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A GA-based feature selection and parameters optimization for support vector machines

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Abstract

Support Vector Machines, one of the new techniques for pattern classification, have been widely used in many application areas. The kernel parameters setting for SVM in a training process impacts on the classification accuracy. Feature selection is another factor that impacts classification accuracy. The objective of this research is to simultaneously optimize the parameters and feature subset without degrading the SVM

classification accuracy. We present a genetic algorithm approach for feature selection and parameters optimization to solve this kind of problem. We tried several real-world datasets using the proposed GA-based approach and the Grid algorithm, a traditional method of performing parameters searching. Compared with the Grid algorithm, our proposed GA-based approach significantly improves the classification accuracy and

has fewer input features for support vector machines.

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*Keywords:* Support vector machines; Classification; Feature selection; Genetic algorithm; Data mining

1. Introduction

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Support vector machines (SVM) were first suggested by [Vapnik (1995)](#_bookmark6) and have recently been used in a range of problems including pattern recognition ([Pontil and Verri,](#_bookmark6) [1998](#_bookmark6)), bioinformatics ([Yu, Ostrouchov, Geist, & Samatova,](#_bookmark6) [1999](#_bookmark6)), and text categorization ([Joachims, 1998](#_bookmark6)). SVM classifies data with different class labels by determining a set of support vectors that are members of the set of training inputs that outline a hyperplane in the feature space. SVM provides a generic mechanism that fits the hyperplane surface to the training data using a kernel function. The user may select a kernel function (e.g. linear, polynomial, or sigmoid) for the SVM during the training process that selects support vectors along the surface of this function.

When using SVM, two problems are confronted: how to choose the optimal input feature subset for SVM, and how to set the best kernel parameters. These two problems are crucial, because the feature subset choice influences the appropriate kernel parameters and vice versa ([Fro¨hlich and Chapelle, 2003](#_bookmark5)).

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Therefore, obtaining the optimal feature subset and SVM

parameters must occur simultaneously.

Many practical pattern classification tasks require learning an appropriate classification function that assigns a given input pattern, typically represented by a vector of attribute values to a finite set of classes. Feature selection is used to identify a powerfully predictive subset of fields within a database and reduce the number of fields presented to the mining process. By extracting as much information as possible from a given data set while using the smallest number of features, we can save

significant computation time and build models that generalize

better for unseen data points. According to [Yang and Honavar](#_bookmark6) [(1998)](#_bookmark6), the choice of features used to represent patterns that are presented to a classifier affects several pattern classification aspects, including the accuracy of the learned classification

algorithm, the time needed for learning a classification function, the number of examples needed for learning, and the cost associated with the features.

In addition to the feature selection, proper parameters setting can improve the SVM classification accuracy. The parameters that should be optimized include penalty

parameter *C* and the kernel function parameters such as

the gamma (g) for the radial basis function (RBF) kernel. To design a SVM, one must choose a kernel function, set the kernel parameters and determine a soft margin constant

*C* (penalty parameter). The Grid algorithm is an alternative to finding the best *C* and gamma when using the RBF kernel function. However, this method is time consuming and does not perform well ([Hsu and Lin, 2002](#_bookmark6); [LaValle and](#_bookmark6) [Branicky, 2002](#_bookmark6)). Moreover, the Grid algorithm cannot

perform the feature selection task.

Genetic algorithms have the potential to generate both the optimal feature subset and SVM parameters at the same time. Our research objective is to optimize the parameters and

feature subset simultaneously, without degrading the SVM classification accuracy. The proposed method performs feature selection and parameters setting in an evolutionary way. Based

on whether or not feature selection is performed independently

of the learning algorithm that constructs the classifier, feature

Eqs. (1) and (2) can be combined into one set of inequalities.

*yi*ðh*w*$*xi*i C *b*ÞK1R 0 c *i* Z 1; .; *m* (3)

The SVM finds an optimal separating hyperplane with the maximum margin by solving the following optimization problem:

Min 1*w*T*w* subject to : *yi*ðh*w*$*xi*i C *b*ÞK1R 0 (4)

*w*;*b* 2

It is known that to solve this quadratic optimization problem one

must find the saddle point of the Lagrange function:

1 T X*m*

*Lp*ð*w*; *b*; aÞ Z 2 *w* $*w*K

ða*iyi*ðh*w*$*xi*i C *b*ÞK1Þ (5)

*i*Z1

subset selection algorithms can be classified into two

categories: the filter approach and the wrapper approach ([John, Kohavi, & Peger, 1994](#_bookmark6); [Kohavi and John, 1997](#_bookmark6)). The wrapper approach to feature subset selection is used in this paper because of the accuracy.

