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The Hybrid Dynamic Prototype Construction and Parameter Optimization with Genetic Algorithm for Support Vector Machine

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Abstract

The optimized hybrid artificial intelligence model is a potential tool to deal with construction engineering and management problems. Support vector machine (SVM) has achieved excellent performance in a wide variety of applications. Nevertheless, how to effectively reduce the training complexity for SVM is still a serious challenge. In this paper, a novel order-independent approach for instance selection, called the dynamic condensed nearest neighbor (DCNN) rule, is proposed to adaptively construct prototypes in the training dataset and to reduce the redundant or noisy instances in a classification process for the SVM. Furthermore, a hybrid model based on the genetic algorithm (GA) is proposed to simultaneously optimize the prototype construction and the SVM kernel parameters setting to enhance the classification accuracy. Several UCI benchmark datasets are considered to compare the proposed hybrid GA-DCNN-SVM approach with the previously published GA-based method. The experimental results illustrate that the proposed hybrid model outperforms the existing method and effectively improves the classification performance for the SVM.

Keywords: Genetic Algorithm (GA), Dynamic Condensed Nearest Neighbor (DCNN), Support Vector Machine (SVM).

1. Introduction

The support vector machine (SVM) was first proposed by Vapnik [1] and has been successful as a high performance classifier in several domains including data mining and the machine learning areas [2]. The decision boundary of SVM only depends on a small part of training instances. Therefore, if only instances near the boundary are selected, the training of SVM can be efficient and thus classification accuracy is kept. However, the performance of SVM is sensitive to how the kernel parameters are set [3]. As a result, the appropriate instance selection and kernel parameters setting must perform simultaneously to improve the SVM classifier.

In the literature, several data reduction algorithms have been proposed that extract a consistent subset of the overall training set including Condensed Nearest Neighbor (CNN), Modified CNN (MCNN), Fast CNN (FCNN), and others [4-7]. These algorithms have been shown to achieve condensation ratios corresponding to a small percentage of the overall training set and to obtain the comparable classification accuracy. However, these papers merely focused on data reduction without dealing with features selection to reduce the irrelevant features for the classifier.

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Feature selection algorithms may be widely categorized into two groups: the filter and the wrapper approaches [8-9]. The filter approaches select highly ranked features based on a statistical score as a preprocessing step. Wrapper approaches, on the contrary, directly use the induction algorithm to evaluate the feature subsets. They generally outperform filter methods in terms of classification accuracy, but are computationally more intensive. Huang and Wang [3] proposed a GA-based feature selection method that optimized both the feature selection and parameters setting for the SVM classifier. Based on the experimental results obtained, the authors claimed that the algorithm may work superior to the conventional grid search algorithm. However, they did not take into account the treatment of these redundant or noisy instances in a classification process. So far, to the best of our knowledge, there is no other research using an evolutionary algorithm to simultaneously deal with these three type problems, including essential training instances extraction, input features selection, and SVM parameters setting as mentioned above.

In this paper, a new data reduction algorithm named dynamic CNN (DCNN) algorithm, which differs from the original CNN in its employments of the voting scheme, is proposed to adaptively construct prototypes with merged rate threshold. Second, the proposed GA-DCNN-SVM model hybridized the prototype construction, feature selection and kernel parameters optimization methods with genetic algorithm, exhibiting high efficiency in terms of classification accuracy for SVM. The rest of this paper is organized as follows. Section 2 describes the related works including the basic SVM, the CNN rule, and GA concepts. Section 3 details the research methodology, the prototype voting scheme, DCNN rule, and the proposed hybrid model in this study. Section 4 contains the experimental results from several UCI benchmark datasets and comparison with the GA-based previously published method. Finally, conclusions are given in section 5.

2. Related Works

2.1. Basic SVM Classifier

SVM starts from a linear classifier and searches the optimal hyperplane with maximal margin. The main motivating criterion is to separate the various classes in the training set with a surface that maximizes the margin between them. It is an approximate implementation of the structural risk minimization induction principle that aims to minimize a bound on the generalization error of a model [2].

Given a training set of instance-label pairs $(x_i, y_i),\ i=1,2,...,m$ where $x_i \in R^n$ and $y_i \in \{+1,-1\}$. The generalized linear SVM finds an optimal separating hyperplane $f(x)=\langle w \cdot x\rangle + b$ by solving the following optimization problem:

$$\begin{aligned} &\underset{w,b,\xi}{\text{Minimize}} \quad \frac{1}{2} w^T w + C\sum_{i=1}^{m}\xi_i \\ &\text{Subject to:} \quad y_i(< w \cdot x_i > + b) + \xi_i - 1 \geq 0 \\ &\qquad\qquad\quad \xi_i \geq 0 \end{aligned} \tag{1}$$

where C is a penalty parameter on the training error, and ξ_i is the non-negative slack variables. This optimization model can be solved using the Lagrangian method, which maximizes the same dual variables Lagrangian $L_D(\alpha)$ as Eq. (2) as in the separable case.

