Chapter 1
An Introduction to the Use of Evolutionary Computation Techniques for Dealing with ECG Signals

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Abstract Evolutionary Computation (EC) has become one of the most developed and successful computational intelligence techniques used for solving real-world problems from different application areas, including engineering, machine learning, signal processing, and data mining, among many others. It is indeed particularly worth noticing the success of the use of EC techniques for dealing with problems that involve the processing, classification, and interpretation of different sources of signals. From them, the treatment of ECG signals represents a challenge for the scientific community since such a problem has not only a high academic impact, but an important social impact, as well. In this chapter we present an introduction to basic EC concepts, including the description (under a unified perspective) of the most representative algorithms within this area. Furthermore, the chapter is aimed to provide the reader with the fundamentals of the most representative EC-based methodologies and other well-known bio-inspired inspired metaheuristics that have been adopted for dealing with the treatment of ECG signals. Additionally, some areas for future research are also identified towards the end of the chapter.

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1.1 Introduction

Evolutionary Computation (EC) techniques have reached an impressive level of development, both from the point of view of basic research as well as from the perspective of practical applications. This has also triggered an important amount of research on other bio-inspired metaheuristics such as Particle Swarm Optimization (PSO), Ant Colony Optimization (ACO), Differential Evolution (DE) and Artificial Immune Systems (AIS), which have also been extensively applied in many real-world problems.

Biomedical signals (biosignals) processing has became a very appealing area for developing and applying Computational Intelligence (CI) techniques. CI can be defined as a broad class of bio-inspired approaches normally used for classification and optimization, which includes EC techniques, artificial neural networks, and fuzzy logic. Among the most relevant biosignals are those represented by raw data collected by different medical instruments such as Electrocardiograms (ECG), Electroencephalograms (EEG), and Electromyogram (EMG); however, in this chapter we will focus specifically on ECG signals.

It is worth emphasizing that the use of CI-based techniques for medical applications is a vast and promising research area that has been kept under continuous development in the last few years. Although (Begg et al., 2008) have observed that neural networks and fuzzy logic are the most developed CI techniques used for medical applications, several important EC techniques have also been applied in this area, too, as we will see in this chapter. Several EC-based tools have been proposed for medical applications, including those that deal directly with the processing of ECG signals. However, there are also EC-based tools aimed to help other techniques to improve their processing of ECG signals (this could be considered as an indirect way of applying EC approaches in this area). Therefore, the aim of this chapter is to show that EC techniques can be considered as useful tools to be used in this application domain. With that goal in mind, this chapter will review the newest and most relevant proposals on the use of EC techniques for biomedical problems, aiming to provide an appealing perspective of this CI technique and its potential use for medical applications.

The rest of the chapter is organized as follows. Section 1.2 provides the main EC concepts necessary to make this chapter self-contained. This includes a brief description of the most representative EC-based algorithms, seen under a unified perspective. In Section 1.3 we give some introductory remarks and definitions on ECG signals. Next, in Section 1.4 we present a brief literature review of applications that use EC techniques as either a primarily or as a secondary tool when dealing with some typical problems related to ECG signals. An additional literature review is given in Section 1.5 that describes the application to ECG signals of other bio-inspired metaheuristics such as PSO, AIS, and ACO. The chapter finishes in Section 1.6 with some

general comments about the state-of-the-art and future research lines in this application domain.

1.2 EC Basics

EC techniques comprise a set of metaheuristics that seek to emulate the mechanism of natural selection described in Charles Darwin's evolutionary theory, with the aim of solving problems. Although the origins of EC can be traced back as far as the early 1930s (Fogel, 1995), it was not until the 1960s that the three main techniques based on this notion were developed: genetic algorithms (Holland, 1962, 1992), evolution strategies (Schwefel, 1965, 1995) and evolutionary programming (Fogel, 1966). These approaches, which are now collectively denominated "evolutionary algorithms," constitute the core of the evolutionary computation field.

Nowadays, there exists a large amount of literature devoted to EC techniques and their applications, see for example (Bäck, 1996; Bäck et al., 2000; Eiben and Smith, 2003; Fogel, 1995; Michalewicz and Fogel, 2004). Modern approximations to the theory and practice of EAs can be found in (De Jong, 2006) as it represents a valuable, comprehensive, and up-to-date source of information about EAs from a unified point of view. Additionally, in (Glover and Kochenberger, 2003), and in (Talbi, 2009), one can find good descriptions of EC techniques in the context of modern metaheuristics. These books also describe other bio-inspired algorithms such as Ant Colony Optimization (ACO), Particle Swarm Optimization (PSO), Bee Colony (BC) based algorithms, and Artificial Immune Systems (AIS).

Considering the most recent perspectives to study EC techniques, we present in the following a general and unified description of EAs that can help readers to better understand their basic operating principles and the ways in which they could be applied in the solution of problems related to the processing of ECG signals.

