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ORIGINAL RESEARCH

Multi-disease prediction model using improved SVM-radial bias technique in healthcare monitoring system

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Abstract
In this digital world, data is an asset, and enormous data was generating in all the fields. Data in the healthcare industry consists of patient information and disease-related information. This medical data and machine learning techniques will help us to analyse a large amount of data to find out the hidden patterns in the disease, to provide personalised treatment for the patient and also used to predict the disease. In this work, a general architecture has proposed for predicting the disease in the healthcare industry. This system was experimented using with reduced set features of Chronic Kidney Disease, Diabetes and Heart Disease dataset using improved SVM-Radial bias kernel method, and also this system has compared with other machine learning techniques such as SVM-Linear, SVM-Polynomial, Random forest and Decision tree in R studio. The performance of all these machine learning algorithms has evaluated with accuracy, misclassification rate, precision, sensitivity and specificity. From the experiment results, improved SVM-Radial bias kernel technique produces accuracy as 98.3%, 98.7% and 89.9% in Chronic Kidney Disease, Diabetes and Heart Disease dataset respectively.

Keywords SVM · Random forest · Decision tree · Data analytics · Chronic kidney disease · Diabetes · Heart disease · Clinical data analytics · Healthcare analytics

1 Introduction

In recent years, due to digitisation, data were growing exponentially in all the fields. Big data is a term, which is massive, and it cannot be processed with regular computers. Big data analytics is a progression of examining large datasets to uncover new insights, value, and hidden patterns. Big Data analytics has used in several applications like weather prediction, fraud and risk detection, Logistic Delivery and Healthcare (Chahal and Gulia 2016).

Machine Learning algorithms will help us to study the algorithms that use large data set to learn, generalise and predict. Machine Learning is closely related to computational statistics and also in making decisions. Machine learning algorithms are used in various applications like predicting the sales of the product, finding the probability of the occurrence of rainfall in a particular region and etc.

Systematic analysis of existing medical data will help the doctors to detect the pattern of the disease and also helps the doctors in diagnosis the disease and its critical level. Systematic analysis with the machine learning algorithms will help us to construct the predictive models for personalized treatment, monitor the harm signs of the patients during their trial run and also helps the doctors to identify the drug for the patients (Chen et al. 2017). In this paper, we proposed an integration framework of decision support system for predicting the disease using machine learning techniques.

The decision support system was implemented with improved SVM- Radial bias kernel technique for predicting the disease and its performance was compared with various machine learning techniques. The remaining paper is organised as follows, Sect. 2 reviews related work in healthcare analytics and disease prediction, Sect. 3 deals with the implementation of healthcare analytical system (Devarajan et al. 2019). Results were compared in Sect. 4, and Sect. 5 concludes with discussions of this research work.

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2 Related works

Different researchers are doing research in clinical data analytics to predict various diseases by using different machine learning algorithms. This section discusses about various studies in health care analytics, chronic kidney diseases, diabetes, heart disease and different machine learning algorithms used in clinical data analytics.

In Li et al. (2019), the authors described the potential advantages of data analytics in the health care industry. The authors also described research opportunities in the healthcare industry to construct predictive modelling, statistical and algorithms to improve the clinical trial design. Data preprocessing will remove unwanted and noisy data from the dataset.

In Johnson et al. (2016), the authors narrated the issues involved in critical care data preprocessing. In this work, the authors classified the challenges in critical care section into three categories (1) classifying the data (2) preprocessing (3) prediction. Hospitals are maintaining the patient`s data in the central repository. In Cooke and Iwashyna (2013) and Black and Payne (2003), the authors proposed the advantages of linking the database with the hospitals for improving the prediction. Quality of the data is significant for constructing the predictive model for any applications. In Nouira and Trabelsi (2012), Imhoff et al. (1998), West et al. (1985) and Becker and Gather (2001), the authors proposed different techniques to remove the outliers in the dataset.