$$\underset{\alpha}{\text{Maximize}} \quad L_D(\alpha) = \sum_{i=1}^{m} \alpha_i - \frac{1}{2}\sum_{i,j=1}^{m} \alpha_i \alpha_j y_i y_j < x_i \cdot x_j >$$

$$\text{Subject to:} \quad 0 \le \alpha_i \le C, \;\; i = 1, 2, \ldots, m \;\; \text{and} \;\; \sum_{i=1}^{m} \alpha_i y_i = 0 \tag{2}$$

To solve the optimal hyperplane, a dual Lagrangian $L_D(\alpha)$ must be maximized with respect to non-negative α_i under the constrains $\sum_{i=1}^{m} \alpha_i y_i = 0$ and $0 \le \alpha_i \le C$. The penalty parameter C is a constant to be chosen by the user. A larger value of C corresponds to assigning a higher penalty to the errors. After the optimal solution α_i^* is obtained, the optimal hyperplane parameters w^* and b^* can be determined. The optimal decision hyperplane $f(x, \alpha^*, b^*)$ can be written as:

$$f(x, \alpha^*, b^*) = \sum_{i=1}^{m} y_i \alpha_i^* < x_i \cdot x > + b^* = \langle w^* \cdot x \rangle + b^* \tag{3}$$

Linear SVM can be generalized to non-linear SVM via a mapping function Φ, which is also called the kernel function, and the training data can be linearly separated by applying the linear SVM formulation. The inner product $(\Phi(x_i) \cdot \Phi(x_j))$ is calculated by the kernel function $k(x_i, x_j)$ for training data. By introducing the kernel function, the non-linear SVM (optimal hyperplane) has the following forms:

$$f(x, \alpha^*, b^*) = \sum_{i=1}^{m} y_i \alpha_i^* < \Phi(x) \cdot \Phi(x_i) > + b^* = \sum_{i=1}^{m} y_i \alpha_i^* k(x, x_i) + b^* \tag{4}$$

Though new kernel functions are being proposed by researchers, there are four basic kernels as follows:

Linear: $k(x_i, x_j) = x_i^T x_j$ (5)

Polynomial: $k(x_i, x_j) = (\gamma x_i^T x_j + r)^d, \gamma > 0$ (6)

Radial Basis Function: $k(x_i, x_j) = \exp(-\gamma \| x_i - x_j \|^2), \gamma > 0$ (7)

Sigmoid: $k(x_i, x_j) = \tanh(\gamma x_i^T x_j + r)$ (8)

Radial basis function (RBF) is a common kernel function as Eq. (7). In order to improve SVM, the kernel parameter in the kernel function should be set appropriately.

2.2. The Condensed Nearest Neighbor (CNN) Algorithm

The nearest neighbor (NN) rule [10-11] assigns an unclassified sample to the same class as the nearest of the N stored labeled samples of the training set. The rule is simple, and with an unlimited number of instances, the risk in making an NN decision is never worse than twice the Bayes risk [12]. But, as all the labeled samples of the training set must be searched to classify a test sample, the NN method imposes large storage and computational requirements. In order to reduce the both storage space and computational time requirements, the Condensed Nearest Neighbor (CNN) rule first introduced by Hart [4] is that patterns in the training set may be very similar and some do not add extra information and thus may be discarded. In the CNN rule, *prototype-subset* ones aim to select a subset of the training set that classifies the remaining data correctly through the NN rule. Using a prototype subset, instead of the entire training set, to implement the NN rule has the additional advantage that it may guarantee better classification accuracy [6]. The concept of the CNN algorithm can be formalized as follow to determine a consistent subset of the original sample set.

The CNN algorithm uses two bins, called training set *S* with *c*-class and prototype subset *P*. Initially, randomly select one sample from *S* to *P* for each class *c*. Then, we pass one by one over the samples in *S* per epoch and classify each pattern $x_i \in S$ using *P* as the prototype set. During the scan, whenever a pattern x_i is misclassified, it is transferred from *S* to *P* and the prototype subset is augmented; otherwise the pattern x_i is called merged into *P* and still left in *S*. The algorithm terminates when no pattern is transferred during a complete pass of *S* and no new prototype is added to *P*. The procedure can be formalized as follows.

Step 1: The first sample is randomly selected and copied from *S* to *P* for each class *c*.

Step 2: Check each pattern $x_i \in S$ using *P* as the prototype subset. If all patterns have been merged into P, terminate the process; otherwise, go to Step 3.

Step 3: For each class *c*, if there are any unmerged samples, randomly select one and add the pattern to *P*; otherwise, no new prototype is added to class *c*. Go to Step 2.

2.3. Genetic Algorithm

Genetic Algorithm (GA) is one of the most effective approaches for solving optimization problem. The basic principles of GA were first proposed by Holland [13] for the formal examination of the mechanisms of natural adaptation, since then, the algorithm has been modified to solve computational problems in research.

The GA is a stochastic search method based on the mechanics of natural selection and the process of evolution. An implementation of a GA begins with a population of random chromosomes which can be represented by binary strings. The members of the population are usually strings which encode a candidate solution to the problem to be solved. Members of the population at each generation are evaluated, and chromosomes are selected for reproduction by calculating the fitness value. The better chromosomes have higher probability to be selected into the recombination pool using the roulette wheel or other tournament selection methods. After selection and reproduction operation, new population is generated by perturbing the current solutions via crossover and mutation. Crossover takes two individuals called parents and produces two new individuals called the offspring by swapping parts of the parents. This operator allows information exchange between candidate solutions and new solution regions in the search space to be explored. Mutation serves to prevent premature loss of population diversity by randomly sampling new points in the search space. The evolutionary process executes many generations until the termination condition is met or by finding an acceptable solution by some criterion.

