퍼지 로직과 유전 알고리즘을 이용한 영상 인식

류상진* · 나철훈**

Image Recognition by Fuzzy Logic and Genetic Algorithms

Ryoo, Sang-Jin* · Na, Chul-Hoon**

요 약

유전자 알고리즘을 이용한 다양한 특징의 분석이 필요한 퍼지 분류기의 설계 방법을 제안한다. 본 논문에서 제안한 퍼지 분류기는 퍼지 논리를 이용한 분류 부분과 유전자 알고리즘을 이용한 규칙 생성 부분으로 구성된다. 유전자 알고리즘을 이용한 규칙 생성 부분에서는 최적의 퍼지 멤버쉽 함수를 결정하고, 각 특징이 규칙에 포함되는지 포함되지 않는지의 여부도 결정하게 된다. 또한, 특정 대상에 대한 인식률을 분석하여 큰 오인식률을 갖는 부분에 세부 특징을 추가하는 방법과 문자열과 population의 최소 크기, 인식률 개선을 위한 반복적 분석 방법을 사용한다. 제안된 퍼지 분류기의 적용 예로서, 아이리스 데이터와 갑상선 종양 세포의 식별을 든다. 본 논문에서 제안한 퍼지 분류기는 아이리스 데이터에 대해 98.67%의 인식률을, 갑상선 종양 세포에 대해서 98.25%의 인식률을 얻었다.

ABSTRACT

A fuzzy classifier which needs various analyses of features using genetic algorithms is proposed. The fuzzy classifier has a simple structure, which contains a *classification part* based on fuzzy logic theory and a rule *generation part* using genetic algorithms. The rule generation part determines optimal fuzzy membership functions and inclusion or exclusion of each feature in fuzzy classification rules. We analyzed recognition rate of a specific object, then added finer features repetitively, if necessary, to the object which has large misclassification rate. And we introduce repetitive analyses method for the minimum size of string and population, and for the improvement of recognition rates. This classifier is applied to two examples of the recognition of iris data and the recognition of Thyroid Gland cancer cells. The fuzzy classifier proposed in this paper has recognition rates of 98.67% for iris data and 98.25% for Thyroid Gland cancer cells.

키워드

Recognition, Fuzzy Logic, Genetic Algorithm

Ⅰ. Introduction

Pattern Recognition Technique has attracted considerable attention in the recent years. This is mostly due because it plays an important role in human visual perception and provides information which is used in recognition and interpretation. Pattern Recognition technique has a wide variety of applications in medical image, remote-sensing, geology, and robotics[1]. An example of application in medical image is the evaluation of roentgenograms to classify normal and abnormal interstitial pulmonary patterns[2].

This paper deals with the cancer cell discrimination that

* 전남대학교
* 목포대학교

접수일자 : 2006. 12. 5

calls attentions to t .e pathologists. The object cell images were Thyroid Glan l cells image that diagnosed as normal cell, follicular neop astic cell, and papillary neoplastic cell, respectively.

The Clinical Cytology which detects the cancer cells by analyze the microscopic images was introduced by Papanicolaou[3]. The Clinical Cytology is the inspection method of detecting the cancer cells by analyzing the microphotographs of cells in medical image processing. Cells are taken from the internal organs of human body and check for the existence of cancer cells. It is a necessary inspection method of detection of the various types of cancers for early diagnosis and treatments. However, discriminations were achieved by human visual system. The digital process of medical image began early 1960' dealing with the microscopic images, X-ray images, and Computer Tomographic(CT) images. Digital image processing methods has been applied to Clinical Cytology[4]. But, the Clinical Cytology has many problems to the engineers. Medical features are difficult to understanding for engineer. And there are various features in every types of cells. The discrimination experiment uses the multiple parameters instead of simple parameters to increase the discrimination rate. The focus of this paper is to find a combination of dominant feature parameters for recognition of cancer cell using fuzzy logic and genetic algorithm.

