GENETIC PROGRAMMING AND BACTERIAL ALGORITHM FOR NEURAL NETWORKS AND FUZZY SYSTEMS DESIGN

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***Abstract* – In the field of control systems it is common to use techniques based on model adaptation to carry out control for plants for which mathematical analysis may be intricate. Increasing interest in biologically inspired learning algorithms for control techniques such as Artificial Neural Networks and Fuzzy Systems is in progress. In this line, this paper gives a perspective on the quality of results given by two different biologically connected learning algorithms for the design of B-spline neural networks (BNN) and fuzzy systems (FS). One approach used is the Genetic Programming (GP) for BNN design and the other is the Bacterial Evolutionary Algorithm (BEA) applied for fuzzy rule extraction. Also, the facility to incorporate a multi-objective approach to the GP algorithm is outlined, enabling the designer to obtain models more adequate for their intended use.** *Copyright © 2003 IFAC.*

Keywords: constructive algorithms, B-splines, genetic programming, bacterial evolutionary algorithm, fuzzy rule base;

1. INTRODUCTION

Current research aims to understand the modelling properties of the various Artificial Neural Networks (ANN) architectures. New algorithms are being developed to improve their fitness for modelling and control applications. Different architectures can be found in the literature, however, B-spline neural networks offer definite advantages over more commonly known neural networks, such as multilayer perceptrons or radial basis function networks. One of the most important advantage is its suitability for on-line adaptive modelling and control applications. Their grid-based structure makes them transparent, which, in contrast to other networks, means that it is easier to understand the knowledge stored in these networks (this is an advantage that is also applies to fuzzy rule-based models over conventional neural networks). It is not surprising that, at a high level, the basic information principles of B-spline networks and fuzzy systems are the same. So, under certain conditions, the low-level algorithms are also identical. For fuzzy systems, the most important task is to find the optimal rule base; this is translated, in terms of BNNs in the determination of the best topology and its parameters values. The rule base might be given by a human expert or might be given a priori by the linguistic description of the modelled system. If neither is available, the system has to be designed by other methods based on numerical data.
Nature inspired some evolutionary optimisation algorithms suitable for global optimisation of even non-linear, high-dimensional, multimodal, and discontinuous problems. The original genetic algorithm (GA) was developed by Holland (Holland, 1992) and was based on the process of evolution of biological organisms. Recently, approaches like genetic programming and bacterial evolutionary algorithm present an alternative to the former algorithms. GP optimisation uses the same operators as GA, though it requires an expression tree for gene representation as a combination of functions. The BEA is a simpler algorithm, and its operations were inspired by the microbial evolution phenomenon.
The current paper focuses on a comparison between the applicability of GP for BNN design and BEA for the optimisation of the fuzzy rule base.
The layout of the paper is as follows: Section 2 and 3 introduce the topology of B-spline neural networks and the Fuzzy Systems concept. In Section 4 and 5 GP for BNN and BEA for fuzzy rule extraction will

be described. Results are presented in Section 6 and conclusions are drawn in Section 7.

2. B-SPLINE NEURAL NETWORKS

B-spline neural networks belong to the class of networks termed *grid or lattice-based associative memories networks* (AMN). This type of networks is composed of three layers: a *normalised input space* layer, a *basis functions* layer and a *linear weight* layer.

2.1. Normalised Input Layer

The normalised input layer can take different forms but is usually a grid on which the basis functions are defined. To define a grid, vectors of *knots* must be defined, one for each input axis. There are usually a different number of knots for each dimension, and they are generally placed at different positions.
The interior knots, for the i^{th} axis, are $\lambda_{i,j}, j = 1,\cdots,r_i$. They are arranged in such a way that:

$$x_i^{\min} < \lambda_{i,1} \le \lambda_{i,2} \le \cdots \le \lambda_{i,r_i} < x_i^{\max}, \tag{1}$$

where $x_i^{\min}$ and $x_i^{\max}$ are the minimum and maximum values of the i^{th} input, respectively.
At each extreme of each axis, a set of k_i *exterior knots* must be given which satisfy:

$$\lambda_{i,-(k_i-1)} \le \cdots \le \lambda_{i,0} = x_i^{\min} \tag{2}$$

$$x_i^{\max} = \lambda_{i,r_i+1} \le \cdots \le \lambda_{i,r_i+k_i} \tag{3}$$

These exterior knots are needed to generate the basis functions that are close to the boundaries.
The j^{th} interval of the i^{th} input is denoted as $I_{i,j}$ and is defined as:

$$I_{i,j} = \begin{cases} [\lambda_{i,j-1} \quad \lambda_{i,j}[\ \textit{for} \ j = 1,\cdots,r_i \\ [\lambda_{i,j-1} \quad \lambda_{i,j}] \ \textit{if} \ j = r_i + 1 \end{cases} \tag{4}$$

