A Combined Approach of Naive Bayes Classifier and Relevance Vector Machine for Breast Cancer Diagnosis

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***Abstract*- Diagnosing cancer manually may have some limitations and it is difficult too. Many researches are still under process for detecting cancer accurately. Many software applications are developed to diagnose the disease and some are developed for analyzing data for effective usage. Machine learning techniques are very popular for developing medical applications. There are many techniques under machine learning for cancer detection which gives appropriate results. This article deals with diagnosing breast cancer in combination of Naïve bayes and Relevance vector machine algorithms. Wisconsin original breast cancer dataset is used for testing and training.**

Keywords- Classification, LDA, Naïve Bayes Classifier, Relevance Vector Machine, RVM

1. INTRODUCTION

Cancer is one of the most dangerous diseases that cause cells in the body to change and grow out of control. Mostly the women are affected by cancer such as breast cancer, cervical cancer, and ovarian cancer. Breast cancer is said to be one of the leading cause of death among women. Breast cancer not only affects female but also affect male, due to lifestyle factors and habits. Treating breast cancer is most painful and there are still many research work undergoing for predicting breast cancer in early stage. Recently breast cancer specialists have introduced new techniques for predicting breast cancer. It is a lab test known as circulating tumor cells, which predicts, which patient may have recurrence of their cancer. Another test is done using images which is called as Scinitimammography also called as molecular breast imaging, in which, a molecular tracer called Technetium Sestamibi is injected into a vein as shown in figure 1. This tracer attaches to breast cancer cells and is detected by a special camera.

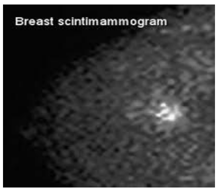


Figure 1. Scinitimammogram Image

Most software is designed by experts for predicting breast cancer in early stages through mammographic images and laboratory test details. This work also deals with predicting breast cancer using Wisconsin original breast cancer dataset. A Graphical User Interface is designed, in which the details of the patient are entered. The system recognizes whether the given data is benign or malignant. The Naïve bayes algorithm in combination with Relevance vector machine is used to design the system, which gives the accuracy of 98%.

2. NAIVE BAYES CLASSIFIER

Bayesian classification can be used to represent statistical and supervised learning method and hence it can be used to solve predictive and diagnostic problems. Naïve Bayes classifier can be used in complex problems to reduce complexity (Jesmin nahar, Yi-Pingphoebechen, & Shawkatali, 2007). The Naïve Bayes algorithm is based on Bayes rule. It assumes that the attributes are conditionally independent. Figure 2 shows the graphical model of independent inputs.

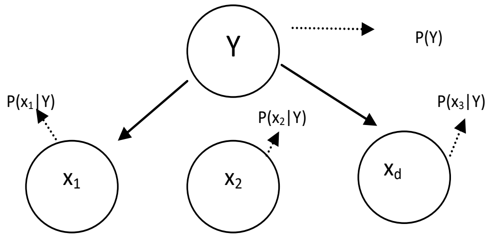


Figure 2. Graphical model of independent inputs

To perform classification when X_i is continuous, then Gaussian distribution can be defined by mean and standard deviation specific to X_i and Y_k. To train Naïve Bayes classifier, mean and standard deviation are estimated. Hence it can be represented as $\mu_{ik=E[Xi|Y=Y_k}$] for mean and $\sigma^2 ik = E[(X_i - \mu_{ik})^2 |Y=yk\ ]$ for standard deviation where X_i = Attribute and Y_k = Possible Values. Priors can be estimated as $\pi_{k=P(Y=y_k\ )}$. Maximum likelihood estimate or Maximum a Posteriori (MAP) can be estimated as $\hat{\mu}_{ik=}\frac{1}{\sum_j \delta(\ Y^j=Y_k)} \sum_j X_i^j \partial(Y^j = Y_k)$ where j=jth training example, k=target. The formula to estimate the probabilities of continuous dataset is P $(v_j|c_i)$ $=\frac{1}{\sqrt{2\pi\sigma_{ji}}} e(-\frac{(v_j-\mu_{ij})^2}{2\sigma^2{}_{ji}})$ where v =variable and c=class.

