

# Parallel Distributed Two-level Evolutionary Multiobjective Methodology for Granularity Learning and Membership Functions Tuning in Linguistic Fuzzy Systems

Miguel A. De Vega, Juan M. Bardallo, Francisco A. Márquez, Antonio Peregrín  
*juanmanuel.bardallo@sic.uhu.es; miguelangelde.vega@sic.uhu.es;*  
*alfredo.marquez@dti.uhu.es; peregrin@dti.uhu.es)*

## Abstract

*This paper deals with the learning of the membership functions for Mamdani Fuzzy Systems – the number of labels of the variables and the tuning of them – in order to obtain a set of Linguistic Fuzzy Systems with different trade-offs between accuracy and complexity, through the use of a two-level evolutionary multi-objective algorithm. The presented methodology employs a high level main evolutionary multi-objective heuristic searching the number of labels, and some distributed low level ones, also evolutionary, tuning the membership functions of the candidate variable partitions.*

## 1. Introduction

Recent research on the design of linguistic fuzzy models (FMs) [1] with genetic algorithms has focused on methods aimed at generating fuzzy rule-based systems (FRBS) with an appropriate trade-off between two usually contradictory features, accuracy and interpretability in the sense of system complexity [2], [3], so as to obtain reliable and understandable models.

One of the recent techniques used to improve the aforesaid trade-off between accuracy and interpretability of linguistic fuzzy systems has been Multi-Objective Evolutionary Algorithms (MOEAs) [4] - [12]. Some of these achieve the set of non-dominated solutions with different trade-off between both features by selecting the set of rules [9], [12] best representing the example data, i.e., providing a set of solutions with different balance between the

complexity of the fuzzy rule base (RB) and system accuracy.

In addition, there are many studies devoted to the design of different elements of fuzzy systems, such as tuning the meanings of the variables used in the rules [13], [14] (tuning of the membership functions), learning the number of labels for each variable (granularity) [15], [16] deriving the linguistic RB [17] - [21], setting up the inference system [22] -[23], and establishing the defuzzification method [24] amongst others. Likewise, there are studies focusing on combinations of some of these techniques [25], [26] to achieve a joint solution where different elements cooperate. These techniques can present major difficulties when we deal with complex models with large data sets (the scaling problem).

In line with these ideas, in this paper we present a methodology for the design of linguistic fuzzy systems aimed at a more readily achievable accuracy by focusing on the learning of one of the most influential elements in this process, the variables membership functions, specifically combining the learning of the number of membership functions with the tuning of them. This is accomplished whilst taking into account the main objective in systems modeling, which is to develop reliable and understandable models by using a multi-objective evolutionary methodology that generates a set of FRBSs with different optimal trade-off between accuracy and complexity.

The evolutionary model proposed deals with large search spaces, in particular when complex models or large data sets are being dealt with. This difficulty is tackled by making a simple, high level, main evolutionary multi-objective search of the number of labels and some low level evolutionary distributed searches which tune the membership functions. Not only does the distributed tuning take advantage of available computer clusters in terms of computing power like [27] (where a two-level methodology for

---

This work was supported by Projects TIN2008-06681-C06-06 and P07-TIC-03179.

J. M. Bardallo, M. A. De Vega, F. A. Márquez and A. Peregrín are with the Department of Information Technologies, University of Huelva, 21819 Palos de la Fra. Huelva, Spain.

granularity and RB learning was proposed in order to have a simple much more cost-effective approach than using individual super-computers of similar performance), but convergence is improved thanks to communications among distributed searches like genetic algorithm island model architecture.

In order to explain how this is achieved, Section II describes the proposed model, Section III shows the experimental study developed, and finally Section IV presents some concluding remarks.

## 2. Proposed Model

This section describes the two-level parallel-distributed methodology proposed in this work. First, we provide an overview of the method, and then give a detailed description of the high level node and the low level nodes in two subsections.

Membership functions learning has been one of the most studied topics for improving the accuracy of system modelling with FRBSs, alongside its effects on interpretability [13]. By other hand, the influence of fuzzy partitions granularity has been studied [16].