This way, within the range of the i^{th} input, there are r_i+1 intervals (possibly empty if the knots are coincident), which means that there are $p' = \prod_{i=1}^{n}(r_i+1)$ *n*-dimensional cells in the grid.

2.2. The basis functions layer

The output of the hidden layer is determined by a set of *p* basis functions defined on the *n*-dimensional grid. The univariate B-spline basis function of order *k* has a support, which is *k* intervals wide. Hence, each input is assigned to *k* basis functions.
The j^{th} univariate basis function of order *k* is denoted $N_k^j(x)$, and it is defined by the following relationships:

$$N_k^j(x) = \left(\frac{x - \lambda_{j-k}}{\lambda_{j-1} - \lambda_{j-k}}\right) N_{k-1}^{j-1}(x) + \left(\frac{\lambda_j - x}{\lambda_j - \lambda_{j-k+1}}\right) N_{k-1}^{j}(x) \tag{5}$$

$$N_1^j(x) = \begin{cases} 1 \ \textit{if} \quad x \in I_j \\ 0 \ \textit{otherwise} \end{cases} \tag{6}$$

Multivariate basis functions are formed by taking the *tensor product* of the univariate basis functions.
The number of basis functions of order k_i defined on an axis with r_i interior knots is r_i+k_i. Therefore, the total number of basis functions for a multivariate B-spline is $p = \prod_{i=1}^{n}(r_i + k_i)$.
This number depends exponentially on the size of the input and because of this, B-splines are only applicable for problems where the input dimension is small (typically ≤ 5).

2.3. The weight layer

The output of an AMN is a linear combination of the outputs of the basis functions. The linear coefficients are the adjustable weights, and as the mapping is linear, finding the weights is just a linear optimisation problem. The output is therefore:

$$y = \sum_{i=1}^{p} \mathbf{a}_i \mathbf{w}_i = \mathbf{a}^T \mathbf{w}, \tag{7}$$

2.4. Sub-Modules

To overcome the "curse of dimensionality", it is common to employ, instead of a single module covering all inputs, a linear sum of smaller sub-modules, each one with a lower input dimensionality. The output of such a network is:

$$y(\mathbf{x}) = \sum_{u=1}^{n_u} S_u(\mathbf{x}_{\underline{u}}) \tag{8}$$

where $S_i(\mathbf{x}_{\underline{i}})$ denotes the i^{th} sub-model, and $\mathbf{x}_{\underline{i}}$ is the set of input variables ($\underline{i}$) which compose sub-model *i*.

3. FUZZY SYSTEMS

The theory of fuzzy logic was first proposed by Zadeh in the 1960s. His main idea was that most of the phenomena of the real world could not be described by two values, so he defined a function which would assign fuzzy truth degrees between zero and one to elements of a universal set. In 1973 he pointed out that the new fuzzy concept could be excellently used for describing very complex problems with a system of fuzzy relations represented by a fuzzy rule base [1].
A fuzzy rule base contains fuzzy rules that map the multivariate fuzzy input set to the univariate output set. Let's denote a rule by R_i,:

R_i: *IF* (x_1 *is* A_{i1}) *AND* (x_2 *is* A_{i2}) *AND*
... AND (x_n *is* A_{in}) *THEN* (*y is* B_i), (9)

where A_{ij} and B_i are fuzzy sets, x_j and *y* are the fuzzy inputs and output, respectively.
The structure of a rule is the following:

IF Premise THEN Conclusion, (10)

where the premise consists of antecedents linked by the *AND* operator.

