Chapter 2
A Medical Decision Support System Based on Ensemble of Complex-Valued Radial Basis Function Networks

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ABSTRACT

The use of machine learning techniques for medical diagnosis has become increasingly common in recent years because, most importantly, the computer-aided diagnostic systems developed for supporting the experts have provided effective results. The authors aim in this chapter to improve the performance of classification in computer-aided medical diagnosis. Within the scope of the study, experiments have been performed on three different datasets, which include heart disease, hepatitis, and BUPA liver disorders datasets. First, all features obtained from these datasets were converted into complex-valued number format using phase encoding method. After complex-valued feature set was obtained, these features were then classified by an ensemble of complex-valued radial basis function (^{E}CVRBF) method. In order to test the performance and the effectiveness of the medical diagnostic system, ROC analysis, classification accuracy, specificity, sensitivity, kappa statistic value, and f-measure were used. Experimental results show that the developed system gives better results compared to other methods described in the literature. The proposed method can then serve as a useful decision support system for medical diagnosis.

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INTRODUCTION

In medical diagnostics, diagnosis of a disease is performed with considering patient's data. However, the increase in the data density and the excessive number of symptoms affecting the disease complicate diagnostic procedures. Amongst one of the most popular topics to emerge in recent years is the use of computers in medical diagnostic. Computer-aided medical diagnostic systems have been developed to help specialists, with such systems aiming to minimising the physician error. Computer-aided classification systems can minimise the potential errors. In addition, these systems facilitate and accelerate in-depth examination of medical data (Cheung, 2001; Das, 2010).

In order to test the effectiveness of newly developed computer-aided medical diagnostic systems, researchers are conducting experiments on datasets that are open to common use. The hybrid method proposed in this study has been tested with three datasets. Those are Statlog heart disease, BUPA liver disorders, and Hepatitis datasets, which are obtained from the UCI machine learning repository (Bache & Lichman, 2013). The common characteristic of these datasets is having a distribution which cannot be separated linearly. There is also a large amount of missing data on the Hepatitis dataset. Information about some of the earlier studies carried out on these datasets is given below.

In the literature, some studies performed on the Statlog heart disease dataset are as follows: Based on many attempts, Cheung (2001) has achieved the highest classification accuracy (81.48%) using the Naive Bayes algorithm among a number of other classification algorithms. Kahramanli and Allahverdi (2008) have achieved 86.8% accuracy rate by using a fuzzy neural network algorithm. Das et al. (2009) have developed an ensemble algorithm which includes three neural networks and an 89.01% classification accuracy has been obtained with the proposed model. Subbulakshmi et al. (2012) have achieved an 87.50% classification accuracy by using the extreme learning machine (ELM) method. Karabulut and Ibrikci (2012) have developed a method based on a rotation forest algorithm, and a 91.20% classification accuracy has been obtained with the proposed method.

In the literature, some studies that have been carried out on the Hepatitis dataset are as follows: Javad et al. (2012) have developed a hybrid method (SVM-SA) which includes SVM and simulated annealing (SA) algorithms. They have obtained a 96.25% accuracy rate. Shao et al. (2015) have proposed a weighted linear loss twin SVM for large-scale classification. They have obtained an 84.99% accuracy rate with the method. Aldape-Pérez et al. (2012) have developed a novel method referred to as an associative memory based classifier (AMBC) and an 85.16% classification accuracy has been obtained. Bashir et al. (2016) have developed an ensemble method

with multi-layer classification using optimized weighting and enhanced bagging, and an 87.04% classification accuracy has been obtained with the method which is entitled HM-BagMoov.

In the literature, some studies have been carried out on the BUPA liver disorder dataset for the identification of liver disorders as follows: Goncalves et al. (2006) have developed a new neuro-fuzzy method entitled the inverted hierarchical neuro-fuzzy BSP System (HNFB). A 73.33% classification accuracy has been obtained using this method. Jin et al. (2007) have proposed a genetic fuzzy feature transformation method for SVMs. They have achieved a 70.80% accuracy rate. Lee and Mangasarian (2001) have developed smooth SVMs (SSVM) and reduced SVMs (RSVM) classifier methods. Using these methods, they have achieved 70.3% and 74.8% accuracy rates, respectively. Chen et al. (2012) have developed a hybrid method in which the 1-NN method and particle swarm optimization (PSO) are used together. A 68.99% classification accuracy has been obtained with the proposed hybrid method. Dehuri et al. (2012) have developed an enhanced PSO-based evolutionary functional link neural network (ISO-FLANN). A 76.8% classification accuracy has been achieved with the method. Shaoa and Deng (2012) have developed a coordinate descent margin based-twin SVM. They have obtained 73.67% classification accuracy with the method. Savitha et al. (2012) have developed a fully complex-valued radial basis function (FC-RBF) network. A 74.6% accuracy rate has been achieved with the proposed method. Mantas and Abellán(2014) have developed an algorithm entitled Credal-C4.5. A 64.53% classification accuracy has been achieved with the Credal-C4.5 method which involves a decision tree based on imprecise probabilities. López et al. (2014) have developed an SVM based method. In this method, a multivariate normalization algorithm was used to train the SVM algorithm. A 72.17% classification accuracy has been achieved with the method.

Recently, the use of complex-valued classifiers for real-valued classification problems is one of the most important research topics (Savitha, Suresh & Sundararajan, 2012; Amin, Islam & Murase, 2009). Complex-valued classifiers have been utilised in the classification stage of many studies, since they provide good results (Peker, 2016; Savitha, Suresh &Sundararajan, 2012; Amin & Murase, 2009; Amin, Islam & Murase, 2009; Li, Huang, Saratchandran & Sundararajan, 2006; Chen, Mclaughlin & Mulgrew, 1994). In this study, a new hybrid method, an ensemble version of a complex-valued radial basis function algorithm has been developed. Bagging and boosting methods have been used as an ensemble algorithm. We believe that the proposed method provides an important contribution to the literature relating to complex-valued classifiers.

