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RESEARCH ARTICLE

Detection of Liver Disorder Using RBF SVM in Comparison with Naïve Bayes to Measure the Accuracy, Precision, Sensitivity and Specificity

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ABSTRACT

Aim: Machine learning techniques are rapidly used in the area of medical research due to its impressive results in diagnosis and prediction of diseases. The objective of this study is to evaluate the performance of SVM classifier in identification of liver disorder by comparing it with Naive Bayes algorithm. **Methods and Materials:** A total of 31619 samples are collected from three liver disease datasets available in kaggle. These samples are divided into training dataset (n = 22133 [70%]) and test dataset (n = 9486 [30%]). Accuracy, precision, specificity and sensitivity values are calculated to quantify the performance of the SVM algorithm. **Results:** SVM achieved accuracy, precision, sensitivity and specificity of 73.64%, 97.82%, 97.56% and 69.77% respectively compared to 57.31%, 41.39%, 94.87% and 37.20% by Naive Bayes algorithm. **Conclusion:** In this study it is found that the RBF SVM algorithm performed better than the Naive Bayes algorithm in liver disorder detection of the datasets considered.

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Introduction

Liver is one of the primary organs of the human body. It is involved in major functions like metabolism and catabolism of complex molecules within our system. If the liver does not work well, it can affect the functioning of the entire body (Haque et al. 2018). Early and accurate detection of liver disorder is a necessity in today's clinical scenario (Naseem et al. 2020; Abdar et al. 2017). This detection process will take more time and also sometimes man made errors lead to wrong prediction of liver disease. Liver diseases are the leading reason behind world death that impacts the huge amount of humans around the world. Machine learning techniques are used both in hospitals and medical industries for large datasets (Biswas et al. 2018). To reduce the risk of life it is very much necessary to detect the liver disorder at the earlier stage.

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The authors (Rabbi et al. 2020) discussed the importance of liver disorder detection using machine learning algorithms.

Recently a lot of researches have been done on a variety of liver diseases using machine learning techniques for liver disease detection. 53 research articles were published in IEEE Xplore and 6490 articles found in Google scholar. In recent times surveys of machine learning algorithms for disease were explored mostly as they predicted 97.10% of output accuracy using Naive Bayes algorithm (M pasha 2017). From the survey, it is observed that many research works involve prevention and treatment of hepatitis disease using wrapper methods and SVM. To reduce noise features in the dataset wrapper method is used (Roslina and Noraziah 2010). (Omar S. Soliman et al, 2014) used hybrid classification technique for diagnosis liver diseases and compared the results with the novel LS-SVM Modified Particle Swarm Optimization algorithm. (Asrani et al. 2019) proposed a classification model for liver diagnosis, with two datasets of liver patients. Eleven data mining algorithms were used, and the classifiers results were tested

for accuracy, precision, and recall. (Fatima and Pasha 2017) performed a survey on diagnosis of various diseases using the SVM algorithm.

Previously our team has a rich experience in working on various research projects across multiple disciplines (Sathish and Karthick 2020; Varghese, Ramesh, and Veeraiyan 2019; S. R. Samuel, Acharya, and Rao 2020; Venu, Raju, and Subramani 2019; M. S. Samuel et al. 2019; Venu, Subramani, and Raju 2019; Mehta et al. 2019; Sharma et al. 2019; Malli Sureshbabu et al. 2019; Krishnaswamy et al. 2020; Muthukrishnan et al. 2020; Gheena and Ezhilarasan 2019; Vignesh et al. 2019; Ke et al. 2019; Vijayakumar Jain et al. 2019; Jose, Ajitha, and Subbaiyan 2020). Now the growing trend in this area motivated us to pursue this project.

Most of the existing works are performed with the data collected from particular ethnic groups. Many of the existing works analysed the performance of machine learning algorithms in a small sample of data. However in the proposed work, SVM algorithm performance is analysed using large dataset collected from samples worldwide.

