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A Fast and Scalable Multi-Objective Genetic Fuzzy System for Linguistic Fuzzy Modeling in High-Dimensional Regression Problems

R. Alcalá, M.J. Gacto, and F. Herrera, *Member, IEEE,*

***Abstract*— Linguistic fuzzy modeling in high-dimensional regression problems poses the challenge of exponential rule explosion when the number of variables and/or instances becomes high. One way of addressing this problem is by learning the used variables, the linguistic partitioning and the rule set together, in order to only evolve very simple but still accurate models. However, evolving these components together is a difficult task involving a complex search space.**

In this work, we propose an effective multi-objective evolutionary algorithm that, based on embedded genetic data base learning (involved variables, granularities and slight fuzzy partition displacements), allows the fast learning of simple and quite accurate linguistic models. Some efficient mechanisms have been designed to ensure a very fast, but not premature, convergence in problems with a high number of variables. Further, since additional problems could arise for datasets with a large number of instances, we also propose a general mechanism for estimating the model error when using evolutionary algorithms, by only considering a reduced subset of the examples. By doing so we can also apply a fast post-processing stage for further refining the learned solutions.

We tested our approach on 17 real-world datasets with different numbers of variables and instances. Three well-known methods based on embedded genetic data base learning have been executed as references. We compared the different approaches by applying non-parametric statistical tests for multiple comparisons. The results confirm the effectiveness of the proposed method in terms of scalability, but also in terms of the simplicity and generalizability of the obtained models.

***Index Terms*— Linguistic fuzzy modeling, Multi-objective genetic fuzzy systems, embedded genetic data base learning, Scalability, High-dimensional regression problems**

I. Introduction

Linguistic fuzzy modeling in high-dimensional and large scale regression datasets is a challenging topic since conventional linguistic Fuzzy Rule-Based Systems (FRBSs) suffer from exponential rule explosion when the number of variables and/or data examples becomes high [1], [2]. Another problem when we deal with high-dimensional datasets is the analysis of algorithm scalability on big databases, emphasizing the training time and the convergence towards compact and interpretable models [3]. In this way, we can distinguish two kinds of problems: high dimensionality when a large number of variables have to be considered, and scalability in datasets with a large amount of data.

A good way to address both problems is by searching for a good and simple global structure within the same process, in order to consider the relationships among the different components defining the Knowledge Base (KB) of the obtained linguistic models. That is, by learning the main components of the KB, a Data Base (DB) containing the definitions of the linguistic fuzzy partitions and a Rule Base (RB) containing the associated set of rules, together. Since this method involves using different coding schemes to represent each solution, Evolutionary Algorithms, particularly Genetic Algorithms (GAs), are useful for this task. These kinds of global search techniques have been successfully applied to learn fuzzy systems in recent years, giving rise to the so called Genetic Fuzzy Systems (GFSs) [3]–[5]. Furthermore, the application of MOEAs to the derivation of compact linguistic FRBSs is a prolific framework in which we can find several interesting and recent works. Some MOEAs were proposed as post-processing techniques [6]–[13] while others were proposed as learning techniques [11], [14]–[18].

However, this method involves a lot of components/parameters that should be determined together: selection of important variables, determination of a good number of linguistic terms or granularities per variable, parametric definition of the Membership Functions (MFs) and associated set of rules. Since it involves using different coding schemes to represent a complete solution and therefore a very complex search space, this is a difficult task. In fact, the balance among problem size, algorithm scalability and solution quality is an important topic for GFSs that is worth studying in depth [3], which has not been directly taken into account in the mentioned evolutionary approaches devoted to linguistic fuzzy modelling.

An efficient way to obtain the whole KB of an FRBS is to obtain the DB and the RB within the same process but separately, based on embedded genetic data base learning [19]–[24]. This is an evolutionary process that learns the DB and wraps a simple method to derive a set of rules for each DB definition. This enables the most adequate context [20] for each fuzzy partition to be learned, which strongly affects the final model complexity. However, this approach cannot solve the following contradictory requirements:

- The obtained linguistic models should be *simple* and *transparent*, but also *competitive* in terms of the general-

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R. Alcalá and F. Herrera are with the Dept. of Computer Science and Artificial Intelligence, University of Granada, 18071 Granada, Spain, (e-mail: {alcala, herrera}@decsai.ugr.es).

M.J. Gacto is with the Dept. of Computer Science, University of Jaén, 23071 Jaén, Spain, (e-mail: mjgacto@ugr.es).

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ization error.

- The evolutionary learning algorithm should be *effective*, but also *scalable*, in terms of the time and memory consumed, in order to be useful for a wide range of high-dimensional or large-scale problems.

In this work, we propose a convenient reduction of the search space for the embedded genetic data base learning (variable selection, granularities and MF parameters) and an effective and efficient Multi-Objective Evolutionary Algorithm (MOEA) as a tool that makes use of some specific mechanisms in order to ensure a fast convergence. To reduce the search space [25], we propose the performance of a slight *lateral displacement of fuzzy partitions* by applying a common displacement parameter to all the MFs at each linguistic variable. This allows a simple pre-screening of promising granularities, which avoids the derivation of very specific systems presenting overfitting, and preserves equidistributed strong fuzzy partitions. In addition, the proposed MOEA includes such concepts as incest prevention and restarting in order to improve the algorithm convergence [26], together with some mechanisms to step up the learning process, such as a rule cropping criterion in the RB generation process.

The proposed method is able to handle dimensionality, however it does not directly solve scalability with respect to the number of available data in the dataset. To deal with this, we also propose a mechanism to avoid using a big percentage of the examples for error computation, estimating it from a reduced subset of the examples. By doing so we can also apply a post-processing stage to further refine the learned solutions. We have applied a previous MOEA [27], [28], namely SPEA2$_{E/E}$, including this new error estimation procedure for fine tuning of the membership functions and rule selection, which will help to significantly improve the performance of the simple global structure (initially based on strong fuzzy partitions) while the complexity is decreased.

We tested our approach on 17 real-world problems with a number of variables ranging from 4 to 85 and a number of samples ranging from 337 to 40,768. When it was possible, depending on the dimensionality, we executed three well-known accuracy-driven single-objective methods based on embedded genetic data base learning in order to have some good performance references. To assess the results obtained by the different algorithms, we have applied non-parametric statistical tests [29]–[32] for multiple comparisons, considering for the MOEA the average of the most accurate solution from each Pareto front. The results obtained demonstrate the effectiveness of the proposed method, particularly in terms of scalability, but also in terms of simplicity and the generalizability of the obtained models.

This contribution is arranged as follows. Section II proposes the lateral displacement of fuzzy partitions. In Section III, we present an effective MOEA to learn FRBSs for high-dimensional problems. Section IV proposes the new method for fast error computation and its application to the proposed algorithm and to a known algorithm for post-processing, SPEA2$_{E/E}$. Section V shows the experimental study on the proposed method and describes a Web page associated with the paper (`http://sci2s.ugr.es/FS-MOGFS/`) that contains complementary material to this study. Finally, section VI draws some conclusions.

II. A Proposal for the Lateral Displacement of Linguistic Fuzzy Partitions

In [25], a new model of tuning of FRBSs was proposed, considering the linguistic 2-tuples representation scheme introduced in [33], which allows the lateral displacement of the support of a label. The main achievement is that, since the 3 parameters usually considered per label [4], [34]–[40] are reduced to only 1 symbolic translation parameter, this proposal decreases the learning problem complexity, facilitating the derivation of optimal models [14], [25], [41]. In any event, an FRBS based on linguistic 2-tuples could be represented as a classical Mamdani FRBS [42], [43]. See [25] or the Web page associated with the paper (`http://sci2s.ugr.es/FS-MOGFS/`) for a more detailed description of this tuning approach.

The lateral tuning of MFs allows a good adaptation for each MF comprising the DB. However, our main aim in this work is to learn a good, simple and general KB in a fast way. Learning all the components of the KB together represents a huge search space when high dimensional problems are considered. To perform a good adaptation for each individual MF while learning the system structure could lead to very complex systems, since it is difficult to obtain the best parameters for each concrete system structure. Once relatively good parameters are obtained for a system structure, convergence starts in this zone and it is difficult to explore other good configurations (with similar accuracy) that could represent more simple and interesting systems.

To solve this problem, we propose the application of a single lateral displacement of linguistic fuzzy partitions by applying a common α displacement parameter to all the MFs at each linguistic variable, i.e., all the MFs are uniformly displaced depending on the displacement parameter associated with each linguistic fuzzy partition. In order to avoid very specific parameters and to preserve the original meanings of the MFs as much as possible, we propose the use of a short displacement interval, $[-0.1, 0.1)$ in our case, as the range to express the relative shifts associated with the labels. In this way, we can represent the translation of a linguistic partition S by the 2-tuple notation as,

$$(S, \alpha),\ \alpha \in [-0.1, 0.1) \Rightarrow (s_i, \alpha),\ \forall s_i \in S.$$

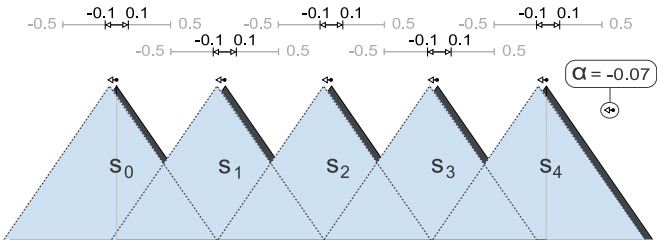

Fig. 1. Lateral displacement in [-0.1, 0.1] of the whole linguistic partition $S = \{s_0, s_1, s_2, s_3, s_4\}$.

Figure 1 shows the lateral displacement of a linguistic partition S for a concrete α value. Some interesting characteristics of this approach are:

- The search space is reduced providing a fast convergence. This makes it easier to explore different granularities that can represent promising linguistic partitions.
- The constrained variation interval avoids a fine adaptation of the MFs, allowing only a simple pre-screening of promising granularities, which avoids the derivation of very specific systems presenting overfitting.

All these properties facilitate a fast derivation of promising models based on uniformly distributed strong fuzzy partitions. Once they are obtained, a fine tuning [6], [7], [25], [37]–[39] (post processing) could be applied easily depending on user preference. We do not consider this possibility in this contribution as we are focused only on the learning stage.