From a Darwinian perspective (De Jong, 2006), the metaphor of adaptation and evolution of an species involves: a) one o more populations of individuals competing for limited resources, b) the notion of dynamically changing populations due to the birth and death of individuals, c) a concept of fitness which reflects the ability of an individual to survive and reproduce, and d) a concept of variational inheritance (*i.e.,* offspring closely resemble their parents, but are not identical). An algorithm designed to fulfill the above characteristics implements a *Darwinian evolutionary system* (De Jong, 2006). Based on the concept of evolutionary systems, several possibilities arise to design advanced algorithms capable of efficiently exploring complex search spaces for solving complex optimization problems. In this regard, it is necessary identify the problem components and the way they can be included in the evolutionary system (*e.g.,* a representation of potential solutions, a fit-

ness function to assess the quality of potential solutions, selection mechanisms for mating and reproduction, and evolutionary operators to create offspring from the individuals selected for reproduction). An EA can be considered an advanced expression of an evolutionary system, mainly devoted to solve optimization problems. In the following, we describe the main components (including some examples) of an EA. Next, it is presented a general outline of an EA that embodies, in a unified manner, the most representative EAs in current use.

1.2.1 Fundamental Components of an Evolutionary Algorithm

When dealing with a particular problem, a potential user or implementer of an EA must carefully make appropriate design decisions in order to achieve an effective and efficient EA to solve the problem at hand. Those decisions are related to the main components of the EA with regards to the following description:

- **Individuals' representation**: With no doubt, this is one of the earliest and most important design decisions that must be made. The type of representation adopted will determine the size of the search space (i.e., the set of all possible solutions) as well as the design of the evolutionary operators that will be used for manipulating these solutions. In the jargon of EAs it is said that an individual[1] encodes (using a particular alphabet) a possible solution for the problem at hand. Many times, the chromosome is an indirect representation of a solution (called genotype) and a decoding process is needed to obtain the solution (called phenotype). However, some other representation encodings directly represent the problem solution, *i.e.,* the EA search space is a phenotypical one. Thus, we will assume that the search space of an EA can be either genotypical or phenotypical. The binary alphabet is the canonical option in EAs, and the most commonly considered is the set $\{0, 1\}$. However, many other encodings are possible as long as we can devise appropriate operators for them. The choice is generally determined by the problem and also by the type of EA that is being implemented. For example, when using Evolution Strategies (Schwefel, 1995), the typical representation is a real valued vector. In contrast, the typical representation in Genetic Programming (Koza, 1992, 1994) is a tree structure. Another important consideration is about the length of the chromosomes. Their length could be fixed or variable. This depends on the problem we are dealing with. For the sake of a simpler discussion, we will assume in this chapter the use of a fixed length $n \in \mathbb{N}$ for all the

[1] The term *chromosome* is also widely adopted and will be used interchangeably in the following.

individuals in an EA.

- **Population of Individuals:** An EA performs an iterative process that manipulates a population of individuals. Accordingly, a structure $P(t)$ is defined to keep the current population of those individuals at time t (variable t represents the iteration number as described in the following section). Usually, the population size is kept fixed during the evolutionary process; however, the use of variable size populations is also possible.

  Definition 1. Let $\mathcal{I}$ be the set of all possible encoded solutions, $P(t) \in \mathcal{I}$ a set of the current population at time t and $m = |P(t)|$ is the population size. The size of $\mathcal{I}$ will depend on n, the length of the chromosome and the cardinality of the alphabet adopted.

  Some examples of possible search spaces regarding the chosen solution representation are the following:

Binary vectors:	$\mathcal{I}_1 = \{(b_1, \ldots, b_n) \vert b_i \in \{0, 1\}\}$
Real vectors:	$\mathcal{I}_2 = \{(r_1, \ldots, r_n) \vert r_i \in [a, b] \text{ with } a, b \in \mathbb{R}\}$
Permutations:	$\mathcal{I}_3 = \{(p_1, \ldots, p_n) \vert p_i \in \{1, \ldots, n\} \text{ and } (\text{ if } p_i = p_j, \text{ then } i = j)\}$
Integer vectors:	$\mathcal{I}_4 = \{(a_1, \ldots, a_n) \vert a_i \in \mathbb{N}\ \}$

- **Fitness Function**: As the emulation of the evolution metaphor implies the survival of the fittest individuals, a measurement mechanism should be defined for assessing the adaptability of the individuals to the environment (*i.e.,* the problem under consideration). The fitness function:

$$F : \mathcal{I} \rightarrow \mathbb{R}^+ \tag{1.1}$$

  assigns to each individual a real positive value that is used for the selection mechanism (next item) to guide the search in forthcoming iterations.