Ⅱ. Fuzzy Classifier

When the similarity between standard pattern P and input pattern I is high, the possibility of inclusion in the specific class is high[5]. This simple fact is the basis of classification algorithms. Fuzzy membership function $\mu(x)$ is defined by equation (1) and is shown Figure 1.

$$\mu(x)=\begin{cases}\dfrac{x-p_M}{P_M-p_L}+1, & where\ p_L \le x \le p_M \\ \dfrac{x-p_M}{P_M-p_R}+1, & where\ p_M \le x \le p_R \\ 0 & , o/w\end{cases} \quad (1)$$

p_L, p_M and p_R are parameters of fuzzy membership function. The standard pattern $\mathrm{P}(i,j)$ in equation (2) is defined by mean values of features in each class. The number of pattern in each class is not same, but feature vectors have same dimension. $\mathrm{I}_k(i,j)$ is $i-th$ class and $j-th$ feature and $k-th$ input pattern.

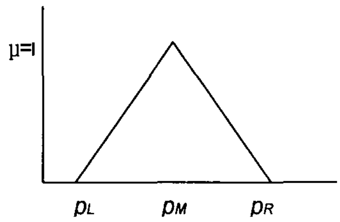


그림 1. 퍼지 멤버쉽 함수
Fig.. 1. Fuzzy membership function.

$$\mathrm{P}(i,j)=\sum_{k=1}^{N_I}\mathrm{I}_k(i,j)/N_I \quad (2)$$

$i=1,2,\cdots,N_C$, $j=1,2,\cdots,N_F$

N_C : Number of class, N_F : Number of feature,

N_I : Number of input patterns in each class.

We apply equation (3) which stands for similarity between standard patterns and input pattern to calculate fuzzy pattern matching[6]in each class. FPM_{ij} is the value of fuzzy pattern matching in $i-th$ class and $j-th$ feature.

$$\begin{aligned}\mathrm{FPM}&=\{FPM_{ij}\mid 1\le i\le N_C, 1\le j\le N_F\} \quad (3)\\ &=\min_{k=1}^{N_I}(1-|\mu_P(x)-\mu_{I_k}(x)|)\end{aligned}$$

$\mu_P(x)$ is a membership function of standard pattern, $\mu_{I_k}(x)$ is a membership function of $i-th$ input pattern. When the similarity between the input patterns between standard pattern is higher, the possibility of inclusion in standard pattern is higher. To calculate the class which include in standard pattern, we define the degree of matching M_i in equation (4). The s_R is a selection bit and means inclusion or exclusion of features in each rule, N is the number of features in each rules.

$$M_i = \sum_{j=1}^{N_F} \frac{FPM_{ij}}{N} \tag{4}$$

The class of input pattern from the membership value of input pattern is obtained equation (5)

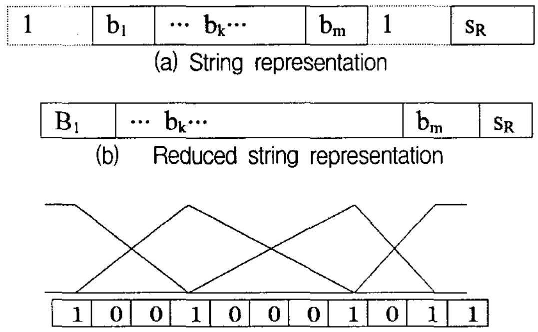
$$If\ \max_{i=1}^{N_C} M_i\ is\ M_C,\ Then\ Class(I)\ is\ c \tag{5}$$

III. Fuzzy Rule Generation using Genetic Algorithms

Genetic algorithms are kinds of stochastic optimization methods modeling native natural evolution phenomena [5]. Usual GAs consist of three kinds of genetic operations; selection, crossover and mutation. They work as stochastic operations on a population to make a change of generation. Crossover combines substructures of parents to produce new individuals. It is the most characteristic operation as an optimization method because other methods as simulated annealing did not use such global multiple search points

3.1. String Representation

To solve any optimization problem using a genetic algorithm, it is necessary to code scheme to encode the parameters of the problem into a string. Genetic algorithms are applied to obtain the shape and number of fuzzy membership function and an inclusion or exclusion of feature for classification. String representation and an example of real fuzzy membership function in genetic algorithms are shown in Fig. 2. The numeral 1 in membership function parts means boundary value in membership function, and 0 and 1 in rule selection part means exclusion and inclusion.



