vector – 904∨864 – 17; Biases: 1 – 1; • Number of outputs = 17, from the set: {0, 1}. Value of "1" assigned to the output (class) with the highest stimulus;
Optimized parameters	
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;
KNN	• The parameter *exponent* affects the calculation of the Minkowski distance from the range [0.01; 100], with resolution 10^{-14}, $50 \cdot 20 = 1000$ values;
PNN	• The parameter *spread* determines the spread of the radial basis function (RBF) of the network kernel from the range [1; 100], with resolution 10^{-14}, $50 \cdot 20 = 1000$ values;
RBFNN	• The parameter *spread* determines the spread of the radial function (RBF) of the network kernel from the range [1; 300], with resolution 10^{-14}, $50 \cdot 20 = 1000$ values;

multi-class problems concerning the recognition of more than two classes. A higher value indicates a better result.

$$\kappa = \left(\sum_{i=1}^{N} \frac{M \sum_{j=1}^{n} m_{j,j} - \sum_{j=1}^{n} (G_j C_j)}{M^2 - \sum_{j=1}^{n} (G_j C_j)} \right) \cdot 100\% / N \tag{12}$$

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 1000 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:

$$C_F = \frac{F_a}{F} \cdot 100\% \tag{13}$$

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 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 5), the sensitivity coefficient (SEN) is equal to the overall accuracy coefficient (Acc) from the literature (de Chazal et al., 2004; da S. Luz et al., 2016). This is because the WTA (Winner-Takes-All) method was used for the classifiers.

3. Results

All combinations of methods (2.4) have been tested on a smaller database containing 744 ECG fragments and 29 patients. This article presents the results for the 8 paths that have achieved the highest sensitivity (SEN): 1 type of normalization x 2 Hamming window widths x 4 types of classifiers. The results obtained were very similar for both variants of databases (744 and 1000 ECG fragments).

The study utilized the MATLAB R2014b environment together with the LIBSVM library (Chang & Lin, 2011). The computations were performed on an Intel Core i7-6700K 4.0 GHz machine with 32GB of RAM (only a single core was used). The total computation times, consisting of the training, testing, and optimization phases, are shown in Tables 3 and 4.

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).

The optimization time needed to obtain the results can be shortened multiple times by parallelization the computation.

3.1. Preprocessing with normalization

In Fig. 2, a comparison of the following ECG signal fragments is presented: **A** – concentration within the classes: normal sinus rhythm (all fragments of the ECG signal, where other colors represent signals from other patients); **B** – separation between all 17 classes (only the first fragments of the ECG signal for each class, where other colors represent the signals from other classes). The graphs show the 10-s fragments of the ECG signals after normalization based on rescaling the signal to the range $[-1, 1]$, reducing the constant component, and performing feature extraction based on the DFT with a Hamming window with a width of 512 samples.

3.2. Experiments

This section presents the results of evolutionary-neural systems, which achieved the highest recognition sensitivity for heart disorders. 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 1000 classifications (in the training sets, in all cases, the sum of the errors equals zero).

Table 3 presents detailed results on 4 types of classifiers (SVM, kNN, PNN and RBFNN), 1 type of signal pre-processing method (rescaling + reduction in constant component) and 2 types of feature extraction (2 widths of the Hamming window: 512 and 1024 samples) for one variant of the cross-validation method - 10-fold cross-validation, and for 1000 ECG signal fragments.

In Figs. 3 and 4, the detailed results for the best classifier - *SVM* from Table 3 - are presented. In Fig. 3, the following coefficient values are presented: the sum of errors (ERR), accuracy (ACC), sensitivity (SEN), and specificity (SPE) for each class. Fig. 4 presents the coefficient value comparison of the sum of errors (ERR), accuracy (ACC), sensitivity (SEN), specificity (SPE), and κ coefficient for the recognition of 17, 15, and 13 classes.