In the literature, only a few algorithms have been proposed

for SVM feature selection ([Bradley, Mangasarian, & Street,](#_bookmark5)

where the ai denotes Lagrange multipliers, hence a*i*R0. The search for an optimal saddle point is necessary because the *Lp* must be minimized with respect to the primal variables *w* and *b*

and maximized with respect to the non-negative dual variable a*i*. By differentiating with respect to *w* and *b*, the following equations are obtained:

*m*

[1998](#_bookmark5); [Bradley and Mangasarian, 1998](#_bookmark5); [Weston et al., 2001](#_bookmark6);

v *L* Z 0; *w* Z X a *y x*

(6)

[Guyon, Weston, Barnhill, & Bapnik, 2002](#_bookmark5); [Mao, 2004](#_bookmark6)). Some other GA-based feature selection methods were proposed ([Raymer, Punch, Goodman, Kuhn, & Jain, 2000](#_bookmark6); [Yang and](#_bookmark6) [Honavar, 1998](#_bookmark6); [Salcedo-Sanz, Prado-Cumplido, Pe´rez-Cruz,](#_bookmark6) [& Bouson˜o-Calzo´n, 2002](#_bookmark6)). However, these papers focused on feature selection and did not deal with parameters optimization

v*w p*

v

*Lp* Z 0;

v*b*

The

Karush Kuhn–Tucker (KTT) conditions for the optimum

*i i i*

*i*Z1

*m*

X

a*iyi* Z 0 (7)

*i*Z1

for the SVM classifier. [Fro¨hlich and Chapelle (2003)](#_bookmark5) proposed a GA-based feature selection approach that used the theoretical bounds on the generalization error for SVMs. The SVM regularization parameter can also be optimized using GAs in Fro¨hlich’s paper.

This paper is organized as follows: a brief introduction to the SVM is given in Section 2. Section 3 describes basic GA

constrained function are necessary and sufficient for a maximum

of Eq. (5). The corresponding KKT complementarity conditions are

a*i*½*yi*ðh*w*$*xi*i C *b*ÞK1] Z 0 c *i* (8)

Substitute Eqs. (6) and (7) into Eq. (5), then *LP* is transformed to the dual Lagrangian *LD*(a):

concepts. Section 4 describes the GA-based feature selection *m m*

and parameter optimization. Section 5 presents the experimen- Max *L* ðaÞ Z X a K1 X a a *y y* h*x* $*x* i

a *D*

tal results from using the proposed method to classify several

real world datasets. Section 6 summarizes the results and draws

*i*

*i*Z1

2 *i*;*j*Z1

*i j i j i j*

*m*

X

(9)

a general conclusion.

1. Brief introduction of support vector machines
   1. *The optimal hyperplane (linear SVM)*

In this section we will briefly describe the basic SVM concepts for typical two-class classification problems. These concepts can also be found in ([Kecman, 2001](#_bookmark6); [Scho˝lkopf](#_bookmark6) [and Smola, 2000](#_bookmark6); [Cristianini and Shawe-Taylor, 2000](#_bookmark5)).

subject to : a*i* R 0 *i* Z 1; .; *m* and a*iyi* Z 0

*i*Z1

To find the optimal hyperplane, a dual Lagrangian *LD*(a) must be maximized with respect to non-negative a*i*. This is a standard

quadratic optimization problem that can be solved by using some standard optimization programs. The solution a*i* for the dual optimization problem determines the parameters *w*\*and *b*\* of the optimal hyperplane. Thus, we obtain an optimal decision hyperplane *f*(*x*,a\*,*b\**) (Eq. (10)) and an indicator decision

function sign [*f*(*x*,a\*,*b\**)].

Given a training set of instance-label pairs (*xi*, *yi*), *i*Z1,

\* \* X*m* \*

\* X \* \*

2,., *m* where *xi*2*Rn* and *y*i2{C1, K1}, for the linearly separable case, the data points will be correctly classified by

*f* ð*x*; a ; *b* Þ Z

*i*Z1

*yi*a*i* h*xi*; *x*i C *b*

Z

*i*2*sv*

*yi*a*i* h*xi*; *x*i C *b*

(10)

h*w*$*xi*i C *b*RC1 for *yi* Z C1 (1)

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h*w*$*xi*i C *b*%K1 for *yi* ZK1 (2)

In a typical classification task, only a small subset of the Lagrange multipliers a*i* usually tend to be greater than zero. Geometrically, these vectors are the closest to the optimal

hyperplane. The respective training vectors having nonzero a*i* are called support vectors, as the optimal decision hyperplane *f*(*x*,a\*,*b\**) depends on them exclusively.

