

Hierarchical-interpolative Fuzzy System Construction by Genetic and Bacterial Programming Algorithms

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Abstract—In this paper a method is proposed for constructing hierarchical-interpolative fuzzy rule bases in order to model black box systems defined by input-output pairs, i.e. to solve supervised machine learning problems. The resulting hierarchical rule base is the knowledge base, which is constructed by using evolutionary techniques, namely, Genetic and Bacterial Programming Algorithms. Applying hierarchical-interpolative fuzzy rule bases is an advanced way of reducing the complexity of the knowledge base, whereas evolutionary methods ensure a relatively efficient learning process. This is the reason of the investigation of this combination.

Index Terms—Hierarchical-interpolative fuzzy systems, Genetic Programming, Bacterial Programming, supervised machine learning

I. INTRODUCTION

This paper proposes a method for constructing hierarchical-interpolative fuzzy rules in order to model black box systems based on input-output pairs, i.e. to solve a certain type of supervised machine learning problem. The resulting hierarchical rule base is constructed by using evolutionary techniques, namely, Genetic and Bacterial Programming Algorithms.

There are two key elements in machine learning systems: the learning architecture including the structure of the knowledge base and the learning algorithm applied during the learning process, i.e. the technique that optimizes the knowledge base according to the particular problem. Hence, in order to establish a learning system having favorable properties (low knowledge complexity, high accuracy, fast learning process, etc.) these elements must be chosen so that they outperform other alternatives of knowledge bases and learning algorithms.

For interpretability purposes, i.e. after the learning process to have a quasi-interpretable knowledge base, this paper considers only knowledge bases realized in the form of fuzzy rule bases.

The classical approaches of fuzzy control deal with dense rule bases where the universe of discourse is fully covered by the antecedent fuzzy sets of the rule base in each dimension, thus for every input there is at least one activated rule. The main problem is the high computational complexity of these traditional approaches.

If a fuzzy model contains k variables and maximum T linguistic terms in each dimension, the order of the number

of necessary rules is $\mathcal{O}(T^k)$. This expression can be decreased either by decreasing T , or k , or both. Of course, these are very different in terms of the efficiency of the complexity reduction. The first way (decreasing T) leads to sparse rule bases and rule interpolation, see e.g. [1], [2]. The second, more effective way (decreasing k) aims at reducing the dimension of the sub-rule bases by using meta-levels or hierarchical fuzzy rule bases (e.g. [3], [4]). The combination of these two methods leads to decreasing of both T and k , and was introduced in [5].

The scope of this paper focuses on this combination of complexity reduction approaches, namely, the application of hierarchical-interpolative fuzzy rule bases as previous papers [6], [7], [8] considered the other ways of complexity reduction.

Nature inspired evolutionary optimization algorithms are suitable for the global optimization of even non-linear, high-dimensional, multi-modal, and non-continuous problems. The original Genetic Algorithm (GA) was developed by Holland [9] and was based on the process of the evolution of biological organisms. Recognized as a powerful global search technique, genetic algorithms have been applied to a wide variety of problems. They exhibit a remarkable balance between search domain exploration and exploitation [10]. On one hand, every part of the domain is searched and on the other hand, the search effort is concentrated around the best solutions and their neighborhood, producing even better solutions. Bacterial Evolutionary Algorithm (BEA) [11] inspired by the microbial evolution phenomenon is similar, but based on results in the literature appearing more effective technique than GA (e.g. [12], [13], [6]). Approaches like Genetic Programming (GProg) [14] and Bacterial Programming (BProg) [15], present an alternative to the former algorithms. These techniques use the same operators as GA and BEA, respectively, though they require expression trees for gene representation, which could model hierarchical fuzzy rule bases, for example.

Evolutionary algorithms are useful tools for identification problems, they can help with finding a good compromise between the accuracy and the complexity of the model. In case of hierarchical but non-interpolative (i.e. dense) rule bases, genetic and bacterial approaches were successfully applied for fuzzy rule based learning during our previous work [7], [8]. This is the reason why Genetic and Bacterial Programming

is applied in our present work as the learning approaches that optimize the knowledge base (instead of using e.g. fuzzy clustering for this purpose like proposed in [16]).

Since so far no method has been invented to obtain the main properties (efficiency, accuracy, etc.) of such complex systems exactly, they can be figured out mostly by simulation. Therefore, in order to discover the capabilities of the established hierarchical-interpolative fuzzy rule based learning systems, simulation runs were carried out.

