Available Online at www.ijcsmc.com

International Journal of Computer Science and Mobile Computing

A Monthly Journal of Computer Science and Information Technology

ISSN 2320–088X

IJCSMC, Vol. 3, Issue. 11, November 2014, pg.102 – 115

RESEARCH ARTICLE

Comparison of Classifiers in Data Mining

Gaurav Taneja[1], Ashwini Sethi[2]
Department of Computer Science, Guru Kashi University, Talwandi Sabo (Bathinda)
taneja132@gmail.com, mtech.gku@gmail.com

Abstract: Hepatitis virus infection substantially increases the risk of chronic liver disease and hepatocellular carcinoma in humans and also affects majority of population in all age groups.
It is the major challenge for many hospitals and public health care services for diagnosing hepatitis. Accurate diagnosis and exact prediction of the disease on time can save many patients life and there health. Hepatitis viruses are the most common cause of hepatitis in the world but other infections, toxic substances (e.g. alcohol, certain drugs), and autoimmune diseases can also cause hepatitis. Using Data mining which is a effective tool to diagnose hepatitis and to predict result. This paper review the many data mining techniques which diagnosis hepatitis virus. I will compare three algorithms. All algorithms use different mechanism. I will analyze the result of all and will conclude the algorithm which gives the maximum accuracy for detection of hepatitis.

Keywords-Hepatitis, Data Mining, NB TREE, NAÏVE BAYES, SMO, Weka Tool

Introduction

1. Naive Bayesian classification

The naive Bayesian classifier, or simple Bayesian classifier, works as follows:

$$P(C_i|X) = \frac{P(X|C_i)P(C_i)}{P(X)}.$$

A) Each data sample is represented by an n-dimensional feature vector, X = (x1, x2,…….. xn), depicting n measurements made on the sample from n attributes, respectively A1,A2,….An.

B) Suppose that there are m classes, C1, C2, ……Cm. Given an unknown data sample, X (i.e., having no class label), the classifier will predict that X belongs to the class having the highest posterior probability, conditioned on X. That is, the naive Bayesian classifier assigns an unknown sample X to the class Ci if and only if :

$$P(C_i|X) > P(C_j|X) \text{ for } 1 \leq j \leq m, j \neq i.$$

Thus we maximize P(CijX). The class Ci for which P(CijX) is maximized is called the maximum posteriori hypothesis. By Bayes theorem

$$P(C_i|X) = \frac{P(X|C_i)P(C_i)}{P(X)}.$$

c) As P(X) is constant for all classes, only P(X/Ci)P(Ci) need be maximized. If the class prior probabilities are not known, then it is commonly assumed that the classes are equally likely, i.e. P(C1) = P(C2) = ……..= P(Cm), and we would therefore maximize P(X/Ci). Otherwise, we maximize P(X/Ci)P(Ci). Note that the class prior probabilities may be estimated by P(Ci) = si/s , where si is the number of training samples of class Ci, and s is the total number of training samples.

D) Given data sets with many attributes, it would be extremely computationally expensive to compute P(XjCi). In order to reduce computation in evaluating P(XjCi), the naive assumption of class conditional independence is made. This presumes that the values of the attributes are conditionally independent of one another, given the class label of the sample, i.e., that there are no dependence relationships among the attributes.

$$P(X|C_i) = \prod_{k=1}^{n} P(x_k|C_i).$$

The probabilities P(x1/Ci), P(x2/Ci)…….. P(xn/Ci) can be estimated from the training samples.

Bayesian belief classification**:**

The naive Bayesian classifier makes the assumption of class conditional independence, i.e., that given the class label of a sample, the values of the attributes are conditionally independent of one another. This assumption simplifies computation. When the assumption holds true, then the naive Bayesian classifier is the most accurate in comparison with all other classifiers. In practice, however, dependencies can exist between variables. Bayesian belief networks specify joint conditional probability distributions. They allow class conditional independencies to be defined between subsets of variables. They provide a graphical model of causal relationships, on which learning can be performed. These networks are also known as belief networks, Bayesian networks, and probabilistic networks.