- **Selection**: The selection mechanism imposes a bias to the search process towards regions of high quality solutions. The aim of this mechanism is to preferably select the fittest individuals that will participate in the reproduction phase. The selection mechanism can be seen as the following function:

$$\mathcal{S}el : 2^{\mathcal{I}} \rightarrow 2^{\mathcal{I}} \tag{1.2}$$

- **Reproductive Mechanisms (or Evolutionary Operators)**: This important component is in charge of generating the offspring from the selected set of parents (function $\mathcal{S}el$). Generally speaking, evolutionary operators promote the exploration of the search space by creating offspring which inherit good genetic material from their parents. Thus, these operators are expected to create, on average, individuals with higher quality

with respect to their parents. Classical evolutionary operators are crossover (eq. (1.3)) and mutation (eq. (1.4)). The general crossover operator presented in eq. (1.3) is defined as a binary operator that takes two parents and returns one offspring. However, other domains and ranges are also possible for this operator, *e.g.,* multiple-parents, and two or more offspring.

$$\chi_c : \mathcal{I} \times \mathcal{I} \rightarrow \mathcal{I} \tag{1.3}$$

$$\chi_m : \mathcal{I} \rightarrow \mathcal{I} \tag{1.4}$$

A classical example of a crossover operator for binary representation is the so-called 1-point crossover. Its application consists in generating a random number $k \in \{1, \ldots, n-1\}$. The offspring inherits the first k bits form the first parent and the last $n-k$ bits from the second one. For example, given the crossover point $k = 3$ and two possible parents $P1$ and $P2$, one of the generated children is the following:

$$\begin{aligned} P1 &= (0\ 0\ 1\ |0\ \ 1\ \ 0\ 1\ \ 1\ 1) \\ P2 &= (\mathbf{1\ 0\ 0}\ |\mathbf{1\ \ 1\ \ 1\ 0\ \ 1\ 0}) \end{aligned}$$

$$\chi_c(P1, P2) = (0\ 0\ 1\ \ \mathbf{1\ \ 1\ \ 1\ 0\ \ 1\ 0})$$

It must be noticed that the original 1-point crossover generates two offspring, by using a very similar procedure to the one described above. In fact, this procedure can be extended to allow the generation of more than two children, to the use of several crossover points and more than two parents.

Following with the binary representation for the individuals, a classical example for the mutation operator is the so-called flip mutation. This simple operator consists of choosing a location $l \in \{1, \ldots, n\}$ that indicates the bit that will undergo mutation. The new value at location l is: $new_val(l) = 1 - old_value(l)$. Let $l = 4$ be the random location generated and $P1$ the individual that undergoes mutation:

$$P1 = (0\ 0\ 1\ \overset{\smile}{0}\ \ 1\ 0\ 1\ 1\ 1)$$

$$\chi_m(P1) = (1\ 0\ 0\ \mathbf{1}\ \ 1\ 1\ 0\ 1\ 0)$$

1.2.2 A general outline of an EA

Having described the main components of an EA, it is now possible to present a general outline of this kind of algorithm. Figure 1.1 displays a schematic representation of an EA's behavior as a composition of the functions $\mathcal{I}nit$ (ap-

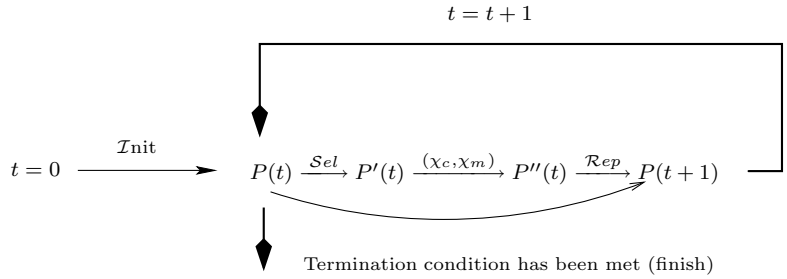
Algorithm 1 General outline of an EA

```
t = 0;
P(t) = Init();
while ( Termination_Condition not met) do
    Eval( P(t) );
    P'(t) = Sel(P(t));
    P''(t) = Apply_Operators(P'(t), χc, χm);
    P(t + 1) = Rep( P(t) , P''(t + 1));
    t=t+1;
end while
```

plied once), $\mathcal{S}el$, χ_c, χ_m, and $\mathcal{R}ep$. Function $\mathcal{I}nit$ is in charge of generating the initial population to be evolved. Several criteria can be used to generate the initial population, but the simpler one is to generate a population completely at random. The last part of the iterative process involves function $\mathcal{R}ep$ which obtains the new population based on the current population ($P(t)$) and the intermediate population ($P''(t)$) generated by applying $\mathcal{S}el$ and operators χ_c and χ_m. In order to have a closer perspective of the implementation of an EA, the corresponding pseudo-code is presented in Algorithm 1.

To conclude this section, it is worth mentioning the importance of hybridization in the field of EAs. Several alternatives to design hybrid EAs can be found in the literature. Such examples illustrate the importance of this topic as an alternative to improve the performance of an EA. A recent comprehensive description of hybrid metaheuristics that can be applied to EAs can be found in (Talbi, 2009). It is also important to highlight that EAs and other related metaheuristics have been widely applied in combination with a large variety of computational intelligence tools as discussed in Section 1.4 within the context of ECG signal processing.

Fig. 1.1 Schematic representation of an EA as a composition of functions: $\mathcal{I}nit$ (applied once), $\mathcal{S}el$, χ_c, χ_m, and $\mathcal{R}ep$.