3. RELEVANCE VECTOR MACHINE

Relevance Vector Machine (RVM) and Support Vector Machine (SVM) have an identical functional form. SVM is a non-probabilistic linear classifier and RVM is a probabilistic classifier and is equivalent to Gaussian process model with covariance function and hence it is formulated as

$$K(x,x') = \sum_{j=1}^{N} \frac{1}{\alpha} \varphi(x,x_j)\varphi(x',x_j) \tag{1}$$

where x refers to input vectors of training set, N is the target. Training RVM involves appropriate weights with proper kernel functions. The symbol φ represents kernel function, α represents variances of prior and x1…xN are input vectors of training data set. The main aim of RVM is to separate input data into their appropriate classes by finding posterior probabilities. One of the main advantage of RVM is that, any kind of kernel function can be used. It can be a simple dot product function or it can be Gaussian Radial Basis function. Other than this RVM classifier can yield decision accuracy and reduction in computational complexity

4. DATA PREPROCESSING

Transforming raw data into understandable format is called as data preprocessing. Generally the real world data are often inconsistent, incomplete and it is likely to have errors and missing values. These are cleaned by using the data preprocessing techniques such as Data cleaning (Filling missing values), Data integration (Using Multiple databases), Data transformation (normalization), Data reduction (Reducing attributes) and Data Discretization (recursively applying partitioning methods). If the data are inconsistent the result will also be inconsistent. Hence data preprocessing plays an important role in data mining.

4. 1. Replacing missing values

The dataset is downloaded from UCI Repository from University of Wisconsin Hospitals, Madison. These dataset are very useful for Data mining. Table 1 shows the details of the attributes.

The dataset consist of totally 11 attributes including sample id number and 699 sample records, out of which 458 records have benign data and 241 records have malignant data. One of the attributes in the dataset consists of missing values. These values must be replaced with new values or those records must be removed. Totally 16 records have missing values. In this work, those values are replaced by data preprocessing method i.e., by finding the mean for that attribute. The dataset is normalized by finding Log10 value for the data in each and every attribute. Data are normalized, so that it improves and speeds up the performance of algorithm and also all the data comes under common scale.

Table 1. Attributes of Wisconsin Dataset

S.No	Attributes/Features	Range of values
1.	Clumpthickness	1-10
2.	Uniformity cell size	1-10
3.	Uniformity cell shape	1-10
4.	Marginal Adhesion	1-10
5.	Single Epithelian Cell size	1-10
6.	Bare Nuclei	1-10
7.	Bland Chromatin	1-10
8.	Normal Nucleoli	1-10
9.	Mitosis	1-10
10.	Class	2-benign 4-Malignant

4. 2. Variable selection using Linear Discriminant Analysis

The purpose of using Linear Discriminant Analysis (LDA) is that, it searches for a linear combination of variables that separates two best classes. LDA performs dimensionality reduction by preserving the class information as much as possible. The variables that are used in this analysis were selected by using Linear Discriminant Analysis (Lorris Nanni & Alessandra lumini, 2010), Different combinations of variables were used and the variables, that gave the highest accuracy were selected for evaluation. Four attributes were selected for diagnosing breast cancer. By considering a set of N dimensional samples such as {α(1, α (2, …, α (N)} where classes are represented by ω1(class 1), ω2(class2) and to obtain scalar y, project the samples α on a line $y = w^t\alpha$ which is the projection of α on w, where w=projection vectors, t=target, α=samples on a line and thus, is a dimensionality reduction . To measure the separation between projections, the arithmetic means of each class are calculated and hence they are specified as μ1, μ2. The mean vector of each class can be calculated as $\mu_{i=\frac{1}{N_i}\sum x\in\omega_i}x$ where x=vector of class ω,where ω_i=class. To find the better separation $|\mu_1 - \mu_2|$ is calculated. Figure 3 shows the two dimensional, two class data projected on w.

