Identification of General Fuzzy Measures by Genetic Algorithms Based on Partial Information

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Abstract—This study develops an identification procedure for general fuzzy measures using genetic algorithms. In view of the difficulty in data collection in practice, the amount of input data is simplified through a sampling procedure concerning attribute subsets, and the corresponding detail design is adapted to the partial information acquired by the procedure. A specially designed genetic algorithm is proposed for better identification, including the development of the initialization procedure, fitness function, and three genetic operations. To show the applicability of the proposed method, this study simulates a set of experimental data that are representative of several typical classes. The experimental analysis indicates that using genetic algorithms to determine general fuzzy measures can obtain satisfactory results under the framework of partial information.

Index Terms—Fuzzy measure, genetic algorithm, identification, partial information.

I. INTRODUCTION

IN multiattribute decision-making reality, fuzzy measures have been widely used to demonstrate the significance of attribute subsets [13], [18], [19], [23], [24], [26], [31]. Compared with other types of fuzzy measures, general fuzzy measures fulfilling the boundary conditions, monotonicity, and continuity provide more useful information, such as the characterization of the coupling coefficient, overlap coefficient, degree of overlap, and necessity coefficient [13], [19]. In recent years, [7]–[10] and [17] extended Shapley's idea [21] to define the interaction between attributes. Based on the Shapley value, they proposed valuable notions involving the importance of attributes, interaction indexes, symmetric attributes, and veto and pass effects.

The identification of general fuzzy measures is a fundamental task to be capable of using them in practice. [13] developed a fuzzy measure learning identification algorithm (FLIA) to determine fuzzy measure values. However, FLIA only considers the overall evaluation of an alternative as the solution objective; thus, the exact patterns of degrees of importance for all subsets

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are still unknown. Thus, [19] took the evaluation of an alternative in each subset into consideration. To reduce the difficulty in data collection, they used, as a convenience, the weighted mean of single-attribute evaluations to replace the evaluation of a subset. Such a way represents that fuzzy measures are additive, but this additivity assumption is quite unnecessary for general fuzzy measures. References [7] and [11] proposed an identification method based on quadratic programming algorithms, and the method produced good results.

Although several studies have been made on general fuzzy measure identification, most of them did not consider the difficulty in data collection. Suppose that the universal set has n attributes. We must collect the data of human-provided measure values of $(2^n - 2)$ subsets to determine general fuzzy measures. From the practical standpoint, this requirement is highly infeasible and is hardly implemented in many realistic problems. Thus, we use a sampling procedure of attribute subsets [1] to capture enough partial information and then develop an identification procedure to acquire the values of general fuzzy measures.

References [15], [28], and [30] used genetic algorithms to determine λ-fuzzy measures [23]. According to their successful experiences, we employ genetic algorithms [3], [6] as the solution strategy for general fuzzy measure identification. Recently, [27] applied genetic algorithms to determine the nonadditive set function. When their method is applied in multiattribute decision making, the situation of information insufficiency may occur in real-life problems. That is, the data provided by the individual information sources cannot certainly cover most of the attribute subsets. The detailed discussion will be clarified later. On the contrary, the author's sampling procedure can not only capture most of the useful information using the fewest samples, but also control the information demand clearly and definitely. Based on the partial information acquired by the sampling procedure, we propose an appropriate procedure to identify general fuzzy measures in this study. We improve the detailed steps to develop a specially designed genetic algorithm that can easily be applied in other research areas.

The rest of this paper is organized as follows. Section II reviews fuzzy measures and fuzzy integrals. Section III introduces the concept of genetic algorithms. Section IV first presents the sampling process of attribute subsets to surmount the difficulty in data collection. Based on the framework of partial information, Section IV then proposes the details of the solution procedure for general fuzzy measures using genetic algorithms. Section V generates the experimental data and discusses the experiment results. Finally, Section VI presents our conclusions.

II. FUZZY MEASURES AND FUZZY INTEGRALS

The purpose of this section is to review the basic concept of fuzzy measures and fuzzy integrals. Let X be a universal set and $\mathcal{P}(X)$ be the power set of X. A fuzzy measure, g, is defined as follows:

$$g\colon \mathcal{P}(X) \to [0, 1].$$

The axioms of fuzzy measures include boundary conditions ($g(\phi) = 0$ and $g(X) = 1$) and monotonicity (for every $A, B \in \mathcal{P}(X)$, if $A \subseteq B$, then $g(A) \leq g(B)$). If the universal set is infinite, we must add an extra axiom of continuity. In practice, it is enough to consider a finite universal set. Let $X = \{x_1, x_2, \ldots, x_n\}$ and $i = 1, 2, \ldots, n$. Fuzzy density, $g(\{x_i\})$, is a fuzzy measure of a subset with a single element x_i, and we denote $g_i = g(\{x_i\})$.

Consider a fuzzy measure g of $(X, \mathcal{P}(X))$ and X a finite set. Let f be a measurable function from X to [0,1] (i.e., $f\colon X \to [0, 1]$). Then, without loss of generality, assume that the function $f(x_j)$ is monotonically nonincreasing with respect to j, that is, $f(x_1) \geq f(x_2) \geq \cdots \geq f(x_n)$. Renumber the elements in X if the inequality does not hold. The Sugeno's fuzzy integral, a widely used type of fuzzy integrals, of f with respect to g is

$$\fint f(x)\, dg = \bigvee_{i=1}^{n} [f(x_i) \wedge g(X_i)] \tag{1}$$

where $X_i := \{x_1, x_2, \ldots, x_i\}$, $i = 1, 2, \ldots, n$. We can use the same fuzzy measure, but the Choquet integral is used instead of the max-min integral [5], [18], [20], [26]. That is,

$$(c) \int f\, dg = f(x_n)g(X_n) + [f(x_{n-1}) - f(x_n)]g(X_{n-1})$$
$$+ \cdots + [f(x_1) - f(x_2)]g(X_1). \tag{2}$$

Even if there is complete information regarding $(2^n - 2)$ subsets, the max-min integral calculation can only determine some interval at which the measure values are possibly located. On the contrary, the unique solution will be obtained if the Choquet integral is used. In addition, using the Choquet integral can obtain more reasonable results than using the fuzzy integral in many cases [29]. Therefore, we use Choquet integrals in this study. Finally, for convenience in applications, we denote an element in the power set $\mathcal{P}(X)$ of X as an "attribute aspect." The collection of all of the aspects that contain i elements is called the ith aspect set, where $i = 1, 2, \ldots, n$.

III. GENETIC ALGORITHMS

Based on Darwin's "survival of the fittest," genetic algorithms use mathematical methods to demonstrate the natural evolutionary process of artificial life under a competitive environment [12]. Since genetic algorithms need only the information of environmental fitness, they can easily be applied in numerous fields, such as programming problems, machine learning, artificial intelligence, etc. [2], [4], [6], [16].

Genetic algorithms propose an innovative idea in that they simultaneously employ a set of chromosomes to conduct an optimal search. In addition, three main genetic operators provide

ways of controlling an optimal search from the parent generation to the offspring, including reproduction, crossover, and mutation. Genetic algorithms randomly produce a certain amount of chromosomes and select a portion of the better ones. Then, these chromosomes will be recombined to bring forth the chromosomes of the next generation with a certain mutation proportion. The above steps are repeated until an approximate chromosome is obtained.

Reference [15] proposed a λ-fuzzy measure [23] identification method based on genetic algorithms. They showed that genetic algorithms could be successfully conducted without the full information of all fuzzy densities. Therefore, if the data collection is really difficult, it would be acceptable to take partial aspects to conduct an investigation for identifying general fuzzy measures.

IV. IDENTIFICATION OF GENERAL FUZZY MEASURES

In this section, we first introduce the design of reducing the information demand of general fuzzy measures. Then, we present a flowchart to explain the solution procedure of measure values using genetic algorithms and list the operational steps in detail.

A. Reducing Information Demand

To resolve the difficulty in data collection of general fuzzy measure identification, the author developed a sampling procedure of attribute aspects through experimental design approaches [1]. To facilitate the experimental design, f must be monotonically nondecreasing. Consider a fuzzy measure g of $(X, \mathcal{P}(X))$, where X is a finite attribute set. Let $f\colon X \to [0, 1]$ and $f(x_j)$ is monotonically nondecreasing with respect to j; i.e., $f(x_1) \leq f(x_2) \leq \cdots \leq f(x_n)$. Let $X_i = \{x_i, x_{i+1}, \ldots, x_n\}$, $i = 1, 2, \ldots, n$, then the overall evaluation, $E(\{x_1, x_2, \ldots, x_n\})$ (or $E_{x_1 x_2 \cdots x_n}$ for convenience), of a particular alternative in X is as follows:

$$E(\{x_1, x_2, \ldots, x_n\}) = (c) \int f(x)\, dg$$
$$= f(x_1)g(X_1) + [f(x_2) - f(x_1)]g(X_2)$$
$$+ \cdots + [f(x_n) - f(x_{n-1})]g(X_n). \tag{3}$$

Besides the importance measure, the given data can be replaced by the synthetic evaluation [27], [29], [30]. That is, the input is the values of synthetic evaluation, while the output is the measure values. This is the inverse problem of synthetic evaluation [29]. In this study, we also solve the inverse problem to determine general fuzzy measures.