1.3 ECG signals

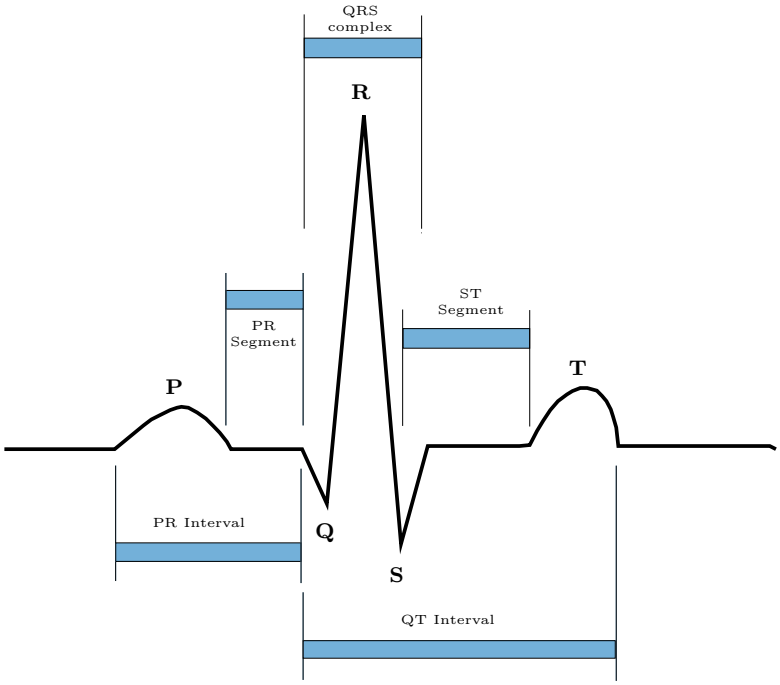
With the advancements of digital technology in general and the technology used in medical instrumentation, in particular, many different types of medical data are continuously collected from patients for different reasons. Consequently, the hospital and clinical databases are continuously growing as they maintain detailed information from different medical instruments and sources of physiological signals (biosignals) that are usually generated by human beings. For example, magnetic resonance imaging, computerized tomography, electrocardiogram (ECG), electroencephalogram (EEG), and electromyogram (EMG) signals. Although ECG, EEG, and EMG signals are usually associated to the analysis of unimodal signals (*i.e.,* one signal is considered at a time), multimodal signal modelling and processing could be also considered (Laguna and Sörnmo, 2009). Particularly, this chapter is devoted to the ECG unimodal signal processing from an evolutionary computation perspective, as an alternative way to deal with some particular problems in this area. In what follows, we first provide the basic concepts and components involved in the processing of ECG signals, and then we discuss the need to use automatic approaches and algorithms for signal processing, as well as the kind of tasks that are more suitable to be solved through the use of EC techniques.

Electrocardiogram (ECG) signal processing conforms one important part of the above mentioned medical data that are widely available and are also easy to obtain due to the lower costs of medical instruments necessary to collect them among patients under different circumstances. Moreover, heart diseases diagnosis and ECG interpretation is an important non-invasive step in the clinical diagnosis process. The ECG is a valuable indicator of cardiac function and it represents the electrical activity of the heart over time. In Figure 1.3 we can observe a normal ECG where the QRS complex and some other waveforms give evidence of mechanical pumping of the heart. Consequently, a correct analysis and interpretation of these waveforms can be extensively used to infer cardiac health as well as cardiac diseases —*e.g.,* arrhythmia, myocardial infarction, and myocardial ischemia; moreover blood and vessels diseases and congenital diseases can also be detected by carefully analyzing the ECG signals. In the next section we cover some of the main tasks that are usually considered when analyzing the ECG signals in search for patterns that could indicate possible heart diseases or malfunctioning.

1.3.1 ECG signal processing

General algorithms for basic ECG signal processing include at least the following components: a) noise filtering, b) QRS detection, and c) wave delineation. In addition to that, d) a data compression module can be added

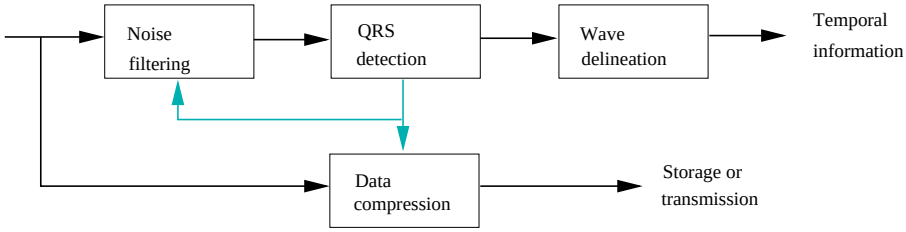
Fig. 1.2 Schematic representation of a normal ECG: QRS Complex; PR and ST segments; and PR and QT intervals.



for further data storage or transmission. (Sörnmo, L. and Laguna, P., 2006) describe the interaction among these components which is recreated in this chapter as shown in Figure 1.3. For further information, an appealing source of introductory information regarding ECG signal processing is precisely the above mentioned book of (Sörnmo, L. and Laguna, P., 2006). In the following, we present a short description of the main modules in ECG signal processing which explains their respective functions and scope in the whole processes:

- One important issue when dealing with the interpretation of recorded signals is the presence of noise as indicated in Figure 1.3 by the respective module in the main sequence of ECG signal processing. In that regard, most of the signal processing aims at extracting the expected signal (*i.e.,* uncorrupted) from a noisy one. According to (Friesen et al., 1990), there exist several sources of noise that can corrupt in different ways the recorded ECG signal. The following can be considered as the most important sources of noise:

Fig. 1.3 A general scheme of a potential algorithm for basic ECG signal processing. Light arrows indicate that the output from QRS complex detection can be used as feedback information in 'Data compression' and 'Noise filtering' modules to improve their respective performance.