2. SMO (Sequential Minimal Optimization)

SVM needs the solution of very large Quadratic Programming (QP).SMO breaks large QP problem into a series of smallest possible QP problems. These small QP problems are solved analytically, which avoids using a time-consuming numerical QP optimization as an inner loop. The amount of memory required for SMO is linear in the training set size, which allows SMO to handle very large training sets. Because matrix computation is avoided, SMO scales somewhere between linear and quadratic in the training set size for various test problems, while the standard chunking SVM algorithm scales somewhere between linear and cubic in the training set size. SMO’s computation time is dominated by SVM evaluation, hence SMO is fastest for linear SVMs and sparse data sets. On real world sparse data sets, SMO can be more than 1000 times faster than the chunking algorithm. Sequential Minimal Optimization (SMO) is a simple algorithm that can quickly solve the SVM QP problem without any extra matrix storage and without using numerical QP optimization steps at all. SMO decomposes the overall QP problem into QP sub-problems, using Osuna's theorem to ensure convergence. Unlike the previous methods, SMO chooses to solve the smallest possible optimization problem at every step. For the standard SVM QP problem, the smallest possible optimization problem involves two Lagrange multipliers, because the Lagrange multipliers must obey a linear equality constraint. At every step, SMO chooses two Lagrange multipliers to jointly optimize, finds the optimal values for these multipliers, and updates the SVM to reflect the new optimal values. The advantage of SMO lies in the fact that solving for two Lagrange multipliers can be done analytically. Thus, numerical QP optimization is avoided entirely. The inner loop of the algorithm can be expressed in a short amount of C code, rather than invoking an entire QP library routine. Even though more optimization sub-problems are solved in the course of the algorithm, each sub-problem is so fast that the overall QP problem is solved quickly.

In addition, SMO requires no extra matrix storage at all. Thus, very large SVM training problems can fit inside of the memory of an ordinary personal computer or workstation. Because no matrix algorithms are used in SMO, it is less susceptible to numerical precision problems. There are two components to SMO: an analytic method for solving for the two Lagrange multipliers, and a heuristic for choosing which multipliers to optimize.

3. NBTree (The Hybrid Algorithm)

The NBTree algorithm is similar to the classical recursive partitioning schemes except that the leaf nodes created are Naïve Bayes categorizers instead of nodes predicting a single class.

A threshold for continuous attributes is chosen using the standard entropy minimization technique as is done for decision trees_ The utility of a node is computed by discretizing the data and computing fold cross validation accuracy estimate of using Naïve Bayes at the node_ The utility of a split is the weighted sum of the utility of the nodes where the weight given to a node is proportional to the number of instances that go down to that node.

TERMINOLOGY

Imagine a study evaluating a new test that screens people for a disease. Each person taking the test either has or does not have the disease. The test outcome can be positive (predicting that the person has the disease) or negative (predicting that the person does not have the disease). The test results for each subject may or may not match the subject's actual status. In that setting:

- True positive: Sick people correctly diagnosed as sick
- False positive: Healthy people incorrectly identified as sick
- True negative: Healthy people correctly identified as healthy
- False negative: Sick people incorrectly identified as healthy

HEPATITIS DATASET

It contains 153 instances and 20 attributes, in which 9 instances are having missing values. It is a health care dataset. It has been taken from UCI Machine Repository(source). The fields (attributes) name are…..

