

# A Multi-Objective Cooperative Coevolutionary Approach to Mamdani Fuzzy System Generation

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## Abstract

A novel multi-objective cooperative coevolutionary approach aimed at generating a set of Mamdani-type fuzzy rule-based systems (FRBSs) with optimal trade-offs between accuracy and interpretability is proposed. Interpretability is measured both in terms of complexity of the rule base (RB) and of integrity of the data base (DB). In the framework of the cooperative coevolutionary approach, multi-objective optimization of RB and DB is performed in two distinct populations. Individuals of the two populations cooperate among them through representatives properly extracted at each generation. Results of the application of our approach to the well-known Mackey-Glass chaotic time series dataset are shown and discussed.

**Keywords:** multi-objective evolutionary algorithms, cooperative coevolution, fuzzy rule-based systems.

## 1 Introduction

In the last years, the issue of automatic generation of Mamdani-type FRBSs from data has been widely studied in the literature and several different approaches have been proposed. A Mamdani-type FRBS consists of a completely linguistic RB, a DB containing the fuzzy sets associated with the linguistic terms used in the RB and a fuzzy logic-based inference engine. A large number of papers have focused on learning techniques that guarantee the generation of FRBSs which are both accurate and interpretable [3]. In the literature, interpretability of an FRBS has been defined in different ways. A

common approach is to distinguish between interpretability of fuzzy partitions, also known as *integrity* [6], and interpretability of rules, also known as *complexity* [5]. Complexity is usually defined in terms of simple measures, such as number of rules in the RB and number of linguistic terms in the antecedent of rules. On the other hand, integrity depends on some properties of the fuzzy partition, such as coverage, distinguishability and normality, which may be difficult to measure [6].

Since accuracy and interpretability are in general conflicting goals, multi-objective evolutionary algorithms (MOEAs) have gained attention in the framework of FRBS generation [10]. Typically, MOEAs search for Pareto-optimum FRBSs by concurrently optimizing accuracy (e.g., increasing classification rate in classification or decreasing error in regression) and some interpretability indices.

Most of the existing MOEAs evaluate interpretability in terms of either complexity of the RB or integrity of the DB; few approaches perform RB and DB identification by taking both the aspects into account [8][9][13]. On the other hand, the RB and DB identification processes can be considered as complementary and interdependent subtasks of the same main problem, i.e., FRBS generation, and, therefore, they should be approached separately, but concurrently.

In this paper, we exploit a multi-objective cooperative coevolutionary algorithm (MOCCA) [12] to achieve a trade-off among three objectives: accuracy, complexity and integrity. Our algorithm concurrently evolves two separate populations (*species*), composed by individuals

which, respectively, encode rules and partitions. The dependencies between the species are managed by selecting proper *representatives* that concur to compute the fitness of the other species. We exploit interpretability measures and chromosome coding defined in our previous works [1][2][5]. Further, we introduce a novel approach to the selection of representatives. To test the effectiveness of our approach, we use the well-known Mackey-Glass (MG) chaotic time series.

The paper is organized as follows. In Section 2, we briefly review previous work on related topics. Section 3 details our proposed algorithm. In Section 4, we show the experimental results. Finally, in Section 5 we draw conclusions.

## 2 Previous Work

Cooperative coevolutionary techniques are based on the observation that splitting complex tasks into subtasks may help concentrate the exploration of the search space around useful niches and prevent loss of diversity in the population [12]. Since the cooperative coevolutionary approach assigns an isolated species to each subtask, splitting must take care of existing dependencies occurring among the subtasks. These dependencies are usually critical to fitness evaluation. *Complete solutions* to a problem are generated by coupling individuals of a species with individuals of the other species. Hence, during the evolution, species cooperate with each other by means of representatives that are used to assess the fitness of complete solutions.