(a) String representation

(b) Reduced string representation

(c) Fuzzy membership function example

그림 2. 문자열의 표현과 그 예
a) 문자열 표현 b) 감소된 문자열 표현 c) 예
Fig. 2. String representation and its example
a) String representation
b) Reduced string representation c) Example

A successive three 1s except 0 in b_k are lower, middle, and upper parameter in membership function. The optimal strings can be produced using genetic algorithms[7][8][9]. Optimal string is an optimal fuzzy membership function and makes the maximum recognition rate. Furthermore, rule selection bit makes better performance by eliminating the bad effect due to non-effective feature. To select effective feature vectors guarantee better recognition rate. We classify feature vectors into dominant, recessive, and extra feature vector. The proposed rule selection bit exclude recessive feature vector and include dominant feature vector to increase recognition rate.

3.2. Fitness Function

A fitness function must be relevant to the problem being optimized. The fitness value of each string is computed from the fitness function. A good string is one that scores a high fitness value. The fitness value is defined in recognition rate *RR*. We classified higher 30% of strings to superior set, all operations, for example, reproduction, crossover, and mutation are conducted superior strings and the other strings.

3.3. Genetic Op rator

A. Reproduction

The reproductior operation is performed as follows:

1) Normalize the fitness value of each string such that the sum of the fitness values of all the strings in the current population is equal to 1.

2) Partition a unit-length scale into population size N slots, where each slot size is in proportion to the normalized fitness value of a string in the current population

3) Generate N random numbers from 0 to 1 and see where the number falls on the scale. The string corresponding to the division where a random number falls is selected to be a member for the new population.

For the better performance, superior string must survive in next generation. String which has better performance has higher selection probability. Crossover operation was conducted in next step. In reproduction procedure, strings for crossover operation are selected in superior strings and other strings. The size of population is 20 and the number of superior strings is 6 in every experiment.

B. Crossover Operation

The crossover operator is the most important operator in genetic algorithms. It is the mating operator that allows production of new strings through a combination of parts of strings. The probability for crossover operation is0.5.

1) Paris of members of the newly reproduced strings are randomly selected for mating.

2) For each pair of selected strings, parts of the strings are swapped to from a pair of new strings. The position of a string to which the swapping takes place is randomly selected.

C. Mutation Operation

Mutation is needed because, even though reproduction and crossover effectively search and recombine extant notions, occasionally they may become overzealous and lose some potentially useful genetic materials. The mutation operator protects against such irrecoverable loss. The probability for mutation operation is 0.05.

Ⅳ. Experimental Results

To show the effectiveness of proposed method, we apply our algorithms 150 IRIS data and 57 gland cancer cells data and we use the 16 feature parameters[10].

4.1. IRIS Data[11][12]

IRIS data which is standard data for pattern classification problem consist of 4 features and 3 classes. To show the effectiveness of proposed method, we show the classification results in Table 1 (a). The size of the string is changed by 1 to 7 except rule selection bit and the maximum recognition result was obtained in 10 times experiments. The result show that the proposed method has 98.67% recognition rate(148 correct classification in 150 patterns)when the size of string is 4 and the number of rule is 1.

표 1. (a) 여러 문자열의 모의시험결과
Table 1. (a) Simulation results with different string size.

String size	With RS bit		Without RS bit	
	No. of patterns	No. of rules	No. of patterns	No. of rules
1	144	1	140	1
2	145	1	144	1
3	147	1	146	1
4	148	1	146	1
5	147	1	146	1
6	146	1	145	1
7	146	1	146	1

표 1 (b) 여러 교배연산의 모의시험결과[11]
Table 1. (b) Simulation results with different crossover operations[11].

Trial number	Uniform crossover		One-point crossover	
	No. of patterns	No. of rules	No. of patterns	No. of rules
1	149	5	149	5
2	149	6	149	5
3	148	6	150	7
4	149	7	149	6
5	149	7	149	6
Average	148.8	6.2	149.2	5.8

Table 1 (b) shows the results used multiple classification rules by Ishibuchi[11]. Ishibuchi has got only one misclassification pattern in 150 patterns using 5 classification rules and has got 100% classification result using 7 rules. And Young could classify 146 patterns using only one rule. This result shows same result when we didn't use rule selection bit.

