

Breast Cancer Prediction Using Naive Bayes Classifier

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Abstract: In this paper we present a predictive model to identify the type of breast cancer as benign or malignant. For this purpose, we developed our own naive bayes classifier which helps oncologist in diagnosing the cancer type with in no time and then helps oncologist in decision making in treatment method for the same purpose, we have taken dataset from uci ml repository which consists of 699 valid instances and 10 attributes on the basis of which we will find out the type of cancer one is suffering from. We have used our own algorithm to clean the data by providing the missing tuple a valid value based on the nearby attribute value. unlike weka which skips the instances with missing tuples. After a series of procedures to cleanse the data, we applied machine learning algorithm: naive bayes. using java net beans interface to predict the type of breast cancer. In this study, we compare the 4 machine learning algorithms:- svm, bayes network, naive bayes, j48 decision to the same data. After comparison with weka, it has been found that our implementation of the machine learning algorithm naive bayes on java net beans interface project builder and provides better accuracy.

Keyword: UCI ML repository, WEKA, Naive Bayes, JAVA Net beans, machine learning

1. Introduction

Breast cancer is a malignant tumor that starts in cells of the breast. A malignant tumor is a group of cancer cells that spread into distant areas of the body [1]. Breast Cancer, one of the commonest malignancies, is a major cause of death among women in developed countries like UK, USA and in developing countries like India[2]. With the growth of developing countries grows the risk of suffering from diseases like breast cancer among its people[3]. An analysis has shown that survival rate is 88% after 5 years of diagnosis and 80% after 10 years of diagnosis .Therefore it is necessary to detect breast cancer at earliest stage possible[4].

The data provided by UCI repository[5] is quite helpful in identifying the attributes that count in investigating the type of breast cancer one is suffering from. The attributes we have taken into account are:

1. Sample code number Id-number
2. Clump thickness 1-10
3. Uniformity of cell size 1-10
4. Uniformity of cell shape 1-10
5. Marginal Adhesion 1-10
6. Single Epithelial cell size 1-10
7. Bare Nuclei 1-10

1. Introduction

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10. Mitoses 1-10

11. Class (2 for benign, 4 for malignant)

After identifying the attributes we have to ap- ply a machine learning algorithm to accurately predict the breast cancer type. So, we imple- mented Naïve Bayes Algorithm and compared our results with results of the tool WEKA [6]. On comparison we found that our model pre- dicted more accurately.

2. Background Study

The Naive Bayes Classifier technique is based on the so-called Bayesian theorem and is par- ticularly suited when the dimensionality of the inputs is high. Despite its simplicity, Naive Bayes can often outperform more sophisticated classification methods [7].

To demonstrate the concept of Naïve Bayes Classification, consider the example displayed in the illustration above. As indicated, the ob- jects can be classified as either GREEN or RED. Our task is to classify new cases as they arrive, i.e., decide to which class label they be- long, based on the currently exiting objects.

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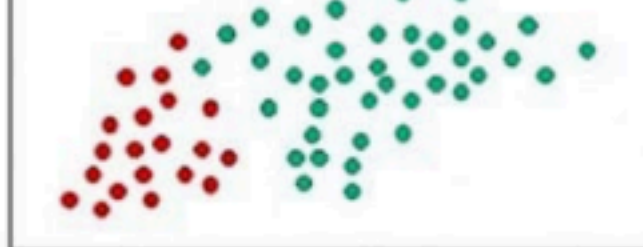


Fig. 1. Objects for Clasification

Since there are twice as many GREEN objects as RED, it is reasonable to believe that a new case (which hasn't been observed yet) is twice as likely to have membership GREEN rather than RED. In the Bayesian analysis, this belief is known as the prior probability. Prior probabilities are based on previous experience, in this case the percentage of GREEN and RED objects, and often used to predict outcomes before they actually happen.

Thus, we can write:

$$\text{Probability for GREEN} \propto \frac{\text{Number of GREEN objects}}{\text{Total number of objects}}$$

$$\text{Probability for RED} \propto \frac{\text{Number of RED objects}}{\text{Total number of objects}}$$