*LD*ðaÞ Z

*m i*Z1

1 *m*

a*i* K

X

X

2

*i*;*j*Z1

a*i*a*jyiyjk*ð*xi*$*xj*Þ

X*m*

(16)

* 1. *The optimal hyperplane for nonseparable data (linear generalized SVM)*

The above concepts can also be extended to the non- separable case, i.e. when Eq. (3) there is no solution. The goal is to construct a hyperplane that makes the smallest number of errors. To get a formal setting of this problem we introduce the non-negative slack variables x*i*R0, *i*Z1,., *m*. Such that

h*w*$*xi*i C *b*RC1Kx*i* for *yi* Z C1 (11)

subject to : 0% a*i* % *C*; *i* Z 1; .; *m* and a*iyi* Z 0

*i*Z1

This optimization model can be solved using the method for solving the optimization in the separable case. Therefore, the optimal hyperplane has the form Eq. (17). Depending upon the applied kernel, the bias *b* can be implicitly part of the kernel function. Therefore, if a bias term can be accommodated within the kernel function, the nonlinear SV classifier can be shown as Eq. (18).

X*m*

h*w*$*xi*i C *b*%K1 Cx*i* for *yi* ZK1 (12)

*f* ð*x*; a\*; *b*\*Þ Z

*i*Z1

*yi*a\**i* hFð*xi*Þ; Fð*x*Þi C *b*\*

In terms of these slack variables, the problem of finding the

hyperplane that provides the minimum number of training errors, i.e. to keep the constraint violation as small as possible,

*m*

Z

X

*i*Z1

*yi*a\**i k*ð*xi*; *x*Þ C *b*\*

(17)

has the formal expression:

*f* ð*x*; a\*; *b*\*Þ Z X *yi*a\**i* hFð*xi*Þ; Fð*x*Þi Z X *yi*a\**i k*ð*xi*; *x*Þ (18)

1 T X*m*

Min

*w*;*b*;x 2

*w w* C *C*

x*i*

*i*Z1

*i*2*sv*

(13)

*i*2*sv*

subject to : *yi*ðh*w*$*xi*i C *b*Þ Cx*i* K1R 0; x*i* R 0

Some kernel functions include polynomial, radial basis

function (RBF) and sigmoid kernel ([Burges, 1998](#_bookmark5)), which

This optimization model can be solved using the Lagrangian method, which is almost equivalent to the method for solving the optimization problem in the separable case. One must maximize the same dual variables Lagrangian *LD*(a) (Eq. (14)) as in the separable case.

X

are shown as functions (19), (20), and (21). In order to improve classification accuracy, these kernel parameters in the kernel functions should be properly set.

Polynomial kernel:

(19)

*d*

*xj*Þ Z ð1 C *xi*$*xj*Þ

*k*ð*xi*;

Radial basis function kernel:

*j*

*x* K*x* jj Þ

Kgjj

*x* Þ Z expð

Max *LD*ðaÞ Z

a

*m i*Z1

a*i* K

1. *m*
2. *i*;*j*Z1

X

a*i*a*jyiyj*h*xi*$*xj*i

X*m*

subject to : 0% a*i* % *C*; *i* Z 1; .; *m* and

*i*Z1

(14)

a*iyi* Z 0

*k*ð*xi*;

*j*

*i*

2

Sigmoid kernel:

*k*ð*xi*;

*xj*Þ Z tanhð*kxi*$*xj* KdÞ

(20)

(21)

To find the optimal hyperplane, a dual Lagrangian *LD*(a) must be maximized with respect to non-negative a*i* under the constrains a*iyi* Z 0 and 0%a*i*%*C*, *i* Z1,.,*m*. The penalty parameter *C*, which is now the upper bound on a*i*, is

P

determined by the user. Finally, the optimal decision hyper- plane is the same as Eq. (10).

* 1. *Non-linear SVM*

The nonlinear SVM maps the training samples from the input space into a higher-dimensional feature space via a mapping function F, which are also called kernel function. In the dual Lagrange (9), the inner products are replaced by the kernel function (15), and the non-linear SVM dual Lagrangian

*LD*(a) (Eq. (16)) is similar with that in the linear generalized case.

ðFð*xi*Þ$Fð*xj*ÞÞ :Z *k*ð*xi*; *xj*Þ (15)

1. Genetic algorithm

Genetic algorithms (GA), a general adaptive optimization search methodology based on a direct analogy to Darwinian natural selection and genetics in biological systems, is a promising alternative to conventional heuristic methods. GA work with a set of candidate solutions called a population. Based on the Darwinian principle of ‘survival of the fittest’, the GA obtains the optimal solution after a series of iterative computations. GA generates successive populations of alter- nate solutions that are represented by a chromosome, i.e. a solution to the problem, until acceptable results are obtained. Associated with the characteristics of exploitation and exploration search, GA can deal with large search spaces efficiently, and hence has less chance to get local optimal solution than other algorithms.