III. A Fast and Scalable Multi-Objective Genetic Fuzzy System for Embedded Genetic Data Base Learning

An alternative to learn an entire KB is Iterative Rule Learning (IRL). However, IRL approaches usually obtain models with too many rules involving all the system variables. For this reason, they are usually devoted to obtaining approximate models, mainly focused on accuracy, in problems with a reasonable number of variables. An example can be found in [44] where a three stage learning process is used to obtain a large set of accurate approximate TSK fuzzy rules. A methodology with a similar philosophy [45] consists of the use of a clustering method for first generating a set of initial TSK local rules in order to subsequently reduce complexity without affecting accuracy too much. Both approaches allow TSK models (approximate FRBSs) to be obtained, considering all the variables in each rule and presenting highly accurate results in problems with a reasonable number of variables.

In the case of linguistic FRBSs (which need the definition of a permanent appropriate grid), an efficient way to learn the whole KB consists of obtaining the DB and RB within the same process but separately, based on embedded genetic data base learning [19]–[24], [46]. This method allows us to learn the most adequate context [20], [46] for each fuzzy partition, which is necessary in different contextual situations (different applications).

Even though different optimization techniques could be considered for the embedded learning of the DB parameters, in this work, we consider an MOEA for this task, which allows different coding schemes to be handled within the same process and to improve both system accuracy and simplicity (essential to handle high-dimensional problems). To this end, we can learn different parts of the DB together (number of labels and parameters), thus considering the relationships among them.

The learning scheme considered to obtain complete KBs is comprised of two main components, DB evolutionary learning and an RB *ad-hoc* rule learning process. In the following, an effective design of the learning process is first discussed and proposed to later present the specific fast MOEA as the most important part of the proposed technique.

A. Convergence and Scalability Discussion for the Embedded Algorithm Design

Some problems arise when high-dimensional datasets are considered (see Figure 2). The two main problems are:

- *The large number of evaluations needed to reach convergence*. We solve this problem in two ways. By learning together the number of labels and single partition displacement parameters for each linguistic variable instead of the three definition points for each MF (reduced search space). And, by developing an advanced MOEA based on the well known SPEA2, we ensure an effective trade-off between exploration and exploitation. This specific MOEA is able to stop the process when convergence is reached. In this way, we can ensure a fast but effective convergence in order to avoid unneeded evaluations.
- *Too much time is required to generate the RB*. This problem is related to the previous one. Each evaluation requires generating an RB based on the coded DB. Even though a fast *ad-hoc* rule generation method is going to be used, this method can take a significant amount of time in high-dimensional problems. Due to the required number of evaluations, it poses a problem. We solve this problem by including a cropping criterion in the RB generation method, thus avoiding the generation of excessively large RBs that expend too much time and make no sense in linguistic fuzzy modeling. Additionally, we enable the removal of unnecessary variables while evolving, thus leading to DBs that do not provoke an excessive number of rules when the RB generation process is applied.

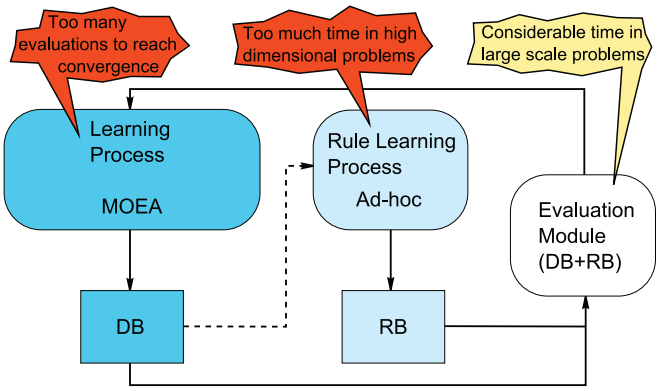

Fig. 2. Learning scheme of the KB.

The two previous problems are directly related to the learning process. However, a third problem arises in large scale problems (datasets with a large number of data) since each evaluation can take a considerable amount of time (see Figure 2). This problem is greatly reduced by solving the two previous ones and is also related to data pre-processing [47] or parallel computation [48], [49]. We address this problem in Section IV, proposing a general scheme for fast error estimation.

1) Embedded Genetic Data Base Learning: Taking into account the previous discussion, the proposed algorithm is comprised of these two main components:

- An effective MOEA based on SPEA2 [50] with two minimization objectives (system error and number of rules) in order to learn promising DBs. In order to improve its search ability and good convergence, this MOEA also implements such concepts as incest prevention and restarting [26]. It allows us to define:
  - The number of labels per variable, which determine the corresponding uniformly distributed strong linguistic partitions. We will enable the possibility of removing unnecessary variables by allowing granularity 1, which means that the corresponding variable is not considered in the final model.
  - The lateral displacements for each linguistic partition.
- A quick *Ad-hoc* data-driven method to learn an RB from each DB definition within the evolutionary process. The cooperative action of both components allows the whole definition of the KB (DB and RB) to be obtained. The simple Wang and Mendel algorithm [51] (WM) will be considered for this task by adding a rule base cropping mechanism.

Due to the importance of the cropping mechanism for high-dimensional data sets, we first explain this approach devoted to shortening the time spent on evaluating nonsensical KBs. Then, the MOEA for evolving DBs that integrates this version of WM is explained in depth.

2) Cropping Mechanism for the Ad-Hoc *WM Algorithm:* The WM process is based on the existence of a predefined DB and a set of input-output training data $E = \{e_1, ..., e_l, ..., e_m\}$ with $e_l = (x^l_1, \ldots, x^l_{N-1}, y^l)$, $l \in \{1, \ldots, m\}$, m being the data set size, and N-*1* being the number of input variables. Since, in high-dimensional problems, WM can take a long time to derive thousands of rules, a cropping criterion has been added to this method. In this way, the RB is generated by means of the following steps, integrating the WM cropping mechanism as the last step of the process:

- Initially the RB is empty and the data randomly ordered (the data is re-ordered at each generation of the evolutionary algorithm).
- For each example e_l in E:
  1) Generate the rule with the labels best covering the example $(x^l_1, ..., x^l_{N-1}, y^l)$.
  2) Compute the covering degree of the complete rule (antecedent and consequent).
  3) If there is no rule with the same antecedent in the RB, add the obtained rule to the RB together with its covering degree.
     Otherwise maintain the consequent and covering degree of the rule with the highest coverage.
  4) Stop the process if the RB reaches a limit of 50 rules and mark the RB as incomplete.

In this contribution, we propose a maximum number of rules of 50 for the rule cropping mechanism, based on some empirical trials. The smaller this number is, the faster the method is and the simpler the solutions are. However, the precision of the models finally obtained is significantly affected with too small values. We detected this phenomenon in values clearly under 50, making this number a good limit for a large variety of problems. Higher values or even those that do not use cropping do not obtain significantly more accurate solutions in terms of generalizability (see the Web page associated with the paper for some examples demonstrating this at `http://sci2s.ugr.es/FS-MOGFS/`).

B. Proposed Multi-Objective Evolutionary Algorithm

This section presents the proposed MOEA for the embedded Genetic DB learning, namely FS-MOGFS (Fast and Scalable Multi-Objective Genetic Fuzzy System). In the following, the components needed to implement this algorithm are explained in depth. They are: DB codification, objectives and incomplete RBs Penalization, initial gene pool, crossover and mutation, incest prevention, restarting and stopping condition.

1) DB Codification: A double coding scheme ($C = C_1 + C_2$) to represent both parts, *granularity* and *translation parameters*, is considered:

- Number of labels (C_1): This part is a vector of integer numbers with size N (with N representing the number of linguistic variables) in which the granularities of the different variables are coded,
$$C_1 = (L^1, \ldots, L^N) \ .$$
Each gene L^i represents the number of labels used by the i-th variable and takes values in the set $\{2, \ldots, 7\}$. Additionally, in the case of input variables, it can take a value equal to 1 to determine that the corresponding variable is not used.
- Lateral displacements (C_2): This part is a vector of real numbers with size N in which the displacements of the different variables are coded. In this way, the C_2 part has the following structure (where each gene is the displacement value of the fuzzy partition of the corresponding linguistic variable and takes values from $[-0.1, 0.1]$),
$$C_2 = (\alpha^1, \ldots, \alpha^N) \ .$$

2) Objectives and Incomplete Rule Bases Penalization: Once a complete KB is obtained the following two objectives are minimized for this problem: the number of rules (simplicity) and the Mean Squared Error (accuracy),

$$\text{MSE} = \frac{1}{2 \cdot |E|} \sum_{l=1}^{|E|} (F(x^l) - y^l)^2,$$

with $|E|$ being the data set size, $F(x^l)$ being the output obtained from the FRBS decoded from a given chromosome when the l-th example is considered and y^l being the known desired output. The fuzzy inference system considered to obtain $F(x^l)$ is the *center of gravity weighted by the matching* strategy as a defuzzification operator and the *minimum t-norm* as implication and conjunctive operators.

In order to obtain a complete KB from a given chromosome, we apply WM to the DB coded by this chromosome, considering a cropping mechanism. Firstly, in order to decode this DB, equidistant strong fuzzy partitions are defined considering the granularity values in C_1. Secondly, the MFs of each variable

are uniformly displaced to their new position considering the displacement values in C_2.

WM is applied to the obtained DB, but it stops if the RB reaches a maximum of 50 rules and marks the RB as incomplete in order to penalize its objective values:

- In the case of the number of rules, we estimate the worst possible value as the product of the number of labels of the input variables in the decoded DB (a pessimistic proportional estimation of the number of rules).
- In the case of the MSE, it is multiplied by 2.0 (if an example is not covered by the incomplete RB, the middle of the output domain is given as the estimated output).

In this way, these solutions are not a problem for the computational time and they compete with each other at secondary Pareto fronts, which is useful for detecting promising combinations of selected variables and granularities at the first stages of the algorithm (i.e., until appropriate combinations of variables and granularities that allow the derivation of RBs with a good number of rules arise, which will dominate those previous incomplete solutions).