Medical instruments used in hospitals and diagnosing centres are generating a massive amount of data. The generated data should be appropriately classified for identifying any diseases. In Zhang and Zhou (2007), the authors proposed Multi-Label lazy approach to sort the data from the unknown category of data to the popular type of data. Here the authors used k- nearest neighbour algorithm to organize the data into the correct group and in Yu et al. (2015) author proposed incremental semi-supervised clustering ensemble framework for clustering high dimensional data. Correlation is a statistical term to find out the relation with others. In medical research, some diseases depend upon other conditions (Iwashyna et al. 2010).

The authors (Mukaka 2012) discussed the guidelines to choose appropriate correlations in medical examination. Support Vector Machine (SVM) is a supervised algorithm which classifies similar features of the dataset in the training model in one category, and dissimilar features of the dataset had grouped into another category. In SVM, classification was performed by finding the appropriate hyperplane to classify the data. The authors Çomak et al. (2007), Anthimopoulos et al. (2016), Son et al. (2010), Verplancke et al. (2008), Yu et al. (2010) and Maglogiannis et al. (2009), have used the SVM algorithm to classify the medical records for improving the models in disease detection.

Shen et al. (2016) have proposed the fruit fly optimization to find out the appropriate parameters for improving the classification accuracy. In Polat et al. (2017), the authors used the SVM algorithm with Best First search engine feature selection method to predict chronic kidney diseases. For this experiments, the authors have used the UCI dataset with 25 features and prediction accuracy of this technique was recorded has 98.5%. In Sinha and Sinha (2015), authors had proposed performance evaluation of KNN and SVM algorithms for predicting Chronic Kidney Diseases. In this work, the authors used the UCI repository data set for predicting the accuracy of the algorithms and it was recorded as 78.75% and 73.75% respectively.

Misir et al. (2017) had reported that, the reduced set features for chronic kidney disease prediction using correlation-based algorithms. In this model, the authors considered only eight factors out of twenty-five factors of the UCI kidney disease dataset to predict the diseases (Fontecha et al. 2019).

The authors in Norouzi et al. (2016) constructed an integrated intelligent fuzzy expert system for predicting renal failure progression. In this model, they used 15 cc/kg/min/1.73 m^2as a GFR threshold value for predicting renal failure. Barakat et al. had proposed SVM based tool for predicting the diabetes disease (Finney et al. 2011). In that experiment, they recorded the prediction accuracy as 94% (Barakat et al. 2010). With this motivation and literature survey, we extended to develop a Health care monitoring system and decision support system for predicting the disease using healthcare data.

3 Healthcare analytical model

The present work has proposed for predicting multiple diseases in the Health care industry. As a test phase, the system has experimented with Chronic Kidney Disease (CKD), Diabetes and Heart diseases from UCI dataset with the guidelines of the National Kidney Foundation, Standards of Medical Care in Diabetes, Cardiovascular Clinical Recommendations and Guidelines respectively.

The main objective of the system is to help the doctors to reduce the diagnosis time so that doctors can start the treatment at earliest. The correctness of the model is computed using the confusion matrix. The confusion matrix is formulated with actual count and predicted count. The confusion matrix represented with the number of correct and incorrect predictions and it is represented in Table 1

True positive Predicting the patient with the disease as yes, and its observation results are yes.

True negative Predicting the patient with no disease and its observation results are negative.

Table 1 Confusion matrix

Actual	Predictor	
	Yes	No
Yes	True positive	False negative
No	False positive	True negative

False positive Predicting the patient with no diseases but with the observation, the patient is having the disease.

False negative Predicting the patient doesn`t have a disease but the patient has the disease.

Evaluation parameters:

A. *Accuracy*: The accuracy of the classifier id described as how many samples were corrected accurately among the total number of samples and it is represented as follows

$$Accuracy = \frac{True\ Positive\ +\ True\ Negative}{Total\ no\ of\ Predctions} * 100 \tag{1}$$

B. *Misclassification rate*: It is described as, the classifier which is not predicting properly and it is also referred to as error rate

$$Miscalssification\ Rate = \frac{False\ Positive\ +\ False\ Negative}{Total\ no\ of\ Predctions} * 100 \tag{2}$$

C. *Recall*: It is described as the classifier which is predicting the positive values to actual positive values

$$Recall = \frac{TruePositive}{TruePositive + FalseNegative} \tag{3}$$

D. *Precision*: The classifier which is predicting the positive values to the total positive values

$$Precision = \frac{TruePositive}{TruePositive + FalsePositive} \tag{4}$$

E. *Specificity*: It is a measurement of predicting actual negatives as negative

$$Specificity = \frac{TrueNegative}{TrueNegative + FalsePositive} \tag{5}$$

In this work, the performance of the system is evaluated with accuracy, sensitivity and specificity.