The proposed model makes use of both these ideas, the learning of the granularity and the tuning of the terms of the variables. These processes are not independent because the tuning is coupled to the granularity previously selected.

We propose to use a high level single search based on a multi-objective algorithm to find a set of optimal granularity combinations of the variables using accuracy and complexity as objectives. Coupled with the abovementioned high level search, in particular with the evaluation of its candidate solutions, the proposed model uses some low level parallel distributed evolutionary search processes to find the best tuning for the membership functions associated with each granularity combination candidate. Figure 1 shows this schema.

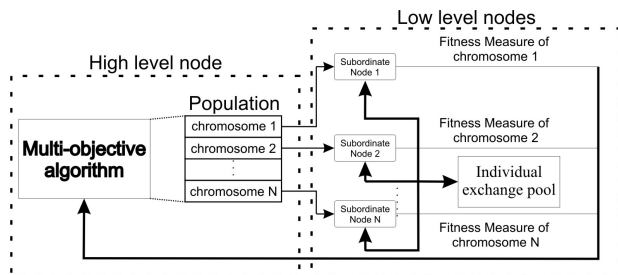


Figure 1. Global scheme

The two-level methodology proposed have an interesting feature taken from the distributed genetic algorithm field that improves its convergence beyond the use of parallel nodes which is the communications

between them though a exchange pool. It will be describe in depth in Section 2.2.

### 2.1. High level multiobjective search: granularity of the variables

As mentioned above, a single node performs a multi-objective search in order to find the granularity of the variables. It uses a multi-objective schema implemented using one of the best-known and frequently-used MOEAs for general multi-objective optimization in the literature: the NSGA-II [28]. It is a parameterless approach with many interesting principles: a binary tournament selection based on a fast non-dominated sorting, an elitist strategy and a crowding distance method to estimate the diversity of a solution. A fuller description may be found in [28].

The two objectives considered by the MOEA are the mean square error (as a measure of accuracy) and the number of rules (as a measure of interpretability in the sense of complexity) of the FRBS obtained.

The coding scheme used in the evolutionary high level search is the one shown in Figure 2. Every chromosome of the multi-objective algorithm encodes the number of linguistic labels for each variable. More specifically, each chromosome has as many genes as the problem has variables. Hence, genes are integer values indicating the number of linguistic terms in their respective variables, likewise for antecedents and consequents. The minimum and maximum number of linguistic terms that each variable may have is predetermined, and they are uniformly distributed in the universe of the variable.

Genes are randomly initiated to a value between the predetermined minimum and maximum values.

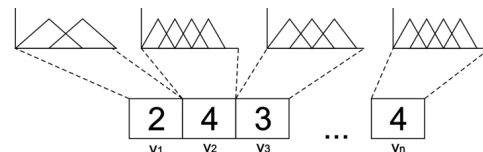


Figure 2. MOEA chromosome coding

### 2.2. Low level distributed search: tuning of membership functions

The evaluation of the population of the MOEA in the high level node is carried out in some subordinate nodes for every chromosome in its population.

The subordinate nodes perform a low level distributed search of the tuning of the membership functions of the variables. It is achieved in three stages: first, each node receives the number of linguistic terms for each variable, then it generates the associated RB

and finally it performs the evolutionary tuning of membership functions in collaboration with other nodes, returning the RB and its accuracy computed with the training dataset to the high level node.

The tuning of the membership functions is performed using LA-tuning [29], which only manages the displacement and the amplitude of a label. This is a good approach because it works with fewer parameters than classic tuning [14] obtaining good results.

In [29], the authors used a real coded CHC [30] to perform the LA-tuning, which presents a good trade-off between exploration and exploitation, making it a good choice in problems with complex search spaces. The genetic model of CHC makes use of a “Population-based Selection” approach.  $N$  parents and their corresponding offspring are combined to select the best  $N$  individuals to form part of the next population.