In Table 4, a comparison of the obtained results for 4 designed classifiers is presented.

Table 3
The results of evolutionary-neural systems for 10-fold cross-validation. In all training sets, in all cases, the sum of the errors equals zero.

Normalization:	Window width:	Classifiers: SVM	kNN	PNN	RBFNN
RESCALING + REDUCTION OF CONSTANT COMPONENT	**512 SAMPLES**	$-g = 3.04e-5$			
		$-n = 0.0118$	*exponent* = 2.88	*spread* = 18.87	*spread* = 154.14
		$\boldsymbol{ERR_{sum} = 98}$	$\boldsymbol{ERR_{sum} = 117}$	$\boldsymbol{ERR_{sum} = 114}$	$\boldsymbol{ERR_{sum} = 115}$
		$ACC = 98.85\%$	$ACC = 98.62\%$	$ACC = 98.66\%$	$ACC = 98.65\%$
		$\boldsymbol{SEN = 90.20\%}$	$\boldsymbol{SEN = 88.30\%}$	$\boldsymbol{SEN = 88.60\%}$	$\boldsymbol{SEN = 88.50\%}$
		$SPE = 99.39\%$	$SPE = 99.27\%$	$SPE = 99.29\%$	$SPE = 99.28\%$
		$\boldsymbol{\kappa = 88.49\%}$	$\boldsymbol{\kappa = 86.38\%}$	$\boldsymbol{\kappa = 86.68\%}$	$\boldsymbol{\kappa = 86.51\%}$
		$C_F = 48.56\%$	$C_F = 49.44\%$	$C_F = 49.74\%$	$C_F = 49.54\%$
		$T_t = 18.7926\ [s]$	$T_t = 0.1280\ [s]$	$T_t = 0.5855\ [s]$	$T_t = 99.7178\ [s]$
		$\boldsymbol{T_c = 0.0023\ [s]}$	$\boldsymbol{T_c = 0.0701\ [s]}$	$\boldsymbol{T_c = 0.0079\ [s]}$	$\boldsymbol{T_c = 0.0076\ [s]}$
		$T_o = about\ 135$ [h]	$T_o = about\ 170$ [h]	$T_o = about\ 135$ [h]	$T_o = about\ 155$ [h]
	1024 SAMPLES	$-g = 2.52e-5$			
		$-n = 0.0207$	*exponent* = 1.57	*spread* = 26.17	*spread* = 174.65
		$\boldsymbol{ERR_{sum} = 115}$	$\boldsymbol{ERR_{sum} = 134}$	$\boldsymbol{ERR_{sum} = 121}$	$\boldsymbol{ERR_{sum} = 119}$
		$ACC = 98.65\%$	$ACC = 98.42\%$	$ACC = 98.58\%$	$ACC = 98.60\%$
		$\boldsymbol{SEN = 88.50\%}$	$\boldsymbol{SEN = 86.60\%}$	$\boldsymbol{SEN = 87.90\%}$	$\boldsymbol{SEN = 88.10\%}$
		$SPE = 99.28\%$	$SPE = 99.16\%$	$SPE = 99.24\%$	$SPE = 99.26\%$
		$\boldsymbol{\kappa = 86.44\%}$	$\boldsymbol{\kappa = 84.33\%}$	$\boldsymbol{\kappa = 85.85\%}$	$\boldsymbol{\kappa = 85.99\%}$
		$C_F = 48.26\%$	$C_F = 49.66\%$	$C_F = 49.09\%$	$C_F = 49.61\%$
		$T_t = 29.1564\ [s]$	$T_t = 0.1290\ [s]$	$T_t = 0.5173[s]$	$T_t = 91.7492\ [s]$
		$\boldsymbol{T_c = 0.0028\ [s]}$	$\boldsymbol{T_c = 0.0680\ [s]}$	$\boldsymbol{T_c = 0.0072\ [s]}$	$\boldsymbol{T_c = 0.0072\ [s]}$
		$T_o = about\ 135$ [h]	$T_o = about\ 170$ [h]	$T_o = about\ 135$ [h]	$T_o = about\ 155$ [h]

Table 4
A comparison of the obtained results for 4 designed classifiers, 1000 ECG fragments, 10-fold cross-validation method, genetic optimization and genetic feature selection. In all training sets, in all cases, the sum of the errors equals zero.