3.1 Experimental setup

In this section, we are discussing the experimental setup of the decision support model to predict the disease as shown in Fig. 1 and the flow diagram of the system is represented in Fig. 2. This system consists of three layers

1. Data sources and data collection
2. Data storage
3. Decision support system.

Data collection In earlier days, hospitals were maintained the patient details in the physical format, and it is tough to analyse. Due to digitisation and technology advancement, now a day's, hospitals were maintaining the patient record in the Electronic Health Record (EHR) format to track the patient details more easily.

With the advancement of technologies, the health care system will collect data from electronic gadgets like mobile phones and smart watches. IoT enabled diagnosis devices were directly sending the data to the cloud-enabled storage centres for further processing. These technologies will allow us to collect data from multiple data sources.

Data storage Hospitals were maintaining the repository to store the patient's record. In the early day's, hospitals were kept the patient's data in their hospitals, and it was minimal to store in nature. With the advancements in storage technology, hospitals were storing the data in the cloud. This feature will enable the doctor to access the patient data at any time and anywhere.

Decision support system Decision support system consists of four sub modules.

A. Data preprocessing model
B. Feature selection model
C. Feature extraction model
D. Predictive model.

A. Data preprocessing

In data analytics, Data preprocessing plays a significant role in removing unwanted and noisy data. Sometimes data sources will capture unwanted data and incomplete data. These issues were addressed during data preprocessing model. In machine learning, missing data are handled with the following techniques.

- Eliminate the missing values by ignoring the missing fields in the dataset.
- Use Mean method to fill the missing value.
- Fill the missing values by using matching respondents with an earlier dataset.
- Fill the missing value by using the most likely value.

Ignoring the missing fields is the commonly used technique in data analytics. This method is suitable only if you have sufficient samples in the dataset.