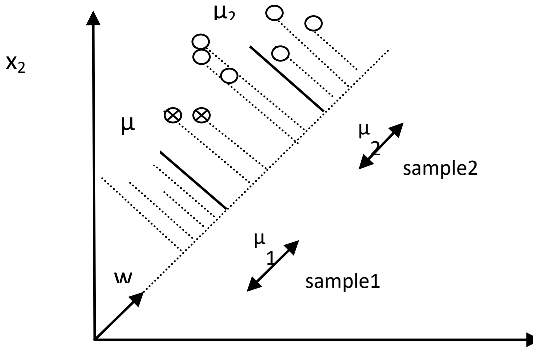
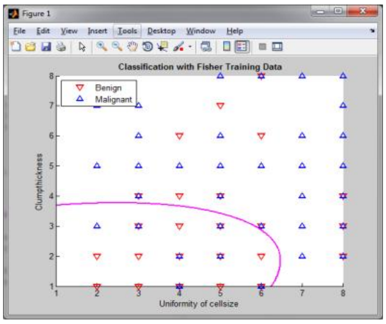
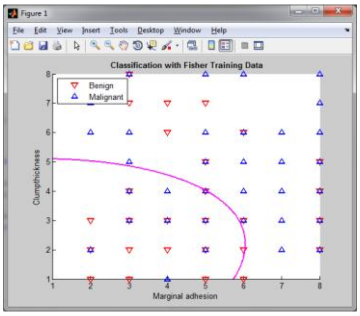
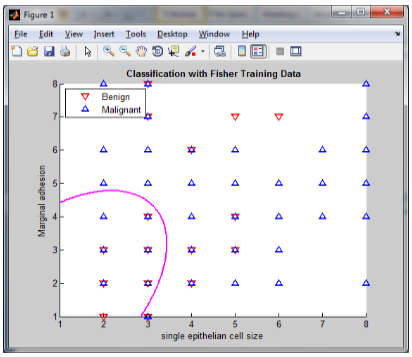
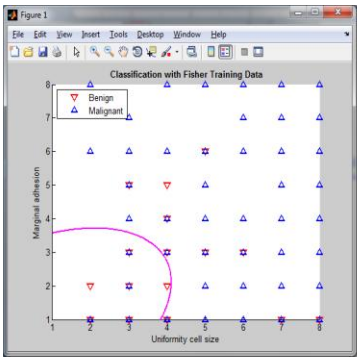


Figure 3. Two class data projected on w

Hence the Linear Discriminant can be calculated by using the formula $D_i = b_0 + \sum_{k=1}^{p} b_k X_k$ where X =raw scores of each predictor, b= constant, p=target. The scoring function of LDA is $C_i = c_1Z_1 + c_2Z_2 + \cdots + c_pZ_p$ where $c_i =$ discriminant function coefficient, Z=score on each predictor, p=target. By using the above function different set of attributes (Di) are created. The group that gives good accuracy is taken for diagnosis. This variable selection is already explained by the same authors in the paper breast cancer detection using Relevance

Vector Machine which has been already published. The following table 2 shows the graphical output classification using LDA. Out of all possible lines, the line that maximizes the scalars seperability is selected.

Table 2. Samples of different outputs with different combination of variables

Name of Algorithm	Output	
Linear Discriminant Analysis	 Figure 1 File Edit View Insert Tools Desktop Window Help Classification with Fisher Training Data Benign Malignant Clumpthickness Uniformity of cellsize (a)	 Figure 1 File Edit View Insert Tools Desktop Window Help Classification with Fisher Training Data Benign Malignant Clumpthickness Marginal adhesion (b)
	 Figure 1 File Edit View Insert Tools Desktop Window Help Classification with Fisher Training Data Benign Malignant Marginal adhesion single epithelian cell size (c)	 Figure 1 File Edit View Insert Tools Desktop Window Help Classification with Fisher Training Data Benign Malignant Marginal adhesion Uniformity cell size (d)

5. LITERATURE REVIEW

The following section explains previous contributions on Naïve Bayes classifier and Relevance Vector Machine (RVM) for breast cancer diagnosis.

S.Kharya and Sunita Soni proposed a new method for a Naïve Bayes classifier by including the weighted approach for classifying breast cancer (Shweta Kharya & Sunita soni, 2016). This approach was done to improve the performance of Naïve bayes classifier. The dataset available in UCI machine learning repository was used. The result of this weighted Naïve Bayes classifier showed better results than the traditional Naïve bayes classifier and the accuracy was 92%. In this work all the features were used for classification.