Materials and Methods

This proposed work involves two groups for liver disorder detection. Total sample size of group1 and group2 is 31,619. The required samples for this analysis is done using G power calculation(Kane, Phar, and BCPS n.d.). Minimum power of the analysis is fixed as 0.8 and maximum accepted error is fixed as 0.5.

Liver disorder dataset collected from kaggle and UCI needs to be processed before applying it to the machine learning model. The processed dataset is given for training and testing. Data processing includes missing data removal, replacement of null values with mean or median values and standardization of data. The preprocessed dataset with features are given as input to SVM and Naive Bayes Classifier. From the total sample size75% of the data is given for training and remaining 25% is given for testing.

In this Indian Liver Patient Dataset (ILDP) is collected from Kaggle with a total of 583 patient records. Out of which the ILDP contains 416 liver patient records and 167 non liver patient records. The records were collected from test samples in North East of Andhra Pradesh, India(Jeevan Nagaraj n.d.). Class label is represented as 'is_patient' in the dataset that divides into groups like liver patient and non liver patient. This data set contains 441 male patient and 142 female patient records. Liver disease Patient Dataset (LDPD) is collected from Kaggle with a total of 30691 patient records. Out of which the LDPD contains 21917 liver patient records and 8774 non liver patient records. The records were collected from across the World LIver Patients(Shrivastava n.d.). Class labels are represented as a 'selector' in the dataset that divides into two groups (liver patient or not). Liver Disorder (LD) dataset is collected from UCI Repository of Machine Learning with total 345 patient records. The records were collected from BUPA Medical Research Ltd ("UCI Machine Learning Repository: Liver Disorders Data Set" n.d.).

The ILDP and LDPD dataset has 10 attributes in common. Common attributes are age, gender, Total Bilirubin, Direct Bilirubin, total proteins, albumin, Albumin and /Glucose ratio, alkaline phosphatase, alanine aminotransferase, and alkaline phosphatase (Alk Phos). The age attribute column is removed for training and testing of the model as it does not contribute much information for classification. The gender attribute which is in categorical form is changed to 0 for male and 1 for female as it contributes information for classification. The LD dataset has 7 attributes such as mean capsular volume, alkaline phosphatase, alanine aminotransferase, aspartate aminotransferase, glutamyl transpeptidase, drinks and selector for Liver Disorder classification. All three datasets used in this proposed work are suitable for binary classification as given in table 1.

Table 1. Samples, features and classes from various Datasets. From LDPD dataset 30691 samples were taken, from ILDP dataset 583 were taken and from LD dataset 345 samples were taken. All the dataset contains 2 classes (with liver disorder and without liver disorder).

Datasets	No of Patients	Features	Classes
Liver disease Patient Dataset (LDPD)	30691	10	2
Indian Liver Patient Dataset (ILDP)	583	10	2
Liver Disorder (LD)	345	7	2

Table 2 represents the statistical features extracted from the data for training the Learning algorithm. The statistical features extracted are mean, standard deviation, minimum, 25% quantile, 50% quantile, 75% quantile and maximum. The learning process of SVM and Naive Bayes classifier is given below.

Table 2. Statistical features of the LDPD dataset - Sample. It contains Age, Gender, TB, DB, Alkphos, Sgpt, Sgot, Proteins, ALB, A/G Ratio as input features.

	count	mean	std	min	25%	50%	75%	max
Age	30689.0	44.107205	15.981043	4.0	32.0	45.0	55.0	90.0
Gender	29789.0	0.261942	0.439699	0.0	0.0	0.0	1.0	1.0
TB	30043.0	3.370319	6.255522	0.4	0.8	1.0	2.7	75.0
DB	30130.0	1.528042	2.869592	0.1	0.2	0.3	1.3	19.7
Alkphos	29895.0	289.075364	238.537589	63.0	175.0	209.0	298.0	2110.0
Sgpt	30153.0	81.488641	182.158850	10.0	23.0	35.0	62.0	2000.0
Sgot	30229.0	111.469979	280.851078	10.0	26.0	42.0	88.0	4929.0
protiens	30228.0	6.480237	1.081980	2.7	5.8	6.6	7.2	9.6
ALB	30197.0	3.130142	0.792281	0.9	2.6	3.1	3.8	5.5
A/G Ratio	30132.0	0.943467	0.323164	0.3	0.7	0.9	1.1	2.8

