Original Article

Detection and Classification of Myocardial Infarction with Support Vector Machine Classifier Using Grasshopper Optimization Algorithm

Abstract

Background: Providing a noninvasive, rapid, and cost-effective approach to diagnose of myocardial infarction (MI) is essential in the early stages of electrocardiogram (ECG) signaling. In this article, we proposed the new optimization method for support vector machine (SVM) classifier to MI classification. **Methods:** After preprocessing ECG signal and noise removal, three features such as Q-wave integral, T-wave integral, and QRS-complex integral have been extracted in this study. After that, different statistical tests have evaluated the matrix of these features. To more accurately detect and classify the MI disease, optimizing the SVM classification parameters using the grasshopper optimization algorithm (GOA) was first used in this study (that called SVM-GOA). **Results:** After applying the GOA on the SVM classifier for all three kernels, the final results of MI detection for sensitivity, specificity, and accuracy were 100% ± 0%, 100% ± 0%, and 100% ± 0%, respectively. The final results of different MI types' classification after applying the GOA on SVM for polynomial kernel were obtained 100% ± 0%, 97.37% ± 0%, and 94.2% ± 0.2% for sensitivity and specificity and accuracy, respectively. However, the results of both linear and RBF kernels that were used for the SVM classifier method have also shown a significant increase after using GOA. **Conclusion:** This article's results show the highly desirable effect of applying a GOA to optimize different kernel parameters used in the SVM classifier for accurate detection and classification of MI. The proposed algorithm's final results show that the proposed system has a relatively higher performance than other previous studies.

Keywords: *Biomedical signal processing, electrocardiogram, grasshopper optimization algorithm, myocardial infarction, support vector machine classifier*

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Introduction

Myocardial Infarction (MI) is permanent and irreversible cell death of the heart muscle that occurs due to the loss of blood flow and severe ischemia in that part of the heart.[1] Despite all advances in the medical sciences and the facilitation of the diagnosis and treatment of cardiovascular disease, unfortunately, the prevalence of this disease increases, so it is a significant concern of the World Health Organization. MI accounts for 15.53% of total deaths by 2015.[2] Electrocardiogram (ECG), clinical trials, echocardiogram imaging, and MRI can use to diagnose this disease.[3] ECG is one of the most widely used noninvasive diagnostic tools for diagnosing heart disease, including MI. Diagnosis of this disease in the early stages can prevent the disease's progression and eventually, MI. Therefore, early detection of this disease has always been the goal of many researchers in this field. Besides, detection using ECG signals is of great importance due to its availability and low cost compared to costly cardiac echocardiogram and MRI methods. There are several methods for diagnosing MI so far, some of which are briefly reviewed in follow. Sugimoto *et al.*, in 2019, presented a method for the diagnosis of MI based on cannulation networks.[4] This method uses an ECG signal with 12 leads. In that study, researchers at first developed a convolution-based model for healthy ECG signals. The computer-aided engineering model is then built for each lead, and if normal ECG data is input, normal ECG data will be restored. Otherwise, the output waveform will be corrupted for inappropriate data. In the next step, the