The rest of the paper is organized as follows. In Section Materials and Methods, information is presented about the datasets and methods used in the study. The

experimental results and discussion section is given in Section Experimental Results and Discussions. In addition, a comparison with the existing methods in the literature have been carried out in this section. General information about the obtained results is presented in Section Conclusion.

MATERIALS AND METHODS

Data Description

Studies have been carried out on three different datasets in order to evaluate the success of the proposed method. The datasets have been taken from the UCI Machine Learning Repository (Bache & Lichman, 2013). These datasets are related to heart, Hepatitis, and liver disorders. The Statlog heart disease dataset relates to 270 people (Bache & Lichman, 2013). The data of 120 of these relate to healthy individuals and 150 relate to patients. The features of this dataset have been presented in Table 1.

The Hepatitis disease dataset was donated by the Jozef Stefan Institute in Slovenia (Bache & Lichman, 2013). The dataset is used to estimate the existence or absence of Hepatitis, based on different medical tests carried out on a patient. The dataset is comprised of 155 samples with 19 features. Target features have been coded as 1 for survivors (123) and 0 for the patients who died (32). Approximately 48.30% of the dataset contains missing value. Features in the dataset have been presented in Table 2.

The BUPA liver disorders dataset contains 345 samples with 6 features and two classes (Bache & Lichman, 2013). Samples are all unmarried men. 200 of these

Table 1. The features of the Statlog heart dataset

ID	Feature	ID	Feature
1	Age	8	Maximum heart rate achieved
2	Sex	9	Exercise induced angina
3	Chest pain type (four values)	10	Old peak = ST depression induced by exercise relative to rest
4	Resting blood pressure	11	The slope of the peak exercise ST segment
5	Serum cholesterol in mg/dl	12	Number of major vessels (0–3) colored by fluoroscopy
6	Fasting blood sugar >120 mg/dl	13	Thal: 3 = normal; 6 = fixed defect and 7 = reversible defect
7	Resting electrocardiographic results (values 0, 1 and 2)		

Table 2. The features of the Hepatitis disease dataset

Feature Number	Feature Description	Values
1	Age	10, 20, 30, 40, 50, 60, 70, 80
2	Sex	Male, Female
3	Steroid	No, Yes
4	Antivirals	No, Yes
5	Fatigue	No, Yes
6	Malaise	No, Yes
7	Anorexia	No, Yes
8	Liver Big	No, Yes
9	Liver Firm	No, Yes
10	Spleen Palpable	No, Yes
11	Spiders	No, Yes
12	Ascites	No, Yes
13	Varices	No, Yes
14	Bilirubin	0.39, 0.80, 1.20, 2.00, 3.00, 4.00
15	Alk Phosphate	33, 80, 120, 160, 200, 250
16	Sgot	13, 100, 200, 300, 400, 500
17	Albumin	2.1, 3.0, 3.8, 4.5, 5.0, 6.0
18	Protime	10, 20, 30, 40, 50, 60, 70, 80, 90
19	Histology	No, Yes

data have been taken from healthy people with no liver disorder. The remaining 145 samples have been obtained from individuals with liver disorder. Five features are blood test results and daily alcohol consumption. Features in the dataset are presented in Table 3.

Table 3. The features of the BUPA liver disorder dataset.

Feature Number	Feature Description	Values
1	MCV (mean corpuscular volume)	Numeric value
2	Alkphos (alkaline phosphatase)	Numeric value
3	SGPT (alanine aminotransferase)	Numeric value
4	SGOT (aspartate aminotransferase)	Numeric value
5	Gamma GT (gamma-glutamyltranspeptidase)	Numeric value
6	Drinks (number of half-pint equivalents of alcoholic beverages drunk per day)	Numeric value

Complex-Valued Radial Basis Function Networks (CVRBF)

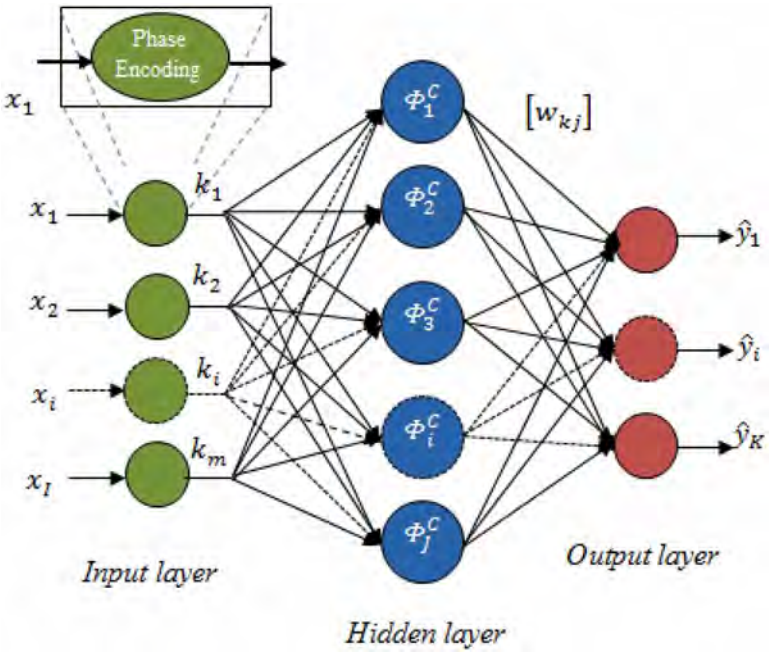
CVRBF was first proposed by Chen et al. (1994). Initially, it was applied to a non-linear signal processing, which includes complex signals. After this, it was used in different classification problems which have complex and real-valued input features (Chen et al., 2008; Babu, Suresh & Savitha, 2012; Savitha, Suresh & Sundararajan, 2012). CVRBF is the complex-valued version of the real-valued RBF neural network. It is structurally similar to the RBF neural network except that the parameters are complex-valued here. The CVRBF sample with a single hidden layer is given in Figure 1.

