

Genetic Fuzzy Markup Language for Diet Application

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Abstract—In this paper, the genetic fuzzy markup language (GFML) is presented to describe the knowledge base and rule base of the diet domain, including ingredients and the contained servings of six food categories of some common food. The domain experts first define the nutrient facts of the common food to construct the fuzzy food ontology. Meanwhile, the involved Taiwanese students of National University of Tainan (NUTN) record their daily meals for a constant period of time. Then, based on the built fuzzy food ontology, a GFML-based learning mechanism combining the genetic learning mechanism with the fuzzy markup language (FML) is carried out to infer the possibility of dietary healthy level for one-day meals. From the experimental results, it is known that the proposed GFML-based learning mechanism is workable for the diet-domain healthcare applications.

Keywords: *Fuzzy Ontology; Fuzzy Markup Language; Genetic Learning; Dietary Healthy Level Assessment*

I. INTRODUCTION

A balanced diet must contain correctly proportioned carbohydrate, protein, fat, vitamins, mineral salts, and fiber because each nutrient plays an important role in supporting humans' everyday physical activities. However, what is a balanced diet? According to [1], eating a balanced diet means choosing a wide variety of foods and drinks from all the food groups. It also means eating certain things in moderation. The goal of the balanced diet is to take in nutrients you need for health at the recommended levels. And, how to begin a balanced diet is also a difficult problem for most of the people. At the present day, the desirable eating habits cannot be obtained easily since our lifestyle is getting diversified. To meet this requirement, some approaches integrating the fuzzy inference mechanism and ontology have been proposed to support the diet assessment for the past few years. For example, Lee *et al.* proposed a type-2 fuzzy ontology to apply to the personal diabetic-diet recommendation [2] and diet assessment [3], [4].

Ontologies have become ubiquitous in information systems. As ontology development becomes increasingly widespread and collaborative, developers are creating ontologies using different tools and languages [6]. For example, Zouaq and Nkambou [7] presented the knowledge puzzle ontology learning tool to extract concept maps from text and export them into a domain ontology. Hisham and Nguyen [8] proposed a new ontology-structure-based technique for measuring the semantic similarity in single ontology and

across multiple ontologies in the biomedical domain within the framework of Unified Medical Language System (UMLS). Ontology also has been extensively studied in many research fields, including the news summarization, multi-agent systems, webservice, natural language processing, medical science, computer game, and e-commerce platforms. For instance, Lee *et al.* proposed a fuzzy ontology to apply to news summarization [9] and diabetes decision support [5]. Chou *et al.* [10] focused on developing an ontology structure of elements for Web-based disaster management systems to assist developers and evaluators of Web sites in such domains. A fuzzy markup language (FML) implementation is based on the employment of tags able to model different parts of the fuzzy controller in a taxonomic way. It can be not only considered a standalone language used to model the fuzzy controllers, but also can effectively describe the knowledge base and rule base of the fuzzy logic system; therefore, the previous studies employed it to incorporate with the fuzzy inference mechanism [3], [4], [11], [12]. There are many FML-based applications, such as Acompra *et al.* [19] proposed an Interoperable and adaptive fuzzy services for ambient intelligence application Lee *et al.* [3] [4] applied FML to diet assessment.

The genetic algorithm (GA) has been applied to various research topics [13]. For example, Lee *et al.* proposed a genetic-based fuzzy image filter and its application to image processing [14] and meeting scheduling decision support system [15]. Khoo and Sugathan [16] presented a GA-based optimization procedure for structural pattern recognition in a model-based recognition system. The GFML-based fuzzy learning mechanism combined GA with FML is proposed and applied to the diet domain in this paper. Based on the proposed food ontology, the developed approach is able to show the involved people the healthy level of the eaten food to make them not only enjoy the delicious food but also eat healthily.

The remainder of this paper is structured as follows. The Taiwanese and Japanese fuzzy food ontologies are introduced in Section II. The GFML and the GFML-based learning mechanism are presented in Section III. The GFML-based learning mechanism on the diet application is introduced in Section IV. Experimental results are shown in Section V. Finally, some conclusions are given in Section VI.

II. FUZZY FOOD ONTOLOGY

It has been widely pointed out that classical ontology is not

sufficient to deal with imprecise and vague knowledge for some real-world applications [2]. On the other hand, fuzzy ontology can effectively help to handle and process uncertain data and knowledge [2], [17]. The fuzzy ontology is an extension of the domain ontology that is more suitable to describe the domain knowledge for solving the uncertainty reasoning problems [2]. In this paper, the Taiwanese fuzzy food ontology is constructed to describe the fuzzy concepts and fuzzy relations for some common Taiwanese food. The proposed *fuzzy ontology* is an extended version of our previous research works [2], [9].

