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Radar target recognition using SVMs with a wrapper feature selection driven by Immune Clonal Algorithm

Xiangrong Zhang, Shuang Wang, Tan Shan, and Licheng Jiao, Senior Member, IEEE *

National Key Lab for Radar Signal Processing, Institute of Intelligent Information Processing
Xidian University, 710071 Xi'an, China

Abstract. A wrapper feature selection method based on Immune Clonal Algorithm for SVM is presented and applied to 1-D images recognition of radar targets in this paper. In the proposed method, the cross-validation is used for feature evaluation in wrapper feature selection step for SVMs. And Immune Clonal Algorithm, which is characterized by rapid convergence to global optimal solution, is applied to find the optimal feature subset. Experimental results on 1-D images of 3 airplanes obtained in a microwave anechoic chamber show the effectiveness of the proposed method.

1 Introduction

1-D images of radar targets are obtained using the scaling model of targets through rotation plan imaging in a microwave anechoic chamber. It is easier to obtain than 2-D images and can reflect exact geometry construction of targets when resolution rate is high enough. Many successful recognition methods for radar targets based on 1-D images have been proposed, for example methods based on matching score concept [1], fractal compression characteristic [2], Hidden Markov Model [3] and so on.

In paper [4], SVMs is used for recognition of 1-D images of radar targets with high dimension. Though SVM has excellent ability for the processing of multi-dimension data, it does not offer automatic detection of internal relevance of data. Irrelevant and redundant information usually contaminate the performance of machine learning algorithm. The removal of it, namely feature selection or dimension reduction, is essential for improving the performance of the classifiers. Feature selection methods based on minimizing the bounds of generation error for SVMs have been proposed [5] [6]. These methods are faster in computation than k-fold cross-validation, but the bounds are the estimation of the generalization error and they have a higher bias than cross-validation in general. In this paper, cross-validation is used for feature evaluation in wrapper feature selection for SVM because it is more robust in practical situations and the computation time is acceptable in present application.

Feature selection is usually considered as an optimization problem. After selecting the evaluation criterion, we need to choose a searching algorithm. Genetic algorithm (GA) is a global searching algorithm and is widely used in feature selection [7]. Unfortunately, GA has the unavoidable disadvantages that the convergence speed is low and the optimal solution cannot be obtained in limited generations since it emphasizes the competition alone and the communication between individuals is ignored. Immune Clonal Algorithm (ICA) overcomes the shortcoming of GA to some

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degree [8][9]. It is based on the artificial immune system, in which competition and cooperation coexist. ICA demonstrates the self-adjustability function by accelerating or restraining the generation of antibodies, which enhances the diversity of the population. Accordingly, ICA is applied to search the optimal feature subset.

2 Wrapper Feature Selection Driven by ICA For SVMs

Feature selection is motivated for three-fold: improve generation error, determine the relevant features and reduce the dimensionality of the input space. Based on the evaluation criterion, feature selection methods can be classified into filter and wrapper methods [10]. In wrapper feature selection method, the classification accuracy is used for the evaluation of the selected feature subset. Because it takes feature selection and classification as a whole and the classifier used in evaluating the feature subset is the same as the one used in classifying unknown patterns, the accuracy of the resulting classification is higher. As a system of machine learning including feature selection and pattern classification, the wrapper method can lead to a more suitable feature subset for given classifier.

2.1 Evaluation of Feature Subset

The goal of feature selection is to achieve the same or better performance using fewer features. Therefore two fundamental issues in feature selection are the number of selected features and quality. The quality of the feature subset is evaluated by the 5-fold cross-validation technique using SVMs in order to minimize the generalization error. Combining the number of feature subset selected and the resulting accuracy, the evaluation of a feature subset is given as

$$Aff = 10^3 Acc - 0.7 \times d \quad (1)$$

where *Acc* is the accuracy that a given feature subset achieves and *d* the number of features included in the corresponding subset. *Acc* is the average accuracy of k-fold cross-validation of the training data here that ranges from 0.5 to 1, then the first term from 500 to 1000. *d* ranges from 1 to the number of the total features *D* (*D* is 64 for 1-D images of radar targets here), and then the second term ranges roughly from 0.7 to 45. The coefficients in formula (1) ensures that the higher the accuracy, the higher the *Aff*. Between the accuracy and the dimension of feature subset selected, the former is the major concern. And in the case that two subsets achieve the same performance, the subset with low dimension is preferred.