3) Initial Gene Pool: The initial population will be comprised of two different subsets of individuals:

- In the first subset, each chromosome has the same number of labels for all the system input variables. In order to provide diversity in the C_1 part, these solutions have been generated by considering all the possible combinations in the antecedent part, i.e., from 2 labels to 7 labels in all the input variables (6 combinations). For each of these combinations, all the possible combinations are generated in the consequent part (6 combinations per each input combination). Additionally, for each of the previous combinations two copies are included with different values in the C_2 part. The first one with random values in $[-0.1, 0.0]$ and the second one with random values in $[0.0, 0.1]$. Thus, a total of 72 ($6{*}6{*}2$) different individuals are generated. If there is no space for these solutions, they are included from the smallest granularities (the most interesting combinations in principle) to the highest possible ones.
- In the second subset, we generate random solutions in order to completely fill the population (values in $\{2, \ldots, 7\}$ for C_1 and values in $[-0.1, 0.1]$ for C_2).

Finally, except in the cases of problems with less than three input variables, an input variable v is removed at random, $L^v = 1$, in the first individual. This action is repeated until no more than 10 variables remain in this individual. If the problem has no more than 10 variables this action is not repeated, thus only one variable is removed at random. This process is applied to all the individuals in the population in order to avoid the generation of solutions that make no sense (because of their exorbitant number of rules).

4) Crossover and Mutation Operators: The crossover operator depends on the part of the chromosome to which it is applied. A crossover point is randomly generated and the classical crossover operator is applied to this point for the C_1 part. The Parent Centric BLX (PCBLX) operator [52], which is based on BLX-α, is applied to the C_2 part (Figure 3 depicts the behavior of these kinds of operators). Specifically, PCBLX is described as follows. Let us assume that $X = (x_1 \cdots x_n)$ and $Y = (y_1 \cdots y_n)$, with $x_i, y_i \in [a_i, b_i] \subset \Re$ and $i = 1 \cdots n$, are two real-coded chromosomes that are going to be crossed. The PCBLX operator generates the following two offspring:

- $O_1 = (o_{11} \cdots o_{1n})$, where o_{1i} is randomly (uniformly) generated in the interval $[l_i^1, u_i^1]$, with $l_i^1 = max\{a_i, x_i - I_i\}$, $u_i^1 = min\{b_i, x_i + I_i\}$, and $I_i = \mid x_i - y_i \mid \cdot \alpha$. In our case, α has been fixed to 0.3.
- $O_2 = (o_{21} \cdots o_{2n})$, where o_{2i} is randomly (uniformly) generated in the interval $[l_i^2, u_i^2]$, with $l_i^2 = max\{a_i, y_i - I_i\}$ and $u_i^2 = min\{b_i, y_i + I_i\}$.

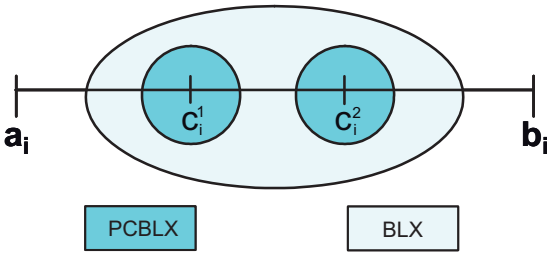

Fig. 3. Scheme of the behavior of the PCBLX and BLX operators.

In this way, four new individuals are obtained by combining the two offspring generated from C_1 with the two offspring generated from C_2. For each of them, the mutation operator is applied with probability P_m. The mutation operator decreases by 1 the granularity in a gene g selected at random ($L^g = L^g - 1$) or randomly determines a higher granularity in $\{L^g + 1, \ldots, 7\}$ with the same probability. No decreasing is performed when it provokes DBs with only one input variable. The same gene is also changed at random in C_2. Finally, after considering mutation, only the two most accurate individuals are taken as descendants.

5) Incest Prevention: An incest prevention mechanism has been included by following the concepts of CHC [26] and by only taking into account the C_2 parts. Following the original CHC scheme (for binary coding), two parents are crossed if their hamming distance divided by 2 is over a predetermined threshold, L. Since C_2 makes use of a real coding scheme, we have to transform each gene considering a Gray Code (binary code) with a fixed number of bits per gene ($BITSGENE$), that is determined by the system expert. In this way, the threshold value is initialized as:

$$L = (\#GenesC_2 \cdot BITSGENE)/4.0.$$

Typically, L is decremented by one when there are no new individuals in the next generation. In order to step up the convergence, in our case, L will be decremented by two at each generation for problems with less than 50 variables. In order to increase the convergence speed for hard high-dimensional data sets, this quantity is increased by two for every 50 additional variables ($L = L - 2 - 2 * \lfloor N/50 \rfloor$). Incest prevention represents a way to provide a good trade-off between exploration and exploitation, avoiding unnecessary crosses of very similar solutions at the earlier stages of the algorithm.

6) Restarting and Stopping Condition: In order to get away from local optima a restarting mechanism [26] (external population is forced to be empty) is applied by including the most accurate individual as a part of the new population and by generating the remaining individuals at random (taking values between 1 and the granularity coded in the most accurate individual for each gene of the C_1 part). This mechanism is applied when the threshold value L is below zero (L is set to its initial value).

The algorithm ends when a maximum number of evaluations are reached or when L is below zero for a second time. That, only two exploration/exploitation stages are needed to reach convergence.

IV. Partial Error Computation on Large Scale Databases for Elitist-Based Evolutionary Algorithms: Evolving with Estimated Errors

As stated in the introduction, considering a post-processing stage on the KBs obtained by the proposed learning algorithm represents a way to enhance the solutions. To this end, we will apply a previous MOEA, namely SPEA2$_{E/E}$ [27], [28], for fine tuning of the MFs and rule selection which will help to significantly improve the performance of the simple global structure (initially based on strong fuzzy partitions) while the complexity is decreased.

While the problem of high dimensionality (high number of variables) is being solved at a first stage by the proposed learning algorithm, there are still two interdependant problems representing a difficult challenge in order to apply this second post-processing stage: the convergence, imposing a minimum number of evaluations needed (which is not a problem itself if the algorithm is well designed); and the large time consumed by error computation in large scale datasets (i.e., datasets with a large amount of data). Since this last problem cannot be solved by their own learning or tuning strategy, and since particularly in the case of tuning it could present high computational times in some datasets, we propose in this section a new general mechanism for fast error computation on large scale datasets. This procedure is based on taking a small percentage of the training examples to estimate the quantity of errors of bad solutions, thus only using all the examples to evaluate good candidate solutions. In what follows, we present the main steps to apply this fast fitness evaluation procedure, which is defined in general as *Evolving with Estimated Errors* with any kind of Elitist-Based Evolutionary Algorithm, either single objective or multiobjective elitist-based ones.

The evaluation process is based on the existence of a set of input-output training data $E = \{e_1, ..., e_l, ..., e_m\}$ with m being the data set size. For a new solution C whose performance is going to be computed, two sets of solutions have to be taken into account: the set of elite solutions (one solution in the case of single objective algorithms) and the solutions previously evaluated at the current generation. Let r^e be the rate of examples used to estimate the error. In any case, *if* $\lfloor r^e * m \rfloor \geq 1000$ *then* $r^e = 1000/m$, i.e., no more than 1000 examples have to be considered. The subset of examples E^e for error estimation is obtained by randomly selecting $\lfloor r^e * m \rfloor$ new examples at each generation. Thus, E^e is kept fixed for a complete generation. After each generation the examples are replaced by random selection from those examples that were not used in the previous generation. In this way, we promote a rotation of the selected examples.

Let S_{elit} and $S_{current}$ be the set of elite solutions and the set of evaluated solutions at the current generation respectively. The fast error computation process is as follows:

1) Compute the error of solution C in E^e (error estimation) and assign this error to C.
2) If by taking into account the estimated error and the solutions in S_{elit} and $S_{current}$, C is candidate to become a member of S_{elit} (i.e., it presents the best error in single objective algorithms or it is a non dominated solution in multi-objective ones) continue to step 3, otherwise go to step 4.
3) Perform a complete evaluation by considering the estimated error and the examples in $E - E^e$. In this way, S_{elit} (the final output of the algorithm) will always contain solutions evaluated considering 100% of the examples.
4) Evaluations = Evaluations + 1 (since this mechanism is proposed for saving time and not for saving evaluations).

The new mechanism for fast performance/error computation has been included in the post-processing algorithm proposed in [27] in order to speed up the fine classic tuning process, giving way to an algorithm with a low computational expense. It has also been included within the proposed learning algorithm FSMOGFS in order to improve the computational time with respect to the number of training data. As regards this algorithm, we have to clarify that the reduced set of examples is only used to estimate the errors, i.e., we do not recommend using this set for the induction of rules. In this way, we always use all the dataset to obtain the rules and the reduced one only to compute/estimate the errors.

V. Experiments and Analysis of Results

In order to evaluate the usefulness of the proposed approach, namely FSMOGFS^e+TUN^e, in high-dimensional problems, we have used 17 real-world problems with different numbers of variables and cases. Table I sums up the main characteristics of the different problems considered in this study and shows the link to the KEEL project webpage [53] from which they can be downloaded. These problems have been selected from minor to major complexity, covering a range from 4 to 85 input variables and from 337 to 40,768 examples (even though each of them is complicated in itself in terms of the modeling task). The more complex problems are ELV, AIL, MV and TIC because of the large number of variables and data. To the best of our knowledge, the problems have never been solved using GFSs o linguistic fuzzy models. This is due to the long time needed to evaluate an individual and to the minimum number of evaluations needed to reach convergence of GFSs. Moreover, a large number of rules would be easily obtained for these kinds of problems, which make no sense in linguistic fuzzy modeling. Then, these problems represent an important challenge for this algorithm.