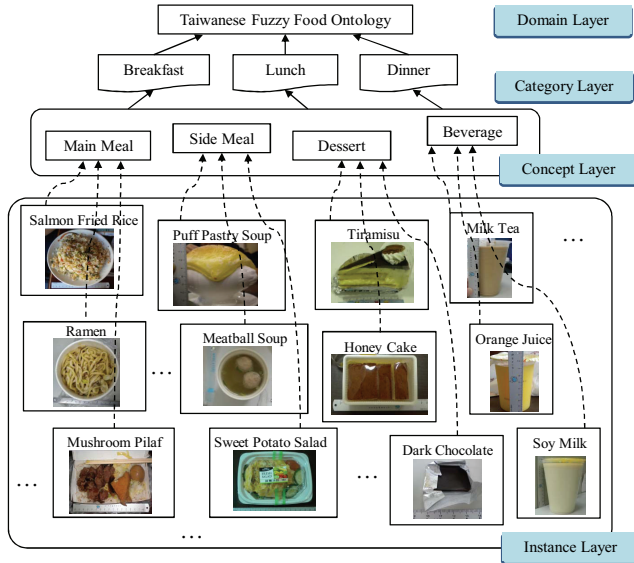


Fig. 1. Taiwanese fuzzy food ontology

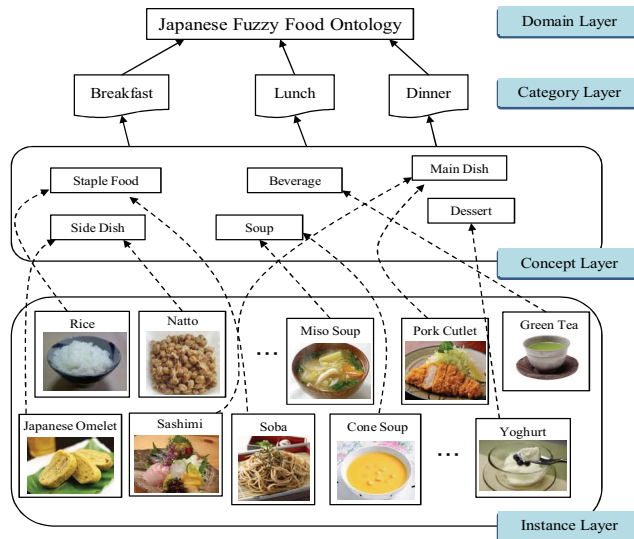


Fig. 2. Japanese fuzzy food ontology [18]

Figs. 1 and 2 show the four-layer fuzzy food ontology for Taiwanese food and Japanese food, respectively. The fuzzy food ontology is composed four layers, including (1) *Domain Layer*: This layer represents the domain name of the ontology. (2) *Category Layer*: In this layer, it comprises various categories defined by domain experts. In this paper, the category in Figs. 1 and 2 is divided into three meals,

Breakfast, *Lunch*, and *Dinner* to simplify the ontology's structure. (3) *Concept layer*: This layer describes some components of the category layer. For Taiwanese fuzzy food ontology, there are concepts such as *Main Meal*, *Side Meal*, *Dessert*, and *Beverage*. On the other hand, for the Japanese food, some concepts like *Staple Food*, *Main Dish*, *Side Dish*, *Soup*, *Beverage*, and *Dessert* make up of this layer. (4) *Instance layer*: This layer consists of lots of instances of each concept in the *concept layer* [18].

There is a relationship between one concept and a lot of instances. For example, ramen is one kind of main meal for the Taiwanese food so Fig. 1 shows a relationship between Instance *Ramen* and concept *Main Meal*. Similarly, miso soup is one kind of soup for the Japanese food so there is a relationship between Instance *Miso Soup* and concept *Soup* in Fig. 2. In addition to showing the relationship among the food, the predefined fuzzy ontology also contains the nutritional information of each food, such as how many grams of carbohydrates, protein, and fat per portion and how many servings of six food groups per portion are contained. In this way, the proposed approach can evaluate how much healthy people's one-day meals are based on the fuzzy food ontology and people's basic personal profile such as height, weight, age, and everyday physical activity.

III. GENETIC FUZZY MARKUP LANGUAGE

In this paper, the genetic learning mechanism is embedded into the fuzzy markup language, and this novel approach is named the genetic fuzzy markup language learning mechanism. The details of the GFML-based learning mechanism like how to encode one GFML ontology into one chromosome and what is the mutation restriction will be introduced in this section.

A. Chromosome Representation of GFML

An example of how to encode the FML ontology into the chromosome is given in this sub-section. The FML ontology is encoded into one chromosome with a lot of genes. The genes on each chromosome are composed of three parts, including the rule-based part, knowledge-based part, and fuzzy-hedged part. The rule-based genes are a collection of the weight of the fuzzy rules. For example, there are four fuzzy rules listed in Table I. The genes of the chromosome about the rule-based part is $\{1\ 0\ 0\ 1\}$.

TABLE I. EXAMPLE ABOUT RULE-BASED GENES

<pre> <RuleBase type="mamdani" activationMethod="MIN" andMethod="MIN" orMethod="MAX" name="RuleBase1"> + <Rule connector="and" operator="MIN" weight="1" name="Rule1"> + <Rule connector="and" operator="MIN" weight="0" name="Rule2"> + <Rule connector="and" operator="MIN" weight="0" name="Rule3"> + <Rule connector="and" operator="MIN" weight="1" name="Rule4"> </RuleBase> </pre>

The type about the knowledge-based genes is a hash table. The key and the value of this hash table are composed of the fuzzy variables' names and the objects with the fuzzy terms of their own fuzzy variables, respectively. The object could be a *TriangularShape*, *TrapezoidShape*, ..., and so on. Take the Table II for an example. The genes about the knowledge-based part contain a dictionary entry, including the key is *CPURate*

and this key's value is $\{ \langle \text{TriangularShape Param1}="0" \text{ Param2}="0" \text{ Param3}="50" \rangle / \langle \text{TriangularShape Param1}="25" \text{ Param2}="50" \text{ Param3}="75" \rangle / \langle \text{TriangularShape Param1}="50" \text{ Param2}="100" \text{ Param3}="100" \rangle \}$. The fuzzy-hedged genes are also described as a hash table whose key is the fuzzy variable names, and the value of the key is represented by the fuzzy terms' hedge of the fuzzy variables. The value of the hedge (δ) is calculated by Eq. (1). For example, the key and the value of the fuzzy-hedged genes listed in Table III are *MemoryRate* and $\{11111\}$, respectively.

