Classification of Faults in Nuclear Power Plant

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Abstract: - In this paper, the performance of traditional Support Vector Machine (SVM) is improved using Genetic Algorithm (GA). GA is used to determine the optimal values of SVM parameters that assure highest predictive accuracy and generalization ability simultaneously. The proposed scheme, called Support Vector Machine Genetic Algorithm (SVM-GA) Scheme, is applied on a beforehand data of a Nuclear Power Plant (NPP) to classify its associated faults. Compared to the standard SVM model, simulation of SVM-GA indicates its superiority when applied on the dataset with unbalanced classes. SVM-GA scheme can gain higher classification with accurate and faster learning speed.

Key-Words: - Support Vector Machine (SVM), fault classification, multi fault classification, Genetic Algorithm (GA), machine learning.

1 Introduction

Research in machine learning has continued to benefit diverse communities including process engineering. Several machine-learning algorithms like support vector machines, face recognition [1], spam categorization [2-3], have found recent applications in data driven modeling, classification and process fault detection [4]. Incorporation of prior knowledge has considerably enhanced the performance of many of these algorithms [5-9]. Prior knowledge has been incorporated in Support Vector Machine Algorithm (SVM-GA) classification algorithm and has been used successfully in faults classification applications [10]. Support Vector Machine Genetic Algorithm (SVM-GA) is introduced in this paper and is exemplified by solving the problem of fault classification in Nuclear Power Plant NPP. There are as many as thirty variables in the process such as pressure, temperature, flow that can be monitored over a period of time. The data reflects a good amount of variability and represents the dynamics of the process. The problem of classifying faults in NPP is tackled in this paper. Various faults in NPP system are generated with the aim to classify them as accurately as possible based on the knowledge of the dataset. This paper investigates the use of GAs [11] to automatically tune the parameters of the binary SVMs contained in common decomposition strategies. Thus, the parameter adjustment problem was formulated as a search for combinations of parameter values able to minimize the error rates obtained in the multiclass problem solution. GA searches for a set of parameter values which will be common to all classifiers in the decomposition. The rest of the paper is organized as follows: Section 2 provides a background of SVM and its application. The data creation of the NPP is scrutinized in section 3. Detailed SVM and GA mathematics are reviewed in section 4. Proposed SVM-GA scheme is described in section 5. Selection of SVM-GA parameters are presented in section 6. Experimental results are discussed in section 7. Finally conclusions are given in section 8.

2 BACKGROUND

Support Vector Machine (SVM) is a relatively new soft computing method based on statistical learning theory [12]. In SVM, original input space is mapped into a high dimensional dot product space called feature space in which the optimal hyper-plane is determined to maximize the generalization ability of the classifier. The optimal hyper-plane is found by exploiting a branch of mathematics, called optimization theory, and respecting the insights provided by the Statistical Learning Theory (SLT), [13]. SLT is based on structure risk minimization and it has a good learning ability even though fewer learning samples are used.   Recently, SVM is widely used in many realms, such as face recognition, nonlinear equalization, and spam categorization. In fault diagnosis area, some researches also have been performed, [14-19]. SVM based fault classifiers are claimed to have better generalization properties than Artificial Neural Network (ANN) ones [20]. SVM was originally designed for binary classification, which is not

suitable for fault diagnosis, because it has several fault classes in addition to health condition. The main aim of an SVM classifier is obtaining a function f(x), which determines the decision boundary or hyper-plane. Kernel-Adatron algorithm was proposed in [21], which could automatically create the decision hyper-plane without testing on a validation data. Unfortunately, this algorithm is ineffective if the data have a flat ellipsoid distribution. Therefore, one possible way to solve the problem is to consider the distribution of the data. Interestingly, various specific functions in SVM, after the learning stage can create the decision hyper-plane of the same type. To solve such a problem, a systematic method for selecting SVM parameters was provided in [22].

3. DATA SET CREATION

The NPP can be subjected to many failures which can affect almost all its state variables. In this study, 30 types of different faults are simulated. Since the performance of any statistical method depends solely on the datasets on which it is trained, it is advisable that datasets should be created such that all possible dynamics of the state variables are captured. The selected features should be as decorrelated as possible to avoid the problem of multicollinearity. To investigate the performance of the proposed algorithm, we use the mathematical model of the Pressurized Water Reactor (PWR) NPP, based on a neurotic process and thermal hydraulic process with the components: reactor core, pressurizer, pump, and steam generator. The list of PWR state variables is given in Table 1. The Simplified block diagram for dynamic model of the primary first loop of the PWR shown in Fig. 1 is implemented to generate the closed loop simulated process data for the different faults as shown in Table 2.

