Hindawi
Mathematical Problems in Engineering
Volume 2020, Article ID 7653946, 18 pages
https://doi.org/10.1155/2020/7653946

Research Article

A Model of High-Dimensional Feature Reduction Based on Variable Precision Rough Set and Genetic Algorithm in Medical Image

Zhou Tao,[1,2] **Lu Huiling**,[2] **Fuyuan Hu**,[3] **Shi Qiu**,[4] **and Wu Cuiying**[5]

[1]*School of Computer Science and Engineering, North Minzu University, Yinchuan 750021, China*
[2]*School of Science, Ningxia Medical University, Yinchuan 750004, China*
[3]*School of Electronic & Information Engineering, Suzhou University of Science and Technology, Suzhou 215009, China*
[4]*Key Laboratory of Spectral Imaging Technology CAS, Xi'an Institute of Optics and Precision Mechanics, Chinese Academy of Sciences, Xi'an 710119, China*
[5]*Human Resources Department, The Second Affiliated Hospital of Xiamen Medical College, Xiamen 361021, China*

Correspondence should be addressed to Lu Huiling; lu_huiling@163.com

Received 29 March 2020; Accepted 20 April 2020; Published 30 May 2020

Guest Editor: Zaoli Yang

Copyright © 2020 Zhou Tao et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Aiming at the shortcomings of high feature reduction using traditional rough sets, such as insensitivity with noise data and easy loss of potentially useful information, combining with genetic algorithm, in this paper, a VPRS-GA (Variable Precision Rough Set--Genetic Algorithm) model for high-dimensional feature reduction of medical image is proposed. Firstly, rigid inclusion of the lower approximation is extended to partial inclusion by classification error rate β in the traditional rough set model, and the ability dealing with noise data is improved. Secondly, some factors of feature reduction are considered, such as attribute dependency, attributes reduction length, and gene coding weight. A general framework of fitness function is put forward, and different fitness functions are constructed by using different factors such as weight and classification error rate β. Finally, 98 dimensional features of PET/CT lung tumor ROI are extracted to build decision information table of lung tumor patients. Three kinds of experiments in high-dimensional feature reduction are carried out, using support vector machine to verify the influence of recognition accuracy in different fitness function parameters and classification error rate. Experimental results show that classification accuracy is affected deeply by different weight values under the invariable classification error rate condition and by increasing classification error rate under the invariable weigh value condition. Hence, in order to achieve better recognition accuracy, different problems use suitable parameter combination.

1. Introduction

Rough set theory was developed by Pawlak in 1982 [1], and it is a mathematical tool to deal with vagueness and uncertainty. The classification ability unchanged in its main idea, decision or classification rules of problem are derived by knowledge reduction [2]. The Variable Precision Rough Set (VPRS) theory, proposed by Ziarko, and is an extension of original rough set model. For inconsistent information system, the VPRS model allows a flexible approximation boundary region by a precision variable β [3]. When $\beta = 0$, Pawlak rough set model is a special case of variable precision rough set model. The main task of variable precision rough set model is to solve the problem of data classification with no function or uncertainty. The hierarchical model of attribute reduction for variable precision rough set is studied by Xiaowei [4]. There is abnormal phenomenon in existing attribute reduction models; therefore, a variable precision rough set attribute reduction algorithm with the property of interval is proposed, and the reduction abnormal problem is transformed into a hierarchical model representation, and the reduction anomaly is gradually eliminated by the layer-by-layer reduction model; Jie and Jiayang [5] puts forward that there may be a reduction

jump phenomenon in variable precision rough set feature reduction, which affects the quality of reduction and brings the problem of attribute reduction of variable precision rough set; Pei and Qinghua [6] proposes an FCM clustering algorithm based on variable precision rough set; according to the threshold characteristics of the variable precision rough set model, the algorithm divides the objects in the edge of the cluster into the positive, negative, and boundary regions, to improve the accuracy of clustering. Two different solutions of variable precision rough set attribute reduction algorithm are proposed by Hao and Junan [7]; based on tolerance matrix and minimal reduction of attribute core, the attribute kernel idea of variable precision rough set is proposed. The experimental results show that the two algorithms can reduce the search space and improve the efficiency of the algorithm.

Feature reduction is one of the core contents of rough set theory; in the condition of keeping the classification ability for knowledge base unchanged, we delete irrelevant or unimportant knowledge, which can reduce the dimension of the decision system, reduce the time complexity, and improve the efficiency of the algorithm [8]. People want to find the minimum reduction, but it has been proved to be an NP-Hard problem [9]; the main research is how to find the second optimal solution. Genetic algorithm is a computational model which is based on the natural selection and evolution mechanism; its core idea is inspired by the natural selection rule of the survival of the fittest, can achieve a highly parallel, random, and adaptive search, is not easy to fall into local optimal [10], can find the global optimal solution with high probability, and has great advantage in solving the NP-Hard problem.

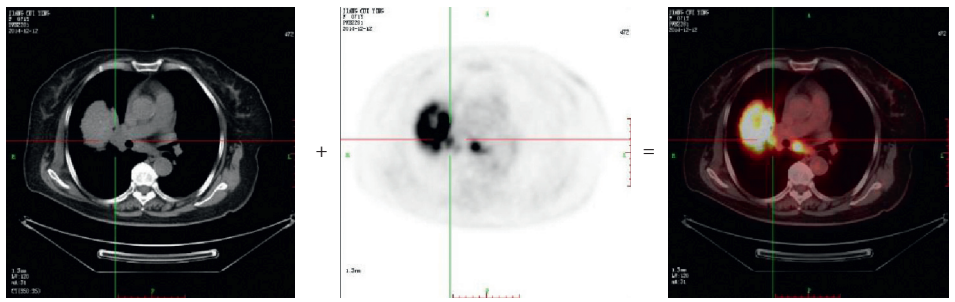
In this paper, a new algorithm of PET/CT high-dimensional feature selection is proposed based on genetic algorithm and variable precision rough set model. On one hand, the algorithm considers the value of chromosome coding, the minimum number of attributes, and the dependency of attributes to construct a general fitness function framework and adjusting weight coefficient of each factor to achieve different fitness function; on the other hand, aiming at the limitation of Pawlak rough set model, introducing the classification error rate of β, it extends rigid inclusion of the lower approximation for traditional rough set to partial inclusion, not only improving the concept of approximate space, but also enhancing the ability to deal with noise data and changing the range of β to achieve different fitness function. Finally, through extracting PET/CT lung cancer ROI 98-dimensional feature to construct the information decision table of lung cancer patients, 8 group experiments of high-dimensional features selection are done by using support vector machine to classify and recognize reduction subsets, to verify the degree of influence on the different weights and different classification error rate, and find a set of parameters suitable for this problem ($\omega 1 = 1, \omega 2 = 1, \omega 3 = 0$; $\beta = 0.6$). The experimental results show that different parameters can be used to get different experimental results, so we should choose the appropriate parameter combination according to different problems so as to get better recognition accuracy.

2. Materials and Methods

2.1. PET/CT. PET/CT is a kind of advanced medical imaging technology, which is a combination of the good performance of PET and CT on the same device, and provides the anatomical and functional metabolism of the subjects under the same conditions [11]. PET is a functional image; it can provide metabolic information of tissue and organ and reflect functional changes of the human body from the molecular level, such as the physiological, pathological, biochemical, and metabolic, but has poor spatial resolution, cannot be accurately located, and cannot display the anatomical information of the lesions [12]. CT belongs to the anatomical structure of images, with high spatial resolution and density resolution; it has unique advantages in displaying the anatomical structure and density of the body [13], it also can provide detailed anatomical information of human organs and tissues, but can not reflect the functional information of tissues and organs [14] (Figure 1).

2.2. Genetic Algorithm. Genetic algorithm is a computational model which is based on the natural selection and evolution mechanism; its core idea is inspired by the natural selection rule of the survival for the fitness, so the search algorithm is an iterative process of survival and detection, is a very effective search and optimization technique, can achieve a highly parallel, random, and adaptive search, cannot easily fall into local optimum, and can find the global optimal solution with high probability and its robustness is good [15]. General use of genetic algorithm for reduction is achieved by a binary coding, 1 indicates that the position selects the corresponding attribute, while 0 indicates that the corresponding attribute is not selected. Genetic algorithm consists of four parts: encoding and decoding, fitness function, genetic operator, and control parameters, genetic operators include selection operator, crossover operator, and mutation operator, The selection operator is generally selected by roulette wheel selection method, according to the selection probability $p_i = (f_i / \sum_{i=1}^{M} f_i)$, crossover operator is a single point crossover, with a certain probability p to select individuals to participate in crossover, mutation operator selects the individual with the probability p and randomly selects the corresponding gene of the variant individuals to operate [16]. The general steps are as follows: determining the initial population and calculating the target value of each individual in the population and the corresponding value of the fitness function, choosing the chromosomes with high fitness value, and forming a matching set (selection), according to certain rules of reproduction (crossover and mutation), to meet the conditions to stop the genetic iteration, or return to step 3 (Figure 2).