Coefficients	Classifiers: kNN	RBFNN	PNN	SVM
Results obtained for the best case (combination of classifier + normalization + window width)				
Normalization	*Rescaling*	*Rescaling*	*Rescaling*	*Rescaling*
Window	512	512	512	512
$\boldsymbol{ERR_{SUM}}$	***117***	***115***	***114***	***98***
ACC	98.62%	98.65%	98.66%	98.85%
SEN	***88.30%***	***88.50%***	***88.60%***	***90.20%***
SPE	99.27%	99.28%	99.29%	99.39%
$\boldsymbol{\kappa}$	***86.38%***	***86.51%***	***86.68%***	***88.49%***
$\boldsymbol{C_F}$	49.44%	49.54%	49.74%	48.56%
$\boldsymbol{T_t}$ ***[s]***	0.1280	99.7178	0.5855	18.7926
$\boldsymbol{T_c}$ ***[s]***	***0.0701***	***0.0076***	***0.0079***	***0.0023***
$\boldsymbol{T_o}$ $[H]$	170	155	135	135
Average result for all cases of experiment				
$\boldsymbol{ERR_{SUM}}$	***125.5***	***117.0***	***117.5***	***106.5***
ACC	98.52%	98.63%	98.62%	98.75%
SEN	***87.45%***	***88.30%***	***88.25%***	***89.35%***
SPE	99.22%	99.27%	99.27%	99.34%
$\boldsymbol{\kappa}$	***85.36%***	***86.25%***	***86.27%***	***87.47%***
$\boldsymbol{C_F}$	49.55%	49.58%	49.42%	48.41%
$\boldsymbol{T_t}$ $[S]$	0.1285	95.7335	0.5514	23.9745
$\boldsymbol{T_c}$ $[S]$	***0.0691***	***0.0074***	***0.0076***	***0.0026***
$\boldsymbol{T_o}$ $[H]$	170	155	135	135

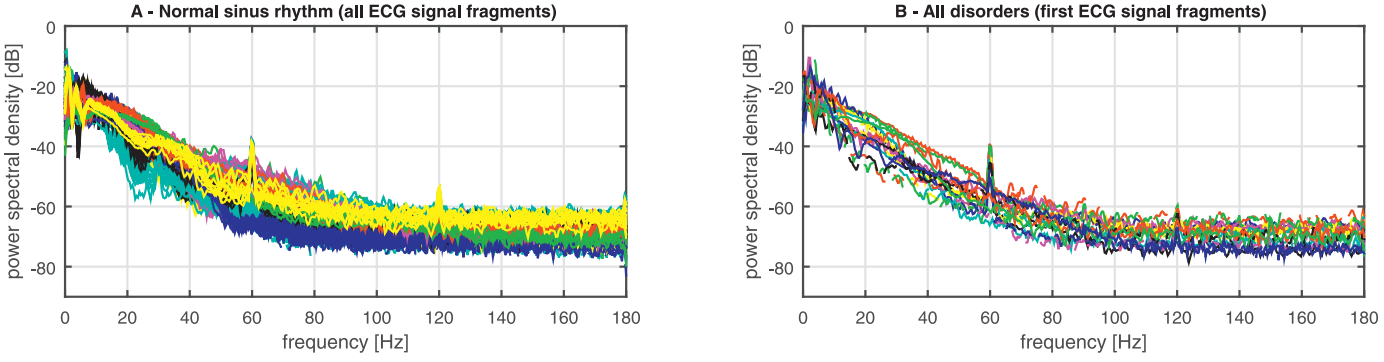

Fig. 2. Comparison of the analyzed classes after applying the DFT and logarithm procedure: **A** – concentration within the classes: normal sinus rhythm (all fragments of the ECG signal, where the other colors represent signals from other patients); **B** – separation between all 17 classes (only the first fragments of the ECG signal for each class, where the other colors represent the signals from other classes).