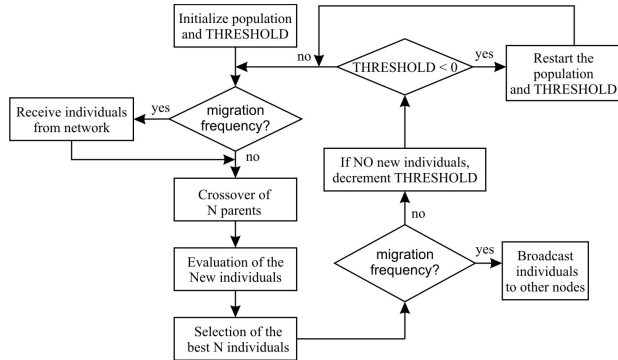
We have modified the CHC model, adding an individuals exchange mechanism whereby each node can share its individuals with other ones. This architecture is known as Multi-deme parallel GA or “island model” GA [31] in the GA area which each node corresponds to a deme.

In our proposal, the goal of such mechanisms is to improve the convergence based on the movement of good quality information about terms tuned among nodes with the same variable granularity. In this way, each node periodically is informed of the best results information (granularity and tuning) stored in an exchange pool and it can use this data that match the granularity of any of its own variables to create a new individual for its own population. Particularly, it generates a hybrid chromosome from the foreign individual and the best individual of its population at that moment.

Each hybrid chromosome competes with a randomly selected individual from the population in a binary tournament selection procedure to determine which remains in the population.

Figure 3 shows a global scheme of a node in the distributed evolutionary model based on the original CHC [30].

Two parameters have to be considered in this scheme: the migration rate and the migration frequency, which respectively represent the percentage of individuals that a node can send/receive to/from the network and how many evaluations are performed in each migration.



**Figure 3. Scheme of a node in the distributed evolutionary model based on CHC**

### 3. Experimental Study

In order to analyze the practical behavior of the proposed methodology, we built several FMs in two real-world problems [32], [33], with different complexities (different number of variables and amount of data).

Table 1 summarizes the different models used in the experimental study, where LA- $t_N$  stands for LA-tuning [29], the method considered as reference, and  $N$  being the granularity selected in all the variables. The  $D_N$  methods are the proposed two level multi-objective distributed models, where  $N$  is the maximum number of labels used by the algorithm. We also decided to test the performance of the two level multi-objective methodology proposed sequentially, which are denoted by  $S_N$ , to study the advantages of the distributed model against the sequential model ( $S$  models do not use chromosome exchange mechanism).

**Table 1. Methods considered for comparison**

Ref.	Method	Description
[29]	LA- $t_N$	LA-tuning with $N$ labels for each variable
-	$S_N$	Two-level Sequential evolutionary multi-objective methodology with up to $N$ labels for each variable
-	$D_N$	Two-level Distributed evolutionary multi-objective methodology with up to $N$ labels for each variable

#### 3.1. Applications and Comparison Method

To evaluate the goodness of the proposed approach, two real-world problems with different complexities were considered:

- An electrical distribution (EL) problem [32] that consists in estimating the maintenance costs of medium voltage lines in a town (1059 cases; 4 input continuous variables; one output variable).
- The Ankara Weather (AW) dataset [33] that concerns the task of trying to predict the mean

temperature in Ankara, Turkey (1609 cases; 9 input continuous variables; one output variable).

We considered a 5-fold cross-validation model, i.e., 5 random partitions of the data, each with 20% (4 with 211 examples, and one with 212 examples, for the EL problem, and 4 with 322 examples, and one with 321 examples for the AW problem) and the combination of 4 of them (80%) as training, with the remaining one as test. We achieved a total of 30 trials for each model, by running the learning methods for each one of the data partitions 6 times with different seeds for the random number generator. We show the average values of the mean square error (MSE), as a standard performance measure (with expression (1)),

$$MSE(S)_B = \left( \frac{1}{2} \sum_{k=1}^P (y_k - S(x_k))^2 \right) / P, \quad (1)$$

where  $S$  denotes the FM selected, computed considering the most accurate solution from each Pareto obtained with the multi-objective algorithm. This measure uses a set of system evaluation data formed by  $P$  pairs of numerical data  $Z_k = (x_k, y_k)$ ,  $k=1, \dots, P$ , with  $x_k$  being the values of the input variables, and with  $y_k$  being the corresponding values of the associated output variables.

