

A GA-based Approach for Mining Membership Functions and Concept-Drift Patterns

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Abstract—Since customers' behaviors may change over time in real applications, algorithms that can be utilized to mine these drift patterns are needed. In this paper, we propose a GA-based approach for mining fuzzy concept-drift patterns. It consists of two phases. The first phase mines membership functions and the second one finds fuzzy concept-drift patterns. In the first phase, appropriate membership functions for items are derived by GA with a designed fitness function. Then, the derived membership functions are utilized to mine fuzzy concept-drift patterns in the second phase. Experiments on simulated datasets are also made to show the effectiveness of the proposed approach.

Keywords—concept drift, data mining, fuzzy association rules, genetic algorithms, membership functions.

I. INTRODUCTION

Association rule mining is commonly used to analyze the transaction database for providing useful relationship between itemsets, and *Apriori* is one of the well-known mining algorithms [2]. Many *Apriori-like* approaches were then proposed for dealing with different types of transactions. Recently, the research about concept drift is very popular. Tsymbal described concept drift as finding patterns that change over time in unexpected ways [23]. For example, assume at time t there is an association rule "if buying milk, then buying bread", and at time $t+k$, there is another rule "if buying milk, then buying apple" mined. The latter rule changes from the former rule in the consequence part along the time. This change is a type of concept-drift patterns.

Based on the definition of concept-drift patterns, classic data mining approaches have been extended for the purpose and applied to various research fields [4, 7, 8, 22, 25]. For classification tasks, when concept drift occurs, a model built by the old data may not be suitable for predicting new data. Thus, Black et al. proposed an algorithm based on decision trees to learn concept-drift rules for dealing with telecom customer call data [4]. Tsai *et al.* proposed an algorithm for mining concept-drift decision rules from data streams [22]. A survey of emerging patterns for classification can be found in [9]. In addition, Pang et al. proposed an approach for detecting emerging anomalous traffic patterns from GPS data [20]. Some other approaches were proposed for mining emerging patterns from high-dimensional datasets [24, 26].

As to association rule mining, Song et al. defined three types of concept-drift patterns, namely emerging patterns, unexpected change and added/perished rules. They also proposed an algorithm for mining concept-drift patterns [21]. It first separated the database into several time blocks and mined association rules from each block. Then, the rules derived from different blocks were compared to discover the concept-drift patterns. Since transactions usually consist of quantitative values, traditional mining approaches can not easily handle them. Thus, some researchers adopted the fuzzy theory to handle quantitative transactions and induce fuzzy association rules [5, 10, 15, 16, 18, 27]. In fuzzy data mining, membership functions, however, have a great influence on the final results, and thus how to get appropriate membership functions is an interesting problem. Several genetic-fuzzy mining (GFM) algorithms have then been proposed for deriving appropriate membership functions for items to mine fuzzy association rules in recent years [1, 6, 11, 13, 14, 17].

To our best knowledge, there has not been research working on deriving membership functions for discovering concept-drift patterns. Thus in this paper, we present a concept-drift GFM algorithm to derive membership functions of items for inducing concept-drift patterns as more as possible from a given transaction dataset. It first encodes the membership functions of items into a chromosome. The fitness value of each individual is then evaluated by the number of concept-drift patterns (emerging patterns, unexpected change and added/perished rules) and the suitability of membership functions in the corresponding chromosome. After the GA process terminates, the membership functions found are then used to find better sets of fuzzy association rules for determining the concept drift in different time. Experimental results on a simulated dataset have also shown the effectiveness of the proposed approach.

II. FUZZY CONCEPT-DRIFT PATTERNS

According to Song's definition [21], the concept-drift patterns mean that the structure of rules are changed along with different periods of times. They defined three patterns, namely emerging patterns, unexpected change and added/perished rules. Assume there are two rules $r_i^t: A \rightarrow B$ with $\text{sup}(A \rightarrow B) = a$ and $r_j^{t+k}: C \rightarrow D$ with $\text{sup}(C \rightarrow D) = b$, where r_i^t is the i -th rule of rule set RS^t at time t , r_j^{t+k} is the j -th rule of rule set RS^{t+k} in time $t+k$, and A, B, C and D are

itemsets. The definitions of the three patterns are given below [21].