To implement a rule set, each of the univariate fuzzy linguistic statements – e.g. *(x_n is A_{in})* – needs to be given and also the operators used to implement the underlying fuzzy logic, such as *AND*, *THEN*, etc., need to be specified. Because no single implementation is correct, many implementation methods have been proposed (Harris *et al.*, 1993).

A crisp input is presented to the network, and the membership functions of the multivariate fuzzy input linguistic variables are computed. The network output is obtained by *defuzzifying* this information.

3.1. RELATIONS BETWEEN FUZZY SYSTEMS AND B-SPLINE NETWORKS MODELS

In the simplest form, fuzzy systems calculate their response by taking a linear combination of the input membership functions, in an analogous way as several neural networks. The relationships between fuzzy and *B-spline* networks, have been addressed by several authors (see, for example (Nelles, 2000; Ruano *et al.*, 2001)). In order to have a strict equivalence between FS and BNN models, the FS must satisfy some assumptions, which are outlined in (Ruano *et al.*, 2001). In the current work, the structure of the Mamdani FS and BNN models are not strictly equivalent, their main differences being:

- The linguistic terms of the rule antecedents and consequents are not modelled by *B-splines*, instead, by trapezoids.
- For the logic connectives such as the conjunction and implication, the *t-norm* used is *not* the algebraic product, but the *min* operator;

Please note that it is not essential that the two model's structures are equivalent, since the main objective of this work is the comparison of the performance between two different optimisation heuristics and not a structure comparison.

4. GENETIC PROGRAMMING

Genetic programming employs the main operators used by a genetic algorithm in its search procedure. The main difference, which, from our point of view is beneficial for this type of neural networks, is that the network parameters are not coded as bit strings, but instead as a tree structure, composed of *function* and *terminal* nodes, is employed. The tree structure, as well as the characteristics of the nodes, evolves from generation to generation.

4.1. Single Objective Genetic Programming

For the case of B-Spline construction, and referring to the previous sections, sub-models must be *added* (+), sub-models of higher dimensionality must be *created* from smaller sub-modules (*), and sub-models of higher dimensionality must be *split* into lower dimensional sub-models (/). These are the set of primitive functions that were implemented.

In contrast with the application of GP to other neural networks, the node terminals do not represent only each *input variable*, but also the *spline order*, the *number of interior knots*, and *their location*.

An example of an expression tree for B-spline networks is presented in the next figure.

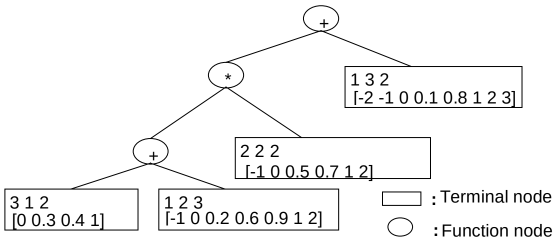


Fig 1: A sample expression tree for B-spline networks.

The evolutionary process involves the following steps:

- The creation of an initial population, and the determination of the size of the population;
- The evaluation of the candidates using **B**ayes **I**nformation **C**riterion (Nelles, 2001), and their fitness assignment;
- The application of genetic operations, such as:
  - <u>Selection</u>: Pairs of parent trees are selected based on their fitness for reproduction;
  - <u>Crossover</u>: A node in the tree is selected at random and exchanging the associated sub-trees produces a pair of offspring trees.
  - <u>Mutation</u>: This is performed by either replacing a node selected at random by a sub-tree generated randomly or by changing its type.
  - <u>Replacement</u>: All parents are replaced by the offspring (generational approach).
- The termination criterion, which is usually the maximum number of generations defined.

The evolution cycle is summarized in Figure 2. Mutation on a function implies the replacement of the tree node with a randomly generated sub-tree of maximum length 2. Mutation on a terminal can be of 6 different types, which are:

1. Full replacement of the terminal.
2. Variable identification replacement.
3. Splines order replacement.
4. Random displacement of an interior knot.
5. Addition of *N* interior knots placed randomly. *N* is fixed to 5.
6. Removal of *N* interior knots. In the absence of interior knots, no operation is executed.

For simplification purposes, the terminal mutation rates will be described as a vector p_m_terminal=[%1 %2 %3 %4 %5 %6], where %i designates the i^{th} type mutation rate.