3. Methods

The original CNN has been used to iteratively select some samples and ignores others that can be absorbed for data reduction algorithm. In this section, we extend this concept to propose the dynamic CNN approach, which differs from the CNN rule in its employment of a strong absorption criterion, to achieve consistency efficiently for classification problems. Some preliminary definitions are described as follows. Assume that we are given a dataset in which $S = \{(x_i, y_i), i = 1, 2, \ldots, m\}$ is a set of *m* number of samples with well-defined class labels. $x_i = (x_{i1}, x_{i2}, \ldots, x_{iD})^T$ is the vector of dataset for the *i*-th sample describing in *D*-dimensional Euclidean space and $y_i \in L = \{c_1, c_2, \ldots, c_q\}$ is the class label associated with x_i, where *q* is the number of classes. The distance between any two vectors x_i and x_j using the distance measure $d(\cdot)$ is:

$$d(x_i, x_j) = \|x_i - x_j\| = \left[\sum_{k=1}^{D}(x_{ik} - x_{jk})^2\right]^{1/2} \tag{9}$$

3.1. The Prototype Voting Scheme (PVS) scheme

Majority vote is one of the simplest and intuitive ensemble combination techniques. Consider the n samples, c-class dataset U from S, given an instance x_i of U, the Nearest Neighbors' Distance Vector (NNDV) of x_i according to a distance d is:

$$NNDV(x_i) = \begin{bmatrix} d_{i,1,c} & d_{i,2,c} & \cdots & d_{i,j,c} & \cdots & d_{i,n-1,c} & d_{i,n,c} \end{bmatrix}, \tag{10}$$

$$d_{i,j,c} = \begin{cases} 1, & d(x_i, x_j) = \min_j d(x_i, x_j) \quad and \quad i \neq j \\ 0, & d(x_i, x_j) \neq \min_j d(x_i, x_j) \quad or \quad i = j \end{cases} \tag{11}$$
$$i = 1, 2, \ldots, n, \quad j = 1, 2, \ldots, n, \quad c \in \{1, 2, \ldots, q\}.$$

We pass one by one over all of the instances in U, the outputs of NNDV in U are first organized into a Decision Prototype Matrix (DPM) as shown in Fig. 1. The column for $d_{1,j,c}$ to $d_{n,j,c}$ represents the support from samples x_1 to x_n for the candidate point x_j, and the row $d_{i,1,c}$ to $d_{i,n,c}$ is the NNDV of x_i. The vote will then result in an ensemble decision for the candidate point x_λ, and the λ value is:

$$\lambda = \arg\max_{j=1}^{n} \sum_{i=1}^{n} d_{i,j,c} \tag{12}$$

$$DPM = \begin{bmatrix} 0 & d_{1,2,c} & \cdots & d_{1,j,c} & \cdots & d_{1,n-1,c} & d_{1,n,c} \\ d_{2,1,c} & 0 & \cdots & d_{2,j,c} & \cdots & d_{2,n-1,c} & d_{2,n,c} \\ \vdots & \vdots & \ddots & \vdots & \iddots & \vdots & \vdots \\ d_{i,1,c} & d_{i,2,c} & \cdots & d_{i,j,c} & \cdots & d_{i,n-1,c} & d_{i,n,c} \\ \vdots & \vdots & \iddots & \vdots & \ddots & \vdots & \vdots \\ d_{n-1,1,c} & d_{n-1,2,c} & \cdots & d_{n-1,j,c} & \cdots & 0 & d_{n-1,n,c} \\ d_{n,1,c} & d_{n,2,c} & \cdots & d_{n,j,c} & \cdots & d_{n,n-1,c} & 0 \end{bmatrix}$$

Fig. 1 Decision Prototype Matrix for the PVS scheme

The candidate point with the highest total support is then chosen as the prototype. The pseudo code of the proposed Prototype Voting Scheme (PVS) algorithm is shown in Fig. 2. The CNN rule is randomly to select candidate point for the prototype construction process. The PVS algorithm differs from CNN, is order-independent and always returns the same consistent prototype subset from the original sample set.

The Prototype Voting Scheme (PVS) scheme
Input: A training set U with c-class from S;
Output: A prototype point λ ;

For all patterns x_i in U
For each candidate x_j in U
If ($x_i \neq x_j$ and $\min\{d(x_i, x_j)\}$ =True) Then
$d_{ij} = 1$;
Else
$d_{ij} = 0$;
End If
End For
End For
For each candidate x_j in U
Summation of d_{ij} to support value;
End For
Choose x_j with the maximum support value ;
Return (λ);

Fig. 2 Pseudo code of the PVS scheme

3.2. The Dynamic Condensed Nearest Neighbor (DCNN) rule

As the CNN rule randomly chooses samples as prototypes and checks whether all samples have been fully merged into prototype subset, the PVS algorithm is used to improve the randomly select process in *Prototype Construction* stage and the adaptively merged rate coefficient θ_m for dynamically tuning the flexible criterion in *Merge Detection* process. Hence, it is called the Dynamic CNN (DCNN) algorithm.