The first application of a single-objective cooperative coevolutionary algorithm for FRBS generation from data has been discussed in [11]. Here, the FRBS generation task is split into two subtasks: learning the DB and learning the RB. The two subtasks are performed by two separate species: individuals in the RB species identify the linguistic rules of the FRBS and individuals in the DB species define the meanings associated with the linguistic terms used in the RB. Thus, solutions to the FRBS generation problem are obtained by composing an individual belonging to the DB species with a representative from the RB species, and vice versa. The repre-

sentatives are selected probabilistically according to their fitness. The approach proposed in [11] takes only accuracy into account and is based on simple elitist single-objective genetic algorithms that evolve the two species concurrently.

In [8], cooperative coevolution for Takagi-Sugeno-type FRBS generation is tackled by using a hierarchical approach. Here, four species at different hierarchical levels encode fuzzy partitions, rules, RBs and FRBSs, respectively. Since individuals of the FRBS species are composed by an RB and a DB identified by individuals at the lower levels, collaboration among species is performed without the need for representatives. Therefore, the fitness of an individual of a given species depends upon the fitness of individuals at higher levels. Similar to [11], the approach proposed in [8] considers accuracy as the only objective of the search process. Some interpretability and complexity properties, however, are enforced by means of constrained optimization.

Multi-objective cooperative coevolutionary approaches to FRBS generation have been recently proposed in [15][16]. In [15], a MOCCA was used to identify systems of classifiers. In [16], a similar algorithm was applied to the generation of Takagi-Sugeno-type FRBSs. In both works, a species is used to evolve the RB and another species is used to evolve parameters of Gaussian-shaped fuzzy sets. Further, in [15], rule selection is performed by using a third species. As in [11], complete solutions are built by selecting representatives from the species. Although both these works take the accuracy-interpretability issue into account, integrity is not an objective of the evolution, but rather a constraint which is enforced by using traditional similarity measures (for instance, during evolution, fuzzy sets similar to a large extent are merged). A similarity-based technique is also exploited for RB simplification. The three objectives of the evolutionary optimization are accuracy and two complexity measures based on number of rules and number of fuzzy sets, which are strongly dependent on the simplification step.

### 3 Proposed approach

Similar to [11][16], our approach exploits two species, namely  $P_1$  and  $P_2$ , which contain individuals encoding, respectively, rules and partitions. Thus,  $P_1$  and  $P_2$  evolve to determine RBs and DBs, respectively. NSGA-II, one of the most popular MOEAs [7], is used to evolve the two species separately, taking accuracy and interpretability into account for each species. Accuracy is measured in terms of mean square error (MSE) between the real and predicted values in both  $P_1$  and  $P_2$ . The interpretability index is species-dependent: in  $P_1$ , it is defined in terms of complexity of the rules as in [5], i.e., by counting the number of linguistic terms in the antecedents of all the rules; in  $P_2$ , it is defined in terms of integrity and measured by averaging the index introduced in [1] over all the partitions. The choice of different objectives for the two species allows effectively exploring the Pareto-optimum fronts on the overall three objectives: accuracy, complexity and integrity.

Individuals in  $P_1$  and  $P_2$  represent partial solutions. A complete FRBS is generated by coupling any of the individuals in  $P_1$  with any of the individuals in  $P_2$ . Obviously, assessing the fitness values of each possible FRBS at each generation is computationally very expensive. Thus, to speed up computation, we limit the fitness evaluation to a subset of possible FRBSs. This subset is obtained by first extracting two individuals from each species and then combining these individuals with all the individuals of the other species. One of the two individuals is chosen randomly, while the other corresponds to the representative (selected as explained below) of the previous generation. Hence, we perform a number of evaluations equal to two times the sum of  $P_1$  and  $P_2$  sizes rather than to the product of the two sizes. Finally, for each population, we select as representative the individual which generates the FRBS with the lowest MSE. The motivation for this single-objective choice of the representative is the same as in [9]: we aim to explore the three-dimensional objective-space so as to focus on a region where FRBSs achieve high accuracy. Further, the use of NSGA-II ranking in each separate species guarantees to obtain FRBSs with few and simple rules and with transparent partitions.