### 3.2. Genetic Algorithms Setup

The MOEA in the high level node used different configurations depending on the maximum number of linguistic terms set up. When a maximum value of 5 labels was selected in the EL problem, the population was fixed to 25 chromosomes and the number of evaluations was 750. On the other hand, when the maximum value of 7 labels for each variable was selected in the EL problem - just as when the maximum value of 5 labels for each variable was selected in the AW problem - the population was fixed at 25 chromosomes and the number of evaluations was 1250. The crossover operator used was HUX- $\alpha$  with  $\alpha = 0.5$ . The mutation operator used was the classic mutation operator with a probability of 0.2. The initial population was randomly initialized within the minimum to maximum range of values for the partitions.

The models based on CHC algorithm used in the low level nodes (both for sequential and distributed models) were set up with a population of 30 chromosomes in all cases. The number of evaluations was fixed to 3000 in the case of the EL problem when the maximum value of 5 labels for each variable was selected, and to 5000 evaluations in both the EL problem when a maximum of 7 labels was selected and in the AW problem. The crossover operator used was BLX- $\alpha$  with  $\alpha = 0.5$ . The threshold to restart the

population was fixed to  $L/4$ ,  $L$  being the length of the chromosome multiplied by the number of bits which codified each gene.

The migration rate and the migration frequency were fixed to 0.1, and the threshold of the binary tournament was set to 0.75 in all cases.

To compare the results obtained we also used non-parametric tests, according to the recommendations made in Demšar [34] which suggests a set of simple, safe and robust non-parametric tests for statistical comparisons of algorithms, one of which is the Wilcoxon signed-ranks test [35] we use in this work. It is analogous to the paired t-test in non-parametrical statistical procedures.

The RB is generated using the well known Wang & Mendel [18] algorithm.

### 3.3. Results and Analysis

The results obtained are shown in Table 2 and 3 for the EL problem and in Table 4 for the AW problem, where MSE are the average MSE, for training and test, and Wil-test are the results of applying the Wilcoxon signed-ranks test [35] (with 95% confidence), with the following interpretation: \* represents the best average result (control algorithm); + means that the best result has better (the same for =) performance than that of the corresponding row; and finally # $R$  is the average number of rules.

It is important to note that Tables 2, 3 and 4 only show the FRBS with the best accuracy of the Pareto front for each multi-objective model. Viewing these Tables we can point out that the distributed models (D) show the best accuracy in all cases with a similar or lower number of rules. They improve the sequential ones (S), which use the same evaluations, so this mechanism improves the convergence of the evolutionary models. Table 7 shows the mean speed-up ratio obtained computed as the time spent by the sequential divided by the execution time of the distributed approach. The higher the value of this ratio, the better. The distributed approach takes advantage of its architecture that uses 25 low level nodes.

Table 5 and 6 show an example of the Pareto front obtained by the models  $S_7$  and  $D_7$  respectively for the EL problem. Their columns show the MSE for training and test, the number of rules, and the chromosomes achieved, that is, the number of linguistic terms found. The first 4 genes on the left of the chromosome belong to the antecedents and the last one on the right belongs to the consequent. Some solutions with different trade-offs have been found among the most and the least accurate. Figure 4 compares the Pareto fronts for  $S_7$  and  $D_7$ .

**Table 2. Results obtained for the EL application with a maximum of 5 labels**

Method	Training		Test		#R
	MSE	Wil-test	MSE	Wil-test	
LA-t <sub>5</sub>	20950,70	+	24851,75	+	65
S <sub>5</sub>	13151,07	+	16017,05	+	32,2
D <sub>5</sub>	<b>11289,87</b>	*	<b>13354,10</b>	*	<b>29,2</b>