To investigate the proficiency of the proposed technique in classifying multiple faults, three types of faults are considered as described in Table 2. Total of 302 points are selected (which represents the true dynamics of the related state variables) amongst which train and test partitions are made (192 and 110, respectively).

Table 1: List of PWR state variables

TPi	Primary water inlet plenum temp.
TP1	First primary water lump temp.
TP2	Second primary water lump temp.

TP3	Third primary water lump temp.
TP4	Fourth primary water lump temp.
TPo	Primary water outlet plenum temp.
TM1	First tube metal lump temp.
TM2	Second tube metal lump temp.
TM3	Third tube metal lump temp.
TM4	Fourth tube metal lump temp.
THL	Hot Leg Average Temp.
TCL	Cold Leg Average Temp.
TUP	Upper Plenum Average Temp.
TLP	Lower Plenum Average Temp.
Td	Down comer Average Temp.
TF	Fuel Average Temp.

Table 2: Description of considered faults in PWRNPP

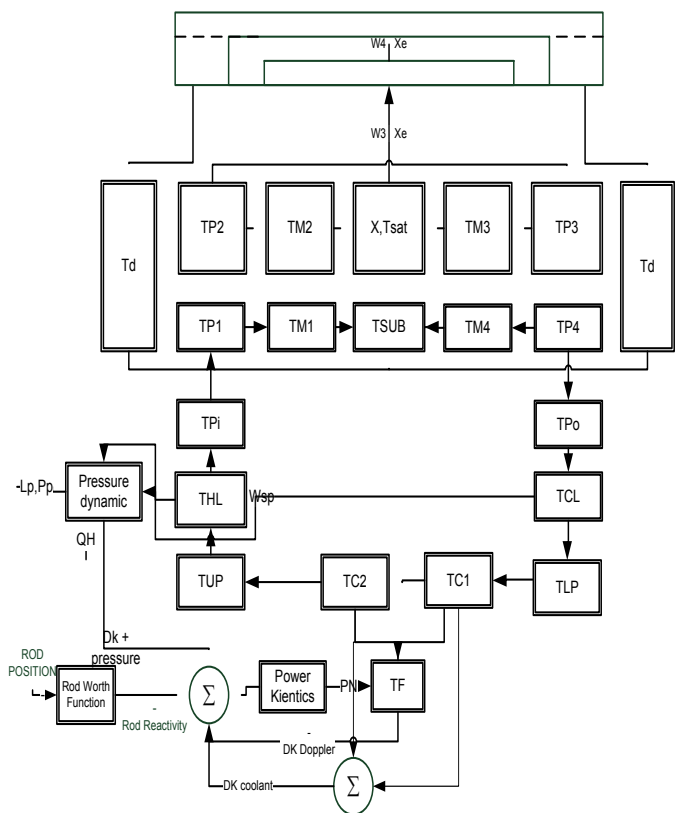| Fault	Type of fault
Fault 1	Step change in reactivity 0.20C
Fault 2	Step change in Inlet Temp. 4F
Fault 3	Step change in feed water Temp. 10F

Fig.1: Simplified block diagram for dynamic model of the primary first loop of the PWR

4. The proposed Approach

The following sections will present both Support Vector Machine, SVM, and Genetic Algorithm, GA.

4.1   Super Vector Machine, SVM

SVM is an effective approach for pattern recognition. The basics of the SVM are found in [13]. For the two classes problem, we assume that we have a dataset, which given m as the amount of the labeled training samples, x_i are the training samples while y_i are the targets or labels in n-dimensional space as:

$$\{x_i, y_i, x_i \in R^n, y_i \in \{-1,1\}, i = 1...m\} \qquad (1)$$

In SVM, the results in a linearly separable problem correspond to a decision function:

$$f(x) = \mathrm{sgn}((w.x) + b) \qquad (2)$$

The set of samples is said to be optimally separated by the hyper-plane if it is separated without error and the margin is maximum, this hyper-plane bisects the shortest line between the convex hull of the two classes, thus, it must satisfy the following constrained minimization as:

$$\min(\frac{1}{2}w^T.w), \ y_i(w.x) + b \ge 1 \qquad (3)$$

This hyper-plane can be constructed by solving quadratic optimization problem which is the solution of w and expand with $w = \sum_i \alpha_i y_i x_i$ in terms of a subset of training pattern that lies on the margin. These training patterns are called support vectors, which provide the important information of classification problems. Then, the decision function can be formulated as:

$$f(x) = \mathrm{sgn}(\sum_i \alpha_i y_i (x.x_i) + b) \qquad (4)$$

For the linearly non separable case, a modification on previous minimization problem needs to be done to recover the misclassification data points. A new penalizing error variable is introduced; ε as the measurement of violation on the constraints:

$$\min\left(\frac{1}{2}w^T.w + C\sum_i^l \varepsilon_i\right), \ y_i(w.x) + b \ge 1 - \varepsilon_i \qquad (5)$$

C is used to weight the penalizing parameter. SVM separates a non-linear separable classification problem by mapping the data into a feature space via a non-linear map. This solution is done by using kernel, K. By using a suitable kernel, the non-linear

separated samples input space will be turn out to be linearly separated after being mapped in feature space. The decision boundaries function for non-linear problems can be formulated as:

$$f(x) = \sum_i \alpha_i y_i K(x, x_i) + b \qquad (6)$$

There are a lot of kernel functions. Some of them are shown in Table 3. Any type of kernel can be chosen according to experiments as it is dependent on the sample data.

Table 3: Types of kernel functions

Kernel function	Classifier
$K(x, x_i) = \exp(- \|x - x_i\|^2 / 2\sigma^2)$	RBF
$k(x.x_i) = (x^T.x_i + 1)^d$	Polynomial
$k(x.x_i) = (x^T.x_i)$	Linear

4.1.1 Multiclass SVM

The original SVM is binary classification method, i.e., it classifies the two-classes problems. However, fault classification requires multiclass classification. There are two methods for multi-classes. One is 'one to one' algorithm, [23]. This algorithm constructs all two-class SVM classifiers between any two classes so
k(k-1)/2 two-class SVM classifiers can be constructed in all for a case of k classes. In the recognition stage, a new sample x is input to the classifier between m class and n class:

$$f^{mn}(x) = \mathrm{sgn}\left\{\sum_{i=1}^l \alpha^{mn} y^{mn} K(x, x_i) + b^{mn}\right\} \qquad (7)$$

If the classifier shows that x belongs to m class, then a ballot is cast for the m class. After recognized by all these k (k-1) / 2 classifiers, x can be judged to belong to the class that has the most ballots. Some disadvantages of this algorithm are: (1) the number k(k-1)/2 of two-class SVM classifiers increases greatly with the class number k, calculation increases greatly as well, and the rate of training and recognition is very slow; (2) when two or more classes have the same ballots, it is hard to judge which class the new sample x belongs to; (3) there is at least a class whose ballots are the most, so a new sample x that does not really belong to any of these k classes would be misjudged to belong to them and the classifying error appears.

The other sub-method is 'one to all' algorithm, [24]. This algorithm takes any one class m of these k classes as a category, takes the rest k - 1 classes as another category, constructs a two-class SVM classifier and names it SVM m. In this way, k two-class SVM classifiers can be constructed in all for a case of k classes. The classifying function of SVM m is:

$$f^m(x) = \text{sgn}\left\{ \sum_{i=1}^{l} \alpha^m y^m K(x, x_i) + b^m \right\} \qquad (8)$$

In the recognition stage, the new sample x is input to all these k classifiers. There are k outputs in all. In this classifier, 1 class represents (class 1) and 0 class represents (classes 2 and 3). Unlike one to one classifier, all data are used in each classifier. To classify an observation, y_{pred} is determined for all classifiers. The test point is identified as the class with maximum y_{pred}, which is class 1 in this example. The new sample x is judged to belong to the class whose classifier has the largest output. Some disadvantages of this algorithm are: (1) all samples have to be taken into the training of all these k classifiers; in the recognition stage, only after all these k classifiers have recognized, the new sample x can the classification result be obtained. Therefore the calculation is very time-consuming and the rate of training and recognition is slow as well; (2) there is at least a two-class SVM classifier whose output is the largest, so a new sample x that does not really belong to any of these k classes would be misjudged to belong to them and the classifying error appears; (3) when two or more classifiers have the same outputs, it is hard to judge which class the new sample x belongs to.