A fitness function assesses the quality of a solution in the evaluation step. The crossover and mutation functions are



Parents

Offspring

Crossover point

**Crossover**



Before

After



**Mutation**

Fig. 3. The chromosome comprises three parts, *C*, g, and the features mask.

|  |  |  |
| --- | --- | --- |
|  |  |  |

system. Therefore, the chromosome comprises three parts, *C*,

g, and the features mask. However, these chromosomes have different parameters when other types of kernel functions are selected. The binary coding system was used to represent the chromosome. [Fig. 3](#_bookmark0) shows the binary chromosome represen-

tation of our design. In [Fig. 3](#_bookmark0), *g*1 w*gnc* represents the value of

1 *n*g *C C*

Fig. 1. Genetic crossover and mutation operation.

parameter C, *g*g w*g*g represents the parameter value g, and

*g*1 w*gnf* represents the feature mask. *n* is the number of bits

*f f c*

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fitness fn

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note

Selection

Replacement

Offspring

|  |  |
| --- | --- |
| Parents | |
| Cros  Mut | sover  ation |

|  |  |
| --- | --- |
| Evaluat | ion |
| Population | |

Fig. 2. Evolutionary cycle.

the main operators that randomly impact the fitness value. Chromosomes are selected for reproduction by evaluating the fitness value. The fitter chromosomes have higher probability to be selected into the recombination pool using the roulette wheel or the tournament selection methods.

[Fig. 1](#_bookmark0) illustrates the genetic operators of crossover and mutation. Crossover, the critical genetic operator that allows new solution regions in the search space to be explored, is a random mechanism for exchanging genes between two chromosomes using the one point crossover, two point crossover, or homologue crossover. In mutation the genes may occasionally be altered, i.e. in binary code genes changing genes code from 0 to 1 or vice versa.

Offspring replaces the old population using the elitism or diversity replacement strategy and forms a new population in the next generation.

The evolutionary process operates many generations until termination condition satisfy. [Fig. 2](#_bookmark0) depicts the GA evolution- ary process mentioned above ([Goldberg, 1989](#_bookmark5); [Davis, 1991](#_bookmark5)).

1. GA-based feature selection and parameters optimization

The chromosome design, fitness function, and system architecture for the proposed GA-based feature selection and parameter optimization are described as follows.

* 1. *Chromosome design*

To implement our proposed approach, this research used the RBF kernel function for the SVM classifier because the RBF kernel function can analysis higher-dimensional data and requires that only two parameters, *C* and g be defined ([Hsu,](#_bookmark5) [Chang, & Lin, 2003](#_bookmark5); [Lin and Lin, 2003](#_bookmark6)). When the RBF kernel

is selected, the parameters (*C* and g) and features used as input attributes must be optimized using our proposed GA-based

representing parameter C, *nr* is the number of bits representing

parameter g, and *nf* is the number of bits representing the features. Note that we can choose *nc* and *n*g according to the calculation precision required, and that *n*g equals the number of features varying from the different datasets.

In [Fig. 3](#_bookmark0), the bit strings representing the genotype of parameter *C* and g should be transformed into phenotype by Eq. (22). Note that the precision of representing parameter depends on the length of the bit string (*nc* and *nr*); and the minimum and maximum value of the parameter is determined by the user. For chromosome representing the feature mask, the bit with value ‘1’ represents the feature is selected, and ‘0’ indicates feature is not selected.

*p* Z min max*p* Kmin*p* X*d* (22)

*p* C *l*

2 K1

*P* phenotype of bit string

min*p* minimum value of the parameter max*p* maximum value of the parameter

*d* decimal value of bit string

*l* length of bit string

* 1. *Fitness function*

Classification accuracy, the number of selected features, and

the feature cost are the three criteria used to design a fitness

function. Thus, for the individual (chromosome) with high classification accuracy, a small number of features, and low total feature cost produce a high fitness value. We solve the multiple criteria problem by creating a single objective fitness function that combines the three goals into one. As defined by formula (23), the fitness has two predefined weights: (i) *WA* for the classification accuracy; (ii) *WF* for the summation of the selected feature (with nonzero *Fi*) multiplying its cost. The weight accuracy can be adjusted to 100% if accuracy is the most important. Generally, *WA* can be set from 75 to 100% according to user’s requirements. Each feature has different feature cost in the dataset from the UCI. If we do not have the feature cost information, the cost *Ci* can be set to the same value, e.g. ‘1’ or another number. The chromosome with high fitness value has high probability to be preserved to the next generation, so user should appropriately define these settings according to his requirements.

fitnessZ*WA*XSVM\_accuracyC*WF*X

*nf i*Z1

X

*Ci*X*Fi*

!K1

(23)

increase SVM accuracy according to our experimental results. Generally, each feature can be linearly scaled to the range [K1, C1] or [0, 1] by formula (24), where *v* is original value, *vt* is scaled value, max*a* is upper bound of

*WA* SVM classification accuracy weight

*SVM*\_*accuracy* SVM classification accuracy

*WF* weight for the number of features

the feature value, and min*a* is low bound of the feature value.