The author termed the aspects, including attribute x_1, as "basic information aspects," and denoted the collection of basic information aspects as $x_1 \sim$. For instance, $x_1 \sim$ of X means that $x_1 \sim := \{A | A \subseteq X, x_1 \in A\}$. According to the proof result in [1], all of the basic information aspects can cover the information of grades of importance of all aspects in X. Thus, denote the data of $x_1 \sim$ as "sufficient information." Based on the framework of sufficient information, the monotonicity axiom of fuzzy measures can be used to design a sampling

procedure regarding the basic information aspects, as shown in Appendix I. According to the sampling procedure, there may be some aspects left unselected or uncovered. Thus, the information collected using this procedure is termed as "partial information." Partial information significantly reduces the amount of the data requirement and the corresponding investigation procedure is effective and feasible in actual applications. Therefore, based on partial information, we use genetic algorithms to develop an identification method for general fuzzy measures.

Reference [27] developed a genetic algorithm to determine nonadditive set functions. The required data in their study include the measurable function of single-element aspects and the universal set. They gave an example ($n = 4$) to show the efficiency of their method. Although a good result was obtained in this case, the data of the example might be not realistic in many multiattribute decision-making applications. In the light of the measurable function (f) toward a specific alternative (e.g., the public attitude toward the nuclear energy usage), subjects may express similar opinions in evaluating the performance of the alternative. If this situation occurs, the ranking of $f(x_i)$'s will seldom vary much such that the calculation of the Choquet integral may only involve a few measure values of specific aspects. For example, let $X = \{x_1, x_2, x_3, x_4, x_5, x_6\}$ and there are three subjects. The subjects give the evaluation values of an alternative in each single-element aspect and the overall evaluation as shown at the bottom of the page.

Then we can list the following three equations by (3)

$$\begin{aligned} 0.5 =\ & 0.1 + (0.3 - 0.1)g(\{x_2, x_3, x_4, x_5, x_6\}) \\ & + (0.4 - 0.3)g(\{x_3, x_4, x_5, x_6\}) \\ & + (0.5 - 0.4)g(\{x_4, x_5, x_6\}) \\ & + (0.7 - 0.5)g(\{x_5, x_6\}) + (0.9 - 0.7)g_6. \end{aligned}$$
(subject 1)

$$\begin{aligned} 0.7 =\ & 0.3 + (0.5 - 0.3)g(\{x_2, x_3, x_4, x_5, x_6\}) \\ & + (0.7 - 0.5)g(\{x_4, x_5, x_6\}) \\ & + (0.8 - 0.7)g(\{x_5, x_6\}) + (0.9 - 0.8)g_6. \end{aligned}$$
(subject 2)

$$\begin{aligned} 0.4 =\ & 0.1 + (0.2 - 0.1)g(\{x_1, x_3, x_4, x_5, x_6\}) \\ & + (0.3 - 0.2)g(\{x_3, x_4, x_5, x_6\}) \\ & + (0.6 - 0.3)g(\{x_4, x_5, x_6\}) \\ & + (0.7 - 0.6)g(\{x_5, x_6\}) + (0.8 - 0.7)g_6. \end{aligned}$$
(subject 3)

From the above input data, we only cover the information of aspects $\{x_2, x_3, x_4, x_5, x_6\}$, $\{x_3, x_4, x_5, x_6\}$, $\{x_4, x_5, x_6\}$,

$\{x_5, x_6\}$, $\{x_6\}$, and $\{x_1, x_3, x_4, x_5, x_6\}$. Except for these six aspects, the information of other 56 aspects remains uncovered. Thus, when most of the subjects give similar opinions, the amount of human-provided information may be too little to secure an approximate pattern of measure values.

Maybe in the case of λ-fuzzy measure identification, the problem of low information is not critical because of the λ-rule. However, there are no consistent rules among general fuzzy measures of each aspect. Thus, it is very difficult to determine the measure values for all aspects using the limited information. Of course, if the human-provided evaluation values can cover distinct ranking situations, then we can anticipate a good solution of general fuzzy measures. Unfortunately, it is impossible to control people's ranking regarding the evaluation values, and thus researchers have not a scheme to master the amount of covered information on the premise of producing a satisfactory solution.

In addition, according to our simulation results toward the cases of $n = 6, 7, 8$, we found that a local optimal solution (i.e., the error of the evaluation values is very small but the pattern of estimated values is totally unlike the actual measure values) was easily obtained under the situation of similar ranking. Someone may argue that this problem could be lessened through collecting the evaluation data of distinct alternatives. However, the measure values depend on the individual alternatives because the attribute importance is relative to the particular alternative under consideration [14], [22], [25]. Viewed in this light, we still apply the author's sampling procedure to rigidly control the necessary data under the requirement of practical feasibility.

B. Genetic Algorithms for Solving General Fuzzy Measures

Since the evaluation value of each sample aspect is the input in our solution procedure, we may encounter a problem of the Choquet integral with an incomplete series of arguments. In general, the subjective evaluation can be obtained through the investigation. When respondents evaluate the performance of an alternative in a particular aspect, they have already given consideration to the overall importance of the attributes in that aspect. Thus, based on the evaluation values, we can employ the equation of Choquet integrals to derive grades of importance.

When we calculate the Choquet integral, the grade of importance of the discussion universe is one (i.e., $g(X) = 1$) because of the boundary condition. However, when a subset, X', of the discussion universe is considered to be evaluated alone, it may be not subject to the condition, $g(X') = 1$, for the aspect X' ($X' \subset X$). Thus, we normalize the fuzzy measure of aspect X' to render a consistent basis for comparison. Namely, the grade of importance $g(X'_i)$ for each $X'_i \subset X'$ will be divided by $\sup_j g(X'_j)$. Because the grades of importance meet the mono-

Subject	$f(x_1)$	$f(x_2)$	$f(x_3)$	$f(x_4)$	$f(x_5)$	$f(x_6)$	Overall evaluation
1	0.1	0.3	0.4	0.5	0.7	0/9	0.5
2	0.3	0.5	0.5	0.7	0.8	0.9	0.7
3	0.2	0.1	0.3	0.6	0.7	0.8	0.4

tonicity axiom, it follows that $\sup_j g(X'_j) = g(X')$. Let $X' = \{x_{i_1}, x_{i_2}, \ldots, x_{i_k}\}$ and $f(x_{i_1}) \leq f(x_{i_2}) \leq \cdots \leq f(x_{i_k})$. In addition, let $X_j = \{x_{i_j}, x_{i_{j+1}}, \ldots x_{i_k}\}$, $j = 1, 2, \ldots, k$. The overall evaluation, $E(\{x_{i_1}, x_{i_2}, \ldots, x_{i_k}\})$ (or $E_{x_{i_1} x_{i_2} \cdots x_{i_k}}$ for convenience), of an alternative in aspect $\{x_{i_1}, x_{i_2}, \ldots, x_{i_k}\}$ is as follows:

$$
\begin{aligned}
E(\{x_{i_1}, &x_{i_2}, \ldots, x_{i_k}\}) \\
&= f(x_{i_2}) + [f(x_{i_2}) - f(x_{i_1})] \cdot \frac{g(X_2)}{g(X_1)} \\
&\quad + [f(x_{i_3}) - f(x_{i_2})] \cdot \frac{g(X_3)}{g(X_1)} + \cdots \\
&\quad + [f(x_{i_k}) - f(x_{i_{k-1}})] \cdot \frac{g(X_k)}{g(X_1)}.
\end{aligned} \tag{4}
$$

In the following, we apply genetic algorithms to determine the values of general fuzzy measures. When genetic algorithms are applied to an optimization procedure, a chromosome is equivalent to a solution during the searching process, while a gene is taken as a variable. Moreover, the population refers to the collection of all chromosomes. Genetic algorithms are based on a parallel structure, and a generation is constructed by continuously conducting a parallel search to the entire population. The optimization process refers to the usage of generation evolution until a generation has matured. Thus, the population is also the collection of all current solutions through a parallel search.

There are three main operators in each generation. First, the reproduction operator reallocates the search domain according to the solution performance. The domain with the better performance will be allocated more search points. Next, the crossover operator is to exchange the partial superior information during the search process. Last, the mutation operator is used to conduct a neighborhood search around each chromosome (i.e., the search point). The solution procedure of genetic algorithms is presented in Fig. 1.

1) *Initialization:* the determination of the initial values of search points.
2) *Calculation of Fitness:* the fitness is defined by the objective and conformance function, where the conformance values are obtained from the constraints. Moreover, fitness determines the weighting during the reproduction operation.
3) *Reproduction Operator:* reallocates the search points according to the fitness.
4) *Crossover Operator:* parts of the variables are exchanged between two chromosomes. The chromosomes with higher fitness can bring out more offspring generations after the reproduction operation.
5) *Mutation Operator:* conducts a local search in the neighborhood of every chromosome.
6) *Parameter Control:* refers to the fact that users can control the proportion in each operator so as to derive the individual effects needed.