A complex-valued input data can be represented as shown in Equation (1). Here, the input value is composed of real and imaginary values.

$$x^C = x_R + ix_I \tag{1}$$

where $\mathrm{i} = \sqrt{-1}$. x^C is the complex input value, x_R is the real value and x_I is the imaginary value. Real-valued feature values in the input layer are normalized between the range of [0, 1] at the initial phase. Normalisation formula has been given in Equation (2).

Figure 1. Structure of the CVRBF classifier



$$x_i^C = \frac{x_i - x_{(min)}}{x_{(max)} - x_{(min)}} \tag{2}$$

where x_i is the input value. $x_{(min)}$ is the minimum and $x_{(max)}$ is the maximum value. At this stage, as can be seen in the attached small picture in Figure 1, normalised values are converted to complex space with phase encoding [0, π] by using the equation '$exp\left(i\pi x\right)$'. The phase encoding method, which assures the conversion of real-valued input values to complex valued number format, has been given in Equation (3).

$$a_i^C = exp\left(i\pi x_i^C\right) \tag{3}$$

where x_i^C is the real-valued input feature normalised between the range of [0, 1]. a_i^C is the complex-valued input feature calculated based on x_i^C.

The example has been given in Figure 1 is a hidden layer with CVRBF structure. The CVRBF has 'j' hidden neurons. These hidden neurons in the hidden layer have a real radially symmetric response around the node centre. The centres of hidden nodes are some of the complex vectors in the input domain. The non-linearity of hidden node is a real function. Equation (4) is used to determine the response of each hidden node.

$$\Phi_j^C = exp\left(-\frac{1}{\sigma_j^2}\left(a_i^C - c_j^C\right)^H \left(a_i^C - c_j^C\right)\right) \tag{4}$$

where σ_j is the width of Gaussian function. a_i^C represents i th complex-valued input vector. c_j^C is the complex-valued centre of gravity of jth Gaussian CVRBF. $\left(\bullet\right)^H = \left(\left(\bullet\right)^T\right)^*$ operator is the Hermitian operation. $\left(\bullet\right)^T$ indicates vector or matrix transpose, while $\left(\bullet\right)^*$ indicates complex conjugate.

The output value of each output neuron is computed as the linear total of weights from the hidden layer to the output layer and the response of each hidden layer neuron. In the study, weights are real-valued in the CVRBF neural network. The response of output neurons is also real-valued. Equation (5) is used for the response of the output neuron.

$$y_k = \sum_{j=1}^{J} w_{kj} \Phi_j^C = \sum_{j=1}^{J} w_{kj} exp\left(-\frac{1}{\sigma_j^2} \left(a_i^C - c_j^C \right)^H \left(a_i^C - c_j^C \right) \right) \tag{5}$$

where w_{kj} is linkage value between k th output neuron and j th hidden neuron. ϕ_j^C is the radial basis function of the j th hidden node.

The error function is given in Equation (6) for CVRBF.

$$e = e_R + ie_I = y^t - \hat{y}^t \tag{6}$$

where e_R and e_I are respectively real and complex components of complex-valued error value e, $\hat{y}^t$ is the calculated output value and y^t is the real output value. In this study, the mean squared error has been used as the error function. The error function is defined as Equation (7).

$$E = \frac{1}{2} \sum_{t=1}^{N} \left(e^{t^H} e^t \right) \tag{7}$$

where H denotes the complex Hermitian operator. To minimise the deviations of the mean squared error, a gradient descent-based learning algorithm has been used. Updating rules based on this learning algorithm are as follows.

$$\Delta v_{kj} = \mu_v e_k y_h^j ;\ k = 1,2,\ldots,n ;\ j = 1,2,\ldots,h \tag{8}$$

$$\Delta \sigma_j = \mu_\sigma y_h^j \left[\sum_{k=1}^{n} \left(v_{kj}^R e_k^R + v_{kj}^I e_k^I \right) \right] . \frac{z - c_j^{\ 2}}{\sigma_j^3} \tag{9}$$

$$\Delta c_j = \mu_c y_h^j \left[\frac{\sum_{k=1}^{n} \left[v_{kj}^R e_k^R \, re\left(z - c_j \right) + i v_{kj}^I e_k^I \, im\left(z - c_j \right) \right]}{\sigma_j^2} \right] \tag{10}$$

where μ_v, μ_c and μ_σ are, respectively, the learning rate parameters for weight, centre and width of Gaussian function. v_{kj}^R and v_{kj}^I are, respectively, the real and imaginary components of v_{kj} weight value.

Ensemble of CVRBF

When ensemble learning methods are used, a single decision is made for the ensemble by gathering the results revealed by multiple classifiers. These methods put the class estimations made by the many different classifiers through voting. As a result of this voting, the best rated class is then presented as class estimation of the ensemble.

Ensemble learning methods increase the accuracy rate of predictions revealed by basic or singular learning algorithms and, for this reason, they are usually more successful than singular/individual learning methods. Bagging and Boosting are the most known and studied ensemble learning algorithms amongst them (Breiman, 1996; Freund & Schapire, 1997). In this study, these two methods are used for the ensemble version of CVRBF algorithm. The ensemble of CVRBF is named as ^{E}CVRBF.

Bagging is basically a bootstrap ensemble algorithm (Das & Sengur, 2010). The bootstrap element ensures separation during training using copies of a dataset. In other words, it means extracting and using data subsets of the dataset by relocation. Each data subset is used in the training of CVRBF. The trained CVRBFs compose an ensemble. The real result is obtained based on an absolute majority of the results of the algorithm. Bagging is simple but powerful ensemble method recommended for improving the stability and accuracy of learning algorithms (Das, Turkoglu & Sengur, 2009). The pseudo-code for the CVRBF ensemble with the Bagging algorithm is given in Figure 2.