Since there is a total of 60 objects, 40 of which are GREEN and 20 RED, our prior probabilities for class membership are:

$$\text{Probability for GREEN} \propto \frac{40}{60}$$

$$\text{Probability for RED} \propto \frac{20}{60}$$

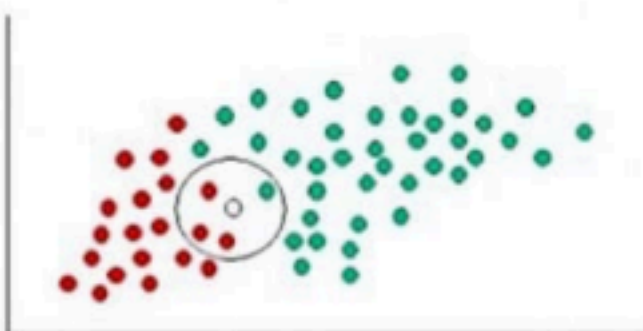


Fig. 2. Classification of newly arrived object

Having formulated our prior probability, we are now ready to classify a new object (WHITE circle). Since the objects are well clustered, it is reasonable to assume that the more GREEN (or RED) objects in the vicinity of X, the more likely that the new cases belong to that particular color. To measure this likelihood, we draw a circle around X which encompasses a number (to be chosen a priori) of points irrespective of their class labels. Then we calculate the number of points in the circle belonging to each class label. From this we calculate the likelihood:

$$\text{Likelihood of X given RED} \propto \frac{\text{Number of RED in the vicinity of X}}{\text{Total number of RED cases}}$$

From the illustration above, it is clear that Likelihood of X given GREEN is smaller than Likelihood of X given RED, since the circle encompasses 1 GREEN object and 3 RED ones. Thus:

$$\text{Probability of X given GREEN} \propto \frac{1}{40}$$

$$\text{Probability of X given RED} \propto \frac{3}{20}$$

Although the prior probabilities indicate that X may belong to GREEN (given that there are twice as many GREEN compared to RED) the likelihood indicates otherwise; that the class membership of X is RED (given that there are more RED objects in the vicinity of X than GREEN). In the Bayesian analysis, the final classification is produced by combining both sources of information, i.e., the prior and the likelihood, to form a posterior probability using the so-called Bayes' rule (named after Rev. Thomas Bayes 1702-1761).

Posterior Probability of X being GREEN \propto

$$\text{Prior probability of GREEN} \times \text{Likelihood of X given GREEN} = \frac{4}{6} \times \frac{1}{40} = \frac{1}{60}$$

Posterior Probability of X being RED \propto

$$\text{Prior probability of RED} \times \text{Likelihood of X given RED} = \frac{2}{6} \times \frac{3}{20} = \frac{1}{20}$$

Finally, we classify X as RED since its class membership achieves the largest posterior probability.

3. Methodology

In this paper, we have implemented naïve Bayes algorithm to predict cancer type by using JAVA Netbeans interface and then compared the result with the other algorithm using WEKA.

To carry out this whole operation we have firstly cleansed the data through data mining techniques [9] and then applied Naïve Bayes algorithm to classify the breast cancer type as benign or malignant[10].

The dataset that we have used in our study is from UCI ML repository and it consists of 699 instances and 10 attributes. It has positive samples and negative samples and every sample has the 10 attributes defined for them.



Fig. I. Objects for Clasification

Since there are twice as many GREEN objects as RED, it is reasonable to believe that a new case (which hasn't been observed yet) is twice as likely to have membership GREEN rather than RED. In the Bayesian analysis, this belief is known as the prior probability. Prior probabilities are based on previous experience, in this case the percentage of GREEN and RED objects, and often used to predict outcomes before they actually happen.

Thus, we can write:

Probability for GREEN $a = \frac{40}{60}$ Probability for RED $a = \frac{20}{60}$

Since there is a total of 60 objects, 40 of which are GREEN and 20 RED, our prior probabilities for class membership are:

Probability for GREEN a^*

Probability for RED a^*





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Having formulated our prior probability, we are now ready to classify a new object (WHITE circle). Since the objects are well clustered, it is reasonable to assume that the more GREEN (or RED) objects in the vicinity of X, the more likely that the new cases belong to that particular color.

To measure this likelihood, we draw a circle around X which encompasses a number (to be chosen a priori) of points irrespective of their class labels. Then we calculate the number of points in the circle belonging to each class label. From this we calculate the likelihood:

Likelihood of X given GREEN = $\frac{\text{Number of GREEN points in circle}}{\text{Total number of points in circle}}$

Figure 2. Classification of newly arrived object

Likelihood of X given RED = $\frac{\text{Number of RED points in circle}}{\text{Total number of points in circle}}$

Figure 2. Classification of newly arrived object

From the illustration above, it is clear that Likelihood of X given GREEN is smaller than Likelihood of X given RED, since the circle encompasses 1 GREEN object and 3 RED ones. Thus: Probability of X given GREEN = $\frac{1}{4}$.

Probability of X given RED = $\frac{3}{4}$;

Although the prior probabilities indicate that X may belong to GREEN (given that there are twice as many GREEN compared to RED) the likelihood indicates otherwise; that the class membership of X is RED (given that there are more RED objects in the vicinity of X than GREEN). In the Bayesian analysis, the final classification is produced by combining both sources of information, i.e., the prior and the likelihood, to form a posterior probability using the so-called Bayes' rule (named after Rev. Thomas Bayes 1702-1761).