### 3.1 The MOCCA

Let species  $P_1(t) = \{p_{1,1}(t), \dots, p_{1,N_1}(t)\}$  and  $P_2(t) = \{p_{2,1}(t), \dots, p_{2,N_2}(t)\}$  be composed by  $N_1$  and  $N_2$  individuals, respectively. We denote the representatives of  $P_1(t)$  and  $P_2(t)$  as  $\hat{p}_1(t)$  and  $\hat{p}_2(t)$ , respectively.

For each generation  $t$ ,  $t = 1..T$ , the steps performed by the MOCCA are detailed in Figure 1. Steps from 1 to 4 are used to select the representatives of the current species, while step 5 implements a customized version of the NSGA-II algorithm for cooperative coevolution. After the species have evolved for  $T$  generations, we generate a three-dimensional Pareto front approximation by extracting non-dominated FRBSs from the set of  $N_1 \cdot N_2$  complete solutions obtained by combining each individual of  $P_1(T)$  with each individual of  $P_2(T)$ .

In the MOCCA, a complete solution represents a Mamdani-type FRBS with  $F$  input variables  $X_1, \dots, X_F$ , one output variable  $X_{F+1}$  and at most  $M_{\max}$  rules in the RB. Let  $U_f$ ,  $f = 1, \dots, F+1$ , and  $O_f = \{A_{f,1}, \dots, A_{f,T_f}\}$  be the universe of variable  $X_f$  and a fuzzy partition of  $T_f$  fuzzy sets on variable  $X_f$ , respectively. We assume to have a data set  $S = \{(\hat{\mathbf{x}}_d, \hat{y}_d)\}$  of  $D$  real-world examples, where  $\hat{\mathbf{x}}_d$  is a vector of  $F$  input values, and  $\hat{y}_d$  is the corresponding output. The MSE used in MOCCA is given by

$$MSE = \frac{1}{2 \cdot D} \sum_{d=1}^D (F(\hat{\mathbf{x}}_d) - \hat{y}_d)^2, \quad (1)$$

where  $F(\hat{\mathbf{x}}_d)$  is the output computed by the Mamdani-type FRBS when  $\hat{\mathbf{x}}_d$  is the input.

In the following, we describe the chromosome coding and the genetic operators used to evolve species  $P_1$  and  $P_2$ . A detailed analysis of all the techniques introduced in the following two Sections can be found in our previous works [1][2][5].

### 3.2 The RB species

The RB of an FRBS is represented by the integer chromosome shown in Figure 2, where  $j_{m,f} \in [1, T_f]$  identifies the index of the fuzzy set (among the  $T_f$  fuzzy sets of partition  $O_f$ ),

which has been selected for the input variable  $X_f$  in rule  $R_m$ . In the experiments, we set  $T_f$  to 5 for all partitions  $O_f$ .

- Set  $t = 1$ . Generate species  $P_1(t)$  and  $P_2(t)$  as described in Sections 3.2 and 3.3. Set  $\hat{p}_1(0)$  and  $\hat{p}_2(0)$  to two individuals randomly chosen in  $P_1(t)$  and  $P_2(t)$ , respectively.
- 1) Randomly extract two individuals,  $\hat{p}_1'(t)$  and  $\hat{p}_2'(t)$ , from  $P_1(t)$  and  $P_2(t)$ , respectively.
  - 2) Generate a set  $C_1(t)$  of  $2 \cdot N_1$  complete solutions obtained by combining  $\hat{p}_1'(t)$  and representative  $\hat{p}_2(t-1)$  of  $P_2(t-1)$  with each individual in  $P_1(t)$ . It follows that
 
$$C_1(t) = \{(\rho_{1,1}(t), \hat{p}_2(t-1)), \dots, (\rho_{1,N_1}(t), \hat{p}_2(t-1)),$$

