Workshop Proceedings of the 9th International Conference on Intelligent Environments
J.A. Botía and D. Charitos (Eds.)

doi:10.3233/978-1-61499-286-8-36

Cardiac Arrhythmia Classification Using KNN and Naive Bayes Classifiers Optimized with Differential Evolution (DE) and Particle Swarm Optimization (PSO)

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Abstract. In the present investigation we are looking for improve the features classification of a cardiac arrhythmias database using metaheuristics (Differential Evolution and Particle Swarm Optimization) and classifiers (KNN and Naive Bayes), with the purpose of select the main features and increase the percentage of classification. The classification percentage in some cases increased until 100% and the number of features was significantly reduced.

Keywords. ECG, Arrhythmia, Classifiers, KNN, Naive Bayes, Differential Evolution, PSO, Feature Reduction.

1. Introduction

Separate the data through different classes is the main function of the classifiers. Exist different applications of classifiers in ECG signals. In Nasiri [21] was performed the arrhythmia classification of EEG signals using Support Vector Machines (SVM) and Genetic Algorithms. In Abdeel-Badeeh [1] was applied the machine learning in a ECG diagnosis. Ramírez [24] propose a dynamic model of cardiac arrhythmia classification trough machine learning with user interface. In Mohamed [19] presented two methods for multiclass arrhythmia classification applying the Principal Component Analysis (PCA), the Fuzzy Support Vector Machine, and the Unbalanced Clustered. Kallas [12] showed the classification of multiclass arrhytmia through Support Vector Machines (SVM) mixed

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with feature extraction through Principal Components Analysis (PCA) in ECG signals. In Thanapatay [34] proposed a new method for ECG classification using Principal Component Analysis (PCA) and Support Vector Machine (SVM). Rabee [25] presented the ECG signal classification using Support Vector Machine and based on the Multiresolution Wavelets analysis. In Shen [29] proposed a classification model using Support Vector Machine (SVM) and Independent Component Analysis and Zellmer [37] obtained the ECG signals classification based on continuous wavelet transform and Support Vector Machines (SVM).

The combination of classifiers with metaheuristics for feature selection on ECG signals is an efficient way to eliminate unnecessary data in the search of abnormal heartbeats. Martínez [17] proposes a classification model using intelligent ECG to detect heart problems using neural networks and Genetic Algorithms. In Melgani [18] was performed ECG signals classification with Support Vector Machine (SVM) algorithm applying PSO (Particle Swarm Optimization) and in Daamouche [5] they are looking for optimize the classification applying PSO algorithm, Support Vector Machines (SVM) and perform noise reduction in ECG signals through Wavelets.

In Fira [7] investigated the results of classification from the compression of ECG signals from different projection matrices. In Vaish [35] were investigated the loads of efficacy and computational efficiency of different algorithms used to recognize the emotional state through cardiovascular signals.

The ability to identify automatically ECG arrhythmia is important for clinical diagnosis and treatment. In Soman [31] have used machine learning systems, Oner, J48 and Naive Bayes to classify the data sets obtained from doctors databases. In Gao [8] was described a system for detecting cardiac arrhythmias in ECG signals, based on a bayesian artificial neural network (ANN) constructed by a logistic regression model and a BackPropagation algorithm.

2. Metaheuristics

In this work we applied several metaheuristics, Differential Evolution and Particle Swarm Optimization, mixed with a different classifiers, KNN and Naive Bayes, to find the best value in the percentage of classification.

2.1. Differential Evolution (DE)

In computer science, differential evolution (DE) is a method that optimizes a problem by iteratively trying to improve a candidate solution with regard to a given measure of quality. Such methods are commonly known as metaheuristics as they make few or no assumptions about the problem being optimized and can search very large spaces of candidate solutions. However, metaheuristics such as DE do not guarantee an optimal solution is ever found.

Differential Evolution is a small and simple mathematic model of a big and complex evolution process, this process is easy and efficient [6]. The first description of differential evolution was performed in 1995 by Price and Storn [23].

2.1.1. Population

Differential Evolution needs an initial population of a 4 individuals at least. Each individual have a vector, each vector contain a component that represent a dimension with values in the continue space, but can be used in the discrete space too.

2.1.2. Function of Adaptation

Given an individual, the adaptation function need to assign a real number, that reflects the level of adaptation to the individual problem.