The DCNN rule has the following advantages. First, it incorporates simply voting scheme in prototype construction process to always return the same consistent training subset independent of the order in which the data is processed and can thus outperform the CNN rule. Second, the employment of the adaptively merged rate coefficient in the Merge Detection process is flexible to edit out noisy instances, to reduce the superfluous instances and makes the machine less sensitive to noises and outliners. The adaptively merged rate coefficient, denoted as $\theta_m \in [0,1]$, is defined as the ratio of the number of instances merged into prototypes to the number of overall dataset and evaluated by Eq. (13). The number of instances merged into prototypes and the number of overall dataset are indicated by N_{merge} and N_{total}, respectively.

$$\theta_m = \frac{N_{merge}}{N_{total}} \times 100\% \tag{13}$$

The proposed DCNN algorithm is described as follows.

Step 1: Prototype Initiation: For each class *c*, adopts the PVS algorithm to select a *c*-sample as a new *c*-prototype.

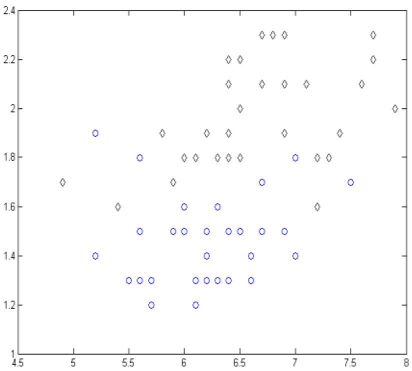
Step 2: Merge Detection: Detect whether all samples have been achieved the user defined merged rate threshold θ_m. If so, terminate the process; otherwise, proceed to the Step 3.

Step 3: Prototype Augmentation: For each *c*, if there are any un-merged *c*-samples, applies the PVS algorithm to construct a new *c*-prototype; otherwise, no new prototype is added to class *c*. Proceed to Step 2.

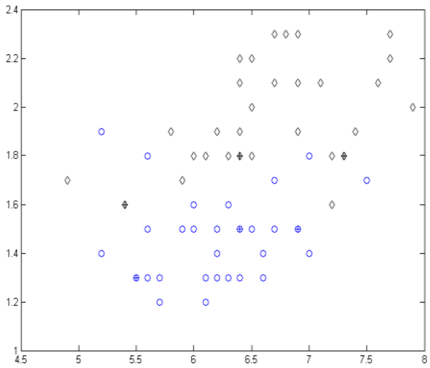
Table 1 The numerical values of the prototype data points with five values of merged rate

No. of data points	$\theta_m = 0.8$	$\theta_m = 0.85$	$\theta_m = 0.9$	$\theta_m = 0.95$	$\theta_m = 1.0$
Class 1 (1)	(5.5,1.3)	(5.5,1.3)	(5.5,1.3)	(5.2,1.4)	(5.2,1.4)
Class 1 (2)	(6.4,1.5)	(5.6,1.5)	(5.6,1.5)	(5.5,1.3)	(5.2,1.9)
Class 1 (3)	(6.9,1.5)	(6.3,1.6)	(5.6,1.8)	(5.6,1.5)	(5.5,1.3)
Class 1 (4)		(6.4,1.5)	(6.3,1.6)	(5.6,1.8)	(5.6,1.5)
Class 1 (5)		(6.9,1.5)	(6.4,1.5)	(6.0,1.5)	(5.6,1.8)
Class 1 (6)		(7.0,1.8)	(6.7,1.7)	(6.3,1.6)	(6.0,1.5)
Class 1 (7)			(6.9,1.5)	(6.4,1.5)	(6.0,1.6)
Class 1 (8)			(7.0,1.8)	(6.7,1.7)	(6.3,1.6)
Class 1 (9)				(6.9,1.5)	(6.4,1.5)
Class 1(10)				(7.0,1.8)	(6.7,1.7)
Class 1(11)					(6.9,1.5)
Class 1(12)					(7.0,1.8)
Class 1(13)					(7.5,1.7)
Class 2 (1)	(5.4,1.6)	(5.4,1.6)	(5.4,1.6)	(4.9,1.7)	(4.9,1.7)
Class 2 (2)	(6.4,1.8)	(5.8,1.9)	(5.8,1.9)	(5.4,1.6)	(5.4,1.6)
Class 2 (3)	(7.3,1.8)	(6.4,1.8)	(6.2,1.9)	(5.8,1.9)	(5.8,1.9)
Class 2 (4)		(6.9,1.9)	(6.4,1.8)	(5.9,1.7)	(5.9,1.7)
Class 2 (5)		(7.1,2.1)	(6.9,1.9)	(6.2,1.9)	(6.1,1.8)
Class 2 (6)		(7.3,1.8)	(7.1,2.1)	(6.4,1.8)	(6.2,1.9)
Class 2 (7)			(7.2,1.6)	(6.9,1.9)	(6.4,1.8)
Class 2 (8)			(7.3,1.8)	(7.1,2.1)	(6.9,1.9)
Class 2 (9)				(7.2,1.6)	(7.1,2.1)
Class 2(10)				(7.3,1.8)	(7.2,1.6)
Class 2(11)					(7.3,1.8)
Class 2(12)					(7.4,1.9)
Class 2(13)					(7.7,2.2)