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classification of healthy and MI data based on model error reconstruction was performed using the K-nearest neighbor (KNN) method. Finally, this classification method's final results are reported higher than other existing methods.[4] Panagiotis Barmpouti *et al.* in 2019 proposed the method based on multi-LEAD ECG signal analysis for the diagnosis of MI through Grassmannian and Euclidean mapping.[5] In this study, the multidimensional signal is first transformed into a third order tensor structure, and feature extraction is performed in both Euclidean and Grassmannian spaces. In addition, two different methods for mapping two various features in a Hilbert space are presented. Finally, this method's final accuracy in the diagnosis of MI is 100%.[5] In 2019, Sharm and Sunkaria proposed a method for diagnosing and localizing MI using optimal features.[6] After preprocessing and noise removal from the ECG signal, the wavelet transforms are used for ECG decomposition in this study. Then energy, entropy, and slope-based features in specific bands of ECG signal were extracted. Finally, the KNN classification method is used to diagnose the disease. According to the authors' report, this method can be effectively used with one lead to detect MI and localize it.[6] In 2018, Ketcham and Muankid presented an algorithm to probe the ECG signal to classify MI. The steps reported in this study include R-wave detection, QRS complex detection, and then MI disease classification.[7] In 2016, Pereira and Daimiwal presented a method for analyzing wavelet transform-based features for the diagnosis of MI.[8] In this study, the 21-lead ECG signal was decomposed using a wavelet transform, and then multiple features were extracted from different subbands. It has been observed that the statistical features extracted from different ECG subbands were differed for the two groups of healthy and diseased and have been used for classification.[8] In 2015, Bhaska *et al.* presented a method for analyzing and diagnosing MI using support vector machine (SVM) algorithms and artificial neural networks. In that study, LIBSVM (A Library for Support Vector Machines) was studied to classify with SVM and artificial neural networks with different hidden layers.[9] Remya *et al.*, in 2016, presented a study for the classification of anterior and posterior MI using wavelet analysis. In this study, the R-peaks and ST-segment amplitude were considered features, and the adaptive threshold was selected for the classification method. The final classification accuracy for anterior MI was 93.22% and posterior MI 83.33%.[10] In 2018, Lui and Chow proposed a method to classify MI based on recursive and convolutional neural networks using one lead of ECG signals. In that study, after preprocessing and noise removal from ECG signals, convolutional neural networks and recursive neural networks were used for classification, and the absolute accuracy was reported as 92.4%.[11] Chang *et al.*, in 2012, presented the method for the classification of MI based on Markov and Gaussian models. In that study, statistical, HMM, and GMM features were extracted

from the multilead ECG signal and then classified by the SVM method. The final accuracy obtained was 85.71%, and the researcher reported it.[12] Baloglu *et al.*, in 2019, presented research to classify MI based on deep neural networks. In that study, the ECG signal was measured using 12 leads, and the convolutional neural network performed the classification. The final accuracy obtained is 99% reported.[13]

Objectives

In this article, we presented the detection and classification of MI using simple morphological features extracted from healthy and MI ECG signals, these signals were obtained from the Physikalisch-Technische Bundesanstalt database.[14] For this article's purposes, the feature matrix of the extracted signals was used for accurate classification by optimizing the SVM classification parameters. In the first part, in the materials and methods section, the proposed algorithm is described in detail in this article. Then, in the results' section, the results of applying this proposed method are investigated. Finally, in the last part of the article, we conclude and discuss our findings and compare them with other previous research in this field.

Materials and Methods

This study proposed a novel method detecting and classifying MI (i.e., anterior, posterior, and inferior MI) by 12-lead ECG signals processing, based on the grasshopper optimization algorithm (GOA). The proposed method consists of four preprocessing steps that called features extraction from ECG signals, statistical analysis of these features, classification, and classifier parameters optimization by the GOA. Figure 1 shows the block diagram of the proposed method in this article. Each of these sections is described in detail below.

Database

The data used in this study is a 12-lead ECG signal set (named I, II, III, AVR, AVL, AVF, V1, V2, V3, V4, V5, and V6), which is download from the free-access PhysioNet database.[14] This database contains 549 ECG signals with a sampling rate of 1000 Hz (averaging 1–5 signals per person) collected from 290 individuals (209 males and 81 females) with a mean age of 17–87 years. This database contains nine datasets, the details of which are described in Table 1.[14] In this study, we used the ECG signals of patients with MI, they are 148 cases (58 subjects were anterior MI, 85 subjects were inferior MI, and 5 subjects were posterior MI) and 52 persons with a health condition.

