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Comments on "Constraining the Optimization of a Fuzzy Logic Controller"

Ming-Da Wu and Chuen-Tsai Sun

Abstract—**Genetic algorithms (GAs) are a highly effective and efficient means of solving optimization problems. Gene encoding, fitness landscape and genetic operations are vital to successfully developing a GA. Cheong and Lai[1] described a novel method, which employed an enhanced genetic algorithm with multiple populations, to optimize a fuzzy controller, and the experimental results revealed that their method was effective in producing a well-formed fuzzy rule-base. However, their encoding method and fitness function appear unnatural and inefficient. This study proposes an alternative method of concise genetic encoding and fitness design.**

Index Terms—**Fuzzy modeling, genetic algorithms, polyploidy.**

I. INTRODUCTION

Designing a fuzzy logic controller involves two major steps: structure identification and parameter identification. Structure identification is the process of choosing a suitable controller structure, such as the size of the fuzzy rule-base, or the number of nodes of a fuzzy neural network. Parameter identification then determines the value of the parameters of a fuzzy controller, such as the shape of the fuzzy membership functions and the contents of the fuzzy rule-base. The previous study proposed a novel method for achieving these two steps simultaneously, and a genetic algorithm was employed to optimize the parameters of a PI-like version of Mamdani FLC, with possible FLC structures being evolved in numerous populations.

Cheong and Lai's study claimed that a well-formed rule-base is important for a FLC, and we strongly agree on this point, since a scrambled rule-base often results in a broken control surface and damages robustness. To construct a comprehensive rule-base, the previous work added a punishment to the fitness function following MacVicar–Whelan's meta-rules [1], and thus a scrambled rule-base always had a worse fitness score and lower survival probability than a well formed rule-base. Fig. 1 (Fig. 4 of Cheong and Lai's study) illustrates the MacVicar–Whelan meta-rules, with the cells of the matrix containing the fuzzy output and their possible range of variation being indicated by the arrow, and with Fig. 2 displaying the probability of scrambled case for each cell in accordance with MacVicar–Whelan's meta-rules. Additionally, since each cell in the Mamdani FLC was directly encoded into a gene, most points in the search space contained
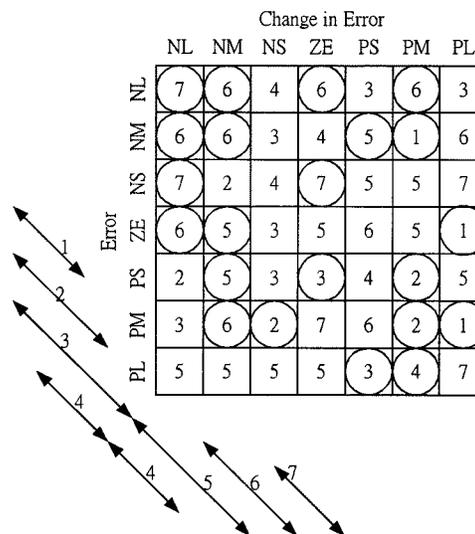
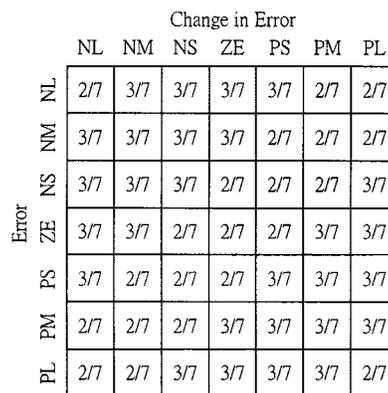Fig. 1. Example of a scrambled rule-base.

Fig. 2. Probability of each cell containing well-formed rule.

a scrambled rule. As displayed in Fig. 2, the probability of a possible 7 to 7 FLC being well formed is less than $(3/7)^{7*7} = 9.1 \times 10^{-19}$. Restated, 99.999 999 999 999 999% of chromosomes are scrambled and thus not desirable. Although the genetic algorithm is effective in searching large spaces, it is time consuming when applied to this case. The previous work of Cheong and Lai restricted the range of the initial population, thus enhancing the efficiency of the search, but this approach is unnatural and does not solve this underlying issue, since there is still high probability of generating offspring with the scrambled rules via crossover and mutation.