The next section gives a brief overview of the algorithms and techniques used. The third section proposes a method for constructing and optimizing hierarchical-interpolative fuzzy rule bases by Genetic and Bacterial Programming approaches. The simulation results and the observed behavior will be discussed in the fourth section. Finally, in the last section we will summarize our work and draw some conclusions.

II. OVERVIEW OF THE TECHNIQUES AND ALGORITHMS

In order to carry out this investigation, it is necessary to have familiarity with some theoretical fields including the concept of interpolative, hierarchical and hierarchical-interpolative fuzzy rule bases, structure constructing evolutionary optimization techniques (GProg, BProg) and machine learning.

The following subsections aim at giving a brief overview of some important points of these theoretical aspects, which will be repeatedly referred to later in the paper.

A. Interpolative fuzzy systems

In case of classical inference techniques (e.g. Mamdani-[17] or Takagi-Sugeno-inference [18]) in order to obtain any conclusion for an arbitrary observation, the fuzzy rules must cover the whole input space in the following sense. For every observation ($x \in X$) there must be at least one rule (in the form ' R_i : if x_1 is A_{i1} and x_2 is A_{i2} and ... and x_k is A_{ik} then y is B_i ') in the rule base ($R = \{R_i\}$) so that $\bigwedge_{j=1}^k A_{ij}(x) \geq \alpha > 0$, i.e. the rule base must be α -dense.

Interpolative fuzzy systems calculate the conclusion by using interpolation, hence the input space need only be partially covered by the rules in the sense that there can be observations ($x \in X$) for which there is no rule in the rule base so that $\bigwedge_{j=1}^k A_{ij}(x) \geq \alpha > 0$, i.e. the rule base can be *sparse*.

The interpolative inference technique considered in this paper is the stabilized KH-interpolation [19]. This method is based on a certain interpolation of a family of distances between fuzzy sets in the rules and in the observation. Unlike the original linear KH-interpolation (cf. [1], [2]), it does not consider only the two closest surrounding rules, but it takes all the rules and computes the conclusion based on the consequent parts weighted by the distances. Furthermore, it contains an exponent determined by the number of input dimensions in the denominator in order to stabilize the interpolation function.

B. Hierarchical fuzzy rule based systems

The basic idea of using hierarchical fuzzy rule bases is the following ([3], [4]). Often the multi-dimensional input space $X = X_1 \times X_2 \times \dots \times X_m$ can be decomposed, so that

some of its components, e.g. $Z_0 = X_1 \times X_2 \times \dots \times X_p$ determine a subspace of X ($p < m$), so that in Z_0 a partition $\Pi = D_1, D_2, \dots, D_n$ can be determined: $\bigcup_{i=1}^n D_i = Z_0$.

In each element of Π , i.e. in each D_i , a sub-rule base R_i can be constructed with local validity. In the worst case, each sub-rule base refers to exactly $X/Z_0 = X_{p+1} \times \dots \times X_m$. The complexity of the whole rule base $\mathcal{O}(T^m)$ is not decreased, as the size of R_0 is $\mathcal{O}(T^p)$, and each R_i , $i > 0$, is of order $\mathcal{O}(T^{m-p})$, $\mathcal{O}(T^p) \times \mathcal{O}(T^{m-p}) = \mathcal{O}(T^m)$.

A way to decrease the complexity would be finding in each D_i a proper subset of $X_{p+1} \times \dots \times X_m$, so that each R_i contains only less than $m-p$ input variables. In some concrete applications in each D_i a proper subset of $X_{p+1}, \dots, X_m$ can be found so that each R_i contains only less than $m-p$ input variables, and the rule base has the structure shown in Table I., where $z_i \in Z_i$, $Z_0 \times Z_i$ being a proper subspace of X for $i = 1, \dots, n$.

TABLE I
HIERARCHICAL RULE BASE

R_0 :	If z_0 is D_1 then use R_1 If z_0 is D_2 then use R_2 ... If z_0 is D_n then use R_n
R_1 :	If z_1 is A_{11} then y is B_{11} If z_1 is A_{12} then y is B_{12} ... If z_1 is A_{1r_1} then y is B_{1r_1}
R_2 :	If z_2 is A_{21} then y is B_{21} If z_2 is A_{22} then y is B_{22} ... If z_2 is A_{2r_2} then y is B_{2r_2}
...	
R_n :	If z_n is A_{n1} then y is B_{n1} If z_n is A_{n2} then y is B_{n2} ... If z_n is A_{nr_n} then y is B_{nr_n}

If the number of variables in Z_i is $k_i < m-p$ and $\max_{i=1}^n k_i = K < m-p$, then the resulting complexity will be $\mathcal{O}(T^{p+K}) < \mathcal{O}(T^m)$, so the structured rule base might lead to a reduction of the complexity.