We present multi-class SVM algorithm here. It is called 'one to others' algorithm [25]. For a data set of k classes:

$$(x_i, y_i), i = 1, 2, \ldots l, x_i \in R^d, y_i \in \{1, 2, \ldots k\}, \qquad (9)$$

Where l is sample number, d is dimension of sample vector, k is class number. First, we have a case of k classes, take a top-priority class from these k classes as a category, and take the rest (k - 1) classes as another category, construct a two-class SVM classifier and name it SVM 1; Next, this top-priority class is excluded, and then we have a case of k - 1 classes, take a top-priority class from those k -1 classes as a category, and take the rest k-1-1 classes as another category, and construct a second two-class SVM classifier and name it SVM 2, and so on and so forth till the last two-class SVM classifier is constructed and named SVM k - 1. In

this way, k- 1 two-class SVM classifiers can be constructed in all for a case of k classes. In the fault diagnosis, the most common or the most dangerous fault can be given top priority. The 'one to others' multi-class SVM classifier is a binary tree composed of several two-class SVM classifiers organized by fault priority as shown is Fig. 2.

GA is a stochastic search algorithm modeled on the process of natural selection, which underlies biological evolution [26]. GA has been successfully applied in optimization and machine learning problems, [27-30]. GA evolves a population of chromosomes as potential solutions to an optimization problem. There are three major design decisions to consider when implementing a GA to solve a particular problem. A representation for candidate solutions must be chosen and encoded on the GA chromosome, fitness function must be specified to evaluate the quality of each candidate solution, and finally GA run parameters must be specified including which genetic operators to use.

4.2 Genetic Algorithm (GA)

The genetic algorithms (GAs) are stochastic adaptive algorithms whose search method is based on simulation of natural genetic inheritance and Darwinian strive for survival. They can be used to find approximate solutions to numerical optimization problems in case where finding an exact optimum is prohibitively expensive. The following sub-sections briefly discuss GA operators.

4.2.1 Initial population

In general, the initial population is generated randomly. In this way, however, we will end up with a population where each individual contains the same number of 1s and 0's on the average. To explore subsets of different numbers of features, the number of 's for each individual is generated randomly. Then, the 's are randomly scattered in the chromosome.

4.2.2 Mutation

Mutation is the genetic operator responsible for maintaining diversity in the population. Mutation operates by randomly "flipping" bits of the chromosome, based on some probability. This probability should usually be set fairly low. If it is set to high, the search will turn into a primitive random search.
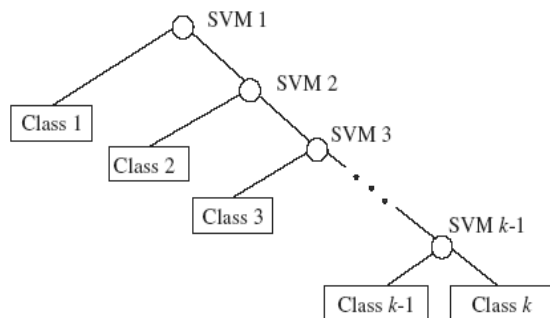
Fig.2: Framework of the 'one to others' SVM algorithm.

4.2.3 Crossover

Crossover is a genetic operator that allows new solution regions in the search space to be explored. It is a random mechanism for exchanging genes between two chromosomes using the one point crossover, two point crossovers, or homologue crossover. Offspring replaces the old population using the elitism or diversity replacement strategy and forms a new population in the next generation. Genetic crossover and mutation operation is shown in Fig. 3.
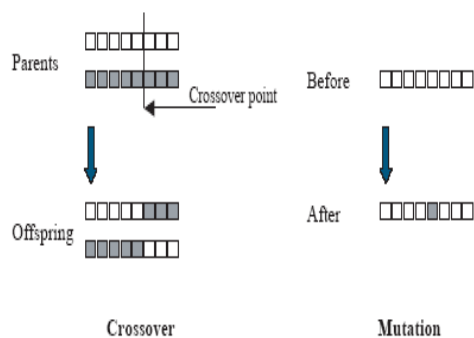
Fig.3: Genetic crossover and mutation operation

4.2.4 Replacement

Replacement schemes determine how a new population is generated. The concept of overlapping populations is used in this work, where parents and offspring are merged, and the best individuals from this union will form the next population.