2.3. Variable Precision Rough Set. Ziarko proposed the variable precision rough set model in 1993, he first proposed the concept of classification error rate; in the case of a given classification error rate, the objects with the same attributes can be classified into classes as many as possible [17].



(a) (b) (c)

Figure 1: The source image of CT, PET, PET/CT.

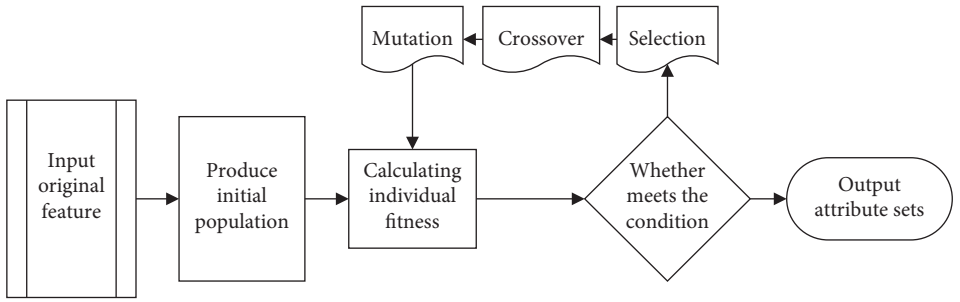


Figure 2: Flow chart of knowledge reduction method based on genetic algorithm.

Definition 1 (equivalence class). Assuming that R is an equivalence relation on K, a collection of all elements equivalent to an element k in K is called an equivalence class of k, denoted as $[k]$.

Definition 2 (indiscernibility relation). If $P \subseteq R$ and $P \neq \phi$, then $\cap P$ is also an equivalence relation, it is called the indiscernibility relation on P, denoted as ind $[P]$.

Definition 3 (upper approximation and lower approximation). The knowledge base of $K = (U, R)$, $X \subseteq U$, R is equivalent to the relationship between U. The lower approximation of X can be understood as all of the classification errors that are not greater than β are included in the R equivalence class in X. The upper approximation of X can be understood as the intersection of all those with classification error not greater than β and equivalence classes with X is not empty [18]. Expressions are as follows:

$$\underline{RX}_{\beta} = \cup \left\{ Y \in \frac{U}{R} \middle| Y \subseteq X \right\},$$
$$\overline{RX}_{\beta} = \cup \left\{ Y \in \frac{U}{R} \middle| Y \cap X \neq \varphi \right\}. \quad (1)$$

Assume that the decision information table $S = (U, A, V, f)$, where U is a sample of the universe and a nonempty finite sample set, $U = \{x1, X2, x3, \ldots, Xn\}$, and Xi represents each sample. $A = P \cup Q$, P represents a collection of conditional attributes, Q represents a set of decision attributes. V represents the range of attribute. f: $U \times A \longrightarrow V$ is an information function that gives an attribute value for each attribute of each x_i, that is, $\forall_a \in A, x \in U, f(x, a) \in V_a$. X and Y represent nonempty set in finite field U. $P, Q \subseteq A$ represents the condition attribute set and decision attribute set; ind (P), ind (Q) is an indiscernibility relation determined by P, Q; ind (P) is a collection of equivalence classes called condition class, expressed in U/P, i.e., $U/\text{ind}(P) = \{P_1, P_2, P_3, \ldots, P_n\}$; ind (P) is a collection of equivalence classes called decision class, expressed in U/Q, that is $U/ind(Q) = \{Q_1, Q_2, Q_3, \ldots, Q_n\}$.

Definition 4 (majority inclusion relation). If there is a $e \in Y$ for each $e \in X$, then Y contains X, denoted as $Y\ X$, then

$$c(X, Y) = \begin{cases} 1 - |X \cap Y|/|X|, & |X| > 0, \\ 0, & |X| = 0, \end{cases} \quad (2)$$

where $|X|$ represents the cardinality of the set X and $c(X, Y)$ is the relative classification error rate of set X on set Y.

Make $(0 \leq \beta < 0.5)$; the majority inclusion relation is defined as $Y \overset{\beta}{\supseteq} X \Longleftrightarrow c(X, Y) \leq \beta$; the "majority" requirement implies that the number of common elements in X and Y is greater than 50% of the number of elements in X.

Definition 5 (β-reduction). Conditional attribute set P is a subset of P for β-reduction or approximate reduction of decision attribute set Q, and the subset is red (P, Q, β) and meets the following two conditions [19]:

(1) $\gamma(P, Q, \beta) = \gamma(\text{red}(P, Q, \beta), Q, \beta)$

(2) To remove any attribute from red (P, Q, β), condition (1) is not valid

2.3.1. Attribute Dependency

Definition 6. The dependency of the decision attribute set Q and the conditional attribute set P is defined as

$$\gamma(P,Q,\beta) = \frac{|\mathrm{pos}(P,Q,\beta)|}{|U|}. \tag{3}$$

$\mathrm{pos}(P,Q,\beta) = \cup_{Y\in U/Q} \underline{\mathrm{ind}(P)}_{\beta} Q$, $|U|$ is the number of objects contained in the domain, $|\mathrm{pos}(P,Q,\beta)|$ is the number of objects contained in the positive domain of all equivalence classes that are not greater than the β classification error, which indicates that the conditional attributes can correctly divide the object to $U|Q$. $\gamma(0 \le \gamma \le 1)$ is the β dependency of the decision attribute Q to the conditional attribute P and is an evaluation of the ability to classify objects with the classification error β.$\gamma = 0$ means that P cannot be used to divide objects into equivalence classes in Q, $\gamma = 1$ means that P can be used to divide objects into equivalence classes in Q completely, $0 < \gamma < 1$ means that P can be used to divide objects into equivalence classes in Q partly.

2.3.2. Attribute Importance

Definition 7. Assume that the decision information table is $S = (U, A, V, f)$, $A = P \cup Q$, $s \in h$, the relative importance of attribute s is

$$Z(s) = \frac{\gamma(P,Q,\beta) - \gamma(P-\{s\},Q,\beta)}{\gamma(P,Q,\beta)} = 1 - \frac{\gamma(P-\{s\},Q,\beta)}{\gamma(P,Q,\beta)}. \tag{4}$$

An attribute is able to distinguish an object; the greater the value, the stronger the ability.

The selection of threshold β for variable precision rough set needs to meet the following requirements.

The choice of β to make the classification accuracy as high as possible:

(1) $0 \le \beta < 0.5$

(2) β makes the attributes contained in the reduction results as little as possible

2.4. SVM. Support vector machine (SVM) is a supervised learning model for data analysis, pattern recognition, and regression analysis in the field of machine learning. The best compromise between model complexity (the learning accuracy of a particular training sample) and learning ability (ability to identify an arbitrary sample without error) should be found based on limited sample information. In order to obtain the best generalization ability, the basic idea is to use the structural risk minimization principle to construct the optimal classification hyperplane in the attribute space. SVM has some advantages such as good generalization ability, simple data structure, low computational complexity, short training time, few parameters selection, high fitting precision, strong robustness, and so on [20, 21]. It has great advantages in dealing with small sample, nonlinear, and high-dimensional pattern recognition. It is often used in pattern recognition [12, 22], regression estimation, and so on.

(1) After the introduction of kernel function and penalty parameter by SVM, the optimal discriminant function model is

$$f(x) = \mathrm{sgn}\left(\sum_{i=1}^{n} a_i y_j k(x_i, x) + b\right). \tag{5}$$

Among it, $0 < a < C$, $y_i \in \{1, -1\}$.

(2) The optimization function of SVM is

$$Q(a) = \sum_{i=1}^{n} a_i - \frac{1}{2}\sum_{i,j=1}^{n} a_i a_j y_i y_j k\left(x_i, x_j\right). \tag{6}$$

(3) The radial basis kernel function is a widely used kernel function; the kernel function is used in this paper:

$$k(x,y) = \exp\left(-g\|x-y\|^2\right). \tag{7}$$

Among them, $g > 0$, g is an important parameter in the kernel function, which affects the complexity of SVM classification algorithm.

The kernel function parameter g and penalty coefficient C of support vector machine (SVM) is an important parameter which affects the performance of SVM classification, so (C, g) is used as the optimization variable. In the process of learning SVM, 5-fold cross validation is used to calculate the optimal classification performance of kernel function parameter and penalty coefficient, and then the diagnosis result of optimization is applied to the SVM classifier for lung cancer, the final selection of the sensitivity, specificity, accuracy, and computation time as the evaluation indexes of related experiments.

3. Results and Discussion

3.1. Main Idea. The main idea of the model is as follows.

3.1.1. Parameters. Population size M, chromosome length N (the number of condition attributes), crossover probability Pc, mutation probability Pm, fitness function $F(x)$, and the maximum number of iterations K are the parameters.

3.1.2. Coding. The binary coding method is used, which is represented by a binary string whose length is equal to the number of condition attributes; each bit corresponds to a condition attribute, a bit of 1 indicates that the corresponding condition attribute is selected, 0 indicates that the condition attribute is not selected, e.g., {00110101} represents a chromosome with a length of 8, and it is known that the corresponding 1, 2, 5, 7 of 0 indicates that the corresponding condition attribute is not selected, then{c3, C4, C6, c8} is the last individual to choose the attributes set.