For a more detailed explanation, please see (Cabrita, *et al.*, 2001).

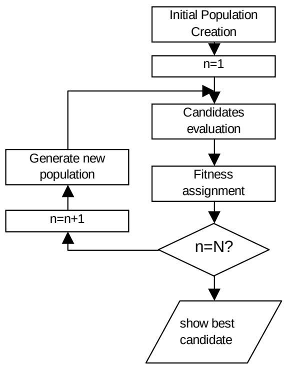


Fig 2: Flowchart for Genetic Programming.

4.2. Multi-objective genetic programming

GP can also be applied in a multi-objective strategy, which is useful for B-spline networks design. For a description on multi-objective optimisation, please refer to (Fonseca, 1998).
In this approach, candidate evaluation consists not only of the objective functions evaluation, but also of a decision process based on priorities and goals associated with every objective. At each generation, fitness is assigned to the candidates according to the result of that decision process. Non-dominated solutions are recorded, and in the end, the decision maker selects the best non-dominated solutions that correspond to the preferred candidates.
Here, the following objectives have been considered:

- Mean Square of Absolute Error for training and validation data (MSE/MSEv).
- Mean Square of Relative Error for training and validation data (MSRE).

$$MSRE = \frac{1}{N\_pat}\sum_{i=1}^{N\_pat}\frac{(t_i - y_i)^2}{y_i^2};$$

- Mean of Relative Error Percentage for training and validation data (PMRE/PMREv).

$$PMRE = \frac{100}{N\_pat}\sum_{i=1}^{N\_pat}\left|\frac{t_i - y_i}{y_i}\right|.$$

Some objectives may have greater priority than others. Objectives with priority greater than 0, together with the corresponding goals, act as constraints that must be satisfied. Lower-priority objectives are only taken into account as long as the remaining ones have their goals satisfied.

5. BACTERIAL EVOLUTIONARY ALGORITHM

A newer approach is the bacterial algorithm. This is based on a process, which can be found in nature. Bacteria can transfer genes to other bacteria. This mechanism is used in the bacterial mutation and in the gene transfer operation. The gene transfer operation substitutes the GA's crossover operation, so the information can be transferred between different individuals (Nawa and Furuhashi, 1999).

5.1. The encoding method

Referring now to Section 3, for a fuzzy system design using BEA, the class of membership function is restricted to a trapezoidal function, described by its four breakpoints. The membership functions are identified by the two indices *i* and *j*, so that, the membership function $A_{i,j}(x_j)$ belongs to the ith rule and the jth input variable. $B_i(y)$ is the output membership function of the ith rule and its shape is the same as for $A_{i,j}(x_j)$ but it is described by different breakpoints (Botzheim, 2001).

The encoding method of a fuzzy system with two inputs and one output, can be observed in Fig. 3.

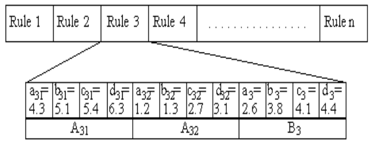


Fig 3: Fuzzy rules encoded in a chromosome.

For example, Rule 3 in Fig. 3 means:

$$\textit{If } x_1 \textit{ is } A_{31} \textit{ and } x_2 \textit{ is } A_{32} \textit{ then } y \textit{ is } B_3 \qquad (11)$$

where $A_{3,1}$ $A_{3,2}$ and B_3 mean the trapezoidal membership function with the breakpoints values shown in the previous figure.

5.2. The algorithm

Generating the initial population. First, the initial bacteria population is created randomly. The population consists of *n* chromosomes (the *bacteria*). The initial number of rules in one chromosome is N_{max}. So, $n(k+1)N_{max}$ membership functions are created, where *k* is the number of input variables in the given problem, and each membership function has four parameters.

Bacterial mutation The bacterial mutation is applied to each chromosome one by one as in (Nawa and Furuhashi, 1999). First, *m* -1 copies (clones) of the rule base are generated. Then a certain part of the chromosome is randomly selected and the parameters of this selected part are randomly changed in each clone (mutation). Next, all the clones and the original bacterium are evaluated by the error criterion. The best individual transfers the mutated part into the other individuals. This cycle is repeated for the remaining parts, until all parts of the chromosome have been mutated and tested. At the end, the best rule base is kept and the remaining *m* -1 are discharged.