4.2.5 Selection

This is the process of choosing parents for reproduction. Usually, it emphasizes the best solutions in the population, but since the replacement scheme employed here already offers enough evolutionary pressure, a random selection approach was chosen.

4.2.6 Random immigrant

This is a method that helps to keep diversity in the population, minimizing the risk of premature convergence works by replacing the individuals whose fitness is under the mean by recently initialized individuals [31]. Random immigrant is invoked when the best individual does not change for a certain number of generations.

4.2.7 Fitness function

The main goal of feature selection is to use fewer features to obtain the same or better performance [30]. Fitness function is one of the most important parts in genetic search. This function is used to evaluate the effectiveness of each individual in a population, so it has an individual as an input and it returns a numerical evaluation that must represent the goodness of the feature subset. The search strategy's goal is to find a feature subset maximizing this function. The crossover and mutation functions are the main operators that randomly impact the fitness value.

5. Proposed Hybrid approach, SVM based on GA

The selection of the SVM parameters plays an important role in the performance of SVM. To design an effective SVM model, values of parameters in SVM have to be chosen carefully in advance [32]. The SVM with RBF includes the following parameters:

a- Regularization parameter C, which determines the trade-off cost between minimizing the training error and

minimizing the complexity of the model [33-37] ;

b- Parameter sigma (σ) of the kernel function which defines the non-linear mapping from the input space to some high-dimensional feature space, which constructs a non-linear decision hyper surface in an input space;

c- Parameter ε is non-negative slack variables and provides the minimum training error.

In this study, GA is used to determine the optimal values of C, σ and ε that assure highest predictive accuracy and generalization ability simultaneously. The proposed model is named SVM-GA. Since three parameters should be optimized, the chromosome should comprise three parts, C, σ and ε as shown in Fig. 4, where the binary coding system was used to represent it.

A fitness function, assessing the performance of each chromosome, should be defined. Many forecasting performance indices can be used as fitness function, such as MSE (Mean-Squared Error), RMSE (Root-Mean-Squared Error), MAE (Mean Absolute Error), and MAPE (Mean-Absolute Percent Error). In this research, ROCC (Rate of Correct Class) is employed as the performance measure. It is defined as:

$$\text{ROCC} = -\frac{1}{l}\left(\sum_{1}^{l}|y_i - y_t|\right) * 100\% \qquad (10)$$

Where l is the number of training data, y_i is the actual output, y_t is the expected output. The scheme of the proposed SVM-GA used to classify NPP (PWR) faults is shown in Fig. 5.

The model with minimum value of ROCC is the most appropriate one, so the optimal model with the maximum value of the fitness function should be obtained.
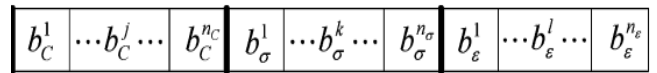

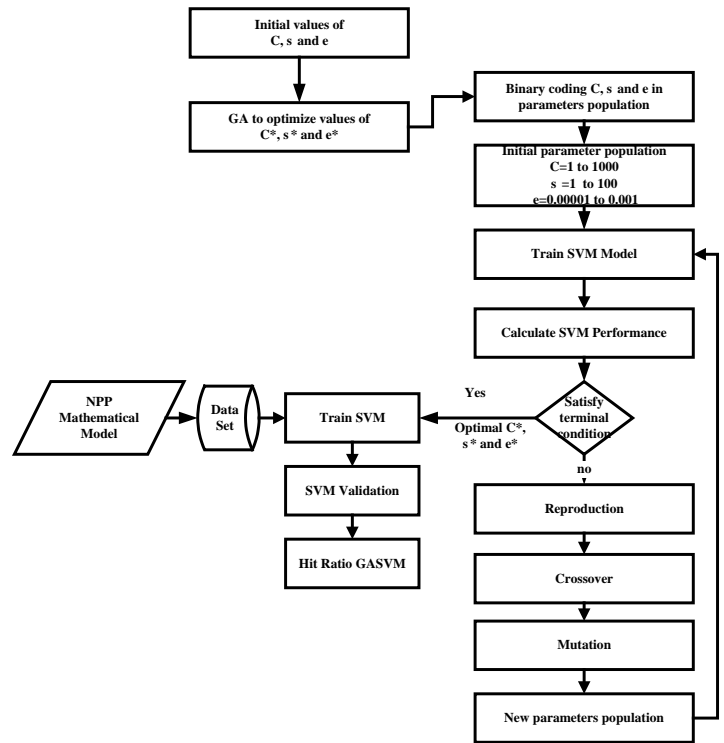Fig. 4: The chromosome comprises three parts C, σ and ε