C. Detail Design

From the boundary conditions of fuzzy measures, the grades of importance of the empty set and universal set are zero and
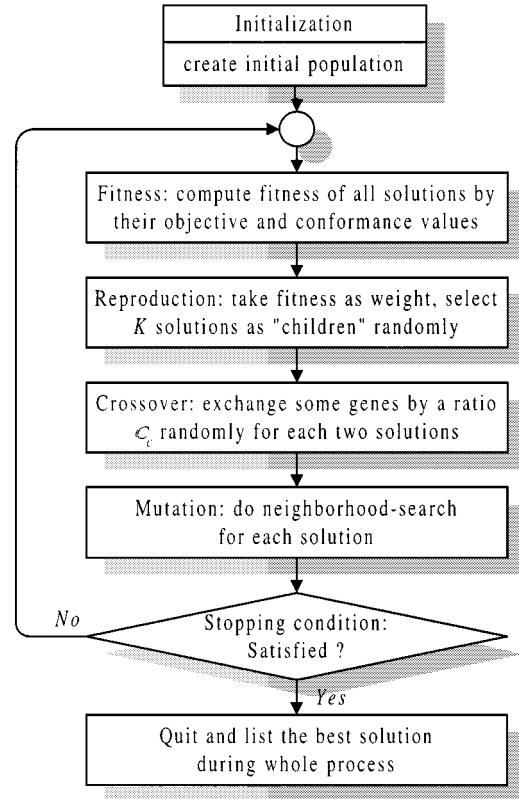

Fig. 1. Solution procedure of genetic algorithms.

one, respectively. Moreover, according to the sampling procedure under partial information, the grades of importance of all aspects in the first aspect set will be investigated. The measure values of the basic information aspects in the second aspect set can be also exactly determined (see Appendix I). Therefore, after the investigation has been conducted, the grades of importance already known include $g(\phi) = 0, g(X) = 1, g_i(i = 1, 2, \ldots, n)$, and $g(\{x_1, x_j\})(j = 2, 3, \ldots, n)$. Nevertheless, the grades of importance for other aspects still remain unknown.

We consider every chromosome as a solution during the searching process, while each gene code represents the grade of importance of an aspect. Thus, the chromosome encoding is denoted as $(\{g(A)|A \in \mathcal{P}(X)\backslash\phi\})$; i.e., each chromosome can be represented by a vector with $(2^n - 1)$ real-valued elements within the interval [0,1].

In the following, we elaborate on the initialization of the population, establishment of the fitness function, and the detailed design of the three genetic operators.

1) *Initialization of Population:* Since it is difficult for a random initialization procedure to locate a solution that is consistent with monotonicity, we propose an efficient method to conduct the initialization procedures regarding each of the chromosomes.

   a) Let $\mathbf{U}^0$ denote the collection of aspects with initial given grades of importance, i.e., $\mathbf{U}^0 = \{\phi, \{x_1\}, \{x_2\}, \ldots, \{x_n\}, \{x_1, x_2\}, \{x_1, x_3\}, \ldots, \{x_1, x_n\}, X\}$. Let $\mathbf{U}$ be the collection of aspects with assigned grades of importance. Thus, $\mathbf{U} = \mathbf{U}^0$ in the very beginning. The collection of aspects

with unknown grades of importance is $\mathbf{U}', \mathbf{U}' = \mathcal{P}(X) \backslash \mathbf{U}$.

b) Select any element U from $\mathbf{U}'$. According to the monotonicity axiom, let $g(U)$ be a continuous random variable, uniformly distributed within the interval $[g^-(U), g^+(U)]$, where

$$g^-(U) = \sup\{g(V)|V \subset U, V \in \mathbf{U}\},$$

and

$$g^+(U) = \inf\{g(V)|V \supset U, V \in \mathbf{U}\}.$$

That is, $g(U) = random\ (g^-(U), g^+(U))$.

c) Classify U into the given collection. Let $\mathbf{U}^{(\mathrm{new})} = \mathbf{U}^{(\mathrm{old})} \cup \{U\}$, $\mathbf{U}'^{(\mathrm{new})} = \mathbf{U}'^{(\mathrm{old})} \backslash \{U\}$, and repeat the aforementioned process until $\mathbf{U}'$ becomes an empty set.

2) *Calculation of Fitness:* Degree of fitness is determined by the objective function and the constraints of a programming model. If any solution is given, the objective function value and constraint values can be attained. The objective function is generally defined as the error sum of squares between the estimated values and the investigated data of evaluations. Let $\hat{E}(A)$ and $E(A)$ respectively represent the human-provided evaluation value (obtained by investigation) and the estimated evaluation value of an alternative in aspect A. For comparison, we use the average error sum of squares to redefine the objective function, which is denoted as Z. Additionally, the constraint is the monotonicity condition.

Since the evaluation values of aspects in the first aspect set and $x_1 \sim$ in the second aspect set can be derived directly from the investigation results, we use the aspects with given evaluations from the third to nth aspect sets to define the solution objective. Let Ξ denote the collection of aspects with investigated data of evaluations from the third to nth aspect sets, while $|\Xi|$ indicates the number of elements in Ξ. Then, the solution objective and constraints for general fuzzy measure identification are as follows:

$$\min Z = \sqrt{\frac{\sum\limits_{A \in \Xi} [E(A) - \hat{E}(A)]^2}{|\Xi|}} \tag{5}$$

subject to $g^-(U) \leq g(U) \leq g^+(U) \quad \forall U \in \mathcal{P}(X)$ (6)

where

$$g^-(U) = \sup\{g(V)|V = U \backslash \{x_i\}, x_i \in U\}, \tag{7}$$

$$g^+(U) = \inf\{g(V)|V = U \cup \{x_i\}, x_i \in X \backslash U\}. \tag{8}$$

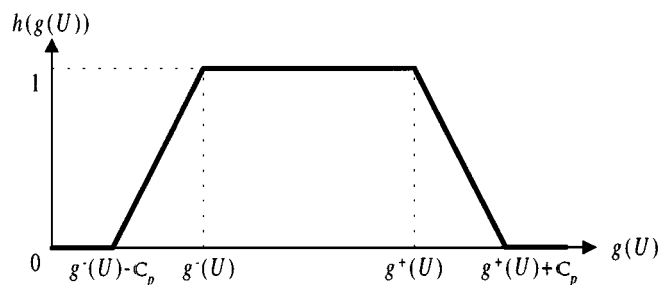Equations (6)–(8) are referring to the monotonicity axiom.

Fig. 2.   Tolerance interval of the conformance function ($\mathbb{C}_p$).

Due to the possibility that crossover and reproduction operators could produce grades of importance that disobey monotonicity, a conformance function h is designated to lower the fitness of an unqualified chromosome. Then, the reproduction operator will filter out the chromosomes with low conformance degrees. To conduct a flexible search, we allow searching outside the feasible domain but still near the boundary by assigning the tolerance interval, $\mathbb{C}_p$, to the conformance. The conformance function used here is a trapezoidal fuzzy number, as indicated in Fig. 2. The tolerance interval $\mathbb{C}_p$ gradually decreases to zero until the search process is completed. Meanwhile, no chromosomes violating the monotonicity constraint will be allowed. The conformance function of the aspect with importance $g(U)$ is denoted as $h(g(U))$, and is defined in (9) at the bottom of the page.

The conformance function values of aspects with unknown grades of importance can be used to define the overall conformance, H, of each chromosome:

$$H = \inf\{h(gU))|U \in \mathcal{P}(X) \backslash \mathbf{U}^0\}. \tag{10}$$

3) *Reproduction Operator:* First, we normalize the objective value of each chromosome and take the conformance function value as the weight. Then, we integrate the objective and the conformance values into the fitness of every chromosome. Next, we conduct a weighted random sampling until the sample number is identical with the amount of the original population. Let $\mathbb{K}$ denote the population size (i.e., the number of chromosomes), and the indicator, k, as the serial number of chromosomes in the population. The detailed steps are as follows.

a) First, we must find the best solution, Z^+, and the worst solution, Z^-, in the current population, where

$$Z^+ = \min_{k \in [1, \mathbb{K}]} Z^k, \quad \text{and}$$

$$Z^- = \max_{k \in [1, \mathbb{K}]} Z^k.$$

$$h(g(U)) = \begin{cases} \dfrac{g(U) - g^-(U) + \mathbb{C}_p}{\mathbb{C}_p}, & g^-(U) - \mathbb{C}_p \leq g(U) < g^-(U); \\ 1, & g^-(U) \leq g(U) < g^+(U); \\ \dfrac{g^+(U) - g(U) + C_p}{\mathbb{C}_p}, & g^+(U) \leq g(U) < g^+(U) + \mathbb{C}_p; \\ 0, & \text{otherwise.} \end{cases} \tag{9}$$

b) The objective value, Z^k, of the kth chromosome and the overall conformance value, H^k, are normalized into fitness, F^k. The significance of the conformance function here is the extent of nonpunishment if the constraint holds:

$$F^k = H^k \cdot \frac{Z^k - Z^-}{Z^+ - Z^-} \ \forall k \in \{1, 2, \ldots, \mathbb{K}\}. \tag{11}$$

c) Calculate the accumulated fitness, $\overline{F}^k$, which represents the total of fitness of the entire population.

$$\overline{F}^k = \sum_{i=1}^{k} F^i \ \forall k \in \{1, 2, \ldots, \mathbb{K}\}. \tag{12}$$

d) Reproduction is implemented as a linear search through a Roulette wheel with slots weighted in proportion to solution fitness values. Let $\mathbb{R}_p$ represent a continuous random variable that is uniformly distributed over the interval $[0, \overline{F}^k]$. If $\mathbb{R}_p \geq \overline{F}^{k-1}$, then all information of the kth chromosome will be added to the next new generation. It is noted that $\overline{F}^0 = 0$.

e) Repeat the above steps until the chromosome number of the offspring generation is the same as that of the parent.