2.1.3. Mutation

The mutation consists in the construction of noise random vectors **NP**, created from three random individuals, called *target vectors*. We could use different methods for the mutation process:

Using the equation OF/RAND/1:

$$temp\overrightarrow{E_i} = \overrightarrow{E_j} + F(\overrightarrow{E_k} - \overrightarrow{E_l}) \tag{1}$$

Using the equation OF/RANK:

$$temp\overrightarrow{E_i} = \overrightarrow{E_i} + F(\overrightarrow{E_j} - \overrightarrow{E_k}) \tag{2}$$

$$temp\overrightarrow{E_i} = \overrightarrow{E_{BEST}} + F(\overrightarrow{E_{BEST}} - \overrightarrow{E_l}) \tag{3}$$

Using the equation DE/CURRET TO BEST/1:

$$temp\overrightarrow{E_i} = \overrightarrow{E_i} + F(\overrightarrow{E_{BEST}} - \overrightarrow{E_i}) + G(\overrightarrow{E_k} - \overrightarrow{E_l}) \tag{4}$$

Where $i \neq j \neq k \neq l$, F (and G for current to best) $\sim$ [0,2] is a basic parameter of input (constant in all time of the execution time), if F is less than 1 then shrinks and if F is more than 1 then grows.

2.1.4. Crosses

When we have the noise random vectors **NP**, the crosses is done randomly through the following equation:

$$tempE_i[j] = \begin{cases} tempE_i[j] & if\ r \leq CR \\ E_i[j] & in\ other\ case \end{cases} \tag{5}$$

Where $CR \sim$ [0,1] is a basic parameter of input (constant in all time of the execution time) and $r \sim$ [0,1] is a random number uniformly distributed.

2.1.5. Differential Evolution Algorithm to Classifier ECG Arrhythmias

Algorithm 1 Differential Evolution Algorithm.

```
Data input: $F \sim [0,2]$, $CR[0,1]$, size of the population, call functions, objective function
-classifier-(1NN, 3NN, Naive Bayes), number of folds.
Start a random population.
Evaluate the first population.
while (no finish call functions) do
    $tempE_i \leftarrow$ (see Equation of Mutation).
    Use sigmoid ($>1 \rightarrow 0$, $<1 \rightarrow 1$)
    for each coordinate $j$ of the individual do
        $r \leftarrow$ uniformly distributed random number between 0 and 1.
        if $r \leq CR$ then
            $tempE_i[j] \leftarrow$ (see Crosses Equation)
        end if
    end for
    if $f(tempE_i)$ better $f(E_i)$ then
        $E_i \leftarrow tempE_i$.
        $f(E_i) \leftarrow f(tempE_i)$.
    end if
end while
```

2.2. Particle Swarm Optimization (PSO)

PSO is a metaheuristic inspired in the social conduct of particles often applied for solving optimization problems. In 1995 Kennedy and Eberhart [14] developed the first algorithm. The algorithm can be used in continues or discrete functions. This proposal was an excellent optimization algorithm to continues no-lineal math functions, but could be applied in binary too.

Basically, PSO works with a set of candidates solutions named *swarm*. Each member of the swarm is a *particle*, and this particle have a solution vector named *position*. Each particle knows the best position in the swarm o *best global*. If you defined subsets of particles in the swarm, each particle is named *neighbourhood*.

To update the velocities of the particles, we need to use the next equation:

$$v_{ij} = wv_i + \phi_1(GBest_i - x_i) + \phi_2(LBest_i - x_i) \tag{6}$$

Therefore, to realize the actualization of the value x_i we need to use a sigmoid, the equation is:

$$\overrightarrow{Sig(V_{ij})} = \frac{1}{1 + \exp^{-vij}} \tag{7}$$

2.2.1. PSO Algorithm to Classifier ECG Arrhythmias

Algorithm 2 PSO Algorithm

```
Data input: $\phi_1[0,1]$, $\phi_2[0,1]$, size of the population, call functions, objective function -classifier-(1NN, 3NN, 5NN, Naive Bayes), number of folds.
Start a random population and generate random velocities $V[0,1]$.
Evaluate the first fitness of each individual, take the Best Individual and the Best Fitness (GBest) and save the first fitness of each individual (LBest).
while (no finish call functions) do
    for each particle i do
        for each member of the particle j do
            Update the velocities (Equation 6) and update the value of $x_i$ (Equation 7).
        end for
        for each member of the particle j do
            Generate a random number $r_{ij}[0,1]$.
            if $r_{ij} < Sig(V_{ij})$ then
                $x_{ij} = 0$
            end if
            if $r_{ij} > Sig(V_{ij})$ then
                $x_{ij} = 1$
            end if
        end for
        Evaluate the fitness of each individual (percentage of classification).
        Update the LBest.
        if $f(x_i) > f(LBest_i)$ then
            $LBest_i = x_i$
        end if
    end for
    Find the best LBest
    if $LBest > GBest$ then
        $GBest_i = LBest_i$
    end if
end while
```

3. Experimental Set-Up

3.1. Experimental Dataset

We need a experimental set to find the percentage of classification. In this research, the experimental dataset consisted of labelled ECG records from the [9] database. The experimental records were obtained from the MIT/BIH arrhythmia set. This set contains 48 recordings of 30 min duration. All the heatbeats were already labelled. However, the AAMI standard [4] recommends the consideration of the following heartbeat types: normal beat (labelled as N), Supraventricular ectopic beat (S), Ventricular ectopic beat

(V), Fusion beat (F), and unknown beat class (Q). Any of these types might be present in any record. A complete description of all the records is included in (see Table 1), showing the equivalence between the AAMI and MIT/BIH labels in the two first rows.

