

A Preliminary Cooperative Genetic Fuzzy Proposal for Epilepsy Identification Using Wearable Devices

E.A. de la Cal, J.R. Villar, P.M. Vergara, J. Sedano and A. Herrero

Abstract The epilepsy is one of the neurological disorders that affects people of all socioeconomic groups and ages. An incorrect treatment or a lack in monitoring might produce cognitive damage and depression. In previous work we presented a preliminary method for learning a generalized model to identify epilepsy episodes using 3DACC wearable devices placed on the dominant wrist of the subject. The model was based on a Fuzzy Finite State Machines to detect the epilepsy episodes in 3DACC time series. The learning model applied was a classical Genetic Fuzzy Finite State Machine. The goal of the present work is to adapt the previous learning scheme to a Cooperative Coevolutionary Genetic Fuzzy Finite State Machine to improve the classification results. The obtained results show that a Cooperative proposal outperform moderately the results of the original proposal.

Keywords Cooperative coevolutionary genetic fuzzy finite state machine • Time series classification • Human activity recognition • Epilepsy identification

1 Introduction

The epilepsy is one of the neurological disorders that affects people of all socioeconomic groups and ages [1]. Basically, there are two main epileptic crisis types: the generalized and the focal crisis. In both of them there are subtypes with or without motor activity: those with motor activity are the most common cases. The motor

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activity can vary from the generalized tonic-clonic crisis to the focal mio-clonic crisis. Where the tonic-clonic episodes includes the following symptoms: losing the consciousness, a short tonic stage followed by a prolonged generalized and repeated clonic movements of the whole body, on the other hand the focal mio-clonic epilepsy typology involves repeated bursting movements of one limb, the upper and lower limbs of one body side or a combination of movements of the limbs and face [2].

Classical methods to treat epilepsy include medication, brain stimulation, surgery, dietary therapy or various combinations of the above, directed toward the primary goal of eliminating or suppressing seizures [3]. But roughly the 30% of patients suffer from medically refractory epilepsy. These cases have lead researchers to investigate the mechanisms of seizures in refractory epilepsy using techniques from many scientific disciplines, like molecular biology, genetics, neurophysiology, neuroanatomy, brain imaging and computer modeling [4]. But computer modeling has been used as a general method to tackle not only refractory epilepsy cases. Traditionally in medicine fields Computer Modeling stands for computer aided mathematical techniques used to obtain neurological models based on scalp and intracranial ElectroEncephaloGram (EEG) signals [4, 5]. But there are other computer models based on other kind of measures like electrocardiography, accelerometry and motion sensors, electrodermal activity, and audio/video captures [6, 7]. Considering the current state of the wearable technology, it can be stated that the use of personal devices with tri-axial accelerometer (3DACC) is a cheap and promising medium to monitor some kind of epilepsy [7–10].

In our previous work [11], a method for recognizing focal mio-clonic epilepsy episodes based on analyzing the motor activity by means of a 3DACC placed on the dominant wrist was presented. The main hypothesis in the previous work was that it is possible to learn general models that may allow us to classify the current activity as an epilepsy onset. It worth to remark that when deploying Activity Recognition (HAR) solutions, it is always feasible to gather data for the specific user so the model can be tuned to fit the current user: it is possible to define a training routine that the user has to accomplish with at the very beginning of using the solution. However, this tuning stage is not longer feasible when the problem is focused on the recognition of an illness episode or onset. Therefore, obtaining generalized models is a main requisite that any proposal that aims to recognize an illness episode or onset should perform.

In the previous work a method based on Genetic Fuzzy Finite State Machines (hereafter referred as to as the original proposal) was proposed to the capture of the generic model. But two main problems of the original proposal are the poor classification results and the so heavy computation cost because of the large search space. Thus in this work it's proposed a Cooperative Coevolutionary (hereafter referred as to as the coevolutionary proposal) scheme [12–14] to outperform the results of the original proposal.

The work is structured as follows: in Sect. 2 a revision of the literature is presented, while in Sect. 3 the Cooperative Coevolutionary proposal is explained. Finally, numerical results and the conclusions and future work are presented.

2 State of Art

2.1 Detect Epilepsy Using 3DACC Devices

Epilepsy detection algorithms involve two main phases: first, apposite quantitative values or features, such as EEG signals, movements, or other biomarkers, must be obtained from the data, second a threshold or model-based criteria must be applied to the features to determine the presence or absence of a seizure [7].