The task of finding such a partition is often difficult, if not impossible, (sometimes such a partition does not even exist), however there are cases when, locally, some variables unambiguously dominate the behavior of the system, and consequently the omission of the other variables allows an acceptably accurate approximation.

C. Hierarchical-interpolative fuzzy systems

Based on [20], [21] and [22] the reduction of both the maximum number of the linguistic terms (T), and the number of variables (k) can be performed as follows when applying stabilized KH-interpolation. Let us assume that the observation on X is A^* and its projections are $A_0^* = A^*/Z_0$, $A_1^* = A^*/Z_1$,

$A_2^* = A^*/Z_2, \dots, A_n^* = A^*/Z_n$. Using stabilized KH-interpolation, the sub-conclusions, obtained from the sub-rule bases $R_1, R_2, \dots, R_n$ are $^{SKH}B^{(1)*}, ^{SKH}B^{(2)*}, \dots, ^{SKH}B^{(n)*}$, respectively. (The superscript shows the reference to the rule bases.) Then, by substituting the sub-conclusions into the meta-rule base we obtain $^{SKH}B_k^*$, the conclusion. The steps of the algorithm are as follows:

- 1) determine the projection A_0^* of the observation A^* to the subspace of the fuzzy partition Π
- 2) determine the distances between A_0^* and the meta-rule antecedents
- 3) for each R_i determine A_i^* the projection of A^* to Z_i and determine the distances between A_i^* and the rule antecedents
- 4) determine the sub-conclusions for each sub-rule base R_i by applying stabilized KH-interpolation
- 5) using the sub-conclusions from step 4, compute the final conclusion $^{SKH}B^*$ by applying stabilized KH-interpolation again

Fig. 1 shows a simple example of the algorithm. In step 3 and 4, in each sub-rule base, a different inference engine can be applied, e.g., if the sub-rule base itself is dense, the Mamdani-algorithm (or one of its variations), or in any case one of the interpolation algorithms can be used.

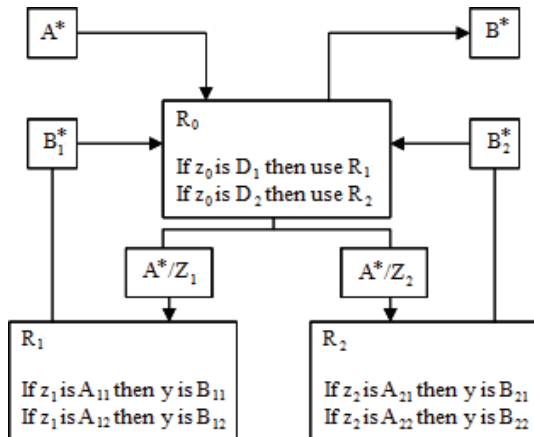


Fig. 1. Interpolation in a hierarchical-interpolative fuzzy system

D. Structure building evolutionary techniques

1) *Genetic Programming*: There are various optimization algorithms, which were inspired by processes in the nature. The advantage of these algorithms is their ability to solve and quasi-optimize problems with non-linear, high-dimensional, multimodal, and discontinuous character. These processes can easily be applied in optimization problems where one individual corresponds to one possible solution of the problem. In the original Genetic Algorithm (GA) [9] an individual is represented by a sequence of numbers, for example a sequence of bits. This sequence is called chromosome. GA uses three operators: selection, crossover, and mutation. A more recent approach is Genetic Programming (GProg) [14],

which uses the same operators as GA, though the individuals are represented by the so called expression tree. This tree is composed of the non-terminal nodes (also called as inner or function nodes) and the terminal nodes (leaves).