Table 5
A comparison of the results under the methods based on the subject-oriented validation scheme and the same database - MIT-BIH Arrhythmia (da S. Luz et al., 2016).

No.	Work	Year	# of classes	Feature set	Classifier	Acc=SEN
1.	Escalona-Moran et al. (2015)	2008	5	Raw wave	RC	98%
2.	Huang et al. (2014)	2014	5	Random projection, RR-intervals	Ensemble of SVM	94%
3.	Llamedo and Martinez (2011)	2011	5	Wavelet, VCG + SFFS	Weighted LD	93%
4.	Lin and Yang (2014)	2014	5	Normalized RR-interval	Weighted LD	93%
5.	Bazi, Alajlan, AlHichri, and Malek (2013)	2013	5	Morphological, Wavelet	SVM, IWKLR, DTSVM	92%
6.	Soria and Martinez (2009)	2009	5	RR-Intervals, VCG, morphological + FFS	Weighted LD	90%
7.	Mar et al. (2011)	2011	5	Temporal Features, Morphological, statistical features + SFFS	Weighted LD, MLP	89%
8.	Zhang and Luo (2014)	2014	5	RR-intervals, morph. features, ECG-inter. and segments, wavelet coeff.	Combined SVM	87%
9.	Zhang et al. (2014)	2014	5	RR-intervals, morphological features, ECG-intervals and segments	Combined SVM	86%
10.	Ye, Kumar, and Coimbra (2012b)	2012	5	Morphological, Wavelet, RR interval, ICA, PCA	SVM	86%
11.	Park et al. (2008)	2008	5	HOS, HBF	Hierarchical SVM	85%
12.	de Lannoy, Francois, Delbeke, and Verleysen (2012)	2012	5	RR-intervals, ECG-segments, morphological, HBF, HOS	Weighted CRF	85%
13.	de Chazal et al. (2004)	2004	5	ECG-Intervals, Morphological	Weighted LD	83%
14.	de Lammoy, Francois, Delbeke, and Verleysen (2010)	2010	5	ECG-Intervals, morphological, HOS, HBF coefficients	Weighted SVM	83%
	Pławiak		**13**	**Frequency components of the power spectral density of the ECG signal**	**Evolutionary-Neural System (based on SVM)**	**95%**
			15			**91%**
			17			**90%**

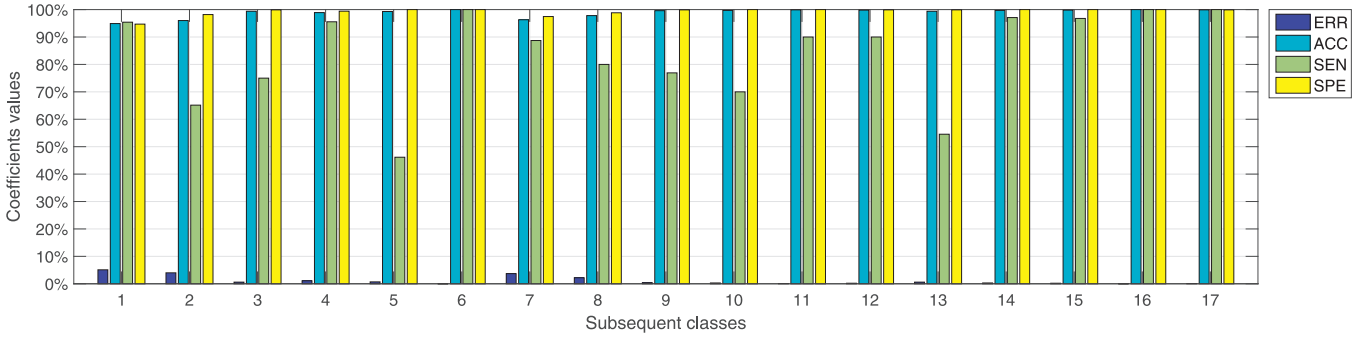

Fig. 3. Comparison of coefficient values for each class.