TABLE II. EXAMPLE ABOUT KNOWLEDGE-BASED GENES

```
<KnowledgeBase>
  <FuzzyVariable domainleft="0" domainright="100" name="CPURate"
    scale="%" type="input">
    <FuzzyTerm name="Low" hedge="Normal">
      <TriangularShape Param1="0" Param2="0" Param3="50" />
    </FuzzyTerm>
    <FuzzyTerm name="Medium" hedge="Normal">
      <TriangularShape Param1="25" Param2="50" Param3="75" />
    </FuzzyTerm>
    <FuzzyTerm name="High" hedge="Normal">
      <TriangularShape Param1="50" Param2="100" Param3="100" />
    </FuzzyTerm>
  </FuzzyVariable>
</KnowledgeBase>
```

$$\delta = \begin{cases} 1, & \text{if linguistic hedge is normal} \\ 2, & \text{if linguistic hedge is very} \\ 0.5, & \text{if linguistic hedge is less or more} \end{cases} \quad (1)$$

TABLE III. EXAMPLE ABOUT FUZZY HEDGE GENES

```
<KnowledgeBase>
  <FuzzyVariable domainleft="0" domainright="100" name="MemoryRate"
    scale="%" type="input">
    <FuzzyTerm name="VeryLow" hedge="Normal">
      <TriangularShape Param1="0" Param2="0" Param3="20" />
    </FuzzyTerm>
    <FuzzyTerm name="Low" hedge="Normal">
      <TriangularShape Param1="0" Param2="20" Param3="40" />
    </FuzzyTerm>
    <FuzzyTerm name="Medium" hedge="Normal">
      <TriangularShape Param1="20" Param2="40" Param3="60" />
    </FuzzyTerm>
    <FuzzyTerm name="High" hedge="Normal">
      <TriangularShape Param1="40" Param2="60" Param3="80" />
    </FuzzyTerm>
    <FuzzyTerm name="VeryHigh" hedge="Normal">
      <TriangularShape Param1="60" Param2="100" Param3="100" />
    </FuzzyTerm>
  </FuzzyVariable>
</KnowledgeBase>
```

B. GFML-based Learning Mechanism

The flowchart of GFML-based learning mechanism, shown in Fig. 3, operates as follows.

• Part 1: Parameter Initialization

- Initialize all of the necessary parameters including (1) crossover probability $p_{crossover}$, (2) mutation probability $p_{mutation}$, (3) generation number $N_{generation}$, (4) maximum evaluation number $N_{generation_max}$, (5) minimum fitness value $fitness_{minimum}$, (6) size of population of chromosomes $S_{population}$, and (7) maximum size of population of chromosomes $S_{population_max}$.

• Part 2: Genetic Population Initialization

- Encode before-learned FML ontology into one chromosome, herein, the FML ontology stores all of the information of the knowledge base and rule base of the FML-based inference mechanism.
- Mutate the generated chromosome based on the mutation probability.
- Decode the after-mutated chromosome into the GFML ontology, herein, the GFML ontology stores all of the information of the knowledge base and rule base of the GFML-based inference mechanism.
- Input the training data to execute the GFML-based inference mechanism to obtain the inferred results.
- Input the desired output, and then execute the fitness function to calculate the fitness value of the after-mutated chromosome, that is, compute the sum of the difference value between the inferred results and desired output of the training data.
- Repeat Part 2 until the size of the population reaches the maximum size of the population.

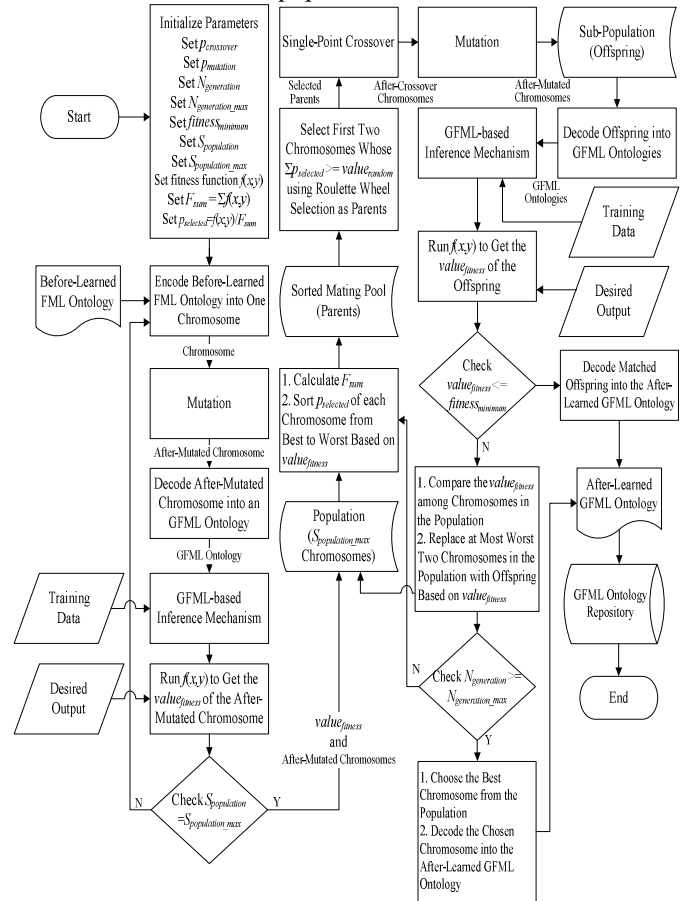


Fig. 3. GFML-based learning mechanism flowchart

• Part 3: Genetic Evolution

- Calculate the sum of the fitness value of all chromosomes in the population.
- Sort the selected probability of all chromosomes in the population from the best to the worst one based on each chromosome's fitness value.