Fig. 5: The scheme of the proposed SVM-GA.

6. Selection of SVM-GA Parameters

A chromosome of GSVM represents a value of C parameter; a value of kernel parameter σ, and the value of ε parameter, a chromosome of SVM-GA consists of 12 bits (genes). The value of C parameter part of a chromosome in SVM-GA is represented by 4 bits. The value of RBF kernel parameter part of a chromosome in GSVM is represented by 4 bits. The value of ε parameter part of a chromosome 4 bits. The operational processes of the GSVM approach can be arranged as the initial population of SVM-GA is consisted of 100 chromosomes, Probability of crossover = 0.7, Probability of mutation=0.3, adjustable range of $C = 1 \rightarrow 1000$, adjustable range of $\sigma = 1 \rightarrow 100$ and the adjustable range of ε $\varepsilon = 0.00001 \rightarrow 0.01$.

7. Experimental Results and Discussions

The multi-fault classifier is trained by 192 training samples, which includes 3 fault classes. The faults and fault number are shown in Table 2. To investigate the proficiency of SVM-GA for classifying multiple classes that are overlapping, NPP simulator was used to generate three classes of faulty data, which correspond to faults 1, 2, and 3 specified by the NPP (Table 2). Faults 2 and 3 are selected because both faults are associated with reactor cooling water inlet temperature, but they are different in terms of type of fault (Step change in Inlet Temp. 4F and step change in feed water Temp. 10F). Fault 1 is associated with criticality of the reactor. These three faults are good representation of overlapping data. For each faulty case, two sets of data were generated. The training data were used to build the models and the testing data were used to validate the model. The training and testing data contain 192 and 110 observations, respectively. Each observation contains 30 process variables. However, only variable 7 (Parallel flow first tube metal lump) and variable 15 (down comer Average temperature) are important in terms of distinguishing the three classes as shown in Fig.9, Fig. 10 and Fig. 11. It makes sense in engineering perspective because faults 2 and 3 are associated with reactor temperature, while fault 1 is associated with reactivity of the reactor, which also affects the reactor temperature. The rest of the 30 variables do not provide important information in terms of classification (i.e. no differences in these 30 variables are observed for faults1, 2, and 3 training and testing datasets). To assess the effectiveness of our proposed method (one to other), we performed a critical comparison with several multi classification methods as shown in Fig. 6, Fig. 7, and Fig. 8.

Our proposed method outperforms all of the other methods. We have described a hybrid GA-SVM multi-class classifier with application to NPP faults classification. Emphasis is placed on the selection of three important SVM

parameters. This hybrid system harnesses the capability of a standard GA to search for the best value for the SVM Gaussian kernel parameter and SVM feature parameters, using the optimized parameters, have shown very good classification results on the 3-class data sets, with average accuracy of at least 95.3125%.
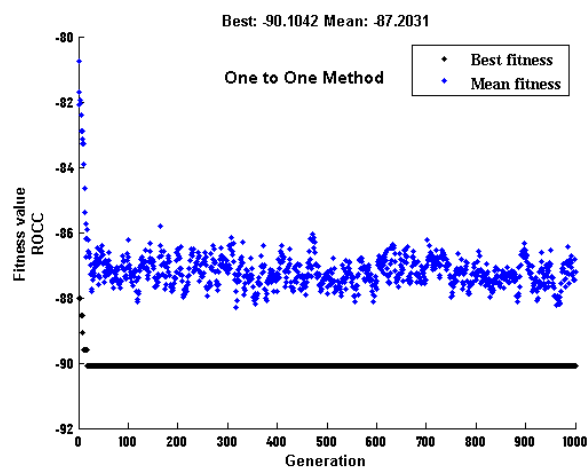