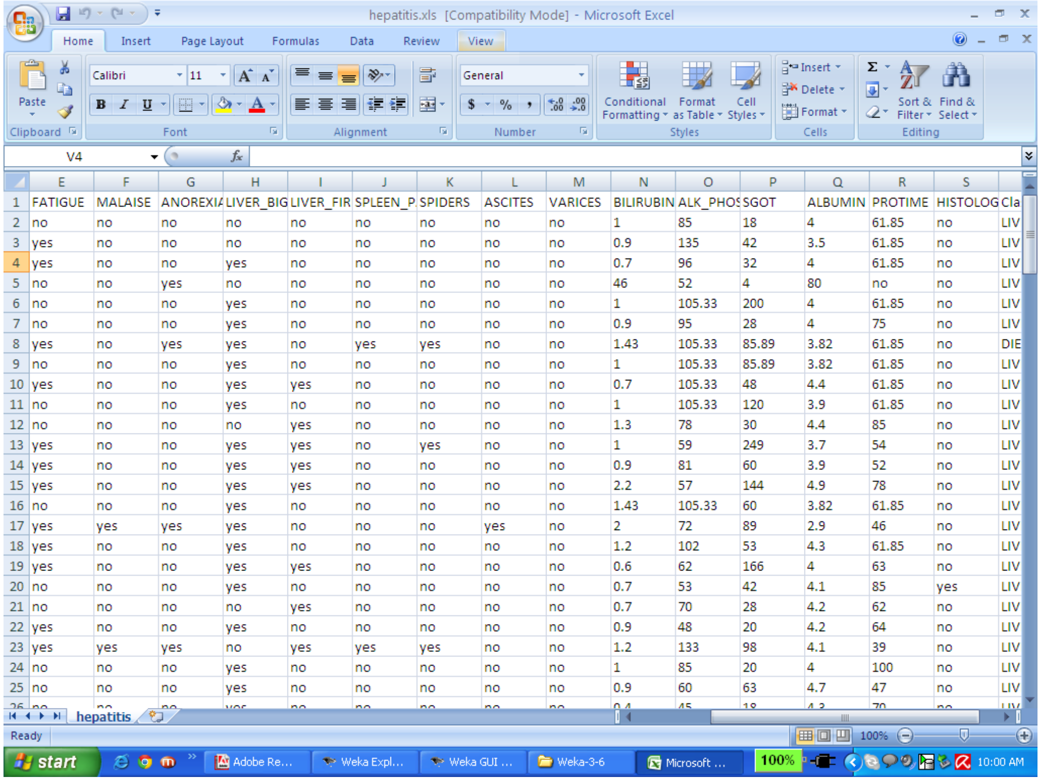
- ➢ AGE
- ➢ SEX
- ➢ STEROID
- ➢ MALAISE
- ➢ PROTIME
- ➢ HISTOLOG
- ➢ CLASS (LIVE/DEAD) etc.

And instances are like-(42,female,yes,no,yes,no,no,yes,yes,………..0.9,0.2,80,dead)

Name	***Type***
1-)AGE	integer
2-)SEX	{ 2, 1}
3-)STEROID	{ 1, 2}
4-)ANTIVIRALS	{ 2, 1}
5-)FATIGUE	{ 2, 1}
6-)MALAISE	{ 2, 1}
7-)ANOREXIA	{ 2, 1}
8-)LIVER_BIG	{ 1, 2}
9-)LIVER_FIRM	{ 2, 1}
10-)SPLEEN_PALPABLE	{ 2, 1}
11-)SPIDERS	{ 2, 1}
12-)ASCITES	{ 2, 1}
13-)VARICES	{ 2, 1}
14-)BILIRUBIN	real
15-)ALK_PHOSPHATE	integer
16-)SGOT	integer
17-)ALBUMIN	real
18-)PROTIME	integer
19-)HISTOLOGY	{ 1, 2}
20-)Class	{ DIE, LIVE}

Figure 12: Attributes and their types [6]