TABLE II
METHODS CONSIDERED FOR THE EXPERIMENTAL STUDY

Ref.	Method	Type of learning
[51]	WM(L)	Ad-hoc data-driven rule generation method with L labels
[19]	GR-MF	Gr. & MF parameters & RB by WM
[20]	GA-WM	Gr. & Scaling fact. & Domains & RB by WM
[54]	GLD-WM	Gr. & Individual Lateral MF parameters & RB by WM
-	FSMOGFS	Gr. & Lateral partition params. & RB by WM
-	FSMOGFS+TUN	FSMOGFS + (Tuning of MF parameters and rule selection by SPEA2$_{E/E}$ [27])
-	FSMOGFS^e	FSMOGFS including fast error estimation
-	FSMOGFS^e+TUN^e	FSMOGFS+TUN including fast error estimation

TABLE I
DATA SETS CONSIDERED FOR THE EXPERIMENTAL STUDY

Problem	Abbr.	Variables	Cases
Electrical Maintenance	ELE	4	1056
Auto MPG6	MPG6	5	398
Auto MPG8	MPG8	7	398
Analcat	ANA	7	4052
Abalone	ABA	8	4177
Stock	STP	9	950
Weather Izmir	WIZ	9	1461
Weather-Ankara	WAN	9	1609
MV Artificial Domain	MV	10	40768
Forest Fires	FOR	12	517
Mortgage	MOR	15	1049
Treasury	TRE	15	1049
Baseball	BAS	16	337
Elevators	ELV	18	16559
Computer-Activity	CA	21	8192
Ailerons	AIL	40	13750
The Insurance Company	TIC	85	9822

Available at `http://www.keel.es/`

This section is organized as follows:

- First, we describe the experimental set-up and we introduce the information shown at the Web page associated to the paper in Section V-A.
- Second, we compare the most accurate solutions of our proposal with respect to three well-known accuracy-oriented single-objective related algorithms in Section V-B.
- Third, we compare both stages including or not the fast error computation procedure in terms of the performance in Section V-C.
- Fourth, we show the computational costs of the different algorithms and we discuss the scalability of the proposed approach in Section V-D.
- Finally, in Section V-E, for each dataset we plot the average Pareto fronts and the average results of the single objective based approaches. These plots provide reliable information on the form and characteristics of the Pareto fronts obtained, allowing us to check the trend and the kind of correlation of the training and the test errors.

A. Experimental Framework

This section describes the experimental set-up, including a brief description of the methods and the non-parametric statistical tests considered for comparisons. It then introduces the contents of the Web page with additional material associated with the paper.

1) Experimental Set-Up: In order to evaluate the effectiveness of the proposed method designed for fast learning and its applicability to large scale problems (with and without a tuning stage; with and without fast error estimation), three well-known single objective-based methods for the learning of accurate KBs have been considered for comparisons, GR-MF [19], GA-WM [20] and a more recent and effective approach, namely GLD-WM [54]. These methods are also based on embedded genetic data base learning. Further, WM [51] is also considered as a reference since all of these approaches are based on it. A brief description of the studied methods is presented in the next three paragraphs while Table II summarizes their main characteristics:

- WM [51] algorithm is considered as a simple rule generation method to quickly obtain RBs from a predefined DB. This method is considered as a reference since the studied algorithms are devoted to obtaining good fuzzy partitions for the application of WM. The initial linguistic partitions for this method are comprised by L *linguistic terms* with uniformly distributed triangular MFs giving meaning to them. In this way, we will refer to this method as WM(L), with L taking values in $\{3,5,7\}$.
- On the other hand, three different GFSs devoted to obtaining a complete KB (by embedded genetic data base learning) are considered for comparisons. Both are accuracy oriented single objective-based algorithms whose main objective is to obtain FRBSs as accurately as possible. The first one, Gr-WM [19], learns the granularity for each fuzzy partition and the MFs parameters (their three definition points). The second one, GA-WM [20], learns the granularity, scaling factors and the domains (i.e., the variable domain or working range to perform fuzzy partitioning) for each system variable. Both methods obtain the RB by means of the WM algorithm. The third one, GLD-WM [54], has been proposed more recently for an effective learning of the KB by obtaining the granularity and the individual lateral displacements of the MFs (i.e., fine parameter adaptation), which will have the benefit of obtaining higher accuracy in the results.
- The proposed method, namely FSMOGFS (see Section III) or FSMOGFS^e when it includes the fast error estimation mechanism (see Section IV), has less freedom degrees

than the other three genetic approaches selected for comparisons, which should obtain the most accurate results from a theoretical viewpoint. Therefore, they represent a good accuracy goal for the proposed algorithm at the first stage in those problems in which they are still applicable (particularly in the case of GLD-WM, which was more recently designed to obtain as accurate as possible linguistic models). The addition of a post-processing technique, namely FSMOGFS+TUN or FSMOGFS^e+TUN^e when it includes the fast error estimation mechanism, gives way to a new procedure/method working at two stages, which presents the same freedom degrees as the approaches selected for comparisons and should obtain the best results.

In all the experiments, we adopted a *5-fold cross-validation model*, i.e., we randomly split the data set into 5 folds, each containing 20% of the patterns of the data set, and used four folds for training and one for testing [1]. For each of the five partitions, we executed six trials of the algorithms (6 different seeds). For each data set, we therefore consider the average results of 30 runs. In the case of FS-MOGFS, the average values are calculated considering the most accurate solution from each obtained Pareto front. Our main aim following this approach is to have the possibility of statistically comparing the single objective approaches (only accuracy) with the most accurate solution found by the proposed MOEA.

In order to assess whether significant differences exist among the results, we adopt statistical analysis [29]–[32] and in particular non-parametric tests, according to the recommendations made in [29] and [30], where a set of simple, safe and robust non-parametric tests for statistical comparisons of classifiers has been analyzed. We will employ different approaches for multiple comparison, including Friedman's test [55], Iman and Davenport's test [56] and Holm's method [57]. For a detailed description of these tests and for detailed explanation of the use of non-parametric tests for data mining and Computational Intelligence see the Website at `http://sci2s.ugr.es/sicidm/`. To perform the tests, we use a level of confidence $\alpha = 0.1$.

The values of the input parameters considered by GR-MF, GA-WM and GLD-WM are: population size of 61, 100,000 evaluations, 0.6 as crossover probability and 0.2 as mutation probability per chromosome. In the case of the SPEA2 based methods (FSMOGFS, FSMOGFS^e, FSMOGFS+TUN and FSMOGFS^e+TUN^e), we have considered an external population size of 61 (the same size used by the named single objective algorithms) and a proportion of 1/3 rounded to 200 as standard population size. The remaining parameters for them are: a maximum of 100,000 evaluations, 0.2 as mutation probability (crossover is always applied in SPEA2), 30 bits per gene for the Gray codification, $r^e = 0.2$ for the fast error computation technique, and the set $\{2, \ldots, 7\}$ as possible numbers of labels in all the system variables for the learning approaches. The same set $\{2, \ldots, 7\}$ has been considered for GR-MF, GA-WM and GLD-WM after comparing this configuration with the original configuration indicated by the authors in the corresponding papers [19], [20], [54] ($\{3, \ldots, 9\}$). See this study as complementary material in the associated Web page at (`http://sci2s.ugr.es/FS-MOGFS/`).

2) Web Page Associated with the Paper: In order to provide additional material to the paper content, we have developed a Web page at (`http://sci2s.ugr.es/FS-MOGFS/`) in which we have included the following information:

- The data sets' partitions employed in the paper. These partitions can be found in a table together with the main characteristics of the used data sets.
- An Excel file with the complete tables of results. We include an Excel file with the training and test results for all the algorithms so that any interested researcher can use them to include their own results and extend the present comparison. A figure with the average Pareto fronts for all the studied datasets.
- Some examples of the influence of the lateral displacements and the rule cropping strategy in the proposed method.
- Some representative models in some of the data sets considered are also depicted to graphically show the kinds of models obtained by the proposed algorithm. Additionally, we have depicted the KB of the most accurate solution from the first data partition and seed in all the datasets and included them in a zip file.
- The results of GR-MF, GA-WM and GLD-WM with the sets $\{2, \ldots, 7\}$ and the original configuration indicated by the authors in the corresponding papers [19], [20], [54], $\{3, \ldots, 9\}$, as possible numbers of labels in all the system variables. We have included these results and the assessment of Wilcoxon's Signed-Ranks test [58], [59] for pair-wise comparison in favour of versions with $\{2, \ldots, 7\}$ in both, test error and number of rules.
- A description of Wilcoxon's Signed-Ranks test [58]–[60] and an explanation on how to apply it in the regression framework.
- An introduction to the lateral tuning of MFs [25] as preliminary information to the paper.

B. Results and Analysis of the Most Accurate Solution

The results obtained by the studied methods are shown in Table III. This table is grouped in columns by algorithms and it shows the average of the results obtained by each algorithm in all the studied data sets. For each one, the first column shows the average number of rules and used variables (R/V). The second and third columns show the average MSE in training and test data (Tra./Tst.) together with their respective standard deviations (SDs). No values are shown with GR-MF, GA-WM and GLD-WM in MV, ELV, CA, AIL and TIC because the large number of variables and cases provoked memory overflow errors after several hours running without finishing the evaluation of the initial population (some memory issues were improved in these methods to solve this problem, which helped to show results in at least some of the data sets with more than 7 variables, but it was impossible to run them in these problems).

[1]The corresponding data partitions (5-fold) for these datasets are available at the KEEL project webpage [53]: `http://sci2s.ugr.es/keel/datasets.php`

TABLE III

AVERAGE RESULTS OF THE DIFFERENT ALGORITHMS IN COMPLEXITY AND ACCURACY (TRAINING/TEST). RESULTS IN THIS TABLE (TRA./TST. AND SD) SHOULD BE MULTIPLIED BY 10^5, 10^{-5} OR 10^{-8} IN THE CASE OF BAS, ELV OR AIL RESPECTIVELY. GR-MF, GA-WM AND GLD-WM WERE NOT APPLICABLE TO MV, ELV, CA, AIL AND TIC BECAUSE OF THE LARGE NUMBER OF VARIABLES AND CASES PROVOKED MEMORY OVER FLOW ERRORS.