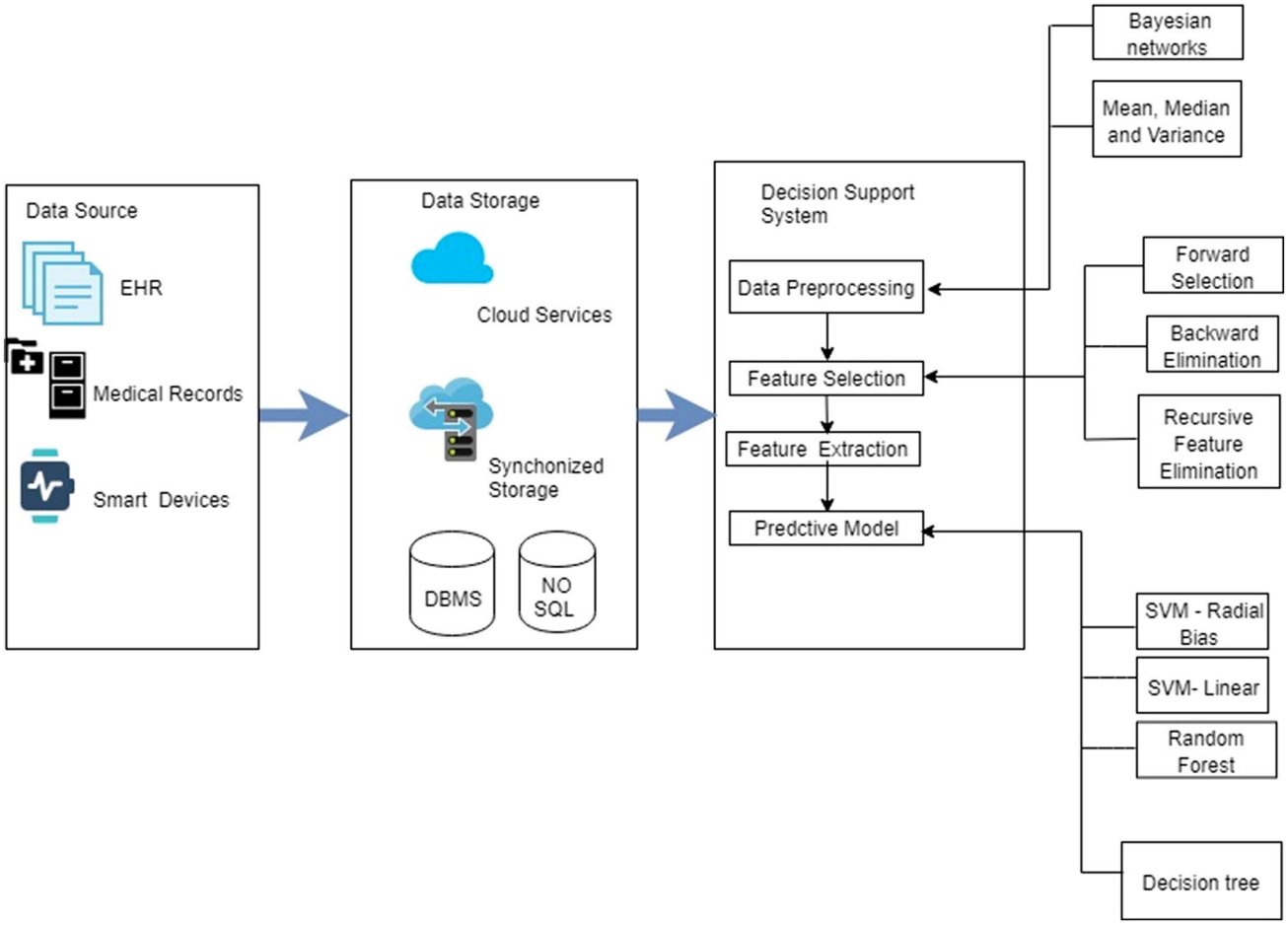

Fig. 1 Decision support system

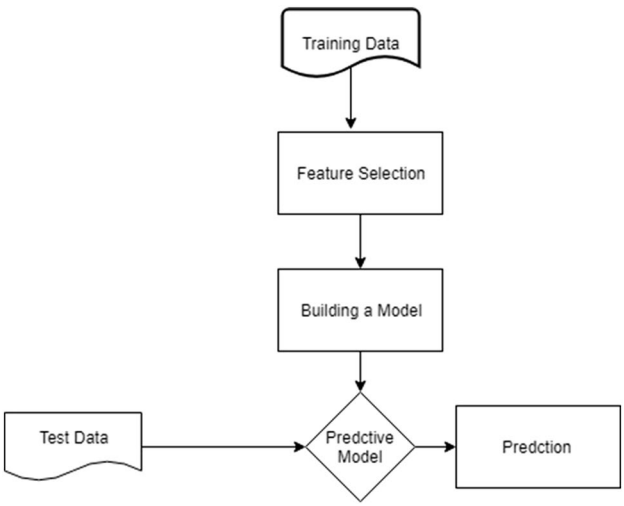

Fig. 2 Flow diagram of decision support system

In the second technique, missing values were filled with the mean value of the features. This technique will be useful if the data set is small in size.

In the third technique, missing values were computed from the historical values. In this technique, similarity will find out with the existing value and it will fill the related values in the missing fields. The last technique was filling the missing values by using computational methods.

We can use linear regression models to fill the missing values. But in this work, we used, "Eliminate the missing values by ignoring the missing fields in the dataset" technique as a data preprocessing technique.

B. Feature selection

It is a process of selecting the most relevant features in the dataset. Data source have generated the data with many attributes. Some of the attributes in the dataset will not affect the performance of the prediction so we can remove this unwanted attributes while constructing the predictive model.

Let us consider the dataset for the model may consist of "N" features with "M" samples and it is denoted as in

Eq. (6). Where "a" is an attribute or feature in the dataset and " N" is the number of features.

$$D = \{a_1, a_2, a_3, a_4, \ldots, a_N\} \tag{6}$$

The accuracy of the classifier may not depend on the complete set of attributes of the dataset "D", and it may depend only the selected features in the dataset. This selected features subset is represented as in Eq. (7). Here the system is proposed with Chi square model to identify best features from the given dataset.

$$Y = \{a_1, a_2, a_3, a_4, \ldots, a_n\}, n < N \tag{7}$$

C. Feature extraction

Feature extraction will create a new subset from the selected features. Feature extraction is a process of transforming the original features of the data into a reduced feature set.