Support Vector Machine (SVM) classifier is used to find an optimal hyperplane that has the ability to classify normal and liver disease. SVM maps the given data into linearly separable and non linearly separable data. If the given data can be separated linearly SVM can easily separate two classes (Devikanniga, Ramu, and Haldorai 2018). If the given data is non-linearly separable then, the datas are mapped into higher dimensions to provide better classification performance. The separating hyperplane for RBF SVM is given by the equation (1)

$$H = W^T X + b \quad (1)$$

Where H - Hyperplane, W - normal vector representing position of hyperplane, X - input data, b - threshold value indicating distance between the hyperplane and origin. The design of the SVM classifier depends on the hyperplane and the associated support vectors. The structure of the RBF SVM is given in Fig 1.

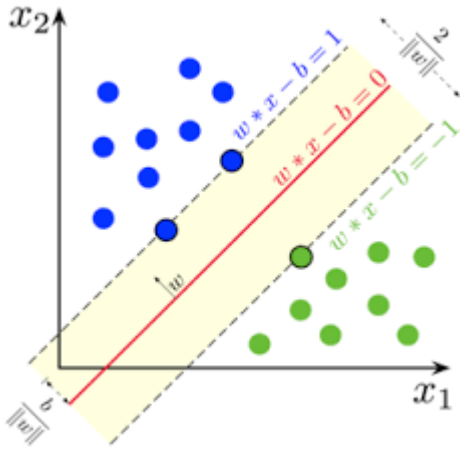

Fig. 1. Representative structure of RBF SVM with linear hyperplane. Illustrates the general classification performed by the SVM algorithm

The margin (γ) between the planes is given as $\gamma = \frac{2}{||w||}$, where $w = \sqrt{W^T W}$ is also called as L2-norm. Maximizing the margin value gives a better classification rate. The maximization of margin value is achieved by minimizing the L2-norm. The minimization of L2-norm is achieved by equation (2)

$$Minimize\ \frac{1}{2}||w||_2^T = \frac{1}{2}w^T w \quad (2)$$

Naive-Bayes (NB) classifier assumes a strong independence within the feature values. It constructs class variables and designs a model classifier based on the features (Wayahdi, Tulus, and Lydia 2020). NB is simple with less computational complexity and better predicting ability. The probability of classifier is given in the equation (3)

$$P\left(\frac{C_i}{X}\right) = \frac{P\left(\frac{X}{C_i}\right)P(C_i)}{P(X)} \quad (3)$$

Where, $P\left(\frac{C_i}{X}\right)$ - Posterior Probability, $P(C_i)$ - Class Prior Probability, $P(X)$ - Predictor Prior Probability, $P\left(\frac{X}{C_i}\right)$ - Likelihood. In NB the assumption of the probability of occurrence of a feature value is independent of all the other features.

The proposed work uses google colab cloud platform for testing the RBF SVM and Naive Bayes algorithm. The Python programming tool is used for execution of the algorithm. This Core i5 processor with 4GB ram.

From the total sample size 75% of the data with features extracted is trained in the RBF SVM and Naive Bayes model. For training the model involves a number of iterations to get better performance. After training the algorithm, random test data is given to the algorithm for accurate identification of classes.