2.2 Wrapper Feature Selection Driven by ICA

2.2.1 A Brief Review of ICA

The clonal selection theory is used by the immune system to describe the basic features of an immune response to an antigenic stimulus; it establishes the idea that the cells are selected when they recognize the antigens and proliferate. When exposed to antigens, immune cells that may recognize and eliminate the antigens can be selected in the body and mount an effective response against them during the course of the clonal selection. The clonal operator is an antibody random map induced by the

affinity and it includes three steps: clone, clonal mutation and clonal selection. The state transfer of antibody population is denoted as follows:

$$C_{MA}: A(k) \xrightarrow{clone} A'(k) \xrightarrow{mutation} A''(k) \xrightarrow{selection} A(k+1)$$

According to the affinity function f, a point $a_i = \{x_1, x_2, \cdots, x_m\}$, $a_i(k) \in A(k)$ in the solution space will be divided into q_i same points $a_i^{'}(k) \in A'(k)$ by using clonal operator. A new antibody population is produced after performing clonal mutation and clonal selection. In ICA, affinity is the reflection of the degree of match between solution and the fitting function, which generally indicates values of objective functions or fitness measurement of the problem.

Derived from traditional evolutionary algorithm, ICA introduces the mechanisms of affinity maturation, clone and memorization. Rapid convergence and good global search capability characterize the performance of the corresponding operators. In this paper, the property of rapid convergence to global optimum of ICA is made use of to speed up the searching of the most suitable feature subset among a huge number of possible feature combinations.

2.2.2 Wrapper Feature Selection Based on ICA

Wrapper feature selection based on ICA can be stated as to identify the d most discriminative measurements out of D ($d \le D$) potentially useful measurements whose performance is the best for SVMs. Here, the performance corresponds to the affinity in ICA, which is evaluated with equation (1).

Encoding

A binary encoding scheme is used to represent the presence or absence of a particular feature. An antibody is a binary string whose length D is determined by the number of total features extracted. Let $(a_{v_1}, a_{v_2}, \cdots, a_{v_D})$ denote an antibody, where a_{v_i} denotes locus, and let $a_{v_i} = 0$ when the associated feature is absent, $a_{v_i} = 1$ when the associated feature is present. When evaluating the affinity of a given antibody, the binary string is decoded to the corresponding features combination through removing the features where $a_{v_i} = 0$ and the new training sample sets are achieved.

Initial Population

The initial antibody population $A(0)$ is generated randomly and each one of N_p (population size) antibodies represents a different feature subset.

Clone

Implement the clonal operator on current parent population $A(k)$, then $A(k)^{'} = \{A(k), A_1^{'}(k), A_2^{'}(k), \cdots, A_{N_p}^{'}(k)\}$. The clonal size N_c of each individual can be determined proportionally by the affinity between antibody and antigen or be a constant integer for convenience.

Clonal Mutation

The clonal mutation operator is only implemented on the cloned part of $A^{'}(k)$, which changes each of the bits based on the probability of mutation $p_m = 1/D$, and then $A^{''}(k)$ is achieved.

Clonal Selection

In subpopulation, if mutated antibody $b = \max\{f(a_{ij}) \mid j = 2,3,\cdots,q_i - 1\}$ exists so as to $f(a_i) < f(b)$, $a_i \in A(k)$, b replaces the antibody a_i and is added to the new parent population, namely, the antibodies are selected proportionally as the new population of next generation $A(k+1)$ based on the affinity. It is a map $I^{N_c(k)+n} \to I^n$, which realizes population compressing through selecting local optimum.

3 Experiments

The real data of three airplanes B-52，J-6 and J-7 obtained through scaling models in a microwave anechoic chamber are used in experiments. Image angles range from 0° to 155°. There are 322 location data for B-52, 311 for J-6 and 451 for J-7. The data consists of 64 attributes, namely, range cells. The 1-D images of the variation with the imaging angles are given in Fig.1.