D. Predictive model

In the decision support system, the prediction accuracy is depending upon the data quality and the algorithm used in the prediction.

3.2 Modeling

A. Support vector machine

Support Vector Machine (SVM) is a supervised machine learning algorithm which classifies the data into positive and negative classes with maximum distance or margin (Burges 1998) and it is represented in (8) and (9)

$$x_i.w + b \geq +1 \quad \text{for all } y_i = +1 \tag{8}$$

$$x_i.w + b \leq -1 \quad \text{for all } y_i = -1 \tag{9}$$

Here x, w are vectors and b is bias.

The hyperplane is defined as $w^T \cdot x = 0$. In SVM, the best hyperplane is considered with a larger distance between the margins.

So to increase the margin between the hyperplane we should decrease the $\| w \|$ and is formulated in (10)

$$\min_{w,b} = \frac{1}{2}||w||^2 \tag{10}$$

In a non-linear condition, the data might not be appropriately classified. To consider the error rate, we used slack variable ζ_i where i = 1,2,3,…,n. and it is associated with C.

When C is large then the error rate is more, and if C is less there is a possibility of fewer errors (Burges Burges 1998) and it is described in (11)

$$\min_{w,b,\zeta} = \frac{1}{2}||w||^2 + C\sum_{i=0}^{n}\zeta_i \tag{11}$$

B. Kernel Tricks in SVM

In SVM, Support vectors decide the margin width of the hyperplane. There are different ways to improve the predicting accuracy of the SVM algorithm. One way is changing the kernel function.

Kernel trick is a mathematical function which transforms non-linear, non-separable data into linearly separable data by converting the data into its higher dimension space (12)

$$K(m,n) = \langle f(m), f(n) \rangle \tag{12}$$

Here K(m,n) is a kernel function. m,n were the dimensional inputs, and f was a map function from the dimension space. Based upon the mathematical functions used in the kernel trick, it has following types

1. Linear Kernel
2. Radial bias Kernel
3. Polynomial Kernel

Linear Kernel is like a normal dot product of two vectors and it is formulated as follows.

$$K(x_1, x_2) = x_1 \cdot x_2 \tag{13}$$

The polynomial kernel function is like a Linear kernel but it has a polynomial degree associated with it.

$$K(x_1, x_2) = (x_1 \cdot x_2 + c)^p \tag{14}$$

Another form of the kernel is, Radial Bias Function and it is represented in (15)

$$K(x_1, x_2) = \exp(-\gamma||x_1 - x_2||^2) \tag{15}$$

where $||x_1 - x_2||$ is a Euclidian distance and γ describes the decision region.

In SVM, Margin (M) and Misclassification (MCR) are directly proportional. ie. If we increase the margin size of hyperplane then the misclassification rate will be increased.

Cost parameter "C" helps the SVM to find out the margin for the hyperplane.

To reduce the misclassification rate, we should decrease the margin size so that all the vectors will be classified into its corresponding space. The relationships between "MCR", "M" and "C" was represented in (16) and (17)

$$MCR \propto M \tag{16}$$

Training Model for SVM

Input: D=[X,Y]; X(array of input with m features), Y(array of class labels)
Y=array(C) // Class label
Output: Find the performance of the system
function train_svm(X,Y, number_of_runs)
initialize:learning_rate=Math.random();
for learning_ rate **in**number_of_runs
error=0;
for i **in** X
if (Y[i] *(X[i]*w))<1 **then**
update : w=w + learning_rate * ((X[i]*Y[i])*(-2*(1/number_of_runs)*w)
else
update: w=w+learing_rate *(-2*(1/number_of_runs)*w)
end if
end
end

Fig. 3 Pseudocode for training the SVM

$$M \propto \frac{1}{C} \tag{17}$$

The training model for the SVM is as shown below (Fig. 3)

4 Results and discussion

The system has experimented with CKD, Diabetes and Heart disease datasets from the UCI repository using R tool. During this experiment, the dataset was split into two parts as 80% for training and 20% for validation. We used Chi square method to identify the important features in each disease dataset.