4) *Crossover Operator:* Generally, the crossover operator deals with two chromosomes at a time, but we will employ a multipoint crossover in this study. In other words, every two adjacent variables might, at any rate, be cut off. The multipoint crossover operator needs only to designate a crossover rate, $\mathbb{C}_c$; then, select any random number, $\mathbb{R}_c$, for every variable. $\mathbb{R}_c$ represents a continuous random variable that is uniformly distributed over the interval $[0,1]$, that is, $\mathbb{R}_c = random(0,1)$. If $\mathbb{R}_c < \mathbb{C}_c$, then exchange. The detailed operation method is as follows:

a) Select any two chromosomes (called the ith and jth chromosomes) from the population, then the grades of importance of any unknown aspect U $(U \in \boldsymbol{\mathcal{P}}(X) \backslash \mathbf{U}^0)$ will be $g^i(U)$ and $g^j(U)$, respectively.

b) Select a random number, $\mathbb{R}_c$, toward every U, and conduct the exchange judgment. That is,

$$g^i(U) = \begin{cases} g^j(U), & \text{if } \mathbb{R}_c = random(0,1) < \mathbb{C}_c \\ g^i(U), & \text{otherwise} \end{cases}$$
$$\forall U \in \boldsymbol{\mathcal{P}}(X) \backslash \mathbf{U}^0. \tag{13}$$

c) Select any two chromosomes from the rest of the population, and repeat the aforementioned steps until all of the chromosomes have been addressed.

5) *Mutation Operator:* The mutation operator toward the real variable involves adding a slight change, and the range of the amount of change is controlled by the mutation rate, $\mathbb{C}_m$. The steps of the mutation operation are as follows.

a) Let $g^k(U)$ denote the grade of importance of the kth chromosome in aspect U. For all $U \in \boldsymbol{\mathcal{P}}(X) \backslash \mathbf{U}^0$, implement the following mutation operation:

$$g^k(U)^{(\text{new})} = g^k(U)^{(\text{old})} + random\ (-\mathbb{C}_m, \mathbb{C}_m)$$
$$\forall U \in \boldsymbol{\mathcal{P}}(X) \backslash \mathbf{U}^0. \tag{14}$$

b) Conduct the aforementioned step to every chromosome until all chromosomes in the population have been addressed.

6) *Parameter Specification:* There are several parameters needed to be specified in genetic algorithms, including population size, stopping conditions, and each rate parameter required in the genetic operation. The population size has influence upon the use of memory space and the stability of sampling. The stopping condition is related to the implementation time and the quality of results. It can be specified by the CPU implementation time, the change of objective values, the expected quality of the solutions, and the maximum generation size. Since the previous three methods are unable to control the actual search steps in different computer hardware, we decided to use the maximum generation size as the stopping condition. Finally, each rate parameter would primarily employ piecewise linear functions. We disclose more details concerning the experiment analysis in the next section.

V. EXPERIMENT ANALYSIS

In this section, we conducted an experimental analysis to test the validity of our proposed method. First, we simulated a set of experimental data according to some requirements. Each attribute is categorized into several selected classes respectively, and these classes refer to distinct characteristics of individual attributes. Then, for facilitating the experimental design, the single-attribute evaluations have to fulfill $f(x_1) \leq f(x_2) \leq \cdots \leq f(x_n)$. The generation process of simulated data will be illustrated in the following.

A. Design of Experimental Data

The experiment illustrates the identification of general fuzzy measures using genetic algorithms for $n = 7$. We use the fuzzy densities and the mean degree of overlapping between an attribute and the other attributes to demonstrate the characteristics of each attribute, where the definition of the degree of overlap, η_i, is cited from [13], [19]. Based on the levels of overlapping and importance, the experimental data was designed to represent several specific classes.

As shown in Fig. 3, according to the degree of overlap and grade of importance, all attributes can be categorized into nine classes. Class 1 indicates that those attributes can provide nonoverlap information and have a great influence on the model structure. In addition, Class 1 has high a grade of importance. Attributes in Class 3 also have their influence, but

	low grade of importance $g_i \in (0, 0.07]$	medium grade of importance $g_i \in (0.07, 0.14]$	high grade of importance $g_i \in (0.14, 1)$
non-overlapping $\eta_i \in [0, 1]$	**Class 3** x_4 $g_4=0.05$ $\eta_4=0.278$	**Class 2** – –	**Class 1** x_5 $g_5=0.15$ $\eta_5=0.102$
low overlapping $\eta_i \in [-0.5, 0)$	**Class 6** – –	**Class 5** x_7 $g_7=0.11$ $\eta_7=-0.240$	**Class 4** x_3 $g_3=0.17$ $\eta_3=-0.299$
high overlapping $\eta_i \in [-1, -0.5)$	**Class 9** x_6 $g_6=0.06$ $\eta_6=-0.501$	**Class 8** x_2 $g_2=0.09$ $\eta_2=-0.538$	**Class 7** x_1 $g_1=0.21$ $\eta_1=-0.545$

Fig. 3. Category of each attribute in the experimental data $(n = 7)$.

TABLE I
ASPECTS WITH ERRORS LARGER THAN 0.01 IN THE THIRD ASPECT SET

Illustration	Aspect (absolute value of the error)		
Aspects with errors larger than 0.0200	$\{x_2,x_4,x_6\}$(0.0270) $\{x_4,x_5,x_6\}$(0.0203)	$\{x_3,x_5,x_7\}$(0.0249)	$\{x_1,x_4,x_7\}$(0.0219)
Aspects with errors larger than 0.0100 and no more than 0.0200	$\{x_1,x_6,x_7\}$(0.0195) $\{x_2,x_4,x_5\}$(0.0157) $\{x_1,x_5,x_7\}$(0.0101)	$\{x_1,x_3,x_6\}$(0.0183) $\{x_2,x_6,x_7\}$(0.0126)	$\{x_1,x_5,x_6\}$(0.0180) $\{x_3,x_5,x_6\}$(0.0109)

the grades of importance are low. Class 7 indicates that the attributes with high grades of importance have a high degree of overlap with other attributes. The attributes in Class 9 make no salient contributions to the provision of nonoverlap information and to the grade of importance. The most common situation is Class 5, which has low overlapping and a medium grade of importance. We first selected the five classes above, and they are respectively represented by one attribute. In addition, for those nonparticular situations in Classes 2, 4, 6, and 8, any two classes are selected and each is represented by one attribute. Thus, seven classes were selected. We simulated the relevant data and the single-attribute evaluations must fulfill $f(x_1) \leq f(x_2) \leq \cdots \leq f(x_7)$ to implement the experimental design. The simulated experimental data are listed in Appendix II and x_5 represents Class 1, x_4 for Class 3, x_3 for Class 4, x_7 for Class 5, x_1 for Class 7, x_2 for Class 8, and x_6 for Class 9. The solution result for the third aspect set is shown in Fig. 9. In general, the error is greater than that in the second aspect set. The aspects with errors (absolute values) larger than 0.0100 are listed in Table I, where aspects $\{x_2, x_4, x_6\}$, $\{x_3, x_5, x_7\}$, $\{x_1, x_4, x_7\}$ and $\{x_4, x_5, x_6\}$ have a little greater difference between the estimated and actual values of the grades of importance. Even so, the error, as a whole, remains to be insignificant and the solution quality is very satisfactory.

B. Sampling Process of Attribute Aspects

After simulating the experimental data (including the measure values of each aspect and the evaluation values of each single-attribute aspect), we conducted the sampling procedure under partial information to determine the sample aspects, as indicated in Fig. 4.

Step 1) for the first aspect set
Since the first aspect set provides the primary information, the fuzzy density g_i $(= \hat{g}_i)$ and evaluation value $f(x_i)$ $(= \hat{f}(x_i))$ of each single-at-

tribute aspect must be investigated in practice, where $i = 1, 2, \ldots, 7$.

Step 2) for $x_1 \sim$ of the second aspect set
The exact solution for $g(\{x_1, x_i\})$ $(i = 2, 3, \ldots, 7)$ can be uniquely derived, so it is necessary to investigate the data of $E_{x_1 x_i}$ $(= \hat{E}_{x_1 x_i})$.

Step 3) for the seventh aspect set
The overall evaluation, $\hat{E}_{x_1 x_2 \ldots x_n}$, of the universal set must be surveyed.