$$(\rho_{1,1}(t), \hat{p}_2'(t)), \dots, (\rho_{1,N_1}(t), \hat{p}_2'(t))\}.$$
  - 3) Generate a set  $C_2(t)$  of  $2 \cdot N_2$  complete solutions obtained by combining  $\hat{p}_1'(t)$  and representative  $\hat{p}_1(t-1)$  of  $P_1(t-1)$  with each individual in  $P_2(t)$ . It follows that
 
$$C_2(t) = \{(\hat{p}_1(t-1), \rho_{2,1}(t)), \dots, (\hat{p}_1(t-1), \rho_{2,N_2}(t)),$$

$$(\hat{p}_1'(t), \rho_{2,1}(t)), \dots, (\hat{p}_1'(t), \rho_{2,N_2}(t))\}.$$
  - 4) Compute the MSEs of all solutions in  $C_1(t)$  and  $C_2(t)$ . Choose as representatives  $\hat{p}_1(t)$  and  $\hat{p}_2(t)$  of species  $P_1(t)$  and  $P_2(t)$  the components  $\rho_{1,a}(t)$  and  $\rho_{2,b}(t)$  of the solutions  $a$  and  $b$  which achieve the lowest MSEs among all solutions in  $C_1(t)$  and  $C_2(t)$ , respectively.
  - 5) Apply NSGA-II to  $P_1(t)$  and  $P_2(t)$  as follows:
    - a) For each individual in  $P_1(t)$  and in  $P_2(t)$ , evaluate complexity and integrity, respectively.
    - b) Combine each individual of  $P_1(t)$  with  $\hat{p}_2(t)$  and each individual of  $P_2(t)$  with  $\hat{p}_1(t)$  and evaluate the MSEs of all the combinations.
    - c) Apply to  $P_1(t)$  and  $P_2(t)$  the species-dependent genetic operators defined in Sections 3.2 and 3.3 so as to generate the offspring species  $Q_1(t)$  and  $Q_2(t)$ , respectively.
    - d) For each individual in  $Q_1(t)$  and in  $Q_2(t)$ , evaluate complexity and integrity, respectively.
    - e) Combine each individual of  $Q_1(t)$  with  $\hat{p}_2(t)$  and each individual of  $Q_2(t)$  with  $\hat{p}_1(t)$  and evaluate the MSEs of all the combinations.
    - f) Use the NSGA-II ranking on MSE and complexity objectives, and on MSE and integrity objectives to assess the ranking of  $P_1(t) \cup Q_1(t)$  and  $P_2(t) \cup Q_2(t)$ , respectively.
    - g) Extract the sets  $B_1(t)$  and  $B_2(t)$  of the best  $N_1 - 1$  and  $N_2 - 1$  ranked individuals in  $P_1(t) \cup Q_1(t)$  and  $P_2(t) \cup Q_2(t)$ , respectively, by adopting the elitist strategy implemented in NSGA-II.
    - h) Set  $P_1(t+1) = B_1(t) \cup \hat{p}_1(t)$  and  $P_2(t+1) = B_2(t) \cup \hat{p}_2(t)$ .
  - 6) Set  $t = t + 1$ . If  $t < T$ , go to step 1; else terminate.