The use of a large number of rules increases the probability of obtaining a scrambled rule base, and also certain bad and redundant rules do not excessively influence the overall behavior of the FLC during the learning phase. The scrambled rule-base problem closely resembles an over-fitting effect, with both of them being caused by excessive learning memory. We believe that most of the scrambled rules can be avoided by modifying the chromosome encoding employed in the Cheong and Lai's work. Actually, the MacVicar–Whelan Rule can be represented in matrix from, as displayed in Fig. 3, and could be further simplified [2], as displayed in Table I. Restated, when solving the low order control problem there is no need to encode each cell in the matrix of Fig. 1 into the chromosome. The optimization of an FLC using a full rule base may result in a scrambled rule base because of the increased likelihood of malformed rules. Table II, which is a generalized form of

Change in Error

		NL	NM	NS	ZE	PS	PM	PL
Error	NL	NL	NL	NL	NL	NM	NS	Z
	NM	NL	NL	NM	NM	NS	Z	PS
	NS	NL	NM	NS	NS	Z	PS	PM
	ZE	NL	NM	NS	Z	PS	PM	PL
	PS	NM	NS	Z	PS	PS	PM	PL
	PM	NS	Z	PS	PM	PM	PL	PL
	PL	Z	PS	PM	PL	PL	PL	PL

Fig. 3. Simplified FLC.

Table I, presents the rule-base we used. Each rule in the rule base use only one input, either the error or the change in error. The system output integrates the output of each rule according to their firing strength.

The following section presents an example of the implementation of the simplified encoding.

II. ILLUSTRATIVE EXAMPLE

Fig. 4 illustrates the chromosome encoding of a Mamdani FLC. Each rule is denoted as two continuous genes, the first one containing the antecedent part of the rule, and the second describing the consequence part. For ease of explanation, two rules are assigned in different axes in the FLC matrix as a rule pair. Since N pairs of rules exist for the simplified $N \times N$ FLC, various distinct FLC structures can be represented as a fuzzy polyploidy [3]. A polyploidy consists of a number of certain units called monoploidy, and each unit shares a homogeneous genetic encoding and phenotype mapping method. In this example, each rule pair is represented as a monoploidy, and the simplified $N \times N$ FLC is represented as the polyploidy with n-units. The crossover and mutation operations in polyploidy employ standard methods.

The encoding of the membership function resembles that in the previous work of Cheong and Lai, and the central apex of the triangular membership function is recorded in a chromosome. The major difference between the encoding method employed herein and that in the Cheong and Lai's investigation is that the range of membership function is not restricted herein. The left and right corners of the triangular membership function are equal to the center points which are closest to the current center in the input space. The membership functions with the leftmost and the rightmost center apexes are modified as illustrated in Fig. 5. Thus, the whole input space can be covered by the sets of membership function in a polyploidy. Fig. 5 presents the mapping relation between the polyploidy chromosomes and fuzzy membership function.