- **Power-line interference:** to diminish this kind of noise, filters are designed to suppress ECG components close to the power-line frequency.
- **Electrode contact noise:** is a transient interference caused when an electrode loses contact with the skin.
- **Motion artifacts:** the electrode-skin impedance can produce artifacts with electrode motion.
- **Muscle contraction:** this causes that millivolt-level potential fields can be generated.
- **Baseline drift:** the beat morphology is suitable for changes that do not have a cardiac origin and can produce important distortions in the collected signal. This type of noise can be generated by the movements of the patient when is being tested.
- **Instrumentation noise:** normally generated by electronic devices used in signal processing, *e.g.,* producing a saturation on the input devices that avoid to reach the ECG signals.
- **Electrosurgical noise:** this type of noise is produced by the instruments that apply electrocauterization and it can completely destroy the ECG signal.

• The QSR wave detection is a very important and determinant step in the ECG signal processing. On the one hand, QRS complex detection is directly associated to heart beat detection. Thus, a poor performance of a potential detector will produce irrecoverable errors in further processing steps, *e.g.,* during the wave delineation. There exists a large number of QRS morphologies that must be detected and certainly, many different

diagnosis tasks that might arise based on the results of the QRS detector. For example, clustering of beat morphologies may be performed for the purpose of characterizing the morphology of a QRS complex, *i.e.,* groups of beats with similar morphology can be assigned to the same cluster.

- Wave delineation is the process through which it is determined the boundaries of each wave within the PQRST complex (see Figure 1.3). This can be done right after the detection of the QRS complex. This process lets us measure the length (or duration) of the waves. From these and other measurements, different characterizations are possible for the waves in the PQRST complex such as amplitude and morphology.
- Data compression implies an efficient use of storage media, transmission under different media; *e.g.,* from the ambulance to the hospital for a rapid diagnostic. Nowadays, the impressive advancements in the creation and improvement of medical instruments to capture huge amounts of data makes necessary to find mechanisms to efficiently transmit, and also store and retrieve the information collected, while avoiding any type of redundancy.

1.3.2 Feature extraction from ECG signals

Once the ECG signal processing has finished, a large amount of raw digital data is available for different analysis and interpretation. For undertaking such analysis and interpretation, it is necessary to present such data to the phase of feature extraction which lets us to identify the most relevant characteristics that could help us to determine possible heart diseases, if any. However, the resulting features from the extraction process can lead us to sub-optimal or redundant sets of characteristics. In the sub-optimal case, a possible approach to learn and determine heart diseases from some data of a patient will probably fail since there is not enough information available to reach a correct or an acceptable decision. In the second case, the learnt prediction model can be very complex and probably inaccurate as well.

The feature extraction problem can be formulated as follows. Let $\mathcal{F}$ be the set of all available features and $n = |\mathcal{F}|$, the number of features. The objective is to select a subset $F \subseteq \mathcal{F}$ with $m = |F| \leq n$ that optimizes a given selection criterion C in regards of $\mathcal{F}$. The feature extraction problem belongs to the class of NP problems. Therefore, computational intelligence (CI) techniques are a suitable alternative for dealing with such problems.

It is also worth noting that from a CI perspective, feature extraction is only one part of the problem, since the main objective is to establish a relationship between the available information (representing the input data) and the corresponding pathology observed in real patients. Here is when EAs or other metaheuristic approaches come to play an important role within ECG signal interpretation as they can be a very useful tools to provide, in a timely manner, high-quality solutions in regards either the feature extraction task

(direct application) or by helping to find more accurate rules in a fuzzy-logic classifier and more efficient neural networks —*e.g.,* optimal weight values or network structure (indirect application). Based on this observation, the next section presents a short review that embodies the most recent research in this area.

1.4 EAs for ECG: a brief review

This section presents a short review of the specialized literature that highlights the application of EAs for solving ECG signal processing related problems. This review also includes tasks such as feature extraction, as well as the design of soft computing tools like those found in the field of fuzzy logic and neural networks. It should be noticed, however, that using EAs as either indirect or direct tool to deal with ECG signals, many different solution search spaces are possible. For example, an EA as indirect application could be designed to find a good combination of kernels in a support vector machine or possibly for evolving a neural network structure. Also, EAs are usually applied in the feature selection process before applying another soft computing tool (*e.g.,* for classification). In this case, a binary string is the most widely used representation for the features to select. In the case of direct applications, it is possible to deal with the problem of segmentation of a ECG signal. For that, a real vector can be used as solution representation to approach this particular problem. Accordingly, the reader should be aware that many schemes for solution representation are possible. Certainly, it will depend on the specific problem at hand when dealing with ECG signals and the way that problem is approached. To better characterize the use of EAs in the field of ECG signal processing, we have split the presentation of the review by considering *indirect* and *direct* application of EAs as was explained in the previous section.