*Ci* cost of feature *i*

*Fi* ‘1’ represents that feature *i* is selected; ‘0’ represents that feature *i* is not selected

*v*0 Z *v*Kmin*a*

max*a* Kmin*a*

(24)

* 1. *System architectures for the proposed GA-based approach*

To precisely establish a GA-based feature selection and parameter optimization system, the following main steps (as shown in [Fig. 4](#_bookmark1)) must be proceeded. The detailed explanation is as follows:

1. *Data preprocess: scaling*. The main advantage of scaling is

to avoid attributes in greater numeric ranges dominating

those in smaller numeric ranges. Another advantage is to avoid numerical difficulties during the calculation ([Hsu et al., 2003](#_bookmark5)). Feature value scaling can help to

1. *Converting genotype to phenotype*. This step will convert each parameter and feature chromosome from its genotype into a phenotype.
2. *Feature subset*. After the genetic operation and converting each feature subset chromosome from the genotype into the phenotype, a feature subset can be determined.
3. *Fitness evaluation*. For each chromosome representing *C*, g and selected features, training dataset is used to train the SVM classifier, while the testing dataset is used to calculate classification accuracy. When the classification accuracy is obtained, each chromosome is evaluated by fitness function— formula (23).

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note

Population

Parameter genes

Phenotype of Feature feature genes genes

Selected feature subset

Training set with selected feature subset

Testing set with selected feature subset

Phenotype of parameter genes

Classfication accuracy for testing set

Trained SVM

classifier

Training SVM

classifier

Converting genotype to phenotype

Testing set

Training set

Genetic

operatation

Scaling

Dataset

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |

Yes

Fig. 4. System architectures of the proposed GA-based feature selection and parameters optimization for support vector machines.

Fitness evaluation

Optimized (C, ) and

feature subset

No

Termination are satisfied?

Table 1

Datasets from the UCI repository

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| No. | Names | No. of classes | No. of instances | Nominal features | Numeric features | Total features |
| 1 | German (credit card) | 2 | 1000 | 0 | 24 | 24 |
| 2 | Australian (credit card) | 2 | 690 | 6 | 8 | 14 |
| 3 | Pima-Indian diabetes | 2 | 760 | 0 | 8 | 8 |
| 4 | Heart disease (Statlog Project) | 2 | 270 | 7 | 6 | 13 |
| 5 | Breast cancer(Wisconsin) | 2 | 699 | 0 | 10 | 10 |
| 6 | Contraceptive Method Choice | 3 | 1473 | 7 | 2 | 9 |
| 7 | Ionosphere | 2 | 351 | 0 | 34 | 34 |
| 8 | Iris | 3 | 150 | 0 | 4 | 4 |
| 9 | Sonar | 2 | 208 | 0 | 60 | 60 |
| 10 | Statlog project: vehicle | 4 | 940 | 0 | 18 | 18 |
| 11 | Vowel | 11 | 990 | 3 | 10 | 13 |

1. *Termination criteria*. When the termination criteria are satisfied, the process ends; otherwise, we proceed with the next generation.
2. *Genetic operation*. In this step, the system searches for better solutions by genetic operations, including selec- tion, crossover, mutation, and replacement.
3. Numerical illustrations
   1. *Experiment descriptions*

To evaluate the classification accuracy of the proposed system in different classification tasks, we tried several real- world datasets from the UCI database ([Hettich, Blake, & Merz,](#_bookmark5) [1998](#_bookmark5)). These data sets have been frequently used as bench- marks to compare the performance of different classification methods in the literature. These datasets consist of numeric and nominal attributes. [Table 1](#_bookmark2) summarizes the number of numeric attributes, number of nominal attributes, number of classes, and number of instances for these datasets.

To guarantee valid results for making predictions regarding

new data, the data set was further randomly partitioned into

training sets and independent test sets via a *k*-fold cross

validation. Each of the *k* subsets acted as an independent

holdout test set for the model trained with the remaining *k*K1 subsets. The advantages of cross validation are that all of the test sets were independent and the reliability of the results could be improved. The data set is divided into *k* subsets for cross validation. A typical experiment uses *k*Z10. Other values may be used according to the data set size. For a small data set, it may be better to set larger *k*, because this leaves more examples in the training set ([Salzberg, 1997](#_bookmark6)). This study used *k*Z10, meaning that all of the data will be divided into 10 parts, each of which will take turns at being the testing data set. The other nine data parts serve as the training data set for adjusting the model prediction parameters.