Preprocessing

The preprocessing procedure is one of the critical steps in signal processing methods. In this study, preprocessing was used to prepare and remove any noises from the ECG signals. Initially, different data of all ECG leads and the
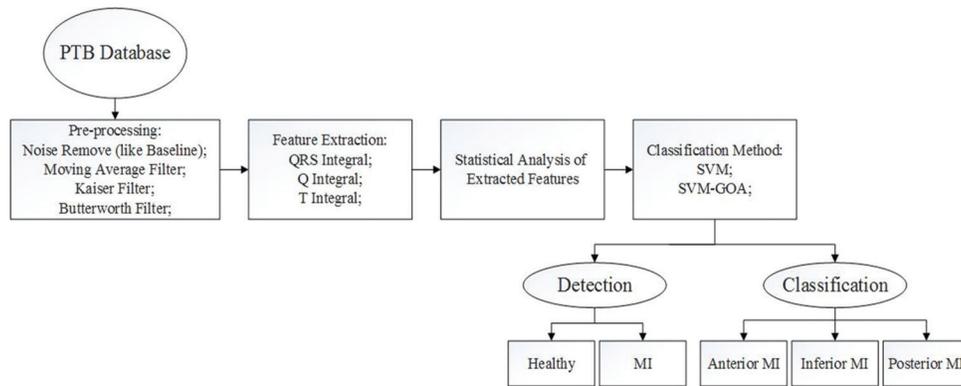
Figure 1: Block diagram of the proposed method in this article

Table 1: Different PTB database groups

Type	Number
Myocardial infarction	148
Cardiomyopathy/heart failure	18
Bundle branch block	15
Dysrhythmia	14
Myocardial hypertrophy	7
Valvular heart disease	6
Myocarditis	4
Miscellaneous	4
Healthy controls	52

filters were designed and applied to the signals to eliminate the deviation from the baseline and eliminate the power line noise from them. In the next step, four smoothing filers which called moving average, Kaiser, Butterworth, and median filters are applied to the ECG signals for smoothing them. The results of these preprocessing are given in the results' section of this article.

Feature extraction

Feature extraction was used to train and design models to classify signals. In this study, three features were extracted from ECG signals, such as QRS-complex integral, T-integral, and Q-integral. At first, the R-wave of each ECG cycle was calculated from the ECG signal. After that, the positive and negative peaks before and after R-peak are considered as Q-wave and S-wave. The integral (the area under the curve) was then calculated from point Q to point S to obtain the integral feature as the QRS-complex. The ECG signal's T-wave was similarly extracted, and the T-wave integral and the Q-wave integral were calculated as two other features. After extracting the mentioned features, all features were saved in each candidate ECG signal's feature matrix. Then, a label was assigned to the extracted features from each person's ECG signals. The first labels included two classes to classify the data of healthy and MI, and the second labels included four categories to classification the normal and MI data that are called anterior, posterior, and inferior MI.

Statistical evaluation of the extracted features' set

At first, before applying the extracted features' matrix to the classification algorithm, statistical analyses were performed on the set of these features. To consider the normality tests of the ECG signals' extracted features, the feature normality test was performed in the SPSS, IBM SPSS Version 20.0. The results of the statistical analysis of the extracted features are given in the results' section of this article. The final classification method presented in this article will be discussing in the next section.

Classification

Since the features mentioned above have been extracted to classify both the classes, in this section, after dividing the data into two train and test sets, the classification is performed using the SVM method. Data validation is performed by the k-fold cross-validation method with $k = 4$; the data were divided into two parts, train and test sets. In other words, 75% of data is selected for training set and 25% of data determined for test set. The SVM classifier classified the extracted feature from ECG signals with three kernels, such as linear, RBF, and polynomial. Then, the most important parameters for these kernels were updated using the GOA method.

Grasshopper optimization algorithm

One of the critical parameters that directly impact the classification performance is the parameter selection of the SVM classifier. In this study, using the GOA presented in 2017 by Saremi *et al.*,[15] the best parameters are selected for different SVM classification kernels. First, we will briefly introduce the GOA. The process of finding the best values for the variables of a particular problem to minimize or maximize an objective function is called optimization.[15] Optimization problems exist in various fields of the study. So far, there are many optimization algorithms such as firefly Algorithm, bat Algorithm, particle swarm algorithm, genetic algorithm, ant colony algorithm, flower pollination algorithm, and grey wolf optimizer[16-22] which have been introduced. However, a few studies have simulated the grasshopper swarm algorithm.[23-27] Grasshoppers are insects

that are considered pests because of damage to crops. Although grasshoppers are usually seen separately in nature, they are in one of all creatures' gigantic swarms. Nature-inspired algorithms rationally divide the search process into two exploration and exploitation trends.[28] In the exploration operation, search agents are encouraged to move abruptly, while they tend to move locally during exploitation. The grasshoppers usually perform these two functions and the target search in the GOA. Therefore, if a mathematical model can found to model with this behavior, a new nature-inspired algorithm can be designed.[28] In the following, we describe this algorithm as presented in previous study.[15]