Considering Epilepsy has an important impact in the motor system, it can be stated that a big part of the works in the literature use a 3DACC [7, 15, 16]. Different proposals on this topic have been present during the last decade: in [17] a review on the extraction of characteristic epileptic patterns from data is presented, and they conclude that typical movements differ on the kind of epilepsy crisis. An study about 8 types of epilepsy crisis using a 3DACC brazelets to detect rhythmical movements in topic-clonic episodes was presented in [9] but the results are not mature to be deployed.

Likewise, in the work [18], the transformation “amount of movement” is used for calculating alarms in sleeping epileptic episodes in a controlled environment. The heuristic is very simple, when the amount of movement surpass a threshold then an epileptic episode is identified. Due to the use of thresholds, the study was limited to reduced movements activities. Also, in [19] an study on detecting epilepsy episodes in sleeping phase is tackled.

An interesting work is [20] where they use a combination of sympathetically mediated electrodermal activity (EDA) and accelerometry measured using a novel wrist-worn biosensor. In this work data are gathered in half-controlled environment, where the patients can do wide range of activities of daily living such as emotionally and physically activating games.

A good reference work on transformations for the data gathered from the sensors to recognize the epileptic episodes can be found in [10].

2.2 Automatic Techniques to Detect Epilepsy Using 3DACC

The second phase to detected epilepsy, called classification, might be as simple as thresholding a value or might require models derived from modern machine learning algorithms.

Several proposal are based on time domain and frequency domain-based algorithms, [21–23] trying to capture the pattern of frequency during crisis episodes. Other works use simple analytic techniques such as: [24] based on linear threshold function to determine nocturnal seizures, in [25] they use standard deviations of moving epochs and uses moving average filter to detect nocturnal seizures. Also [9, 19] try to obtain motor patters using different mathematical techniques. And finally

in [26], an algorithm based on a time series comparison using Dynamic time warping (DTW) is presented.

All these works have a common restriction, they output specific models for each patient. Besides it can be stated the lack of application of intelligent analysis of data in above problem. Thus, in our previous work [11] we presented a general model to detect epilepsy based on Genetic Fuzzy Systems, but the results can be improved using an new model based on coevolutionary techniques.

2.3 Coevolutionary GFFS to Detect Epilepsy

Our preliminary proposal was based on a Fuzzy Rule Base System (FRBS) using a Pittsburg approximation [27, 28], so the search space in this kind of solution is huge. Thus, as Casillas et al. recommend in [12] a coevolutionary scheme for this kind of problem is suitable. Let's review how a Cooperative Coevolutionary FRBS (Fuzzy Rule Base System) works [12]. First it's important to define what a FRBS is [29]: basically is a set of IF-THEN fuzzy rules, whose antecedents and consequents are composed of fuzzy statements, related with the dual concepts of fuzzy implication and compositional rule of inference. Here the aim is to derive an appropriate knowledge base (KB) about the problem being solved. The KB stores the available knowledge in the form of fuzzy IF-THEN rules. It consists of the rule base (RB), comprised of the collection of rules in their symbolic forms, and the data base (DB), which contains the linguistic term sets and the membership functions defining their meanings. One of the most used automatic methods to perform the derivate task is the Genetic Algorithms (GA) [13]. When only the derivation of the RB is tackled, methods operate in only one phase. And the DB is commonly obtained from the expert information. However, methods that design both RB and DB are preferable since the automation is higher. These methods presents two different approaches: simultaneous derivation (RB and DB are evolved at the same time) and sequential derivation (the learning process is divided in several stages). In most cases, a sequential process by firstly learning the RB and then tuning the DB is considered

When the RB and the DB are simultaneously derived, the high dependency of both components make derivation process considerably more complex because the search space grows and the selection of a suitable technique is key. The direct decomposition of the KB derivation process (thus obtaining two interdependent components, learning of the RB and DB) makes coevolutionary algorithms with a cooperative approach [30] very useful for this purpose.

3 A Cooperative Coevolutionary Genetic Fuzzy Finite Machine to Detect Epilepsy in Time Series

In our previous work [11], it was presented a preliminary method for learning a generalized model to identify epilepsy episodes using 3DACC wearable devices placed on the dominant wrist of the subject. The model used in this proposal was based on Fuzzy Finite State Machines using one-population Genetic Algorithm [31]. The goal of the present work is to adapt the previous learning scheme to a Collaborative Coevolutionary Genetic Fuzzy System [12, 32] to improve the former results.

