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Prediction Analysis Of Chronic Kidney Disease Using Novel Decision Tree Algorithm By Comparing Naive Bayes For Obtaining Better Accuracy

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ABSTRACT

Aim: Individuals at high-hazard of cardiovascular sickness are no doubt defenseless against ongoing kidney diseases, and historical clinical records can assist with turning away complicated kidney issues. The main objective of this study aims to find the best-suited algorithm that will give us the most ideal prediction. We will be comparing Novel Decision Tree with Naive Bayes to find out which of these can give us the best accuracy. **Material and Methods:** The study used 540 samples with Novel Decision Tree and Naive Bayes is executed with varying training and testing splits for predicting the accuracy for kidney disease prediction with the G-power value of 80% and the kidney datasets were collected from various web sources with recent study findings and threshold 0.05%, confidence interval 95% mean and standard deviation. The performance of the classifiers are evaluated based on their accuracy rate using the chronic kidney disease dataset. **Results:** The accuracy of predicting kidney disease in Novel Decision Tree (96.66%) and Naive Bayes (90.83%) is obtained. There is a statistical significant difference in accuracy for two algorithms is 0.001 ($p<0.05$) by performing independent samples t-tests. **Conclusion:** This study concludes that the Prediction of Kidney disease using the Novel Decision Tree (DT) algorithm appears to be significantly better than the Naive Bayes (NB) with improved accuracy.

Keywords

Chronic Kidney Disease, Novel Decision Tree, Naive Bayes, Machine learning, Classification, Diabetes.

Imprint

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INTRODUCTION

Right now, kidney illness is a significant issue. Since there are countless individuals with this disease having diabetes. Kidney infection is very dangerous in the event that it is not quickly treated on schedule, and might be lethal. Assuming the specialists have a decent instrument that can distinguish patients who are prone to have kidney disease, diabetes ahead of time, they can treat the patients on schedule (Lee et al. 2022). In this paper, 12 supervised AI algorithms were utilized to investigate and review electronic clinical information on chronic kidney sickness. The review designated 544 short-term patients although 48 neglected to meet the standards and a few other 21 cases had missing qualities and were rejected from the review. (Singh, Asari, and Rajasekaran 2022) presented a computer-aided diagnosis implementation based on analyzing images. This system is helpful in detecting various stages of Chronic Kidney Disease. The K-means clustering was used to detect after the image processing step using a novel decision tree. (Provenzano et al. 2021) used Gradient Boosting (GB) classifier and got an accuracy of 92.32%. Data mining strategies are utilized to produce decisions by eliciting hidden data from ongoing chronic kidney datasets. This calls for the capacity and control of a lot of organized, unstructured, and semistructured information using novel decision trees. The job of big data for the equivalent is vital (Lees et al. 2022). Kidney harm because of diabetes is persistent and a sluggish cycle, yet significant affects the patient. High glucose levels in the blood upset the kidney from working actually. It has applied affiliation rule mining to predict diabetes mellitus in a given dataset by producing synopsis rules. This has utilized the decision hypothesis to approve the clustering information mining method (Dutta and Bandyopadhyay, n.d.). Kidneys have a huge number of tiny blood vessels to filter blood from waste products and having the diabetes. In some occurrences, this filtration system separates and kidneys lose their capacity to filter waste products, which brings about kidney disease.

A lot of research has been done based on the classification of the chronic kidney using machine learning

algorithms. More than 150 articles were published in IEEE explore and nearly 1525 articles were found in google scholar. This used Python as a high-level interpreted programming language for developing our system. In this review, the initial step intends to fabricate a relapse model to anticipate the worth of creatinine from 23 elements (Vassalotti 2020), and afterward consolidate the anticipated worth of creatinine with the first 23 highlights to assess the risk of CKD(Sinha, Sinha, and BUIT 2015). Adding a creatinine test into routine health assessment could identify CKD. Missing values are usually seen in real-life medical situations because patients may miss some measurements for various reasons (Wesson et al. 2022). As more things for extensive assessment implies greater expense (Dutta and Bandyopadhyay, n.d.), creatinine testing is excluded from the standard health assessment in numerous nations. A calculation in view of normal test results, without creatinine test, to assess the gamble of CKD will build the opportunity of its initial location and treatment (Ventrella et al. 2021). Data preprocessing, a mechanism for managing missing values, data aggregation, and feature extraction are all part of the current study's methodology for predicting CKD status using clinical data (Senan et al. 2021).Our team has extensive knowledge and research experience that has translate into high quality publications(Chellapa et al. 2020; Lavanya, Kannan, and Arivalagan 2021; Raj R, D, and S 2020; Shilpa-Jain et al. 2021; S, R, and P 2021; Ramadoss, Padmanaban, and Subramanian 2022; Wu et al. 2020; Kalidoss, Umapathy, and Rani Thirunavukkarasu 2021; Kaja et al. 2020; Antink et al. 2020; Paul et al. 2020; Malaikolundhan et al. 2020)

The existing research study predicts the classification using images but it does not group them. Another research paper has the random forest calculation beat any remaining applied calculations, arriving at an exactness, accuracy, review, and F1-score of 100 percent for all actions. CKD is a not kidding perilous infection, with high rates of dreariness and mortality. Therefore the study aims to increase the accuracy of predicting the likelihood of kidney failure, diabetes and improve the prediction model using the Novel Decision tree.