Figure 1: The steps of the MOCCA

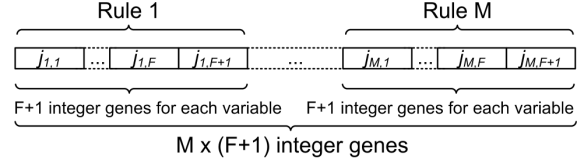


Figure 2: Chromosome for species  $P_1$

As regards the RB species evolution, we exploit the classical one-point crossover and three ad-hoc mutation operators [5]. The first mutation operator adds  $\gamma$  rules to RB, where  $\gamma$  is randomly chosen in  $\{1, \dots, \gamma_{\max}\}$ . The upper bound  $\gamma_{\max}$  (5 in the experiments) is fixed by the user. The second mutation operator removes  $\lambda$  rules from the RB, where  $\lambda$  is randomly chosen in  $\{1, \dots, \lambda_{\max}\}$ . In the experiments, we used  $\lambda_{\max} = \min(\phi_{\max}, M - M_{\min})$ , where  $\phi_{\max}$  (5 in the experiments) is fixed by the user, and  $M$  and  $M_{\min}$  are, respectively, the number of rules of the individual and the minimum number of rules allowed for all individuals. The third mutation operator randomly changes  $\delta$  elements of the chromosome. The number  $\delta$  is randomly generated in  $\{1, \dots, \delta_{\max}\}$ . The upper bound  $\delta_{\max}$  (5 in the experiments) is fixed by the user.

The probability of applying the crossover operator is 0.05. When the application of the crossover operator is selected, the mutation is applied with probability 0.01, otherwise it is always applied. When the application of the mutation is selected, the three operators are applied with a probability of 0.85, 0.05 and 0.1 respectively.

The initial population of the RB species was generated by executing the RB identification algorithm based on NSGA-II introduced in [5]. In the experiments, NSGA-II was executed for 2000 generations on fuzzy partitions composed of five uniformly distributed trapezoidal fuzzy sets. Further, the same crossover and mutation operators, and the same above-mentioned crossover and mutation probabilities were used.

The complexity of an RB is computed as the sum of the conditions which compose the antecedents of the rules. Since FRBSs with a high number of rules are generally of scarce interest,

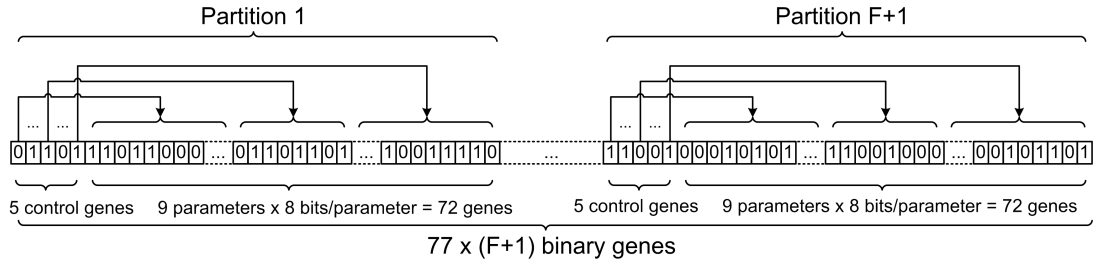


Figure 3: Chromosome for species  $P_2$

in order to constrain the search space, we set the maximum number  $M_{\max}$  of rules to 25.

### 3.3 The DB species

To represent the DB species, we exploit the same operators introduced in [2]. For each linguistic variable  $X_f$ ,  $f = 1, \dots, F + 1$ , we start from a partition  $\bar{O}_f$  composed by  $T_f$  trapezoidal fuzzy sets uniformly distributed in the  $[0, 1]$  universe. We obtain the tuned partition  $O_f$  by applying the following operators: a non-linear scaling function and four fuzzy modifiers, namely the *core-width modifier*, the *core-position modifier*, the *support-width modifier* and the *generalized positively modifier*.

Each modifier acts on the core, on the support or on the boundary elements of the fuzzy sets, thus allowing generating a wide range of configurations of  $O_f$  with few tuning parameters. To actually tune  $\bar{O}_f$ , we need to determine which operators should be applied and the values of their parameters. We remark that the operators are applied with the same intensity on the overall partition, i.e., a single value of each parameter is needed for all the fuzzy sets in a partition. Thus, each individual in  $P_2$  is represented by a chromosome composed by  $F + 1$  strings of 77 bits, where each string encodes five control genes and nine 8-bit parameters. The first five bits, one for each operator, control whether the corresponding operator is applied or not on each fuzzy partition  $\bar{O}_f$ . The other 72 bits are organized in sub-strings of 8 bits: each sub-string determines the value of a different parameter, via Gray decoding and quantization. Figure 3 shows the structure of the chromosome of an individual of the DB species.

