Multi-objective Optimization Evolutionary Algorithms applied to Paroxysmal Atrial Fibrillation diagnosis based on the k-nearest neighbours classifier

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Abstract. In this paper, multi-objective optimization is applied to determine the parameters for a k-nearest neighbours classifier that has been used in the diagnosis of Paroxysmal Atrial Fibrillation (PAF), in order to get optimal combinations of *classification rate*, *sensibility* and *specificity*. We have considered three different evolutionary algorithms for implementing the multi-objective optimization of parameters: the *Single Front Genetic Algorithm* (SFGA), an improved version of SFGA, called *New Single Front Genetic Algorithm* (NSFGA), and the *Strength Pareto Evolutionary Algorithm* (SPEA). The experimental results and the comparison of the different methods, done by using the hypervolume metric, show that multi-objective optimization constitutes an adequate alternative to combinatorial scanning techniques.

1 Introduction

Most real-world optimization problems are multi-objective in nature, since they normally have several (usually conflicting) objectives that must be satisfied at the same time. These problems are known as MOP (*Multi-objective Optimization Problems*) [1].The notion of *optimum* has to be re-defined in this context and instead of aiming to find a single solution; a procedure for solving MOP should determine a set of good compromises or *trade-off* solutions, generally known as *Pareto optimal solutions* from which the decision maker will select one. These solutions are optimal in the wider sense that no other solution in the search space is superior when all objectives are considered.

Evolutionary Algorithms (EAs) have the potential to finding multiple Pareto optimal solutions in a single run and have been widely used in this area [2] Recently the importance of *elitism*, supported experimentally [2,3], *secondary population* and adequate *diversity maintaining techniques* has focused the attention of researches [4]. In that sense, some of the authors have presented elsewhere the SFGA [5] and the NSFGA[6] that continue exploring the benefits of the aforementioned concepts.

The Atrial Fibrillation is the heart arrhythmia that causes most frequently embolic events that may generate cerebrovascular accidents. In this paper is described how the aforementioned techniques are applied to an open real world problem: Paroxysmal Atrial Fibrillation Diagnosis based on Electrocardiogram (ECG) traces without

explicit Atrial Fibrillation episodes [7]**.** Recently has finished an international initiative that addressed this problem concluding that an automatic PAF diagnosis scheme is possible with a reasonable efficiency. The different proposed diagnosis approaches within the Computers in Cardiology Challenge 2001 [7] were focused on achieving high classification rates. But the use of ECGs (non invasive exploration method) for the diagnosis motivates the possibility of using this diagnosis scheme in routinely cardiac examinations. If the application reaches high accuracy detecting PAF patients (high sensibility), even with a lower capability of accurate diagnosis with healthy subjects (lower specificity), positive diagnosis would motivate more complete explorations. Therefore it can be considered a MOP in which is has interest to optimize the **classification rate** and the **sensibility** (see section 2).

In this paper section 2 describes the PAF diagnosis problem, Section 3 reviews both SFGA and NSFGA. Experimental results for SFGA, NSFGA and SPEA which is one of the State-of the-art evolutionary algorithms for MOPs, are given in section 4. Finally concluding remarks are summarized in Section 5.

2 PAF Diagnosis based on the K-nearest neighbor classifier

A public database for PAF diagnosis applications is available [8]. It is composed by registers obtained of 25 healthy individuals and 25 patients diagnosed with PAF. An automatic algorithm capable of discriminating registers of these two groups with a certain accuracy is the challenge addressed in the present paper. For this purpose 48 parameters have been extracted of each ECG register [9] obtaining a 48 component vector that characterizes each subject (p_1, …, p_{48}).

A modular classification algorithm based on the K-nearest neighbours has been used for this application and described in detail in [10]. The labelled vectors work as references of the classification system. For each new non-labelled vector, the Euclidean distances to the labelled vectors are calculated. The labels of the K-nearest neighbours are consulted and the final label is calculated through a voting scheme as the label of the majority of the K-nearest neighbours. In this way the classification algorithm is modular, new parameters can be added easily, only the dimension considered in the Euclidean distance calculation step has to be modified. The modularity of the classification algorithm enables automatic parameter scanning techniques. Using the 48 parameters in the classification scheme is highly inefficient, therefore a parameter selection stage is necessary to select a subset of parameters with which the best classification performances are reached.

In order to be able to automatically modify the selection of the different parameters in the classification scheme the input pattern has been multiplied by a filter vector (F), i.e. I=(p_1 f_1, …, p_{48} f_{48}). Where the filter components f_i lie within the interval [0,1]. These filter components represent the chromosome of the different solutions optimized by the evolutionary algorithms.