This result shows the proposed method is superior to any other results aspect the recognition result versus the number of rules. Ishibuchi has used 441 string size and 50 population size, but we used only 1~7 string size and 20 population size.

4.2. Recognition of Thyroid Gland Cancer Cells

Thyroid Gland cancer cells has two types of papillary and follicular cancer cells[10]. The selection rule classifying cancer cells and normal cells by expert is subjective and too complicated to explain. The input pattern which has 16 features 16 normal cells, 16 papillary cancer cells and 25 follicular cancer cells. Table 2 ~ Table 8 show the recognition rates when the size of the feature vector was changed 4 ~ 1 and rule selection bit was used or not. The number in parenthesis is the number of misclassification patterns. The maximum recognition results were obtained when the number of selected features is 10 or 16 and the size of string is 3 using rule selection bit. The number of misclassification pattern is only one. When we didn't use rule selection bit, we can get maximum recognition rates in the number of features is 12 or 16 and string size is 2 or 3. And the number of misclassification pattern is 4.

The maximum recognition rate was 96.49% and 94.74% when the string size was 2 and 5, respectively. The maximum recognition rate was 88.75% and 90.0% in reference [10].

표 2. 특징 갯수 4일 때 문자열의 크기와 규칙선택 비트의 사용 유, 무에 따른 인식률
Table 2. String size and recognition rates with/without RS bit, Feature size : 4.

String size	With RS bit	Without RS bit
1	75.44% (14)	73.68% (15)
2	75.44% (14)	73.68% (15)
3	78.95% (12)	73.68% (15)
4	77.19% (13)	77.19% (13)
5	74.44% (14)	75.44% (14)
6	77.19% (13)	77.19% (13)
7	75.44% (14)	75.44% (14)

표 3. 특징 갯수 6일 때 문자열의 크기와 규칙선택 비트의 사용 유, 무에 따른 인식률
Table 3. String size and recognition rates with/without RS bit, Feature size : 6.

String size	With RS bit	Without RS bit
1	84.21% (12)	78.95% (12)
2	87.72% (7)	78.95% (12)
3	85.96% (8)	78.95% (12)
4	84.21% (9)	80.70% (11)
5	85.96% (8)	78.95% (12)
6	87.72% (7)	78.95% (12)
7	85.96% (8)	80.70% (11)

표 4. 특징 갯수 8일 때 문자열의 크기와 규칙선택 비트의 사용 유, 무에 따른 인식률
Table 4. String size and recognition rates with/without RS bit, Feature size : 8.

String size	With RS bit	Without RS bit
1	87.72% (7)	80.71% (11)
2	94.74% (3)	85.96% (8)
3	92.98% (4)	85.96% (8)
4	91.23% (5)	84.21% (9)
5	92.98% (4)	84.21% (9)
6	91.23% (5)	85.96% (8)
7	87.72% (7)	82.46% (10)

표 5. 특징 갯수 10일 때 문자열의 크기와 규칙선택 비트의 사용 유, 무에 따른 인식률
Table 5. String size and recognition rates with/without RS bit, Feature size : 10.

String size	With RS bit	Without RS bit
1	89.47% (6)	85.96% (8)
2	92.98% (4)	89.47% (6)
3	98.25% (1)	89.47% (6)
4	94.74% (3)	85.96% (8)
5	91.23% (5)	84.21% (9)
6	91.23% (5)	87.72% (7)
7	91.23% (5)	84.21% (9)

표 6. 특징 갯수 2일 때 문자열의 크기와 규칙선택 비트의 ,사용 유, 무에 따른 인식률
Table 6. Str ng size and recognition rates with/withoLt RS bit, Feature size : 12.

String size	With RS bit	Without RS bit
1	91.23% (5)	87.72% (7)
2	94.74% (3)	91.23% (5)
3	94.74% (3)	92.98% (4)
4	94.74% (3)	89.47% (6)
5	92.98% (4)	89.47% (6)
6	91.23% (5)	89.47% (6)
7	91.23% (5)	87.72% (7)

표 7. 특징 갯수 14일 때 문자열의 크기와 규칙선택 비트의 사용 유, 무에 따른 인식률
Table 7. String size and recognition rates with/without RS bit, Feature size : 14.