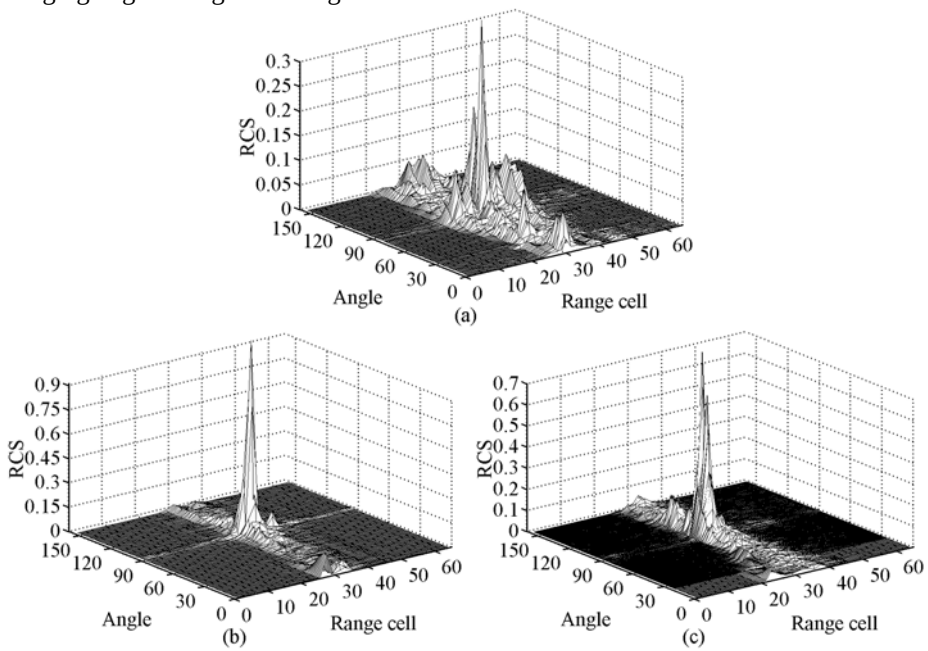

Fig.1: The 1-D images of 3 airplanes under different angles (a) B-52 (b) J-6 (c) J-7

Due to the property that 1-D images of radar target can reflect exactly the geometry structure of the target, the 1-D images are resemble each other if the associated airplanes are with the similar shape. For example, the 1-D images of J-6 and J-7 are similar, as shown in Fig.1. On the other hand, the 1-D images depend on the imaging angles strongly. As a result, the 1-D images of one target under different angles may be different absolutely and those of different targets under different angles may be similar. Of course, the 1-D images of the same target present the similarity when the angles change little.

In the first experiment, we divided these examples into two groups. The imaging angle of the first group is from 0 to 100° and the second from 80 to 155°. The average recognition rates of 10 runs obtained by SVMs only and SVMs with wrapper feature selection driven by ICA are shown in Table 1. In addition, further experiments are carried out on the samples under 0°~155° for comparison, in which filter feature selection with ICA, wrapper feature selection with GA and wrapper feature selection with ICA are performed respectively for finding the most discriminative feature subset from the 64 attributes for classification. In both experiments, SVMs with RBF kernel are used for radar targets recognition based on the selected features. And approximate 1/5 data of each data set are selected for training and the rest for test. The data are normalized first because 3 magnitude gaps exist between the maximum and minimum of the data of the same airplane. 5-fold cross-validation is used for feature subset evaluation in wrapper feature selection. In filter feature selection, *Acc* in equation (1) can be substituted by the distance measure, and the Bhattacharyya distance criterion [11] is used in this experiment. The parameters in ICA are defined as follows. The antibody population size N_p is 5 and the length of each antibody is 64, then the mutation probability $p_m = 1/64$. The clonal size N_c of each individual is a constant integer 5 for convenience. In GA, the size of initial population is 10, crossover probability 0.8 and mutation probability 0.01. The termination criterions for both ICA and GA are triggered whenever the maximum number of generations, 20, is attained. We carry out the experiments 10 times independently. And the recognition results of the 1-D images with angles from 0 to 155° are shown in Table 2, where the results listed is the average of 10 runs.

		0°~100°		80°~155°	
		SVMs	Proposed method	SVMs	Proposed method
Data dimension		64	28.4	64	28.5
Recognition rates (%)	B-52	94.40	96.80	93.33	95.41
	J-6	93.87	97.00	93.62	95.57
	J-7	99.38	97.23	99.14	97.38
Average recognition rates (%)		95.88	97.01	95.36	96.12

Table 1: The recognition results of the 1-D images under 0°~100° and 80°~155°

		SVMs	Filter feature selection with ICA +SVMs	Wrapper feature selection with GA+SVMs	The proposed method
Data Dimension		64	34.4	30	27.8
Recognition rates (%)	B-52	94.57	96.40	96.74	98.22
	J-6	94.38	96.87	96.79	96.47
	J-7	99.86	98.25	97.45	98.28
Average recognition rates (%)		96.27	97.17	96.99	97.66

Table 2: The recognition results of the 1-D images under 0°~155°

The results in Table 1 validate the efficiency of the proposed method. And the results in Table 2 imply that the method using SVMs with a wrapper feature selection driven by ICA outperforms the other two methods for radar targets recognition because higher accuracy is got with fewer features selected. The fact that recognition results of the proposed method are better than those with filter feature selection driven by ICA is attributed to the matter that the former putts the performance of classifier, SVMs, into consideration in feature selection. And the characteristic of ICA, rapid convergence to global optimum, ensures that better feature subset can be got in limited number of generalizations using ICA than GA.

4 Conclusion

A wrapper feature selection based on ICA for SVM is proposed and is applied to 1-D images recognition of radar targets. Because the k-fold cross-validation technique used in wrapper feature selection has lower bias in generalization error for SVMs and the ICA can converge to global optimum rapidly, the most discriminative attributes of 1-D images of radar targets are selected before classification using SVMs though the wrapper feature selection is more time-consuming than filter one. The validity of the method is well verified by 3 airplanes data.

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