- Based on the roulette wheel selection, choose the first two chromosomes whose sum of the selected probability is over the random created value as parents.
- Based on the crossover probability, make the single-crossover for the selected parents to generate the after-crossover chromosomes.
- Based on the mutation probability, mutate the after-crossover chromosomes to generate the offspring.
- Put the generated offspring into the sub-population.
- Decode the offspring into the GFML ontologies.
- Input the training data to execute the GFML-based inference mechanism to obtain the inferred results.
- Input the desired output, and then execute the fitness function to calculate the fitness value of the after-mutated chromosomes.
- Check if the fitness value of any one of offspring is less than the minimum fitness value.
- If it is positive, then decode the matched offspring into the after-learned GFML ontology, store it into the GFML ontology repository, and finally terminate the GFML-based learning mechanism.
- If it is negative, then compare the fitness value of all chromosomes in the population and replace at most worst two chromosomes in the population with the offspring.
- Check if the generation number is over the maximum generation number.
- If it is positive, then choose the best chromosome from the population, decode the chosen chromosome into the after-learned GFML ontology, store it into the GFML ontology repository, and eventually terminate the GFML-based learning mechanism.
- If it is negative, repeat Part 3 until the generation number reaches the maximum generation number or the minimum fitness value is matched.

C. Mutation Restriction

In this sub-section, the mutation restriction about the knowledge-based genes is introduced by Table IV. The membership functions of the fuzzy variables *Low* and *High* are depicted by Fig. 4.

TABLE IV. EXAMPLE ABOUT KNOWLEDGE-BASED GENES' MUTATION

<pre> <KnowledgeBase> <FuzzyVariable domainleft="Domain Left" domainright=" Domain Right" name="SampleFML, " scale="%" type="input"> <FuzzyTerm name="Low" hedge="Normal"> <TriangularShape Param1="A" Param2="B" Param3="C" /> </FuzzyTerm> <FuzzyTerm name="High" hedge="Normal"> <TriangularShape Param1="A'" Param2="B'" Param3="C'" /> </FuzzyTerm> </FuzzyVariable> </KnowledgeBase> </pre>

The key of the knowledge-based genes is *SampleFML*, and the value of this key is $\{ \langle \text{TriangularShape Param1}="A" \text{ Param2}="B" \text{ Param3}="C" \rangle / \langle \text{TriangularShape Param1}="A'" \text{ Param2}="B'" \text{ Param3}="C'" \rangle \}$. The genes' mutation restriction of the knowledge-based part is to randomly select the values of parameters in order within a reasonable range. For example, the mutation value of *A* is a random value between *Domain Left* and *B*, and then the mutation value of *B* is a random value between the

mutation-generated *A* and *A'*. Likely, the other parameters also are mutated in the same way as parameters *A* and *B*. After the mutation, the new genes about the knowledge-based part with the new parameters are obtained and correctly decoded it into the GFML ontology.

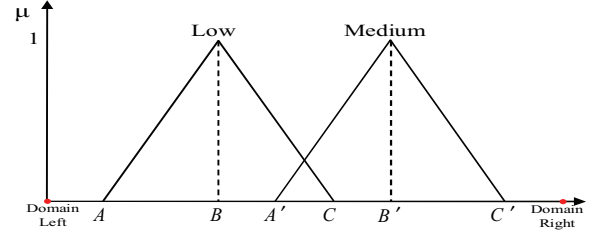


Fig. 4. Membership functions of the fuzzy variables *Low* and *High*

IV. GFML-BASED LEARNING MECHANISM ON DIET APPLICATION

A. Structure

The proposed diet healthy assessment system was introduced in previous work [3], [18]. Fig. 5 shows an overview of the GFML-based diet application and its procedures are as follows: (1) Nutrition facts of some popular food are gathered from the Internet, convenient stores, or fast food stores. (2) Domain experts, like dietitians, verify and define the detailed nutrient facts for each food item. (3) The fuzzy food ontology is constructed via the provided GFML editor. (4) The involved subjects record and input the daily eaten meals through the constructed platform. (5) The healthy-level evaluation of the eaten food is carried out by the GFML-based learning mechanism based on each subject's personal information and built fuzzy food ontology. Then, the output is stored into the dietary healthy level repository. (6) Finally, the involved subjects get the feedback and evaluated results from the domain experts via the provided interface.