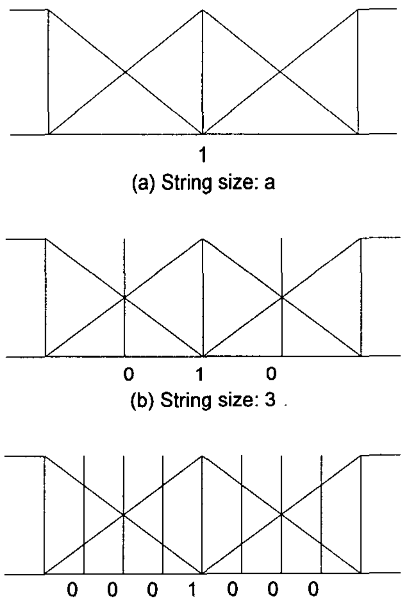
String size	With RS bit	Without RS bit
1	91.23% (5)	89.47% (6)
2	94.74% (3)	91.23% (5)
3	96.49% (2)	91.23% (5)
4	94.74% (3)	91.23% (5)
5	92.98% (4)	87.72% (7)
6	92.98% (4)	89.47% (6)
7	92.98% (4)	87.72% (7)

표 8. 특징 갯수 16일 때 문자열의 크기와 규칙선택 비트의 사용 유, 무에 따른 인식률
Table 8. String size and recognition rates with/without RS bit, Feature size : 16.

String size	With RS bit	Without RS bit
1	92.98% (4)	91.23% (5)
2	96.49% (2)	92.98% (4)
3	98.25% (1)	92.98% (4)
4	94.74% (3)	91.23% (5)
5	94.74% (3)	91.23% (5)
6	94.74% (3)	91.23% (5)
7	92.98% (4)	89.47% (6)

V. Performance of repetitive analysis and dominant features

The size of the string is the important part to determine the shape of fuzzy membership function and has direct relationship in the performance of recognition rates. When we guarantee proposed method search all space, bigger size of string means better recognition rates. But it is impossible or not effective to guarantee these conditions. We will use repetitive analysis method which increases the search space in small volume to larger one. Fig. 3 shows some examples when the string size is 1, 3, and 7. When the string size is 1, the optimal membership function is a part of those in string size is 3. Therefore recognition rate in string size 3 must be same at least or greater than in string size 1. The increment of string is shown in Fig. 3. After saturation in recognition rates occurs, the size of string will be doubled as like Fig. 3.



(a) String size: a

(b) String size: 3

(c) String size: 7

그림 3. 각 문자열 크기에 대한 퍼지 멤버쉽 함수 a) 문자열 크기 : a b) 문자열 크기 : 3 c) 문자열 크기 : 7
Fig. 3. Fuzzy membership functions for each string size.

$$L_{string}(n+1) = 2L_{string}(n) + 1 \tag{7}$$

Initial string size L_{string} is 1, 2, 4, 6, 8, ... When string size is doubled, recognition rate will not decrease any more. The recognition rate by proposed method is shown table 9 and 10.

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표 9. 규칙선택 비트의 사용 유, 무에 따른 아이리스 데이터 반복적 분석법의 인식률
Table 9. Recognition rates with/without RS bit uusing repetitive analyses method for Iris data.

String size	With RS bit	Without RS bit
1	96.00% (6)	93.33% (10)
2	96.67% (5)	96.00% (6)
3	98.00% (3)	97.33% (4)
4	98.67% (2)	97.33% (4)
5	98.00% (3)	97.33% (4)
6	97.33% (4)	96.67% (5)
7	98.00% (3)	97.33% (4)
8	98.00% (3)	97.33% (4)
9	98.67% (2)	97.33% (4)

표 10. 규칙선택 비트의 사용 유, 무에 따른 갑상선 암세포의 인식률(특징 갯수 10)
Table 10. Recognition rates with/without RS bit using repetitive analyses method for Gland Cancer cells data (Feature size:10).