Our implementation was carried out on the Matlab 6.5

development environment by extending the Libsvm which is originally designed by [Chang and Lin (2001)](#_bookmark5). The empirical evaluation was performed on Intel Pentium IV CPU running at

1.6 GHz and 256 MB RAM.

The Grid search algorithm is a common method for searching for the best *C* and g. [Fig. 5](#_bookmark2) shows the process of Grid algorithm combined with SVM classifier. In the Grid algorithm, pairs of (*C*,

g) are tried and the one with the best cross-validation accuracy is

chosen. After identifying a ‘better’ region on the grid, a finer grid search on that region can be conducted ([Hsu et al., 2003](#_bookmark5)).

This research conducted the experiments using the proposed GA-based approach and the Grid algorithm. The results from

Training set

Initializing

(C, )

New (C,  )

Termination criteria

No

Yes

Average accuracy

Grid search

Training SVM

classifier using k-fold cross validation

Testing set

Optimized (C,  )

Fig. 5. Parameters setting using Grid algorithm.

Table 2

A 2X2 contingency table

Target (or disease)

C K

*5.3. Experimental results and comparison*

The detail parameter setting for genetic algorithm is as the following: population size 500, crossover rate 0.7, mutation

Predicted (or Test) C True Positive (TP) False Positive (FP)

K False Negative (FN) True Negative (TN)

the proposed method were compared with that from the Grid algorithm. In all of the experiments 10-fold cross validation was used to estimate the accuracy of each learned classifier. Some empirical results are reported in the following sections.

*5.2. Accuracy calculation*

Accuracy using the binary target datasets can be demon- strated by the positive hit rate (sensitivity), the negative hit rate

(specificity), and the overall hit rate. For the multiple class datasets, the accuracy is demonstrated only by the average hit rate. A two by two table with the classification results on the left side and the target status on top is as shown in [Table 2](#_bookmark3). Some cases with the ‘positive’ class (with disease) correctly classified as positive (TPZTrue Positive fraction), however, some cases with the ‘positive’ class will be classified negative (FNZFalse Negative fraction). Conversely, some cases with the ‘negative’ class (without the disease) will be correctly classified as negative (TNZTrue Negative fraction), while some cases with the ‘negative’ class will be classified as positive (FPZFalse Positive fraction). TP and FP are the two important evaluation performances for classifiers ([Woods and](#_bookmark6) [Bowyer, 1997](#_bookmark6)). Sensitivity and specificity describe how well the classifier discriminates between case with positive and with negative class (with and without disease).

*Sensitivity* is the proportion of cases with positive class that are classified as positive (true positive rate, expressed as a percentage). In probability notation for sensitivity: P TC DC ZTP= TPCFN . *Specificity* is the proportion of cases with the negative class, classified as negative (true negative rate, expressed as a percentage). In probability notation: P TK DK ZTN= TNCFP . The overall hit rate is the overall accuracy which is calculated by (TPCTN)/(TNC FPCFNCFP).

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The *SVM*\_*accuracy* of the fitness in function (23) is measured by sensitivityXspecificity for the datasets with two classes (positive or negative), and by the overall hit rate for the datasets with multiple classes.

rate 0.02, two-point crossover, roulette wheel selection, and elitism replacement. We set *nc*Z20 and *nr*Z20; the value of *nf* depends on the experimental datasets stated in Section 5.1. According to the fitness function of Eq. (23), *WA* and *WF* can influence the experiment result. The higher *WA* is; the higher

classification accuracy is. The higher *WF* is; the smaller the

number of features is. We can compromise between weight *WA* and *WF*. Taking the German and Australia datasets, for example, as shown in [Figs. 6 and 7](#_bookmark3), the accuracy (measured by overall hit rate) is high with large numbers of features when high *WA* and low *WF* are defined. We defined *WA*Z0.8 and *WF*Z0.2 for all experiments. The user can choose different weight values; however, the results could be different.

The termination criteria are that the generation number

reaches generation 600 or that the fitness value does not

improve during the last 100 generations. The best chromosome is obtained when the termination criteria satisfy. Taking the German dataset, for example, the positive hit rate, negative hit rate, overall hit rate, number of selected features, and the best pairs of (*C*, g) for each fold using GA-based approach and Grid algorithm are shown in [Table 3](#_bookmark4). For GA-based approach, its average positive hit rate is 89.6%, average negative hit rate is 76.6%, average overall hit rate is 85.6%, and average number of features is 13. For Grid algorithm, its average positive hit rate is 88.8%, average negative hit rate is 46.2%, average overall hit rate is 76.0%, and all 24 features are used. Note that the weight *WA* and *WF* are 0.8 and 0.2 in all of our experiments. [Table 4](#_bookmark4) shows the summary results for the positive hit rate, negative hit rate, overall hit rate, number of selected features, and running time for the 11 UCI datasets using the two approaches. In [Table 4](#_bookmark4), the accuracy and average number of features are illustrated with the form of ‘averageGstandard deviation.’ The GA-based approach generated small feature subsets while Grid algorithm uses all of the features.