All analyses are conducted using SPSS("SPSS Software" n.d.) and python tools. Descriptive statistics (mean, standard deviation and standard error) is carried out for SVM and Naive Bayes algorithm. Independent variables in this study are the input variables (age, gender, Total Bilirubin, Direct Bilirubin, total proteins, albumin, Albumin and /Glucose ratio, alkaline phosphatase, alanine aminotransferase, and alkaline phosphatase (Alk Phos)). The dependent variables are output variables (Accuracy, precision, sensitivity, specificity). Independent t-test is performed to compare the performance of algorithms.

Results

In Table 3, it was observed that for LDPD dataset detection accuracy, precision, sensitivity and specificity performance of SVM was significantly better than Naive Bayes. In the LD dataset it was observed that detection accuracy, precision and specificity performance of svm was significantly better than Naive Bayes except sensitivity. In the ILDP dataset it was observed that the detection accuracy and sensitivity performance of SVM was significantly better than Naive Bayes except precision and specificity 0.001. From the three dataset, it was clearly evident that the SVM algorithm performed significantly better than Naive Bayes algorithm.

Table 3. Comparison between RBF SVM and Naïve Bayes. Accuracy, Precision, Sensitivity and Specificity values obtained for SVM and Naive Bayes algorithms are compared for various datasets.

DATA SET	SVM		NAÏVE BAYES	
Liver disease patient dataset (LDPD) (30691,10)	Accuracy	73.64	Accuracy	57.31
	Precision	97.82	Precision	41.39
	Sensitivity	97.56	Sensitivity	94.87
	Specificity	69.77	Specificity	37.20
Liver Disorder (LD) (345,7)	Accuracy	68.96	Accuracy	63.21
	Precision	56.52	Precision	48.07
	Sensitivity	43.33	Sensitivity	82.33
	Specificity	82.87	Specificity	52.63
Indian liver patient Dataset (ILDP) (583,10)	Accuracy	65.06	Accuracy	59.58
	Precision	65.97	Precision	86.53
	Sensitivity	97.38	Sensitivity	46.39
	Specificity	74.30	Specificity	85.71

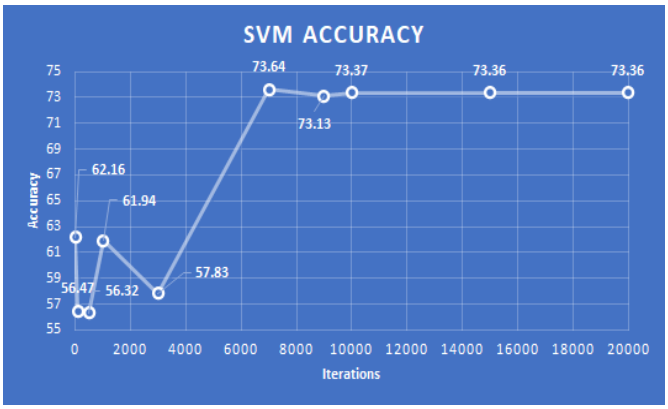

Fig. 2. Accuracy performance of SVM in different iterations. Initially there are fluctuations in accuracy before 6500 iteration, later it becomes constant after 7000 iterations

From Fig 2, it was observed that the increase in iteration increased the accuracy of the algorithm. At the 7000th iteration, SVM was found to achieve an accuracy of 73.64%. Further increase in the iteration values, showed constant accuracy by the classifier. Hence the analysis was restricted to 7000 iterations.

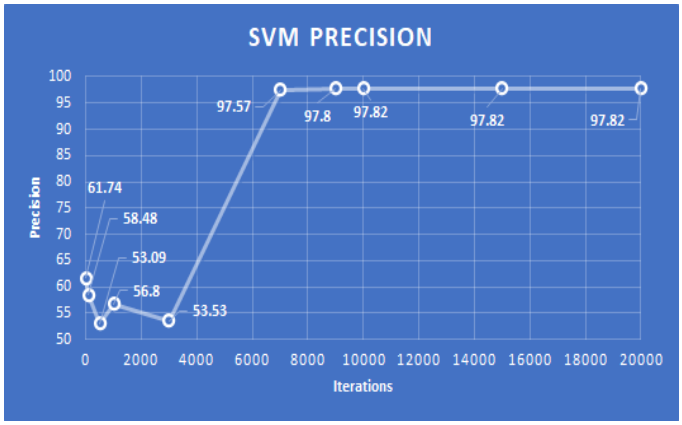

Fig. 3. Precision performance of SVM in different iterations. Initially precision increases as the iteration increases and above 7000 iterations the precision remains constant