String size	With RS bit	Without RS bit
1	89.47% (6)	85.96% (8)
2	92.98% (4)	89.47% (6)
3	98.25% (1)	89.47% (6)
4	94.74% (3)	85.94% (8)
5	94.74% (4)	89.47% (6)
6	91.23% (5)	87.72% (7)
7	98.25% (1)	89.47% (6)
8	94.74% (4)	87.72% (7)
9	94.74% (3)	85.94% (8)

When rule selection bit is applied to classification, additional 1.06% recognition rate in IRIS data and 6.44% recognition rate in gland cancer cell were obtained. Rule selection bit is more effective when input feature is grater. Table 11 shows 16 input features in gland cancer cell recognition.

The dominant input features and fuzzy membership functions by proposed method is shown in table 12, when three 98.25% maximum recognition rates were obtained. We could get same dominant features although fuzzy membership functions are changed. This result shows that selection of dominant feature is very important in classification problem.

Ⅵ. Conclusion.

In this paper, a new method of recognition for medical image analysis was studied which using the pattern recognition techniques. The focus of this paper is the automatic recognition of cells into normal and abnormal cells. The object cells image used in this paper was microscopic image of Thyroid Gland cells. And new technique for recognition of cells image which uses Fuzzy Logic and Genetic Algorithm was proposed.

표 11. 암세포의 특징변수[10].
Table 11. Feature parameters of cancer cells[10].

No.	Symbol	Features
1	SX	Nuclear X-Size
2	SY	Nuclear Y-Size
3	MS	Average of SX and SY
4	DS	Denseness
5	PM	Perimeter
6	GM	Gray Level Mean of Nucleus
7	SD	Standard Deviation
8	AR	Nuclear Area
9	VR	Valid Rate
10	AP	Averaged Power of Necules
11	AC	Autocorrelation
12	ET	Entropy
13	IN	Inactivity
14	AV	Absolute Value
15	ID	Inverse Difference
16	RP	Ratio of (PM / MS)

표12. 멤버쉽 함수의 변수와 우세특징
Table 12. Membership function parameters and Dominant features.

No.	Content of Strings	No.	Content of Strings	No.	Content of Strings
1	01110010110	1	11100110000	1	1011011010
2	10100101010	2	10101001110	2	10011001110
3	00001111100	3	01101011100	3	10000011100
4	11011000001	4	11010000001	4	11111000001
5	00011101011	5	00010101001	5	00011101011
6	00111100011	6	00111010011	6	00111010011
7	11001111101	7	11001111101	7	11001111001
8	00100000011	8	01100000011	8	01110100011
9	10110000011	9	01110000111	9	01110000111
10	10111010111	10	10100110101	10	10111110101
11	01011110110	11	00011110110	11	01101110110
12	10110010111	12	01111010101	12	11110010111
13	00000010110	13	00011111010	13	00011111100
14	00110011011	14	01010010011	14	01110010011
15	01000101111	15	01000101011	15	10100101011
16	01110111010	16	11110111000	16	01111111000

The fuzzy classifier has a simple structure, which contains a classification part based on fuzzy logic theory and a rule generation part using genetic algorithms. The rule generation part determines optimal fuzzy membership functions and inclusion or exclusion of each feature in fuzzy classification rules. We analyzed recognition rate of a specific object, then added finer features repetitively, if necessary, to the object which has large misclassification rate. And we introduce repetitive analyses method for the minimum size of string and population, and for the improvement of recognition rates. This classifier is applied to two examples of the recognition of iris .data and the recognition of Thyroid Gland cancer cells. The fuzzy classifier proposed in this paper has recognition rates of 98.67% for iris data and 98.25% for Thyroid Gland cancer cells.

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저자소개

류 상 진(Sang-Jin Ryoo)

1991년 2월 전남대학교 전자공학과 학사
1994년 2월 전남대학교 전자공학과 석사
1999년 3월~현재 전남대학교 전자공학과 박사과정
※관심분야 : MIMO System, OFDM, AMC, 이동통신

나 철 훈(Cheol-Hun Na)

1985년 2월 전남대학교 전기공학과 학사
1987년 2월 전남대학교 전기공학과 석사
1994년 2월 전남대학교 전기공학과 박사
1995년 9월~현재 목포대학교 교수
※관심분야 : Digital Image Processing, 통신시스템, Medical Image Processing