1.4.1 Indirect Application of EAs

- (Wiggins et al., 2006) describe the application of a GA for evolving a Bayesian network devoted to classify patients' ages based on features extracted from ECG signals. The evolutionary process is aimed to produce a high quality network structure for the classification process by evolving a population of chromosomes represented by integer vectors. The GA is compared with K2, a greedy hill-climbing algorithm considering the classification accuracy. The same authors present in (Wiggins et al., 2008) an extended study of (Wiggins et al., 2006) in which both the GA and K2 are compared with two naïve Bayesian approaches. The results show that

the GA largely outperforms K2 and is also able to achieve an improved performance when compared to the two naïve Bayesian approaches.

- (Chua and Tan, 2007) use a GA to evolve a non-singleton fuzzy logic system (NSFLS) designed for handling uncertainties in cardiac arrhythmias classification which is a particular pattern classification problem that usually arises when dealing with ECG signals. The NSFLS is supposed to work better than a singleton fuzzy logic system (SFLS) when applied to a noisy environment as it models uncertainty, imprecision, or inaccuracy of the inputs which is a usual situation in ECG signals. In the GA, each possible fuzzy logic system is represented by a binary string (chromosome) which decodes values representing, respectively, 3 membership functions (for each value, it decodes both the mean and the standard deviation) and 9 possible rules. As the fuzzy logic system is intended to classify three cardiac arrhythmias —*i.e.,* Ventricular Fibrillation (VF), Ventricular Tachycardia (VT), and Normal Sinus Rhythm (NSR), the respective fitness function is calculated as the weighted average on these three correctly classified classes. NSFLS and SFLS are tested and compared on a set of well known instances of ECG signals (Goldberger et al., 2000). The results show superiority of NSFSL with respect to SFLS regardless of the inputs given.
- (Nasiri et al., 2009b) present the Genetic-ESVM, a novel classification system based on a GA, which is designed to improve the generalization performance of the so-called Emphatic Support Vector Machine (ESVM) classifier. The first stage of the Genetic-ESVM is aimed at finding the best subset of features by applying a GA. In order to achieve this goal, each chromosome is represented by a binary vector of length n_f (n_f number of all possible features that can be selected for further classification). The second stage (last) classifies the ECG signals either using a classical SVM (Genetic-SVM) or the proposed ESVM (Genetic-ESVM). The experimental study compares a classical SVM without using the genetic feature extraction and the two genetic based algorithms: Genetic-SVM and Genetic-ESVM. The dataset MIT-BIH (Goldberger et al., 2000) was considered to assess the algorithms' performance. From the reported results, it can be observed that Genetic-EVSM (with linear kernels) outperformed the other algorithms compared. A related work presented by the same authors (see Nasiri et al., 2009a) compares the performance of a classical SVM, the Genetic-SVM (described above), and PCA-SVM, which is an SVM combined with Principal Component Analysis (PCA). These approaches aim to obtain the subset containing the best possible features for classification. The experimental results show that the feature selection found by the Genetic-SVM greatly improves the quality of classification with respect to the other algorithms studied.
- (Jiang et al., 2005) explore the benefit of applying a GA to simultaneously find the internal structure and associated weights of evolvable Block-based Neural Networks (BbNNs). The evolved BbNNs are applied to classify heart beat patterns from ECG signals. The features of BbNNs make them good candidates to deal with patterns of heart beats (*e.g.,* these patterns vary

for different individuals and, for the same individual, some changes in the pattern can take place at different times of the day as well as in different situations that the individual is experiencing). One of the features of BbNNs is the flexibility of their internal structure which can be adapted as the conditions of the environments change. Additionally, a BbNN can be implemented, for example, through a Field Programmable Gate Array (FPGA) which allows on-line partial reorganization of its internal structure. Ten records collected from different patients provided by the MIT-BIH Arrhythmia database (see Goldberger et al., 2000) were considered in order to assess the behavior of the evolved BbNN which produced a classification accuracy of more than 90%.

- A novel hybrid method based on the Ant Colony Optimization (ACO) metaheuristic and an evolutionary algorithm is presented by (Bursa and Lhotska, 2007). The proposed algorithm, called ACO-DTree is designed to automatically find a classification tree via an evolutionary process which incorporates concepts of the ACO metaheuristic. The main structure of ACO-DTree corresponds to a traditional ACO algorithm. However, the population of solutions found by the colony undergo an evolutionary step (more precisely, the application of a mutation operator) aimed to produce a renewed set of solutions. After that, the usual cycle of the ACO algorithm continues normally by selecting the best solution to proceed with the pheromone evaporation step. The experimental study includes the well-known database MIT-BIH (Goldberger et al., 2000) as well as the Iris data set taken from the UCI repository (Frank and Asuncion, 2010). However, the Iris data set is only considered as part of the preliminary parameter estimation of the algorithm. A comparison of results between an EA and ACO-DTree shows a clear benefit of using the hybrid approach (*i.e.,* ACO-DTree) to automatically build high quality classification trees on the ECG signals data set considered.