The mathematical model used to simulate the grasshopper's swarm behavior is as Eq. 1:[15]

$$X_i = S_i + G_i + A_i \tag{1}$$

In the above relation, X_i defines the grasshopper of i, the S_i is a function of social interaction, G_i is the force of attraction in i grasshopper, and A_i represents the wind prediction. The equation can formulate to represent random behavior by $X_i = r_1 S_i + r_2 G_i + r_3 A_i$, where r_1, r_2, and r_3 are random numbers in the interval (0, 1). The method of calculating the social interaction function is described in Eq. 2.[16]

$$S_i = \sum_{\substack{j=1 \\ j \neq i}}^{N} S(d_{ij}) \hat{d}_{ij} \tag{2}$$

In this equation, d_{ij} is the distance between the grasshoppers i and j and is calculated as $d_{ij} = |x_j - x_i|$, s is a function to define the social interaction function shown in Eq. 2, and $\hat{d}_{ij} = x_j - x_i$ is a single vector from the grasshopper i to grasshopper j. The function s, which defines social forces, is calculated as Eq. 3:

$$S(r) = f e^{\frac{-r}{l}} - e^{-r} \tag{3}$$

In this equation, f represents the absorption intensity, and l represents the longitudinal scale of absorption.[15] In this article, to find the best SVM classification kernel parameters, a grasshopper optimization method with five grasshoppers and 100 iterations was used for three linear kernel types, RBF, and polynomial.

In this algorithm, we can set parameter "c" (the limiting parameter, which exists in MATLAB software as BoxConstrate, and by default, has a value of 1) to set SVM classifier parameters. Other parameters relate to the classification kernel function that we intend to optimize are "σ" and "q". Suppose we use the RBF (Gaussian) or polynomial kernel functions. In these cases, it has a parameter "σ" (like in the Gaussian equation) for optimization in RBF kernel, and we are parameter as "q" when we use the polynomial kernel function. Therefore, in this paper, if the linear kernel function is used, the we

can use "c" parameter, and σ for the RBF kernel function, and the parameters c and q for using in polynomial kernel function, and these parameters can be optimized by the GOA algorithm. In this article's optimization process, a range from 1 to 10 (integers) is assumed for the value of parameter q. The interval between a positive number close to 1 and 1000 is considered for c and σ parameters. Then, by applying the relationships of the GOA, the grasshopper positions in different iterations are calculated to reach the final minimum value of predefined target functions eventually (i.e., optimizing the parameters of the SVM classifier kernel functions).

Results

The purpose of this study was to detect MI and the classification of its types using ECG signal processing. For this purpose, after preprocessing and noise removal from the ECG signals, the three features such as Q-wave integral, T-wave integral, and QRS-complex integral were extracted from two cleaned healthy signals and with MI subjects. The results of the signal preprocessing section are mentioned in the following.

Figure 2 shows the result of the preprocessing of a sample ECG signal after using these filters introduced before.

In terms of normality, performance, and differentiation, these features were evaluated by various statistical tests. The results of the statistical section are given in the following.

Table 2 summarizes the results of the extracted features from all the signals used in the database (data from healthy and MI subjects).