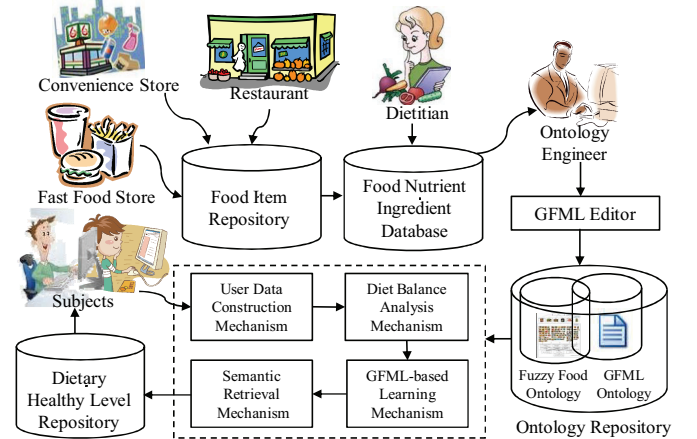


Fig. 5. Structure of the GFML-based diet application

B. Considered Factors for Dietary Healthy Level

Based on the collected meal records and the pre-defined fuzzy food ontology, everyday meals' Percentage of Calories from Carbohydrate (*PCC*), Percentage of Calories from Protein (*PCP*), Percentage of Calories from Fat (*PCF*), the Percentage of Caloric Ratio (*PCR*), and Food Group Balance (*FGB*) are acquired. The detailed information about these five fuzzy variables is described as followings.

In order to support one-day energy, it is necessary to consume the enough calories via the everyday diet. However, the main source of the calories is decided by the fact how many grams of the carbohydrate, protein, and fat that the food contains. As a result, to eat healthily, it is necessary for people to consider the balance of these three main nutrients, namely the carbohydrate, protein, and fat, when consuming your one-day meals. For this reason, this paper sets *PCC*, *PCP*, and *PCF* to represent the percentage of calories from carbohydrate, protein, and fat, respectively. According to [1], it indicates that (1) the suggested percentages of the daily intake for carbohydrate, protein, and fat are 55%~65%, 10%~20%, and 25%~35%, respectively, and (2) the contained calories for each gram of the carbohydrate, protein, and fat is 4kcal, 4kcal, and 9kcal, respectively. Based on the above-mentioned discussions, the *PCC*, *PCP*, and *PCF* are calculated by Eqs. (2), (3), and (4), respectively.

$$PCC(\%) = \frac{\text{Contained Grams of Carbohydrate} \times 4}{\text{Total Consumed Carloies}} \times 100\% \quad (2)$$

$$PCP(\%) = \frac{\text{Contained Grams of Protein} \times 4}{\text{Total Consumed Carloies}} \times 100\% \quad (3)$$

$$PCF(\%) = \frac{\text{Contained Grams of Fat} \times 9}{\text{Total Consumed Carloies}} \times 100\% \quad (4)$$

Besides considering the balance of the three main nutrients, the ratio of actual calories people consume to the planned caloric intake set by nutritionists is also an important factor to affect the healthy diet, especially for the fat and the slim. According to the involved domain experts' opinions, the one-day actually consuming calories for common people should be between 90% and 110% of the planned calories set by the dieticians. The domain experts set a planned goal for each person according to individual's height, weight, and daily physical activities. Based on the planned goal and the actual acquiring energies, the value of *PCR* is obtained by Eq. (5).

$$PCR(\%) = \frac{\text{Actual Consuming Calories}}{\text{Planned Consuming Calories}} \times 100\% \quad (5)$$

The balance of six food groups, including grains & starches, vegetables, fruits, milk, meats & proteins, and fats, is the most important factor to decide how much healthy level the eaten meals are. This is because the lack of some beneficial nutrients for our bodies such as fiber cannot be known if we only consider the balanced intake of carbohydrate, protein, and fat. So, in addition to planning the daily calories, the dieticians also plan one-day unique consuming servings of each food group for each person. Moreover, the contained quantity of sugar also affects the balance of intake-in food. Owing to the present-day living style, most people purchase the processed food as their usual meals from the shopping mall. However, unfortunately, the processed food frequently contains much more sugar than the natural food, and it is harmful for our bodies if too much sugar is eaten by people. The suggested percentage of daily sugar's intake is less than 10% of the planned caloric intake each day. The value of *FGB* is calculated by Eq. (6). With the retrieved information, including the values of *PCC*, *PCP*, *PCF*, *PCR*, and *FGB*, from the collected one-day meals, the dietary healthy level (*DHL*) is obtained after implementing the proposed approach.

$$FGB = BL_{\text{Grains\&Starches}} + BL_{\text{Vegetables}} + BL_{\text{Fruits}} + BL_{\text{Milk}}$$

$$+ BL_{\text{Meats\&Proteins}} + BL_{\text{Fats}} - CL_{\text{Sugar}} \quad (6)$$

where (1) $BL_{\text{Grains\&Starches}}$, $BL_{\text{Vegetables}}$, BL_{Fruits} , BL_{Milk} , $BL_{\text{Meats\&Proteins}}$, and BL_{Fats} represent the balanced level of the food groups grains & starches, vegetables, fruits, milk, meats & proteins, and fats, respectively. The higher the value is, the healthier the meals are; (2) CL_{Sugar} denotes the contained level of sugar for the meals. The lower the value is, the healthier the meals are; and (3) *FGB* value lies in the interval [0, 6].

C. GFML-based Inference Mechanism

In order to make the proposed system much more suitable to apply to the particular diet application, so the GFML is proposed in the paper. The GFML ontology is composed of the knowledge base and the rule base. Therefore, the GFML-based inference mechanism cannot be carried out until the GFML ontology is defined. Based on the above-discussed descriptions, the shapes and parameters of each factor's membership function are decided. Next is to design the rule base consisting of the 243 fuzzy rules. The involved dieticians regard that the *FGB* plays the most important role on the dietary healthy level. But, the *FCR* is as important as the *FGB* when people those who people are losing weight or gaining weight are neglected. As for *PCC*, *PCP*, and *PCF*, generally speaking, these three factors are equally important, but the dietary healthy level will be affected much when the *PCF* is not within the balanced range. Eventually, the fuzzy relation ratio of *PCC:PCP:PCF:PCR:FGB* (1:1:2:3:3) is determined by the involved domain experts.