DATASET	Measure	WM(3)			WM(5)			WM(7)			GR-MF			GA-WM			GLD-WM			FSMOGFS^e			FSMOGFS^e+TUN^e		
($V/Size$)		R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.
ELE	Mean	27/4	192241	192647	65/4	56135	56359	103/4	53092	55495	97/4	16645	18637	47/4	17230	18977	33/4	11483	13384	9/2	16153	16338	**8/2**	**9665**	**10548**
(4/1056)	SD		9658	14436		1498	4685		1955	9452		2319	3386		2501	3195		1085	1978		450	1162		823	1150
MPG6	Mean	43/5	13.552	14.649	115/5	4.136	6.096	194/5	2.642	6.382	243/5	**1.423**	28.93	186/5	1.879	8.824	82/5	2.294	**4.387**	39/3	3.894	4.866	**20/3**	2.860	4.562
(5/398)	SD		1.239	3.204		0.317	2.416		0.11	2.126		0.073	8.633		0.235	6.079		0.249	0.899		0.212	0.644		0.218	0.714
MPG8	Mean	71/7	12.709	13.739	161/7	4.143	7.195	223/7	2.372	9.811	262/7	**1.356**	49.36	214/7	1.563	15.22	135/7	1.709	4.782	43/3	3.885	**4.695**	**23/3**	2.757	4.747
(7/398)	SD		1.885	2.528		0.317	2.731		0.152	1.646		0.104	16.2		0.183	9.13		0.170	1.445		0.312	1.168		0.342	1.235
ANA	Mean	72/7	0.187	0.189	124/7	0.027	0.03	171/7	0.012	0.017	148/7	0.005	0.017	150/7	**0.003**	0.008	92/7	0.006	0.008	23/3	0.006	0.006	**10/3**	**0.003**	**0.003**
(7/4052)	SD		0.001	0.005		0	0.002		0	0.003		0.001	0.008		0.001	0.005		0.001	0.004		0.000	0.001		0.000	0.001
ABA	Mean	68/8	8.407	8.422	199/8	3.341	3.474	368/8	3.057	3.268	498/8	**2.358**	2.885	143/8	2.433	2.549	31/8	2.487	2.545	15/3	2.670	2.708	**8/3**	2.445	**2.509**
(8/4177)	SD		0.443	0.545		0.13	0.247		0.084	0.185		0.052	0.263		0.052	0.163		0.078	0.170		0.139	0.216		0.114	0.184
STP	Mean	123/9	8.852	8.951	265/9	1.576	1.624	378/9	0.611	1.488	343/9	0.4	1.543	344/9	0.389	2.192	217/9	**0.299**	**0.435**	43/3	1.393	1.456	**23/3**	0.764	0.912
(9/950)	SD		0.508	1.193		0.09	0.09		0.029	1.634		0.019	2.484		0.017	3.168		0.025	0.067		0.077	0.159		0.139	0.181
WIZ	Mean	105/9	6.944	7.368	399/9	3.107	5.961	652/9	2.036	10.56	331/9	1.176	9.602	218/9	1.233	3.529	107/9	**0.926**	1.150	17/2	1.519	1.571	**10/2**	0.929	**1.011**
(9/1461)	SD		0.72	0.909		0.27	2.498		0.048	2.197		0.077	8.879		0.065	4.023		0.041	0.123		0.094	0.168		0.057	0.164
WAN	Mean	156/9	16.063	16.393	457/9	4.878	6.305	853/9	2.692	6.538	397/9	1.406	7.381	279/9	1.522	2.82	133/9	**1.111**	2.075	11/2	1.897	2.151	**8/2**	1.441	**1.635**
(9/1609)	SD		0.961	1.7		0.405	1.052		0.11	2.101		0.067	5.404		0.065	2.825		0.077	1.407		0.208	0.916		0.178	0.582
FOR	Mean	246/12	2030	3793	375/12	1435	34235	401/12	340	1E+05	396/12	113	3300	395/12	**47**	3693	377/12	49	3847	35/3	1892	**2449**	**10/3**	1418	2628
(12/517)	SD		531	2340		505	4356		147	4708		17	2207		24	2787		18	2714		505	2146		539	2108
MOR	Mean	78/15	0.985	0.973	199/15	0.128	0.134	257/15	0.095	0.137	209/15	0.03	0.176	160/15	0.02	0.093	78/15	**0.016**	0.022	11/2	0.033	0.034	**7/2**	**0.016**	**0.019**
(15/1049)	SD		0.129	0.09		0.005	0.012		0.006	0.056		0.002	0.28		0.003	0.147		0.002	0.005		0.004	0.007		0.003	0.006
TRE	Mean	75/15	1.636	1.631	196/15	0.401	0.405	261/15	0.17	0.176	189/15	0.066	0.144	136/15	0.045	0.064	70/15	**0.033**	0.045	15/3	0.046	0.052	**9/3**	0.034	**0.044**
(15/1049)	SD		0.121	0.181		0.014	0.055		0.009	0.017		0.011	0.191		0.007	0.046		0.005	0.015		0.005	0.010		0.003	0.015
BAS	Mean	181/16	1.921	3.695	253/16	0.782	6.198	264/16	0.316	10.6	262/16	0.255	12.44	262/16	0.202	11.71	244/16	**0.138**	3.610	28/6	1.706	**2.483**	**17/6**	1.413	2.613
(16/337)	SD		0.109	0.739		0.047	0.686		0.006	1.339		0.02	2.177		0.031	2.562		0.014	0.621		0.124	0.372		0.197	0.585
MV	Mean	3812/10	12.404	12.62	24472/10	4.031	5.019	30616/10	1.963	24.83										16/3	0.159	0.160	**14/3**	**0.158**	**0.158**
(10/40768)	SD		0.245	0.228		0.027	0.076		0.002	1.352											0.031	0.032		0.038	0.037
ELV	Mean	530/18	1.723	1.73	4132/18	1.141	1.215	7769/18	0.995	1.461										15/3	1.000	1.000	**8/3**	**0.900**	**0.900**
(18/16559)	SD		0.109	0.064		0.018	0.022		0.008	0.038											0.100	0.100		0.100	0.100
CA	Mean	425/21	40.384	40.956	1539/21	8.449	12.44	2774/21	5.327	19.14										29/5	6.201	6.320	**14/5**	**5.021**	**5.216**
(21/8192)	SD		3.115	4.637		0.351	1.148		0.06	2.807											0.455	0.489		0.422	0.483
AIL	Mean	1074/40	3.539	3.581	6581/40	2.508	2.995	8593/40	**1.381**	4.678										32/4	2.343	2.367	**15/4**	**1.955**	**2.000**
(40/13750)	SD		0.225	0.259		0.025	0.084		0.011	0.198											0.222	0.236		0.268	0.274
TIC	Mean	5802/85	0.015	0.05	6598/85	0.007	0.09	6732/85	**0.007**	0.098										43/7	0.027	0.028	**20/7**	**0.027**	**0.028**
(85/9822)	SD		0	0.001		0	0.001		0	0											0.000	0.002		0.000	0.002

As stated above, we have included WM as a reference on different fixed granularities. By contrast, we want to compare all the studied GFSs in order to determine whether or not the proposed approach with and without tuning is working properly in terms of the test error and the number of rules. We do not include the methods without fast error estimation here since we are proposing this mechanism based on the fact that the results are almost the same and in order to speed up the process with these kinds of complex problems. In any case, since their counterparts without fast error computation are also a good alternative, they will also be analyzed in the following subsections.

Focusing on the number of rules, it is clear that the proposed algorithms have the advantage since they consider feature selection. What is remarkable about the effect of the post-processing mechanism is that it is able to significantly reduce the number of rules while the system error is decreased.

In case of the test error, we adopt a statistical analysis. Since we will compare more than two algorithms together, we use non-parametric tests for multiple comparison. In order to perform a multiple comparison, it is necessary to check whether any of the results obtained by the algorithms present any inequality. In the case of finding some we can find out, by using a post-hoc test, which algorithms' partners' average results are dissimilar. We will use the results obtained in Tst., defining the control algorithm as the best performing algorithm (which obtains the lowest value of ranking, computed through a Friedman test [55]). In order to test whether significant differences exist among all the mean values we use Iman and Davenport's test [56]. Finally, we use Holm's [57] post-hoc test to compare the control algorithm with the remainder.

TABLE IV

RANKINGS THROUGH FRIEDMAN'S TEST ON TST APPLYING ONE OR BOTH STAGES OF THE PROPOSED ALGORITHM.

Only first stage: FSMOGFS^e		Complete algorithm: FSMOGFS^e+TUN^e	
Algorithm	Ranking on Tst.	Algorithm	Ranking on Tst.
GLD-WM	1.58	FSMOGFS^e+TUN^e	1.17
FSMOGFS^e	1.75	GLD-WM	2.08
GA-WM	3.0	GA-WM	3.08
GR-MF	3.67	GR-MF	3.67

TABLE V
HOLM'S POST-HOC TEST FOR THE STUDIED METHODS WITH $\alpha = 0.1$ ON Tst. APPLYING ONE OR BOTH STAGES OF THE PROPOSED ALGORITHM

Control Algorithm: GLD-WM						Control Algorithm: FSMOGFS^e+TUN^e					
i	Algorithm	z	p	α/i	Hypothesis	i	Algorithm	z	p	α/i	Hypothesis
3	GR-MF	4.74	7.72E-5	0.03	Rejected	3	GR-MF	4.74	2.10E-6	0.03	Rejected
2	GA-WM	3.64	0.007	0.05	Rejected	2	GA-WM	3.64	2.76E-4	0.05	Rejected
1	FSMOGFS^e	1.74	0.75	0.1	Accepted	1	GLD-WM	1.74	0.082	0.1	Rejected
Comparison						Comparison					
5	FSMOGFS^e vs. GR-MF	3.637	2.762E-4	0.02	Rejected	4	GLD-WM vs. GR-MF	3.004	0.003	0.025	Rejected
3	FSMOGFS^e vs. GA-WM	2.372	0.018	0.033	Rejected	3	GLD-WM vs. GA-WM	1.897	0.058	0.033	Accepted

Table IV shows the rankings of the different methods considered in this study when we only apply the first stage of our algorithm (first study on FSMOGFS^e, left part of the table) and when we apply both stages (second study on FSMOGFS^e+TUN^e, right part of the table). ImanDavenport's test tells us that significant differences exist among the observed results in all data-sets, with p-values (8.974E-7 and 1.622E-9) on Tst for both studies respectively. The best rankings are obtained by GLD-WM when only the first stage is considered and by FSMOGFS^e+TUN^e when the complete algorithm is considered.

We now apply Holm's test to compare the best ranking method with the remaining methods for each study, and to obtain the results on FSMOGFS^e VS. GR-MF and FSMOGFS^e VS. GA-WM (for the first study) and on GLD-WM vs. GR-MF and GLD-WM vs. GA-WM (for the second study). Table V presents these results. In this table, the algorithms are ordered with respect to the z-value obtained for each study.

In the case of only using the first stage of the algorithm (first study in the left part of the table), Holm's test rejects the hypothesis of equality with the rest of the methods ($p < \alpha/i$) but FSMOGFS^e in Tst., indicating that GLD-WM outperforms the previous approaches but not FSMOGFS^e. Further, when we check the statistical results with the same test on FSMOGFS^e VS. GR-MF and FSMOGFS^e VS. GA-WM in the bottom part of table V it is clear that FSMOGFS^e also outperforms GR-MF and GA-WM. From this analysis we can state that FSMOGFS^e outperforms the previous methods but GLD-WM in accuracy while, of course, it outperforms all of them in complexity and scalability.