Data set used for example



	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	
1	FATIGUE	MALAISE	ANOREXIA	LIVER_BIG	LIVER_FIR	SPLEEN_P	SPIDERS	ASCITES	VARICES	BILIRUBIN	ALK_PHOS	SGOT	ALBUMIN	PROTIME	HISTOLOG	Cla
2	no	no	no	no	no	no	no	no	no	1	85	18	4	61.85	no	LIV
3	yes	no	no	no	no	no	no	no	no	0.9	135	42	3.5	61.85	no	LIV
4	yes	no	no	yes	no	no	no	no	no	0.7	96	32	4	61.85	no	LIV
5	no	no	yes	no	no	no	no	no	no	46	52	4	80	no	no	LIV
6	no	no	no	yes	no	no	no	no	no	1	105.33	200	4	61.85	no	LIV
7	no	no	no	yes	no	no	no	no	no	0.9	95	28	4	75	no	LIV
8	yes	no	yes	yes	no	yes	yes	no	no	1.43	105.33	85.89	3.82	61.85	no	DIE
9	no	no	no	yes	no	no	no	no	no	1	105.33	85.89	3.82	61.85	no	LIV
10	yes	no	no	yes	yes	no	no	no	no	0.7	105.33	48	4.4	61.85	no	LIV
11	no	no	no	yes	no	no	no	no	no	1	105.33	120	3.9	61.85	no	LIV
12	no	no	no	no	yes	no	no	no	no	1.3	78	30	4.4	85	no	LIV
13	yes	no	no	yes	yes	no	yes	no	no	1	59	249	3.7	54	no	LIV
14	yes	no	no	yes	yes	no	no	no	no	0.9	81	60	3.9	52	no	LIV
15	yes	no	no	yes	yes	no	no	no	no	2.2	57	144	4.9	78	no	LIV
16	no	no	no	yes	no	no	no	no	no	1.43	105.33	60	3.82	61.85	no	LIV
17	yes	yes	yes	yes	no	no	no	yes	no	2	72	89	2.9	46	no	LIV
18	yes	no	no	yes	no	no	no	no	no	1.2	102	53	4.3	61.85	no	LIV
19	yes	no	no	yes	yes	no	no	no	no	0.6	62	166	4	63	no	LIV
20	no	no	no	yes	no	no	no	no	no	0.7	53	42	4.1	85	yes	LIV
21	no	no	no	no	yes	no	no	no	no	0.7	70	28	4.2	62	no	LIV
22	yes	no	no	yes	no	no	no	no	no	0.9	48	20	4.2	64	no	LIV
23	yes	yes	yes	no	yes	yes	yes	no	no	1.2	133	98	4.1	39	no	LIV
24	no	no	no	yes	no	no	no	no	no	1	85	20	4	100	no	LIV
25	no	no	no	yes	no	no	no	no	no	0.9	60	63	4.7	47	no	LIV
26	no	no	no	yes	no	no	no	no	no	0.4	45	18	4.3	70	no	LIV

RESULTS

(A) Table: 1 ACCURACY OF BINARY CLASSIFIERS

Parameters	SMO	NB TREE	NAÏVE BAYES
TP	112	115	106
FP	5	2	11
FN	9	2	8
TN	18	25	19
Accuracy	0.9027	0.9722	0.8680

TP/FP/FN/TN/Accuracy of classifiers

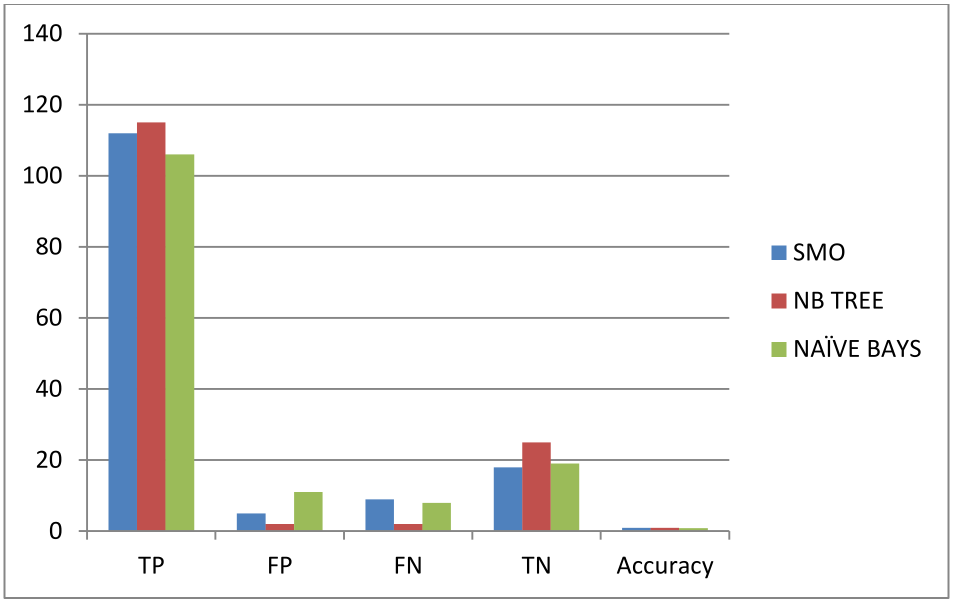


FIGURE 1: TP/FP/FN/TN/Accuracy of Classifiers

(B) **Table 2: LIVE Class - Precision/TPR/TNR/FPR**

Parameters	**SMO**	**NB TREE**	**NAÏVE BAYES**
TPR(Recall/Sensitivity)	0.957	0.983	0.906
TNR(Specificity)	0.7826	0.9259	0.6333
FPR	0.333	0.074	0.296
PRECISION	0.926	0.983	0.93