3.1 The Original Work

First of all, it's important to review the parts of the previous methodology proposed. Our methodology follows the typical stages in the methods to detect epilepsy [7]:

- Feature computation
 - Preprocessing or filtering
 - Feature computation
 - Feature reduction or extraction
- Model learning

Feature computation The data gathered from a 3DACC sensor are the three acceleration components (known as raw data (RD)), and includes both the gravity acceleration (G) and the body acceleration (BA) components. The BA depicts the real acceleration that the part of the body where the sensor is located is being affected. The relevance of each of these components or even of the RD varies according to the current problem and whether the sensor is placed. When the sensor is placed on the limbs, the variable that gets the focus is the BA as long as it resembles the current body movements.

It is worth mentioning that these features have been mainly documented for HAR using 3DACC, with different sensor number and body's placement. The transformations include, among others, (i) the first to fourth moment statistics -mean, standard deviation, skewness and kurtosis-, (ii) the *Mean Absolute Deviation* ($MAD_t(s)$) computed for the RD, (iii) the *Root Mean Square* ($RMS_t(s)$) for the RD, (iv) the *sum of the absolute values* of the BA, (v) the *vibration of the sensor* ($VoS_t(s)$), (vi) the *tilt of the body* for the RD, (vii) the *Signal Magnitude Area* ($SMA_t(s)$) for the BA, (viii) the *Amount of Movement* ($AoM_t(s)$) for the BA, (ix) the *Delta coefficients* for estimating the first order time derivate of each of the G signal components, (x) the *Shifted Delta Coefficients* for estimating the first order time derivate of each of the BA signal components, (xi) the *Average Energy* using the FFT, (xii) the *correlation between axes*, (xiii) the *Intensity of the movement* ($IoM_t(s)$) as the mean first derivative of the raw acceleration data, (xiv) the *Time Between Peaks* measured for any possible

variable as the number of peaks that occurs within the current window, and (**xv**) the *histogram* of the values of the considered acceleration for the current window. An interested readers can find studies of these transformations in [10, 33].

A problem that arises with all these transformations is that, for each concrete problem -where a number of sensors and their locations are specifically chosen-, only the most suitable transformations should be selected for the modeling stage. Thus, the feature domain reduction step is the very first stage that should be analyzed in Time Series (TS) classification.

Furthermore, we are interested on the movements of the limb, which is measured using the BA so, we only consider the modulus of BA and its related transformations.

The tilt of the body has no point as long as it only measures the relevance of two components, thus this feature is more interesting when the sensor is placed centered with the body. Similarly, the correlation between axes was disregarded as well. The VoS only considers the raw data acceleration and the G, both of them have been neglected for this problem. Furthermore, the sum of absolute values and the SMA represent the same transformation with different scaling factor.

After applying different selection criteria like disregarding by computational restrictions, histogram comparison and visual analysis, following three transformations based on BA were selected:

- Signal Magnitude Area (SMA).
- Amount of Movement (AoM).
- Time between peaks (TbP).

The model The problem to detect the state that better resembles the current sliding windows of an acceleration samples Time Series, can be tackled with a Fuzzy Finite State Machine (FFSM). Following the reason proposed in [31], it can be assumed the problem of identifying the class can be represented by means of a $FFSM = \{Q, X, f, Y, g\}$, where $Q = \{q_1, \dots, q_p\}$ is the set of p fuzzy states, X is the set of input variables of the system, $f : Q \times X \rightarrow Q$ is the set of transition mapping functions, Y is the set of outputs, and $g : Q \times X \rightarrow Y$ is the output function. Let's define the elements of our FFSM:

- The fuzzy states to represent Q are $\{EPILEPSY, NO_EPILEPSY\}$ and are defined as $S(t)$, where $S[t] = (s_1[t], \dots, s_p[t]) = (s_1, \dots, s_p)$ is the membership value of current state at time t to each of the available states q_i , with $s_k \in [0.0, 1.0]$ and $\sum_{k=1}^p s_k[t] = 1, \forall t$.
- X is the set of features that best describes the evolution of the class for the different time series. In our problem X is $\{SMA, AoM \text{ and } TbP\}$.
- The transitions functions $f_r, \forall r \in \{1, \dots, R\}$ are represented by means of Fuzzy rules (FR) with the form depicted in Eq. 1, where \otimes is the t-norm for aggregation of the antecedents of the rule, \oplus is the t-conorm for aggregation of the different fuzzy sets involved in the rule for an input variable.

$$\mathbf{IF} (S[t] \text{ is } S_r^a) \otimes C_r^1 \otimes \dots \otimes C_r^N \mathbf{THEN} S_r \quad (1)$$

In this Eq. 1, S_r^a and S_r are the state from which the rule r fires and the destination state, respectively, where C_r^n is the combination of fuzzy sets for variable x_n that are involved in rule r as an antecedent. We have decided to use 3 fuzzy trapezoidal partitions for each fuzzy set.