As shown in Table 2, the sig (*P*-value) results for all three feature sets extracted in both healthy and MI groups were equal to zero, indicating non-normal features (as statistical). Furthermore, the skewness results of each of the three features' sets indicate that they are abnormal. Since the data of all three feature groups in both the healthy and the patients with MI classes are not a normal distribution, and they do not have the same variances, nonparametric analyses should use to investigate the feature independence. For achieving this matter, the correlation status should examine first because the extracted features are in the three groups and are also quantitative. For this purpose, the Pearson correlation test was used to calculate the correlation coefficient. The Pearson correlation test results showed that the correlation of each of the three groups of features was significant with the other two groups with a 99% significance level and 1% error. After examining the correlation of the extracted features' sets, Friedman's nonparametric test was used to determine whether there were statistically significant differences between the three extracted features' sets. The Friedman nonparametric test results show a statistically significant difference between the three groups of extracted features concerning *P* value <0.01. The Chi-square value of the Friedman test
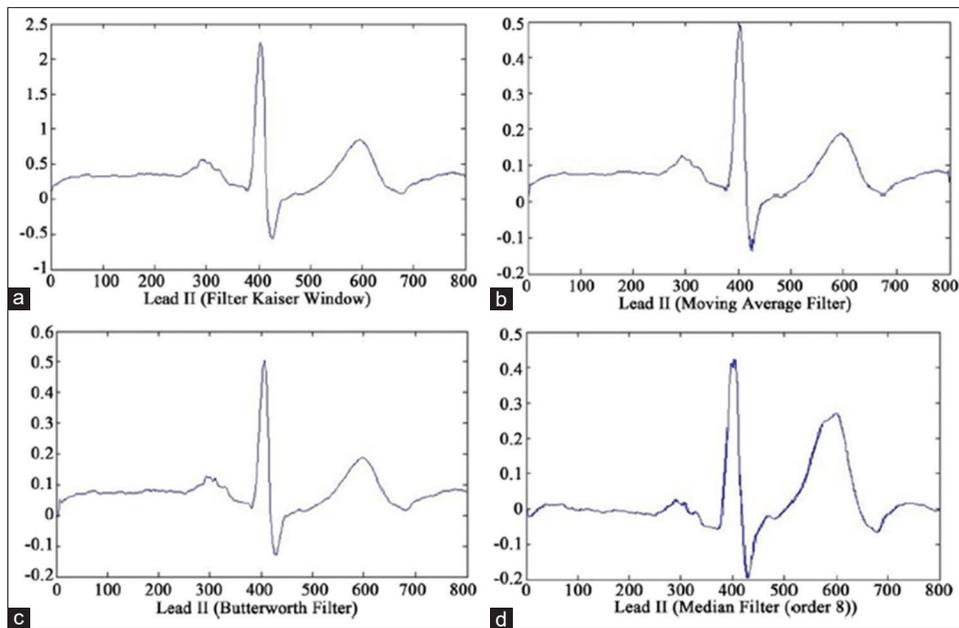
Figure 2: Result of the pre-processing operation of the Lead II of ECG signals as one sample; (a) Results of Kaiser filter; (b) Results of Moving Average filter; (c) Results of Butterworth filter; (d) Results of Median filter

Table 2: Results of the first features' set analysis

	Kolmogorov-Smirnov[a]			Shapiro-Wilk			Statistics			
	Statistic	df	Significance	Statistic	df	Significance	Variance	Skewness	Kurtosis	Mean
Q_Integral	0.328	214	0.000	0.286	214	0.000	14,392.2	−8.772	92.114	−43.99
QRS_Integral	0.111	214	0.000	0.892	214	0.000	456,371.5	−1.597	8.059	125.67
T_Integral	0.218	214	0.000	0.855	214	0.000	931,858.0	−0.620	10.160	−29.90

[a]Lilliefors significance correction

with <1% error and a confidence level of 99% is confirmed. Finally, considering that there is a statistically significant difference between different groups of extracted features, it has been concluded that this set of features can be reliably used as input to classification algorithms.

Then, considering the abnormalities of the extracted features [shown in the results of Table 2], nonparametric analyses were used to evaluate the independence of the features in two healthy and MI classes. At this stage, since the healthy and the MI groups represent two completely independent groups, so in this article, Mann-Whitney and Kolmogorov–Smirnov tests were used to investigate the independence of features in two groups of healthy and MI cases. The results of the above two tests for all three extracted features in two independent classes are shown in Table 3. According to Table 3, the results indicate a statistically significant difference between all three features in the healthy and the MI groups. Therefore, it has been concluded that selecting this set of features can help distinguish between healthy and MI patients.