Gene transfer operation. The gene transfer operation allows the recombination of genetic information between two bacteria.

First, the population must be divided into two halves. The better bacteria are called superior half, the other bacteria are called inferior half.
One bacterium is randomly chosen from the superior half, this will be the source bacterium, and another is randomly chosen from the inferior half, this will be the destination bacterium.
A "good" part from the source bacterium is chosen and this part can overwrite a not-so-good part of the destination bacterium or simple be added. A good part can be a fuzzy rule with a high degree of activation value. The activation value of a fuzzy rule is calculated as follows:

$$\overline{w_i} = \frac{1}{P}\sum_{j=1}^{P} w_i^{(j)} \qquad (12)$$

where $\overline{w_i}$ is the mean activation value of the i^{th} rule, $w_i^{(j)}$ is the activation value of the i^{th} rule for the j^{th} pattern, P is the number of patterns. So the best part of the source bacterium is the rule which has the greatest mean activation value.

Gene transfer is repeated for $N_{\inf}$ times, where $N_{\inf}$ is the number of "infections" per generation.

Stop condition. If the population satisfies a stop condition or the maximum generation number is reached, then the algorithm ends. Otherwise it returns to the bacterial mutation step.

5.3. *Definition of the error function*

The error function used for training is defined as follows:

$$e_{rel} = \frac{1}{n}\sum_{patterns}\frac{|y-\hat{y}|}{I_{\max}-I_{\min}} \qquad (13)$$

where I_{max} is the upper and I_{min} is the lower bound of the interval of the output variable, so the error is normalised by the length of the output interval rather than the actual value of the output.

6. RESULTS

Three different examples have been experimented with GP and BEA. Both algorithms were set to run for 10 sessions of 40 generations and the results obtained relate to the following specifications: ***M**ean **S**quare of the absolute **E**rror*, ***M**ean **S**quare of the **R**elative **E**rror*, ***M**ean **R**elative **E**rror **P**ercentage*, and *structure **Comp**lexity* (number of basis functions) for both training and validation data (using ***v*** subscript). The training and validation sets contained the same number of patterns and some of the patterns were identical. 110 patterns were used for the pH problem, 101 patterns for the ICT problem and 200 patterns for the six-dimensional generic function.
For GP, the population size is 10, the initial population creation method is ramped-half-and-half, the fitness assignment is exponential ranking with selective pressure 5, and the crossover rate, the mutation rate and the number of generations are 0.5, 0.8, 40, respectively. The terminal mutation rate is [5% 10% 5% 10% 60% 10%].
For BEA, the population size and number of clones are 10, the number of infections and rules is 5 and 7, respectively.

6.1. *pH problem*

The aim of this example is to approximate the inverse of a titration-like curve. This type of non-linearity relates the *pH* (a measure of the activity of the hydrogen ions in a solution) with the concentration (*x*) of chemical substances.

6.2 *Inverse Coordinate Transformation Problem (ICT)*

This example illustrates an inverse kinematic transformation between 2 Cartesian coordinates and one of the angles of a two-links manipulator.
For a more complete description on the above examples refer to (Ruano et. al, 2001).

6.3 *A sixth input generic function*

This example is widely used as a target function and the output is given by the following expression (see Botzheim et. al, 2001):

$$y = x_1 + x_2^{0.5} + x_3x_4 + 2e^{2(x_5-x_6)} \qquad (14)$$

6.4 *Comparison between SOGP and Bacterial Algorithm*

The values shown from Table 1 to Table 4 refer to results obtained from the 10 different sessions, and show mean values of specifications for the best candidates from each run, for the PH, ICT and sixth input generic function, respectively.

Table 1: Results for the PH problem.

Alg	MSE	MSRE	%MRE	Comp	MSEv	%MREv
GP	$3.3\text{x}10^{-7}$	$2.4\text{x}10^{-2}$	2.4	69	2.710^{-2}	7.2
BEA	$5.8\ \text{x}10^{-4}$	$9.4\ \text{x}10^{-2}$	12.5	28	$7.6\ \text{x}10^{-4}$	23.1

Table 2: Results for the ICT problem.