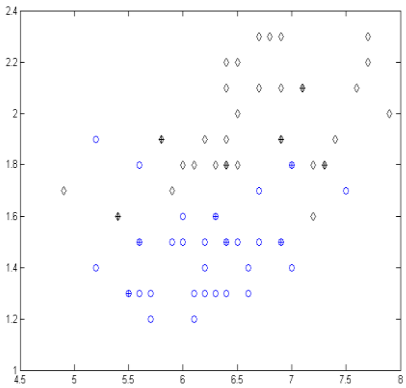
In order to illustrate the behavior of the proposed DCNN algorithm, a set of data points in R^2 space is considered. The numerical values of the prototype data points with five merged rate value of θ_m (θ_m =0.8, 0.85, 0.9, 0.95 and 1.0) using the proposed algorithm are listed in Table 1. The simulation results are shown in Fig. 3, where "◇" and "O" denote the positive class and negative class respectively, the data points with "+" inner symbols are prototypes. The results show that the higher the value of θ_m, the larger the number of prototypes, and vice versa. This property makes the DCNN algorithm flexible to tackle those training samples misclassified in the overlapped region or outliers on the different distributions of dataset. Thus, we can apply SVM to post-process the set of prototypes from DCNN, to improve the outlier sensitivity problem of the standard SVM and yield an effectively hybrid classifier.



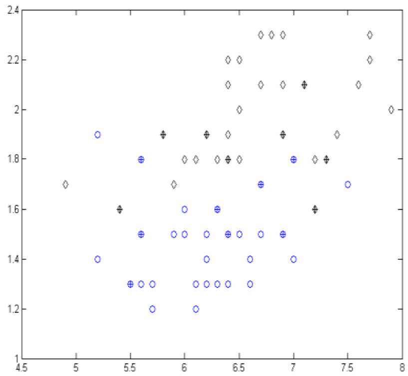
(a) The result of original dataset



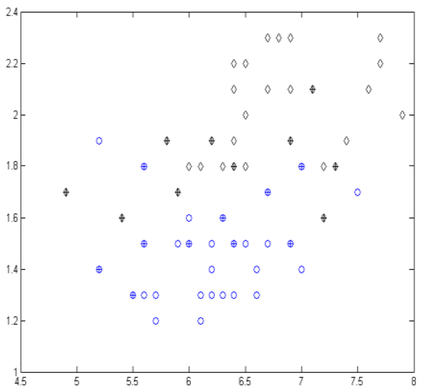
(b) The result of $\theta_m = 0.8$



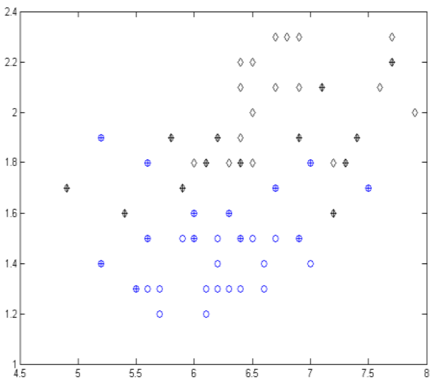
(c) The result of $\theta_m = 0.85$



(d) The result of $\theta_m = 0.9$



(e) The result of $\theta_m = 0.95$



(f) The result of $\theta_m = 1.0$

Fig. 3 The simulation results

3.3. The GA-DCNN-SVM hybrid model

This section detailed the proposed novel hybrid framework, which integrates the prototype construction, feature selection and parameter optimization for the SVM. The chromosome representation, fitness definition and system procedure for the proposed hybrid model are described as follows.

3.3.1. Chromosome Representation

This research used the RBF kernel function (defined by Eq. (7)) for the SVM classifier to implement our proposed method. The RBF kernel function requires that only two parameters, C and γ should be set. Using the adaptively merged rate for DCNN and the RBF kernel for SVM, the parameters θ_m, C, γ and features used as input attributes must be optimized simultaneously for our proposed GA-DCNN-SVM hybrid system. The chromosome therefore, is comprised of four parts, θ_m, C, γ and the features mask. Fig. 5 shows the chromosome representation of our design.

$$\left[b^{\theta_m}_{n_{\theta_m}-1} b^{\theta_m}_{n_{\theta_m}-2} \ldots b^{\theta_m}_{0}, b^{c}_{n_c-1} b^{c}_{n_c-2} \ldots b^{c}_{0}, b^{r}_{n_r-1} b^{r}_{n_r-2} \ldots b^{r}_{0}, b^{f}_{n_f-1} b^{f}_{n_f-2} \ldots b^{f}_{0} \right]$$

Fig. 4 Chromosome representation in θ_m, C, γ and features mask

In Fig. 4, $b^{\theta_m}_{n_{\theta_m-1}} \sim b^{\theta_m}_{0}$ indicates the parameter value θ_m and the bit string's length is n_{θ_m}, $b^{c}_{n_c-1} \sim b^{c}_{0}$ represents the parameter value C and the bit string's length is n_c, $b^{\gamma}_{n_\gamma-1} \sim b^{\gamma}_{0}$ denotes the parameter value γ and the bit string's length is n_γ, $b^{f}_{n_f-1} \sim b^{f}_{0}$ stands for the features mask and n_f is the number of features that varies from different datasets. Furthermore, we can choose different length for each n_{θ_m}, n_c and n_γ parameter according to the calculation precision required.