According to the above table results, it is clear that with a 99% confidence level and error <1%, the three extracted features have a statistically significant difference between the healthy and the patient groups. Since there is a

statistically significant difference in the extracted features between different groups, it can conclude that these features are highly differentiable. Hence, they can be reliably used for this set of features to apply them to the input classification algorithms for calculation of the accuracy, sensitivity, and specificity criteria.

In the final step, the feature set matrix is used as input of the SVM classification method to diagnose MI and its variants. Since SVM classification parameters play an essential role in this system's performance, the GOA optimized these parameters, and the best metrics were obtained. Tables 4 and 5 show the results of MI's data detection and classification and its types using the SVM method before the optimization process, respectively.

Tables 6 and 7, respectively, show the results of the detection and classification of the cardiac MI types using an SVM classifier after applying the GOA on various kernel parameters of the SVM method.

Figure 3 shows the comparison of the SVM classifier results before and after the optimization for the classification of MI. The SVM-GOA hybrid system's performance is higher in all three indicators of accuracy, specificity, and sensitivity.

Discussion and Conclusion

In this study, a method has been proposed to diagnose MI and its different types using ECG signal processing. For this purpose, the features of Q-wave integral, T-wave integral, and QRS-complex integral of signals from healthy and MI subjects have been used. The grasshopper optimization method for optimizing SVM classification parameters was the first used in this study. The final results show that after optimizing the parameters, this system has a higher performance and has increased accuracy in diagnosing MI and the classification of its variants.

In the best results of applying various kernels of SVM classifiers such as linear, RBF, and polynomial for MI detection, the sensitivity, specificity, and accuracy before using the optimization process are $100\% \pm 0\%$, $100\% \pm 0\%$, and $100\% \pm 0\%$, respectively, for the linear kernel. Still, the results of the RBF and polynomial kernels were slightly lower. These values for sensitivity, specificity, and accuracy are $100\% \pm 0\%$, $100\% \pm 0\%$, and $100\% \pm 0\%$ for all three kernels for MI detection after applying the grasshopper optimization process on SVM kernel parameters, which indicates the excellent performance of the proposed method in this article.

In addition, in the best results of applying linear, RBF, and polynomial kernels used in SVM classifiers to classify different types of MI disease, the best sensitivity, specificity, and accuracy before applying the optimal process were equal to $95.24\% \pm 0.01\%$, $100\% \pm 0\%$, and $66.67\% \pm 0.23\%$ for the use of linear kernel in SVM classifier, respectively. These values obtained to classify different MI types after applying GOA on SVM kernel parameters were equal to $100\% \pm 0\%$, $97.37\% \pm 0\%$, and $94.2\% \pm 0.2\%$ for sensitivity, specificity, and accuracy, respectively, for the polynomial kernel. It should be noted that the results of both linear kernels and RBF have also increased significantly after applying the GOA. The sensitivity, specificity, and accuracy of the polynomial kernel optimization algorithm increased by 10%, 10%, and 40%, respectively, indicating the proposed method's high efficiency and effectiveness introduced in this article.

According to the results of this study, it can be concluded that the ECG signals of healthy individuals and patients have statistically significant differences in the type of MI
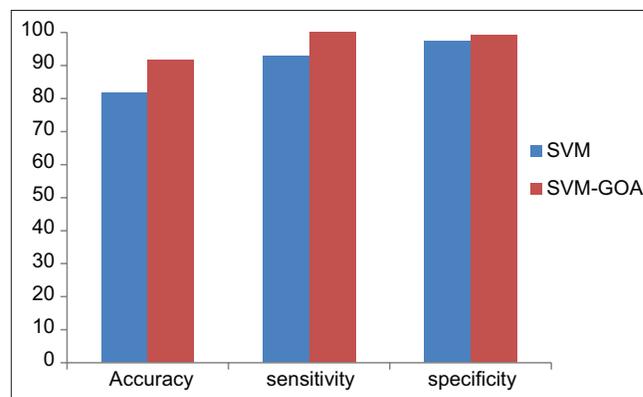
Table 3: Results of mean±standard deviation value, and *P* value of the Mann-Whiteny and Kolmogorov-Smirnov tests on the three extracted features from the electrocardiogram signals in the database in two independent groups of healthy subjects and subjects with myocardial infarction