The evolutionary process involves the following steps:

- a) creation of an initial population
- b) evaluation of the candidates
- c) application of genetic operators:
 - **selection**: pairs of trees are selected based on their fitness for reproduction
 - **crossover**: nodes in the trees are selected at random and the sub-trees belonging to the selected nodes are exchanged producing a pair of offspring trees
 - **mutation**: this is performed by either replacing a node selected at random by a sub-tree generated randomly or by changing the inner properties of the node
 - **replacement**: substituting the created offsprings to the population
- d) test of the termination criteria (e.g. reaching the maximum number of generations, or the time limit) and if any of the termination criteria is achieved, the algorithm stops, otherwise it continues from step b)

The cycle of evolution is summarized in Fig. 2.

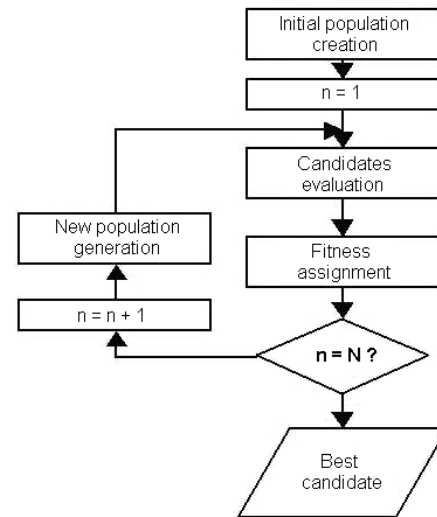


Fig. 2. Flowchart of Genetic Programming

2) *Bacterial Programming*: An evolutionary technique being slightly different compared to GA is called Bacterial Evolutionary Algorithm (BEA). This algorithm was introduced by Nawa and Furuhashi in [11]. The first version of this algorithm was called Pseudo-Bacterial Genetic Algorithm (PBGA) [23] which proposed a modified mutation operator called bacterial mutation, based on the natural phenomenon of microbial evolution. Bacterial Evolutionary Algorithm introduced a new operator called gene transfer operator. While PBGA incorporates

bacterial mutation and crossover operator, the BEA substitutes the classical crossover with the gene transfer operation. Both of these new operators were inspired by bacterial evolution. Bacteria can transfer genes to other bacteria. The bacterial mutation performs local optimization whilst the gene transfer allows the bacteria to directly transfer information to the other individuals in the population.

Based on these bacterial operations, but using the tree structures similar to the ones in the Genetic Programming, a new technique was proposed, named Bacterial Programming (BProg) [15].

The evolutionary process of BProg involves the following steps:

- a) creation of an initial population
- b) application of bacterial operators:
 - **bacterial mutation**: this is performed by either replacing a node selected at random by a sub-tree generated randomly or by changing the inner properties of the node
 - **gene transfer**: nodes in the trees are selected at random in the selected superior individual and the sub-trees belonging to the selected nodes are copied to the selected inferior individual
- c) test of the termination criteria (e.g. reaching the maximum number of generations, or the time limit) and if any of the termination criteria is achieved, the algorithm stops, otherwise it continues from step b)

The cycle of evolution is summarized in Fig. 3.

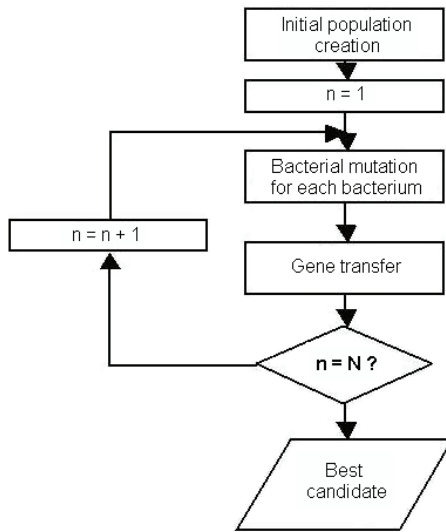


Fig. 3. Flowchart of Bacterial Programming

E. Supervised machine learning

Supervised machine learning [24] means a process where parameters of a 'model' are being adjusted so that its behavior becomes similar to the behavior of the 'system', which is to

be modeled. Since the behavior can be characterized by input-output pairs, the aim of the learning process can be formulated so that the model should give similar outputs for the input as the original system does.

The model can be, for example, a simple function (e.g. a polynomial function), where the parameters are the coefficients, or it can be a neural network, where the parameters are the weights, or it can be a hierarchical fuzzy rule base together with an inference engine [25]. In this case the parameters determine the structure of the rule base as well as the membership functions of the rules in the rule base. In our work we applied a hierarchical fuzzy rule base containing trapezoidal membership functions.