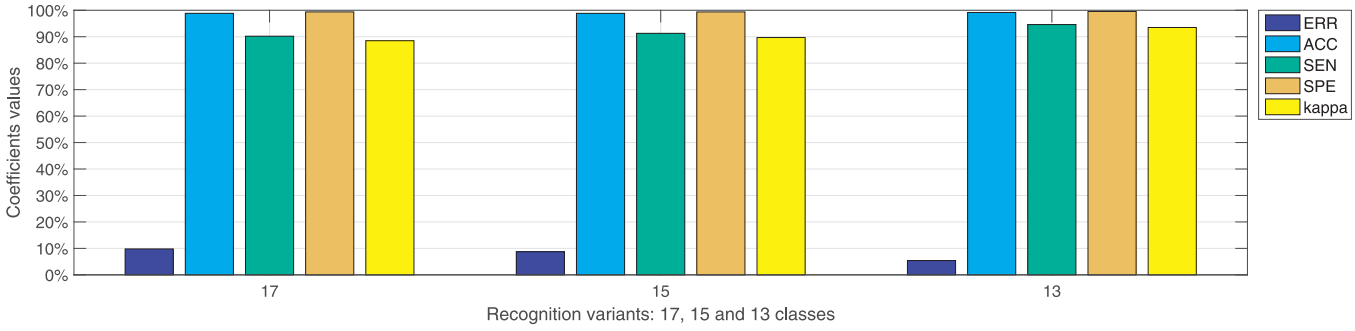

Fig. 4. Comparison of coefficient values for the recognition of 17, 15, and 13 classes.

In Table 5, 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 in our work is presented. The summary is based on the same database - MIT-BIH Arrhythmia, and the more objective subject-oriented validation scheme (Afkhami et al., 2016; da S. Luz et al., 2016) and includes information about the applied ECG signal analysis methods.

4. Discussion

4.1. Hypothesis

The results obtained in all experiments confirmed the thesis: the application of the proposed methodology will enable the automatic, efficient, universal, low computational complexity and fast

Algorithm 1: Evolutionary-neural system.

Data:
X – matrix with raw data;
R – matrix with reference answers;
$svm_{type} \leftarrow 1$ – defining the type of *SVM* on $\nu - SVC$;
$kernel_{type} \leftarrow 2$ – defining the type of kernel function on *RBF*;
Result:
B – vector of the form $[f_p, g_1, g_2, c_1, \ldots, c_{4001}]$, with associated values of the fitness function (f_p); the determined optimal parameters of the *SVM* classifier, γ and ν; and the selected features;
O_L and O_T – matrices with the classifier responses of the *SVM*;
CF – confusion matrix with the classifier responses of the *SVM*; and
E – vector with the calculated evaluation coefficients of the *SVM*;

```
Perform one type of signal pre-processing based on X
Perform one type of feature extraction
Create training and test sets and reference matrices based on R
Set genetic algorithm parameters (Table 2);
GENETIC ALGORITHM:
Create an initial population of individuals
for i ← 1 to 20 (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 c ← 1 to 10 (number of set combinations) 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_f)
        Save the related values B for the fitness function (f_f), classifier parameters and selected features as well as the matrices with classifier responses: O_L and O_T
    end
    if f_f == 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
```

recognition of heart disorders based on ECG signal analysis and the evolutionary-neural system.