Fig. 6: the best fitness value vs. the number of generations in the GA for one to one method
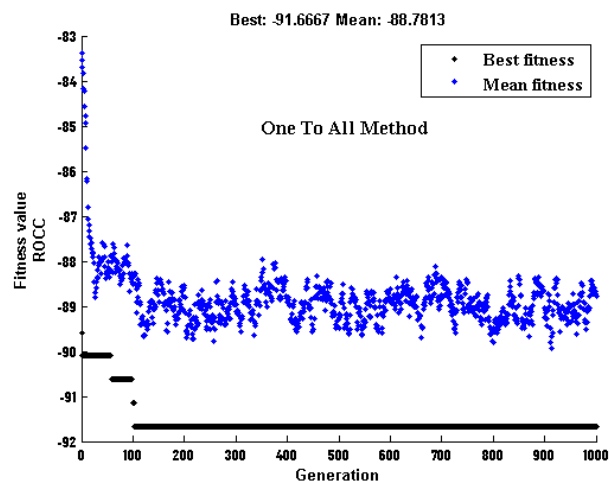

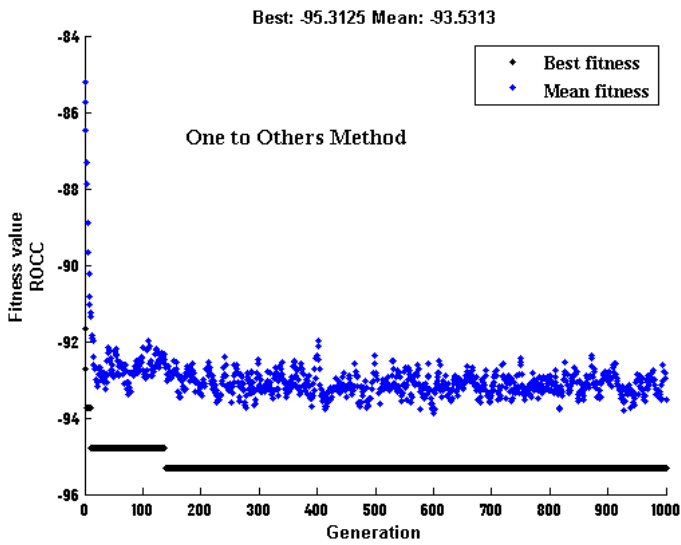Fig. 7: the best fitness value vs. The number of generations in the GA for one to all method

Fig. 8: the best fitness *value vs. the number of generations in the GA for one to other method*
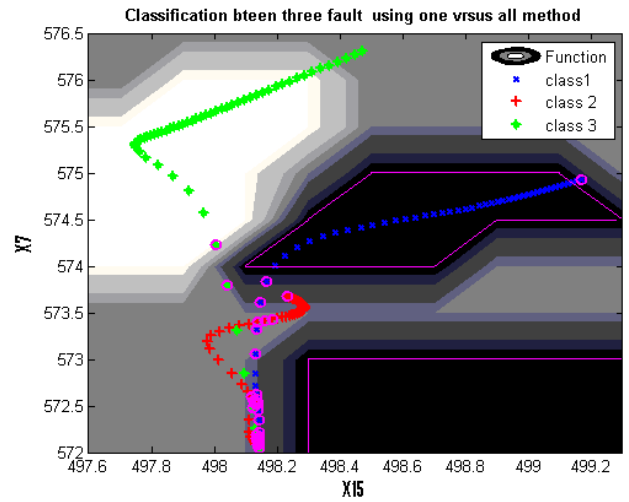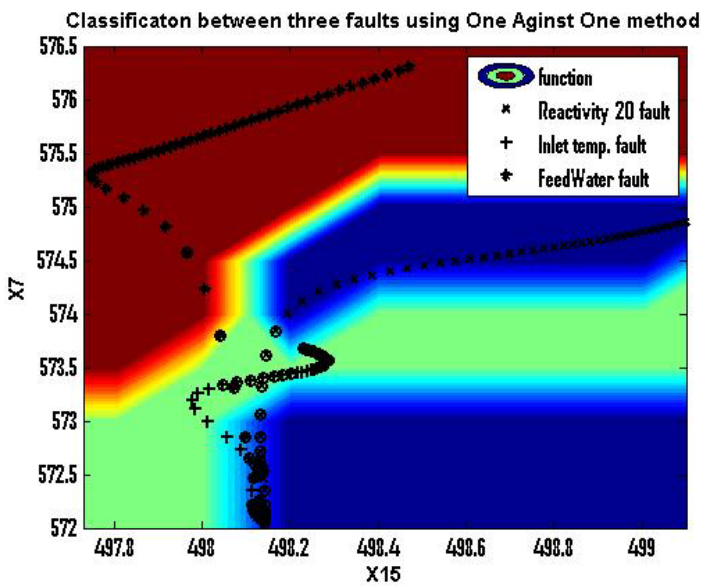