3.1.3. The Initial Population. Assuming the population size M (the number of chromosomes in the population is M), M length of Lr chromosome (0, 1) is the randomly generated as the initial population.

3.1.4. Genetic Operators. Genetic operators include selection operator, crossover operator, and mutation operator. The selection operator generally uses the roulette wheel selection method, according to the selection probability $p_i = (f_i / \sum_{i=1}^{M} f_i)$ to select. Crossover operator uses a single-point crossover, with a certain probability Pc to select the individual uniform crossover. The mutation operator selects the individuals with the probability Pm to carry on the variation, and randomly selects the corresponding bit of the nonnuclear attribute.

3.1.5. Fitness Function. The fitness function is the core of the genetic algorithm, the fitness value is the only index to evaluate the fitness function; this paper from the gene encoding value, the minimum number of attributes reduction, attribute dependency, and other aspects constructs a fitness function framework, by adjusting the weights of various factors and changing the classification error rate to achieve different fitness function. The fitness function is set as follows:

target1. Attribute dependency: $\gamma(P, Q, \beta) = (|\mathrm{pos}_P^{\beta}(Q)|/|U|)$, it represents the β dependency of decision attribute Q for conditional attribute P.

target2. Attributes reduction Length: $|C\_\mathrm{reduct}| = ((|P| - |\mathrm{Lr}|)/|P|)$, $|P|$ is the number of condition attributes represented by 0, 1. $|\mathrm{Lr}|$ represents the number of 1 in attribute P, the shorter the better results.

target3. Gene coding weight function: i.e., Penalty function, $\mathrm{target3} = \sum \mathrm{abs}(r \times (r-1))/|r|$. Gene values can only take 0 and 1, but the chromosome will show not 1 and not 0, such that the value is less than 0 or greater than 1. The value must be punished; therefore, the gene coding weight function is constructed. If the gene is 0, $r \times (r-1) = 0$, but the gene is 1, $r \times (r-1) = 0$. So do not punish the genes of 0 or 1, but if there is a chromosome with a length of 6: $r = [0\ 0\ -2\ -1\ 2\ 1]$, $(r-1) = [-1\ -1\ -3\ -2\ 1\ 0]$, $r \times (r-1) = [0\ 0\ 6\ 2\ 2\ 0]$, then $\sum \mathrm{abs}(r \times (r-1)) = 10$, length is 6, so $\mathrm{target3} = 10/6 = 1.67$.

Therefore, the fitness function constructed in this paper is

$$F(x) = -\omega 1 \times \mathrm{target}\,1 - \omega 2 \times \mathrm{target}\,2 + \omega 3 \times \mathrm{target}\,3, \quad (8)$$

where ω is the weight coefficient of fitness function, $\omega = (0, 1, 2, 3)$, because the genetic algorithm can only find the minimum value, and the bigger the fitness value, the better it is, so the objective function is minus and the penalty function is plus.

Flow chart about this model is given in Figure 3.

3.2. Model Concrete Steps

Input: A decision information table $S = (U, A, V, f)$

Output: $\mathrm{red}(P, Q, \beta)$

generate (M), $\mathrm{Lr} = 98$//Initial population M, 01 sequence of Chromosome length 98

Setting β, ω, crossover probability Pc, mutation probability Pm, iteration number K

Begin

for $i = 1 : K$

target1 = $(|\mathrm{pos}_P^{\beta}(Q)|/|U|)$

target2 = $((|P| - |Lr|)/|P|)$

target3 = $(\sum \mathrm{abs}(r \times (r-1))/|r|)$

Fitness function = $-\omega 1 \times \mathrm{target}1 - \omega 2 \times \mathrm{target}2 + \omega 3 \times \mathrm{target}3$; //Fitness function

$P = \mathrm{Select}\ (M, 2, \mathrm{Pc})$;//Crossover probability Pc

$Q = \mathrm{Crossover}\ (P, 2, \mathrm{Pc})$;//Crossover algorithm

$Q' = \mathrm{Mutation}\ (Q, \mathrm{Pm})$;//Mutation algorithm

End

3.3. Experimental Environment and Data

3.3.1. Hardware Environment. Intel Core i5 4670-3.4 GHz with 8.0 GB memory and 500 GB hard disk were used.

3.3.2. Software Environment. Matlab R2012b, LibSVM, and Windows 7 operating system were used.

3.3.3. Experimental Data. The PET/CT images of 2000 lung cancer patients were collected as the study samples (1000 cases of benign lung tumor, 1000 cases of malignant lung tumor). Firstly, ROI was extracted from the lung tumor and pretreated; then 8-dimensional shape features, 7-dimensional gray features, 3-dimensional Tamura features, 56-dimensional GLCM features, and the 24-dimensional frequency domain features were extracted from the lung tumor ROI, and 98-dimensional feature vectors are discreted and normalized. In the decision attribute, 1 represents the lung malignant tumor and −1 represents the lung benign tumor. Figure 4(a) shows four PET/CT images, ROI of Lung malignant tumor, and Figure 4(b) shows four PET/CT images' ROI of lung benign tumor. Table 1 gives the feature values of two patients with lung cancer (one patient was a malignant tumor and the other was a benign tumor).

3.4. Analysis of Experimental Results. In this paper, 3 kinds of experiments are designed according to the weight value $\omega = (0, 1, 2, 3)$ of the fitness function and the classification error rate $\beta = \{0.4, 0.2, 0\}$ (namely, the inclusion degree $1 - \beta = \{0.6, 0.8, 1\}$). For first type of experiments, $1 - \beta = 0.6$, according to the different values of ω to do the three groups of experiments totally. For second type of experiments, $\omega 1 = 1, \omega 2 = 1, \omega 3 = 0$, according to the different values of β to do three groups of experiments. For third type of experiments, $1 - \beta = 0.6$, by increasing the ω

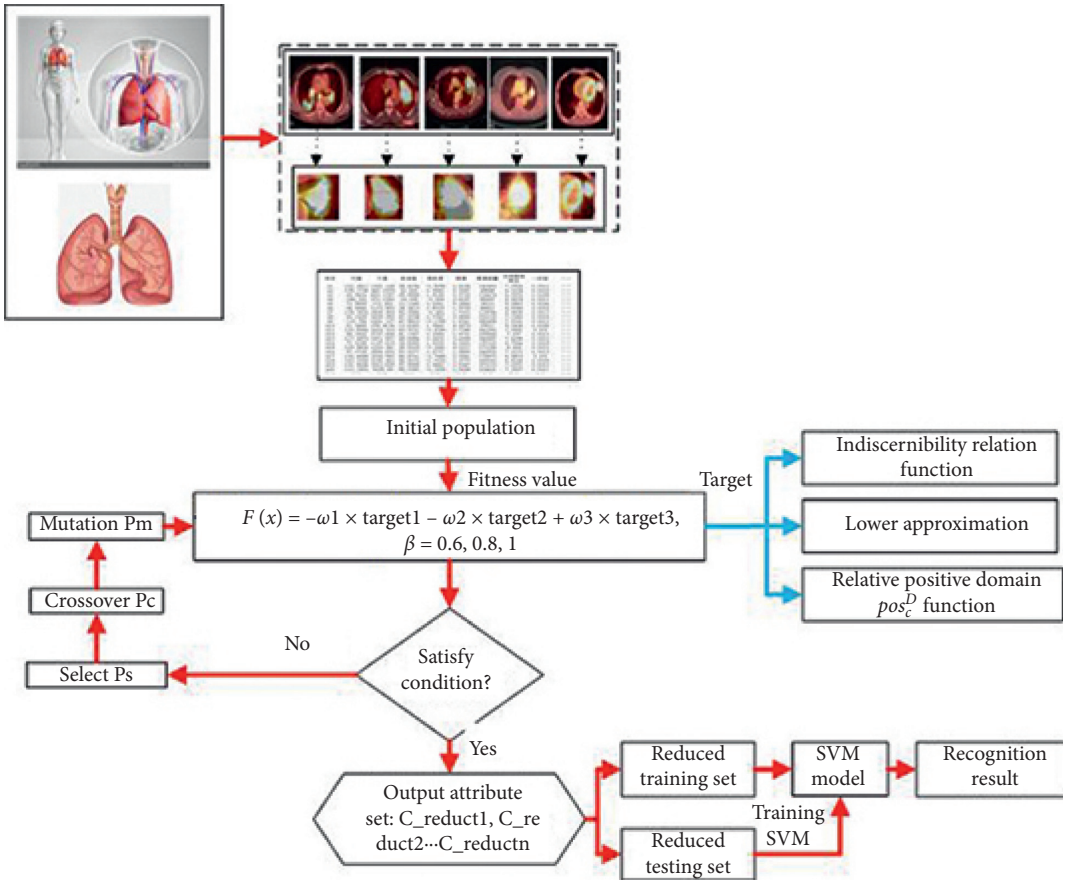
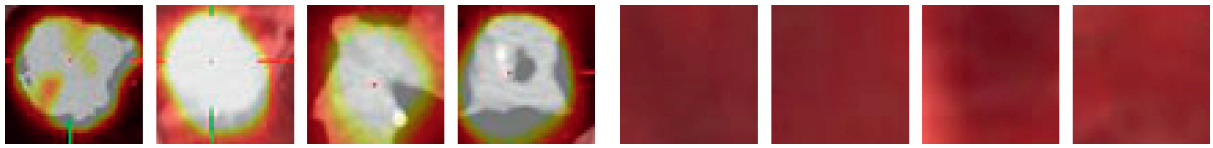


Figure 3: Flow chart of high-dimensional feature selection based on genetic algorithm and variable precision rough set.