Since each rule in a Mamdani FLC has a fuzzy output, an extra defuzzification process is necessary to transform the output from fuzzy to crisp. Using centroid defuzzification and sum-product composition [5] provides a more feasible means of implementation. The crisp output in this approach is equivalent to the weighted average of centroids of consequent membership functions, and the weighted factor equals the firing strength of each rule multiplied by the area of the its consequent membership function [3], as displayed in (1), where w_i is the firing strength of the ith rule, a_i is the area of the consequent membership of the ith rule, and z_i is the centroid of the consequent membership of the ith rule. This approach provides a more efficient means for achieving defuzzification.
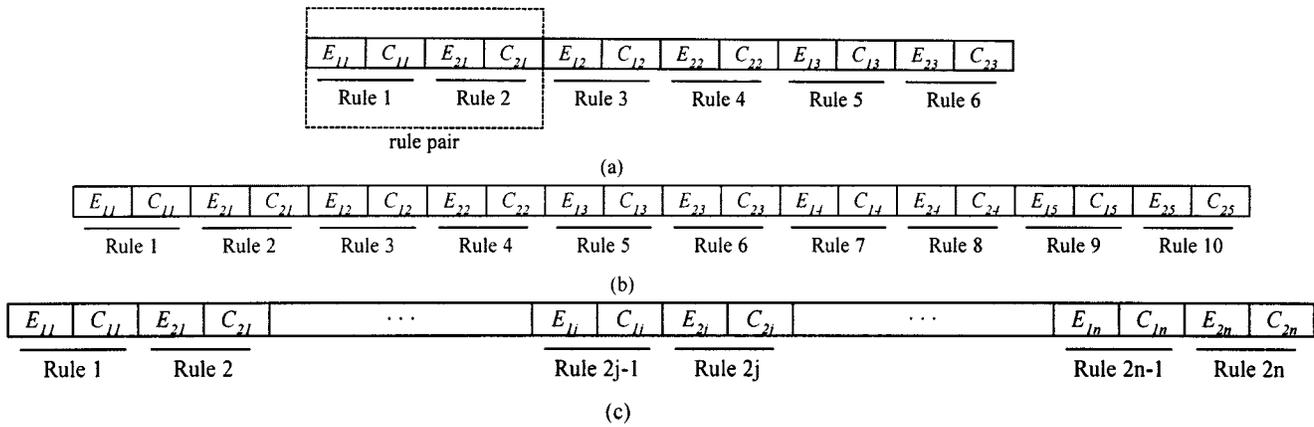
Crisp output
$$= \frac{w_1 \cdot a_1 \cdot z_1 + w_2 \cdot a_2 \cdot z_2 + \cdots + w_k \cdot a_k \cdot z_k}{w_1 \cdot a_1 + w_2 \cdot a_2 + \cdots + w_k \cdot a_k} \quad (1)$$

TABLE I
SIMPLIFIED MACVICAR–WHELAN FUZZY RULE BASE

RULE 1:   **IF** the error is Z
          THEN the change of the control is Z
RULE 2:   **IF** the change of the error is Z
          THEN the change of the control is Z
RULE 3:   **IF** the error is NL
          THEN the change of the control is NL
RULE 4:   **IF** the change of the error is NL
          THEN the change of the control is NL
RULE 5:   **IF** the error is NM
          THEN the change of the control is NM
RULE 6:   **IF** the change of the error is NM
          THEN the change of the control is NM
RULE 7:   **IF** the error is NS
          THEN the change of the control is NS
RULE 8:   **IF** the change of the error is NS
          THEN the change of the control is NS
RULE 9:   **IF** the error is PS
          THEN the change of the control is PS
RULE 10: **IF** the change of the error is PS
          THEN the change of the control is PS
RULE 11: **IF** the error is PM
          THEN the change of the control is PM
RULE 12: **IF** the change of the error is PM
          THEN the change of the control is PM
RULE 13: **IF** the error is PL
          THEN the change of the control is PL
RULE 14: **IF** the change of the error is PL
          THEN the change of the control is PL

TABLE II
FUZZY RULE BASE OF A SIMPLIFIED $N \times N$ FLC

RULE 1:   **IF** the error is E_{11}

          THEN the change of the control is C_{11}

RULE 2:   **IF** the change of the error is E_{21}

          THEN the change of the control is C_{21}

          .

          .

          .