AAMI	N					S				V		F		Q	
MIT	N	L	R	e	j	A	a	J	S	V	E	F	f	P	Q
Code	1	2	3	34	11	8	4	7	9	5	10	6	38	12	13
Class	0000	1010	0111	1011	0101	0010	1000	0110	1100	0001	1101	1001	0100	0011	1110
100	2237					33				1					
101	1858					3									2
102	99									4			56	2026	
103	2080					2									
104	163									2			666	1378	18
105	2524									41					5
106	1505									520					
107										59				2076	
108	1738				1	4				16		2			
109		2490								38		2			
111		2121								1					
112	2535					2									
113	1787						6								
114	1818					10		2		43		4			
115	1951														
116	2300					1				109					
117	1532					1									
118			2164			96				16					
119	1541									444					
121	1859					1				1					
122	2474														
123	1513									3					
124			1529		5	2		29		47		5			
200	1742					30				825		2			
201	1623				10	30	97	1		198		2			
202	2059					36	19			19		1			
203	2527						2			444		1			4
205	2569					3				71		11			
207		1457	85			106				105	105				
208	1585								2	992		372			2
209	2619					383				1					
210	2421						22			194	1	10			
212	922		1824												
213	2639					25	3			220		362			
214		2001								256		1			2
215	3194					2				164		1			
217	244									162			260	1540	
219	2080					7				64		1			
220	1952					94									
221	2029									396					
222	2060				212	208		1							
223	2027			16		72	1			473		14			
228	1686					3				362					
230	2253									1					
231	314		1252			1				2					
232			396		1	1381									
233	2229					7				830		11			
234	2698							50		3					
TOTAL	74986	8069	7250	16	229	2543	150	83	2	7127	106	802	982	7020	33

The first row corresponds to the labels used according to the AAMI standard, and the second row lists the labels used in the MIT/BIH database.
The third row corresponds to the numerical code of these last labels.
The first column is the name of the records, whereas the others contain the number of heartbeats of each type.

Table 1. Set of recordings of the MIT/BIH database used in the experiments.

3.2. Feature Extraction

Feature extraction consists in obtain the main features of the arrhythmia signal to classify after. For the feature extraction in this research, we took like a reference the extraction of Rodríguez-Sotelo [28]. The initial input feature vectors $x_j = \{x_{ij}, x_{2j}, \dots, x_{pj}\}$, with $p = 100$ were composed of:

$x_{1j} = l_j - l_{j-1}$ (RR interval)
$x_{2j} = l_{j-1} - l_{j-2}$ (pre-RR interval)
$x_{3j} = l_{j+1} - l_j$ (post-RR interval)
$x_{4j} = x_{1j} - x_{2j}$
$x_{5j} = x_{3j} - x_{1j}$
$x_{6j} = (\frac{x_{3j}}{x_{1j}})^2 + (\frac{x_{2j}}{x_{1j}})^2 - (\frac{1}{3} \sum_{k=1}^{3} x_{kj}^2 log(x_{kj}^2))$

x_{7j} quantifies the morphological dissimilarity between current QRS-complex, and a linearly averaged QRS-complex of the last 10 complexes [32] by means of a dynamic time warping (DTW) approach.

$x_{8j} = \mid \frac{max\{QRS_j[t]\}}{min\{QRS_j[t]\}} \mid$
$x_{9j} = \sum_{k=0}^{L_j} QRS_j[t]^2$

x_{10j} to x_{19j} correspond to the Hermite coefficients.

4th-level coefficients of a Daubechies-2, (dB2), Wavelet heartbeat decomposition (A-Amplitude, D-Detail)
x_{20j} to $x_{25j} \Leftarrow A_4$
x_{26j} to $x_{31j} \Leftarrow D_4$
x_{32j} to $x_{42j} \Leftarrow D_3$
x_{43j} to $x_{58j} \Leftarrow D_2$
x_{59j} to $x_{90j} \Leftarrow D_1$
x_{91j} to $x_{95j} = var\{A_4, D_4, D_3, D_2, D_1\}$
x_{95j} to $x_{100j} = max\{A_4, D_4, D_3, D_2, D_1\}$

4. Experiments and Results

We made different experiments for the classification. In the case of PSO we used the next parameters: $\phi_1 = 0.3$, $\phi_2 = 0.5$ y w=0.7. In the case of Differential Evolution, the parameters were $F = 0.9$ and $cr = 0.5$.