Posterior Probability of X being GREEN = Prior probability of GREEN x Likelihood of X given GREEN = $\frac{1}{2} \times \frac{1}{4} = \frac{1}{8}$

Posterior Probability of X being RED = Prior probability of RED x Likelihood of X given RED

$= \frac{1}{2} \times \frac{3}{4} = \frac{3}{8}$

Figure 2. Classification of newly arrived object

Finally, we classify X as RED since its class membership achieves the largest posterior probability.

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In this paper, we have implemented naive Bayes algorithm to predict cancer type by using JAVA Netbeans interface and then compared the result with the other algorithm using WEKA.

To carry out this whole operation we have firstly cleansed the data through data mining techniques (91 and then applied Naive Bayes algorithm to classify the breast cancer type as benign or malignant (10).

The dataset that we have used in our study is from UCI ML repository and it consists of 699 instances and 10 attributes. It has positive samples and negative samples and every sample has the 10 attributes defined for them.

The Naïve Bayes technique depends on the famous Bayesian approach following a simple, clear and fast classifier [11]. A naive Bayes classifier is a simple probabilistic classifier based on applying Bayes' theorem with strong (naive) independence assumptions. A more descriptive term for the underlying probability model would be "independent feature model". A naive Bayes classifier assumes that the presence (or absence) of a particular feature of a class is unrelated to the presence (or absence) of any other feature, given the class variable.

The different parameters that are computed are

$$\text{Accuracy} = (TP+TN)/(TP+FP+TN+TP) \text{--- (1)}$$

$$\text{Sensitivity} = TP/(TP+FP) \text{--- (2)}$$

$$\text{Selectivity} = (TP+FP)/(TP+FP+TN+TP) \text{--- (3)}$$

$$\text{Specificity} = TN/(TN+FP) \text{--- (4)}$$

$$\text{Missed Alarm Rate} = FN/(TP+FN) \text{--- (5)}$$

$$\text{False Alarm Rate} = FP/(TP+FP) \text{--- (6)}$$

From the confusion matrix to analyze the performance criterion for the classifiers in detecting breast cancer, accuracy, precision (for multiclass dataset), sensitivity and specificity have been computed to give a deeper insight of the automatic diagnosis [12]. Accuracy is the percentage of predictions that are correct. The precision is the measure of accuracy provided that a specific class has been predicted. The sensitivity is the measure of the ability of a prediction model to select instances of a certain class from a data set. The specificity corresponds to the true negative rate which is commonly used in two class problems. Accuracy, precision, sensitivity and specificity are calculated using the equations given above, where TP is the number of true positives, TN is the number of true negatives, FP is the number of false positives and FN is the number of false negatives[13].

4. Experimental Study

In this paper, accuracy of our own implemented naïve Bayes is compared with accuracy of four different algorithms on WEKA. Here, our goal is to have high accuracy, besides high precision and recall metrics.

5. RESULT AND DISCUSSION

Table 1 reflects the result that we are getting from our implemented algorithm. As reflected in the table our implemented algorithm pro-

vided better results when compared with other existing algorithm of WEKA (i.e. SMO, J-48 Decision etc.)

