

A Comparative Study of Classification Algorithms to Analyse Biological Data sets

Kommareddy Roja Rani & Dr G Lavanya Devi ¹ M.Tech CST-Bioinformatics, CS&SE Department, Andhra University, Visakhapatnam rojarani.kr@gmail.com ²Assistant Professor, CS&SE Department, Andhra University, Visakhapatnam

lavanyadevig@yahoo.co.in

Abstract:

Data mining is an area of computer science with a huge prospective and it is the process of discovering or extracting information from large database or data sets. Classification also can be *implemented through different number of approaches* or algorithms. The main theme is applying classification algorithms on the considered breast cancer data set. The theme explains about Decision Bayesian classification, Support vector tree, machines and K-Nearest neighbor algorithms and comparison between these four algorithms can be done with the help of R Programming language, which is a open source software. For the comparison of the results, we have used accuracy, error rate, sensitivity, and specificity to find out from the confusion matrix or error matrix. Keywords

Classification; Decision tree; Naïve bayes; Knearest neighbor; Support vector machines; Breast cancer

1. Introduction

Breast cancer is the second leading cause of death among women and it is the second stage of lung cancer [1]. The health and medical sector is more in need of data mining today. By using various data mining methods, valuable information can be extracted from large data base and that can help the medical practitioner to take decision, and improve health services. There are few arguments that can support the use of data mining in health sector for breast cancer like early detection, early avoidance, and indication based medication, rectifying hospital data errors [2]. For statistical analysis, graphical representation and reporting, a programming language named R is used, which provides a software environment. It is freely available under the GNU General Public License, and pre-compiled binary versions are provided for various operating systems like Mac, Linux and Windows. The main reason behind using R programming is helps researchers like us to implement and compare data

mining techniques very easily on real or synthetic data. R is free software distributed under a GNU-style copy left, and an official part of the GNU project called GNU's.

Breast cancer is a malignant or benign tumor, inside breast, wherein cells divide and grow without control [4]. Scientists have tried to know the exact reason behind breast cancer, as there are few risk factors which increase the like childhood of a woman developing breast cancer. Age, Genetic and Hereditary problems are some factors being considered for breast cancer [3].

Treatments of breast cancer are divided into two types, local and systematic. Surgery and radiation are comes under local type of treatments whereas chemotherapy and hormone therapies are examples of systematic therapies. For getting best results, both treatments are used together in different variations as per the patient and disease intensity [9].

2. Classification Algorithms

A. Decision Tree

Decision tree is powerful classification algorithm in data mining. There are several popular decision algorithms such as Quinlan's ID3, C4.5, C5 and CART [8]. A decision tree is a tree structure, where each branch represents an outcome of the test, each internal node denotes a test on an attribute, and each leaf node holds a class label [5]. This technique separates observation into branches to construct tree on repetition basis. In most cases, tree classifiers perform classification in two stages: tree-growing and tree-pruning. The tree-growing is top down approach. In this stage, the tree is split in a recursive manner called recursive partitioning. It is completed when the subset at a node has all the same value of the target variable, or when splitting no longer adds value to the predictions. In the tree-pruning, the tree will be fully grown, fully grown tree is cut back to avert over fitting data and this way it improves the correctness of the tree in bottom up manner. This technique is used to improve the estimate and correctness of the algorithm by minimizing the over fitting. Decision tree is widely used in various areas



because it is strong enough for data distribution.

Here, in this used ID3 classifier for the dataset. It is a collection of pruned decision tree. ID3 has been well established for relatively small datasets. Efficiency becomes an issue of concern when these algorithms are applied to the mining of very large real-world databases. The pioneering decision tree algorithms that we have discussed so far have the restriction that the training tuples should reside in memory [6].