Figure 4 shows the important features for Diabetes disease dataset, Fig. 5 shows the important features for Heart disease dataset and Fig. 6 shows the important features for CKD disease dataset.

From the reduced features identified as important features from feature selection phase, we implemented with SVM-Linear, SVM-Polynomial, Random forest method, Decision tree method and Improved SVM- Radial method. Here SVM-Radial bias method was fine-tuned using variance reduction technique, with "C" and "gamma" values as 1 and 0.60 respectively. The tested results are evaluated with accuracy, misclassification rate, sensitivity, precision and specificity. Table 2 shows the prediction Accuracy, Misclassification rate, Specificity, Precision and sensitivity of CKD, Heart Disease and Diabetes dataset using various machine learning algorithms. From the results, we found that Improved SVM-Radial bias kernel technique was

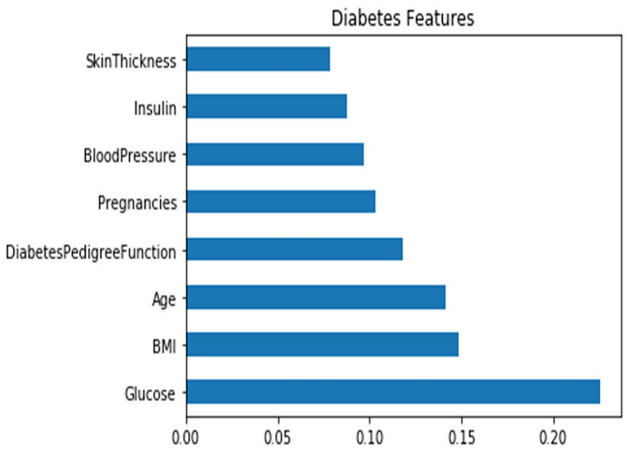

Fig. 4 Important features in diabetes

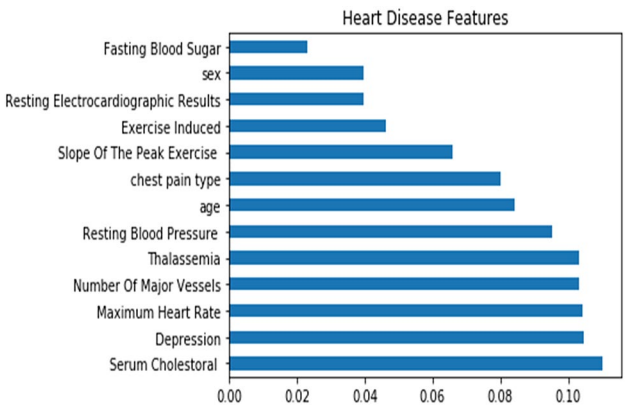

Fig. 5 Important features in heart disease

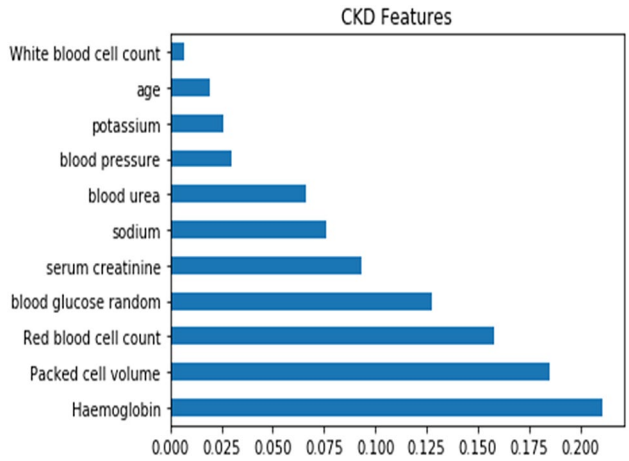

Fig. 6 Important features in CKD disease

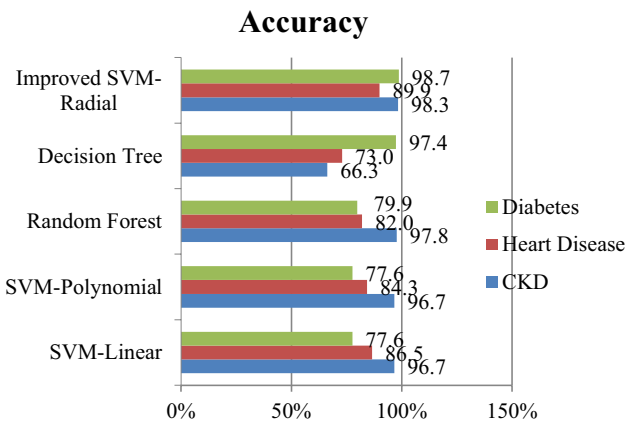

Fig. 7 Comparison of accuracy using improved SVM-Radial Bias Kernel, decision tree, random forest, SVM-polynomial

generating better results well while comparing to other methods in these three diseases.

Figure 7 shows that Improved SVM-Radial bias kernel method is predicting more accurately in all these three datasets while comparing to other methods.

Figure 7 shows that Improved SVM-Radial method is predicting more accurately in these tree datasets while comparing to other methods. Figure 8 shows that Improved SVM- Radial method has less misclassification rate while comparing to other methods.