Definition 1 (Emerging Patterns). If a rule r_k is an emerging pattern, then the following two conditions should be satisfied: (1)The conditional and the consequent parts of rules r_i^t and r_j^{t+k} are the same. That is, $A = C$ and $B = D$; (2) Supports of rules r_i^t and r_j^{t+k} are different. That is $\text{sup}(A \rightarrow B) \neq \text{sup}(C \rightarrow D)$.

Definition 2 (Unexpected Change). If a rule r_k is an unexpected change, then the following two conditions should be satisfied: (1) the conditional parts of rules r_i^t and r_j^{t+k} are the same. That is $A = C$; (2) the consequent parts of rules r_i^t and r_j^{t+k} are different. That is $B \neq D$.

Definition 3 (Added/Perished Rules). If r_j^{t+k} is an added rule, it means that the conditional part C and the consequent part D of r_j^{t+k} are different from those of any r_i^t in RS^t . If r_i^t is a perished rule, it means that the conditional part A and the consequent part B of r_i^t are different from those of any r_j^{t+k} in RS^{t+k} .

In the following, an example illustrates how to extract the concept-drift patterns from the two databases at time t and $t+k$. Assume there are two databases shown in Table 1.

TABLE 1. DATABASES AT DIFFERENT TIME

Database D^t		Database D^{t+k}	
TID	Items	TID	Items
1	A, B, C, D	1	A, B, D
2	A, C, D	2	C, D
3	B, C	3	A, B, C
4	A, D	4	B, D

When the minimum support was set at 0.5, by using the *Apriori* algorithm, two association rule sets R^t and R^{t+k} are derived and shown in Table 2.

TABLE 2. ASSOCIATION RULES DERIVED FROM TWO DATABASES

Rule Set RS^t			
r_i^t	Rules	r_j^{t+k}	Rules
1	$A \rightarrow C$	8	$D \rightarrow C$
2	$C \rightarrow A$	9	$A, C \rightarrow D$
3	$A \rightarrow D$	10	$A, D \rightarrow C$
4	$D \rightarrow A$	11	$C, D \rightarrow A$
5	$B \rightarrow C$	12	$A \rightarrow C, D$
6	$C \rightarrow B$	13	$C \rightarrow A, D$
7	$C \rightarrow D$	14	$D \rightarrow A, C$
Rule Set RS^{t+k}			
1	$A \rightarrow B$	3	$B \rightarrow D$
2	$B \rightarrow A$	4	$D \rightarrow B$

Take r_1^t of R^t and r_1^{t+k} of R^{t+k} as examples. Since the conditional parts of them are the same and the consequent parts of them are different, it is an unexpected change. In this example, there are six unexpected changes, six perished rules and no emerging pattern or added rule. By extending the definitions of the three concept-drift patterns, the fuzzy emerging patterns, fuzzy unexpected change and added/perished fuzzy rules are defined. Assume there are two fuzzy rules $fr_i^t: A \rightarrow B$ with $\text{sup}(A \rightarrow B) = a$ and $fr_j^{t+k}: C \rightarrow D$ with $\text{sup}(C \rightarrow D) = b$, where fr_i^t is the i -th rule of the fuzzy rule set RS^t at time t and fr_j^{t+k} is the j -th rule of the fuzzy rule set RS^{t+k} in time $t+k$, and A, B, C and D are fuzzy itemsets. A fuzzy n -itemset consists of n fuzzy regions, where a fuzzy

region is represented as R_{il} meaning that the l -th linguistic term of item I_i .

III. COMPONENT OF PROPOSED ALGORITHM

In this section, the related components of the proposed approach are stated, including chromosome representation, fitness evaluation and genetic operations.

A. Chromosome Representation

Currently, there are two common methods for encoding membership functions for items. According to [19], the first one is to encode each membership function as a pair (c, w) , where c indicates the center abscissa of a membership function, and w represents half the spread of a membership function. Thus, the set of membership functions MF_j for the item I_j are represented as a substring of $c_{11}w_{11} \dots c_{1|I_j|}w_{1|I_j|}$, where $|I_j|$ is the number of membership functions of I_j . It is shown in Fig. 1.