Please note that all the values shown above in tables have been obtained by applying mentioned classification techniques in weka.

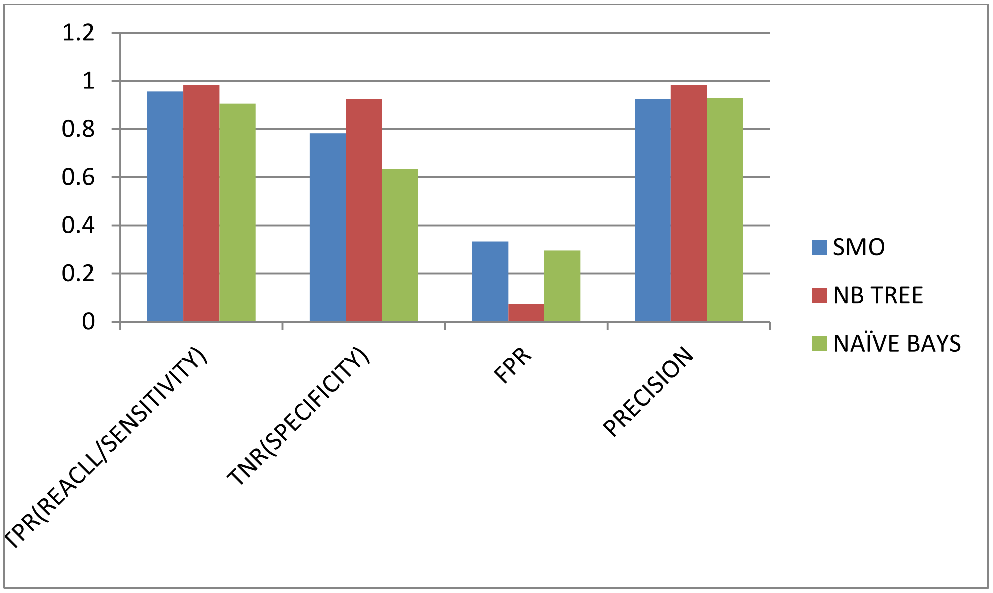


Figure 2: Bar chart showing parameters among classifiers

Table 3: DIE Class Precision/TNR/TPR/FPR

Parameters	**SMO**	**NB TREE**	**NAÏVE BAYES**
TPR(Recall/Sensitivity)	0.667	0.926	0.704
TNR(Specificity)	0.7826	0.9259	0.45
FPR	0.043	0.017	0.094
PRECISION	0.783	0.926	0.633