**Table 3. Results obtained for the EL application with a maximum of 7 labels**

Method	Training		Test		#R
	MSE	Wil-test	MSE	Wil-test	
LA-t <sub>7</sub>	15537,62	+	18461,97	+	103
S <sub>7</sub>	9306,01	+	11271,95	+	<b>42,8</b>
D <sub>7</sub>	<b>8594,57</b>	*	<b>10234,54</b>	*	<b>42,8</b>

**Table 4. Results obtained for the AW application with a maximum of 5 labels**

Method	Training		Test		#R
	MSE	Wil-test	MSE	Wil-test	
LA-t <sub>5</sub>	1,40	+	4,50	+	851,2
S <sub>5</sub>	1,15	+	1,51	=	151,4
D <sub>5</sub>	<b>1,12</b>	*	<b>1,42</b>	*	<b>146,1</b>

**Table 5. A Pareto front example obtained by the model S<sub>7</sub> for the EL problem**

S <sub>7</sub>				
MSE <sub>TRA</sub>	MSE <sub>TST</sub>	#R	Chromosome	
9553.92	12159.94	45	2-2-6-7-7	
9606.33	12442.81	37	3-2-5-4-7	
10102.26	13573.44	31	2-3-5-4-7	
12604.47	13681.52	26	2-3-4-4-6	
12908.61	18126.73	25	2-2-4-4-7	
14490.37	15342.72	17	2-2-6-2-7	
19378.72	21058.12	11	2-2-3-2-6	
30418.25	44803.99	9	2-2-2-2-6	

**Table 6. A Pareto front example obtained by the model D<sub>7</sub> for the EL problem**

D <sub>7</sub>				
MSE <sub>TRA</sub>	MSE <sub>TST</sub>	#R	Chromosome	
7711.17	8833.75	45	2-2-6-7-7	
9443.36	12332.92	31	2-3-5-4-7	
10729.20	14029.50	25	2-2-4-4-7	
13678.55	14107.97	17	2-2-6-2-7	
17268.90	22846.77	14	2-2-4-2-6	
19398.57	21578.84	11	2-2-3-2-6	
23510.23	33407.38	9	2-2-2-2-6	

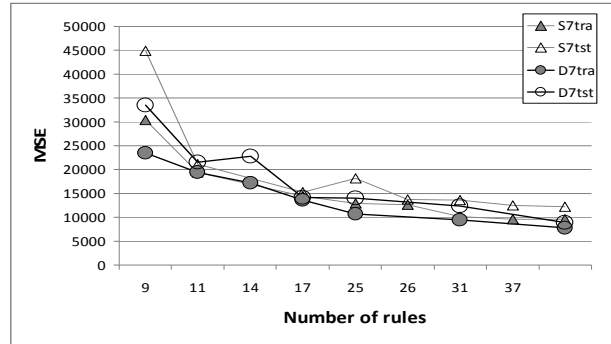
**Table 7. Speed-up values using 25 nodes**

Dataset	Speed-up
EL with a maximum of 5 labels	12.52
EL with a maximum of 7 labels	12.75
AW with a maximum of 5 labels	13.79

## 4. Conclusions

The use of multi-objective algorithms in the design of FRBSs gives a set of solutions with different levels of conciliation between accuracy and complexity. In this work we have proposed an evolutionary two-level parallel distributed multi-objective learning methodology where the number of membership

functions is learnt, as well as their tuning. The distributed methodology proposed deals with more complex models with larger data sets, taking advantage of the available computing resources, and improving their convergence at the same time as was showed in the experimental study developed.