	Mean±SD	Mann-Whiteny	Kolmogorov-Smirnov
Q_Integral	−43.995±119.968	0 (S)	0.001 (S)
QRS_Integral	125.673±675.553	0 (S)	0 (S)
T_Integral	−29.906±965.328	0 (S)	0 (S)

SD – Standard deviation; S – Significant

Table 4: Results mean±standard deviation of detection the myocardial infarction and healthy electrocardiogram signals, before applying the optimization process on support vector machine kernel parameters

Method SVM	Sensitivity (%)	Specificity (%)	Accuracy (%)
Linear	100±0	100±0	100±0
RBF	88.67±0.06	100±0	96.85±0.02
Polynomial	91.33±0.28	99.69±0.01	97.37±0.08

SVM – Support vector machine; RBF – Radial basis function

Table 5: Results mean±standard deviation of classification the various types of myocardial infarction and healthy electrocardiogram signals, before applying the optimization process on support vector machine kernel parameters

Method SVM	Sensitivity	Specificity	Accuracy
Linear	95.24±0.01	100±0	66.67±0.23
RBF	92.31±0.01	95.65±0.1	56.67±0.06
Polynomial	90±0.32	87.91±0.31	55.33±0.14

SVM – Support vector machine; RBF – Radial basis function

Figure 3: Comparison of SVM and SVM-GOA Results for classification of MI

Table 6: Results of detection the myocardial infarction and healthy electrocardiogram signals, after applying the optimization process on support vector machine kernel parameters

Method	Kernel	Grasshopper Papulation	Number of GOA runs	Iteration	Sensitivity	Specificity	Accuracy
SVM classifier	Linear	5	100	100	100±0	100±0	100±0
	RBF	5	100	100	100±0	100±0	100±0
	Pol	5	100	100	100±0	100±0	100±0

SVM – Support vector machine; GOA – Grasshopper optimization algorithm; RBF – Radial basis function

disease in different processing domains. However, the diagnosis of other types of MI was not possible in this study. Tables 8 and 9 compare the results of this study with other previous studies. According to the table, it is clear that the optimization of different kernel parameters of the SVM classifier is very efficient, and results from other studies are more accurate.

Then, the results of the proposed algorithm were analytical compared with the best results of other previous studies. In the study,[28] two integral morphological features of the ECG signals were used. Still, the best MI detection results were much higher than the best results for MI classification reported. These results in the previous study[28] indicate that the introduced features in that study only well perform to detect MI compared to healthy signals but do not perform well for classification MI type. In the study,[4] the incidence of cannulation networks and the KNN method has been used but still has very high accuracy in the diagnosis of MI. In contrast, the final results of that method show

lower values than the final results of the process presented in this article. In the study,[6] although it utilized wavelet transforms and extracted linear and nonlinear features, and paid very high to detect MI, these results were still lower than this algorithm's final results presented in this article.

Comparing the final results of the classification of different types of cardiac MI, according to Table 9, it is clear that the best results presented in this article are higher and better than the results of all studies of classification of the various types of MI. These results suggested that the method presented in this article could be a new and useful step toward a more accurate diagnosis of heart MI through a low-cost, noninvasive, and pure signal recording method done on the standard ECG signals. The reason for the higher output values of the proposed algorithm in this article than the other previous methods may depend on the fact that prior arrangements classify traditional and modern class methods. However, in this article's presented method, using the most recent meta-heuristic for the optimization process (GOA),

Table 7: Results of classification the various types of myocardial infarction and healthy electrocardiogram signals, after applying the optimization process on support vector machine kernel parameters

Method	Kernel	Grasshopper papulation	Number of GOA runs	Iteration	Sensitivity	Specificity	Accuracy
SVM classifier	Linear	5	100	100	100±0	100±0	75.5±0.2
	RBF	5	100	100	100±0	98.72±0.02	80±0.02
	Pol	5	100	100	100±0	97.37±0	94.2±0.2