Step 4) for $x_1 \sim$ of the kth aspect set, $k = 4, 5, 6$.
a) Select aspect $\{x_1, x_2, x_3, x_5, x_6, x_7\}$ from $x_1 \sim$ of the sixth aspect set, and this aspect covers the information for aspects $\{x_1, x_2, x_3, x_5, x_6\}$, $\{x_1, x_2, x_3, x_5, x_7\}$, $\{x_1, x_2, x_3, x_6, x_7\}$, $\{x_1, x_2, x_5, x_6, x_7\}$, and $\{x_1, x_3, x_5, x_6, x_7\}$ in the fifth aspect set.
b) Select aspect $\{x_1, x_2, x_4, x_5, x_6\}$ from the unmarked aspects in x_1 of the fifth aspect set, and this aspect covers the information for aspects $\{x_1, x_2, x_4, x_5\}$, $\{x_1, x_2, x_4, x_6\}$, $\{x_1, x_2, x_5, x_6\}$, and $\{x_1, x_4, x_5, x_6\}$ in the fourth aspect set.
c) Examine other aspects (including those marked aspects) in the fifth aspect set. Two additional aspects, which can cover the information of four unmarked aspects in the fourth aspect set are selected, including $\{x_1, x_2, x_3, x_4, x_7\}$ and $\{x_1, x_3, x_5, x_6, x_7\}$.
d) Continue to examine other aspects in the fourth aspect set. Aspects $\{x_1, x_3, x_4, x_5\}$, $\{x_1, x_2, x_3, x_6\}$, $\{x_1, x_2, x_4, x_7\}$, and $\{x_1, x_5, x_6, x_7\}$ are also selected from the fourth aspect set.

Step 5) for x_1 of the third aspect set
Because the investigated data in the lower aspect set are relatively accurate, we hope to capture all of the aspect information of the third aspect set. Thus, those aspects uncovered by the selected samples of the fourth aspect set must be explored in practice, including $\{x_1, x_2, x_5\}$, $\{x_1, x_3, x_7\}$, and $\{x_1, x_4, x_6\}$.

According to the results from aspect sampling, we can calculate the evaluation values of sample aspects using the simulation data. Those evaluation values are considered as the objective upon which the subsequent solution procedure can be based. The details of the evaluation values are listed in Appendix II.

C. Experiment Results

To show the feasibility and applicability of the solution procedure for general fuzzy measures using genetic algorithms, we applied the proposed method to the experimental data. Besides the boundary conditions, the input data include g_i $(i = 1, 2, \ldots, 7)$, $g(\{x_1, x_j\})$ $(j = 2, 3, \ldots, 7)$, $f(x_i)$ $(i = 1, 2, \ldots, 7)$, $E_{x_1 x_h}$ $(j = 2, 3, \ldots, 7)$, and the evaluation values of twelve sample aspects.

According to the sampling procedure, we selected twelve sample aspects: $\{x_1, x_2, x_5\}$, $\{x_1, x_3, x_7\}$, $\{x_1, x_4, x_6\}$, $\{x_1,$
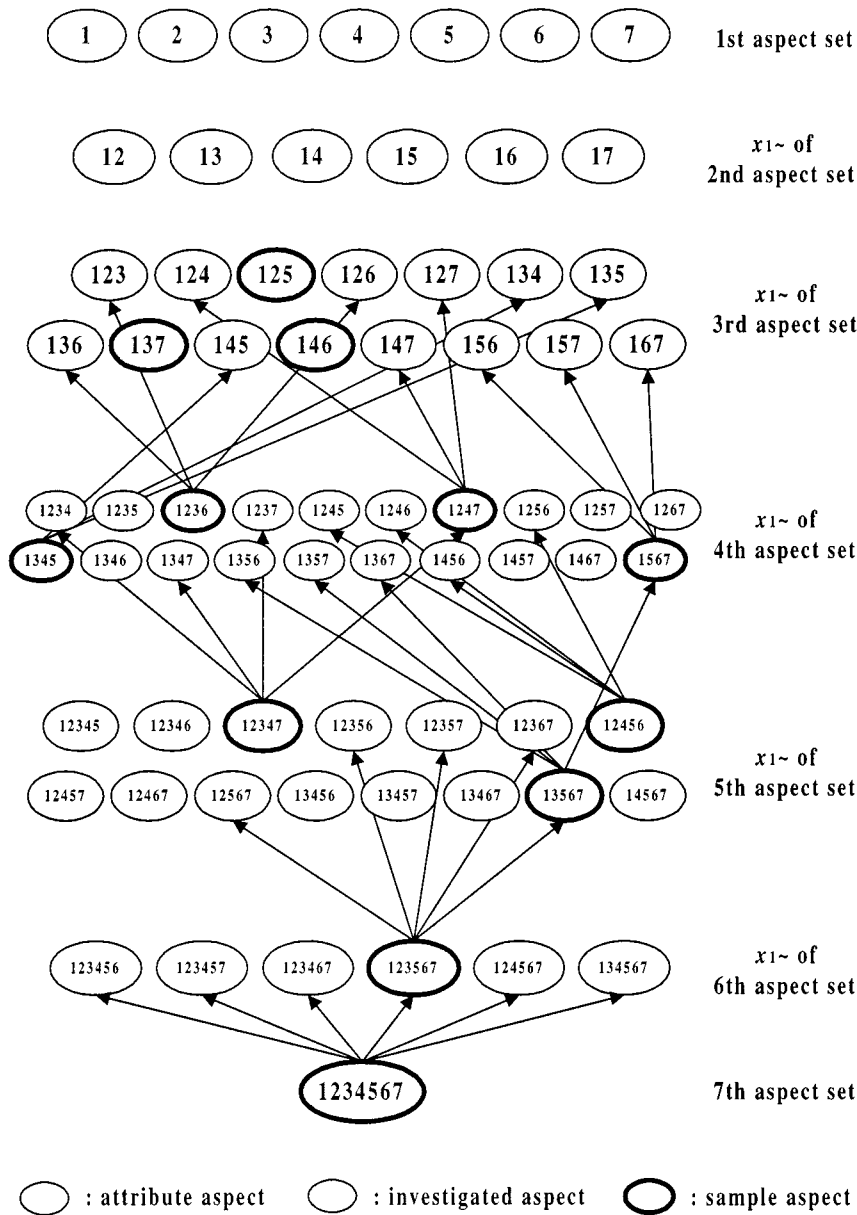
Fig. 4. Sampling procedure of attribute aspects ($n = 7$).

$x_2, x_3, x_6\}$, $\{x_1, x_2, x_4, x_7\}$, $\{x_1, x_3, x_4, x_5\}$, $\{x_1, x_5, x_6, x_7\}$, $\{x_1, x_2, x_3, x_4, x_7\}$, $\{x_1, x_2, x_4, x_5, x_6\}$, $\{x_1, x_3, x_5, x_6, x_7\}$, $\{x_1, x_2, x_3, x_5, x_6, x_7\}$, and $\{x_1, x_2, x_3, x_4, x_5, x_6, x_7\}$. The actual evaluation values of these aspects can be obtained through the investigation in practice. We used the twelve aspects to specify the objective equation, i.e., minimal average error sum of squares.

In using genetic algorithms to solve general fuzzy measures with the proposed procedure, there are some parameters for users to control. To determine the favorable range of parameter values and obtain desirable performance within such a range, we conducted pilot tests on the experimental data. According to the trial-and-error results, the population size, $\mathbb{K}$, is designated as 30. Let $\mathbb{G}$ be the generation number. The stopping condition is specified by defining the maximum of generation size, $\mathbb{G}^{\max}$, which is 100. In regard to each of the rate parameters needed in
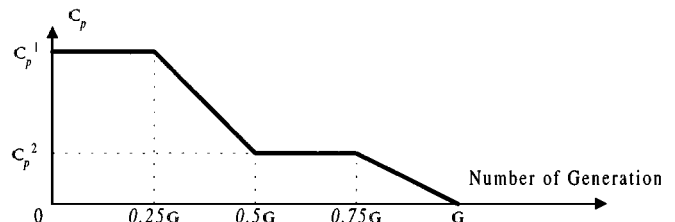
Fig. 5. Tolerance interval of the conformance function ($\mathbb{C}_p$).