(a) (b)

Figure 4: Part of lung tumor PET/CT image ROI. (a) Part of the lung malignant tumor PET/CT-ROI. (b) Part of the lung benign tumor PET/CT-ROI.

value to achieve the best fitness function, to achieve the best results.

3.4.1. Experiment 1—Research on Different Weight Coefficients under the Condition in the Same Classification Error Rate. ω values and β values of experiment 1 are shown in Table 2, and $1 - \beta = 0.6$.

(1) 1st Group Experiment. $\{\omega 1, \omega 2, \omega 3\} = \{1, 0, 0\}$: The algorithm is run 5 times according to this group weights; the results of the 5 groups are given in Table 3, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency degree, and the time. The convergence of VPRS-GA under the variation for fitness function value in one time is shown in Figure 5.

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples; the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by 800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 4.

The weight value in this group experiment is $\{\omega 1, \omega 2, \omega 3\} = \{1, 0, 0\}$, attribute dependency degree are

Table 1: ROI feature values of lung tumor PET/CT image.

Types of disease	Shape feature	Gray feature	Tamura texture	Texture features of GLCM				Texture feature of wavelet		
				0 degree	45 degrees	90 degrees	135 degrees	Norm	Standard deviation	Energy
	6.0000	122.2810	14.7000	0.0808	0.0779	0.0790	0.0611	649.2580	37.1752	1.0000
	0.0012	1491.1500	30.9650	2.8937	2.9067	2.8989	3.1284	26.9473	3.8486	0.0017
	0.0000	38.6154	0.2326	0.2576	0.2820	0.2653	0.4490	9.3520	1.3355	0.0002
	0.0000	−0.5056		0.1668	0.1676	0.1659	0.1649	16.8200	2.4025	0.0007
	0.0000	2.4166		0.0792	0.0759	0.0772	0.0566	27.1143	3.8693	0.0017
	0.0000	140453		0.2576	0.2820	0.2653	0.4490	20.3163	2.9020	0.0010
Lung malignant	0.0000	7.0524		16.4110	16.4469	16.3584	16.4431	13.1755	1.8818	0.0004
tumor	0.0000			2.7089	2.7072	2.7100	2.8066	18.3441	2.6199	0.0008
				0.5755	0.6007	0.5810	0.7345			
				210.9390	211.7900	209.5780	208.8250			
				0.3064	0.3351	0.3135	0.3950			
				−0.6779	−0.6708	−0.6775	−0.5696			
				0.0000	0.0000	0.0000	0.0000			
				0.7625	0.7802	0.7658	0.8001			
	4.0000	50.3912	10.1616	0.8087	0.7915	0.8077	0.7864	379.9170	2.6741	1.0000
	0.0033	6.0006	1.8835	0.4324	0.4732	0.4370	0.4840	5.7551	0.8211	0.0002
	0.0000	2.4496	2.6329	0.0433	0.0621	0.0469	0.0679	1.1745	0.1677	0.0000
	0.0000	0.5649		9.4899	7.8127	9.2429	9.2429	3.4684	0.4955	0.0001
	0.0000	2.8589		0.8082	0.7905	0.8072	0.7853	2.0823	0.2972	0.0000
	0.0000	3283		0.0433	0.0621	0.0469	0.0679	2.1821	0.3117	0.0000
Lung benign	0.0000	3.2559		7.8367	7.8363	7.8396	7.8363	0.8937	0.1276	0.0000
tumor	0.0000			0.4024	0.4301	0.4045	0.4370	2.2387	0.3197	0.0000
				0.1782	0.2326	0.1894	0.2481			
				55.5257	55.0899	55.5291	54.9831			
				0.0596	0.0873	0.0650	0.0958			
				−0.4707	−0.3295	−0.4351	−0.2911			
				0.0000	0.0000	0.0000	0.0000			
				2.0429	2.1172	2.0651	2.1394			

Table 2: Fitness function weight proportion and β value.

Experiment times	$1-\beta=0.6$		
	$\omega1$	$\omega2$	$\omega3$
First group experiment	1	0	0
Second group experiment	1	1	0
Third group experiment	1	1	1

Table 3: Results of VPRS-GA running 5 times when 1-$\beta=0.6$, $\{\omega1=1,\omega2=0,\omega3=0\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{4 5 8 9 11 12 13 17 20 22 23 24 27 30 32 33 35 38 42 48 49 52 57 59 61 62 63 64 65 68 70 72 73 75 77 78 80 87 88 91 92}	41	−0.9705	0.9705	971.9144
2	{1 2 3 4 5 8 11 12 13 14 16 17 19 23 24 25 26 27 28 30 32 36 38 39 40 42 43 44 46 47 52 53 55 61 63 66 67 69 71 72 73 77 79 80 82 84 85 87 92}	49	−0.9685	0.9685	1007.6907
3	{4 6 11 12 15 17 18 24 25 26 28 29 31 36 38 39 42 43 45 47 49 53 56 65 68 69 72 76 77 79 80 81 83 85 88 91 92}	37	−0.9695	0.9695	1043.2000
4	{4 8 9 11 12 13 14 15 17 23 29 34 35 39 40 43 47 48 50 53 55 56 60 61 64 68 70 75 80 81 82 83 84 86}	34	−0.9790	0.9790	947.3111
5	{3 4 6 8 10 11 12 13 15 17 19 20 21 24 26 29 31 39 42 44 45 48 50 53 54 56 59 64 68 77 83 84 87 89 92}	35	−0.9775	0.9775	964.5092
	Average value	39.2	−0.9730	0.9730	986.9251

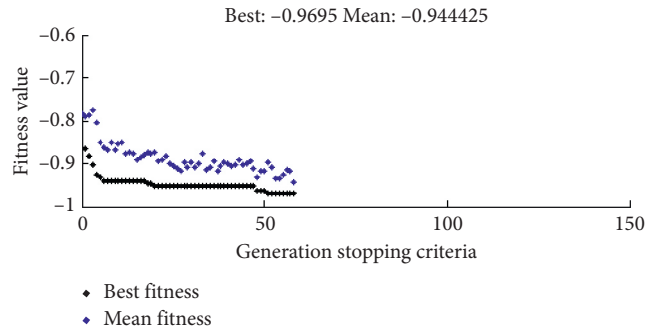


Figure 5: The variation of fitness function value in a running process for Experiment 1-first group.

Table 4: The statistical results of the first group for experiment 1 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	92.50	86.00	99.00	33.2607
	2	97.25	97.50	97.00	34.5051
	3	99.00	99.00	99.00	35.8677
	4	98.00	99.50	96.50	35.1075
	5	99.25	100.00	98.50	35.5948
	Average value	97.20	96.40	98.00	34.8672
Reduction 2	1	93.25	87.00	99.50	43.6533
	2	97.25	98.00	96.50	44.5900
	3	98.75	98.50	99.00	43.9506
	4	97.50	99.00	96.00	44.5064
	5	99.25	100.00	98.50	44.8513
	Average value	97.20	96.50	97.90	44.3103
Reduction 3	1	92.75	87.50	98.00	32.6916
	2	95.75	97.50	94.00	33.7209
	3	98.00	98.00	98.00	34.0701
	4	97.00	98.50	95.50	33.3174
	5	98.50	99.50	97.50	33.3257
	Average value	96.40	96.20	96.60	33.4251
Reduction 4	1	93.75	88.50	99.00	30.6485
	2	96.50	97.50	95.50	31.9240
	3	97.50	97.00	98.00	32.4082
	4	97.75	99.00	96.50	32.5419
	5	99.00	100.00	98.00	36.1516
	Average value	96.90	96.40	97.40	31.8806
Reduction 5	1	94.00	89.00	99.00	31.9557
	2	96.50	97.50	95.50	33.6909
	3	97.25	97.00	97.50	33.0159
	4	97.75	99.00	96.50	39.9980
	5	99.00	100.00	98.00	32.5692
	Average value	96.90	96.50	97.30	34.2459

regarded as fitness function. The average attribute dependency degree is 0.973, the average length of reduction is 39.2, and the average optimal fitness value is −0.973. The average recognition accuracy of the experiment is 96.92%. The premature phenomena are shown in Figure 5, and evolution progress is terminated early.