RULE 2n-1: **IF** the error is E_{1n}

          THEN the change of the control is C_{1n}

RULE 2n: **IF** the change of the error is E_{2n}

          THEN the change of the control is C_{2n}

Fig. 4. Encoding of FLC. (a) 3×3 FLC, (b) 5×5 FLC, and (c) $N \times N$ FLC.
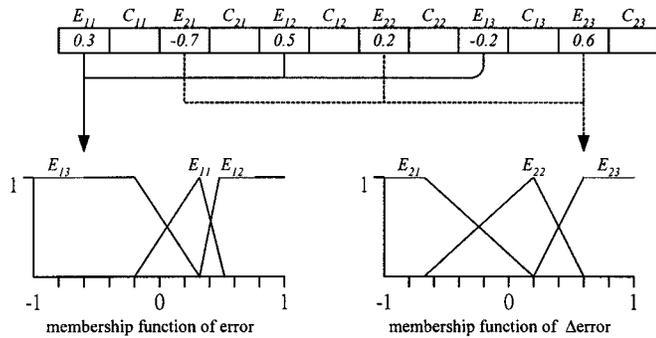
Fig. 5. Decoding of membership function.

Fig. 6. Time response graph of best chromosome. (a) plant B. (b) Plant C.

For ease of implementation, the consequence of each rule is restricted herein to a triangular membership function with the same height and width. Thus, the membership functions have the same areas. To reduce the cost of defuzzification, the centroid of triangle representing the consequent membership function is directly encoded in the polyploidy instead of the apex of triangle representing the membership function. Therefore, defuzzification can be calculated only by the firing strength and the centroid of triangle representing the membership function for each rule. Since the consequent of each rule has the same area, the crisp output can be calculated by (2).
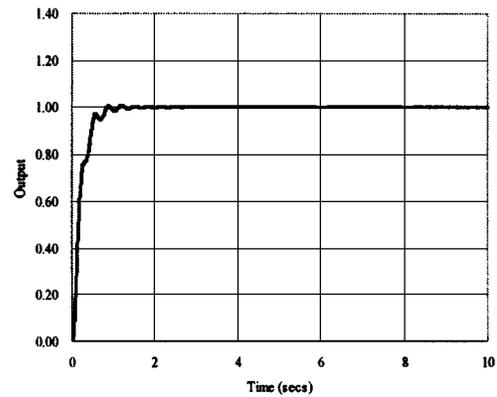
$$\text{Crisp output} = \frac{w_1 \cdot z_1 + w_2 \cdot z_2 + \cdots + w_k \cdot z_k}{w_1 + w_2 + \cdots + w_k}. \qquad (2)$$

Since each rule in a simplified FLC is necessary, any confusing rule will compromise the overall performance of the FLC. Restated, the performance measures of a polyploidy with a scrambled rule-base will be worse than those with a well-formed chromosome. Additionally, the previous work employed ITAE and a strategy of punishment as the fitness measure. The strategy of punishment is less necessary now because most of the scrambled chromosomes have higher ITAE value. Thus, the fitness function is now defined as follows:

$$\text{fitness} = \frac{1}{\text{ITAE}}. \qquad (3)$$

To confirm the usefulness of the concise encoding method, we test the plant B and plant C of the investigation of Cheong and Lai. For convenience of implementation, this work employed the polyploidy GA model with structure expansion [3], rather than the parallel GA with population migration described in the previous work of Cheong and

Lai. We believe the structure migration method from the previous work synthesizing the concise encoding presented herein should produce results equal to or better than those of our simulation. The population size of the simulation is set at 100, the crossover rate is 0.3, and the mutation rate is 0.05. The experiment employs one-point crossover and rank selection [4]. Fig. 6 presents the time-response graph of the best polyploidy (five units) after the 500th generation, and the result closely resembles the best results of the Cheong and Lai's investigation. The concise encoding is also effective in producing an optimized FLC for controlling the previous test plant.

III. Conclusion

This work demonstrates that the control problem described in a previous study of Cheong and Lai can be solved by employing the concise encoding without compromising FLC performance. The concise encoding reduces the search space from $O(n^2)$ to $O(n)$ and hence the search efficiency is markedly enhanced. Furthermore, the penalty term of the fitness function is unnecessary because the rule-base only preserves the vital rules, and the scrambled rule-base can be avoided because of its higher natural error rate. Initial population, fuzzy membership function and fitness function do not need to be restricted in the proposed encoding, and thus implementing the GA becomes more intuitive and natural.

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