Figure 9 shows the comparative analysis with respect to sensitivity.

Figure 10 shows that the precision analysis of Improved SVM-Radial, Decision Tree, Random Forest, SVM-Polynomial, and SVM-Linear.

Figure 11 shows the performance analysis of Improved SVM-Radial, SVM-Linear, SVM-Polynomial, Decision Tree and Random Forest concerning specificity.

5 Conclusion

In this work, we proposed a general architecture decision support system to predict multiple diseases in medical diagnosis. The system has experimented with CKD, Heart Disease and Diabetes disease datasets from UCI repository. For this experiment, essential features were identified using Chi

Table 2 Analyzing the prediction accuracy and misclassification rate of CKD, heart disease and diabetes using machine learning algorithms

Model		SVM-linear (%)	SVM-polynomial (%)	Random forest (%)	Decision tree (%)	Improved SVM-radial (%)
Evaluation parameters	Disease					
Accuracy	CKD	96.7	96.7	97.8	66.3	98.3
	Heart Disease	86.5	84.3	82.0	73.0	89.9
	Diabetes	77.6	77.6	79.9	97.4	98.7
Misclassification	CKD	3.3	3.3	2.2	33.7	1.7
	Heart Disease	13.5	15.7	18.0	27.0	10.1
	Diabetes	22.4	22.4	20.1	2.6	1.3
Sensitivity	CKD	100.0	100.0	100.0	65.9	100.0
	Heart Disease	91.9	86.8	80.5	71.1	97.2
	Diabetes	61.9	69.2	67.4	96.1	95.5
Precision	CKD	90.0	90.0	94.7	65.9	95.0
	Heart Disease	79.1	78.6	80.5	83.3	81.4
	Diabetes	59.1	40.9	66.0	96.1	100.0
Specificity	CKD	95.2	95.2	96.3	66.7	97.6
	Heart Disease	82.7	82.4	83.3	74.5	84.9
	Diabetes	83.6	79.4	85.2	98.1	100.0

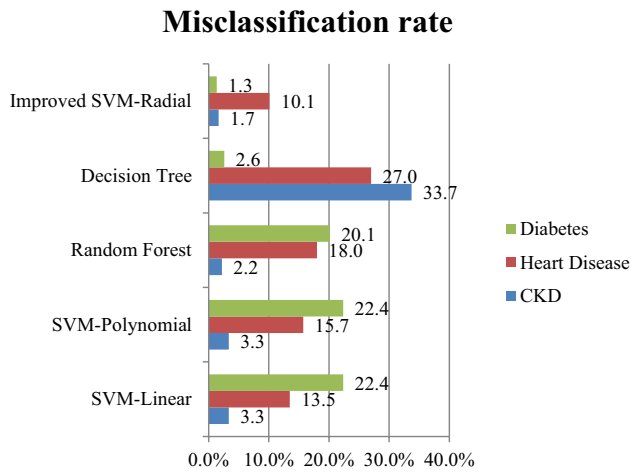

Fig. 8 Comparison of improved SVM-Radial bias Kernel, decision tree, random forest, SVM-polynomial, and SVM-linear with respect to misclassification rate