In Boosting, as in Bagging, each CVRBF is trained on a different bootstrap sample. However, in Boosting, the existing CVRBF focuses more on previously misclassified data points. A typical application of the Boosting method is the AdaBoost method (Freund & Schapire, 1997). In the AdaBoost method, classification is usually performed by aggregating CVRBFs via weighted voting with the weight

Figure 2. The bagging algorithm for ^{E}CVRBF

Input : Training dataset $D = \{x_i, y_i\}_{i=1}^{N}, y_i \epsilon \{-1,1\}$;
Base learning model CVRBF;
Number of iterations T;

Process :

For $t = 1,2,\ldots,T$;
$D_t = Bootstrap(D)$; % Generate a bootstrap sample from D
$h_t = CVRBF(D_t)$; % Train a base learner h_t from the bootstrap sample
End
Compute $H(x) = argmax_{y \epsilon Y} \sum_{t=}^{T} 1\left(y = h_t(x)\right)$; % Majority voting

Output : $H(x)$

in the formula. The pseudo-code for the CVRBF ensemble with Boosting algorithm is given in Figure 3.

The Proposed Method

In the initial step, features were converted into a complex number format using the phase encoding method. The features obtained have been classified by the ensemble of the CVRBF algorithm. The block diagrams of the proposed method based on Bagging and Boosting ensemble learning algorithm are given in Figures 4 and 5, respectively.

EXPERIMENTAL RESULTS AND DISCUSSIONS

All experiments were performed under MATLAB environment using a computer with an Intel(R) Core™ i7-2670QM (2.2 GHz) processor and 8 GB RAM. 10-fold cross-validation method was used for training and testing data. The experiments have been repeated 5 times for the reliability of the results and the averages of obtained results have been reported.

The required parameter values to obtain high efficiency from CVRBF algorithm were found by experimentally. Accordingly, the optimal multi-layer network structures

Figure 3. The boosting algorithm for ^{E}CVRBF

Input : Training dataset $D = \{x_i, y_i\}_{i=1}^{N}, y_i \epsilon \{-1,1\}$;
Base learning model CVRBF;
Number of iterations T;

Process :

$D_1(i) = 1/N$; % Initialize the weight distribution
For $t = 1,2,\dots,T$;
$h_t = CVRBF(D, D_t)$; % Train a base learner h_t from D using D_t
$\varepsilon_t = \Pr_{i\sim D_i}[h_t(x_i \neq y_i)]$; % Measure the error of h_t
$\sigma_t = \frac{1}{2}\ln\frac{1-\varepsilon_t}{\varepsilon_t}$; % Determine the weight of h_t
$D_{t+1}(i) = \frac{D_t(i)}{Z_t} x \begin{cases} exp(-\sigma_t)\ if\ h_t(x_i) = y_i \\ \exp(\sigma_t)\ if\ h_t(x_i) \neq y_i \end{cases}$ % Update the distribution, where
$= \frac{D_t(i)exp(-\sigma_t y_i h_t(x_i))}{Z_t}$; % Z_t is a normalization factor which enables $D_t(i)$ to % be a distribution
End
Compute $H(x) = sign(f(x)) = sign\sum_{t=1}^{T}\sigma_t h_t(x)$; % Weighted majority voting

Output : $H(x)$

Figure 4. ^{E}*CVRBF method with bagging*

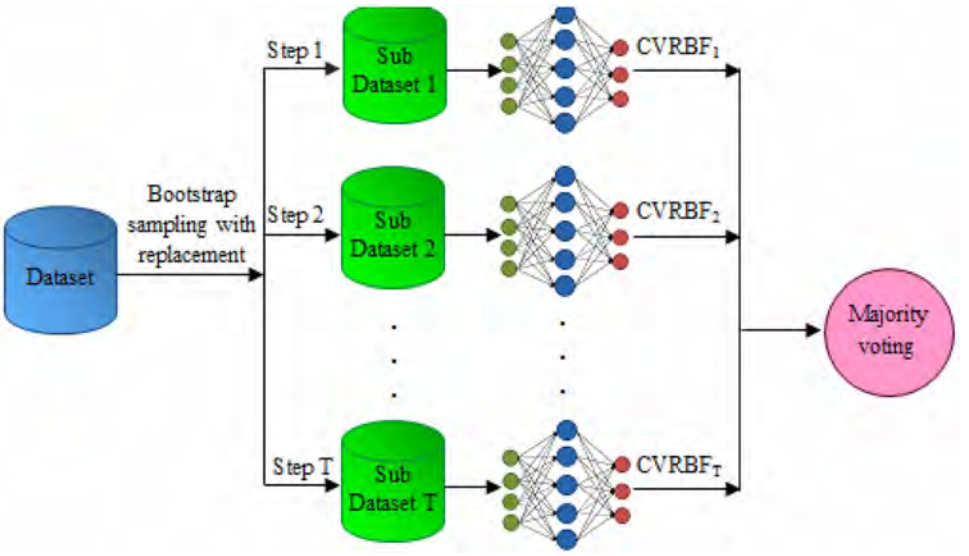
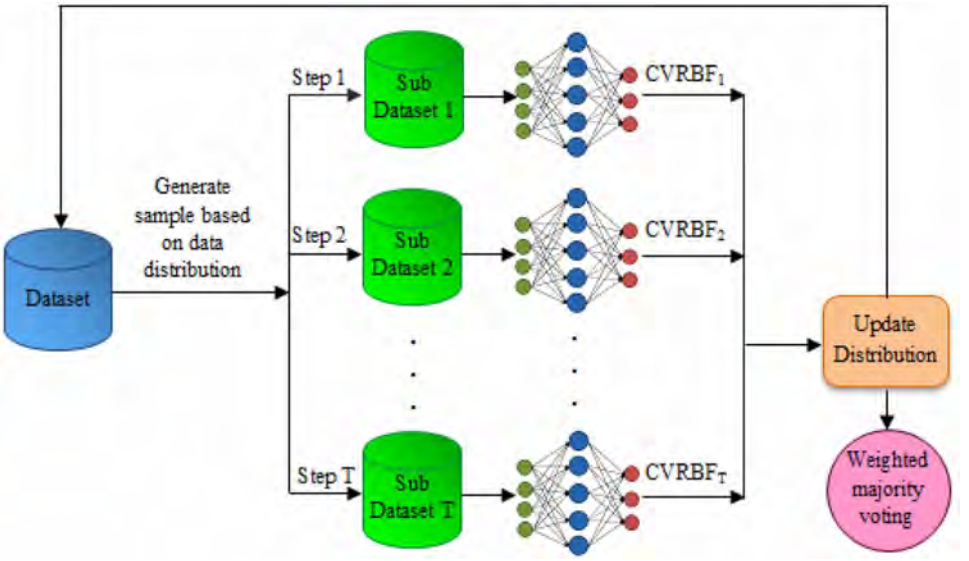