Murat Karabatak classified breast cancer by using Weighted Naïve Bayesian classfier (Murat Karabatak, 2015). The 5-fold cross validation was done and various performance evaluation techniques were used. The experiment showed that weighted Naïve Bayes worked better than Naïve bayes classfier and the accuracy was up to 98% and all the variable were used.

Shweta Kharya et al. designed a Graphical User Interface for detecting the possibility of occurring breast cancer in future (Shweta Kharya, Shika Agrawal, & Sunita Soni, 2014). The dataset was taken from UCI repository and the result was obtained by mining the dataset. The author proved that Naïve bayes classifier performed good and it gave an accuracy of 93% with less computational cost.

Mahmut Kaya et al. classified breast cancer by using Mammographic images (Mahmut kaya, Oktay, Yıldız, & Hasan Sakir Bilge, 2013). Since there were more missing values, to resolve it K-Nearest Neighborhood algorithm was used and the performance was evaluated by using traditional Naïve bayes classifier which gave an accuracy of 81.69%

Gouda I. Salama et al., used various classifiers for detecting breast cancer (Gouda, Salama, M.B.Abdelhalim, & Zeid, 2012). Each and every classifier was applied in various datasets such as Wisconsin Prognostic Breast Cancer dataset (WPBC), Wisconsin Diagnostic Breast Cancer dataset (WDBC) and original dataset. Features were selected by using Principal Component Analysis (PCA). Out of the different classifiers used Naïve bayes showed the best accuracy of 95%.

Diana Dumitru has done investigation for predicting recurrent and non-recurrent events of breast cancer using Naïve Bayes classifier (Diana Dumitru, 2009). The result showed that the performance of Naïve Bayes was good and it worked equivalent to other machine learning techniques and also the computational cost was low. The accuracy of this work was 72.24%. The dataset used for this work was Wisconsin Prognostic dataset, which was taken from UCI Repository.

Daniele Soria had reviewed different supervised machine learning techniques such as C4.5 tree classifier, Naïve Bayes and Multilayer perceptron (Daniele Soria, Jonathan, Garibaldi, & Elia Bianzoli, 2008). From these algorithms, it was found that Naïve bayes worked better than other two, even if the normality of data strongly violated. The dataset used for this work was taken from Nottingham Tenovus primary breast cancer Carcinoma series. The authors reduced the attributes from 25 to 10 and the accuracy was 93.1%.

B.M.Gayathri and C.P.Sumathi proposed a machine learning algorithm using RVM for detecting breast cancer (B.M.Gayathri & C.P.Sumathi, 2015), (B.M.Gayathri & C.P.Sumathi, 2016). Wisconsin Original dataset was used for analysis. In this work the features were reduced by using Linear Discriminant Analysis (LDA). The accuracy of this algorithm was 97%.

A.Bharathi, K.Anandakumar developed an effective machine learning approach using Relevance Vector Machine (A.Bharathi & K.Anandakumar, 2015). The aim of the authors was to diagnose the investigational value using three site of origin such as Lymphoma, Leukemia and Small Round Blue Cell Tumors (SRBCT) and apply these in three different machine learning algorithms such as Fast Support Vector machine learning, Fast Extreme Machine Learning, and Relevance vector machine learning. Out of these algorithms Relevance vector machine learning gave good accuracy than the other algorithms. The features were selected using Analysis of Variance (ANOVA) by specifying ranking scheme.

Elie Tcheimegni et al. proposed Relevance vector machine for diagnosing various diseases such as breast cancer, liver disorders and diabetes (Elie Tcheimegni, Manohar Mareboyana, ClaudeTurner, & Kofi Nyarko, 2013). The datasets used were from various hospitals. For example Breast cancer dataset was got from Wisconsin Hospital Madrid, Liver disorders dataset from BUPA medical research Ltd. and Diabetes dataset from US National Institute of Diabetes and Kidney diseases. For all these datasets Relevance Vector Machine worked in an efficient way and for breast cancer diagnosis it gave an accuracy of 65.52%.

A.Bharathi and A.M.Natarajan have done cancer classification using Relevance Vector Machine and Support Vector Machine in combination with Analysis of variance (ANOVA) for gene selection (A.Bharathi & A.M.Natarajan, 2011). The genes that were selected using ANOVA were applied to RVM and SVM and accuracy of RVM was 97.21%, which worked better than Support Vector Machine.