In the case of using the complete algorithm (second study in the right part of the table), Holm's test rejects the hypothesis of equality with the rest of the methods in Tst. ($p < \alpha/i$). From this analysis we can state that FSMOGFS^e+TUN^e outperforms the previous methods in accuracy and, of course, in complexity and scalability. On the other hand, we can check in the bottom part of table V that GLD-WM outperforms GR-MF and is very close to outperforming GA-WM (the hypothesis is accepted because of the low quantity of datasets available in the regression framework, which makes it more difficult to assess the differences in this case).

Analyzing the results shown in Table III and the statistical evidence obtained we can highlight that:

- FSMOGFS^e+TUN^e obtained the best results in the test error with FSMOGFS^e being the key point in these results and TUN^e a good complementary stage. Even though FSMOGFS^e has been designed to obtain simpler models it is still preferable with respect to the previous approaches (obtaining not so great results in accuracy with respect to GLD-WM but simpler solutions based on strong equally distributed fuzzy partitions).
- The larger the granularities are, and therefore the more rules obtained, the more the overfitting increases. It is particularly clear in the most complex data sets when taking into account the results from WM (granularities from 3 to 7).
- Both single objective-based GFSs (GR-MF and GA-WM) overfit in most of the data sets, even though we selected the versions with the best test values to give them the possibility of competing in the best conditions. This is probably due to the low proportion of data with respect to the number of variables in these kinds of large scale data sets. However, this is not the case with GLD-WM (one of the state-of-the-art algorithms in terms of accuracy for linguistic fuzzy modeling), which presents very competitive results in both, training and test sets.

To sum up, the proposed method obtained very simple solutions in general without significant overfitting, i.e., highly correlated values in training and test in all the data sets before and after fine tuning of the MFs. Another interesting aspect of the algorithm is the number of variables it considers in the different data sets (a value of around 3-4 in most of them). In this sense, and taking into account that MPG6 is the same data set as MPG8 without the two variables removed by experts, it seems that the method is good for removing these variables, obtaining practically the same results in number of rules and accuracy. Then, the proposed approach seems good even in the case that variables without interesting additional information are initially included in the data sets. This property makes the method scalable for high-dimensional problems, for which it is still able to obtain good solutions from the point of view of the accuracy-interpretability trade-off.

C. Analysis of the Use of Partial Performance Computation

In this section we present the results of the different versions of the proposed technique in order to check the effects of the fast error estimation mechanism. These results in the first stage (only fast learning) and in the complete process (including post-processing) are shown in Table VI separately. The best results are shown in boldface for each of the parts.

Taking into account the results in this table, we can observe that very similar results were obtained in the number of rules and in both kinds of errors for both parts. In any

TABLE VI

AVERAGE RESULTS OF THE PROPOSED ALGORITHMS WITHOUT AND WITH FAST FITNESS COMPUTATION IN COMPLEXITY AND ACCURACY (TRAINING/TEST). RESULTS IN THIS TABLE (TRA./TST. AND SD) SHOULD BE MULTIPLIED BY 10^5, 10^{-5} OR 10^{-8} IN THE CASE OF BAS, ELV OR AIL RESPECTIVELY.

Data set	Measure	FSMOGFS			FSMOGFS^e			FSMOGFS+TUN			FSMOGFS^e+TUN^e		
NAME$_{(V/Size)}$		R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.	R/V	Tra.	Tst.
ELE$_{4/1056}$	Mean	10/2	16018	**16083**	**9/2**	16153	16338	9/2	8803	9842	**8/2**	9665	10548
	SD		314	1108		450	1162		739	1391		823	1150
MPG6$_{5/398}$	Mean	**38/3**	3.85	**4.82**	39/3	3.894	4.866	22/3	2.778	**4.548**	**20/3**	2.860	4.562
	SD		0.198	0.772		0.212	0.644		0.220	1.047		0.218	0.714
MPG8$_{7/398}$	Mean	**40/3**	3.827	**4.453**	43/3	3.885	4.695	24/3	2.725	**4.381**	**23/3**	2.757	4.747
	SD		0.274	1.049		0.312	1.168		0.294	0.909		0.342	1.235
ANA$_{7/4052}$	Mean	25/3	0.006	**0.006**	**23/3**	0.006	**0.006**	17/3	0.003	**0.003**	**10/3**	0.003	**0.003**
	SD		0	0.001		0.000	0.001		0.000	0.001		0.000	0.001
ABA$_{8/4177}$	Mean	17/3	2.682	**2.697**	**15/3**	2.670	2.708	10/3	2.393	**2.454**	**8/3**	2.445	2.509
	SD		0.149	0.204		0.139	0.216		0.092	0.163		0.114	0.184
STP$_{9/950}$	Mean	44/3	1.361	1.46	**43/3**	1.393	**1.456**	25/3	0.724	**0.892**	**23/3**	0.764	0.912
	SD		0.095	0.156		0.077	0.159		0.112	0.154		0.139	0.181
WIZ$_{9/1461}$	Mean	23/3	1.469	**1.567**	**17/2**	1.519	1.571	15/3	0.867	**1.011**	**10/2**	0.929	**1.011**
	SD		0.08	0.223		0.094	0.168		0.040	0.177		0.057	0.164
WAN$_{9/1609}$	Mean	12/2	1.81	**1.823**	**11/2**	1.897	2.151	11/2	1.313	**1.581**	**8/2**	1.441	1.635
	SD		0.06	0.143		0.208	0.916		0.174	0.580		0.178	0.582
FOR$_{12/517}$	Mean	**34/4**	1873	**2254**	35/3	1892	2449	33/3	1593	**2406**	**10/3**	1418	2628
	SD		497	2265		505	2146		570	2161		539	2108
MOR$_{15/1049}$	Mean	12/2	0.032	**0.033**	**11/2**	0.033	0.034	9/3	0.015	**0.018**	**7/2**	0.016	0.019
	SD		0.005	0.008		0.004	0.007		0.004	0.005		0.003	0.006
TRE$_{15/1049}$	Mean	17/3	0.046	**0.049**	**15/3**	0.046	0.052	11/3	0.030	**0.040**	**9/3**	0.034	0.044
	SD		0.004	0.01		0.005	0.010		0.004	0.012		0.003	0.015
BAS$_{16/337}$	Mean	33/6	1.673	2.575	**28/6**	1.706	**2.483**	21/6	1.305	2.699	**17/6**	1.413	**2.613**
	SD		0.103	0.521		0.124	0.372		0.172	0.620		0.197	0.585
MV$_{10/40768}$	Mean	20/3	0.531	0.531	**16/3**	0.159	**0.160**	16/3	0.159	0.160	**14/3**	0.158	**0.158**
	SD		0.06	0.062		0.031	0.032		0.031	0.032		0.038	0.037
ELV$_{18/16559}$	Mean	21/3	1.024	1.025	**15/3**	1.000	**1.000**	8/3	0.900	**0.900**	**8/3**	0.900	**0.900**
	SD		0.065	0.063		0.100	0.100		0.200	0.200		0.100	0.100
CA$_{21/8192}$	Mean	**28/5**	6.046	**6.135**	29/5	6.201	6.320	15/5	4.763	**5.063**	**14/5**	5.021	5.216
	SD		0.456	0.474		0.455	0.489		0.404	0.760		0.422	0.483
AIL$_{40/13750}$	Mean	33/4	2.305	**2.308**	**32/4**	2.343	2.367	20/4	1.864	**1.905**	**15/4**	1.955	2.000
	SD		0.21	0.206		0.222	0.236		0.221	0.233		0.268	0.274
TIC$_{85/9822}$	Mean	44/8	0.027	**0.027**	**43/7**	0.027	0.028	25/7	0.026	**0.027**	**20/7**	0.027	0.028
	SD		0	0.001		0.000	0.002		0.000	0.002		0.000	0.002

case, we can find some slight differences. FSMOGFS^e and FSMOGFS^e+TUN^e show a small increment in the test error with respect to their counterparts. Besides, they also show a small decrement in the number of rules, showing that the proposed mechanism helps to obtain models with a little bit less complexity (in all the 17 datasets for the last stage) and a little bit less accuracy (in 12 of the 17). In any event, by checking one by one the results in each part of the table and taking into account the differences shown in Table III for the different methods, we can consider that the mechanism is very useful in both stages, FSMOGFS^e and TUN^e, since it allows almost equivalent results with respect to the original counterparts to be obtained even though FSMOGFS^e+TUN^e also includes the slight differences derived from FSMOGFS^e.

D. Computational Times and Scalability of the Proposed Algorithm

With respect to scalability it is very important to analyze the running times of the different methods (these times were obtained in an Intel Core 2 Quad Q9550 2.83GHz, 8 GB RAM by using only one of the four cores). Table VII shows the running times of the fast WM algorithm (*Ad-Hoc* method) and its cropped version. Of course, WM is practically instantaneous in many of the datasets. However, it is very interesting to see the times this simple method can take in the case of MV, ELV, CA, AIL and TIC (more than one minute in most of the cases). Since each individual evaluation in the genetic approaches is based on running WM, it represents a time computing problem for the embedded algorithms. This is one of the main reasons why we propose the rule cropping strategy included in FSMOGFS, which is needed to ensure a maximum computing time for the WM module independently of the number of cases in any data set (only lineal with respect to the number of variables). In fact, it can be seen from the table that while the original version is mainly dependent on the number of examples, the cropped version is more dependent on the number of variables. The strong time reductions show why the cropping strategy is able to apply these kinds of techniques

TABLE VII
AVERAGE TIME OF A RUN OF WM AND ITS CROPPED VERSION — MINUTES AND SECONDS (M:S) - (S')

Method	MV	ELV	CA	AIL	TIC
WM(3)	00:47 - 0.0003	00:05 - 0.0002	00:18 - 0.0009	00:16 - 0.0007	01:55 - 0.0049
WM(5)	05:10 - 0.0003	00:39 - 0.0006	00:19 - 0.0009	01:46 - 0.0018	02:09 - 0.0062
WM(7)	06:12 - 0.0005	01:10 - 0.0006	00:35 - 0.0010	02:13 - 0.0019	02:10 - 0.0068