(2) 2nd Group Experiment. $\{\omega 1, \omega 2, \omega 3\} = \{1, 1, 0\}$: This experiment introduces an objective function to control the length of reduction (the shorter the length of reduction, the better it is), the influence degree of the objective function which controls the reduction on the fitness function and the final recognition accuracy is verified. The algorithm is run 5 times according to this group weights, and the results of the 5 groups are given in Table 5, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The convergence of VPRS-GA under the variation for fitness function value in one time is shown in Figure 6.

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples, the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by

Table 5: Results of VPRS-GA running 5 times when $1 - \beta = 0.6$, $\{\omega 1 = 1, \omega 2 = 1, \omega 3 = 0\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{5 9 14 20 26 41 43 46 48 54 55 57 64 66 74 79 86 90}	18	−4.6487	0.9965	1072.4072
2	{1 4 11 12 14 24 34 40 42 43 56 60 61 65 67 68 71 72 85}	19	−4.0109	1	632.8122
3	{2 13 27 29 39 42 45 56 59 63 68 70 75}	13	−4.6512	0.9990	1102.3967
4	{1 3 4 7 9 11 12 15 30 34 38 42 46 48 55 62 65 77 79}	19	−4.9674	1	879.4670
5	{3 9 11 13 29 39 41 42 43 46 50 55 65 c77 85 86}	16	−4.4114	0.9815	1507.5539
	Average value	17	−4.5379	0.9954	1038.9274

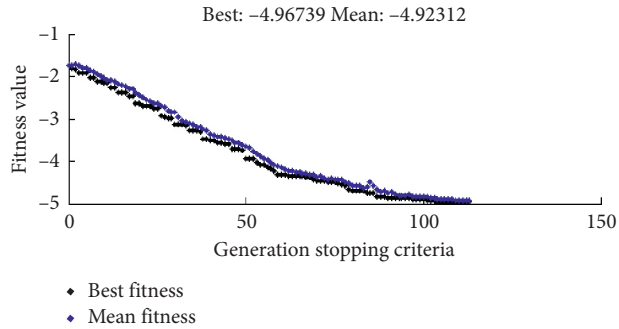


Figure 6: The variation of fitness function value in a running process for experiment 1-second group.

800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 6.

The experimental weight of this group is $\{\omega 1, \omega 2, \omega 3\} = \{1, 1, 0\}$; attribute dependency degree and the length of reduction are regarded as fitness function. As can be seen from Table 5, the reduction length is 13, 17, and so on. The average length of reduction was 17, which was significantly reduced compared with the average length of the reduction in Table 3 in the experiment of the first groups, which reduced the time, improved the efficiency of the algorithm, and increased the attribute dependency of the algorithm, even up to 1. The average recognition accuracy of the experimental group was 96.98%, which was increased by 0.06% compared with that in the first groups.

(3) 3rd Group Experiment. $\{\omega 1, \omega 2, \omega 3\} = \{1, 1, 1\}$: On the basis of attribute dependency degree and attribute reduction length, this experiment introduces gene coding weight function, in order to verify the effect of gene coding weight function on fitness function and the final recognition accuracy. The algorithm are run 5 times according to this group weights, the results of the 5 groups are given in Table 7, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The convergence of VPRS-GA under the variation for fitness function value in one time is shown in Figure 7.

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples; the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by 800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 8.

The experimental weight of this group is $\{\omega 1, \omega 2, \omega 3\} = \{1, 1, 1\}$; attribute dependency degree, the length of reduction, and gene coding weight value are regarded as fitness function. However, the premature phenomena are shown in Figure 7, and evolution progress is terminated early. From Table 7, we can see that the attribute dependency decreases gradually and even the attribute dependency of Reduction 1 is reduced to 0.759. The average recognition accuracy of the experimental group was 96.85%. The accuracy of recognition was decreased compared with the second groups, and hence, using gene encoding weight function in the fitness function to improve recognition accuracy is useless, only for the samples with different results, to analyze specific issues. The 3 experiment runs of experiment 1 verified the necessity of the fitness function, by continuously introducing fitness objective function, such as target1, target2, and target3, the conclusion is that the fitness function is better when it is not bigger, but after the introduction of target3, the accuracy declines; therefore, the introduction of target1 and target2 in this algorithm can get better results.

Table 6: The statistical results of the second group for experiment 1 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	93.00	86.00	100.00	11.6488
	2	96.25	96.00	96.50	12.5511
	3	98.50	99.00	98.00	13.1509
	4	97.25	98.50	96.00	13.4468
	5	99.25	100.00	98.50	14.4839
	Average value	96.85	95.90	97.80	13.0563
Reduction 2	1	94.25	89.00	99.50	12.1096
	2	97.25	97.00	97.50	12.8636
	3	98.00	98.00	98.00	13.5677
	4	97.50	98.00	97.00	13.8196
	5	98.75	99.00	98.50	13.6691
	Average value	97.15	96.20	98.10	13.2059
Reduction 3	1	93.00	87.50	98.50	8.7757
	2	97.25	97.50	97.00	10.3424
	3	97.75	98.00	97.50	10.7411
	4	97.75	98.50	97.00	11.2344
	5	99.00	100.00	98.00	11.3006
	Average value	96.95	96.30	97.60	10.4788
Reduction 4	1	93.75	87.50	100.00	14.6417
	2	96.50	97.50	95.50	15.4736
	3	97.50	97.00	98.00	15.7621
	4	98.00	99.00	97.00	16.1355
	5	99.25	100.00	98.50	16.3381
	Average value	97.00	96.20	97.80	15.6702
Reduction 5	1	92.50	86.50	98.50	12.4933
	2	96.75	98.00	95.50	14.0057
	3	98.00	98.00	98.00	14.5194
	4	98.00	99.00	97.00	14.5792
	5	99.50	99.50	99.50	15.0400
	Average value	96.95	96.20	97.70	14.1275

Table 7: Results of VPRS-GA running 5 times when $1 - \beta = 0.6$, $\{\omega 1 = 1, \omega 2 = 1, \omega 3 = 1\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{4 5 7 26 27 34 35 41 47 54 55 71 74 75 78 80 83 90}	18	−1.4192	0.7590	688.8635
2	{4 15 16 19 22 27 28 29 30 35 38 42 45 50 52 53 59 61 62 64 65 70 71 72 77 87 88}	27	−1.5232	0.8640	812.4857
3	{6 17 19 24 28 31 33 34 38 39 43 45 47 48 49 51 55 56 66 67 69 70 71 72 76 77 78 80 81 84 87 89 91 92}	34	−1.3545	0.7950	952.1511
4	{3 6 8 9 16 17 19 20 24 25 28 35 37 39 41 42 46 49 51 52 54 59 63 65 66 74 83 86}	28	−1.4703	0.8365	871.4839
5	{1 7 8 15 17 19 20 23 29 37 45 48 54 60 62 70 73 75 77 78 79 86}	22	−1.4990	0.7995	779.7617
	Average value	25.8	−1.4532	0.8108	820.9492

3.4.2. Experiment 2—Research on Different Classification Error Rates under the Condition in the Same Weight Coefficient. According to experiment 1, we can see that when $\omega 1 = 1$, $\omega 2 = 1$, $\omega 3 = 0$, the experimental results are the best, so in experiment 2, the case of the weight value of was unchanged, $\omega 1 = 1$, $\omega 2 = 1$, $\omega 3 = 0$, and the β value was changed, and they are shown in Table 9.

(1) 1st Group Experiment. $1 - \beta = 0.6$: The algorithm is run 5 times according to this group weights; the results of the 5 groups are shown in Table 5, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The convergence of VPRS-GA under the variation for fitness function value for one time is shown in Figure 6 (i.e., not repeated in the second group of experiment 1).

(2) 2nd Group Experiment. $1 - \beta = 0.8$: The algorithm are is 5 times according to this group weights, the results of the 5 groups are given in Table 10, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The

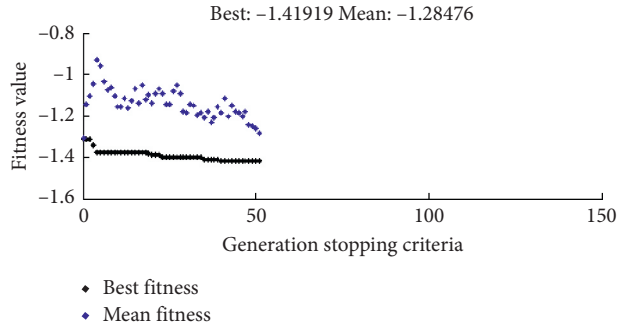


Figure 7: The variation of fitness function value in a running process for experiment 1-third group.