Take one fuzzy rule for an example. Assume there is one fuzzy rule, and the if-part is "IF *PCC* is *Medium* AND *PCP* is *Medium* AND *PCF* is *Medium* AND *PCR* is *Medium* AND *FGB* is *Medium*." Computed by Eq. (7), this fuzzy rule's score (*S*) can be obtained according to Table V.

$$S = \frac{1 \times 2 + 1 \times 2 + 2 \times 2 + 3 \times 2 + 3 \times 1}{1 + 1 + 2 + 3 + 3} = 1.7 \quad (7)$$

TABLE V. THE FUZZY RELATION OF EACH INPUT FUZZY VARIABLE

No	Fuzzy Variable	Fuzzy Relation	Fuzzy Term (Score)		
1	PCC	1	Low (1)	Medium (2)	High (1)
2	PCP	1	Low (1)	Medium (2)	High (1)
3	PCF	2	Low (1)	Medium (2)	High (0)
4	PCR	3	Low (1)	Medium (2)	High (1)
5	FGB	3	Low (0)	Medium (1)	High (2)

After the normalization, the normalized rule score (S_N) is acquired by Eq. (8), where the S_{min} and S_{max} are the minimum and maximum rule scores, respectively. Based on the normalized rule score, the then-part of the fuzzy rule could be determined by Table VI. Finally, the completed fuzzy rule is represented as "IF *PCC* is *Medium* AND *PCP* is *Medium* AND *PCF* is *Medium* AND *PCR* is *Medium* AND *FGB* is *Medium* THEN *DHL* is *VeryHigh*." The dietary healthy level is then inferred by carrying out the proposed method to indicate how much healthy, namely very high, high, medium, low, or very low, the eaten meals are. The before-learned membership functions of the fuzzy variables *PCC*, *PCP*, *PCF*, *PCR*, *FGB*, and *DHL* are illustrated in Fig. 6 and the partial before-learned fuzzy rules are shown in Table VII.

$$S_N = \frac{S - S_{min}}{S_{max} - S_{min}} = 0.83 \quad (8)$$

TABLE VI. S_N RANGE OF THE OUTPUT FUZZY VARIABLE

Fuzzy Term	VeryLow	Low	Medium	High	VeryHigh
S_N Range	[0, 0.2]	(0.2, 0.4]	(0.4, 0.6]	(0.6, 0.8]	(0.8, 1.0]

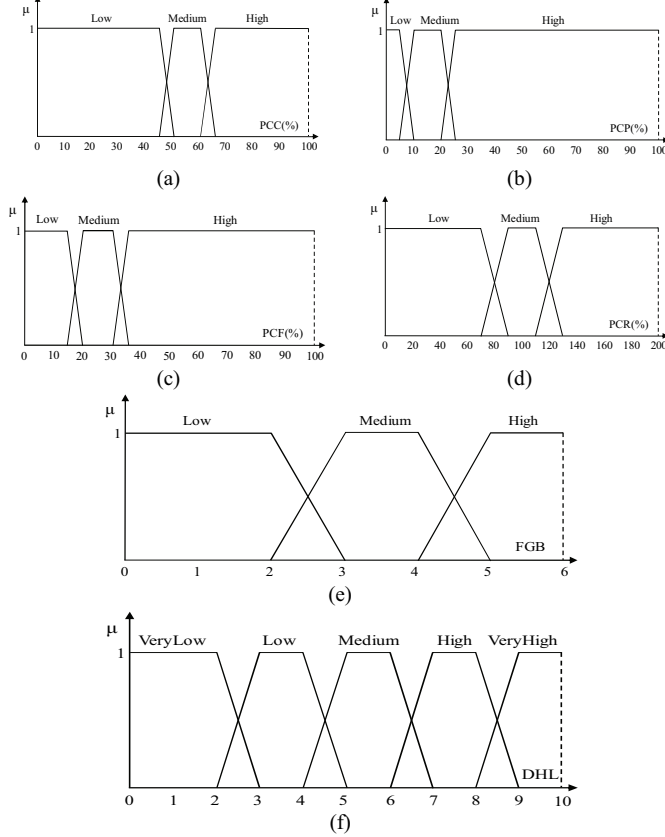


Fig 6. Before-learned membership functions of the fuzzy variables (a) PCC, (b) PCP, (c) PCF, (d) PCR, (e) FGB, and (f) DHL

TABLE VII. PARTIAL BEFORE-LEARNED FUZZY RULES

No	PCC	PCP	PCF	PCR	FGB	DHL
1	Low	Low	Low	Low	Low	VeryLow
2	Low	Low	Low	Low	Medium	Low
3	Low	Low	Low	Low	High	Medium
4	Low	Low	Low	Medium	Low	Low
5	Low	Low	Low	Medium	Medium	Medium
6	Low	Low	Low	Medium	High	High
7	Low	Low	Low	High	Low	VeryLow
8	Low	Low	Low	High	Medium	Low
9	Low	Low	Low	High	High	Medium
10	Low	Low	Medium	Low	Low	Low
11	Low	Low	Medium	Low	Medium	Medium
12	Low	Low	Medium	Low	High	High
13	Low	Low	Medium	Medium	Low	Medium
14	Low	Low	Medium	Medium	Medium	High
15	Low	Low	Medium	Medium	High	VeryHigh
16	Low	Low	Medium	High	Low	Low
17	Low	Low	Medium	High	Medium	Medium
18	Low	Low	Medium	High	High	High
19	Low	Low	High	Low	Low	VeryLow
20	Low	Low	High	Low	Medium	VeryLow
...						
224	High	High	Low	High	Medium	Low
225	High	High	Low	High	High	Medium
226	High	High	Medium	Low	Low	Low