6. NAÏVE BAYES-RVM

In this review it is found that the algorithm Naïve Bayes and RVM were used separately and extensively and has yielded good results. In this work it was experimented to test if the combined approach could yield better results than used individually. Both Naïve bayes and Relevance vector machine are probabilistic classifier, which are easy to implement with less computational cost.

6. 1. Research objective

The objective of this research is to develop a user friendly environment for detecting breast cancer and to implement the Naïve Bayes classifier in combination with Relevance Vector Machine to get more accurate results with less features and computational cost. The GUI is designed using MATLAB software which is more useful for analyzing data, developing algorithms and creating application models. Figure 4 shows the model flowchart of proposed classifier.

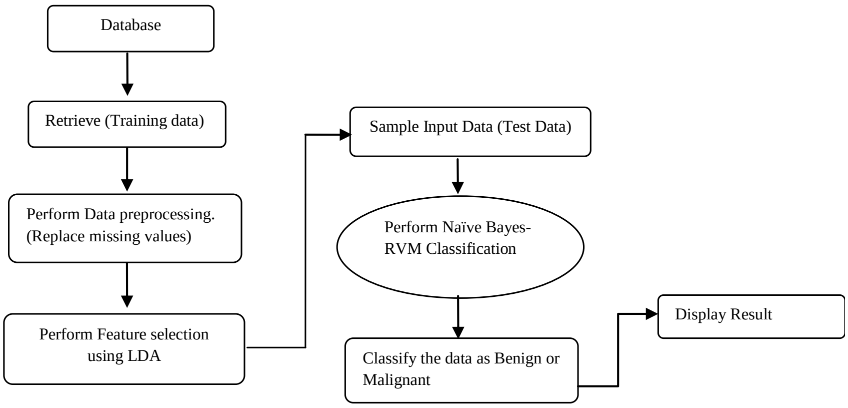
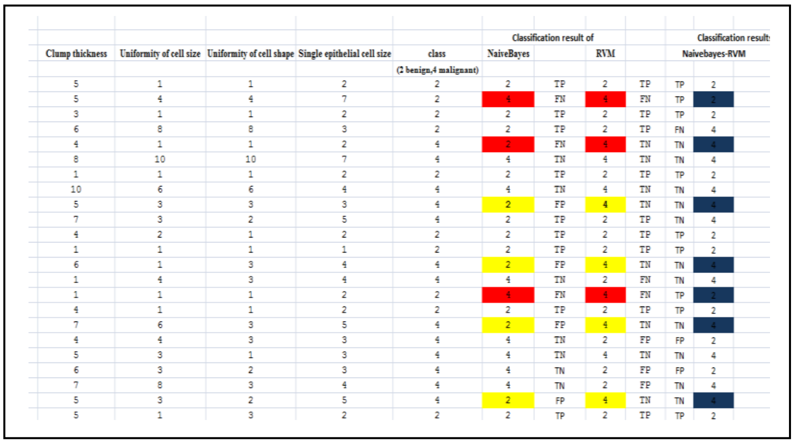

Database
Retrieve (Training data)
Perform Data preprocessing. (Replace missing values)
Perform Feature selection using LDA
Sample Input Data (Test Data)
Perform Naïve Bayes-RVM Classification
Classify the data as Benign or Malignant
Display Result

Figure 4. Model Flow Chart of Naïve Bayes-RVM classification

7. IMPLEMENTATION AND OUTPUT

The Naïve Bayes-RVM algorithm is designed to reduce the computational complexity and predict whether the cancer is benign or malignant. The interface is designed using GUIDE (GUI builder) in MATLAB. The dataset is stored in database and 50% of data were retrieved for training. The dataset contains 699 samples with 16 missing values. It had nine attributes which represent the characteristics of tumor (for eg. Clumpthickness, Uniformity cell size, shape, Marginal adhesion etc.) out of which only four attributes were selected by using one of the data preprocessing method called Linear Discriminant Analysis and the missing values are replaced by median method. The best four attributes were selected for classification. Remaining 50% of data were entered manually in GUI for testing. The following tables table 3 to table 8 shows the sample classification result for 30 records. The accuracy of Naïve Bayes, RVM and Naïve-Bayes-RVM were verified and it showed that NaiveBayes-RVM classifies better when combined, than classifying separately. This is explained by using confusion matrix for all the three algorithms. In figure 5, the values that are bold shows the difference between the results.