Alg	MSE	MSRE	%MRE	Comp	MSEv	%MREv
GP	$8.\ \text{x}10^{-4}$	$2.7\text{x}10^{12}$	$3.8\text{x}10^{7}$	34.3	1.2	3.7
BEA	$7.6\ \text{x}10^{-1}$	$1.5\ \text{x}10^{14}$	$6.8\ \text{x}10^{7}$	56	1.3	21.2

Table 3: Results for the sixth input generic function.

Alg	MSE	MSRE	%MRE	Comp	MSEv	%MREv
GP	1.1	$2.2\text{x}10^{-2}$	9.8	25.7	1.5	11.1
BEA	1.1	$3.2\ \text{x}10^{-2}$	10.1	168	5.0	16.8

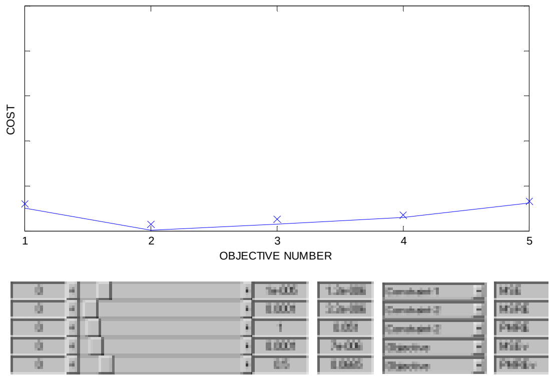
From the previous tables, it can be observed that, with the exception of the pH problem, GP optimising the BNN results in better accuracy between the desired output and estimated output, than the BEA does for the FS rule extraction, for all the specifications,. The results from the validation set uphold the training values and sometimes, as is the case of the ICT problem, present lower specification values. It can also be seen that the complexity of the structure is important, because it gives an idea about the generalisation capabilities of the models: in general, the lower is the complexity, the better the generalisation capability.

6.5 *Multi-objective GP approach*

Supposedly the mean values for the training data for GP, in Table 2 are not as good as expected. A way of establishing a compromise between the training and validation set specifications is using the multi-objective approach for the ICT problem. It should be stressed that this could also be done with any of the other problems. 10 sessions were executed using the parameters in Table 4. Every non-dominated solution from every session was saved and in the end, the decision maker showed the preferred solutions from all the sessions based on the goal and priorities vector shown in the 3rd and 4th column.

Table 4: Multi-objective parameters specification for ICT

Numb. Individuals	Numb. Generations	Priority Vector	Goal Vector
10	40	[1 2 2 0 0]	[10^{-4} 10^{5} 10^{3} 10^{-4} 10^{-2}]



0	1e+005	1.2e-006	Constraint 1	MSE
0	0.0001	2.2e-006	Constraint 2	MSPE
0	1	0.051	Constraint 2	PMPE
0	0.0001	7e-006	Objective	MSEv
0	0.5	0.0065	Objective	PMPEv

Fig 4: Best trade-off curve for the ICT problem.

The results shown in Fig. 4 allow the designer to deduce that it is possible to get good models simultaneously, for the training and validation set, as is the case. Please note that the values in the 3rd column represent the position of the crosses, i.e, approximately the values obtained for each objective. The specifications for the training data have been optimised and its values are much lower than the goals set. One should emphasize that this is not always the case because some other conflicting objectives can be imposed, for e.g. the complexity of the network (the preferred solution presented shows a complexity value of 56) or the condition of the model.

7. CONCLUSIONS

Two recent new methodologies for optimising the structure of neural networks and fuzzy models were subject to comparison. It was observed that the output accuracy attained with the neural network structure, optimized with GP, was better than the one achieved with the fuzzy system, optimized by BEA. One can deduce it might be from the fuzzy structure, which is not identical to the BNN, however, from the point of view of modelling, if the model from the NN and FS are to be seen as a black box, then the GP has better performance. Also, the facility to incorporate a multi-objective approach in GP allows the designer the freedom to obtain models more adequate to their intended use.
As future work, it may be helpful to try and use GP for FS optimisation or to use BEA to optimise a FS whose structure is identical to the BNN, or to optimise the BNN structure itself.

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