Fig. 9: Classification between three faults by Gaussian function using one versus one method

Fig. 10: classification between three faults by Gaussian function using one versus all method method
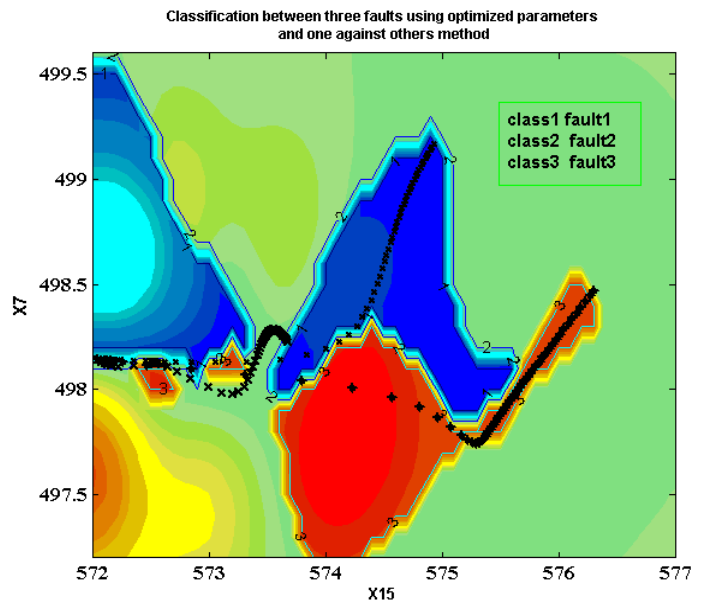

Fig. 11: Classification between three faults by Gaussian function using one to other one

Table 4: The comparison Among the three methods

Classification method	One to One +GA	One to All + GA	One to Other +GA
Training data	192	192	192
Testing data	110	110	110
SVM kernel	RBF	RBF	RBF
Optimized σ parameter	1.1	1.1	1.2
Optimized ε parameter	0.001	0.004	0.002
Optimized C parameter	880.9	291.8	789.6
No. of classifiers	3	3	2
Rate Of Correct Class (ROCC)	90.1%	91.6%	95.3%

Finally the classification task was done and evaluated. We tested and compared SVM-GA system to the different methods, one to one method and one to all method. As shown in table 4, the optimal method is one to other because the rate of training and testing is very high, the computation time is very low, the rate of correct class very high and the number of classifiers less than the other method. The optimal parameters (C, σ, ε) are (789.6, 1.2, 0.002) and the optimal ROCC is 95.3%.

8 Conclusion

In our work, we proposed a framework for NPP fault classification based feature extraction using SVM-GA for feature selection. To assess the effectiveness of our proposed method (one to other), we performed a critical comparison with several multi classification methods. Our proposed method outperforms all of the other methods. We have described a hybrid SVM- GA multi-class classifier with application to the nuclear power plant faults classification. Emphasis is placed on the selection of three important SVM parameters. This hybrid system harnesses the capability of a standard GA to search for the best value for the SVM Gaussian kernel parameter and SVM feature parameters, using the optimized parameters, have shown very good classification results on the 3-class data sets, with average accuracy of at least 95.3%. Finally the classification task was done and evaluated. We tested the SVM-GA system to the different methods for one to one method and one to all method. The optimal method is one to other method and the optimal parameters (C, σ, ε) are (789.6, 1.2, 0.002) and the optimal ROCC is 95.3%.

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