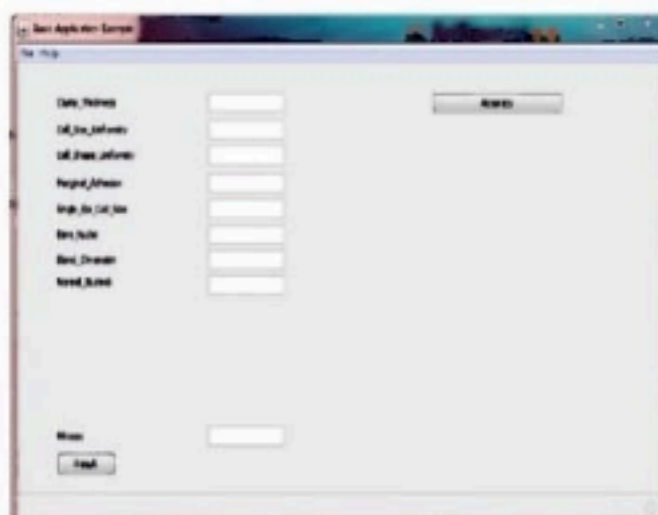


Fig.3. Application Interface

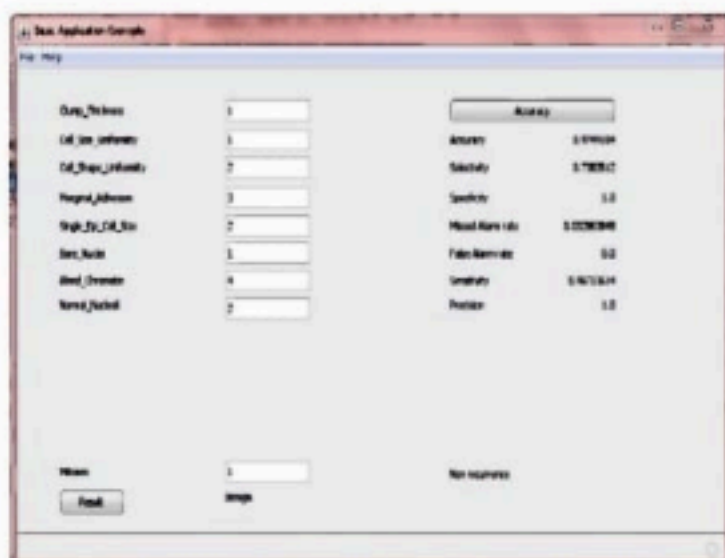


Fig.4. Integrated Application Interface showing result

Table 1. Result From Study

Accuracy	0.975
Precision	1.0
Sensitivity	0.967
Selectivity	0.738
Specificity	1.0
Missed Alarm Rate	0.0328
False Alarm Rate	0.0

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The different parameters that are computed are

Accuracy = $(TP + TN) / (TP + FP + TN + FN)$ --- (1)

Sensitivity = $TP / (TP + FN)$ ----- (2)

Selectivity = $TN / (TN + FP)$ ----- (3)

Specificity = $TN / (TN + FP)$ ----- (4)

Missed Alarm Rate = $FN / (TP + FN)$ ----- (5) False Alarm Rate = $FP / (TP + FP)$ --- (6)

From the confusion matrix to analyze the performance criterion for the classifiers in detecting breast cancer. accuracy, precision (for multiclass dataset). sensitivity and specificity have been computed to give a deeper insight of the automatic diagnosis [12]. Accuracy is the percentage of predictions that are correct. The precision is the measure of accuracy provided that a specific class has been predicted. The sensitivity is the measure of the ability of a prediction model to select instances of a certain class from a data set. The specificity corresponds to the true negative rate which is commonly used in two class problem. Accuracy, precision, sensitivity and specificity are calculated using the equations given above, where TP is the number of true positives, TN is the number of true negatives, FP is the number of false positives and FN is the number of false negatives [13].

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In this paper, accuracy of our own implemented naive Bayes is compared with accuracy of four different algorithms on WEKA. Here, our goal is to have high accuracy, besides high precision and recall metrics.

5- RESULTS AND DISCUSSION

Table I reflects the result that we are getting from our implemented algorithm. As reflected in the table our implemented algorithm provides better results than WEKA in terms of Accuracy, Sensitivity, and Specificity. Also, the implemented algorithm provides better results when compared with other existing algorithms

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Fig.3. Application Interface

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Fig.4. Integrated Application Interface showing result

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Accuracy	Precision	Sensitivity	Specificity
94.762%	0.948	0.961	0.935
96.19%	0.962	0.97	0.948
95.714%	0.957	0.962	0.935
93.80%	0.938	0.940	0.897

Conduction and Future Work

implemented using machine learning in diagnosing cancer type into decision taking for cancer patients we have implemented Naïve Bayes using JAVA Net beans interface. Results show that our approach provides better accuracy in cancer type as benign and malignant.

Our results are better for our implemented Naïve Bayes algorithm as compared to other machine learning algorithm – SMO, Bayes Net, J-48 Decision.

We apply data cleaning algorithm to include the records with missing values on the basis of value of which are not included in case of missing values.

We include experimenting other machine learning algorithm using JAVA Net beans interface. The hybrid algorithm which is a combination of two or more algorithms to model which can predict with better accuracy. Table 2 reflects the result that we are achieved.

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Table 2. Result from WEKA

Conduction and Future Work

Algorithm Accuracy Precision Naive Bayes This Study Implemented using machine learning

technique is helpful in diagnosing cancer type into assist oncologist in decision taking for cancer patient. For this purpose we have implemented Naive Bayes algorithm using JAVA Net beans interface. The experimental results show that our approach performs better and provides better accuracy in predicting the cancer type as benign or malignant.

This study shows that results are better for our implemented Naive Bayes algorithm as compared to other machine learning algorithm - SMO, Bayes Network, Naive Bayes, J48 Decision Tree.

In this work, we apply data cleaning algorithm to clean the data and to include the records with missing data as well on the basis of value of nearby attribute, which are not included in case of WEKA.

Future work will include experimenting other machine learning algorithm using JAVA Net beans interface to make hybrid algorithm which is a combination of existing two or more algorithms to create a predictive model which can predict with higher accuracy. Table 2 illustrates the result that we are getting using tool WEKA.

References

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