If the system is denoted by $\phi(x)$ and the model is denoted by $f(x, p)$, where $x \in X$ is the input vector and p is the adjustable parameter vector, the previous requirement can be expressed as follows:

$$\forall x \in X: \phi(x) \approx f(x, p) \quad (1)$$

In a supervised case the learning happens using a set of training samples (input-output pairs). If the number of samples is m , the input in the i^{th} sample is x_i , the desired output is $d_i = \phi(x_i)$ and the output of the model is $y_i = f(x_i, p)$, the following formula can be used:

$$\forall i \in [1, m]: d_i \approx y_i \quad (2)$$

The error (ε) shows how similar the model to the system is (see Fig. 4). It is the function of the parameter vector, so it can be denoted by $\varepsilon(p)$. A widely applied definition for the error is the Mean Squared Error (MSE):

$$\varepsilon(p) = \frac{\sum_{i=1}^m (d_i - y_i)^2}{m} \quad (3)$$

Obviously, the task is to minimize this $\varepsilon(p)$ function. It can be done by numerical optimization algorithms.

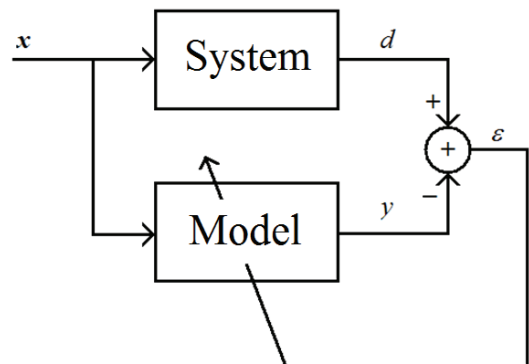


Fig. 4. Supervised machine learning

This way machine learning problems can be traced back to optimization problems.

III. THE ENCODING METHOD

This section describes the method how the hierarchical fuzzy rule bases are represented by the individuals, i.e. how the rule bases are encoded.

The non-terminal (inner) nodes hold the antecedent parts of one or more rules. In case of each non-terminal node the number of considered input dimensions (number of *decision variables*) is a random value, whose maximum can be parameterized. A decision variable can only be such a dimension, which has not been decision variable in the ancestors of the current node. (This way the size of the expression tree becomes limited.) The consequent part of a rule is a child node of the particular node, which can be either a non-terminal or a terminal node. Thus, the number of rules a non-terminal node holds is determined by the number of the children of the particular node. The number of children of the nodes is a random value, whose maximum, i.e. the maximum number of rules belonging to a node, can be parameterized.

Each terminal node (leaf) holds one single fuzzy set, as a conclusion (output) set.

There can be non-terminal nodes as well as terminal nodes on the same level, hence meta-rules and rules can appear together (see Fig. 5).

Since a decision variable cannot be such a dimension, which has already been a decision variable in any ancestor of the current node, in case of crossover in GProg the transferred nodes change their decision variables so that the new decision variables be such dimensions, which have not been decision variables in the ancestors. The same solution of this technical difficulty is applied in gene transfer in BProg, too.

In case of mutation in GProg and bacterial mutation in BProg there are no technical difficulties: only new sub-trees or nodes must be generated with the consideration of the above described encoding rules.

The applied inference algorithm is a simple extension of one of the first interpolation techniques, namely the stabilized KH-interpolation method [19]. This extension is necessary, because there are child nodes in the consequent parts of the rules. Since the conclusions of sub-trees are fuzzy sets (specially, the contents of terminal nodes can also be considered as conclusions), they can be substituted into the consequent parts of the rules of the parent nodes. This can be performed recursively.

IV. SIMULATION RESULTS

Simulation runs were carried out in order to discover the important properties of the established learning systems (speed of learning, accuracy of the resultant knowledge base, etc.).

In our work a six dimensional learning problem was applied that was also used in [11] to evaluate the performance of Bacterial Evolutionary Algorithm. This problem is to approximate the following function:

$$f_{6dim} = x_1 + \sqrt{x_2} + x_3x_4 + 2e^{2(x_5-x_6)} \quad (4)$$

$$x_1, x_2 \in [1, 5], \quad x_3 \in [0, 4], \quad x_4 \in [0, 0.6],$$

$$x_5 \in [0, 1], \quad x_6 \in [0, 1.2].$$

In the simulations the parameters had the following values, because after a number of test runs these values seemed to be suitable. The number of individuals in a generation was 8 in both Genetic and Bacterial Programming algorithms. The maximum number of rules belonging to a node, i.e. the maximum number of children of a node, was set to 4 and the maximum number of decision variables in a node was 3. In case of genetic techniques the selection rate was 0.3 and the mutation rate was 0.1, in case of bacterial techniques the number of clones was 5 and 4 gene transfers were carried out in each generation. The genetic methods applied elitist strategy.