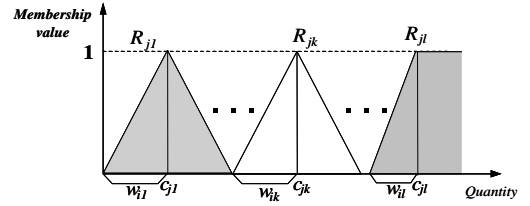


Fig. 1. Membership functions of an item I_j using the center-spread representation model

The second encoding approach is by using the 2-tuple linguistic representation model [1]. Take the set of membership functions MF_j for the item I_j as an example. They are encoded as a substring of $c_{j1}LR_{j1} \dots c_{jk}LR_{jk} \dots c_{j|I_j|}LR_{j|I_j|}$, where c_{jk} and LR_{jk} are the center abscissa and lateral displacement of k -th membership function for item I_j . The scheme are shown in Fig. 2.

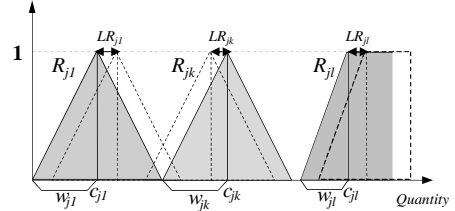


Fig. 2. Membership functions of an item I_j using the 2-tuple linguistic representation model

Note that the half spreads of membership functions are predefined in the second encoding method. Assume there are m items, the entire membership functions for all items are encoded by concatenating substrings of $MF_1, MF_2, \dots, MF_j, \dots, MF_m$. In this paper, the first encoding approach is used in the proposed approach.

B. Fitness Evaluation

The goal of the proposed approach is to derive a good set of membership functions from the given transaction database for mining fuzzy concept-drift patterns. In order to achieve this purpose, an evaluation function is designed to measure the goodness of the derived membership functions. The fitness values of the membership function sets are then fed back to the evolution process to control how the solution space is searched to improve the quality of the membership functions.

Therefore, we define the evaluation function as shown in Equation (1).

$$f(C_q) = \frac{\text{numEP}(C_q) + \text{numUE}(C_q) + \text{numAPR}(C_q)}{\text{suitability}(C_q)}, \quad (1)$$

where $\text{numEP}(C_q)$ is the number of emerging patterns of chromosome C_q , $\text{numUE}(C_q)$ is the number of unexpected changes of chromosome C_q , and $\text{numAPR}(C_q)$ is the number of added/perished rules of chromosome C_q . Assume there are two transaction databases D^t and D^{t+k} , the number of emerging patterns of chromosome C_q is defined in Equation (2):

$$\text{numEP}(C_q) = \text{countEPRule}(RSc_q^t, RSc_q^{t+k}), \quad (2)$$

where the two fuzzy rule sets $RSc_q^t = \{fr_1^t, fr_2^t, \dots, fr_h^t\}$ and $RSc_q^{t+k} = \{fr_1^{t+k}, fr_2^{t+k}, \dots, fr_n^{t+k}\}$ are mined from transaction databases D^t and D^{t+k} with membership functions in C_q by using fuzzy rule mining approach [10]. The number of emerging patterns of chromosome C_q can be calculated according to the definition 1. In the same way, the number of unexpected changes of chromosome C_q is given in Equation (3):

$$\text{numUE}(C_q) = \text{countUERule}(RSc_q^t, RSc_q^{t+k}). \quad (3)$$

According to definition 2, the number of unexpected changes of chromosome C_q can be calculated with the derived rule sets RSc_q^t and RSc_q^{t+k} . Then, the number of added/perished rules of chromosome C_q is defined in Equation (4):

$$\text{numAPR}(C_q) = \text{countAPRule}(RSc_q^t, RSc_q^{t+k}). \quad (4)$$

By using definition 3, the number of add/perished rules can be calculated with the derived rule sets, Rc_q^t and Rc_q^{t+k} . Besides, the $\text{suitability}(C_q)$ is used to reduce the occurrence of the two bad kinds of membership functions, and shown in Equation (5).

$$\text{suitability}(C_q) = \sum_{j=1}^m [\text{overlapFactor}(C_{qj}) + \text{coverageFactor}(C_{qj})], \quad (5)$$

where the overlap factor is used to avoid membership functions too overlapping (redundant). The coverage factor is used to avoid membership functions too separate. More details of it can be found in [16]. Through the designed fitness function, it will lead the evolution process to find appropriate membership function sets that can generate larger number of concept-drift patterns from the transaction databases.