1.4.2 Direct Application of EAs

- A genetic segmentation of ECG signals is proposed by (Gacek and Pedrycz, 2003). The genetic approach is aimed to produce a segmentation of lossy signal compression through evolved geometric constructs (linear functions) which capture the real segments in the ECG signal. The chromosome is represented by a sequence of real numbers which correspond to the respective segments' ending-points and the fitness function measures the level on monotonicity of the ECG data analyzed within the segments based on the extreme estimated derivative values (maximum and minimum). In the experimental study, the authors considered three classes of instances of ECG signals taken from the MIT-BIH database (Goldberger et al., 2000) including: normal beats, left bundle branch block beats, and premature

ventricular contraction. Although the results are encouraging by using a linear model to approximate the real signal, the authors indicate that more sophisticated approximation models should be considered, *e.g.,* quadratic or polynomials of higher order.

- (de Toro et al., 2006) present a methodology consisting in applying either a multimodal[2] or multiobjective evolutionary algorithms for the adjustment of medical diagnostic schemes dealing with biosignal analysis and processing. The evolutionary approach is used in two situations: i) in the process of feature selection and ii) the selection of best parameter setting for different diagnosis schemes as for example KNN used in this work. Three different objectives were considered related to the quality of the possible diagnosis achieved: 1) classification accuracy, 2) sensitivity, and 3) coverage level. In the case of the multimodal EA, the only objective considered out of the three previously mentioned is the classification accuracy. From the multiobjective perspective, SPEA (Zitzler and Thiele, 1999) is the algorithm applied and two different objective combinations were considered: a) classification accuracy and sensitivity, and b) classification accuracy and coverage level. The proposed methodology was successfully applied on the diagnosis of Paroxysmal Atrial Fibrilation (PAF) on the data set found in (PhysioBank, 2001). The authors claim the their proposal provides to the specialists with a set of different solutions to be used in the diagnostic decision (solutions that include different selected features). Therefore, the specialists have certain freedom to select the parameters for the diagnostic decision process according to the possibilities (*e.g.,* availability of medical instrumentation involved in the features selected).
- (Jatoth et al., 2009) present a PSO-based evolutionary tool for extraction of diminished-noise signal from fetal ECGs which allows an effective extraction and further appropriate analysis. The proposed PSO-based tool is intended to optimize the weight vector involved in an adaptive noise cancelation system. This cancelation system aims at minimizing the mean square error between the real and the estimated fetal ECG signal. The estimated signal is referred to as LMS (Least Mean Square) estimation. Although the authors claim that the PSO-based tool outperformed LMS, the experimental study was unfortunately conducted on only one instance of the problem. This makes necessary an extended study of the proposed algorithm to better assess its potential for noise cancelation in fetal ECG.

1.5 Other Nature Inspired Metaheuristics for ECG

Although EAs are the most extensively used and studied bio-inspired metaheuristics in the current literature, other bio-inspired metaheuristics are also

[2] The authors use here the term 'multimodal' to refer to single-objective problems that have several optima.

being applied, with different degrees of success, in a variety of real-world problems. The processing, analysis, and interpretation of ECG signals is one of the real-world problems in which an important number of research has been conducted through the use of ACO, PSO, and AISs, just to mention a few. Accordingly, this section is aimed at showing some recent results in this regard, by providing a short review of the literature focused on the aforementioned bio-inspired metaheuristics.

- (Bursa and Lhotska, 2008b) propose an Ant Colony inspired clustering algorithm (called Ant Colony Clustering) for arrhythmia diagnosis from the analysis of ECG signals. The authors present a comparative study of their proposal with other clustering algorithms, including: ACO-DTree from the same authors (Bursa and Lhotska, 2007), Radial Basis Function Neural Networks (two versions, which are trained by ACO and PSO algorithms, respectively), Kohonen's Self-Organizing Maps (SOMs), Hierarchical Clustering, and k-means. Two versions of Ant Colony Clustering were implemented: one using Euclidean Distance (or L2) and another one using the Dynamic Time Warping (DTW) metric. The reported results show a fairly good performance of the Ant Colony Clustering approach with respect to some of the other algorithms studied in the experimental study. A similar proposal from the same authors (see Bursa and Lhotska, 2008a) involves the comparison of ACO-DTree, as described in (Begg et al., 2008), but using concepts taken form PSO to improve the solutions and applied at each iteration of the ACO algorithm on the set of solutions previously found. The benefit of the proposed algorithm are demonstrated when compared with a Random Tree Generation method (implemented in the WEKA toolkit). The databases considered include ECG signals instances and also Electroencephalogram (EEG) signals. As a general conclusion, the authors claim that their proposal is suitable for biological data clustering (such as ECG and EEG signals). They also claim that their approach has the advantage of producing readily structures (the decision trees) which have a possible clinical use.
- (Korürek and Doĝan, 2010) investigate the use of PSO-RBFNN, an algorithm that evolves radial basis function neural networks (RBFNNs) for ECG beat classification. The evolutionary process is based on PSO and is aimed to find a high quality structure for the neural network. Besides the number of neurons, a RBFNN architecture includes three parameters: a) center of the neurons (c_i), b) the respective bandwidth (σ_i), and c) the weights between the hidden layer and the output layer. In this work, only the center and the respective bandwidth associated to it are considered in the evolutionary process, where each particle in the population is formulated as in (Korürek and Doĝan, 2010): $net = [(c_1, \sigma_1), \ldots, (c_n, \sigma_n)]$, where n is the number of neurons. The authors present several experiments considering the MIT-BIH arrhythmia database (Goldberger et al., 2000). Preliminary experiments were carried out to determine the most appropriate number of neurons before presenting the main part of the ex-