The numbers of training samples were 200 in the learning processes.

Two type of simulation were carried out, which differed in the termination criteria. The runs applying the first criterion stopped after reaching the maximum number of generations, which was 2000 generations, whereas the other optimization processes stopped after reaching the time limit, which was 2000 seconds.

At the end of each optimization processes the accuracy of the resultant rule bases was measured by using three error definitions:

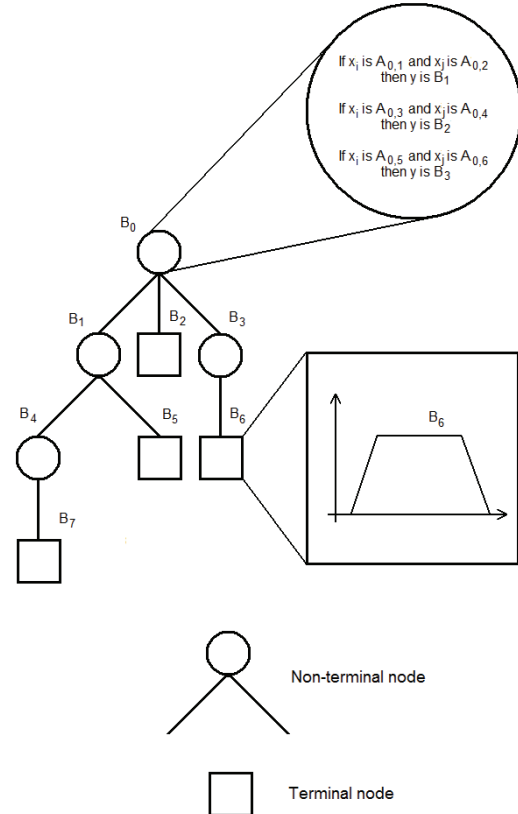


Fig. 5. Tree of a hierarchical rule base (rules and meta-rules appear together on the same levels)

- *Mean Squared Error (MSE)*:

$$\frac{1}{m} \sum_{i=1}^m (d_i - y_i)^2 \quad (5)$$

- *Mean Squared Relative Error (MSRE)*:

$$\frac{1}{m} \sum_{i=1}^m \frac{(d_i - y_i)^2}{y_i^2} \quad (6)$$

- *Mean Relative Error Percentage (MREP)*:

$$\frac{100}{m} \sum_{i=1}^m \left| \frac{d_i - y_i}{y_i} \right| \quad (7)$$

The MSE, MSRE, and MREP values were calculated on the test samples.

The computation time and the number of executed generations were also observed.

In case of both algorithms for each parameterization 10 runs were carried out. Then we took the mean of the obtained values.

During the runs the fitness values of the best individuals were monitored. These fitness values were calculated based on the MSE values (measured on the training samples) as follows:

$$F = \frac{10}{\text{MSE} + 1} = \frac{10m}{\sum_{i=1}^m (d_i - y_i)^2 + m} \quad (8)$$

The means of the fitness values of the best individuals during the runs were presented in Fig. 6 and Fig. 7 to get a better overview. The horizontal axes show the executed number of generations and the elapsed computation time in seconds, respectively, and the vertical axes show the fitness values of the best individuals at the current time.

In the figures the dashed lines show the results of GProg and the solid lines present the graph of BProg. For comparing purposes the results obtained in case of non-interpolative (dense) hierarchical rule bases (which can be found in our previous work [7]) are also presented in the figures (drawn with dotted and dotted-dashed lines).

The results of the simulation runs are presented in Table II and Table III. In Table II ‘Comp. time’ denotes the mean of the computation time (in seconds) the optimization processes required and in Table III ‘No. of gen.’ denotes the mean of the number of executed generations. In both tables ‘No. of rules’ denotes the mean of the number of rules in the resulting hierarchical rule bases (including meta-rules).

Again, for comparing purposes the results obtained in case of non-interpolative hierarchical rule bases are also presented in the tables (in columns named ‘Hierarchical’).