227	High	High	Medium	Low	Medium	Medium
228	High	High	Medium	Low	High	High
229	High	High	Medium	Medium	Low	Medium
230	High	High	Medium	Medium	Medium	High
231	High	High	Medium	Medium	High	VeryHigh
232	High	High	Medium	High	Low	Low
233	High	High	Medium	High	Medium	Medium
234	High	High	Medium	High	High	High
235	High	High	High	Low	Low	VeryLow
236	High	High	High	Low	Medium	VeryLow
237	High	High	High	Low	High	Low
238	High	High	High	Medium	Low	VeryLow
239	High	High	High	Medium	Medium	Low
240	High	High	High	Medium	High	Medium
241	High	High	High	High	Low	VeryLow
242	High	High	High	High	Medium	VeryLow
243	High	High	High	High	High	Low

V. EXPERIMENTAL RESULTS

In this section, some experimental results are given. The proposed GFML-based learning mechanism is implemented with the C# programming language. The research performance presented in this paper is a research project involving with the National University of Tainan (NUTN) and National Cheng Kung Hospital in Taiwan. With the support of the involved domain experts, the proposed method is applied to the diet domain. There are seven students involved in this research project. The involved students of NUTN are responsible for routinely recording their meals and three involved domain experts evaluate the proposed method performance. For the involved students, the meal records are collected through Monday to Friday for one month so that the total collected records are 140. Table VIII shows the partial before-learned FML ontology for the diet application in this paper.

TABLE VIII. PARTIAL BEFORE-LEARNED FML ONTOLOGY

```

<?xml version="1.0"?>
<FuzzyController ip="localhost" name="">
  <KnowledgeBase>
    <FuzzyVariable domainleft="0" domainright="100" name="PCC"
scale="percentage" type="input">
      <FuzzyTerm name="Low" hedge="Normal">
        <TrapezoidShape Param1="0" Param2="0" Param3="45" Param4="50" />
      </FuzzyTerm>
      <FuzzyTerm name="Medium" hedge="Normal">
        <TrapezoidShape Param1="45" Param2="50" Param3="60" Param4="65" />
      </FuzzyTerm>
      <FuzzyTerm name="High" hedge="Normal">
        <TrapezoidShape Param1="60" Param2="65" Param3="100" Param4="100" />
      </FuzzyTerm>
    </FuzzyVariable>
    ...
  </KnowledgeBase>
  <RuleBase activationMethod="MIN" andMethod="MIN" orMethod="MAX"
name="RuleBase1" type="mamdani">
    <Rule name="Rule1" connector="and" weight="1" operator="MIN">
      <Antecedent>
        <Clause>
          <Variable>PCC</Variable>
          <Term>Low</Term>
        </Clause>
        <Clause>
          <Variable>PCP</Variable>
          <Term>Low</Term>
        </Clause>
        <Clause>
          <Variable>PCF</Variable>
          <Term>Low</Term>
        </Clause>
        <Clause>
          <Variable>PCR</Variable>
          <Term>Low</Term>
        </Clause>
        <Clause>
          <Variable>FGB</Variable>

```

```

<Term>Low</Term>
</Clause>
<Antecedent>
<Consequent>
<Clause>
<Variable>DHL</Variable>
<Term>VeryLow</Term>
</Clause>
</Consequent>
</Rule>
...
</RuleBase>
</FuzzyController>

```

In order to implement the genetic learning mechanism based on GFML, one-student 20 records are used as the training data listed in Table IX, and the rest of six-student 120 records are the testing data. In Table IX, the columns DHL_{DO} and DHL_{GFML} represent the desired output from the dieticians and the inferred results from the proposed method, respectively. In this paper, the values of the $N_{generation_max}$, $P_{crossover}$, $P_{mutation}$, $fitness_minimum$, and $S_{population}$ are 1000, 0.9, 0.1, 0, and 100, respectively. Fig. 7 shows the after-learned membership functions for fuzzy variables PCC , PCP , PCF , FCR , FGB , and DHL .

TABLE IX. PARTIAL TRAINING DATA WITH DESIRED OUTPUT AND INFERRED RESULTS

Meal ID	PCC (%)	PCP (%)	PCF (%)	FCR (%)	FGB	DHL_{DO}	DHL_{GFML}
1	48.29	16.44	35.28	128.43	0.71	4	4.14
2	50.17	14.95	34.88	112.98	1.81	4.67	5.26
3	47.59	20.35	32.06	90.91	1	4	0
4	44.44	17.04	38.52	108.67	0.35	4.67	0
5	51.4	13.69	34.91	96.17	0.75	5	2.23
6	57.28	14.86	27.86	100.42	2.34	5	4.14
7	49.77	17.65	32.58	114.51	0.5	5	0
8	51.84	12.06	36.1	147.93	0	2.67	0
9	37.25	18.79	43.96	113.78	1	4.33	4.13
10	56.26	14.27	29.47	84.02	1.47	3.67	2.15
11	58.26	13.22	28.51	135.11	1	3.67	1.66
12	56.95	11.81	31.24	117.92	0.22	3.33	0
13	53.13	14.35	32.52	115.58	2.36	3.33	4.13
14	35.66	18.72	45.62	86.9	0.25	3.67	0
15	40.51	19.9	39.59	113.21	2.1	4.33	5.54
16	56.24	13.15	30.61	137.11	0	3.67	0
17	37.93	17.56	44.51	107.39	1	4	4.13
18	55.02	12.21	32.77	130.91	0.8	2.67	1.66
19	55.94	13.62	30.43	107.26	1	4	1.66
20	45.97	14.38	39.64	115.87	1	4.33	4.13