**Figure 4. Example of the Pareto front with Sequential and Distributed models for EL**

## 5. References

- [1] F. Herrera. "Genetic Fuzzy Systems: Taxonomy, current research trends and prospects", *Evolutionary Intelligence*, vol. 1, 2008, pp. 27–46.
- [2] J. Casillas, O. Cordón, F. Herrera and L. Magdalena. *Interpretability issues in fuzzy modeling*. Springer-Verlag, 2003.
- [3] J. Casillas, O. Cordón, F. Herrera and L. Magdalena. *Accuracy improvements in linguistic fuzzy modeling*. Springer-Verlag, 2003.
- [4] H. Ishibuchi, "Multiobjective Genetic Fuzzy Systems: review and future research directions", in *Proc of Fuzz-IEEE'07 Int Conf on Fuzzy Syst*, London, 2007, pp. 1–6.
- [5] M. Cococcioni, P. Ducange, B. Lazzarini, and F. Marcelloni, "A pareto-based multi-objective evolutionary approach to the identification of Mamdani fuzzy systems", *Soft Comput*, vol.11, 2007, pp. 1013–1031.
- [6] H. Ishibuchi and T. Yamamoto. "Fuzzy rule selection by multi-objective genetic local search algorithms and rule evaluation measures in data mining". *Fuzzy Sets and Syst*, Vol. 141, 2004, pp. 59–88.
- [7] K. Narukawata, Y. Nojima, and H. Ishibuchi. "Modification of evolutionary Multiobjective optimization algorithms for Multiobjective design of fuzzy rule-based classification systems", in *Proc of Fuzz-IEEE'05 Int Conf on Fuzzy Syst*, Reno, 2005, pp. 809–814.
- [8] P. Pulkkinen, H. Koivisto. "Fuzzy Classifier Identification Using Decision Tree and Multi-Objective Evolutionary Algorithms", *Int J Approx Reason*, vol. 48, 2008, pp 526–543.
- [9] M.J. Gacto, R. Alcalá, and F. Herrera. "Adaptation and application of Multi-Objective Evolutionary Algorithms for Rule Reduction and Parameter Tuning of Fuzzy