					Classification result of					Classification result:
Clump thickness	Uniformity of cell size	Uniformity of cell shape	Single epithelial cell size	class	NaiveBayes		RVM			Naivebayes-RVM
				(2 benign,4 malignant)						
5	1	1	2	2	2	TP	2	TP	TP	2
5	4	4	7	2	4	FN	4	FN	TP	2
3	1	1	2	2	2	TP	2	TP	TP	2
6	8	8	3	2	2	TP	2	TP	FN	4
4	1	1	2	4	2	FN	4	TN	TN	4
8	10	10	7	4	4	TN	4	TN	TN	4
1	1	1	2	2	2	TP	2	TP	TP	2
10	6	6	4	4	4	TN	4	TN	TN	4
5	3	3	3	4	2	FP	4	TN	TN	4
7	3	2	5	4	2	TP	2	TP	TN	4
4	2	1	2	2	2	TP	2	TP	TP	2
1	1	1	1	2	2	TP	2	TP	TP	2
6	1	3	4	4	2	FP	4	TN	TN	4
1	4	3	4	4	4	TN	2	FN	TN	4
1	1	1	2	2	4	FN	4	FN	TP	2
4	1	1	2	2	2	TP	2	TP	TP	2
7	6	3	5	4	2	FP	4	TN	TN	4
4	4	3	3	4	4	TN	2	FP	FP	2
5	3	1	3	4	4	TN	4	TN	TN	4
6	3	2	3	4	4	TN	2	FP	FP	2
7	8	3	4	4	4	TN	2	FP	TN	4
5	3	2	5	4	2	FP	4	TN	TN	4
5	1	3	2	2	2	TP	2	TP	TP	2

Figure 5. Sample of classified dataset

Table 3. Confusion matrix for Naïve Bayes

Dataset		30
Condition positive	10(TP)	4(FN)
Condition Negative	7(FP)	9(TN)

Table 4. Performance evaluation of Naïve Bayes classifier

Algorithm	Dataset	Recall rate	Precision Rate	Accuracy
Naïve Bayes	30	71.4%	56%	63.3%

Table 5. Confusion Matrix for RVM

Dataset	30	
Condition positive	11(TP)	3(FN)
Condition Negative	3(FP)	17(TN)

Table 6. Performance evaluation of RVM

Dataset	Sensitivity	Specificity	Accuracy
30	78.7%	85%	82.3%

Table 7. Confusion Matrix for Naïve Bayes - RVM

Dataset	30	
Condition positive	11(TP)	3(FN)
Condition Negative	3(FP)	17(TN)