The bit string $b_{l-1}b_{l-2}\ldots b_0$, where $b_i \in \{0,1\}, i = 0,1,\ldots,l-1$, representing the genotype format of the parameters θ_m, C and γ, should be transformed into phenotype z by Eq. (14). Note that the precision of representing parameter depends on the length of the bit string l (such as n_{θ_m}, n_c and n_γ), and the minimum and maximum value $[z_{\min}, z_{\max}]$ of the parameter is determined by the user. The features mask is Boolean that '1' represents the feature is selected, and '0' indicates the feature is not selected.

$$z = z_{\min} + \frac{(z_{\max} - z_{\min})}{2^l - 1} \sum_{i=0}^{l-1} b_i \cdot 2^i \tag{14}$$

3.3.2. Fitness Definition

Fitness function is the guide of GA's operation to search for optimal solutions. For maximizing the classification accuracy and minimizing the number of selected features, the fitness function F is a weighted sum with w_A for the classification accuracy weight and w_F for the selected features as defined by Eq. (15). A_{cc} is the SVM classification accuracy, f_i is the value of feature mask－'1' represents the feature *i* is selected and '0' indicates that feature *i* is not selected, and n_f is the total number of features. Thus, for the chromosome with high classification accuracy and a small number of features produce a high fitness value.

$$F = w_A \times Acc + w_F \times \left(\sum_{i=1}^{n_f} f_i \right)^{-1} \tag{15}$$

Considering the tradeoff between the classification accuracy and selected feature number, the two weights w_A and w_F can be adjusted according to the preference of classifier designers. The weight accuracy can be tuned to a high value (such as 100%) if accuracy is the most important.

3.3.3. The proposed hybrid GA-DCNN-SVM algorithm

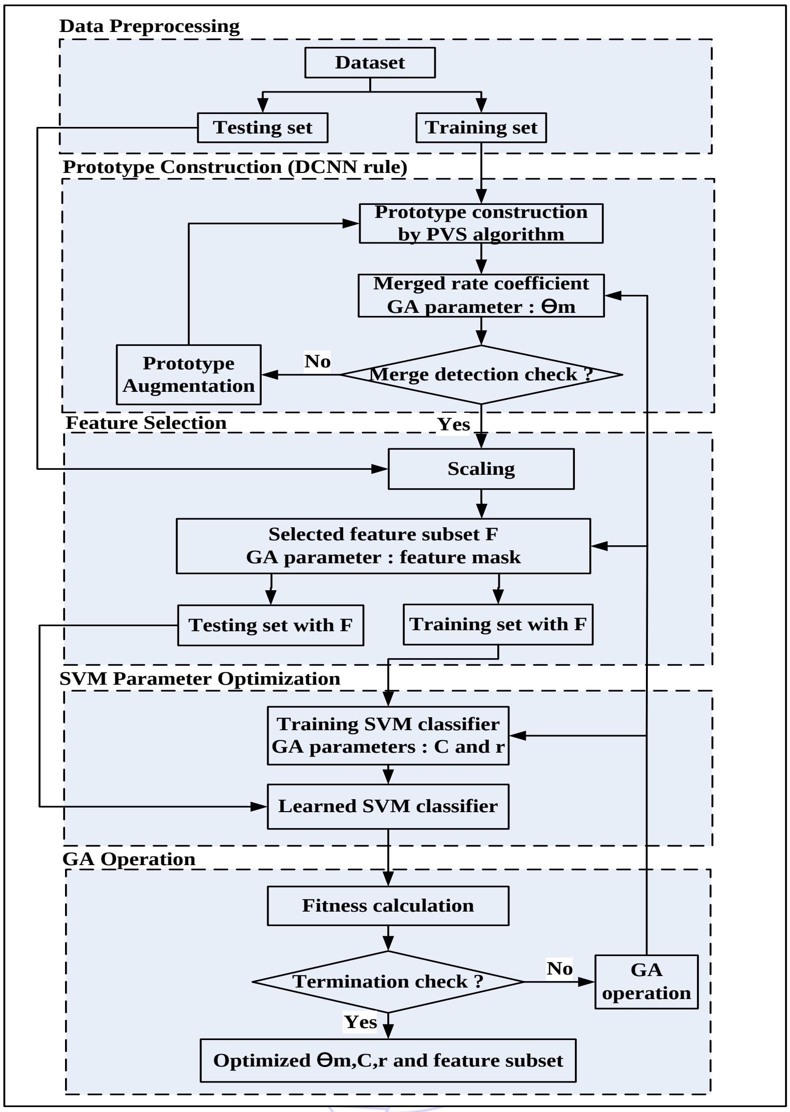


Fig. 5 The flowchart of the proposed hybrid GA-DCNN-SVM algorithm

Fig. 5 shows the system architecture of our proposed hybrid model. Based on the chromosome representation and fitness definition mentioned above, detailed descriptions of the novel GA-DCNN-SVM procedure are illustrated as follows.