The confirmation of this statement is given by the obtained results, summarized in Tables 3–5 and in Sections 4.11, 4.9. The presented results show that the recognition **sensitivity** of the 17 classes for the best evolutionary-neural system based on the *SVM* classifier (rescaling + 512 samples) is ***SEN*** = **90.20**% (*ACC* = 98.85%, *SPE* = 99.39%). This result is higher than the average sensitivity of the results presented in the current scientific literature, which is **88.86%** (Table 5). The obtained result is one of the best in the scientific literature, where the three best results are ***Acc/SEN*** = **98%** (Escalona-Moran, Soriano, Fischer, & Mirasso, 2015), **94%** (Huang et al., 2014) and **93%** (Lin & Yang, 2014; Llamedo & Martinez, 2011) (Table 5). It should be noted that the results obtained in our work include the recognition of 17 classes (a recognition sensitivity for 15 and 13 classes of 91% and 95%; Fig. 4). In contrast, the results presented in the scientific literature include the recognition of only 5 classes (for the subject-oriented validation scheme (da S. Luz et al., 2016)).

The obtained classification time for the ECG signal fragments, $\boldsymbol{C_k}$ = **0.0023 [s]**, for the best evolutionary-neural system based on the *SVM* classifier is also very important.

4.2. Machine learning algorithms

Based on the results obtained in research and presented in Tables 3 and 4, we find that the best classifier was the **SVM** classifier (ERR_{sum} = 98 errors and average = 106.5 errors; *SEN* = 90.20% and average = 89.35%); the other classifiers obtained worse results, respectively: **PNN** (ERR_{sum} = 114 errors and average = 117.5 errors; *SEN* = 88.60% and average = 88.25%), **RBFNN** (ERR_{sum} = 115 errors and average = 117.0 errors; *SEN* =88.50% and average = 88.30%) and **kNN** (ERR_{sum} = 117 errors and average = 125.5 errors; *SEN* = 88.30% and average = 87.45%).

4.3. Preprocessing with normalization

Based on the results obtained in research, we find that the best signal normalization method was the **rescaling** method (ERR_{sum} = 98 errors and average = 116.63 errors; *SEN* = 90.20% and average = 88.34%); the other methods obtained lower results, respectively: **standardization** (average *SEN* lower by about 1.0% from rescaling) and **no normalization** (average *SEN* lower by about 1.5% from rescaling).

4.4. Feature extraction

Based on the results obtained in research and presented in Tables 3 and 4, we find that the greatest efficiency for feature extraction was based on Hamming windows with widths of **512 samples** (ERR_{sum} = 98 and average = 111.00 errors; *SEN* = 90.20% and average = 88.90%) and **1024 samples** (ERR_{sum} = 115 and average = 122.25 errors; *SEN* = 88.50% and average = 87.78%); other Hamming window widths obtained lower results, respectively: **256 samples** (average *SEN* lower by about 1.5% from 512 samples), and **128 samples** (average *SEN* lower by about 2.5% from 512 samples).

The obtained result indicates that the best result was achieved under one of the widest Hamming windows: 512 samples. This width corresponds to an analysis window with a duration of approximately 1.25 [s] (approximately 2 heart evolutions), assuming that one evolution of the heart corresponds to approximately 310 samples of the ECG signal. The obtained result confirms the validity of the research methodology based on the analysis of longer (10-s) fragments of the ECG signal because the results for the narrower Hamming windows (256 samples) corresponding to a single evolution of the heart were characterized by lower recognition efficiency for heart disorders.

4.5. Feature selection

In research tested the effect of the applied genetic selection of the features. The applied feature selection increased the recognition sensitivity of heart pathology due to the removal of redundant or misleading information. Another positive effect of its utilization was the reduction in the length of the input feature vector.

This resulted in an increased effect of the knowledge generalization achieved by the classifiers, reduced effect of over-fitting and reduced training, and classification times. The aim of the genetic selection of features was to eliminate the frequency components corresponding to noise, measurement errors, network voltage components, baseline wandering, and redundant information.