To compare the overall hit rate of the proposed GA-based approach with the Grid algorithm, we used the nonparametric

Wilconxon signed rank test for all of the datasets. As shown in [Table 4](#_bookmark4), the *p*-values for diabetes, breast cancer, and vehicle are larger than the prescribed statistical significance level of 0.05, but other *p*-values are smaller than the significance level of 0.05. Generally, compared with the Grid algorithm, the

Accuracy Fitness

Feature Number

1

0.8

0.6

0.4

0.2

0

1.0 0.9 0.8 0.7 0.6 0.5 0.4 0.3 0.2 0.1

Accurcay Weight

20

15



10

5

0

1.0 0.9 0.8 0.7 0.6 0.5 0.4 0.3 0.2 0.1

Accuracy Weight

***acer***

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Fig. 6. Illustration of the classification accuracy versus the accuracy weight, *WA*, for fold #4 of German dataset.

Table 3

Experimental results for German dataset using GA-based approach and Grid algorithm

Fold # GA-based approach Grid algorithm

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Positive hit rate | Negative hit rate | Overall hit rate% | Optimized *C* | Optimized g | Selected features |  | Positive Negative  hit rate hit rate | Overall hit rate% | Optimized  *C* | Optimized  g |
| 1 | 0.863 | 0.7407 | 83 | 170.9992278 | 0.00491136 | 16 |  | 0.8493151 0.55555556 | 77 | 2048 | 0.000488 |
| 2 | 0.8592 | 0.7931 | 84 | 9.29520704 | 0.5189297 | 13 |  | 0.8591549 0.44827586 | 74 | 8 | 0.007813 |
| 3 | 0.9028 | 0.75 | 86 | 171.9769019 | 0.05343727 | 11 |  | 0.875 0.5 | 77 | 512 | 0.001953 |
| 4 | 0.8919 | 0.8462 | 88 | 60.24731324 | 0.05299713 | 11 |  | 0.9324324 0.46153846 | 81 | 8192 | 0.000122 |
| 5 | 0.9091 | 0.7059 | 84 | 174.4961022 | 0.02207236 | 13 |  | 0.9545455 0.32352941 | 74 | 512 | 0.000122 |
| 6 | 0.8904 | 0.7778 | 86 | 20.99907683 | 0.04938617 | 15 |  | 0.890411 0.48148148 | 78 | 128 | 0.000488 |
| 7 | 0.9041 | 0.7778 | 87 | 219.8157576 | 0.03912631 | 12 |  | 0.9452055 0.44444444 | 81 | 32768 | 0.000035 |
| 8 | 0.9155 | 0.7931 | 88 | 95.16782536 | 0.12330259 | 11 |  | 0.8309859 0.44827586 | 72 | 8 | 0.007813 |
| 9 | 0.871 | 0.7632 | 83 | 255.9134212 | 0.27580662 | 15 |  | 0.8225806 0.44736842 | 68 | 2048 | 0.000122 |
| 10 | 0.9538 | 0.7143 | 87 | 174.313561 | 0.01230963 | 13 |  | 0.9230769 0.51428571 | 78 | 512 | 0.000122 |
| Average | 0.89608 | 0.76621 | 85.6 |  |  | 13 |  | 0.8882708 0.46247552 | 76 |  |  |

Table 4

Experimental results summary of GA-based approach and Grid algorithm on the test sets

Names GA-based approach Grid algorithm *p*-value for Wilcoxon

testing

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Number of original features | Number of selected features | Average positive hit rate | Average negative hit rate | Average overall hit rate% | Average positive hit rate | Average Average negative hit overall hit rate rate% | | |
| German | 24 | 13G1.83 | 0.89608 | 0.76621 | 85.6G1.96 | 0.888271 | 0.462476 76G4.06 0.005\* | | |
| Australian | 14 | 3G2.45 | 0.8472 | 0.92182 | 88.1G2.25 | 0.885714 | 0.823529 | 84.7G4.74 | 0.028\* |
| Diabetes | 8 | 3.7G0.95 | 0.78346 | 0.87035 | 81.5G7.13 | 0.592593 | 0.88 | 77.3G3.03 | 0.139 |
| Heart disease | 13 | 5.4G1.85 | 0.94467 | 0.95108 | 94.8G3.32 | 0.75 | 0.909091 | 83.7G6.34 | 0.005\* |
| breast cancer | 10 | 1G0 | 0.9878 | 0.8996 | 96.19G1.24 | 0.98 | 0.944444 | 95.3G2.28 | 0.435 |
| Contraceptive | 9 | 5.4G0.53 | N/A | N/A | 71.22G4.15 | N/A | N/A | 53.53G2.43 | 0.005\* |
| Ionosphere | 34 | 6G0 | 0.9963 | 0.9876 | 98.56G2.03 | 0.94 | 0.9 | 89.44G3.58 | 0.005\* |
| Iris | 4 | 1G0 | N/A | N/A | 100G0 | N/A | N/A | 97.37G3.46 | 0.046\* |
| Sonar | 60 | 15G1.1 | 0.9863 | 0.9842 | 98G3.5 | 0.65555 | 0.9 | 87G4.22 | 0.004\* |
| Vehicle | 18 | 9.2G1.4 | N/A | N/A | 84.06G3.54 | N/A | N/A | 83.33G2.74 | 0.944 |
| Vowel | 13 | 7.8G1 | N/A | N/A | 99.3G0.82 | N/A | N/A | 95.95G2.91 | 0.02\* |