Here we follow the original proposal by Alvarez et al. [31] using the *min* function as t-norm, and the Lukasiewicz t-conorm ($\vee_{Luk}(a, b) = \min(a + b, 1)$). Besides, we adopt the inference mechanism, the authors proposed computing the new state with their proposal of formula to calculate the strength of one rule.

- As for the original study, [31] $Y[t] = g(S[t], X[t]) = S[t]$

When a problem is focused using this FFMSM representation several design decisions must be taken, like the specific input feature domain, the partitioning of the variables, the parameterization of the FR, etc. Once all these issues have been defined, it is possible to propose a method for learning either the partitioning, or the FR Base or both simultaneously. According to [31], the GFFSM has been found valid for learning TS classification models in the context of HAR. However, the approach should be adapted to the specific problem as explained in [33]. In our previous work a classical GFFSM scheme was used.

3.2 The New Proposal

In this new proposal, a Cooperative Coevolutionary Genetic Fuzzy Finite State Machine is applied following the proposal of Casillas et al. [12] but adapted to a FFMSM. Let's define F_{ij} as the FRBS composed by the individuals i and j of the species 1 (RBs) and 2 (DBs) respectively. The fitness function is the Mean Absolute Error (MAE), which is calculated using Eq. 2. In this equation, N is the number of datasets in the corresponding fold, T is the number of examples in each data set, and $si[t]$ and $si^*[t]$ are the degree of activation obtained from a designed FRBS F_{ij} and the expected degree of activation, respectively, for state qi at time step $t = e$. Let's $s_d[t] = F(t)$

$$MAE(F) = \frac{1}{N} \frac{1}{T} \sum_{d=1}^N \sum_{e=0}^T |s_d[t] - s_d^*[t]| \tag{2}$$

Each individual of species RB y DB are evaluated with corresponding fitness functions $f1$ and $f2$ (see Eq. 3) :

$$\begin{aligned} f1(i) &= \min_{j \in C2} MAE(F_{ij}) \\ f2(j) &= \min_{i \in C1} MAE(F_{ij}) \end{aligned} \tag{3}$$

where i and j are the individuals of species RB and DB respectively. And C_1 and C_2 are sets individuals selected at random from the previous population (generation = $t - 1$). The summary of fitnesses $f1$ and $f2$ evaluation is showed in Fig. 1.

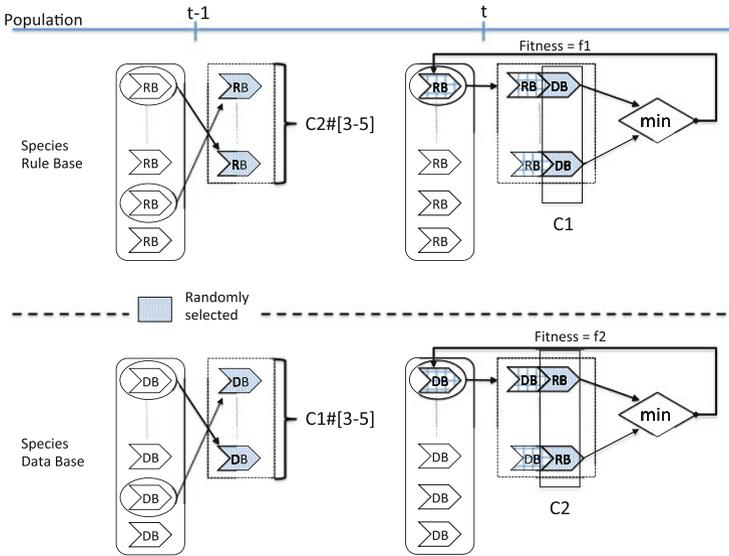


Fig. 1 Cooperative coevolutionary Fitness calculation scheme

The genotype of both species As three input variables are used, the SMA, the AoM and TbP, everyone considered linguistic variables with 3 labels each. Ruspini trapezoid membership functions are used, so we need to learn 4 parameters for each input variable. A GA evolves the partitions and the rules in a Pittsburg style: up to 36 binary genes coding the rules (the RB species) and 12 real-coded genes for the membership function parameters (the DB species).