the genetic operation, the tolerance interval, $\mathbb{C}_p$, concerning the conformance function is as indicated in Fig. 5, where $\mathbb{C}_p^1 = 0.1$ and $\mathbb{C}_p^2 = 0.01$. The specification of the crossover rate, $\mathbb{C}_c$, is as shown in Fig. 6, where $\mathbb{C}_c^1 = 0.1$ and $\mathbb{C}_c^2 = 0.5$. Moreover, the specification of the mutation rate, $\mathbb{C}_m$, is as seen in Fig. 7, where $\mathbb{C}_m^1 = 0.1$ and $\mathbb{C}_m^2 = 0.01$.
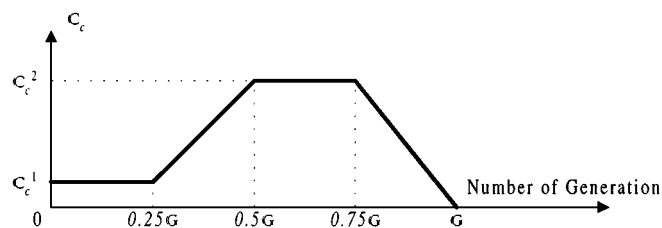
Fig. 6. Parameter specification of the crossover rate, $\mathbb{C}_c$. Parameter specification of the mutation rate, $\mathbb{C}_m$.
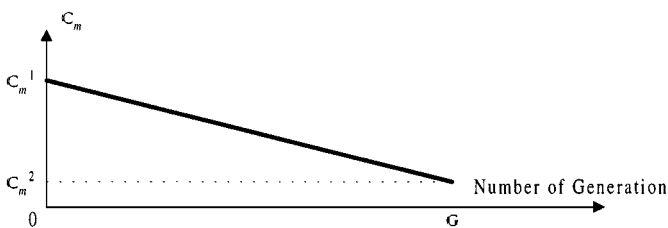
Fig. 7. Parameter specification of the mutation rate, $\mathbb{C}_m$.
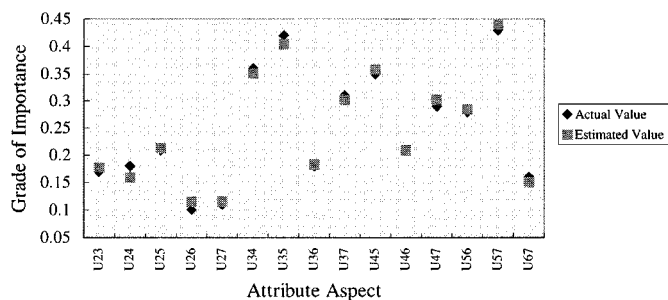
Fig. 8. Solution result of grades of importance in the second aspect set.
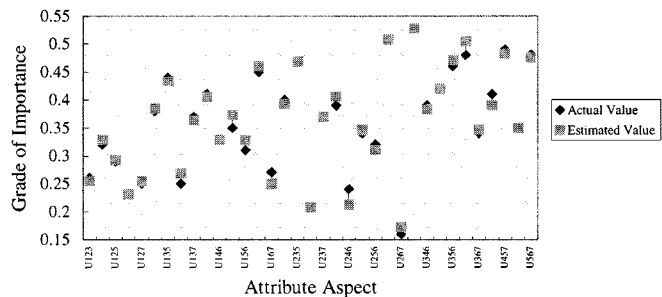
Fig. 9. Solution result of grades of importance in the third aspect set.

Fig. 10. Solution result of grades of importance in the fourth aspect set.

TABLE II
ASPECTS WITH ERRORS LARGER THAN 0.01 IN THE FOURTH ASPECT SET

Illustration	Aspect (absolute value of the error)
Aspects with errors larger than 0.0400	$\{x_1,x_2,x_3,x_4\}(0.0574)$ $\{x_2,x_3,x_5,x_7\}(0.0445)$
Aspects with errors larger than 0.0300 and no more than 0.0400	$\{x_2,x_5,x_6,x_7\}(0.0377)$ $\{x_1,x_3,x_5,x_7\}(0.0310)$
Aspects with errors larger than 0.0200 and no more than 0.0300	$\{x_2,x_3,x_4,x_6\}(0.0282)$ $\{x_1,x_3,x_5,x_6\}(0.0249)$ $\{x_1,x_2,x_3,x_5\}(0.0247)$ $\{x_2,x_3,x_4,x_5\}(0.0237)$ $\{x_3,x_4,x_6,x_7\}(0.0224)$ $\{x_2,x_4,x_5,x_7\}(0.0219)$ $\{x_1,x_4,x_5,x_7\}(0.0208)$
Aspects with errors larger than 0.0100 and no more than 0.0200	$\{x_2,x_4,x_6,x_7\}(0.0191)$ $\{x_1,x_3,x_4,x_7\}(0.0166)$ $\{x_1,x_2,x_4,x_6\}(0.0154)$ $\{x_1,x_3,x_6,x_7\}(0.0153)$ $\{x_2,x_3,x_4,x_7\}(0.0149)$ $\{x_1,x_2,x_4,x_7\}(0.0135)$ $\{x_3,x_4,x_5,x_7\}(0.0133)$ $\{x_1,x_2,x_3,x_7\}(0.0114)$ $\{x_3,x_4,x_5,x_6\}(0.0111)$ $\{x_1,x_4,x_5,x_6\}(0.0105)$
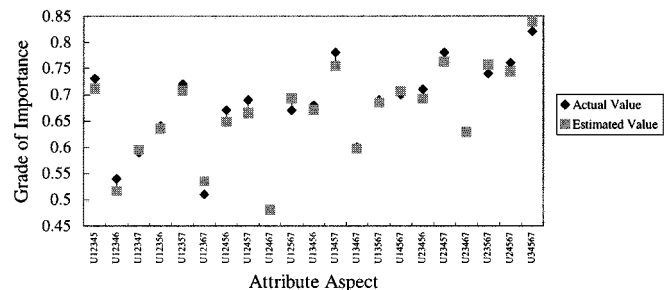
Fig. 11. Solution result of grades of importance in the fifth aspect set.

TABLE III
ASPECTS WITH ERRORS LARGER THAN 0.01 IN THE FIFTH ASPECT SET

| Illustration	Aspect (absolute value of the error)	
Aspects with errors larger than 0.0200 and no more than 0.0300	$\{x_1,x_3,x_4,x_5,x_7\}(0.0259)$	$\{x_1,x_2,x_3,x_6,x_7\}(0.0252)$
	$\{x_1,x_2,x_4,x_5,x_7\}(0.0250)$	$\{x_1,x_2,x_3,x_4,x_6\}(0.0232)$
	$\{x_1,x_2,x_5,x_6,x_7\}(0.0228)$	$\{x_1,x_2,x_4,x_5,x_6\}(0.0220)$
Aspects with errors larger than 0.0100 and no more than 0.0200	$\{x_1,x_2,x_3,x_4,x_5\}(0.0183)$	$\{x_2,x_3,x_4,x_5,x_6\}(0.0183)$
	$\{x_2,x_3,x_4,x_5,x_7\}(0.0179)$	$\{x_3,x_4,x_5,x_6,x_7\}(0.0178)$
	$\{x_2,x_4,x_5,x_6,x_7\}(0.0166)$	$\{x_2,x_3,x_5,x_6,x_7\}(0.0162)$
	$\{x_1,x_2,x_3,x_5,x_7\}(0.0121)$	

The solution results of measure values are exhibited in Appendix III, where an attribute aspect is indicated by U. For example, U237 stands for aspect $\{x_2,x_3,x_7\}$ and U13467 represents aspect $\{x_1,x_3,x_4,x_6,x_7\}$. For most aspects, the difference between the estimated and actual values of the grade of importance is rather slight. Thus, the identification procedure using genetic algorithms has an excellent performance in solving general fuzzy measures.

Fig. 8 shows the solution result for aspects exclusive of $x_1\sim$ in the second aspect set. Here, we only consider the absolute value of errors. The aspect with the greater difference between the estimated and actual values of the grade of importance is $\{x_2,x_4\}$ with error 0.0209, seconded by $\{x_3,x_5\}$ with error 0.0157, then $\{x_2,x_6\}$ with error 0.0149, and next $\{x_4,x_7\}$

with error 0.0119. As for the other aspects, the difference is extremely slim. This indicates that the estimated results for grades of importance are very close to the actual values.

As for the fourth aspect set, Fig. 10 shows that the difference between the estimated and actual values becomes large, where the error 0.0574 in $\{x_1,x_2,x_3,x_4\}$ and 0.0445 in $\{x_2,x_3,x_5,x_7\}$ are most prominent. The aspects with errors lying within (0.0300,0.0400], (0.0200,0.0300] and (0.0100,0.0200] are listed in Table II. The errors of the remaining aspects in this aspect set are very slim.

The solution result of the fifth aspect set is indicated in Fig. 11. Additionally, the aspects with errors lying within (0.0200,0.0300] and (0.0100,0.0200] are listed in Table III.
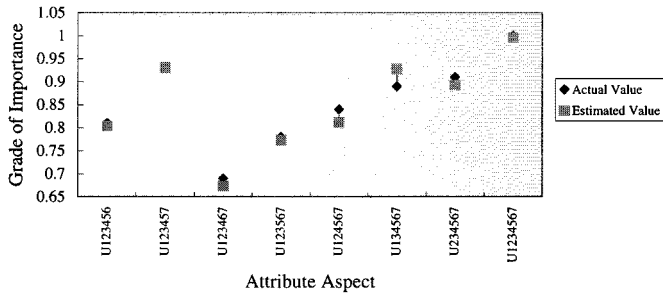
Fig. 12. Solution results of grades of importance in the sixth and seventh aspect sets.