Procedure GA-DCNN-SVM hybrid model

Step 1: Data preparation

Given a dataset S is considered using the 10-fold cross-validation process to split the data into ten groups. Each group contains training and testing sets. The training and testing sets are represented as S_{TR} and S_{TE} , respectively.

Step 2: GA initialization and parameters setting

Set the GA parameters including the number of iterations, population sizes, crossover rate, mutation rate, and weight for fitness calculation. Generate initial chromosomes comprised of the parameters including θ_m , C , γ , and feature mask.

Step 3: Converting genotype to phenotype

Convert each parameter (θ_m , C and γ) from its genotype into a phenotype.

Step 4: Prototype construction by using the DCNN algorithm

The DCNN algorithm computes a prototypes subset, denoted by P, from the training set S_{TR} according to the merged rate parameter θ_m which is represented in the chromosome and calculated from Step 3. Once the prototypes subset P is computed, the new training set $S_{TR}^{'}$ is set to P.

Step 5: Scaling

The purpose of feature scaling is to properly describe the interactions between feature attributes and to avoid attributes in greater numeric ranges dominating those in smaller numeric ranges [3, 14]. Attributewise normalization by Eq. (16) can be linearly scaled to the range [-1, +1] or [0, 1], where $a_j(x_i)$ is the original attribute value of feature x_i, $a_j^{'}(x_i)$ is scaled value, $\max_j$ and $\min_j$ correspond to the maximum and minimum values for attribute a_j over all samples.

$$a_j^{'}(x_i) = \frac{a_j(x_i) - \min_j}{\max_j - \min_j}, \quad \forall i \tag{16}$$

Step 6: Selected features subset

Select input features for training set $S_{TR}^{'}$ and testing set S_{TE} according to the feature mask which is represented in the chromosome from Step 2, then the features subset can be determined. We denote the $S_{TR}^{'}$ and S_{TE} datasets with selected features as $FS_{TR}^{'}$ and FS_{TE}, respectively.

Step 7: SVM model training and testing

Based on the parameters C and γ which are represented in the chromosome and calculated from Step 3, to train the SVM classifier on the training dataset $FS_{TR}^{'}$, then the classification accuracy A_{cc} on the testing dataset FS_{TE} can be evaluated.

Step 8: Fitness evaluation

For each chromosome, evaluate its fitness value by Eq. (15) when the classification accuracy A_{cc} is obtained from previous step. The optimal fitness value will be stored to provide feedback on the evolution process of GA to find the increasing fitness of chromosome in the next generation.

Step 9: Termination check

When the maximal evolutionary epoch is reached, the process ends; otherwise, go to the next step.

Step 10: GA operation

In the evolution process, standard GA operators such as selection, crossover and mutation based on elitist strategy may be applied to search for better solutions.

4. Experimental Results

4.1. System Implementation Descriptions

To verify the effectiveness of the proposed hybrid system, we tried several real benchmark data sets which are cited from the UCI Machine Learning Repository [15].

Six real data sets are considered, namely, the Australian data set, the German data set, the Heart disease data set, the Iris data set, the Vehicle data set, and the Vowel data set. In the above datasets, Table 2 summarizes the number of numeric attributes, number of nominal attributes, number of classes, and number of instances.

Table 2 Datasets from the UCI Machine Learning Repository

Names	Num. classes	Num. instances	Nominal features	Numeric features	Total features
Australian	2	690	6	8	14
German	2	1000	0	24	24
Heart	2	270	7	6	13
Iris	3	150	0	4	4
Vehicle	4	940	0	18	18
Vowel	11	990	3	10	13

The datasets considered are partitioned using the 10-fold cross validation. Each initial data set S, is randomly divided into ten disjoint sets of equal size T_1, …, T_{10}. We maintain the original class distribution (before partitioning) within each set when carrying out the partition process, and then conduct ten pairs of training and testing sets, (S_{TR}^i, S_{TE}^i), i=1, …, 10. Ten trials were run for each data set, and the advantage of cross validation is that all of the testing sets were independent and the reliability of the results could be improved.

Our implementation platform was carried out on Matlab 2013, a mathematical development environment by extending the LIBSVM which is originally designed by Chang and Lin [16]. The GA-based previously published method by Huang [3], namely GA-SVM with non-DCNN version, for searching the best C, γ, and features subset. The existing GA-SVM with non-DCNN version method deals solely with feature selection and parameters optimization by means of genetic algorithm, and the treatment of these redundant or noisy instances in a classification process did not taken into account. Our proposed GA-DCNN-SVM hybrid model has been tested fairly extensively and compared with the non-DCNN version approach using three criteria, namely, the classification accuracy rate, the number of selected feature, and the non-parametric Wilcoxon signed rank test. In all of the experiments, 10-fold cross validation was used to estimate the classification accuracy of each learning algorithm. We report the empirical results in the following section.