SVM – Support vector machine; GOA – Grasshopper optimization algorithm; RBF – Radial basis function

Table 8: Results of this study compared with previous studies in the diagnosis of healthy subjects from cases with heart disease (myocardial infarction detection)

Researcher	Year	Method	Database	Specificity (%)	Accuracy (%)	Sensitivity (%)
Safdarian *et al.*[28]	2014	Extracted T-wave integral and total integral of one ECG cycle Features Classification using PNN, KNN, MLP neural network, naive bayes methods	PhysioNet PTB	-	94.74	-
Sugimoto *et al.*[4]	2019	Cannulation networks KNN method	PhysioNet PTB	99.59	99.87	99.91
Barmpouti *et al.*[5]	2019	Grassmannian and euclidean mapping Hilbert transform	PhysioNet PTB	100	100	100
Sharma and Sunkaria[6]	2020	Wavelet transform Extraction energy, entropy, and slope-based as features KNN classification method	PhysioNet PTB	99.40	99.00	98.62
Ketcham and Muankid[7]	2016	R wave detection and QRS complex detection	PhysioNet PTB	77.78	75	80
Pereira and Daimiwal[8]	2016	Wavelet transform-based Features Extraction multiple features from different sub-bands	PhysioNet PTB	70.94	82.14	83.93
Proposed method	2020	Extraction simple morphological features such as Q-wave integral, T-wave integral, and QRS-complex integral from ECG signals Apply some statistical analyses on extracted features GOA-SVM using 3 kernels for classification	PhysioNet PTB	100	100	100

PTB – Physikalisch-Technische Bundesanstalt; SVM – Support vector machine; GOA – Grasshopper optimization algorithm; ECG – Electrocardiogram; PNN – Probabilistic neural network; KNN – K-nearest neighbor; MLP – Multilayer perceptron

Table 9: Best results of this study compared to previous studies in the classification of different types of myocardial infarction (classification of myocardial infarction)

Researcher	Year	Method	Database	Specificity (%)	Accuracy (%)	Sensitivity (%)
Lui and Chow[11]	2018	Classification using convolutional neural networks and recursive neural networks	PhysioNet PTB	97.2	92.4	97.7
Chang et al.[12]	2012	Extracted statistical, HMM and GMM features Classification based on Markov and Gaussian models	Clinical ECG data	79.82	82.50	85.71
Safdarian et al.[28]	2014	Extracted T-wave integral and total integral of one ECG cycle features Classification using PNN, KNN, MLP neural network, naive bayes methods	PhysioNet PTB	-	76.67	-
Baloglu et al.[13]	2019	Classification based on deep neural networks	PhysioNet PTB	-	99	-
Proposed method	2020	GOA-SVM-liner		100 ± 0	75.5 ± 0.2	100
		GOA-SVM-RBF	PhysioNet PTB	98.72 ± 0.02	80 ± 0.02	100 ± 0
		GOA-SVM-polynomial		97.37 ± 0	94.2 ± 0.2	100 ± 0

PTB – Physikalisch-Technische Bundesanstalt; SVM – Support vector machine; GOA – Grasshopper optimization algorithm; ECG – Electrocardiogram; PNN – Probabilistic neural network; KNN – K-nearest neighbor; MLP – Multilayer perceptron; HMM – Hidden Markov model; GMM – Gaussian mixture model, RBF – Radial basis function

we have been able to optimize the traditional SVM classifier parameters with different kernel types. Finally, with these optimal values, we report the maximum accuracy in both outputs of detection and classification of different cardiac MI types. Another advantage of the proposed method is that it has accurately detected heart disease in different individuals with simple morphological features extracted from ECG signals of healthy and MI individuals. The final results of applying the proposed method in this article can be added as a module to existing cardiac signal recording devices to diagnose heart MI at various stages accurately. This capability can promote the technology of products marketed and encourage technology development in diagnosing heart disease.

Compliance with ethical standards

Financial support and sponsorship

Conflicts of interest

There are no conflicts of interest.

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