TABLE VIII
AVERAGE TIME OF A RUN OF THE DIFFERENT GFSS — HOURS, MINUTES AND SECONDS (H:M:S)

Method	ELE	MPG6	MPG8	ANA	ABA	STP	WIZ	WAN	FOR	MOR	TRE	BAS	MV	ELV	CA	AIL	TIC
GR-MF	09:30	08:01	23:43	2:58:27	3:26:09	32:50	58:22	1:19:12	17:40	41:06	40:47	13:29	-	-	-	-	-
GA-WM	07:27	07:49	10:45	1:46:41	2:02:47	34:43	43:34	1:16:59	21:03	40:29	39:52	16:46	-	-	-	-	-
GLD-WM	09:48	04:22	13:04	1:32:41	1:14:35	39:18	44:16	53:18	37:06	40:25	42:58	32:09	-	-	-	-	-
FSMOGFS	00:08	00:07	00:10	00:50	01:38	00:24	00:35	00:33	00:26	00:38	00:38	00:22	17:31	12:18	08:28	24:14	29:28
FSMOGFS+TUN	02:05	01:46	01:49	09:45	12:10	03:32	04:20	03:51	01:29	02:09	02:24	01:55	2:01:51	54:54	42:18	43:19	59:19
FSMOGFS^e	00:04	00:04	00:23	00:23	00:37	00:12	00:14	00:14	00:17	00:16	00:16	00:11	04:59	03:38	02:45	05:17	09:23
FSMOGFS^e+TUN^e	00:42	01:00	01:31	05:17	03:54	01:31	01:08	00:57	01:07	00:38	00:46	00:58	12:16	09:39	11:55	10:02	20:45

TABLE IX
AVERAGE NUMBER OF COMPLETE EVALUATIONS PER RUN OF THE PROPOSED APPROACH WITHOUT AND WITH PARTIAL EVALUATIONS (EVOLVING WITH ESTIMATED ERRORS)

Method*	ELE	MPG6	MPG8	ANA	ABA	STP	WIZ	WAN	FOR	MOR	TRE	BAS	MV	ELV	CA	AIL	TIC
FSMOGFS	4094	4868	6466	6432	7026	7816	7805	7784	9970	12374	12367	12947	8706	14608	16651	30588	32191
FSMOGFS+TUN	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000	100000
FSMOGFS^e	4085	4877	6441	6429	7028	7795	7786	7787	9979	12367	12317	12960	8711	14592	16682	30641	32287
FSMOGFS^e+TUN^e	30349	47398	40319	46799	38121	41673	33883	32268	64323	34051	35994	50598	31960	42736	43200	55383	67857

* (a maximum of 100000 individuals have been evaluated in all the fourth algorithms)

within an evolutionary process.

On the other hand, the running times of the studied GFSs are shown in Table VIII. In this case, except for the very complex data sets, the proposed method is able to obtain solutions taking only seconds or around 1 minute. The times for the remaining data sets are also very good, taking into account the kinds of problems they represent and the evolutionary nature of this algorithm. From these times we can highlight the following facts:

- No more than 30 minutes in the worst case of FSMOGFS and no more than 2 hours and 2 minutes in the worst case of FSMOGFS+TUN. This last is obtained in MV with 40,768 examples, thus showing a significant increase that is dependent on the large number of examples due to the additional time required by the second stage for fine tuning.
- No more than 10 minutes in the worst case of FSMOGFS^e and no more than 21 minutes in the worst case of FSMOGFS^e+TUN^e. As fast error estimation is considered, the large quantity of data of the MV problem does not affect the overall two stage approach, solving this problem in 12 minutes and 16 seconds, which in this case represents 89.83% with respect to not using the mechanism. In fact, FSMOGFS^e+TUN^e needs less time than the initial learning algorithm without tuning, FSMOGFS, in the most complex datasets (MV, ELV, AIL and TIC).

In order to show the real reason for the great time savings, Table IX shows the average number of evaluations per run in the different versions of the proposed approach. For the learning stage we will compute the number of evaluations by adding 1 per solution evaluated in all cases FSMOGFS and FSMOGFS^e. In this way, in the case of using post-processing as a second stage, this will proceed from the number of evaluations that the learning process (first stage) consumed. In the case of FSMOGFS^e+TUN^e, in order to show how the fast error computation affects the times, we consider in the table the total number of examples used throughout the process (until reaching the stopping criterion) divided by the total number of training examples to count part of the second stage, TUN^e. This is only to show the method's behavior since for the stopping criterion we always consider 100,000 trials, i.e., evaluated individuals independently of the kind of evaluation (partial or complete).

E. Analysis of the Pareto fronts: Average solutions

This section analyzes the performance of the proposed algorithm in the remaining solutions that it obtains in the Pareto fronts. To do that, we plot the average Pareto fronts

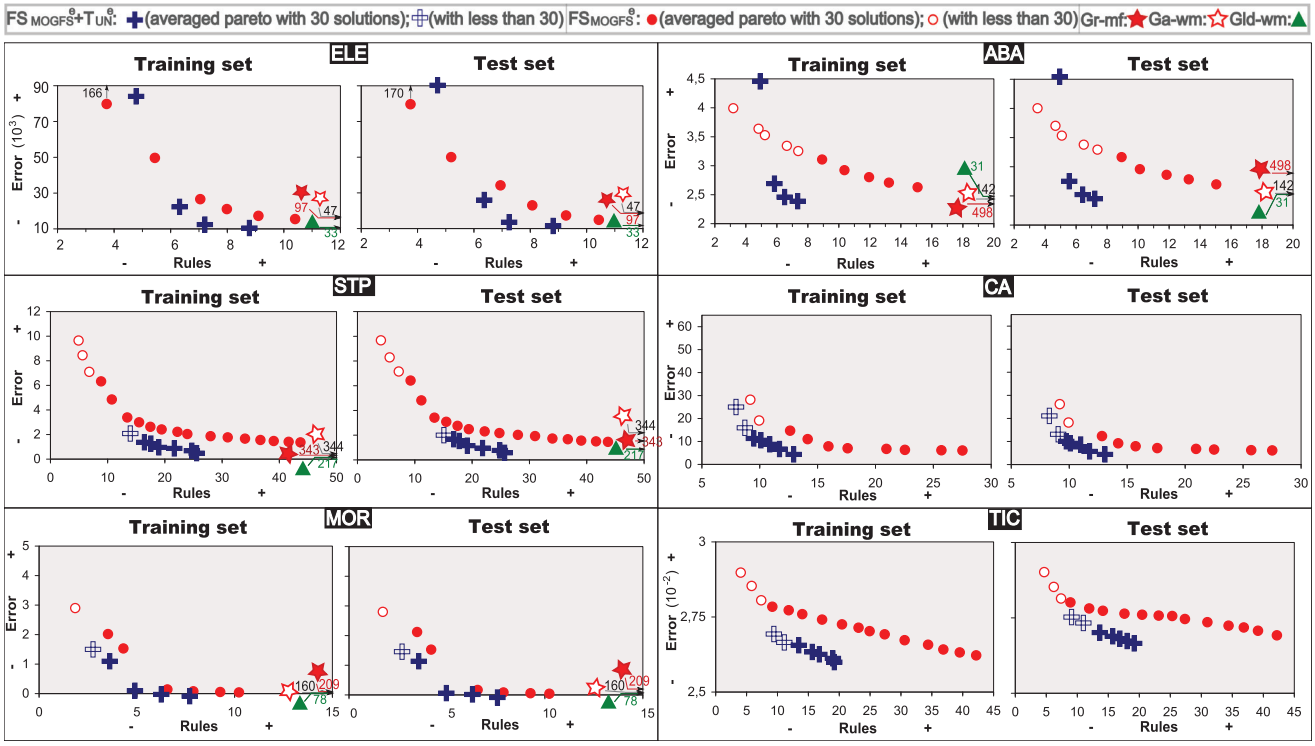

Fig. 4. Average Pareto fronts obtained by FSMOGFS^e and FSMOGFS^e+TUN^e and average solutions obtained by GR-MF, GA-WM and GLD-WM on the different data sets.

composed by the average values of the obtained solutions in each of the thirty Pareto fronts. The first average solution that we want to plot is the one shown in the previous sections, i.e., the average of the most accurate solutions obtained in each of the thirty Pareto fronts. The second average solution is obtained in the same way but considering the second most accurate solutions in each of the thirty Pareto fronts. This process is repeated until no more solutions remain in any of the thirty Pareto fronts. We should remark that there will be a moment at which any of the Pareto fronts will have no more solutions to compute the average of 30 solutions, i.e., the $i-th$ most accurate solution is not available in all the Pareto fronts. In this case, the $i-th$ average solution is calculated considering the $i-th$ solutions of those Pareto fronts in which these solutions are available.

We can find then two different parts in the average Pareto fronts, *the statistically trusted zone* (the one ensuring that there will be those solutions in all the Pareto fronts) and *the non statistically trusted zone* (the one showing that some other solutions are available in some of the thirty runs performed). Thus, we can analyze the correlation and differences between the different solutions obtained by the FS-MOGFS algorithm in terms of the Pareto fronts obtained with the average values, which provide more reliable information than the solutions obtained in a simple run. This method represents an extension of the idea of analyzing the most accurate solutions in the Pareto fronts (first, second, ...) presented in [7], a post-processing mechanism where the search is focused on the most accurate solutions only. The average Pareto fronts represent what a user should statistically expect when he is choosing the $i-th$ most accurate solution obtained from FS-MOGFS.

The average Pareto fronts obtained in a representative set of the studied data sets are shown in Figure 4. This figure also includes the average solutions obtained by the two single objective based GFSs considered for comparisons. We can see that in most of the data sets, many solutions in the trusted zone present better results in test than those obtained by the single objective (accuracy oriented) based approaches.

A really important characteristic of the proposed method is the very high correlation among the values in training and the values in test. For each of the data sets considered we can appreciate that the average solutions in test are a mimic of the solutions obtained in training. The main interest of this characteristic is that it makes the selection of any solution of the obtained Pareto fronts by a standard user very easy. That is, by taking into account the final number of rules/variables and the training error (test errors are not available at the selection moment), any solution could be selected depending on the necessities of the final user expecting similar behavior in test, i.e., similar behavior when the model is applied in real life to solve a problem. This is not the typical situation since usually the solutions obtained in the Pareto front present not totally correlated errors in training and test, which makes it very difficult to select a proper solution with the desired generalizability.