The confirmation of the presented findings is given by the obtained results. From the results, it follows that the applied feature selection increased the recognition effectiveness of heart dysfunctions (average *SEN* higher by about 1.0%) and decreased the sample training and classification times (about 2-fold).

Based on the obtained results presented in Tables 3 and 4, it can be observed that the average number of accepted features is $\boldsymbol{C_F}$ = **49.24%**. This means that the optimal results (highest sensitivity) were obtained after rejecting about half of the features (the frequency components of the ECG signal power spectral density) from the input vector.

4.6. Cross-validation

Based on the obtained results, it can be stated that higher sensitivity (average *SEN* higher by about 2.0%) were achieved under **10-fold cross-validation**, than under a 4-fold cross-validation method.

The 4-fold cross-validation method is less computationally complex, but based on the obtained results, the method achieves a lower efficiency. Because fewer classifiers models were created based on this method and because the created models learned on fewer elements of the training set, the models produced a worse fit to the recognition classes.

4.7. Parameter optimization

Based on the obtained results, it can be stated that higher sensitivity (average *SEN* higher by about 1.5%) were obtained under the **genetic algorithm**, than under the grid search method.

The obtained result is as expected. By using a genetic algorithm, it was possible to search a much larger solution space compared to the grid search method. Another advantage was the much higher resolution (smaller step size) for the tested parameters. These two features resulted in the substantially better GA score.

4.8. Dysfunctions/classes

One of the biggest difficulties in analyzing the ECG signal observed during this research is the variability of the morphological and dynamic features within a given class (disorder) for different patients. This problem was presented for the *normal sinus rhythm* class for 23 different patients in Fig. 2A for ECG signals after the DFT was applied. The variability of the signals within one class for different patients is very large and comparable to the variability of the shapes of the ECG signals for different classes, as presented in Fig. 2B.

In Fig. 3, the recognition efficiency for each class is presented with the best classifier - *SVM*. Based on this, we can observe a high recognition efficiency for practically all classes: ***SEN* over 65%**. The worst results were obtained for *supraventricular tachyarrhythmia* (*SEN* over 46%) and *fusion of ventricular and normal beat* (*SEN* over 55%).

Based on the obtained results presented in Fig. 3, we removed dysfunctions with the smallest value of the *SEN* coefficient. As a result, two other recognition cases were considered: **15 classes** (after removing the *supraventricular tachyarrhythmia* and *fusion of ventricular and normal beat* classes) and **13 classes** (after removing the *premature ventricular contraction*, *supraventricular tachyarrhythmia*, *ventricular tachycardia* and *fusion of ventricular and normal beat* classes). The best classifier, *SVM*, obtained the following sensitivity for heart dysfunction recognition for **17, 15 and 13 classes**, respectively: ***SEN*** = **90.20%**, **91.28%**, and **94.60%** and κ = **88.49%**, **89.69%**, and **93.49%**.

4.9. Times

4.9.1. Parameter optimization

Research confirms the superiority of the genetic algorithm over grid search. GA achieved better results in a comparable amount of time. It should also be noted that the **training and classification times were significantly shortened** (about 2-fold) when was applying the **feature selection**.

4.9.2. Classifiers

Based on Table 4, we can state that the **training** of the **kNN** classifier was the **fastest** and that the **training** of the **RBFNN** classifier was the **slowest**: average T_t [s] = 0.1285 and 95.7335, respectively. The **classification** of the ECG signal fragments by the **SVM** classifier was the **fastest**, and the **classification** by the **kNN** classifier was the **slowest**: average T_c [s] = 0.0026 and 0.0691, respectively. The **optimization** of the **SVM** and **PNN** classifiers was the **fastest**, and the **optimization** of the **kNN** classifier was the **slowest**: average T_o [h] = 135 and 170, respectively.