Parents to be mated are chosen by standard binary tournament selection, as proposed in the

original version of NSGA-II [7]. Then, the offspring population is generated by applying uniform crossover and uniform mutation operators to parents, with a mutation rate of 0.05.

The initial population is composed as follows. The first individual encodes a uniform partition defined in  $U_f$ . One-fifth of the population is generated by applying the uniform mutation operator to the first individual with a mutation rate of 0.1. The rest of the population is randomly generated.

The integrity of a DB is evaluated by means of the index  $\bar{\Phi}_y$  defined in [1]. The index takes coverage, distinguishability and ordering of fuzzy sets into account and, therefore, guarantees an evaluation of the actual integrity which approximates the human perception more faithfully than simple similarity-based approaches. We recall that  $\bar{\Phi}_y$  ranges in  $[0, 1]$ : in our experiments,  $\bar{\Phi}_y = 0$  corresponds to the maximum degree of integrity, and  $\bar{\Phi}_y = 1$  corresponds to the minimum degree of integrity.

## 4 Experimental results

We tested our approach on one of the most popular regression datasets, namely the MG chaotic time series. The MG differential delay equation

$$\frac{dx(t)}{dt} = \frac{ax(t-\tau)}{1+x^{10}(1-\tau)} - bx(t) \quad (2)$$

has been used by a number of researchers for comparing the learning and generalization capabilities of different models [4]. The MG dataset was generated by extracting 500 points from the series generated by solving equation (2) with the Runge-Kutta method. As in previous works available in the literature, we predicted  $x(t+6)$

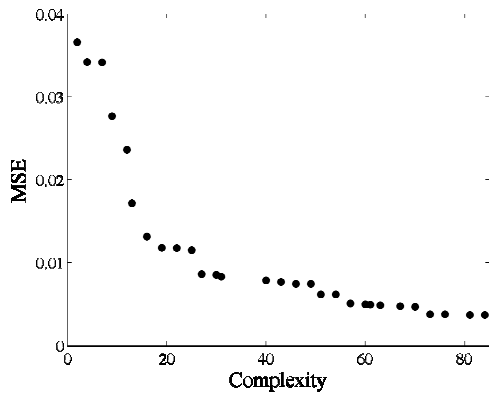


Figure 4: Final RB species (training set)

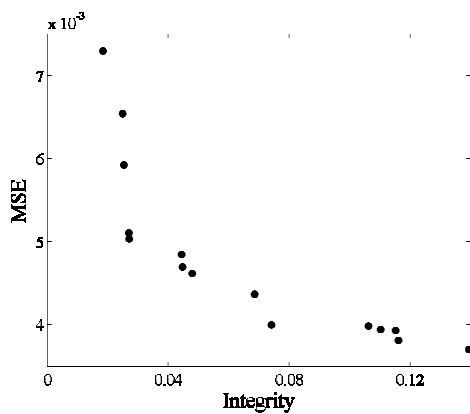


Figure 5: Final DB species (training set)