The mean square error (MSE) is utilized to evaluate the performance of the proposed method in this paper. The MSE is calculated by Eq. (9) and the lower MSE is, the better the performance is. Fig. 8 shows the distribution of the number when MSE_{GFML} is less than or equal to MSE_{FML} , $Count(MSE_{GFML} \leq MSE_{FML})$, and the number when MSE_{GFML} is bigger than MSE_{FML} , $Count(MSE_{GFML} > MSE_{FML})$, for the training data and the testing data. Fig. 8 indicates that the performance of the proposed approach is better than the FML-based inference mechanism for the training data. On the other hand, for the testing data, the FML-based inference mechanism is superior to the GFML-based inference mechanism. In addition, we also need to further use more number of training and testing subjects to demonstrate the performance of the proposed system in the future.

$$MSE = \frac{1}{n} \sum_{i=1}^n e_i^2, e_i = Y_i - \hat{Y}_i \quad (9)$$

where, Y_i represents the inferred results via the FML-based inference mechanism (DHL_{FML}) or the GFML-based learning mechanism (DHL_{GFML}), $\hat{Y}_i$ denotes the desired output recommended from the dieticians (DHL_{DO}), and n is the number of the meal records.

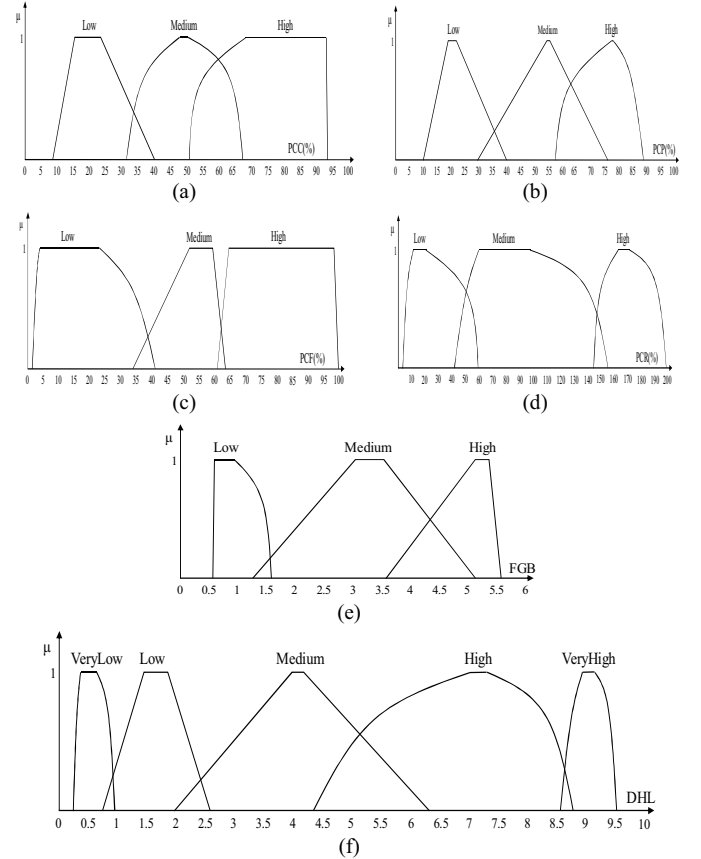


Fig. 7. After-learned membership functions for fuzzy variables (a) PCC , (b) PCP , (c) PCF , (d) PCR , (e) FGB , and (f) DHL

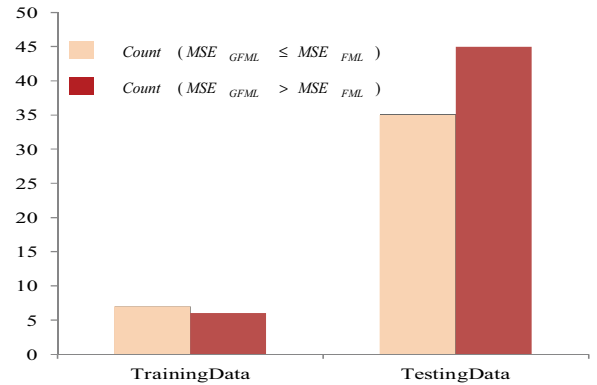


Fig. 8. Distribution for the training data and testing data

VI. CONCLUSIONS

The GFML-based learning mechanism combined the FML with the genetic learning mechanism is presented and applied

to the diet domain to infer the dietary healthy level of one-day eaten food. The effectiveness of the proposed method is verified by comparing with the results of dieticians' assessment. However, some noises such as the gray-marked records in Table IX are generated after executing the GFML-based learning mechanism; therefore, in the future, creating more training data and making some comparisons with other combinations of training and testing subjects are necessary to further improve the performance of the proposed method. Additionally, it is also feasible to introduce the proposed approach to other countries' diet in the future.

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