Genetic operators: A generational scheme is followed in both species. Tournament selection procedure of 4 individuals together with an elitist mechanism (that ensures to select the best individual of the previous generation) are used. A two-point crossover for the RB species and BLX- α ($\alpha = 0.5$) crossover for the DB species applied twice for obtaining two new pairs of chromosomes and a classical bitwise mutation for the rule base (RB species) and uniform mutation for the real-coded part (DB species). It has used a probability of crossover and mutation of 1.0 and 0.1 respectively.

4 Experimentations and Results

4.1 Experimentation

A set of experiments have been run in order to obtain the data for training and testing. To do so, a bracelet including a 3DACC has been delivered to every subject being involved in these experiments; each bracelet was placed on the subject's dominant

wrist. The bracelets have wireless capabilities, transferring the data to a computer at a sample rate of 16 Hz, the range of the sensors fixed to $2 \times g$.

Nevertheless in current work a simple protocol with two similar activities (EPILEPSY and SAWING) simulated by a group of subjects has been defined in order to gather realistic data.

Up to 6 individuals with ages between 22 and 47 years, have successfully completed this experimentation, all of them healthy subjects. Every subject has carried out at least 10 runs per kind of activity.

To run the training and test computation process a 5×2 Cross Validation procedure has been performed with all datasets taken from all the subjects.

The main goal in this paper is to compare our Coevolutionary proposal against the original proposal from the previous work. Thus, the parameters population size (ps) and number of generations (g) in both learning schemes have been adjusted in order to perform the same number of fitness evaluations in the whole training process. So, let's define the number of fitness evaluations (NFE) for the whole generations in both learning schemes (see Eq. 4).

$$\begin{aligned}
 g_{\text{original}} &= \text{Number of generations (50)} \\
 ps_{\text{original}} &= \text{Population Size (50)} \\
 np_{\text{original}} &= \text{Number of populations(1)} \\
 NFE_{\text{original}} &= g_{\text{original}} * ps_{\text{original}} * np_{\text{original}} \\
 NFE_{\text{original}} &= 2500
 \end{aligned} \tag{4}$$

Considering the NFE_{coevol} must be equal to NFE_{original} (2500), the g and the ps have to be adjusted. If ps is fixed to 20 then we have to calculate g_{coevol} (see Eq. 5).

$$\begin{aligned}
 g_{\text{coevol}} &= \text{Number of generations} \\
 ps_{\text{coevol}} &= \text{Population Size(20)} \\
 np_{\text{coevol}} &= \text{Number of populations(2)} \\
 cn &= \text{Number of Cooperators(3,5)} \\
 NFE_{\text{coevol}} &= g_{\text{coevol}} * ps_{\text{coevol}} * np_{\text{coevol}} * nc \\
 NFE_{\text{coevol}} &= g_{\text{coevol}} * 20 * 2 * [3 - 5] \\
 g_{\text{coevol}} * 20 * 2 * [3, 5] &= 2500 \\
 g_{\text{coevol}} &= [2500/(40 * 5), 2500/(40 * 3)] \\
 g_{\text{coevol}} &= [12.5, 20.83]
 \end{aligned} \tag{5}$$

Consequently, we have three types of experiments attending to the number of generations: the original proposal with 50 generations and the coevolutionary proposal with 3 cooperators (20 generations) and 5 cooperators (12 generations).

On the other hand, since the search space in this problem is huge it has been decided to inject in the initial population an expert individual in order to guide the evolution of the genetic algorithm. This expert individual is a manually selected good solution

but not the best. Besides, two percentage of elite individuals, 10 % and 50 %, have used in order to promote the expert individuals. The original proposal was run only with 50 % of elite individuals, while the new proposal was run with 10 % and 50 %.

Thus, we will compare different combination of genetic parameters for the coevolutionary proposal against the original proposal using a fixed set of parameters (see Table 1).

4.2 Numerical Results

Considering the 5 sets of schemes/parameters in Table 1, a 5×2 fold cross validation procedure has been run for each one using the 60 % of the available datasets. The remaining datasets have been kept to reduce the computation time.