Table 8: The statistical results of the third group for experiment 1 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	92.75	86.00	99.50	9.2492
	2	97.25	97.50	97.00	10.7461
	3	98.50	98.50	98.50	11.3811
	4	97.75	99.00	96.50	11.5560
	5	98.75	100.00	97.50	11.7022
	Average value	97.00	96.20	97.80	10.9269
Reduction 2	1	93.50	87.50	99.50	14.8245
	2	97.00	96.50	97.50	16.1535
	3	97.75	98.50	97.00	16.6452
	4	98.00	98.50	97.50	17.5450
	5	98.75	99.50	98.00	17.2348
	Average value	97.00	96.10	97.90	16.4806
Reduction 3	1	91.25	83.00	99.50	20.1904
	2	96.50	97.00	96.00	21.8535
	3	98.00	98.00	98.00	21.9605
	4	96.25	99.00	93.50	22.3091
	5	98.25	100.00	96.50	23.6896
	Average value	96.05	95.40	96.70	22.0006
Reduction 4	1	93.00	87.00	99.00	16.5454
	2	96.75	96.00	97.50	17.2432
	3	98.75	98.50	99.00	17.9301
	4	98.00	99.00	97.00	18.9560
	5	99.00	99.50	98.50	18.5249
	Average value	97.10	96.00	98.20	17.8399
Reduction 5	1	92.75	86.00	99.50	14.1173
	2	97.25	98.00	96.50	16.1295
	3	99.00	99.50	98.50	15.8992
	4	97.75	99.50	96.00	16.4876
	5	98.75	100.00	97.50	16.6070
	Average value	97.10	96.60	97.60	15.8481

Table 9: Fitness function weight proportion and β value.

Experiment times	$\omega 1 = 1, \omega 2 = 1, \omega 3 = 0$		
	$1 - \beta = 0.6$	$1 - \beta = 0.8$	$1 - \beta = 1$
First group experiment	○		
Second group experiment		○	
Third group experiment			○

convergence of VPRS-GA under the variation for fitness function value for one time is shown in Figure 8.

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples; the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by 800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by

Table 10: Results of VPRS-GA running 5 times when $1-\beta=0.8$, $\{\omega1=1,\omega2=1,\omega3=0\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{8 9 11 12 15 16 17 18 25 26 29 31 35 39 40 41 42 48 58 65 67 68 70 83 84 91}	26	−6.7816	0.9490	1000.2827
2	{1 6 8 9 11 12 15 17 21 23 26 28 30 31 34 44 50 56 58 59 62 63 64 68 71 75 77 82 89 92}	30	−6.7797	0.9615	947.7387
3	{6 8 12 14 15 16 17 21 28 35 38 39 45 49 55 58 61 62 64 65 77 82 85}	23	−6.8694	0.9070	1286.6181
4	{4 6 7 8 11 12 13 16 17 20 25 26 31 32 34 35 41 42 44 49 50 55 58 68 72 74 76 78 79 85 89 92}	32	−6.7225	0.9540	1051.0220
5	{3 6 8 9 10 16 17 26 27 34 36 37 38 40 42 44 46 51 52 62 66 67 84 86 87}	25	−6.5892	0.8405	846.9324
	Average value	27.2	−6.7484	0.9224	1026.5188

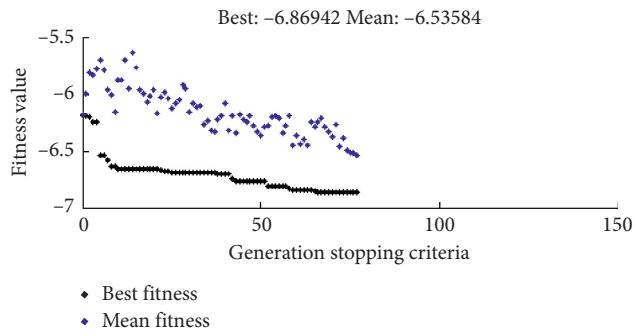


Figure 8: The variation of fitness function value in a running process for experiment 2-second group.

changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 11.

In the case of constant weight ϖ and classification error rate of $\beta=0.2$ (which contains $1-\beta=0.8$), the classification error rate is changed on the basis of the attribute dependency and the length of control reduction. The premature phenomena are shown in Figure 8, and evolution progress is terminated early, such that the attribute dependency of reduction 5 was 0.8405, appeared in attribute dependency on less than 0.9, compared with first groups of experiment 2 attribute dependency declined. The average recognition accuracy of the experimental group was 96.74%. Compared with the classification error rate of 0.4 and inclusion degree of 0.6, the accuracy was decreased by 0.24%.

(3) 3rd Group Experiment. $1-\beta=1$: The algorithm is run 5 times according to the group weights, and the results of the 5 groups are shown in Table 12, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The convergence of VPRS-GA under the variation for fitness function value for one time is shown in Figure 9.

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples, the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by 800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 13.

In the case of constant weight ϖ and classification error rate of $\beta=0$ (which contains $1-\beta=1$), the classification error rate is reduced and the inclusion degree is improved on the basis of the attribute dependency and the length of control reduction. The premature phenomena are shown in Figure 9, and evolution progress is terminated early. The average recognition accuracy of the experimental group was 95.73%, which was decreased by 0.06% compared with that in the second group. In experiment 2, the effect of changing the classification error rate on the recognition accuracy was verified by the 3 groups of experiments. By continually reducing the classification error rate, the final recognition accuracy has been declining, when inclusion degree is 1, $\beta=0$; variable precision rough set becomes Pawlak rough set, the recognition accuracy of the recognition accuracy of is minimum, which was verified the advantages of variable precision rough set.

3.4.3. Experiment 3—Research on Increasing the Weight Coefficient under the Condition in the Same Classification Error Rate. According to experiment 1 and experiment 2, we can know that when $\beta=0.6$, $\omega1=1$, $\omega2=1$, $\omega3=0$, the recognition accuracy is the best; therefore, in the third experiment, by increasing the weight of ω, 3 groups of experiments are performed, fitness goals: target 1 (attribute

Table 11: The statistical results of the second group for experiment 2 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	93.00	86.50	99.50	22.8007
	2	95.75	97.00	94.50	23.7646
	3	97.00	96.00	98.00	23.3250
	4	97.50	98.50	96.50	24.4491
	5	99.25	100.00	98.50	24.4816
	Average value	96.50	95.60	97.40	23.7642
Reduction 2	1	93.75	88.00	99.50	25.2403
	2	96.25	97.50	95.00	26.5289
	3	98.00	97.00	99.00	26.5523
	4	98.00	99.00	97.00	26.8212
	5	99.50	100.00	99.00	27.5880
	Average value	97.10	96.30	97.90	26.5461
Reduction 3	1	92.75	87.50	98.00	18.0780
	2	96.75	97.50	96.00	19.2992
	3	97.00	96.00	98.00	18.7243
	4	97.75	99.50	96.00	20.8482
	5	98.75	100.00	97.50	20.3507
	Average value	96.60	96.10	97.10	19.4601
Reduction 4	1	92.00	86.50	97.50	25.7260
	2	97.00	97.50	96.50	27.3024
	3	97.75	96.50	99.00	27.2316
	4	97.50	99.00	96.00	28.1554
	5	99.00	100.00	98.00	29.1471
	Average value	96.65	95.90	97.40	27.5125
Reduction 5	1	92.75	87.50	98.00	14.3715
	2	96.75	96.00	97.50	15.2637
	3	97.50	98.00	97.00	15.8929
	4	97.75	99.00	96.50	16.2997
	5	99.50	100.00	99.00	16.6792
	Average value	96.85	96.10	97.60	15.7014

Table 12: Results of VPRS-GA running 5 times when $1 - \beta = 1$, $\{\omega 1 = 1, \omega 2 = 1, \omega 3 = 0\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{15 44 68 73 79 84}	6	−2.7313	0.7965	1144.9901
2	{34 51 54 75 80 90}	6	−2.7047	0.8460	969.9391
3	{2 34 49 70 71 72 76 81}	8	−3.4057	0.7535	1123.3489
4	{12 25 78 85}	4	−2.2872	0.9285	1166.8133
5	{6 7 12 13 42 44 55 57 65 66 69 77 81 86 87}	15	−3.3230	0.8665	1323.6077
Average value		7.8	−2.8903	0.8382	1145.7398

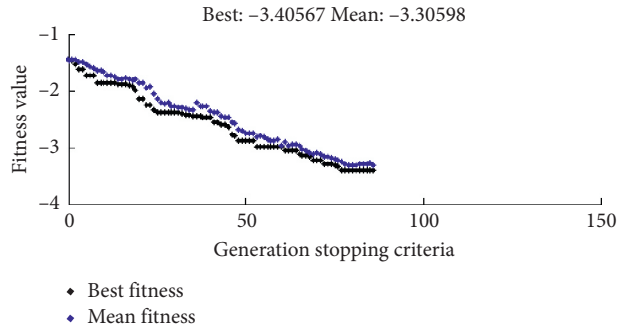


Figure 9: The variation of fitness function value in a running process for experiment 2-third group.