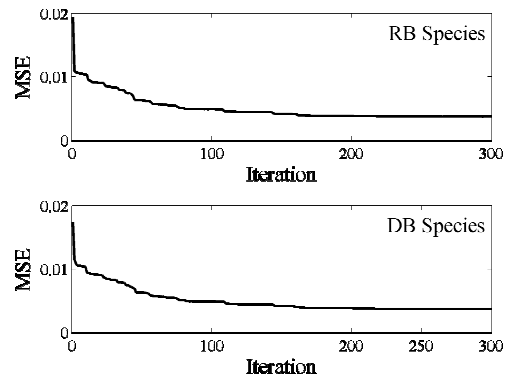


Figure 6: Representatives errors

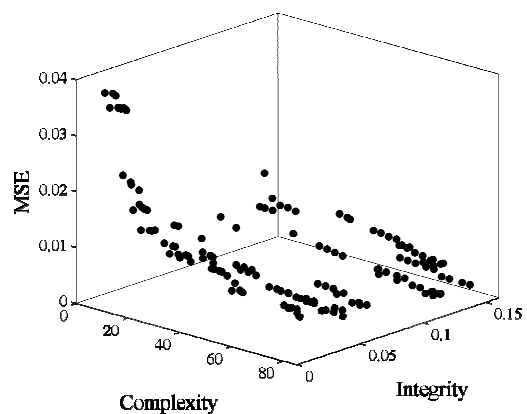


Figure 7: Three-dimensional Pareto front approximation on training set

using the input variables  $x(t)$ ,  $x(t-6)$ ,  $x(t-12)$  and  $x(t-18)$ . The dataset was randomly divided into a training set and a test set of the same size.

We executed the MOCCA algorithm for 300 iterations with species sizes  $N_1 = N_2 = 30$ . Figures 4 and 5 show the non-dominated partial solutions in the final RB and DB species, respectively (MSEs are computed by using the representatives of the last generation). In Figure 6, we plot the MSEs achieved by the two representatives of RB and DB against the generations. We note that the trend of MSE is monotonically decreasing. This behavior is typically observed for the best individual in single-objective genetic algorithms. On the other hand, selection of representatives is guided only by the MSE.

In Figure 7, we show the final three-dimensional Pareto front approximation obtained by extracting non-dominated FRBSs from the set of

$N_1 \cdot N_2$  complete solutions. As expected, systems with high complexity and low integrity, i.e., high values of  $\bar{\Phi}_Y$ , are associated with low MSEs, and, vice-versa, systems with low complexity and high integrity are associated with high MSEs.

Figures 8 and 9 show the projections of the Pareto front approximation on the complexity-MSE plane and on the integrity-MSE plane, respectively. For the sake of readability, we report only the solutions which are non-dominated in the plane.

To show the significance of a well-managed DB optimization to MSE reduction, we performed 300 further iterations of NSGA-II starting from  $P_1(1)$  and continuing the RB identification process with uniform partitions, that is, without DB optimization. Figure 10 compares the Pareto front approximation provided by NSGA-II with the solutions obtained by our approach on the test set. We note that the Pareto front approximation provided by our approach is wider and

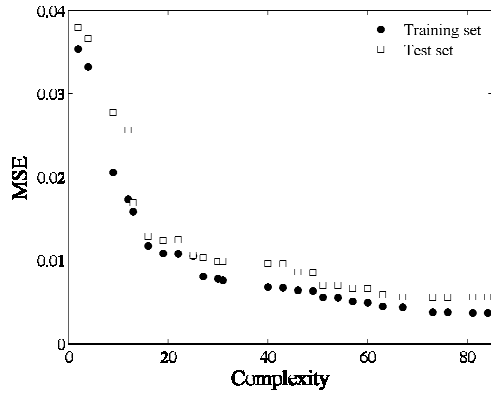


Figure 8: Non dominated solutions on the complexity-MSE plane

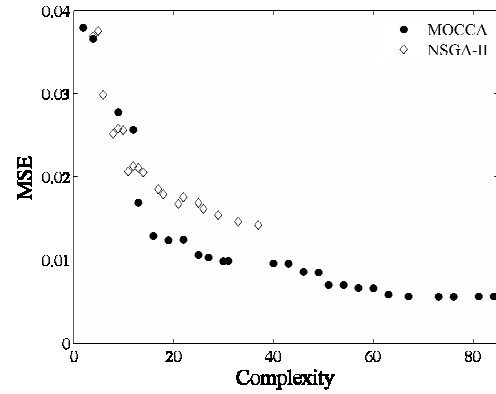


Figure 10: NSGA-II vs. MOCCA on the complexity-MSE plane (test set)