Table 8. Performance evaluation of Naïve Bayes –RVM classifier

Dataset	Sensitivity	Specificity	Accuracy
30	91.6%	88.8%	0.90%

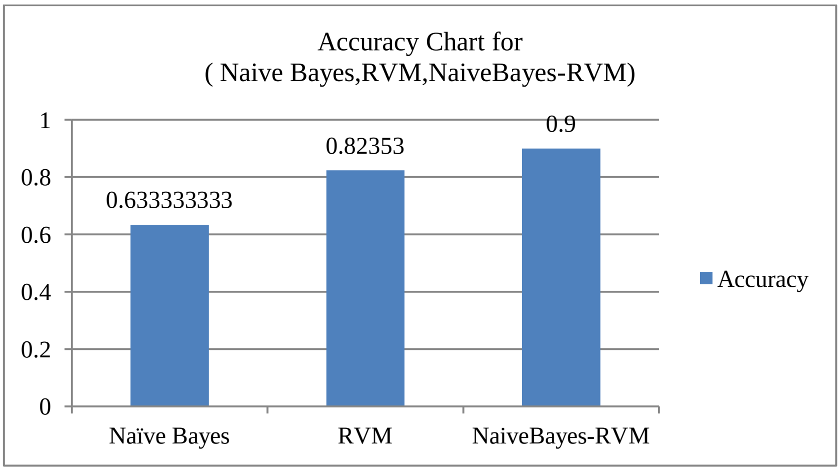


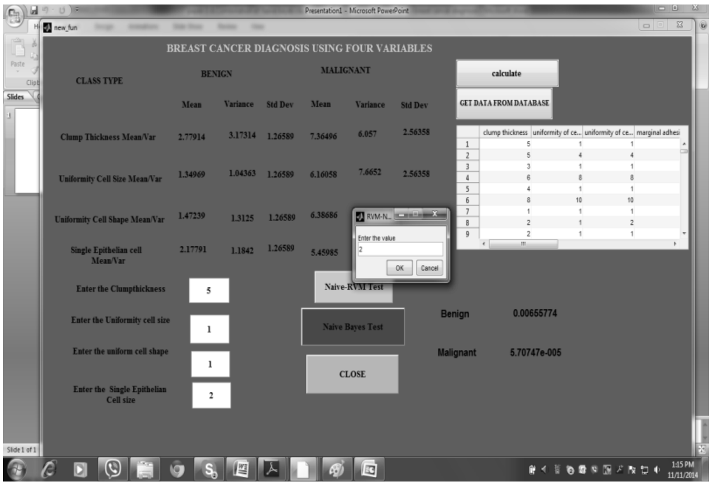
Figure 6. Accuracy chart

Figure 6 shows the accuracy chart of Naivebayes-RVM, when combined together gives more accuracy than NaiveBayes and RVM algorithms for the sample dataset. Figure 7 is the sample interface screen shots.

The following table 9 shows the True Positive, True Negative, False Positive and False Negative classification of Naïve-RVM classifier and table 10 shows the performance evaluation of Naïve bayes –RVM classifier for 300 dataset.

Table 9. Confusion Matrix for Naïve Bayes-RVM

Dataset	300	
Condition positive	98.3%(TP)	2%(FN)
Condition Negative	1.6%(FP)	98%(TN)



BREAST CANCER DIAGNOSIS USING FOUR VARIABLES

CLASS TYPE	BENIGN			MALIGNANT		
	Mean	Variance	Std Dev	Mean	Variance	Std Dev
Clump Thickness Mean/Var	2.77914	3.17314	1.26589	7.36496	6.057	2.56358
Uniformity Cell Size Mean/Var	1.34969	1.04363	1.26589	6.16058	7.6652	2.56358
Uniformity Cell Shape Mean/Var	1.47239	1.3125	1.26589	6.38686		
Single Epithelian cell Mean/Var	2.17791	1.1842	1.26589	5.45985		

	clump thickness	uniformity of ce...	uniformity of ce...	marginal adhesi
1	5	1	1	
2	5	4	4	
3	3	1	1	
4	6	8	8	
5	4	1	1	
6	8	10	10	
7	1	1	1	
8	2	1	2	
9	2	1	1	

Enter the value: 2

Enter the Clumpthickness: 5

Enter the Uniformity cell size: 1

Enter the uniform cell shape: 1

Enter the Single Epithelian Cell size: 2

Benign 0.00655774

Malignant 5.70747e-005

Figure 7. GUI Interface design for Naïve Bayes-RVM

Table 10. Performance evaluation of Naïve Bayes -RVM

Algorithm	Dataset	Recall rate	Precision Rate	Accuracy
Naïve Bayes-RVM	300	98.3%	98%	98%

8. CONCLUSION

In Machine learning techniques, Naïve Bayes acts as a simple probabilistic classifier and Relevance Vector Machine works as a powerful statistical tool for classifying data. The tables 3 to 8 shows the confusion matrix and performance evaluation for the sample of 30 records for Naïve Bayes, RVM and also both combined together. Out of these NaïveBayes-RVM gives better result. The analysis for same dataset for 300 records, was done for Naïve Bayes and RVM separately and their accuracies was 96% and 97% respectively. In this work, the testing is done for 300 records and it gave the accuracy of 98%. Table 9 and 10 shows the confusion matrix and performance evaluation of the proposed algorithm. While performing classification separately, these classifiers work in a better way but when combined, it gives better result than classifying separately. The system is trained and tested using Wisconsin Original dataset and this work can also be expanded to other dataset (such as real life data) from any of the cancer hospital in future.

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