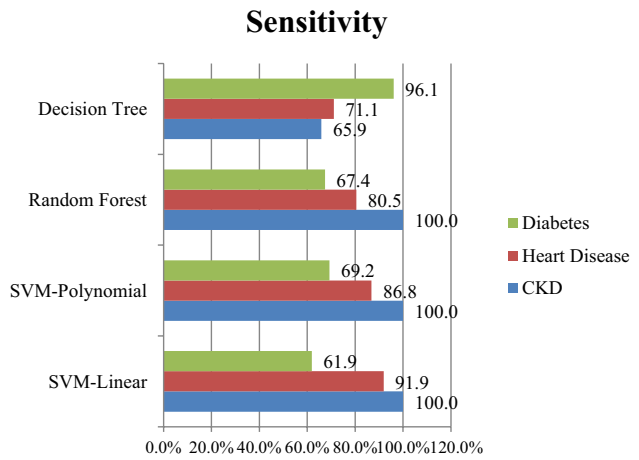

Fig. 9 Comparison of improved SVM-Radial bias Kernel, decision tree, random forest, SVM-polynomial, and SVM-linear with respect to sensitivity

Square method. With identified features we experimented with SVM-Linear, SVM-Polynomial, Improved SVM-Radial bias kernel, Random forest and Decision Tree methods in these datasets. The experimental results show that the Improved SVM-Radial bias kernel method with Cost value "C" of 1 and gamma value of "Γ" 0.6 yields better accuracy while comparing to other methods. Improved SVM-Radial produces 98.3%, 89.9% and 98.7% on CKD, Heart Disease and Diabetes disease dataset respectively.

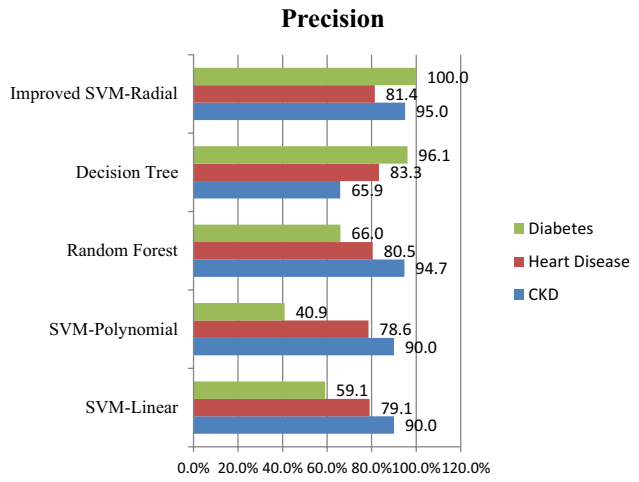

Fig. 10 Comparison of improved SVM-Radial bias Kernel, decision tree, random forest, SVM-polynomial, and SVM-linear concerning precision

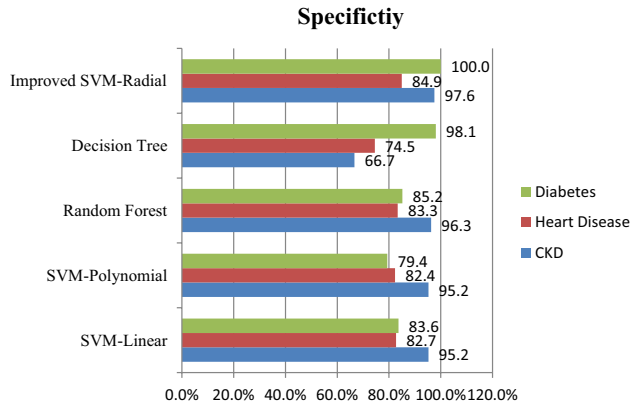

Fig. 11 Comparison of improved SVM-Radial bias Kernel, decision tree, random forest, SVM-polynomial, and SVM-linear with respect to specificity

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