4.9.3. Cross-validation

Based on obtained results, we can state that, as expected, training, classification, and optimization **lasted much longer** (2.5 times) **under 10-fold cross-validation** than under 4-fold cross-validation.

4.10. Enlarged database

Based on obtained results, i.a. Table 4, we can state that, enlarging the database from **744** to **1000 ECG fragments** and increasing the **number of patients** from **29** to **45** practically did not affect on the effectiveness of the classification of cardiac disorders and all the dependencies between the tested methods were retained. For the best case (classifier: SVM + normalization type: rescaling + Hamming window width: 512 samples) obtained a slightly higher value of sensitivity (*SEN*) for the enlarged database, respectively, for 1000 and 744 fragments of the ECG signal: $\boldsymbol{ERR_{sum}}$ = 98 and 73 errors; ***SEN*** = **90.20%** and **90.19%**.

4.11. Computational complexity

The proposed approach has the huge advantage of **lower computational complexity**. 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. Computational complexity are only high on training and optimization stages, while the classification stage is much less computationally complex than the classical approach (based on QRS complex detection). This opens the possibility to use the solution in practice, in mobile devices (less CPU and memory load, lower power consumption, longer battery life).

5. Conclusion

The aim of the conducted research was to develop a new methodology that enables the efficient recognition of myocardium dysfunctions (17 classes: normal sinus rhythm + pacemaker rhythm + 15 heart disorders), based on analysis of 10-s fragments of ECG signals and an evolutionary-neural system. In this

research, 1000 fragments of ECG signals were analyzed from the MIH-BIH Arrhythmia database for one lead, MLII, from 45 patients. Four experiments were conducted, during which many methods were applied and tested concerning the following: signal preprocessing and normalization, feature extraction and selection, cross-validation, machine learning algorithms (SVM, kNN, PNN, and RBFNN classifiers), parameter optimization and enlarged database.

The best evolutionary-neural system based on the SVM classifier obtained a recognition sensitivity of 17 myocardium dysfunctions at a level of 90.20% (98 errors per 1000 classifications, accuracy = 98.85%, specificity = 99.39%, time of classification for one sample = 0.0023 [s]). Against the background of the current scientific literature, these results represent some of the best results obtained.

The obtained results fully confirm the validity of the conducted research and prove that the aims (Section 1) was realized - we developed a novel methodology for the automatic, efficient (Table 5), universal (Table 1), low computational complexity (Section 4.11) and fast (Section 4.9) recognition of heart pathologies.

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) not applying the QRS complex detection and segmentation of the ECG signal, and 5) not applying signal filtering. To the disadvantages we can include: 1) not applying completely subject-oriented validation scheme (inter-patient paradigm), due to insufficient number of appropriate ECG signals in MIT-BIH database, 2) no possibility of analyzing ECG signals fragments that contain more than one class type (except of normal sinus rhythm).

This research is worth continuing in order to: increase the recognition sensitivity for heart disorders and overcome the limitations. Further research will focus on: 1) testing the feature extraction based on wavelet analysis, 2) testing ensembles of classifiers and deep learning methods, 3) analyzing fragments of ECG signals from more leads (2–12), 4) testing more types of windows (e.g. rectangular, Kaiser, Gaussian), 5) analyzing ECG signals fragments that contain more than one class type, 6) collecting more number of appropriate ECG signal fragments.

Future research will also include the construction of a prototype of mobile device for recording ECG signals with implemented algorithms for diagnosing heart disorders. This will allow to use the proposed solution in clinical trials. The ultimate aim of the research will be to design a tele-medicine system for patient self-control and prevention applications.

Acknowledgments

We thanks Professor R. Tadeusiewicz and Professor Z. Tabor for their valuable advice and guidance on the preparation of this paper.

Supplementary material

Supplementary material associated with this article can be found, in the online version, at 10.1016/j.eswa.2017.09.022

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