Observing the results given by the hierarchical-interpolative systems it can be seen that BProg outperformed GProg in both simulation types from the point of view of both fitness values (see Fig. 6 and Fig. 7) and the final error values (see Table II and Table III).

Compared to previous results produced by dense hierarchical, Mamdani-inference based learning systems [7], the results

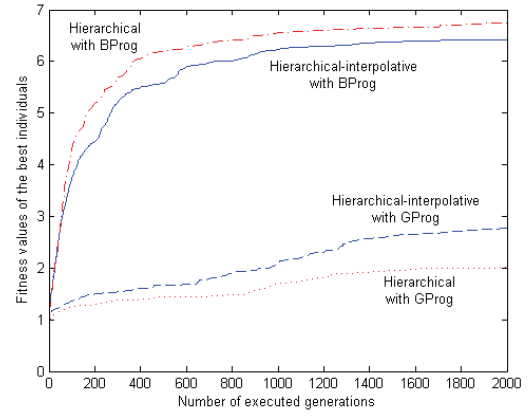


Fig. 6. Results for the six-dimensional learning problem in case of generation limit

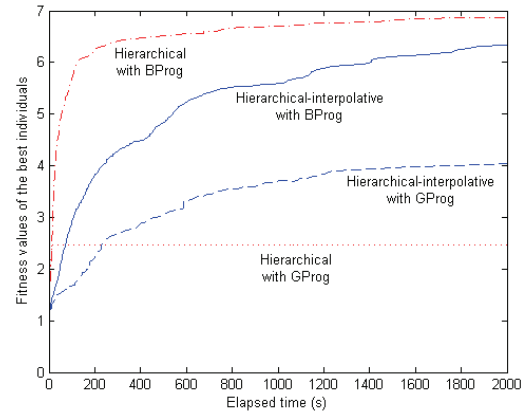


Fig. 7. Results for the six-dimensional learning problem in case of time limit

TABLE II
RESULTS FOR THE SIX DIMENSIONAL LEARNING PROBLEM IN
CASE OF 2000 GENERATIONS

	Hierarchical		Hierarchical-interpolative	
	GProg	BProg	GProg	BProg
MSE	4.7773	1.2189	3.7690	1.2176
MSRE	0.0711	0.0161	0.0500	0.0159
MREP	19.8608	9.5621	16.8610	9.3132
Comp. time	1.4	182.7	90.2	3601.6
No. of rules	3	6.8	5.4	7.2

TABLE III
RESULTS FOR THE SIX DIMENSIONAL LEARNING PROBLEM IN
CASE OF THE 2000 SECONDS TIME LIMIT

	Hierarchical		Hierarchical-interpolative	
	GProg	BProg	GProg	BProg
MSE	3.4850	1.0240	1.5846	1.0335
MSRE	0.0558	0.0155	0.0202	0.0136
MREP	17.7449	9.4368	11.0189	8.8223
No. of gen.	1914618	34627	52685	1611
No. of rules	4.2	6.4	6	6.8

given by the established hierarchical-interpolative learning systems are convincingly better in case of GProg, however it is not so unambiguous in case of BProg, because the non-interpolative hierarchical system gave higher fitness values during the learning processes (see Fig. 6 and Fig. 7), but most often the hierarchical-interpolative system had lower errors on the test samples after learning (see Table II and Table III, where bold numbers present the best error values).

In case of the time limited runs GProg with the dense hierarchical system stuck in local optima and its convergence speed became zero in 20 seconds, whereas the other combinations had a positive convergence speed even after 2000 seconds and continued advancing to better fitness values (see Fig. 7).

V. CONCLUSION

Our work proposed a method for constructing hierarchical-interpolative fuzzy rule bases in order to solve supervised machine learning problems. The rule bases were constructed by using Genetic and Bacterial Programming algorithms.

Simulation runs were carried out in order to discover the properties of the obtained learning systems and to compare them with previous results on non-interpolative hierarchical systems [7]. Bacterial Programming outperformed Genetic Programming in both executed simulation types. The results given by the established hierarchical-interpolative learning systems combined with GProg were unambiguously better than previous results produced by the corresponding non-hierarchical, Mamdani-inference based learning system, however in case of the systems with BProg optimization technique neither the interpolative nor the non-interpolative system showed overwhelmingly better properties.

Further research may aim at improving both the encoded learning architecture and the applied optimization methods (e.g. using gradient steps during the optimization process) and to compare the established hierarchical fuzzy systems with non-hierarchical ones.

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