proposed GA-based approach has good accuracy performance with fewer features.

The ability of a classifier to discriminate between ‘positive’ cases (C) and ‘negative’ cases (K) is evaluated using Receiver

Operating Characteristic (ROC) curve analysis. ROC curves can also be used to compare the diagnostic performance of two or more diagnostic classifiers ([DeLeo and Rosenfeld, 2001](#_bookmark5)). For every possible cut-off point or criterion value we select to discriminate between the two populations (with positive or negative class value) there will generate a pair of sensitivity and specificity. An ROC curve shows the trade-off between

sensitivity and specificity, and demonstrates that the closer the curve follows the left-hand border and then the top border of the ROC space, the more accurate the classifier. The area under the curve (AUC) is the evaluation criteria for the classifier.

Taking fold #4 of German dataset, for example, ROC curve of GA-based approach and Grid algorithm are shown in [Fig. 8](#_bookmark5), where AUC is 0.85, 0.82, respectively. For the ROC curve for the other nine folds can also be plotted in the same manner. In short, the average AUC for the 10 folds of testing dataset of German dataset are 0.8424 for

Accuracy Fitness

Feature Number

1

0.8

0.6

0.4

0.2

0

1.0 0.9 0.8 0.7 0.6 0.5 0.4 0.3 0.2 0.1

Accuracy Weight

20

15

10

5

0

1.0 0.9 0.8 0.7 0.6 0.5 0.4 0.3 0.2 0.1

Accuracy Weight

Fig. 7. Illustration of the classification accuracy versus the accuracy weight, *WA*, for fold #3 of Australia dataset.

1

GA-based approach Grid search

0.9

0.8

0.7

0.6

Sensitivity

0.5

0.4

0.3

0.2

0.1

0

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

1-Specificity

Fig. 8. ROC curve for fold #4 of German Credit Dataset.

Table 5

Average AUC for datasets with two classes

GA-based approach Grid algorithm

German 0.8424 0.7886

Australian 0.9019 0.8729

Diabetes 0.8298 0.7647

Heart disease 0.9458 0.8331

breast cancer 0.9423 0.9078

Contraceptive 0.7701 0.6078

Ionosphere 0.9661 0.8709

Iris 0.9756 0.9572

Sonar 0.9522 0.8898

Vehicle 0.8587 0.8311

Vowel 0.9513 0.9205

GA-based approach and 0.7886 for Grid algorithm. We summarize the average AUC for other datasets with two classes in [Table 5](#_bookmark5). The average AUC shows that GA-based approach outperforms the Grid algorithm.

The average running time for GA-based approach is slightly inferior to that of the Grid algorithm; however, the software environment for the two approaches and the predefined searching precision of the Grid algorithm affect the running time. The Grid algorithm is performed under the Python, while the proposed GA-based approach is implemented by using the Matlab in our research. Generally, compared with other systems, the running time is much longer when using the Matlab. Although the proposed approach performed under the Matlab did not outperform the Grid algorithm, it significantly improves the classification accuracy and has fewer input features for support vector machines.

1. Conclusion

SVM parameters and feature subsets were optimized simul- taneously in this work because the selected feature subset has an influence on the appropriate kernel parameters and vice versa. We proposed a GA-based strategy to select the feature subset and set

the parameters for SVM classification. As far as we know, previous researches did not perform simultaneous feature selection and parameters optimization for support vector machines.

We conducted experiments to evaluate the classification accuracy of the proposed GA-based approach with RBF kernel and the Grid algorithm on 11 real-world datasets from UCI database. Generally, compared with the Grid algorithm, the proposed GA-based approach has good accuracy performance with fewer features.

This study showed experimental results with the RBF kernel. However, other kernel parameters can also be optimized using the same approach. The proposed approach can also be applied to support vector regression (SVR). Because the kernel parameters and input features heavily influence the predictive accuracy of the SVR with different kernel functions; we can use the same GA-based feature selection and parameters optimiz- ation procedures to improve the SVR accuracy.

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