For biomedical diagnosis applications, the final diagnostic of a specific disease for a patient can be **ill** (suffering of a certain pathology) or **healthy** (free of this concrete pathology). This means that the classification result for PAF diagnosis can be:

True Positive (TP). The algorithm classifies as PAF patient a real PAF patient.

True Negative (TN). The algorithm classifies a healthy subject as healthy.

False Positive (FP). The algorithm classifies as PAF patient a healthy subject

False Negative (FN). The algorithm classifies as healthy subject a PAF patient.

With these cases different functions of interest can be defined (1) : *Classification rate* (CR), *Sensibility* (SE) and *Specificity* (SP).

$$CR = \frac{TP + TN}{TP + TN + FP + FN} \;;\; SE = \frac{TP}{TP + FN} \;;\; SP = \frac{TN}{TN + FP} \qquad (1)$$

Note that the *Sensibility* represents the ratio between the detected ill patients and the total ill patients. While the *Specificity* represents the ration between the detected healthy subjects and the total healthy subjects.

Due to the small size of the training database (25 patients and 25 healthy subjects), the evaluation of the classification rate is calculated in 50 cycles with the method *leaving one out*. In this way, in each cycle, one vector is selected as test element. This vector is classified according to the scheme described above with the other 49 labelled vectors as classification references. In each cycle are actualised the classification results in four counters: True_Positive (TP), True_Negative (TN), False_Positive (FP) and False_Negative (FN). The final classification rate (CR), the sensibility (SE) and the specificity (SP) are finally calculated with these counters that accumulate the classification results of the 50 cycles

It is worthy to mention that MOEAs generate a population of different solutions. This must be seen as an added advantage because some of these solutions will be more appropriate than other for certain patients suffering from other cardiac pathologies. This other current pathologies may invalidate some solutions based on certain parameters that are unreliable for these patients. Therefore a population of solutions instead of a single one is desirable.

3 Single Front Evolutionary Algorithms

The *Single front Genetic Algorithm* (SFGA) [5], previously proposed by some of the authors, implements a elitist selection procedure in which only the non-dominated (and well-diversified) individuals in the current population are copied to the mating pool for recombination purposes (see Figure 1.a) The preservation of diversity in the population is ensured by means of a filtering function, which prevents the crowding of individuals by removing individuals according to a given *grid* in the *objective* space. The filtering function uses the distance evaluated in the objective space. That approach has been proved very effective when applied to Zitzler test functions in comparison to other similar algorithms using a more complex selection scheme to produce the mating pool **.**

In the *New Single front genetic algorithm* (Figure 1.b) [6], some features has been added to the original SFGA. Firstly an external archive keeps track of the best-ever solutions found during the running of the algorithm. A selection procedure produces a mating pool of size *S* by randomly choosing individuals from the external set and the filtered current population. The variation operators produces the offspring that is copied to the next population. The updating procedure adds the first front of ND individuals in the current population and deleting from the archive the dominated individuals.

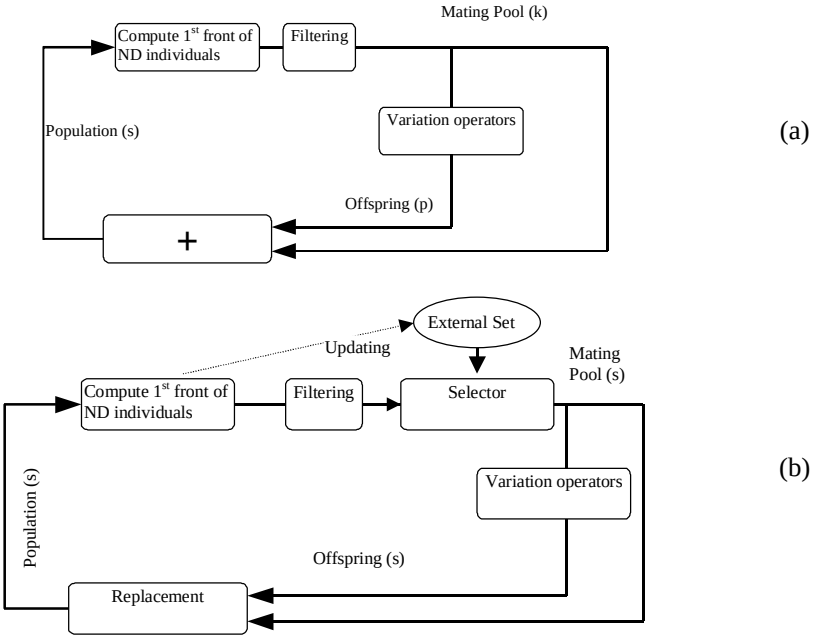

Fig. 1.: Description of SFGA (a) and NSFGA (b).