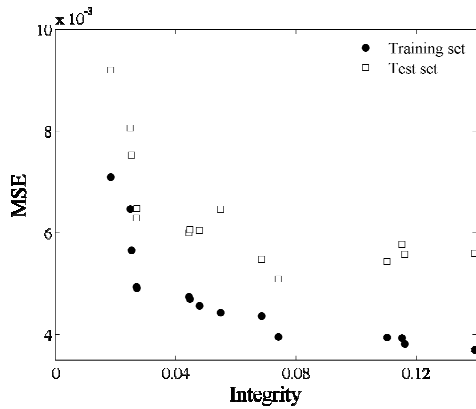


Figure 9: Non-dominated solutions on the integrity-MSE plane

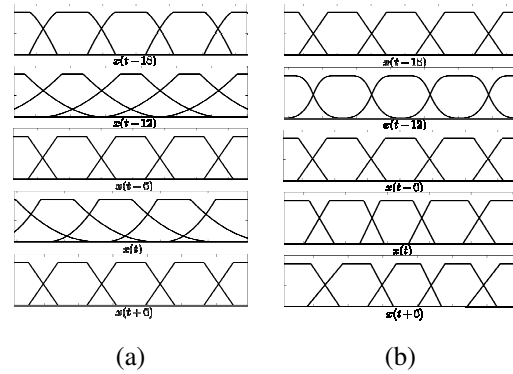


Figure 11: Fuzzy partitions of the FRBSs with the lowest MSE (a) and the lowest  $\bar{\Phi}_Y$  (b)

more accurate than the one generated by NSGA-II. Further, we have also compared our results with the learn-by-example technique proposed in [14], using the same uniform partitions that we exploited in NSGA-II. The FRBS provided by this technique achieves MSEs of 0.00746 and 0.00838 on the training and on the test sets, respectively, and comprises 44 rules for a total complexity of 176. We observe that this FRBS is Pareto-dominated by all solutions shown in Figure 8. Finally, in Figure 11, we show the fuzzy partitions generated by our MOCCA for two FRBSs: the FRBS, which achieved the lowest MSE (Figure 11a), and the FRBS, which achieved the highest integrity on the final species (Figure 11b). The effects of the modifiers are evident in Figure 11a, where non-adjacent fuzzy sets in partitions  $x(t-12)$  and  $x(t)$  overlap and, therefore, the overall value of  $\bar{\Phi}_Y$  is high. However, thanks to the effects of the cooperative algorithm and to the use of our index,

all the partitions show good integrity even when the value of  $\bar{\Phi}_Y$  increases.

## 5 Conclusion

We have introduced a multi-objective cooperative coevolutionary approach aimed at generating a set of Mamdani-type fuzzy rule-based systems (FRBSs) with optimal trade-offs between accuracy and interpretability. Interpretability is evaluated in terms of both complexity of the RB and integrity of the DB. Thanks to coevolution, RB and DB evolve separately within different species. This has allowed us to adopt RB generation and DB tuning techniques we proposed in our previous works. Unlike standard approaches to cooperative coevolution, which adopt single-objective optimization of species, we use a multi-objective optimization. Thus, for each of the two species, we determine a Pareto-optimum set of possible solutions, that

is, a set of RBs and a set of DBs. At the end of the execution of the algorithm, by combining all the possible RBs with all the possible DBs we obtain a set of FRBSs with different trade-offs between accuracy, complexity and integrity. Experiments carried out on the Mackey-Glass dataset have shown that our approach is very promising. Nevertheless, we think that some aspects of the algorithm, such as the strategy for selecting the representatives of the species and the dependencies between individuals of the two species, deserve further investigation.

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