Figure 5. ^{E}*CVRBF method with boosting*



(the number of input-hidden and output neurons) have been determined as 11-10-1, 9-5-1 and 7-10-1 for heart disease, Hepatitis and BUPA liver disorder datasets, respectively. The learning rate during training process has been determined as 0.25, 0.5 and 0.15, respectively. The maximum number of iterations is set to 1000 for all

datasets. The real and imaginary parts of the complex-valued weights have been initiated with the random numbers taken from a uniform distribution $\left(\mathrm{U}\left(-0.5, 0.5\right)\right)$. A gauss activation function was used. In the ensemble of CVRBF to select data subsets, a 75% random sample has been selected with a replacement of the original training dataset. That is, if a training dataset consists of 1000 parts, 750 parts will be drawn randomly with a replacement to create a subset.

The success of the ^{E}CVRBF method has been tested using six different performance evaluation criterions. These are accuracy, specificity, sensitivity, f-measure, the area under an ROC curve (AUC), and kappa statistic values. In order to see the effect of the classifiers, comparative analysis has been performed. The results obtained for each dataset are given in Table 4.

Table 4. The comparative analysis of ^{E}RBF and ^{E}CVRBF ensembles with bagging and boosting

Dataset	Performance Metrics	^{E}RBF		^{E}CVRBF	
		Bagging	Boosting	Bagging	Boosting
Heart	ACC	83.33 ± 9.56	80.37 ± 11.45	90.92 ± 4.36	91.11 ± 5.66
	Sensitivity	84.76 ± 9.10	83.44 ± 8.32	91.94 ± 5.52	90.90 ± 4.97
	Specificity	81.51 ± 10.25	89.95 ± 5.20	89.25 ± 5.85	91.37 ± 5.60
	f-measure	0.8203	0.6475	0.9163	0.9210
	Kappa	0.6622	0.6041	0.8128	0.8195
	AUC	0.8810	0.8610	0.9160	0.9670
Hepatitis	ACC	86.45 ± 7.95	87.74 ± 6.35	96.12 ± 3.85	96.77 ± 3.18
	Sensitivity	70.37 ± 12.44	74.07 ± 11.86	96.42 ± 3.25	99.88 ± 0.11
	Specificity	89.84 ± 4.87	90.62 ± 4.22	96.06 ± 3.72	96.09 ± 3.65
	f-measure	0.6440	0.6779	0.9002	0.9152
	Kappa	0.5611	0.6029	0.9364	0.9471
	AUC	0.8610	0.8440	0.9490	0.9500
BUPA liver disorder	ACC	66.08 ± 11.54	65.79 ± 9.23	87.82 ± 6.15	86.95 ± 7.98
	Sensitivity	64.28 ± 14.85	60.46 ± 13.95	88.72 ± 5.87	87.31 ± 6.95
	Specificity	66.80 ± 10.44	68.98 ± 12.76	87.26 ± 6.55	86.72 ± 7.16
	f-measure	0.5185	0.5693	0.8489	0.8387
	Kappa	0.2716	0.2873	0.7473	0.7295
	AUC	0.6790	0.6800	0.9440	0.9430

When the results in Table 4 are examined, we may observe that the ^{E}CVRBF methods give better results in terms of accuracy, sensitivity and specificity values than the ^{E}RBF methods for all three datasets. ^{E}CVRBF method also gives better results in f-measure, AUC, and kappa statistic values, as well. The superiority of the Bagging to the Boosting method can also vary in the ^{E}RBF methods. The standard deviations of ^{E}CVRBF methods are lower than the ^{E}RBF methods, demonstrating that the proposed method is more robust and reliable. In addition, the same results are given graphically in Figures 6-8.

Figures 9-11 shows ROC curves with different methods were incorporated in the evaluation for heart disease dataset, Hepatitis disease dataset and BUPA liver disorder dataset, respectively. In this phase, the number of algorithms for the comparisons are also increased. These methods are: typical CVRBF; ^{E}CVRBF with Bagging; ^{E}CVRBF with Boosting; original dataset + SVM; original dataset + RBF; and original dataset + Decision Tree. When these graphics are examined, we have seen that the best results have been obtained with ^{E}CVRBF method for three different datasets. We have also seen that, with the ^{E}CVRBF algorithm, in some cases better results were obtained with Bagging, while in some cases better results were obtained