4.2. Results and Comparisons

In computation works, we set GA parameters to the same values to compare the performance using the two different algorithms. The detail parameter setting for GA is as the following: population size 200, generation number 300, crossover rate 0.7, mutation rate 0.05, two point crossover, roulette wheel selection and the elitism replacement. The bit string's length for each parameter n_{θ_m}, n_c, n_γ is configured as 20, and the value of n_f varies from different datasets described in Table 2. According to the fitness function defined by Eq. (15), set the accuracy's weight $w_A = 0.8$ and the feature's weight $w_F = 0.2$ for all experiments. The termination criterion is that the generation number achieves generation 300, and the best chromosome is obtained when the termination criterion satisfies.

Taking the Heart disease dataset, for example, the classification accuracy A_{cc}, number of selected features n_f, and the best parameters θ_m, C, γ for each fold using GA-DCNN-SVM algorithm and GA-SVM with non-DCNN approach are shown in Table 3. For the GA-DCNN-SVM method, average classification accuracy rate is 96.10%, and average number of features is 5.0. For the GA-SVM with non-DCNN approach, its average classification accuracy rate is 94.81%, and average number of features is 5.6. Table 4 shows the summary results for the average classification accuracy rate Avg_A_{cc} and the average number of selected features Avg_n_f for the six UCI datasets using the two different approaches. In Table 4, the classification accuracy rate and number of features are represented as the form of 'average ± standard deviation'. It should be mentioned that in the case of six UCI datasets, the Avg_A_{cc} always increased when the DCNN philosophy was employed.

Table 3 Experimental results for Heart disease dataset comparison from GA-DCNN-SVM and GA-SVM algorithms

	GA-DCNN-SVM algorithm					GA-SVM algorithm			
Fold#	*Acc*	n_f	Optimize θ_m	Optimized *C*	Optimized γ	*Acc*	n_f	Optimized *C*	Optimized γ
1	93.8	4	0.91762668	52.8991662	0.54895732	92.4	5	5.5801297	0.57708836
2	98.2	6	0.95872936	162.8651756	0.02765115	98.1	7	60.2411283	0.01708658
3	100.0	7	0.96772981	133.6631785	0.02488665	100.0	7	171.3113128	0.21574369
4	94.6	4	0.92086954	26.9159661	0.10925755	92.6	4	95.2776294	0.05706643
5	98.5	6	0.94607836	82.7895272	0.33687129	98.4	7	267.4913877	0.33562374
6	93.7	4	0.91765053	165.9553541	0.18916658	92.6	6	53.6696245	0.07895168
7	94.6	4	0.94782197	20.6576587	0.06485473	92.1	4	216.8613768	0.12075873
8	97.6	6	0.92492187	9.7715546	0.08432751	97.5	6	170.5518422	0.45896385
9	93.8	4	0.92642064	216.8693786	0.21982678	90.7	4	75.5779491	0.08705219
10	96.2	5	0.93052900	88.8319034	0.46812314	93.7	6	83.6912762	0.11775911
Average	**96.10**	**5.0**				**94.81**	**5.6**		

To highlight the advantage, the non-parametric Wilcoxon signed rank test is used for all of the datasets. As shown in Table 4, the *p*-value for Iris is equal to 1.0, but other *p*-values are smaller than the statistical significance level of 0.05. Due to time considerations, the average execution time for GA-DCNN-SVM approach requires more computing time than the non-DCNN version. It is reasonable that the DCNN rule can achieve optimization merged rate for training data to improve SVM performance. Generally, compared with the GA-based with non-DCNN version algorithm, the proposed GA-DCNN-SVM hybrid approach has good classification accuracy performance with fewer features and it effectively improves the classification accuracy and has fewer input features for support vector machine.

Table 4 Experimental results of GA-DCNN-SVM algorithm and GA-SVM method on six UCI datasets

Name	GA-DCNN-SVM		GA-SVM		*p*-value for Wilcoxon testing
	Avg_A_{cc}	Avg_n_f	Avg_A_{cc}	Avg_n_f	
Australian	90.3±1.42	4.3±0.82	88.2±1.81	4.5±1.08	0.028*
German	87.4±0.97	12.6±0.84	85.6±1.80	13.1±1.59	0.022*
Heart	96.1±2.32	5.0±1.15	94.8±3.32	5.6±1.26	0.008*
Iris	100±0	1±0	100±0	1±0	1.0
Vehicle	85.9±1.85	8.6±0.97	84.0±2.40	9.7±1.70	0.007*
Vowel	99.2±0.75	7.1±0.74	98.5±0.89	7.9±0.88	0.011*

*Statistical significance level is 0.05.

5. Conclusions

In this work, an order-independent algorithm for data reduction, called the Dynamic Condensed Nearest Neighbor (DCNN) rule, is proposed to adaptively construct prototypes in the training dataset and to reduce the redundant or noisy instances in a classification process for the SVM. Furthermore, a hybrid model based on the genetic algorithm is proposed to simultaneously optimize the prototype construction, the feature selection, and the SVM kernel parameters setting for solving the classification problems. The experimental results illustrate that the proposed method is capable of producing good classification accuracy with a small number of features on several UCI repository of machine learning datasets. Generally, the proposed GA-DCNN-SVM hybrid approach outperforms the existing GA-based method without the DCNN scheme and improves the classification accuracy with fewer features for the SVM. Extending the proposed hybrid framework to other learning tasks, such as SVM ensemble strategy constitutes a feasible approach and useful modification of the regular SVM, is other possible directions to pursue.

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