C. Genetic Operations

Genetic operators are used to generate diverse solutions for the specific GA applications. For crossover operation, the *max-min-arithmetical (MMA) crossover* proposed in [12] is utilized here. For mutation operation, when the first encoding method is adopted, the *one-point* mutation operator will create a new membership function by adding a random value ε to the center and to the spread of an existing linguistic term, say R_{jk} . The center and the spread of the newly formed membership function will be changed to $c \pm \varepsilon$ and $w \pm \varepsilon$ by the mutation operation. The selection strategy used in the proposed approach can be the elitist or the roulette-wheel strategy. Here, the elitist strategy is used in the proposed approach.

IV. PROPOSED MINING ALGORITHM

In this section, the proposed approach that combines concept drift, genetic algorithm, and fuzzy data mining is described as follows:

The concept-drift genetic-fuzzy mining algorithm:

INPUT: Two quantitative transaction databases D^t consists of n quantitative transactions and m items at time t , and D^{t+k} consists of w quantitative transactions and m items at time $t+k$. The parameters include a support threshold α , a confidence threshold λ , a population size P , a crossover rate p_c , a mutation rate p_m , and a number of linguistic terms for items h .

OUTPUT: A set of membership functions and its corresponding concept-drift patterns.

- STEP 1: Randomly generate a population of P individuals. Each individual is a set of membership functions for items in transactions.
- STEP 2: For each chromosome, mine the fuzzy association rule sets RS^t and RS^{t+k} from D^t and D^{t+k} by using fuzzy rule mining algorithm with the support threshold α and the confidence threshold λ [10].
- STEP 3: Count the number of emerging patterns from rule sets RS^t and RS^{t+k} by using Equation (2).
- STEP 4: Count the number of unexpected changes from rule sets RS^t and RS^{t+k} by using Equation (3).
- STEP 5: Count the number of add/perished rules from rule sets RS^t and RS^{t+k} by using Equation (4).
- STEP 6: Calculate the suitability of each chromosome by Equation (5).
- STEP 7: Set the fitness value of each chromosome by using Equation (1).
- STEP 8: Generate the next population by using the elitist strategy.
- STEP 9: Execute the crossover operation on the population.
- STEP 10: Execute the mutation operation on the population.
- STEP 11: If the termination criterion is not satisfied, go to Step 2; otherwise, output the set of membership functions with the highest fitness value and concept-drift patterns.

V. AN EXAMPLE

In the following, an example is given to illustrate how to apply the proposed algorithm on the two databases for driving membership functions for mining concept-drift patterns. Two databases at time t and $t+k$ are shown in Table 3.

TABLE 3. TWO DATABASES FOR THIS EXAMPLE

Database D^t		Database D^{t+k}	
TID	Items	TID	Items
1	(A, 9)(B, 3)(C, 10)(D, 7)	1	(A, 5)(B, 4)(D, 3)
2	(A, 5)(C, 2)(D, 3)	2	(C, 2)(D, 1)
3	(B, 6)(C, 5)	3	(A, 7)(B, 3)(C, 7)
4	(A, 8)(D, 1)	4	(B, 2)(D, 2)

STEP 1: The initial population is generated randomly. Assume the $pSize$ was set at 4 and the first encoding method was used, the results are shown in Table 4.

TABLE 4. INITIAL POPULATION

C_q	Membership Functions
C_1	3, 3, 6, 3, 9, 3, 3, 3, 6, 3, 9, 3, 3, 3, 6, 3, 9, 3, 3, 3, 6, 3, 9, 3
C_2	2, 2, 5, 3, 7, 2, 2, 2, 5, 3, 7, 2, 2, 2, 5, 3, 7, 2, 2, 2, 5, 3, 7, 2
C_3	1, 1, 3, 1, 6, 2, 1, 1, 3, 1, 6, 2, 1, 1, 3, 1, 6, 2, 1, 1, 3, 1, 6, 2
C_4	2, 1, 8, 3, 9, 2, 2, 1, 8, 3, 9, 2, 2, 1, 8, 3, 9, 2, 2, 1, 8, 3, 9, 2

STEP 2: The fuzzy association rule sets RS^t and RS^{t+k} from D^t and D^{t+k} are induced by using fuzzy rule mining algorithm with the predefined support and the membership functions in the chromosome. In this example, the minimum support was set at 0.03. Take chromosome C_1 as an example. The results are shown in Table 5.