Figure 2 depicts box plots for the error (MAE) of individuals with the best fitness in the testing partitions. The best fitness individual for a fold is the combination of the best sub-individual in each species (the Rule Base population and the Data Base population) in this fold.

Table 1 Experiments and configuration summary, where CV is Cross Validation, PS is Populations Size, CN is Cooperators Number, Gen is the number of generations, Cross./Mut. P. are the crossover/mutation probability and Elite P. is the elite probability

| Scheme | PS | CN | Gen. | Cross./Mut. P. | Elite P. |
|----------------|----|----|------|----------------|----------|
| Original | 50 | - | 50 | 1.0/0.1 | 50 % |
| Coevolutionary | 20 | 3 | 20 | 1.0/0.1 | 10 % |
| Coevolutionary | 20 | 3 | 20 | 1.0/0.1 | 50 % |
| Coevolutionary | 20 | 5 | 12 | 1.0/0.1 | 10 % |
| Coevolutionary | 20 | 5 | 12 | 1.0/0.1 | 50 % |

We think that box plots don't allow to conclude statistically that coevolutionary proposals (Coevol. Cooper. box plots) are much better than the original proposal (Evolutionary labeled boxplot). Maybe the configuration Coevol. Cooper with 5 cooperators and 50 % of elite individuals shows better behavior having the best median of the whole configurations. Anyway the statistical results are not determining. It seems that a bigger number of cooperators improves slightly the results. Also we think that a new coevolutionary fitness function considering a mixture of random and elite selected cooperators could improve the results. In current coevolutionary proposal all the cooperators are selected at random.

Considering the best coevolutionary proposal is the one with 5 cooperators and 10 % of elite probability, let's compare the evolution of this proposal against the original proposal in training partitions. Figure 3 shows the evolution of the fitness for the best individual in the original proposal (square marker) combined with the evolution of the fitness for two best sub-individuals in coevolutionary species (circle and triangle

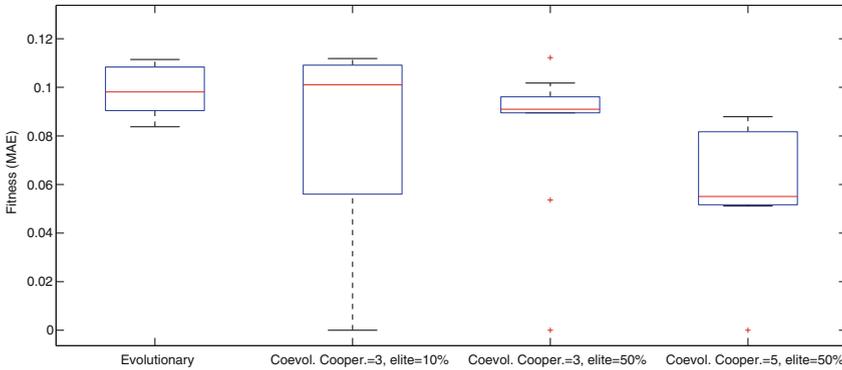


Fig. 2 Testing boxplots for 5×2 CV for original proposal (Evolutionary) vs coevolutionary proposal (Coevol. Cooper.)

markers). It can be stated that coevolutionary best solutions in both species outperform evolutionary solution during the 12 generations. The evaluation of fitness for the coevolutionary sub-individuals was performed taken the best combination with the cooperators in each generation (see Fig. 1).

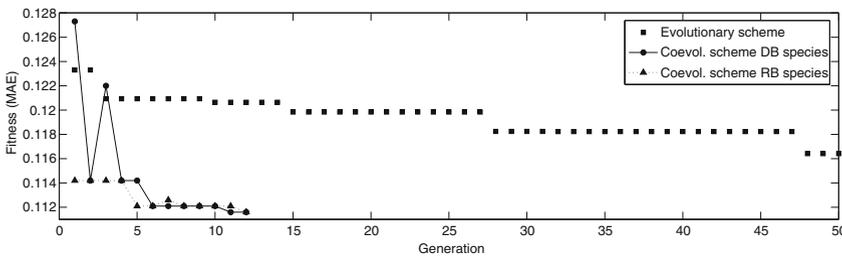


Fig. 3 Training best fitness evolution, original proposal (Evolutionary scheme, 50 generations) vs Coevol. Cooper. proposal (Coevolutionary scheme, 12 generations)

Finally, let's analyze the evolution of the coevolutionary proposal being evaluated with testing datasets. Figure 4 shows the fitness values for the coevolutionary proposal with the four sets of parameters. The fitness function has been calculated for the combination of the best sub-individuals of the both species in each generation using the testing datasets. It's not clear which configuration is better, may be the ones with 5 cooperators (solid line curves) with present a more regular behavior. Also, it can be observed that testing results are better than training results, and this is due to the distribution of EPILEPSY datasets. The datasets are not balanced.