Fig 1: Decision Tree

B. Bayes classification

Bayesian classifier is a statistical classifier as well as a supervised learning method. It will predict class membership probabilities. It provides useful perception for understanding and assessing many learning algorithms. It calculates explicit probabilities for hypothesis and it is robust to noise in input data. When Bayesian classifier is applied to large database, it shows high accuracy and speed. The values of other attributes as the attribute value on a given class are independence to each other, the effect of this can be assumed by the naive Bayesian classifiers. This assumption is called classconditional independence. For this purpose, the Naive Bayesian classification is used for testing [6]. The determination of the posterior probability is best defined using Bayes' theorem.

$$P(H|X) = P(X|H) P(H) / P(X)$$

C. Support Vector Machines

The data set teaches support vector machine to classify the new data as for classification or regression problems, supervised machine learning algorithm also known as support vector machine (SVM) is been used. It works by classifying the data into different classes by finding a line (hyper plane) which separates the training data set into classes. To maximize the distance between the various classes that are involved in linear hyper planes, the support vector algorithm is been used and this is referred as margin maximization.

SVM's are classified into two categories:

- Linear SVM's In linear SVM's the training data i.e. classifiers are separated by a hyper plane.
- Non-Linear SVM's In non linear SVM's it is not possible to separate the training data using a hyper plane. For example, the training data for face detection consists of group of images that are faces and another group of images that are not faces (in other words all other images in the world except faces). The training data is too complex to find a representation for every feature vector which is not possible under this condition. Dividing the set of faces sequential from the set of non-face is a complex task.

D. K-Nearest Neighbor

K-Nearest Neighbor (K-NN) classifier is also known as a distance based classifier. Nearest neighbor classifiers are based on analogy learning. So that means, it is comparing given test tuples with training tuples that are similar to it. The unknown tuple is assigned to most common class among its K-nearest neighbors. When K = 1, the unknown tuple is assigned the class of the training tuple that is closest in the pattern space. It is also used for numeric prediction, that is, it returns realvalue prediction for unknown tuple [5]. This method is also called the lazy learner method.



Fig 2: K-Nearest Neighbor

3. Implementation

A. Data mining in breast cancer comparison

Four different classification algorithms i.e. Decision tree (ID3), Naïve Bayes, K-Nearest Neighbor, and Support Vector Machine have been used to analyze data.

B. Data source

To evaluate these data mining classification,



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we have used dataset of UCI Machine Learning Repository [8]. This dataset has 569 instances. It contains 31 attributes and 1 class attribute. As we did class distribution, there are 357(62.7%) benign class distribution and 212(37.25%) malignant class distribution. No missing values are there in the dataset. To gives description of attributes of breast cancer dataset [11].

C. Performance study of Algorithms on dataset

- Number of instances: 569
- Number of attributes: 32 (ID, diagnosis, 30 real-valued input features)
- Attribute information

1) ID number

2) Diagnosis (B = benign, M = malignant)

Ten real-valued features are computed for each cell nucleus:

- a)Radius
- b) Texture

c) Perimeter
d) Area
e) Smoothness
f) Compactness
g) Concavity
h) Concave points

- i) Symmetry
- j) Fractal dimension

Several of the papers listed above contain detailed descriptions of how these features are computed [12].

All feature values are recoded with four significant digits.

- Missing attribute values: none
- Class distribution: 357 benign, 212 malignant

4. Comparison between the Different Classifiers

As shown in Table 1, based on different criteria, the comparison between the four algorithms Table 1 Comparison of Classifiers

Fields	Decision Tree	Bayes Classification	K-Nearest Neighbor	Support Vector Machine
Major	Decision tree algorithms used to build tree, if then-else rules to classify the data items.	It works on probabilistic representation of attribute values.	It is distance based algorithm.	It is classifying the data into different classes by finding a line (hyper plane).
Classifier works	It recursively partitions data set using depth-first greedy approach or breadth-first approach. It will repeat items are not assigned to some class.	It learns from training data, the independent conditional probability of each attribute.	For unknown sample, it searches the pattern space from the training samples which is close to the unknown samples.	The margin of separation Kernel function.
Different phases of work	Tree building. Tree pruning.	Posterior probability. Prior probability.	Finding distance. Assigning class to maximum class amongst k.	Linear SVM's Non –Linear SVM's.
Advantages	Domain knowledge not required. Works with huge dimensional data.	Achieves high speed and accuracy for large dataset. Calculation work easy.	Implementation easy for parallel implementation work with local info.	It offers best classification performance on the training data.
Disadvantages	Categorical output. One output attribute.	Conditional independence in class for rules.	Requires large storage area may be slow in classifying tuples.	Speed and size, both training and testing.