4 Experimental Results

For performance comparison, the hypervolume metric [3] for maximization problems has been used. For the sake of simplicity just S metric is shown. S(Ai) is the volume of the space that is *dominated* [1] by the set Ai. All of the algorithms were executed with the same initial population. The filter parameter, ft, is set to 0.01, the mutation probability per gene is 0.01 and the crossover probability is 0.6. Each Algorithm (see Table 1) is executed for 3 objectives (section 4.1) and 2 objectives (section 4.2). All algorithms are executed 100 iterations except where indicated.

4.1 Three objectives: Classification rate, sensibility and specificity.

Although these three objectives are linearly dependent, this section can illustrate the performance gain obtained by selecting two of these objectives in section 4.2.

In this case, best Performance was obtained by SPEA with K=1, (the average of the three best Classification rates was 86% with 88% as average Sensibility and 81.3% average Specificity).The results are similar to the ones obtained by combinatorial scanning techniques [10]**.**

Table1. Performance of the algorithms for 3 and 2 objectives

Popsize	K	$SFGA_3$	$SFGA_2$	$NSFGA_3$	$NSFGA_2$	$SPEA_3$	$SPEA_2$
100[1]	1	0.53632	0.68640	0.66259	**0.82720**	**0.68147**	0.77360
	3	0.44256	0.73600	**0.65910**	0.75280	0.58732	**0.78800**
	5	0.47980	0.65120	0.61958	0.77200	**0.68371**	**0.83680**
	7	0.53262	0.65280	0.55104	**0.77200**	**0.59222**	0.73920
	9	0.46086	0.62400	**0.59136**	0.72080	0.57862	**0.72160**
100	1	0.49795	0.65360	0.66259	0.72160	**0.68147**	**0.73840**
	3	0.44256	**0.71760**	0.50048	**0.71760**	0.57203	**0.71760**
	5	0.47804	0.63520	0.52041	0.67120	**0.64313**	**0.73520**
	7	0.51200	0.62400	**0.55104**	0.68880	**0.55104**	**0.72000**
	9	0.45907	0.60800	**0.55104**	0.67200	0.53504	**0.69840**
50	1	0.49612	0.80960	0.63571	**0.82800**	**0.68147**	0.70560
	3	**0.50048**	**0.75440**	**0.50048**	0.69920	0.44460	0.65920
	5	0.55936	0.59200	0.42150	0.61920	**0.61203**	**0.65040**
	7	**0.51558**	0.63840	0.46364	0.63840	0.51072	**0.65360**
	9	0.44179	0.59040	**0.53267**	**0.67200**	0.53260	0.63840
30	1	0.68806	0.65600	0.61958	0.68880	**0.73449**	**0.70560**
	3	0.45926	0.69920	**0.48672**	**0.71520**	0.46700	0.64400
	5	0.48838	0.60480	0.53446	**0.67120**	**0.53632**	0.63840
	7	0.51072	0.59200	0.48153	**0.65520**	**0.51200**	0.61840
	9	0.43776	**0.66880**	0.46086	0.56080	**0.55212**	**0.66800**

4.2 Two objectives: Classification rate and Sensibility.

The whole diagnosis scheme is based on ECG traces, therefore on a non invasive exploration process. In this context, a high sensibility is more desired than a high specificity for the same classification rate. This means, that such an automatic PAF diagnosis application could be applied in routinely explorations, in this way, positive PAF diagnosis would motivate more complex diagnosis processes. Because of that we have focused on optimizing the classification rate and sensibility of the algorithm.

In the two objectives optimization scheme the best Performance was obtained by SPEA with K=5, (the average of the three best Classification rates was 82% with 94.7% as average Sensibility, for these solutions the a posteriori calculated Specificity average is 69.3%). In this case, it is observed that the Sensibility increases significantly, although the classification rate decreases, this can be of interest to detect possible PAF patients among the general population in preventive examinations.

[1] 1000 iterations

5 Concluding Remarks

Optimization of the three algorithms can be seen as a global optimization, while when only two performance indicators are taken into account (CR and SE) the process is focused on optimizing SE (although this would produce a decrease in SP) and CR. The obtained results are of the same range to the ones reached by combinatorial scanning processes [10] but the techniques applied in this paper have two intrinsic advantages: the search space covers uniformly the whole parameter space, and the generation of a population of different solutions instead of a single one. These two characteristics are common to all the evolutionary algorithms applied in this paper.

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