From Fig 3, it was observed that the increase in iteration, increased the precision of the algorithm at a certain level. At 10000th iteration, SVM was found to achieve a high precision of 97.82%. Further increase in the iteration, it was found to give constant precision by the classifier.

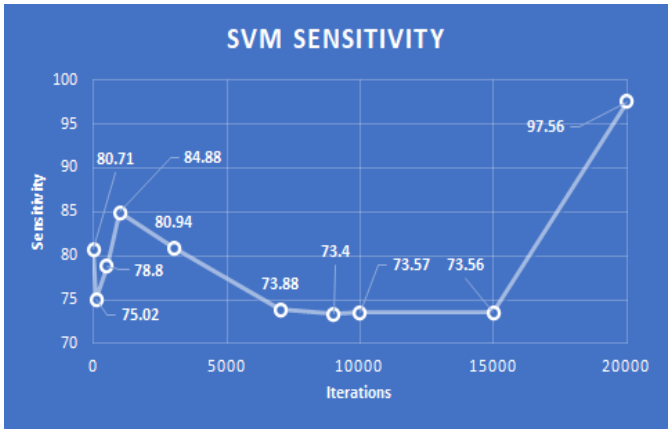

Fig. 4. Sensitivity performance of SVM classifier in different iterations. Initially sensitivity increases as the iteration increases then gradually decreases and becomes constant after 7000 iterations. Sensitivity gradually increases after 15000 iterations

From Fig 4, it was observed that the increase in iterations showed different Sensitivity values at different levels in the Support Vector algorithm. At the 20000th iteration, SVM was found to achieve a sensitivity of 97.56%.

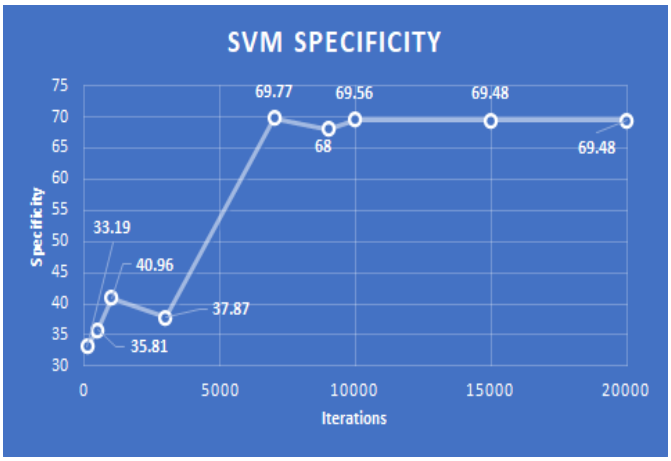

Fig. 5. Specificity analysis of SVM classifier in different iterations. As the iterations increases above 10000, the specificity becomes constant

From Fig 5, it was observed that the increase in iteration, increased the Specificity of the SVM algorithm. At the 7000th iteration, SVM was found to achieve a Specificity of 69.77%. Further increase in the iteration, the algorithm was found to produce constant precision.

In performing statistical analysis of 10 samples, SVM obtained 0.44 standard deviation with 0.14 standard error while Naive bayes obtained 0.51 standard deviation with 0.16 standard error (Table 4). The significance value smaller than 0.001 showed that our hypothesis holds good. With respect to changes in the input values (independent variables) the corresponding output values (dependent variables) also changes (Table 5).