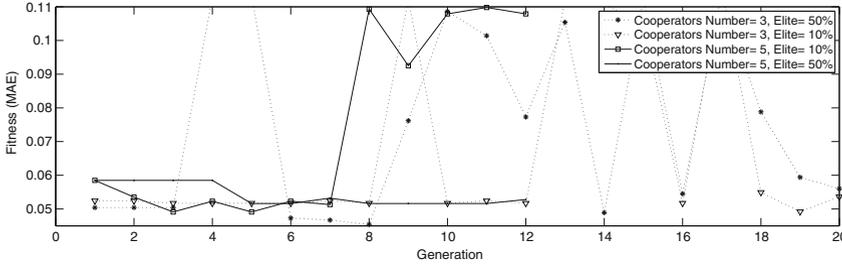


Fig. 4 Testing best fitness evolution, Coevolutionary proposal with 3 (20 generations) and 5(12 generations) cooperators

4.3 Time Performance

As it's said in previous Sect. 2.3, coevolutionary schemes are suitable for problems with a huge space of search. So, if we take a look to Table 2 we can conclude that the extra time (see formula 6) spent by coevolutionary proposals (Coevol. Cooperators/Elite) respect to the original proposal (with speedups between 0.90 % and 0.93 %) is affordable. Also it can be observed that the reduction of generations allow to each coevolutionary scheme to invest more time in the fitness evaluation (Fit. Eval). Note that coevolutionary proposal has to evaluate the fitness for two populations considering that the fitness for coevolutionary individuals is more complex due to the use of the cooperators.

$$SpeedUp = \frac{T_{old}}{T_{new}} \tag{6}$$

Table 2 Time data obtained with the execution of the different proposals for 1 fold (Time measured in seconds). Fit. Eval. stands for the time invested in fitness evaluation in one generation, Total Fit. Eval = Generations*Fit. Eval, Remaining Ops. is the time invested in the genetic operations (initialize the population, crossover operations, etc.), but the Fitness function

| Scheme | Generations | Fit.Eval | Total Fit.Eval. | Remaining Ops. | Total Time | SpeedUp |
|--------------|-------------|----------|-----------------|----------------|------------|---------|
| Evolutionary | 50 | 285,00 | 14249,81 | 332,41 | 14582,22 | - |
| Coevol 3/10 | 20 | 766,24 | 15324,79 | 753,30 | 16078,09 | 0,91 |
| Coevol 3/50 | 20 | 748,31 | 14966,13 | 749,32 | 15715,45 | 0,93 |
| Coevol 5/10 | 12 | 1228,66 | 14743,94 | 1217,54 | 15961,48 | 0,91 |
| Coevol 5/50 | 12 | 1249,46 | 14993,57 | 1248,23 | 16241,79 | 0,90 |

5 Conclusions and Future Work

In a previous work we got a generalized model based on a GFFSM to identify epilepsy episodes using 3DACC wearable but the results could be improved. Thus, in current paper a Cooperative Coevolutionary proposal based on Genetic Fuzzy Systems is presented. It can be stated that the statistical results obtained for the whole configurations of new proposal don't outperform clearly the original proposal ones, since all the bloxplots are not determining (see Fig. 2). Only the best median of MAE error from the different coevolutionary configurations (5 cooperators and 50 % elite got a median of 5.8 %) outperforms the original proposal MAE of 9.8 %. The remaining coevolutionary boxplots overlap the original proposal boxplot.

Besides, as we can see in Sect. 4.3, the time spent by the coevolutionary proposals don't surpass the original proposal in more than a 10 %, what is a modest overtime that can be assumed.

As current paper only analyze datasets from only two typologies of activities EPILEPSY and SAWING, more activities like WALKING and RUNNING must be included in future works in order to obtain a more general model. Also we think that a new coevolutionary fitness function considering a mixture of random and elite selected cooperators could improve the results; current coevolutionary proposal all the cooperators are selected at random. Besides a more extended study of the genetic parameters is needed.

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