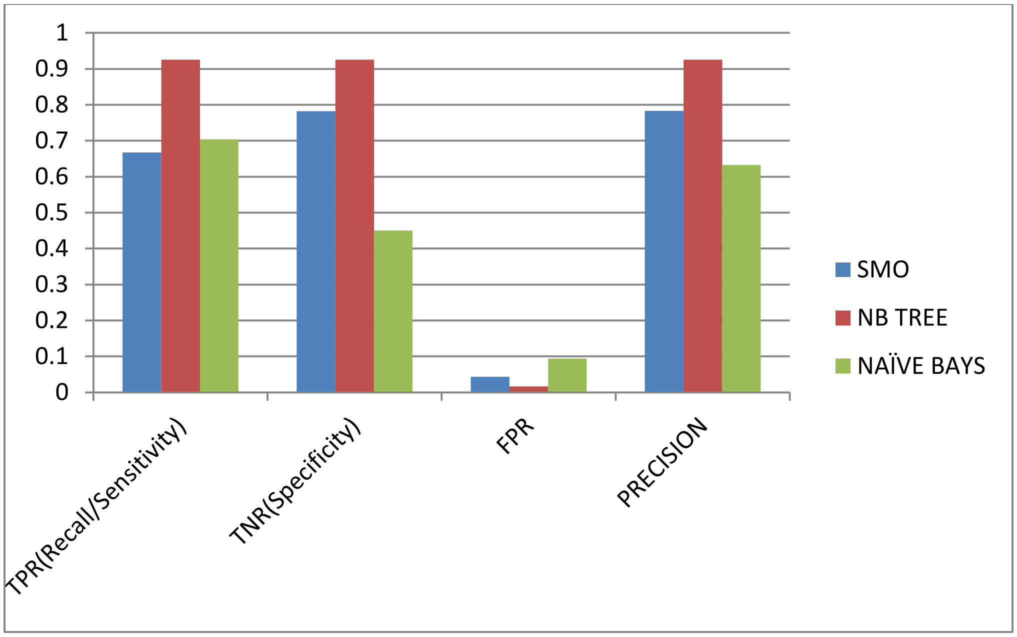


Figure 3:Bar chart for die class

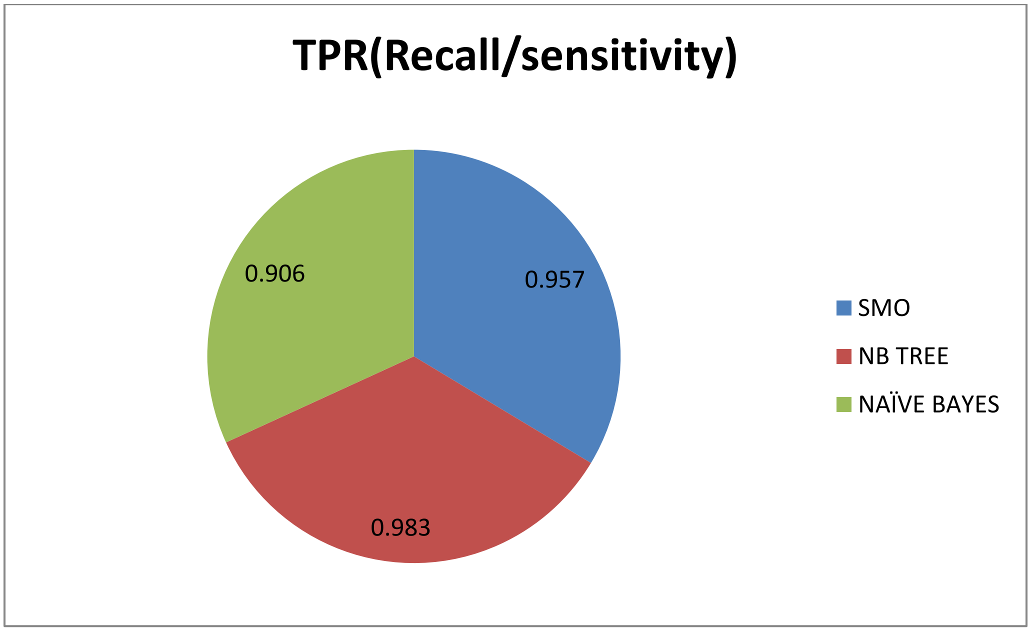


Figure 4: Pi chart for Live Class Sensitivity(TPR)