Figure 6. The results for the heart disease dataset

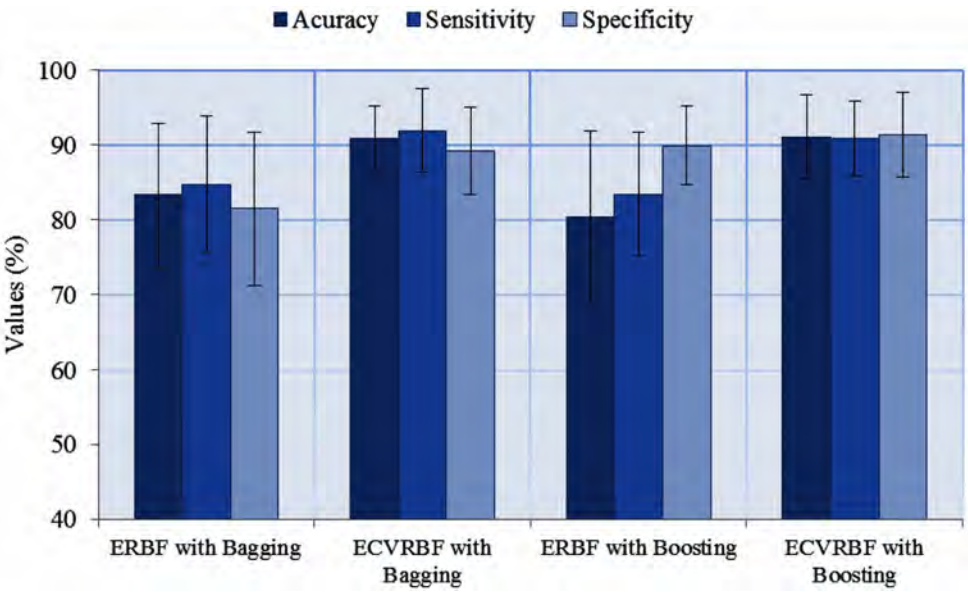


Figure 7. The results for the Hepatitis disease dataset

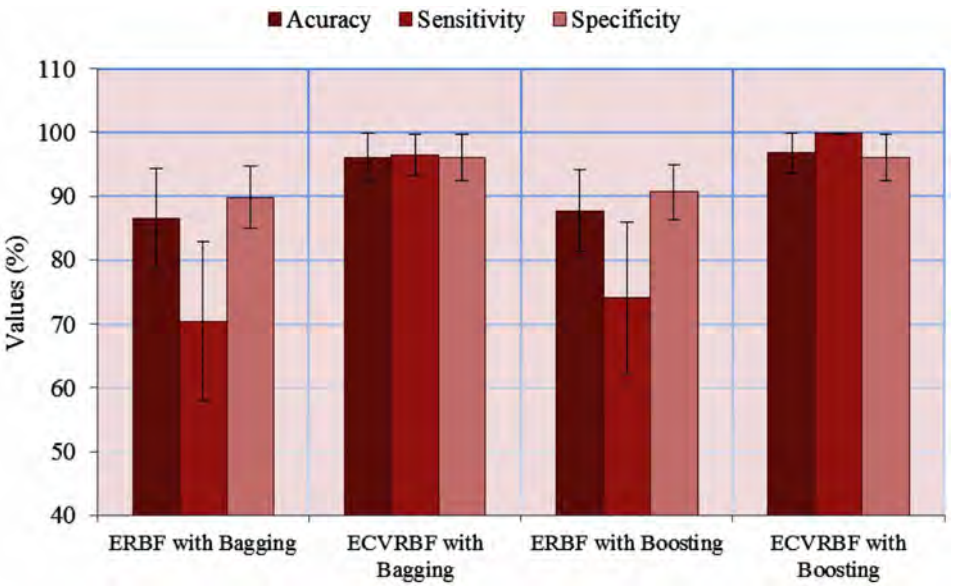


Figure 8. The results for the BUPA liver disorder dataset

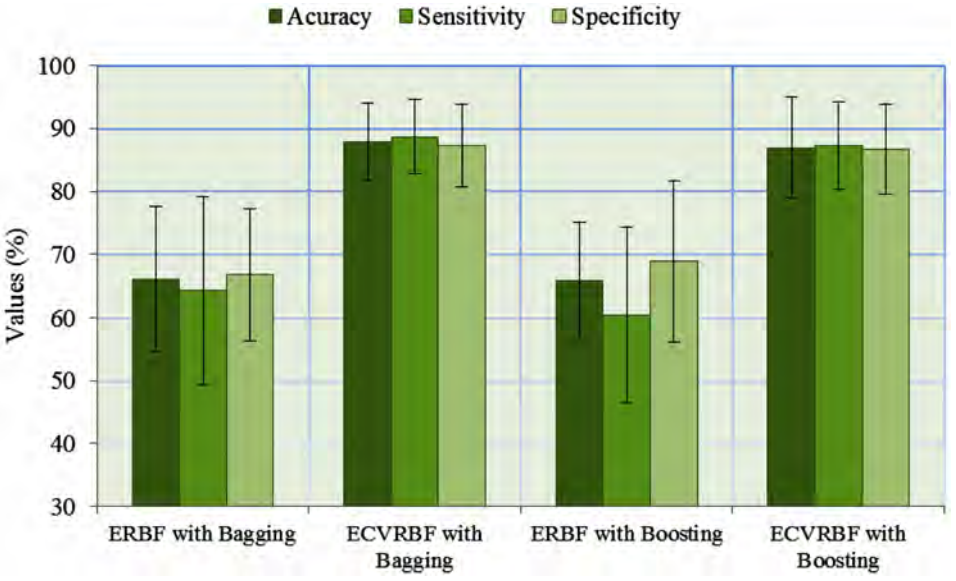


Figure 9. ROC curves for the Statlog heart disease dataset

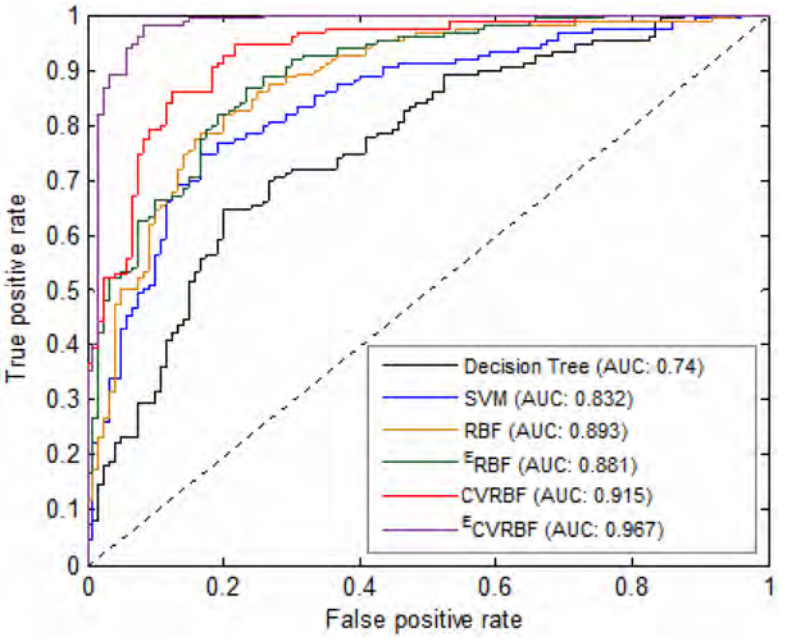


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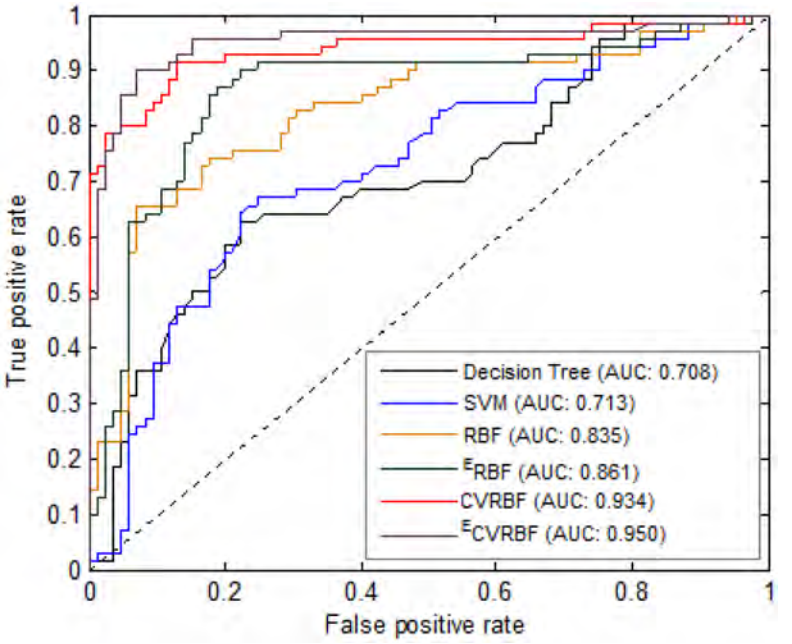
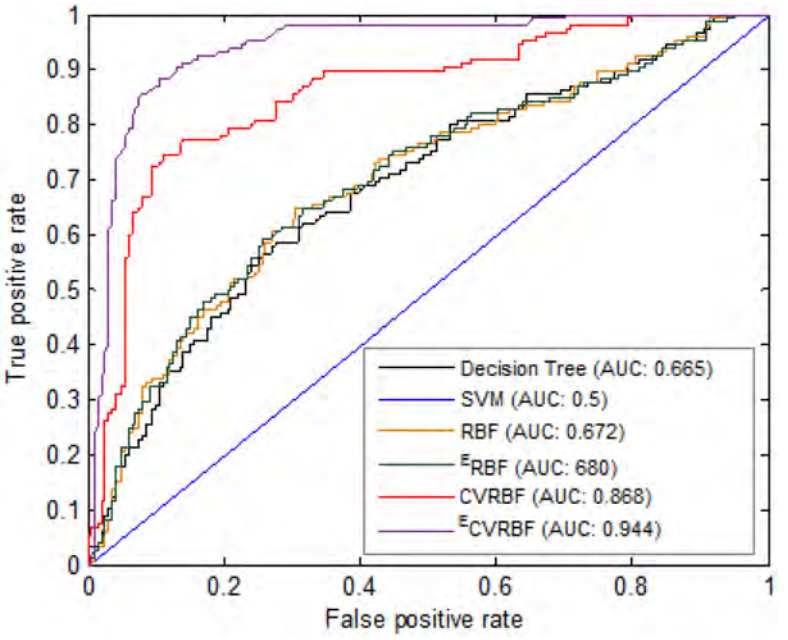
Figure 10. ROC curves for the Hepatitis disease dataset



**For a more accurate representation see the electronic version.*

Figure 11. ROC curves for the BUPA liver disorder dataset



**For a more accurate representation see the electronic version.*

with Boosting. Better results have been obtained with complex valued classifiers, compared to real-valued classifiers. Considering the real-valued classifiers, we have seen that the RBF algorithm is more effective for three datasets.

The performance analysis of the proposed method was then compared with the previous studies from the literature, as listed in Tables 5 to 7. In Table 5, the analysis for the heart disease dataset is given. When the table is examined, we may observe that accuracy values in the range of 80-88% have generally been achieved by other researchers. A 91.11% accuracy rate has been obtained with the developed method for the dataset. In Table 6, the comparative analysis carried out with previous studies for the Hepatitis disease dataset is given. As seen in the table, accuracy values, generally in the range of 79-96%, have been obtained by other researchers. Compared to the other studies, the proposed method has yielded a better result with a 96.77% accuracy value. In Table 7, the comparative analysis for the BUPA liver disorder dataset is given. When we examine the table, we see that an 87.82% classification accuracy has been obtained in this study, while accuracy values in the 60-85% range have generally been obtained by other researchers. In general, the proposed method has provided better results compared to the existing methods from the literature.