TABLE IV
ESTIMATED RESULT OF EVALUATIONS FOR SAMPLE ASPECTS

Aspect	Estimation	Error	Aspect	Estimation	Error
$\{x_1,x_2,x_5\}$	0.2783	-0.0007	$\{x_1,x_5,x_6,x_7\}$	0.3708	0.0012
$\{x_1,x_3,x_7\}$	0.2692	0.0008	$\{x_1,x_2,x_3,x_4,x_7\}$	0.2882	0.0001
$\{x_1,x_4,x_6\}$	0.2853	-0.0002	$\{x_1,x_2,x_4,x_5,x_6\}$	0.2970	0.0004
$\{x_1,x_2,x_3,x_6\}$	0.2267	0.0017	$\{x_1,x_3,x_5,x_6,x_7\}$	0.3317	0.0014
$\{x_1,x_2,x_4,x_7\}$	0.3294	-0.0009	$\{x_1,x_2,x_3,x_5,x_6,x_7\}$	0.3261	0.0028
$\{x_1,x_3,x_4,x_5\}$	0.2900	-0.0003	$\{x_1,x_2,x_3,x_4,x_5,x_6,x_7\}$	0.3179	0.0001

Comparing Figs. 10 and 11, the error in the fifth aspect set is smaller than that of the fourth aspect set on average.

Finally, with respect to the sixth and seventh aspect sets (Fig. 12), the error 0.0379 in aspect $\{x_1,x_3,x_4,x_5,x_6,x_7\}$ comes out the highest, trailed by $\{x_1,x_2,x_4,x_5,x_6,x_7\}$ with error 0.0283, $\{x_2,x_3,x_4,x_5,x_6,x_7\}$ with error 0.0172, and $\{x_1,x_2,x_3,x_4,x_6,x_7\}$ with error 0.0168.

In regard to the solution objective, the average error sum of squares is $Z = 0.0009$, indicating excellent performance using genetic algorithms to solve general fuzzy measures under partial information. The estimated evaluation values and errors of the 12 sample aspects are listed in Table IV. The aspect with the highest error is $\{x_1,x_2,x_3,x_5,x_6,x_7\}$, and the difference between the estimated value and the actual datum is 0.0028, trailed by aspect $\{x_1,x_2,x_3,x_6\}$ with error 0.0017. As a whole, the error of each aspect is negligible.

To summarize, the experiment result using genetic algorithms to solve general fuzzy measures under partial information is desirable. This indicates that even with a lack of complete information, as long as the sampling procedure under partial information is employed, most information can be adequately captured with the least number of sample aspects. Then, genetic algorithms can be used as a solution strategy for identifying general fuzzy measures to obtain a satisfactory estimated result.

VI. CONCLUSIONS

To resolve the difficulty that general fuzzy measures expose in data collection and identification, we applied genetic algorithms to develop a solution procedure for fuzzy measure values based on partial information. The corresponding detailed design was also proposed to facilitate high efficiency of genetic algorithms, including the initialization of the population, establishment of the fitness function, and detailed design of the three genetic operators.

To show the applicability of our proposed method, we simulated the experimental data that are representative of several typ-

ical classes. The experiment results showed that using genetic algorithms to identify general fuzzy measures under partial information performs very well. Moreover, the average error sum of squares, Z, is only 0.0009, showing a satisfactory solution quality.

APPENDIX I
SAMPLING PROCEDURE

The first author developed a sampling procedure to surmount the data collection difficulty when using general fuzzy measures [1]. She used the concept that any aspect of the kth aspect set can, at most, cover the information of $(k-1)$ unrepeated aspects in the $(k-1)$th aspect set. To reduce the sample size, the information of each aspect would be covered by no more than one aspect (excluding itself). The sampling procedure for each aspect set is described as follows.

Step 1) First aspect set

This aspect set provide the essential information, so the fuzzy density g_i $(= \hat{g}_i)$ and evaluation value $f(x_i)$ $(= \hat{f}(x_i))$ of each attribute must be investigated, where $i = 1, 2, \ldots, n$.

Step 2) $x_1 \sim$ of the second aspect set

Since the exact solution of $g(\{x_1, x_j\})$ $(j = 2, 3, \ldots, n)$ can be uniquely determined, it is necessary to investigate the data of $E(\{x_1, x_j\})$ $(= \hat{E}(\{x_1, x_j\}))$. From (4), we know that for $j = 2, 3, \ldots, n$,

$$f(x_1) + [f(x_j) - f(x_1)] \cdot \frac{g_j}{g(\{x_1, x_j\})} = \hat{E}(\{x_1, x_j\}).$$

Since $g_j, f(x_1), f(x_j)$, and $\hat{E}(\{x_1, x_j\})$ are given, $g(\{x_1, x_j\})$ can be derived:

$$g(\{x_1, x_j\}) = \frac{[f(x_j) - f(x_1)] \cdot g_j}{\hat{E}(\{x_1, x_j\}) - f(x_1)}.$$

Step 3) nth aspect set

Investigate the overall evaluation, $\hat{E}(\{x_1, x_2, \ldots, x_n\})$, of the alternative in X.

Step 4) $x_1 \sim$ of the kth aspect set, $k = 4, 5, \ldots, n-1$

a) Select any aspect randomly in the $(n-1)$th aspect set. In the $(n-2)$th aspect set, $(n-2)$ aspects whose information can be covered by the preceding selected aspect are marked.

b) For $k = n-2, n-3, \ldots, 4$, conduct the following steps:

c) First, select any unmarked aspect in the kth aspect set, and $(k-1)$ aspects whose information can be covered in the $(k-1)$th aspect set are marked.

d) Continue to examine other aspects in the kth aspect set (the previously marked aspects are also taken into consideration). If an aspect can cover the information of $(k-1)$ aspects in

TABLE V
EXPERIMENTAL DATA IN THE FIRST ASPECT SET ($n = 7$)

Aspect set	Aspect	Grade of importance	Evaluation
1st aspect set	$\{x_1\}$	$g_1 = \hat{g}_1 = 0.21$	$f(x_1) = \hat{f}(x_1) = 0.13$
	$\{x_2\}$	$g_2 = \hat{g}_2 = 0.09$	$f(x_2) = \hat{f}(x_2) = 0.20$
	$\{x_3\}$	$g_3 = \hat{g}_3 = 0.17$	$f(x_3) = \hat{f}(x_3) = 0.21$
	$\{x_4\}$	$g_4 = \hat{g}_4 = 0.05$	$f(x_4) = \hat{f}(x_4) = 0.36$
	$\{x_5\}$	$g_5 = \hat{g}_5 = 0.15$	$f(x_5) = \hat{f}(x_5) = 0.39$
	$\{x_6\}$	$g_6 = \hat{g}_6 = 0.06$	$f(x_6) = \hat{f}(x_6) = 0.41$
	$\{x_7\}$	$g_7 = \hat{g}_7 = 0.11$	$f(x_7) = \hat{f}(x_7) = 0.45$

TABLE VI
EXPERIMENTAL DATA IN THE SECOND ASPECT SET ($n = 7$)

Aspect set	Aspect	Grade of importance	Overlap coefficient*	Aspect	Grade of importance	Overlap coefficient
2nd aspect set	$\{x_1,x_2\}$	0.22	-0.889	$\{x_3,x_4\}$	0.36	0.737
	$\{x_1,x_3\}$	0.23	-0.882	$\{x_3,x_5\}$	0.42	0.400
	$\{x_1,x_4\}$	0.30	0.444	$\{x_3,x_6\}$	0.18	-0.833
	$\{x_1,x_5\}$	0.27	-0.600	$\{x_3,x_7\}$	0.31	0.214
	$\{x_1,x_6\}$	0.21	-1.000	$\{x_4,x_5\}$	0.35	0.750
	$\{x_1,x_7\}$	0.22	-0.909	$\{x_4,x_6\}$	0.21	0.667
	$\{x_2,x_3\}$	0.17	-1.000	$\{x_4,x_7\}$	0.29	0.722
	$\{x_2,x_4\}$	0.18	0.444	$\{x_5,x_6\}$	0.28	0.538
	$\{x_2,x_5\}$	0.21	-0.333	$\{x_5,x_7\}$	0.43	0.607
	$\{x_2,x_6\}$	0.10	-0.833	$\{x_6,x_7\}$	0.13	-0.667
	$\{x_2,x_7\}$	0.11	-1.000			

*: The definition of the overlap coefficient is cited from [13], [19].