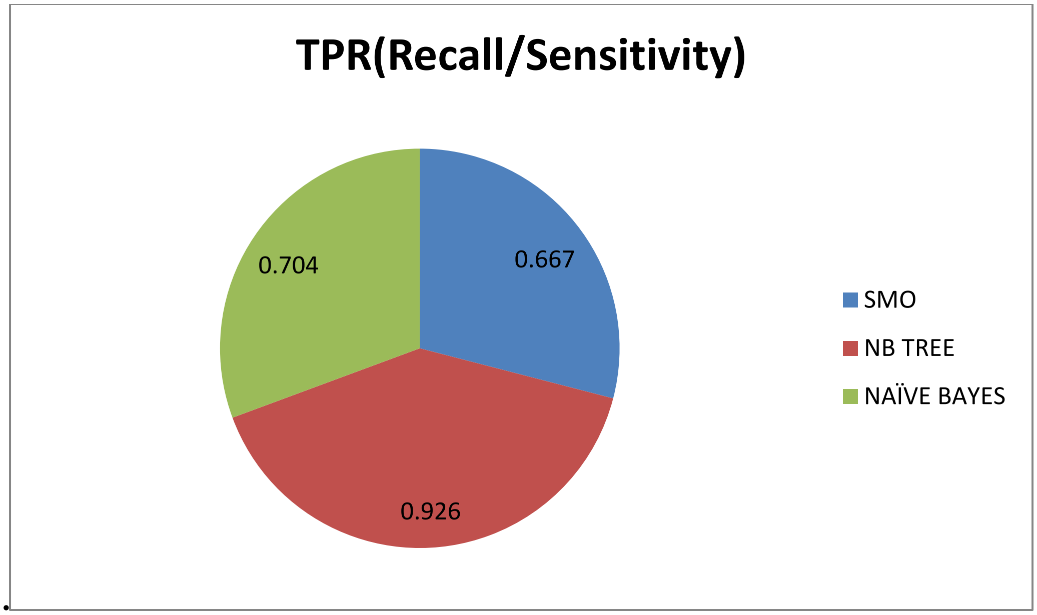


Figure 5: Pi chart showing TPR(Recall/Sensitivity) for DIE Class

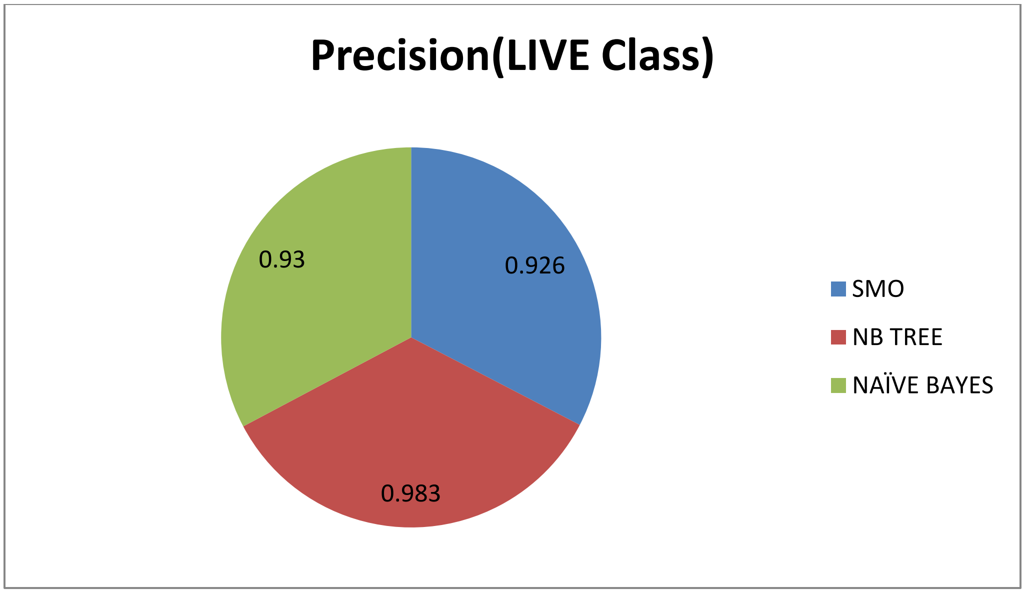


Figure 6: Pi chart showing precision for live class (Hepatitis)