- Rule-Based Systems”. *Soft Computing*, vol. 13, no. 5, 2009, pp. 419–436.
- [10] M. Antonelli, P. Duccange, F. Marcelloni and B. Lazzarini. “Learning Concurrently partition granularities and rule bases of Mamdani Fuzzy Systems in A Multi-Objective Evolutionary Framework”, *Int J Approx Reason*, vol. 50 no. 7, 2009, pp 419–436.
- [11] R. Alcalá, P. Ducange, F. Herrera, B. Lazzarini, F. Marcelloni. “A Multi-Objective Evolutionary Approach to Concurrently Learn Rule and Data Bases of Linguistic Fuzzy Rule-Based Systems”. *IEEE Trans Fuzzy Syst*, DOI: 10.1109 / TFUZZ. 2009. 2023113.
- [12] A.A. Márquez, F.A. Márquez, and A. Peregrín. “Cooperation between the Inference System and the Rule Base by using Multiobjective Genetic Algorithms”, in *Proc of HAIS’08 Int Conf of Hybrid Artificial Intelligence Syst*, Burgos, 2008, pp. 739–746.
- [13] J. Casillas, O. Cordón, M.J. Del Jesus, and F. Herrera, “Genetic tuning of fuzzy rule deep structures preserving interpretability for linguistic modelling”, *IEEE Trans Fuzzy Syst*, vol. 13, no. 1, 2005, pp. 13–29.
- [14] C. Karr, “Genetic algorithms for fuzzy controllers”, *AI Expert* vol. 6, no. 2, 1991, pp. 26–33.
- [15] W. H. Au, K. C. C. Chan, and A. K. C. Wong, “A fuzzy approach to partitioning continuous attributes for classification”, *IEEE Trans Knowl Data Eng*, vol. 18, no. 5, 2006, pp. 715–719.
- [16] O. Cordón, F. Herrera, and P. Villar, “Analysis and guidelines to obtain a good fuzzy partition granularity for fuzzy rule-based systems using simulated annealing”, *Int J Approx Reason*, vol. 25, no. 3, 2000, pp. 187–215.
- [17] J. Casillas, O. Cordón, and F. Herrera. “COR: A methodology to improve ad hoc data-driven linguistic rule learning methods by inducing cooperation among rules”, *IEEE Trans Syst, Man, Cybern. Part B: Cybern*, vol. 32, no. 4, 2002, pp. 526–537.
- [18] L.X. Wang, and J.M. Mendel. “Generating fuzzy rules by learning from examples”, *IEEE Trans Syst, Man, Cybernetics*, vol. 22, no. 6, 1992, pp. 1414–1427.
- [19] M.J. Del Jesus, P. González, F. Herrera, and M. Mesonero, “Evolutionary fuzzy rule induction process for subgroup discovery: a case study in marketing”, *IEEE Trans Fuzzy Syst*, vol. 15, no. 4, 2007, pp.578–592.
- [20] M. Kaya, “Multi-objective genetic algorithm based approaches for mining optimized fuzzy association rules”, *Soft Comput*, vol. 10, no. 7, 2006, pp. 578–586.
- [21] P. Thrift, “Fuzzy logic synthesis with genetic algorithms”, in *Proc of ICGA’91 Int Conf on Genetic Algorithms*, 1991, pp 509–513.
- [22] J. Alcalá-Fdez, F. Herrera, F. Márquez, and A. Peregrín, “Increasing fuzzy rules cooperation based on evolutionary adaptive inference systems”, *Int J Intell Syst*, vol. 22 no. 9, 2007, pp. 1035–1064.
- [23] K. A. Crockett, Z. Bandar, and D. Mclean, “On the optimization of T-norm parameters within fuzzy decision trees”, in *Proc of Fuzz-IEEE’07 Int Conf on Fuzzy Syst*, London, 2007, pp. 103–108.
- [24] D. Kim, Y. Choi, and S. Lee, “An accurate COG defuzzifier design using Lamarckian co-adaptation of learning and evolution”, *Fuzzy Sets and Syst*, vol. 130, no. 2, 2002, pp. 207–225.
- [25] A. Homaifar, and E. McCormick, “Simultaneous design of membership functions and rule sets for fuzzy controllers using genetic algorithms”. *IEEE Trans Fuzzy Syst*, vol. 3, no. 2, 1995, pp. 129–139.
- [26] F. A. Márquez, A. Peregrín, and F. Herrera, “Cooperative evolutionary learning of linguistic fuzzy rules and parametric aggregation connectors for Mamdani fuzzy systems”, *IEEE Trans Fuzzy Syst*, vol. 15, no. 6, 2007, pp. 1168–1178.
- [27] J.M. Bardallo, M.A. De Vega, F.A. Márquez, A.Peregrín. “Parallel Evolutionary Multi-Objective Methodology for Granularity and Rule Base Learning in Linguistic Fuzzy Systems” in *Proc of Fuzz-IEEE’09 Int Conf on Fuzzy Syst*, Korea, 2009, pp. 1700–1705.
- [28] K. Deb, A. Pratap, S. Agarwal, and T. Meyarivan. “A fast and elitist multiobjective genetic algorithm: NSGA-II”. *IEEE Trans Evolut Comput*, vol. 6, no 2, 2002, pp. 182–197.
- [29] R. Alcalá, J. Alcalá, M.J. Gacto and F. Herrera. *Rule base reduction and genetic tuning of fuzzy systems based on the linguistic 3-tuples representation*. Springer-Verlag, 2006.
- [30] L. J. Eshelman, “The CHC adaptive search algorithm: How to have safe search when engaging in nontraditional genetic recombination”, in *Foundations of genetic Algorithms 1, Rawlin G (Ed.) Morgan Kaufman*, 1991, pp. 265–283.
- [31] E. Cantú-Paz, D.E. Goldberg, “Efficient parallel genetic algorithms: theory and practice” *Comput. Methods Appl. Mech. Engrg*. 186, 2000, pp. 221-238.
- [32] O. Cordón, F. Herrera, and L. Sánchez., “Solving electrical distribution problems using hybrid evolutionary data analysis techniques”, *Appl Intell*, vol. 10, 1999, pp. 5–24.
- [33] M. Erdem Kurul and E. Tuzun. Available:www.wunderground.com; <http://www.wunderground.com/global/stations/17128>.
- [34] J. Demšar, Statistical comparisons of classifiers over multiple data sets, *J Mach Learn Res*, vol. 7, 2006, pp. 1–30.
- [35] D.J. Sheskin, *Handbook of Parametric and Nonparametric Statistical Procedures*, CRC Press, Boca Raton, FL, 2003.