Vector

Machine

K-

Nearest

Neighbo r

%

%

0% % Basis % % (rbfdot) 99.43 96.66 3.3 91.98

3%

Confusion matrix or error matrix:

A confusion matrix is obtained to calculate accuracy, error rate, Sensitivity and Specificity. Confusion matrix is a matrix representation for the classification [6]. It is shown in Table 2

- True Positives (TP): these are in which we \triangleright predicated yes, and they do have the disease.
- \geq True Negatives (TN): we predicted no, and they don't have the disease.
- False Positives (FP): We predicted yes, but \triangleright they don't actually have the disease.
- \geq False Negatives (FN): We predicted no, but they actually do have the disease.

The formula shown below is used to calculate accuracy, error rate, sensitivity, and specificity.

	Classified as Healthy	Classified as not Healthy
Actual Healthy	ТР	FN

FP

Accuracy = (TP + TN) / (TP + FP + TN + FN)Error rate = (FP+FN)/(TP+FP+TN+FN)

TN

Actual

Healthy

Not

Sensitivity=TP / (TP-FN) Specificity=TN/ (TN-FP)

TABLE 2. Confusion Matrix

5. Results Table 3. Performance Study of Algorithms of Total

Data

Classifie r(569 instance s)	Algorit hms implem ented	Accu racy	Err or rate	Sensit ivity	Specif icity
Bayes	Naïve	94.02	5.9	94.24	93.62
Classific	Bayes	%	7%	%	%
ation					
Support	Radial	98.24	1.7	99.90	95.20

Table 3 represents the accuracy, error rate, sensitivity, and specificity for different classification techniques that have been implemented on total data set. Figure 3 represents the Support Vector Machines is superior algorithm compare to other three.

%





Table 4. Performance Study of Algorithms of Training Data

Classifi er(569 instanc es)	Algorit hms implem ented	Accu racy	Error rate	Sensi tivity	Spec ificit y
Decisio n Tree	ID3	97.20 %	2.76 %	97.16 %	97.3 5%
Bayes Classifi cation	Naïve Bayes	94.47 %	5.50 %	95.01 %	93.4 3%
Suppor t Vector Machin e	Radial Basis (rbfdot)	99.24 %	0.70 %	98.84 %	99.9 0%

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Table 4 represents the accuracy, error rate, sensitivity, and specificity for different classification techniques that have been implemented on training data set (70%). Figure 4 represents the Support Vector Machines is superior algorithm compare to other three.



Fig 4: Comparison of Accuracy, Error rate, Sensitivity, Specificity of Training Data.

Table 5.	Performance	Study	of Algorithms	of Test
		Data		

Classifi er(569 instance s)	Algorit hms implem ented	Accu racy	Err or rate	Sensit ivity	Specif icity
Decisio	ID3	92.98	7.0	96.33	87.09
n Tree		%	0%	%	%
Bayes	Naïve	92.39	7.6	91.42	93.93
Classifi	Bayes	%	0%	%	%
cation					
Support	Radial	95.90	4.0	95.14	97.07
Vector	Basis	%	9%	%	%
Machin	(rbfdot)				
e					
K-		97.07	2.9	96.90	97.40
Nearest		%	0%	%	%
Neighb					
or					

Table 5 represents the accuracy, error rate, sensitivity, and specificity for different classification techniques that have been implemented on test data set (30%). Figure 5 represents the Support Vector Machines is superior algorithm compare to other three.



Fig 5: Comparison of Accuracy, Error rate, Sensitivity, Specificity of Test Data.

CONCLUSION

Several data mining classification techniques can be applied for the identification and prevention of breast cancer among patients. In this, we used four different data miming classification methods for prediction of breast cancer. Comparison is done using different parameters for the prediction of cancer. But for superior prediction, we focus on accuracy, error rate, sensitivity, and specificity. Our studies filtered all the algorithms based on accuracy and error rate. We came up with conclusion that support vector machine is a superior algorithm.

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