TABLE 5. FUZZY ASSOCIATION RULES DERIVED FROM TWO DATABASES

Rule Set RS^t			
Rule ID	fr_i	Rule ID	fr_i
1	A.High \rightarrow B.Low	2	B.Low \rightarrow A.High
3	A.High \rightarrow C.High	4	C.High \rightarrow A.High
5	B.Low \rightarrow C.High	6	C.High \rightarrow B.Low
Rule Set RS^{t+k}			
1	B.Low \rightarrow D.Low	2	D.Low \rightarrow B.Low
3	C.Low \rightarrow D.Low	4	D.Low \rightarrow C.Low

STEPS 3 to 7: The number of emerging patterns, unexpected changes and add/perished rules are discovered from rule sets RS^t and RS^{t+k} . In this example, there are two unexpected changes, three added ruled, four perished rules and no emerging pattern. Since the suitability of C_1 is 4, the fitness value of C_1 is 2.25 (= 9/4). In the same way, the fitness values of other chromosomes could be calculated.

STEPS 8 to 11: The genetic operations are executed on the population, including crossover and mutation operations. Take chromosomes C_1 and C_2 as an example. When the MMA crossover operator is executed, the four candidate chromosomes are shown as follows:

$$\begin{aligned}
C_1': & 3, 3, 6, 3, 9, 3, 3, 3, 6, 3, 9, 3, 3, 3, 6, 3, 9, 3, 3, 3, 6, 3, 9, 3 \\
C_2': & 2, 2, 5, 3, 7, 2, 2, 2, 5, 3, 7, 2, 2, 2, 5, 3, 7, 2, 2, 2, 5, 3, 7, 2 \\
C_3': & 1, 1, 3, 3, 5, 2, 2, 2, 5, 4, 8, 3, 3, 2, 4, 3, 6, 2, 3, 2, 7, 3, 5, 2 \\
C_4': & 2, 1, 5, 2, 7, 3, 1, 1, 3, 2, 4, 2, 4, 2, 5, 3, 8, 3, 1, 1, 5, 3, 6, 2
\end{aligned}$$

By repeating STEPS 3 to 6, the fitness values of the four candidate chromosomes are calculated as 2.25, 2.5, 2.7 and 2.1, respectively. The chromosomes C_2' and C_3' are used to replace C_1 and C_2 . In this example, since the fitness of the chromosome C_3' is the best, it will be outputted and utilized to mine concept-drift patterns.

VI. EXPERIMENTAL RESULTS

In this section, the results of the experiments to show the performance of the *CDGFM* are described. The experiments were implemented in Java on a personal computer with Intel i7-2600 (3.4GHz) and 4GB RAM. A simulation dataset containing 64 items and 10,000 transactions was used in the experiments. In the data set, the number of purchased items in transactions was first randomly generated, and the purchased items and their quantities in each transaction were then generated. An item could not be generated twice in a transaction. Here, we selected 1000 transactions from the simulated dataset, and divided them into two datasets as databases D^t and D^{t+k} , where each dataset thus has 500 transactions. The initial population size P was set at 20, the crossover rate p_c was set at 0.8, and the mutation rate p_m was

set at 0.01. The parameter d of the crossover operator was set at 0.35 according to Herrera *et al.* [12], and the minimum support was set at 0.04 (4%). Firstly, the convergence of the proposed approach is shown in Fig. 3 after 100 generations.

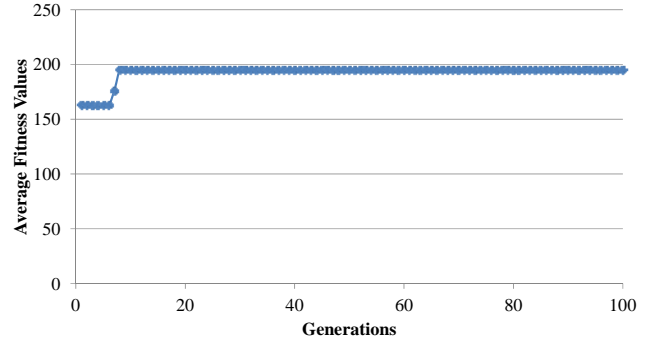


Fig. 3. Convergence of the proposed approach

From Fig. 3, it can be observed that the average fitness value of the proposed approach is increasing along with the increasing of generations, and converge to a certain value. The comparison of the initial membership functions and the derived membership functions for two among all items are shown in Fig. 4.