Table 13: The statistical results of the third group for experiment 2 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	92.25	84.50	100.00	8.1271
	2	95.50	97.00	94.00	9.4583
	3	95.75	94.00	97.50	8.8198
	4	96.00	98.00	94.00	9.3754
	5	97.25	99.00	95.50	9.8691
	Average value	95.35	94.50	96.20	9.1299
Reduction 2	1	92.00	84.50	99.50	6.4894
	2	96.25	95.50	97.00	8.0198
	3	95.25	93.00	97.50	7.7337
	4	96.00	97.50	94.50	7.6012
	5	98.00	100.00	96.00	8.2763
	Average value	95.50	94.10	96.90	7.6241
Reduction 3	1	92.00	84.50	99.50	6.4894
	2	96.25	95.50	97.00	8.0198
	3	95.25	93.00	97.50	7.7337
	4	96.00	97.50	94.50	7.6012
	5	98.00	100.00	96.00	8.2763
	Average value	95.50	94.10	96.90	7.6241
Reduction 4	1	92.75	85.50	100.00	6.7264
	2	96.75	96.00	97.50	7.8467
	3	96.00	94.50	97.50	7.3022
	4	95.75	97.50	94.00	7.9460
	5	98.00	100.00	96.00	8.4184
	Average value	95.85	94.70	97.00	7.6479
Reduction 5	1	92.00	84.50	99.50	11.4719
	2	96.25	97.50	95.00	12.8705
	3	98.50	99.00	98.00	13.2049
	4	97.75	99.50	96.00	13.3513
	5	98.50	100.00	97.00	13.3144
	Average value	96.60	96.10	97.10	12.8426

dependency), target 2 (the minimum number of attributes reduction), and target 3 (gene encoding weight function), the three objective functions play an important role in the evaluation of fitness function. However, the importance of fitness function is reduced in these three objectives. Therefore, in this experiment, when the other conditions are unchanged, the weight coefficient of the target 1 is increased, to verify the influence of the change in the weight coefficient on the experimental results, and they are shown in Table 14.

(1) 1st Group Experiment. $\omega 1 = 1$, $\omega 2 = 1$, $\omega 3 = 0$: The algorithm are run 5 times according to this group weights, the results of the 5 groups are given in Table 5, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency and the time. The convergence of VPRS-GA under the variation for fitness function value in one time is shown in Figure 6 (i.e., not repeated for the second group of experiment 1).

(2) 2nd Group Experiment. $\omega 1 = 2$, $\omega 2 = 1$, $\omega 3 = 0$: The algorithm is run 5 times according to this group weights, the results of the 5 groups are given in Table 15, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The convergence of VPRS-GA under the variation for fitness function value in one time is shown in Figure 10.

Table 14: Fitness function weight proportion and β value.

Experiment times	$1 - \beta = 0.6$		
	$\omega 1$	$\omega 2$	$\omega 3$
First group experiment	1	1	0
Second group experiment	2	1	0
Third group experiment	3	1	0

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples, the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by 800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 16.

The experimental group in the case of $1 - \beta = 0.6$ unchanged, the weight of $\omega 1$ was increased. The attribute dependency and the optimal fitness function are relatively high; the average precision of reduction 1, reduction 2, and reduction 3 in Table 16 is more than 97% and that of reduction 2 is even up to 97.25%. The average recognition accuracy of the experimental group is 97.03%, which is higher than that of the first group.

Table 15: Results of VPRS-GA running 5 times when $1 - \beta = 0.6$, $\{\omega 1 = 2, \omega 2 = 1, \omega 3 = 0\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{2 3 4 5 11 13 16 18 24 30 34 37 39 41 42 51 55 64 70 77 78 82}	22	−3.4859	0.9060	2151.5464
2	{8 9 11 12 14 15 23 25 26 29 30 33 37 42 43 45 46 50 60 61 69 74 80 87 89}	25	−3.0845	0.9390	4276.1634
3	{8 11 12 13 16 18 19 24 29 36 37 43 64 65 68 71 86 91 92}	19	−3.5039	0.9150	2619.7164
4	{2 3 4 8 10 11 12 13 15 16 19 23 25 30 48 55 64 65 68 74 77 80 81 83 84 86 89}	27	−2.9150	0.9575	4427.1631
5	{5 8 9 11 12 15 17 23 25 29 31 36 39 41 48 54 59 63 80 83 86 89}	22	−2.9920	0.9525	4316.1464
Average value		23	−3.1962	0.9340	3558.1471

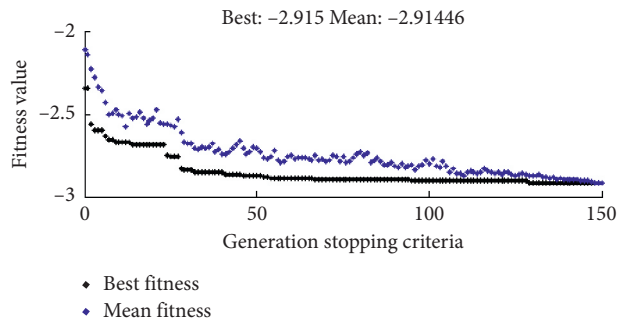


Figure 10: The variation of fitness function value in a running process for experiment 3-second group.

Table 16: The statistical results of the second group for experiment 3 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	92.75	86.00	99.50	18.8497
	2	97.25	98.00	96.50	15.7162
	3	98.50	99.00	98.00	15.8691
	4	98.00	99.00	97.00	16.4603
	5	99.50	100.00	99.00	16.1914
	Average value	97.20	96.40	98.00	16.6173
Reduction 2	1	94.50	89.50	99.50	19.0813
	2	96.75	98.00	95.50	20.0251
	3	97.75	98.00	97.50	19.7008
	4	98.50	99.00	98.00	20.0924
	5	98.75	99.00	98.50	20.9245
	Average value	97.25	96.70	97.80	19.9648
Reduction 3	1	94.00	88.00	100.00	13.1369
	2	97.25	98.00	96.50	14.4797
	3	98.00	98.00	98.00	14.2662
	4	97.25	98.50	96.00	14.7190
	5	99.25	100.00	98.50	14.8799
	Average value	97.15	96.50	97.80	14.2963
Reduction 4	1	93.50	87.50	99.50	24.0456
	2	97.00	97.50	96.50	25.2082
	3	98.00	98.00	98.00	25.1175
	4	97.75	99.50	96.00	27.0188
	5	98.25	100.00	96.50	26.7471
	Average value	96.90	96.50	97.30	25.6274
Reduction 5	1	93.25	88.00	98.50	18.0959
	2	96.00	98.00	94.00	19.6563
	3	97.50	97.50	97.50	19.6723
	4	98.00	99.00	97.00	20.7829
	5	98.50	99.50	97.50	21.9703
	Average value	96.65	96.40	96.90	20.0355

Table 17: Results of VPRS-GA running 5 times when $1-\beta=1$, $\{\omega 1=1, \omega 2=1, \omega 3=0\}$.

Experiment times	C_ reduction	Reduction length	Optimal fitness value	Attribute dependency degree	Time (s)
1	{3 4 5 8 9 11 12 17 19 29 34 35 38 46 52 53 55 59 63 66 72 75 77 78 79 87 92}	27	−3.8867	0.9550	2898.1789
2	{4 8 9 11 12 15 17 29 33 37 38 39 42 43 48 55 67 73 78 81 83 84 88 89 90}	25	−3.8167	0.9715	5578.3772
3	{2 3 4 8 9 10 11 12 13 15 16 19 24 25 30 36 49 54 55 60 64 67 68 70 74 77 83 85 86 91}	30	−3.8807	0.9530	3483.1096
4	{4 5 7 11 12 14 15 17 25 29 33 36 39 41 42 47 48 50 55 56 58 62 67 69 72 74 77 84 86 90 91}	31	−3.9430	0.9665	3574.2822
5	{3 4 5 8 9 11 12 17 19 29 34 35 38 46 52 53 55 59 63 66 72 75 77 78 79 87 92}	27	−3.8867	0.9550	2791.9582
Average value		28	−3.8827	0.9602	3665.1812

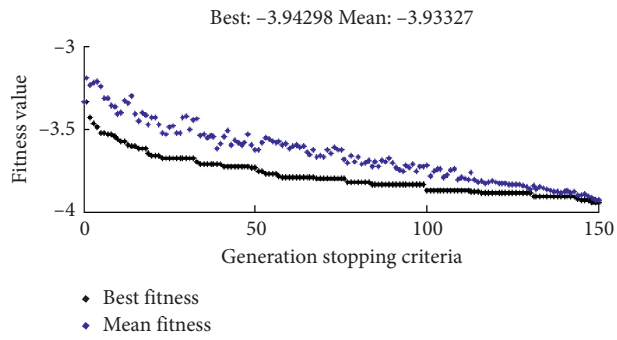


Figure 11: The variation of fitness function value in a running process for experiment 3-third group.

Table 18: The statistical results of the Second group for experiment 3 with the SVM classifier.