Table 5. Performance comparison for the Statlog heart disease dataset

Study	Method	Classification Accuracy (%)
Kahramanli and Allahverdi (2008)	Hybrid system using ANN and FNN (10-fold CV)	86.80
Subbulakshmi et al. (2012)	Extreme learning machine (70-30% training-testing)	87.50
Shao and Deng (2015)	Coordinate descent margin based-twin SVM (10 fold CV)	84.44
Mantas and Abellán (2014)	Decision tree based on imprecise probabilities (Credal C4.5) (10 fold CV)	80.33
Duch et al. (2001)	k-NN, k=28, 7 features (10-fold CV) k-NN, k=28, Manhattan (10-fold CV) FSM, 27 fuzzy rules SSV, 3 rules	84.60–85.60 82.20–83.40 82 80.20–83.40
Tian et al. (2009)	Cooperative coevolutionary algorithm - elliptical basis function neural network (50-25-25% training-validation-testing)	82.45
Ahmad et al. (2013)	Improved hybrid genetic algorithm-multilayer perceptron network (75- 25% training-testing)	86.30
Torun and Tohumoglu (2011)	Simulated annealing and subtractive clustering based fuzzy classifier (10 fold CV)	81.11
Al-Obeidat et al. (2011)	Particle swarm optimization for PROAFT (10 fold CV)	84.27
Jaganathan and Kuppuchamy (2013)	Neural network threshold selection (10 fold CV)	85.19
Lim and Chan (2015)	Bandlerkohout-interval-valued fuzzy sets (BK-IVFS weighted) (5 fold CV)	85.56
Yang et al. (2013)	Fuzzy class – label SVM (y_i - SVM) and Fuzzy SVM (F-SVM)	85.19
Our study	**CVRBF ensemble with Bagging**	**90.92**
Our study	**CVRBF ensemble with Boosting**	**91.11**

CONCLUSION

In this study, ensembles of complex-valued radial basis function networks have been proposed. To investigate the effect of the proposed method, three benchmark medical datasets were used. The common characteristics of these datasets are having a distribution, which cannot be separated linearly and a large amount of missing data. In turn, 91.11%, 96.77% and 87.82% accuracy values were achieved respectively for Statlog heart disease, Hepatitis disease and BUPA liver disorder datasets using

Table 6. Performance comparison for the Hepatitis dataset

Study	Method	Classification Accuracy (%)
Shao et al. (2015)	Weighted linear loss twin support vector machine – 10 fold CV	84.39
Mantas and Abellán (2014)	Decision tree based on imprecise probabilities (Credal C4.5) (10 fold CV)	79.99
Yang et al. (2013)	Fuzzy class – label SVM (y_i - SVM) and Fuzzy SVM (F-SVM)	85.19
De Bock et al. (2010)	Generalized additive models (GAM) ensemble classifiers – 2 fold CV	89.20
Bascil and Oztekin (2012)	Probabilistic Neural Network – 10 fold CV	91.25
Bascil and Temurtas (2011)	Multilayer Neural Network with Levenberg Marquardt Training Algorithm - 10 fold CV	91.87
Moradi and Rostami (2015)	Integration of graph clustering with ant colony optimization (GCACO) and SVM - training set (2/3 of dataset) and test set (1/3 of dataset).	84.52
Pan et al. (2015)	K-nearest neighbor based structural twin support vector machine (KNN-STSVM) – 5 fold CV	87.54
Zhang et al. (2015)	Sparse-response backpropagation algorithm (SRBP) – 10 fold CV	84.25
Our study	**CVRBF ensemble with Bagging**	**96.12**
Our study	**CVRBF ensemble with Boosting**	**96.77**

Table 7. Performance comparison for the BUPA liver disorder dataset

Study	Method	Classification Accuracy (%)
Goncalves et al. (2006)	Inverted hierarchical neuro-fuzzy binary space partitioning system	73.33
Lee and Mangasarian (2001)	Reduced SVMs (10-fold CV)	74.90
Dehuri et al. (2012)	Improved swarm optimized functional link artificial neural network (10-fold CV)	76.80
Shao and Deng (2012)	Coordinate descent margin based-twin SVM (10-fold CV)	72.80
Savitha et al. (2012)	Fully complex valued RBF (10 fold CV)	74.60
Mantas and Abellán(2014)	Decision tree based on imprecise probabilities (Credal C4.5)	64.53
López et al. (2014)	Mahalanobis SVM	72.17
Torun and Tohumoglu (2011)	Simulated annealing and subtractive clustering based fuzzy classifier (10 fold CV)	74.13
Al-Obeidat et al. (2011)	Particle swarm optimization for PROAFT (10 fold CV)	69.31
Yang et al. (2013)	Fuzzy class – label SVM (y_i - SVM) and fuzzy SVM (F-SVM)	74.78
Van Gestel et al. (2002)	SVM with GP (10-fold CV)	69.70
Wang et al. (2014)	Spiking neural networks (SNNs)	56.60
Li et al. (2011)	A fuzzy-based nonlinear transformation method + SVM	70.85
Our study	**CVRBF ensemble with Bagging**	**87.82**
Our study	**CVRBF ensemble with Boosting**	**86.95**

the ^{E}CVRBF algorithm. The received results in this study are higher than the results obtained in many studies, carried out for the same data in the literature. In an important issue such as medical diagnosis, even a slight increase in classification accuracies is very important. Hence, the method proposed here will contribute significantly to the medical diagnostics. In conclusion, the system can also be used as computer-aided medical diagnosis system to help doctors.

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KEY TERMS AND DEFINITIONS

Classification: It is a kind of supervised machine learning in which an algorithm "learns" to classify novel observations from samples of labeled data.

Complex-Valued Neural Network: It is a variety of neural network and its parameters such as input, output, weight, and bias values consist of complex numbers.

Decision Support System: It is a computer-based information system that supports organizational or business decision-making activities.

Ensemble Methods: It is a set of classifiers whose individual decisions are integrated in some way to classify novel examples.

Machine Learning: It is the notion that a computer program can learn and adapt to novel data without human interference.

Medical Diagnosis: It is a classification operation including the decision-making process based on available medical data.

ROC Curve: It is a graphical method which assess the success of a binary classifier system.