Table 4. Statistical analysis of RBF SVM and Naïve Bayes. Mean accuracy value, Standard deviation and Standard Error Mean for SVM and Naive Bayes algorithms are obtained for 10 iterations. It is observed that the SVM algorithm performed better than the Naive Bayes algorithm

	Groups	N	Mean	Std. Deviation	Std. Error Mean
ACCURACY	SVM	10	72.6750	0.44498	0.14071
	NAIVE BAYES	10	56.2040	0.51655	0.16335

Table 5. Independent sample test for significance and standard error determination. P value is less than 0.05 considered to be statistically significant and 95% confidence intervals were calculated

Leven's Test for Equality of Variance				t-test for Equality of Variance					95% Confidence Interval of the difference	
Accuracy		F	sig.	t	dif	sig(2-tailed)	Mean difference	Std. Error Difference	lower	upper
	Equal Variance assumed	0.706	0.412	74.211	18	0.000	16.57000	0.2232B	16.100900	17.03910
	Equal variance not assumed			74.211	16.217	0.000	16.57000	0.2232B	16.09717	17.04283

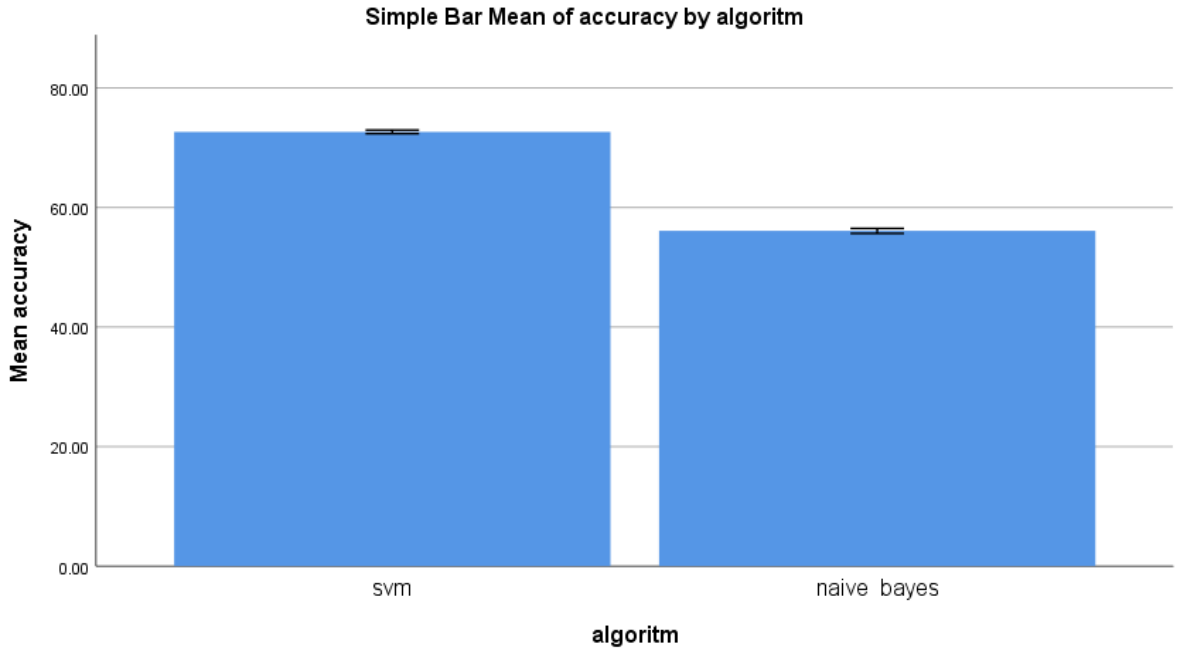

Fig. 6. Comparison of SVM algorithm and Naive Bayes classifier in terms of mean accuracy. The mean accuracy of SVM is better than Naive Bayes and the standard deviation of SVM is slightly better than Naive bayes. X Axis: SVM vs Naive bayes Algorithm Y Axis: Mean accuracy of detection ± 1 SD

Independent t-test was used to compare the accuracy of two algorithms and a statistically significant difference was noticed P < 0.001 The SVM model obtained 73.64% accuracy (Fig 6). Decision tree (Jin, Kim, and Kim 2014), NB tree (Alfisahrin and Mantoro 2013), and decision stump(Nahar and Ara 2018) techniques obtained an accuracy of 69.40%, 67.01% and 70.67% respectively. When compared with the other algorithms performance of the proposed SVM technique achieved better performance than naive bayes classifier.