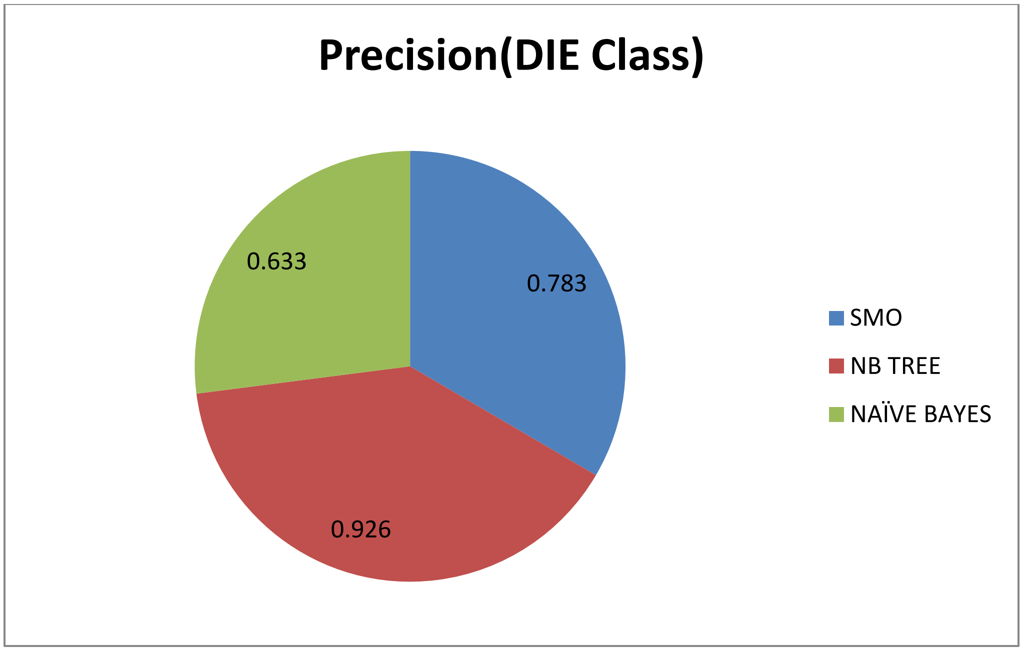


Figure 7: Pi chart precision for die class

OBSERVATION:

- It has been observed (from Table :1)that TP and TN values of NB Tree are high than other classifiers, which is a desirable point,
- The accuracy of NB Tree (0.9722) is high in compare to SMO and NAÏVE BAYES Classification algorithms, which is a important point during classification of Hepatitis patients, we may easily guess that NB Tree is quite sufficient to judge Hepatitis symptoms.
- It is giving very less false positive, it has shown only 2 out of 153 instances which is a desirable point.
- TPR (Recall/Sensitivity) is high(0.983) than others i.e. there are very few chances of Disease undetection, means maximum cases have been detected(refer Table:2,3).
- Since TNR(Specificity) of NB Tree is high(0.9259),means this algorithms has given maximum true result, means very few patients will be labled as sick(refer table:2,3).

- In ideal condition FPR should be zero,NB Tree has only 0.074 false positive rate which indicates that this algorithm does very minor mistake to judge Heaptitis, means most of the time it has given true result.
- Precision answers that" how likely it is that patients have the disease, given that there test's results were positive"?,from table2 and 3 we can say that precision of NB Tree is high which shows that results are positive out of all positive results however result is affected as number of Hepatitis patients increases time to time in world.
- According to experiments and results in this work ,NB Tree gives a satisfying and promising results for the task of classification of class label (LIVE/DIE) in Hepatitis dataset in Healthcare industry. It gives better result in both cases(live class as well as die class).

CONCLUSION

According to above classification techniques result, we can find the best technique for our hepatitis dataset by comparing output of confusion matrix and summary statistic. So the following results are achieved,

Name of the algorithm	**Summary**	**Confusion Matrix**
SMO	Correctly Classified Instances 130 90.2778 % Incorrectly Classified Instances 14 9.7222 % Ignored class unknown instance 2	a b 112 5 | a = DIE 9 18 | b = LIVE
NB TREE	Correctly Classified Instances 140 90.2222% Incorrectly Classified Instances 4 2.7772 % Ignored class unknown instances 2	a b 115 2 | a = DIE 2 25 | b = LIVE

NAÏVE BAYES	Correctly Classified Instances 125 86.8056 % Incorrectly Classified Instances 19 13.1944 % Ignored class unknown instances 2	a, b 106 11| a = DIE 8 19 | b = LIVE

From above conclusion we can say that NB Tree gives the more efficient result than others classifiers .But we may get also more promising result by applying other classifiers.

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