TABLE VII
EXPERIMENTAL DATA IN THE THIRD AND FOURTH ASPECT SETS ($n = 7$)

Aspect set	Aspect	Grade of importance	Aspect	Grade of importance	Aspect	Grade of importance	Aspect	Grade of importance
3rd aspect set	$\{x_1,x_2,x_3\}$	0.26	$\{x_1,x_4,x_5\}$	0.41	$\{x_2,x_3,x_7\}$	0.37	$\{x_3,x_4,x_7\}$	0.42
	$\{x_1,x_2,x_4\}$	0.32	$\{x_1,x_4,x_6\}$	0.33	$\{x_2,x_4,x_5\}$	0.39	$\{x_3,x_5,x_6\}$	0.46
	$\{x_1,x_2,x_5\}$	0.29	$\{x_1,x_4,x_7\}$	0.35	$\{x_2,x_4,x_6\}$	0.24	$\{x_3,x_5,x_7\}$	0.48
	$\{x_1,x_2,x_6\}$	0.23	$\{x_1,x_5,x_6\}$	0.31	$\{x_2,x_4,x_7\}$	0.34	$\{x_3,x_6,x_7\}$	0.34
	$\{x_1,x_2,x_7\}$	0.25	$\{x_1,x_5,x_7\}$	0.45	$\{x_2,x_5,x_6\}$	0.32	$\{x_4,x_5,x_6\}$	0.41
	$\{x_1,x_3,x_4\}$	0.38	$\{x_1,x_6,x_7\}$	0.27	$\{x_2,x_5,x_7\}$	0.51	$\{x_4,x_5,x_7\}$	0.49
	$\{x_1,x_3,x_5\}$	0.44	$\{x_2,x_3,x_4\}$	0.40	$\{x_2,x_6,x_7\}$	0.16	$\{x_4,x_6,x_7\}$	0.35
	$\{x_1,x_3,x_6\}$	0.25	$\{x_2,x_3,x_5\}$	0.47	$\{x_3,x_4,x_5\}$	0.53	$\{x_5,x_6,x_7\}$	0.48
	$\{x_1,x_3,x_7\}$	0.37	$\{x_2,x_3,x_6\}$	0.21	$\{x_3,x_4,x_6\}$	0.39		
4th aspect set	$\{x_1,x_2,x_3,x_4\}$	0.47	$\{x_1,x_2,x_6,x_7\}$	0.34	$\{x_1,x_4,x_6,x_7\}$	0.39	$\{x_2,x_4,x_5,x_7\}$	0.60
	$\{x_1,x_2,x_3,x_5\}$	0.51	$\{x_1,x_3,x_4,x_5\}$	0.62	$\{x_1,x_5,x_6,x_7\}$	0.55	$\{x_2,x_4,x_6,x_7\}$	0.39
	$\{x_1,x_2,x_3,x_6\}$	0.30	$\{x_1,x_3,x_4,x_6\}$	0.45	$\{x_2,x_3,x_4,x_5\}$	0.64	$\{x_2,x_5,x_6,x_7\}$	0.58
	$\{x_1,x_2,x_3,x_7\}$	0.41	$\{x_1,x_3,x_4,x_7\}$	0.50	$\{x_2,x_3,x_4,x_6\}$	0.44	$\{x_3,x_4,x_5,x_6\}$	0.62
	$\{x_1,x_2,x_4,x_5\}$	0.49	$\{x_1,x_3,x_5,x_6\}$	0.53	$\{x_2,x_3,x_4,x_7\}$	0.51	$\{x_3,x_4,x_5,x_7\}$	0.66
	$\{x_1,x_2,x_4,x_6\}$	0.38	$\{x_1,x_3,x_5,x_7\}$	0.58	$\{x_2,x_3,x_5,x_6\}$	0.57	$\{x_3,x_4,x_6,x_7\}$	0.48
	$\{x_1,x_2,x_4,x_7\}$	0.40	$\{x_1,x_3,x_6,x_7\}$	0.43	$\{x_2,x_3,x_5,x_7\}$	0.61	$\{x_3,x_5,x_6,x_7\}$	0.56
	$\{x_1,x_2,x_5,x_6\}$	0.35	$\{x_1,x_4,x_5,x_6\}$	0.54	$\{x_2,x_3,x_6,x_7\}$	0.42	$\{x_4,x_5,x_6,x_7\}$	0.63
	$\{x_1,x_2,x_5,x_7\}$	0.56	$\{x_1,x_4,x_5,x_7\}$	0.59	$\{x_2,x_4,x_5,x_6\}$	0.52		

TABLE VIII
EXPERIMENTAL DATA IN THE FIFTH AND SIXTH ASPECT SETS ($n = 7$)

Aspect set	Aspect	Grade of importance	Aspect	Grade of importance	Aspect	Grade of Importance
5th aspect set	$\{x_1,x_2,x_3,x_4,x_5\}$	0.73	$\{x_1,x_2,x_4,x_5,x_7\}$	0.69	$\{x_1,x_4,x_5,x_6,x_7\}$	0.70
	$\{x_1,x_2,x_3,x_4,x_6\}$	0.54	$\{x_1,x_2,x_4,x_6,x_7\}$	0.48	$\{x_2,x_3,x_4,x_5,x_6\}$	0.71
	$\{x_1,x_2,x_3,x_4,x_7\}$	0.59	$\{x_1,x_2,x_5,x_6,x_7\}$	0.67	$\{x_2,x_3,x_4,x_5,x_7\}$	0.80
	$\{x_1,x_2,x_3,x_5,x_6\}$	0.64	$\{x_1,x_3,x_4,x_5,x_6\}$	0.68	$\{x_2,x_3,x_4,x_6,x_7\}$	0.63
	$\{x_1,x_2,x_3,x_5,x_7\}$	0.72	$\{x_1,x_3,x_4,x_5,x_7\}$	0.78	$\{x_2,x_3,x_5,x_6,x_7\}$	0.74
	$\{x_1,x_2,x_3,x_6,x_7\}$	0.51	$\{x_1,x_3,x_4,x_6,x_7\}$	0.60	$\{x_2,x_4,x_5,x_6,x_7\}$	0.76
	$\{x_1,x_2,x_4,x_5,x_6\}$	0.67	$\{x_1,x_3,x_5,x_6,x_7\}$	0.69	$\{x_3,x_4,x_5,x_6,x_7\}$	0.82
6th aspect set	$\{x_1,x_2,x_3,x_4,x_5,x_6\}$	0.81	$\{x_1,x_2,x_3,x_5,x_6,x_7\}$	0.78	$\{x_1,x_3,x_4,x_5,x_6,x_7\}$	0.89
	$\{x_1,x_2,x_3,x_4,x_5,x_7\}$	0.93	$\{x_1,x_2,x_4,x_5,x_6,x_7\}$	0.84	$\{x_2,x_3,x_4,x_5,x_6,x_7\}$	0.91
	$\{x_1,x_2,x_3,x_4,x_6,x_7\}$	0.69				

TABLE IX
EVALUATION VALUES OF THE SAMPLE ASPECTS ($n = 7$)

Aspect set	Sample of $x_1\sim$	Evaluation
2nd aspect set	$\{x_1,x_2\}$	$E_{x_1,x_2} = \hat{E}_{x_1,x_2} = 0.1586$
	$\{x_1,x_3\}$	$E_{x_1,x_3} = \hat{E}_{x_1,x_3} = 0.1891$
	$\{x_1,x_4\}$	$E_{x_1,x_4} = \hat{E}_{x_1,x_4} = 0.1683$
	$\{x_1,x_5\}$	$E_{x_1,x_5} = \hat{E}_{x_1,x_5} = 0.2744$
	$\{x_1,x_6\}$	$E_{x_1,x_6} = \hat{E}_{x_1,x_6} = 0.2100$
	$\{x_1,x_7\}$	$E_{x_1,x_7} = \hat{E}_{x_1,x_7} = 0.2900$
3rd aspect set	$\{x_1,x_2,x_5\}$	$\hat{E}_{x_1,x_2,x_5} = 0.2790$
	$\{x_1,x_3,x_7\}$	$\hat{E}_{x_1,x_3,x_7} = 0.2684$
	$\{x_1,x_4,x_6\}$	$\hat{E}_{x_1,x_4,x_6} = 0.2855$
4th aspect set	$\{x_1,x_2,x_3,x_6\}$	$\hat{E}_{x_1,x_2,x_3,x_6} = 0.2250$
	$\{x_1,x_2,x_4,x_7\}$	$\hat{E}_{x_1,x_2,x_4,x_7} = 0.3303$
	$\{x_1,x_3,x_4,x_5\}$	$\hat{E}_{x_1,x_3,x_4,x_5} = 0.2903$
	$\{x_1,x_5,x_6,x_7\}$	$\hat{E}_{x_1,x_5,x_6,x_7} = 0.3696$
5th aspect set	$\{x_1,x_2,x_3,x_4,x_7\}$	$\hat{E}_{x_1,x_2,x_3,x_4,x_7} = 0.2881$
	$\{x_1,x_2,x_4,x_5,x_6\}$	$\hat{E}_{x_1,x_2,x_4,x_5,x_6} = 0.2966$
	$\{x_1,x_3,x_5,x_6,x_7\}$	$\hat{E}_{x_1,x_3,x_5,x_6,x_7} = 0.3303$
6th aspect set	$\{x_1,x_2,x_3,x_5,x_6,x_7\}$	$\hat{E}_{x_1,x_2,x_3,x_5,x_6,x_7} = 0.3233$
7th aspect set	$\{x_1,x_2,x_3,x_4,x_5,x_6,x_7\}$	$\hat{E}_{x_1,x_2,x_3,x_4,x_5,x_6,x_7} = 0.3178$

APPENDIX II
EXPERIMENTAL DATA

See Tables V–IX.

APPENDIX III
EXPERIMENTAL RESULT

See Figs. 8–12.

the $(k - 1)$th aspect set, select that aspect; otherwise bypass it and the other aspects that remain to be examined. Repeat the above steps until there are no more aspects in the aspect set to be selected.

Step 5) $x_1\sim$ of the third aspect set

Since the investigated data in the lower aspect set are relatively accurate, those aspects uncovered by the selected samples in the fourth aspect set have to be surveyed.

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