First tests were with the classifiers 1NN, 3NN and Naive Bayes, without metaheuristics. We considered all characteristics to take an initial parameter and to can compare an improvement. Next, we test with the same classifiers, but with the PSO and with Differential Evolution Algorithms.

We can see the Medium of the Percentage of Classification obtained (see Table 2) and the Medium of the Number of Characteristics used in the classification (see Table 3).

Classifier	KNN (1NN)	KNN (3NN)	Naive Bayes	Naive Bayes	Naive Bayes
Population	5	5	5	5	10
Fold	2	2	2	10	10
Call Functions	20	20	20	20	50
without algorithm	94.11%	94.71%	9.72 %	9.93 %	9.93%
PSO	93.38%	94.59%	17.24 %	21.80 %	28.0%
Differential Evolution	93.94%	94.07%	19.50 %	17.46 %	15.75%

Table 2. Medium of Classification Percentage.

Classifier	KNN (1NN)	KNN (3NN)	Naive Bayes	Naive Bayes	Naive Bayes
Population	5	5	5	5	10
Fold	2	2	2	10	10
Call Functions	20	20	20	20	50
without algorithm	100	100	100	100	100
PSO	36.8	53.8	28.6	34.6	31.2
Differential Evolution	50	45.6	29.2	38.4	39.4

Table 3. Medium of Number of Characteristics Used in the Classification.

4.1. Weight of the Characteristics

Taking as 50 the maximum number of times that each feature could be chosen, these are the results for each characteristic:

Characteristic	**Number of Times Selected**	**Characteristic**	**Number of Times Selected**
1	19	26	22
2	18	27	21
3	24	28	22
4	24	29	19
5	20	30	21
6	19	31	22
7	29	32	15
8	24	33	16
9	22	34	20
10	14	35	20
11	12	36	20
12	22	37	23
13	19	38	27
14	14	39	18
15	19	40	19
16	19	41	22
17	27	42	20
18	21	43	22
19	19	44	21
20	18	45	19
21	20	46	18
22	20	47	13
23	19	48	21
24	23	49	22
25	28	50	20

Table 4. Weight of the Characteristics (1 to 50).

Characteristic	Number of Times Selected	Characteristic	Number of Times Selected
51	20	76	22
52	21	77	15
53	19	78	18
54	20	79	4
55	19	80	11
56	14	81	17
57	21	82	25
58	17	83	17
59	16	84	18
60	22	85	20
61	24	86	14
62	17	87	26
63	18	88	23
64	16	89	22
65	24	90	22
66	18	91	16
67	17	92	15
68	12	93	21
69	20	94	19
70	19	95	18
71	17	96	23
72	16	97	13
73	19	98	16
74	19	99	21
75	25	100	16

Table 5. Weight of the Characteristics (51 to 100).

4.2. Non Parametric Wilcoxon Signed-Rank

Using the non-parametric Wilcoxon Signed-Rank, and seeing the Table 2, we can observe that:

In the comparative of methods Without Algorithm (T^-) and PSO (T^+), because T=min(T^-, T^+)=(5, 10)=5 y $T_0 = 1$, we can't conclude that $T \leq T_0$, and we can't accept the alternative hypothesis H_A. Is not possible determined if the PSO Algorithm or the method without algorithm is more nearly to the right.

In the comparative of methods Without Algorithm (T^-) and Differential Evolution (T^+), because T=min(T^-, T^+)=(9, 6)=6 y $T_0 = 1$, we can't conclude that $T \leq T_0$, and we can't accept the alternative hypothesis H_A. Is not possible determined if the Differential Evolution Algorithm or the method without algorithm is more nearly to the right.

In the comparative of methods PSO (T^-) and Differential Evolution (T^+), because T=min(T^-, T^+)=(12, 3)=3 y $T_0 = 1$, we can't conclude that $T \leq T_0$, and we can't accept the alternative hypothesis H_A. Is not possible determined if the PSO Algorithm or the method Differential Evolution is more nearly to the right.

5. Conclusions

After performing different tests applying PSO and Differential Evolution mixed with KNN and Naive Bayes Classifiers, although the features reduction was excellent, and in some cases the increase in the classification rate becomes even higher than 100%, the statistical tests, non parametric signals Wilcoxon test, tell us that we can't determined what algorithm is better PSO, AG or without algorithm, but feature reduction guarantee significant savings in time classification, which is essential in this topic.

As future work, we would propose a new classification algorithm, features reduction through principal component analysis, propose a new metaheuristic or improve the already proposed.

Acknowledgements

Thanks to Consejo Nacional de Ciencia y Tecnología (CONACyT), for their support to carry out this research, and thanks to the project 4573.12-P of DGEST.

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