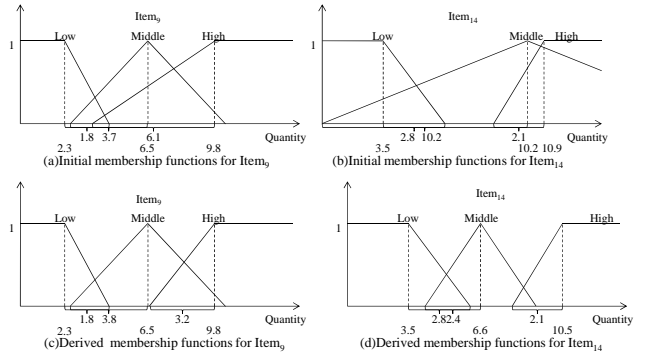


Fig. 4. The initial and derived membership functions

From Fig. 4(a) and 4(b), we can see that the membership functions for the two items overlap too much. Besides, Fig. 4(c) and 4(d) show that the bad types of membership functions don't appear after the evolution process. At last, in order to show the merit of the proposed approach, experiments were then made to compare the proposed approach with the uniform membership functions in terms of the number of concept-drift patterns. The two sets of uniform membership functions are shown in Fig. 5.

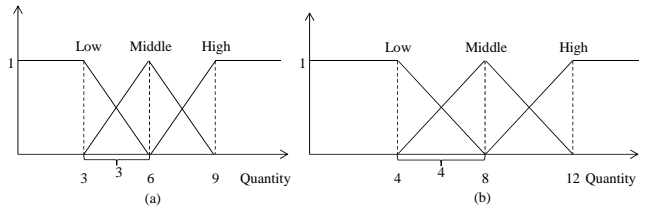


Fig. 5. The two sets of uniform membership functions

By using the two sets of membership functions and the derived membership functions, the numbers of each kind of concept-drift patterns of them are shown in Table 6.

TABLE 6. INITIAL POPULATION

	Number of Emerging Patterns	Number of Unexpected Changes	Number of Add/Perished Rules
<i>Proposed Approach</i>	70	39	255
<i>Uniform MFs(Fig. 5(a))</i>	6	20	72
<i>Uniform MFs(Fig. 5(b))</i>	27	31	165

From Table 6, the number of derived concept-drift patterns for emerging patterns, unexpected changes and add/perished rules are 70, 39 and 255, respectively. Comparing the results with those derived by the uniform membership functions, we can know that the proposed approach is better than others. The results thus indicate the proposed approach is effective in deriving appropriate membership functions for discovering concept-drift patterns.

VII. CONCLUSION AND FUTURE WORKS

In this paper, a concept-drift genetic-fuzzy mining approach has been proposed for deriving membership functions for mining concept-drift patterns. It first encodes membership functions for items into a chromosome. Since the fuzzy concept-drift patterns contains three types, including emerging patterns, unexpected change and added/perished rules, the fitness value of a chromosome is evaluated by the number of concept-drift patterns and the suitability of membership functions. Thus, the goal of the proposed approach is to derive appropriate membership functions that can not only get as more concept-drift patterns as possible but also avoid bad types of membership functions. Experiments on the simulated dataset were made to show the effectiveness of the proposed approach. Firstly, experiments show that the designed fitness function is effective. Secondly, when compared with those from the concept-drift pattern mining approach with predefined membership functions, the results by the proposed approach show that the derived membership functions can discover more concept-drift patterns than those by uniform membership functions. Because the evaluation of a chromosome is time-consuming, in the future, we will try to design other efficient approaches that can speed up the evolution process based on the proposed one.

ACKNOWLEDGMENT

This research was supported by the Ministry of Science and Technology of the Republic of China under grant MOST 103-2221-E-032-029 and 103-2221-E-006-271.

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