Discussion

In this study, we observed that RBF SVM appears to be better than Naive Bayes classifier with an accuracy of 73.64 % ($p<0.05$). In this analysis, performance of SVM and NB is analyzed in classifying liver disease from the dataset obtained from Kaggle and UCI repository. These datasets contain different attributes to define the disease condition and also have varying ratios of normal and affected people. The proposed work signifies that RBF SVM performs better classification compared to NB classifier.

For the datasets considered in this study, the SVM algorithm is able to classify liver disorders with moderate accuracy. Minhas et al proposed a multiclass linear SVM in classifying fatty liver diseases and found to achieve 95% accuracy(Minhas et al. 2012). The direct comparison between the proposed work and previous works poses a great difficulty because of the difference in the type of liver disease, total number of classes and also amount of data present in the dataset. The analysis performed by Huang et al utilized a balanced dataset for classifying liver disease and found to achieve 87.5% sensitivity (Huang et al. 2010). Zhou et al utilized an imbalanced dataset containing 52 normal and 69 liver diseased images and achieved an 81% sensitivity (Zhou, Wang, and Wang 2012). From the above articles it can be observed that the performance of the methods varies depending on balanced or imbalanced dataset used for analysis. Wang et al performed classification on the imbalanced dataset containing 24 normal and 59 liver disease images and achieved sensitivity of 92% (Wang et al. 2013). Indicating that the increased ratio of diseased data to the normal data could increase the sensitivity value of the algorithm in detecting diseased subjects precisely. In our analysis we utilized around 21917 data values of normal subjects and 8774 data of diseased subjects respectively. It is observed that the methods used in our analysis both SVM and NB are found to have the ability to handle the imbalanced dataset and provide better sensitivity 97% and 94% respectively.

In the analysis made by Ribeiro et al they have used images of 40 normal and 35 liver disease subjects. Their results indicate that SVM has produced sensitivity of 93.54% (Ribeiro, Tato Marinho, and Sanches 2012). This indicates that even with the imbalanced dataset the number of non-diseased subjects is considered to be high compared to diseased subjects. This above article is in pair with the proposed analysis as the data ratio of normal to disease subjects is high.

Our institution is passionate about high quality evidence based research and has excelled in various fields ((Vijayashree Priyadharsini 2019; Ezhilarasan, Apoorva, and Ashok Vardhan 2019; Ramesh et al. 2018; Mathew et al. 2020; Sridharan et al. 2019; Pc, Marimuthu, and Devadoss 2018; Ramadurai et al. 2019). We hope this study adds to this rich legacy.

SVM fails to perform when the target classes are overlapping. It takes a huge amount of time to train when the dataset size is large. SVM is not computationally efficient

when the dataset is very large.In future the SVM algorithms accuracy can be improved by adding more data in the training sets, using multiclass SVM, and by combining it with other ANN methods. Also, multi dimensional data can be converted into binary data to improve accuracy.

Conclusion

Accurate detection of liver disease reduces the risk of life threat. From the present study, it suggests that SVM provides significantly better performance in detecting liver disease when compared to Naive Bayes. SVM produced an accuracy of 73.64% compared to the Naive bayes accuracy of 57.31% from the three datasets.

Declarations

Conflict of Interests

No conflict of interest in this manuscript.

Author Contributions

Author MS was involved in data collection, data analysis and manuscript writing. Author KG was involved in conceptualization, data validation, and critical review of manuscript.

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