Experiment times		Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
Reduction 1	1	92.00	87.00	97.00	21.8717
	2	97.50	97.50	97.50	21.0550
	3	98.50	98.50	98.50	20.3206
	4	98.00	99.00	97.00	22.1164
	5	99.25	100.00	98.50	27.2536
	Average value	97.05	96.40	97.70	22.5235
Reduction 2	1	94.00	88.50	99.50	23.3123
	2	95.75	97.50	94.00	24.3349
	3	97.50	97.00	98.00	24.4202
	4	97.75	99.00	96.50	25.6607
	5	99.00	99.50	98.50	25.9071
	Average value	96.80	96.30	97.30	24.7270
Reduction 3	1	92.75	86.50	99.00	25.2584
	2	96.25	97.50	95.00	26.2412
	3	97.75	98.00	97.50	26.0127
	4	97.75	99.00	96.50	26.8670
	5	98.75	100.00	97.50	26.5387
	Average value	96.65	96.20	97.10	26.1836
Reduction 4	1	91.50	85.50	97.50	25.3231
	2	96.25	97.50	95.00	26.4943
	3	97.50	97.00	98.00	27.5283
	4	98.00	99.50	96.50	32.2954
	5	98.25	99.50	97.00	27.7432
	Average value	96.30	95.80	96.80	27.8769
Reduction 5	1	92.00	88.00	96.00	19.5196
	2	97.00	97.00	97.00	21.4889
	3	98.25	98.00	98.50	20.3612
	4	98.50	100.00	97.00	21.3361
	5	99.00	99.00	99.00	22.5526
	Average value	96.95	96.40	97.50	21.0517

(3) 3rd Group Experiment. $\omega 1 = 3$, $\omega 2 = 1$, $\omega 3 = 0$: The algorithm is run 5 times according to the group weights, and the results of the 5 groups are given in Table 17, including the reduction of the conditional attributes, the length of reduction, the optimal fitness value, the attribute dependency, and the time. The convergence of VPRS-GA under the variation for fitness function value for one time is shown in Figure 11.

Each reduction is classified by SVM classifier, using the method of 5-fold cross validation, through changing the training samples and test samples; the results of the five groups were obtained, including accuracy, sensitivity, specificity, and time (training samples are constructed by 800 malignant samples and 800 benign samples; testing samples are constructed by 200 malignant samples and 200 benign samples; the experiment is repeated 5 times by changing training samples and testing samples). Finally, the average values of these five groups are obtained as the final result of the reduction and shown in Table 18.

The experiment in the case of $1 - \beta = 0.6$ unchanged, increase the weight of the $\omega 1$. $\omega 1 = 3$, $\omega 2 = 1$, $\omega 3 = 0$. In Table 18, the recognition accuracy of reduction 1 is over 97% only. The average recognition accuracy of the experimental group is 96.75%, and the accuracy is decreased by 0.28% compared with that in the other second groups. The three groups of experiment 3, the purpose is to verify whether the experimental accuracy is influenced by increasing the weight. The experimental results show that the accuracy of second group for experimental weight {2, 1, 0} compared with first group experiment when {1, 1, 0} is high, but the third groups of experimental weight was {3, 1, 0}, and the accuracy declined; therefore, the weight of {2, 1, 0} is the best choice for this experiment.

4. Conclusions

Aiming at the deficiency of the traditional rough set model, this paper proposes a new feature selection model based on genetic algorithm and variable precision rough set; by introducing the β value, the rigid inclusion of the approximation for the traditional rough set is relaxed, and then we design the 3 kinds of experiments by constructing the decision information table of the PET/CT feature for lung tumor ROI. The first type of experiment is the inclusion of $1 - \beta = 0.6$, and different values of ω made a total of three groups of experiments; the experimental results show that the better recognition accuracy can be obtained when the weight is {1, 1, 0}, and the results show that the gene coding weight function has no effect on the fitness function. For the second type of experiments, $\omega 1 = 1, \omega 2 = 1, \omega 3 = 0$, according to the different values of β to do three groups of experiments, the results show that the recognition accuracy of $1 - \beta = 0.6$ is the best, which shows that the larger the β value is, the lower approximate cardinality will be larger, then the relative accuracy will increase. For the third type of experiments, $1 - \beta = 0.6$, ω value is increased to achieve the best fitness function, in order to achieve the best results. The experimental results show that the recognition accuracy is better than the others when the weight value is {2, 1, 0}, so it is better to solve the problem by increasing the proportion of attribute dependency. Through the above experiments, it is shown that the high-dimensional feature selection algorithm based on genetic algorithm and variable precision rough set can solve the multiobjective optimization problem well. However, when the fitness function and its parameters are applied in the specific application, it is necessary to analyze the specific problems.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare no conflicts of interest.

Acknowledgments

This work was supported by National Natural Science Foundation of China (Grant nos. 61561040 and 61876121), First-Class Disciplines Foundation of Ningxia (No. NXYLXK2017B09).

References

[1] S. Luo, D. Miao, Z. Zhang, Y. Zhang, and S. Hu, "A neighborhood rough set model with nominal metric embedding," *Information Sciences*, vol. 520, pp. 373–388, 2020.

[2] B. Barman and S. Patra, "Variable precision rough set based unsupervised band selection technique for hyperspectral image classification," *Knowledge-Based Systems*, vol. 1936, Article ID 105414, 2020.

[3] Y. Chenyi and L. Jinjin, "Approximate attribute reduction under variable precision rough set β," *Journal of Shandong University*, vol. 11, pp. 17–21, 2011.

[4] S. Xiaowei, *Research on Hierarchical Model of Attribute Reduction in Variable Precision Rough Set*, Central South University, Changsha, China, 2013.

[5] Z. Jie and W. Jiayang, "Analysis of reduction feature of variable precision rough set model," *Computer Application Research*, vol. 7, pp. 12–15, 2007.

[6] Z. Pei and Z. Qinghua, "FCM clustering algorithm based on variable precision rough set," *Journal of Shanxi University*, vol. 3, pp. 342–348, 2016.

[7] C. Hao and Y. Junan, "Attribute kernel and minimum attribute reduction algorithm of variable precision rough set," *Acta Sinica Sinica*, vol. 5, pp. 1011–1017, 2012.

[8] S. Xu, X. Yang, H. Yu, D.-J. Yu, J. Yang, and E. C.C. Tsang, "Multi-label learning with label-specific feature reduction," *Knowledge-Based Systems*, vol. 104, pp. 52–61, 2016.

[9] I. Maryam and G. Hassan, "Feature space discriminant analysis for hyperspectral data feature reduction," *ISPRS Journal of Photogrammetry and Remote Sensing*, vol. 102, pp. 1–13, 2015.

[10] S. Q. Wang, C. Y. Gao, C. Luo, G. M. Zheng, and Y. N. Zhou, "Research on feature selection/attribute reduction method based on rough set theory," *Procedia Computer Science*, vol. 154, pp. 194–198e, 2019.

[11] A. W. Omar, M. Azzam, O. Hadi, and B. Jamal, "CEAP: SVM-based intelligent detection model for clustered vehicular ad

hoc networks," *Expert Systems with Applications*, vol. 50, pp. 40–54, 2016.
[12] H. Lee and Y.-P. P. Chen, "Image based computer aided diagnosis system for cancer detection," *Expert Systems with Applications*, vol. 42, no. 12, pp. 5356–5365, 2015.
[13] J. A. Guy and P. L. Harold, "After detection: the improved accuracy of lung cancer assessment using radiologic computer-aided diagnosis," *Academic Radiology*, vol. 23, no. 2, pp. 186–191, 2016.
[14] E. Kiyonori, T. Shodayu, J. Binghu et al., "Pleural invasion by peripheral lung cancer: prediction with three-dimensional CT," *Academic Radiology*, vol. 3, pp. 310–319, 2015.
[15] B. Koohestani, "A crossover operator for improving the efficiency of permutation-based genetic algorithms," *Expert Systems with Applications*, vol. 1511, Article ID 113381, 2020.
[16] N. K. Lee, X. Li, and D. Wang, "A comprehensive survey on genetic algorithms for DNA motif prediction," *Information Sciences*, vol. 466, pp. 25–43, 2018.
[17] S. Shibao and Y. Leilei, "Research on variable precision rough set model and its application," *Computer Engineering and Application*, vol. 07, pp. 10–13, 2009.
[18] T. Xiaolong, *Several Problems of Multi Granularity Variable Precision Rough Set*, Guangxi University For Nationalities, Nanning, China, 2015.
[19] W. Xueming, *Research on Several Rough Set Models and Neural Network*, University of Electronic Science and Technology of China, Chengdu, China, 2013.
[20] T. Sun, J. Wang, X. Li et al., "Comparative evaluation of support vector machines for computer aided diagnosis of lung cancer in CT based on a multi-dimensional data set," *Computer Methods and Programs in Biomedicine*, vol. 111, no. 2, pp. 519–524, 2013.
[21] Z. Yang, T. Ouyang, X. Fu, and X. Peng, "A decision-making algorithm for online shopping using deep-learning-based opinion pairs mining and q -rung orthopair fuzzy interaction Heronian mean operators," *International Journal of Intelligent Systems*, vol. 35, no. 5, pp. 783–825, 2020.
[22] W. Chen, C. Lin, C. Li et al., "Tracing the evolution of 3D printing technology in China using LDA-based patent abstract mining," *IEEE Transactions on Engineering Managemen*, vol. 36, pp. 1–11, 2020.