This means that there are very simple solutions that could be selected without losing a high degree of accuracy. In any case, as mentioned before, a user could select any solution in

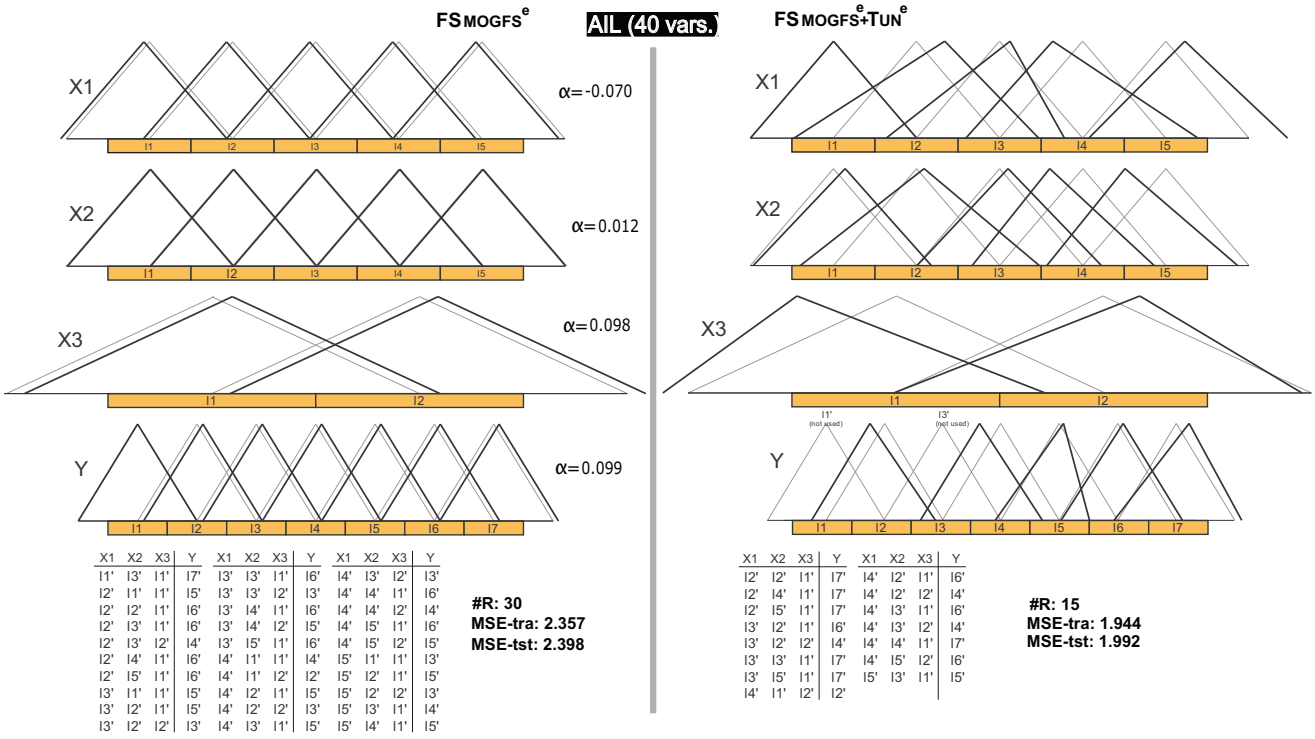

Fig. 5. Pareto fronts obtained by FSMOGFS^e and FSMOGFS^e+TUN^e on the data set Ailerons.

the Pareto front if the training error is acceptable to solve the problem. Moreover, we can see that there is no overfitting in any of the different parts of the obtained Pareto fronts.

The said behavior can also be checked for the remaining datasets in a figure with the plots of the average Pareto fronts together with the global result excel files on the Web page associated with the paper at (`http://sci2s.ugr.es/FS-MOGFS/`). In Figure 5, we show two representative KBs (the results of a single trial) on the dataset Ailerons. Additionally, we have depicted the KB of the most accurate solution from the first data partition and seed in all the datasets. These graphics have been included in a zip file on the Webpage associated with the paper together with a brief analysis of some KB examples as complementary material to the paper.

VI. CONCLUSIONS

In this work, we have proposed an effective MOEA for the learning of linguistic KBs in high-dimensional regression problems, namely FSMOGFS. This method, based on embedded DB learning, allows a slight uniform displacement of the linguistic fuzzy partitions and includes some effective mechanisms in order to enable the derivation of simple and accurate linguistic FRBSs in problems that are difficult to solve with standard evolutionary methods. A post-processing stage performing a rule selection and a tuning of the MFs has been also applied for further refinement of the simple learned solutions. This helps to significantly improve the performance of the simple global structure (initially based on strong fuzzy partitions) while the complexity is significantly decreased.

In order to also take into account datasets with a large amount of data, large scale problems, we have also proposed a mechanism to avoid using a big percentage of the examples for error computation, estimating it from a reduced subset of the examples, but maintaining the performance and general behavior of the methods. This mechanism has been defined in general for *Evolving with Estimated Errors* for use with any kind of Elitist-Based Evolutionary Algorithm, either single objective or multiobjective elitist-based ones. By doing so we can also apply a post-processing stage to further refine the learned solutions. We have included this new error estimation procedure in both the learning and the post-processing stages.

The results obtained in 17 data sets of different complexities confirm the effectiveness of the proposed method, particularly in terms of the simplicity and generalizability of the obtained models but also in terms of dimensionality and scalability (particularly when using the fast error estimation mechanism). We have shown that the scalability of both FSMOGFS^e and FSMOGFS^e+TUN^e is a key characteristic of these approaches, which are able to solve problems with more than 40,000 cases or more than 80 variables in a very fast way. Additionally, FSMOGFS^e+TUN^e is able to obtain promising linguistic models, avoiding overfitting and keeping uniformly distributed strong fuzzy partitions in its first stage and refined ones in its second stage, with very competitive results in terms of accuracy.

The obtained KBs are the result of the application of the well-known WM algorithm, which, based on covering criteria, provides highly meaningful rules at each region of the modeled surface. Further, because of this and because

FSMOGFS^e considers uniformly distributed fuzzy partitions, the models obtained by this method are able to be further post-processed (approximate tuning, linear consequents learning, etc...) becoming a starting point for these kinds of techniques.

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Rafael Alcalá received the M.Sc. degree in Computer Science in 1998 and the Ph.D. degree in Computer Science in 2003, both from the University of Granada, Spain. From 1998 to 2003, he was with Department of Computer Science, University of Jaén. He is currently an Associate Professor in the Department of Computer Science and Artificial Intelligence at the University of Granada, where he is a Member of the Soft Computing and Intelligent Information Systems Research Group.

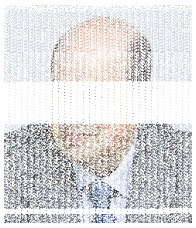
He has published over 75 papers in international journals, book chapters and conferences. He has worked on several research projects supported by the Spanish government and the European Union. As edited activities, he has co-edited the IEEE Transactions on Fuzzy Systems Special Issue on "*Genetic Fuzzy Systems: What's next*", the Evolutionary Intelligence Special Issue on "*Genetic Fuzzy Systems: New Advances*" and the Soft Computing Special Issue on "*Evolutionary Fuzzy Systems*". He currently serves as member of the editorial/reviewer board of the journals: International Journal of Computational Intelligence Research, Journal of Advanced Research in Fuzzy and Uncertain Systems, Journal of Universal Computer Science and Applied Intelligence.

He is a member of the Fuzzy Systems Technical Committee (FSTC) at the IEEE Computational Intelligence Society (CIS), and president of the "Genetic Fuzzy Systems" Task Force from January 2009. He was Program Co-Chair at GEFS 2010, General Co-Chair at GEFS 2011 and Area Co-Chair at FUZZ-IEEE 2011.

His current research interests include multi-objective genetic algorithms and genetic fuzzy systems, particularly the learning/tuning of fuzzy systems for modeling and control with a good trade-off between accuracy and interpretability, as well as fuzzy association rules.

María José Gacto received the M.Sc. degree in Computer Science in 1999 and the Ph.D. degree in Computer Science in 2010, both from the University of Granada, Spain. She is a Member of the Intelligent Systems and Data Mining Research Group in the Department of Computer Science at the University of Jaén.

She has over 30 international publications. She has worked on several research projects supported by the Spanish government and the European Union. Her research interests include, multi-objective genetic algorithms and genetic fuzzy systems, particularly the learning/tuning of fuzzy systems for modeling and control with a good trade-off between accuracy and interpretability.



Francisco Herrera received the M.Sc. degree in Mathematics in 1988 and the Ph.D. degree in Mathematics in 1991, both from the University of Granada, Spain.

He is currently a Professor in the Department of Computer Science and Artificial Intelligence at the University of Granada. He has published more than 200 papers in international journals. He is coauthor of the book "*Genetic Fuzzy Systems: Evolutionary Tuning and Learning of Fuzzy Knowledge Bases*" (World Scientific, 2001).

As edited activities, he has co-edited five international books and co-edited twenty one special issues in international journals on different Soft Computing topics. He currently acts as Editor in Chief of the international journal Progress in Artificial Ingelligence (Springer) and serves as area editor of the Journal Soft Computing (area of evolutionary and bioinspired algorithms). He acts as associated editor of the journals: IEEE Transactions on Fuzzy Systems, Information Sciences, Advances in Fuzzy Systems, and International Journal of Applied Metaheuristics Computing; and he serves as member of several journal editorial boards, among others: Fuzzy Sets and Systems, Applied Intelligence, Knowledge and Information Systems, Information Fusion, Evolutionary Intelligence, International Journal of Hybrid Intelligent Systems, Memetic Computation, Swarm and Evolutionary Computation.

He received the following honors and awards: ECCAI Fellow 2009, 2010 Spanish National Award on Computer Science ARITMEL to the "Spanish Engineer on Computer Science", International Cajastur "Mamdani" Prize for Soft Computing (Fourth Edition, 2010).

His current research interests include computing with words and decision making, bibliometrics, data mining, data preparation, instance selection, fuzzy rule based systems, genetic fuzzy systems, knowledge extraction based on evolutionary algorithms, memetic and genetic algorithms.