perimental study. The main conclusion of the experimental study indicates a reduction on the network size without compromising the quality of the results expressed in terms of 'sensitivity' and 'specificity'.

- (Bereta and Burczyński, 2007) designed an Artificial Immune System (AIS) which implements the immune metaphor based on both, negative and clonal selection for evolving subsets of features well suited for classification. According to the authors, this proposed algorithm is considered a hybrid AIS as it simultaneously incorporates both selection mechanisms, *i.e.,* negative selection and clonal selection. The hybrid AIS manages binary and real-valued encoding for the subpopulations of detectors (T-lymphocytes). Both versions of the hybrid AIS were compared by using different types of samples taken from the MIT-HIS database (Goldberger et al., 2000), representing normal and pathological ECG signals. The real-coded hybrid AIS showed the best performance regarding computational complexity, while having a lower level of misclassified signals, and a lower number of detectors.
- (Korürek and Nizam, 2010) investigate an integrated approach based on a combination of wavelets coefficients of the Discrete Wavelet Transform (DWT) and time domain coefficients for feature selection. In addition, Principal Component Analysis (PCA) is applied on the DWT coefficients in order to decrease the number of features. The resulting subset of features is considered by an ACO algorithm for clustering analysis of ECG arrhythmias instances taken from the MIT-BIH Arrhythmia Database (Goldberger et al., 2000). The design of the ACO algorithm is straightforward, since the number n of elements in the data set determines the number of nodes in the construction graph; m ants are distributed on m nodes to proceed with the search (find the cluster). The ants move from one node to another one by applying rules that depend on the amount of pheromone trails and on information of the nearest neighborhood. An exploration rule is applied to promote exploration by particular ants which are forced to visit the farthest nodes. At each move, an amount of pheromone trail is deposited in the respective connection. The clustering is obtained at the final stage of the algorithm (*i.e.,* when the maximum number of iteration is reached) by considering the final accumulated amount of trail in the whole set of edges in the construction graph. The final step (aimed at improving the clustering) combines small clusters into big ones according to the respective distance from the centroid. The main part of the experimental study includes a comparison of the proposed integrated approach with a similar one except that the clustering is obtained by a Neural Network. As a general conclusion, the authors claim that their proposed approach based on the ACO metaphor slightly outperforms the one based on a Neural Network. In addition, both approaches (ACO and NN-based clustering) can be considered suitable options to accurately classify ECG arrhythmias.
- (Poungponsriand and Yu, 2009) investigate the use of a hybrid search algorithm for training a Wavelet Neural Network (WNN) for ECG signal mod-

eling and noise reduction. The hybrid algorithm consists of the so-called Adaptive Diversity Learning Particle Swarm Optimization (ADLPSO) (Chen et al., 2006) for global exploration and a gradient descendent algorithm for fine-tuning purposes. The proposed hybrid algorithm can successfully model the ECG signal and remove high-frequency noise.

Finally, a recent publication from (Karpagachelvi et al., 2010) presents an interesting survey of different approaches for ECG feature extraction. Such literature review includes an important number of schemes based on Artificial Neural Networks, Genetic Algorithms, Support Vector Machines, and other computational intelligence techniques.

1.6 Conclusions

In this chapter, we have presented some introductory concepts of evolutionary computation techniques, focused on the so-called evolutionary algorithms (EAs). The chapter also provides a short introduction to ECG signal processing which highlights aspects that could be addressed by evolutionary techniques and other related approaches. In addition to that, we also presented a literature review on the use of EAs and other bio-inspired metaheuristics for dealing with ECG signals. This aims to provide an up-to-date perspective of the recent and ongoing research in this area.

As discussed by (Begg et al., 2008) we also believe that the oncoming research in this area will focus on the development of tree-breed approaches coming from i) supervised learning, ii) fuzzy logic, and iii) evolutionary computation. However, the third research area should be extended to include a number of other bio-inspired algorithms as well as local search based algorithms. The reason for that is that such approaches have shown a lot of potential to deal with complex real-world problems, exhibiting, in many cases, a similar or even better performance than traditional evolutionary computation techniques such as genetic algorithms.

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