Materials And Methods

This research study was carried out in the Artificial Intelligence Laboratory at the Department of Computer Science and Engineering, Saveetha School of Engineering, Saveetha Institute of Medical and Technical Sciences, Chennai. This research study uses two groups, the Novel Decision Tree (DT) algorithm, and Naive Bayes (NB) algorithm. Each sample size was predicted using the g-power tool with version 3.1.10 and resulting in 540 total sample sizes and 270 sample sizes per group with 80% of G power values, 95% confidence (Senan et al. 2021).

The data set used for this experiment is obtained from the kaggle open-access dataset (https://www.kaggle.com/mansoordaku/ckdisease?select=kidney_disease.csv) one of the most popular if not the most popular online communities for data scientists and machine learning practitioners. It allows users to search and find datasets that they require and also provides a customizable Jupyter notebook environment with free GPU and 6 hours of runtime. The dataset has 401 rows and 26 columns which consists of data for the symptoms that relate to chronic kidney disease which also includes duplicate, null and missing values. Pre-processing of the datasets is done to remove the duplicate and null values with the help of functions that are provided by Microsoft excel. The dataset that is collected consists of all numerical forms; there is no need to convert the data. The unwanted attributes that are not necessary for the prediction are removed.

The testing setup uses Core i5 with 2.25 GHz with 8 gigabytes of random access memory. In this proposed system 50GB hard disk and 8GB RAM for the execution of the Algorithm. The system type used was a 64-bit Operating System, X64 and it is a windows operating system. To use a machine-learning algorithm one of the Integrated Development Environment called Spyder software with pre-installed libraries or Google collab can be used for replacement. The proposed system for the classification of heart disease prediction involves the following steps: correlation between columns, Exploratory data analysis (EDA), feature extraction, and classification.

Novel Decision Tree Algorithm

Novel Decision Tree falls under the category of supervised algorithms. Novel Decision Trees can be used for both classification and regression. In the classification Novel Decision Tree, the decision variable is categorical. For implementing a Novel Decision Tree, the cost function used to evaluate the binary splits called the Gini Index should be calculated. The split creation is done with help of calculating the Gini score, splitting the dataset, and evaluating them all splits. Once this is done and the root node is created It can start building the tree by first deciding when to stop the

growth of the tree by creating the terminal node by setting the maximum tree depth and second, by using recursive splitting. The terminal node is used for the final prediction and recursive splitting is a method used to build the tree.

Pseudocode for Novel Decision Tree is shown below:

Step 1: from sklearn.tree import DecisionTreeClassifier

Step 2: seed = 7

Step 3: kfold = model_selection.KFold(n_splits=45, random_state=seed)

Step 4: model = DecisionTreeClassifier()

Step 5: model.fit(X_train,Y_train)

Step 6: accuracy_score(Y_test,model.predict(X_test))

Naive Bayes Algorithm

The Naive Bayes algorithm is a supervised learning algorithm, which is based on the Bayes theorem and is used for solving classification problems. It is mainly used in text classification that includes a high-dimensional training dataset. Naïve Bayes Classifier is one of the simplest and most effective Classification algorithms which helps in building fast machine learning models that can make quick predictions. Table 3 contains the pseudocode of the Naive Bayes Algorithm.

Pseudocode for Naive Bayes is shown below:

Step 1: from sklearn.naive_bayes import GaussianNB

Step 2: gnb = GaussianNB()

Step 3: gnb.fit(X_train, Y_train)

Step 4: NY_predict=gnb.predict(X_test)

Step 5: accuracy_score(Y_test,NY_predict)

Statistical Analysis

The statistical analysis is applied using Statistical Package for Social Sciences (SPSS) for descriptive statistical analysis such as mean, standard deviation and standard error were carried out for each group (Ilyas et al. 2021). The test was performed to compare variables across the study groups. Hence the independent variable in this study is mean, entropy, variance, and contrast. The dependent variables are accuracy, bp, rbc. The independent sample t-test is performed to compare the accuracy performance of both Group-1 and Group-2 using the DT and the NB algorithms.

RESULTS

The Novel Decision Tree classifier (DT) takes input in the form of symptoms from the dataset and produces output with an accuracy value of around 96.66%. The mean accuracy and loss values using the T-test for both the algorithms along with the standard derivation are shown in Table 6. Here Novel Decision Tree and logistic regression algorithms are used. The DT algorithm and NB algorithm are compared with 10 samples by applying 70% of training data and 30% of testing datasets. The performances of the classifiers are measured by accuracy value.

Table 1 contains the accuracy for the Novel Decision Tree classifier with N = 10

Table 1

Novel Decision Tree Accuracy and Loss for N = 10.The accuracy of predicting kidney disease using Novel Decision Tree (96.66%) is obtained.

Iterations	Accuracy (%)
1	96.66
2	95.12
3	96.78
4	94.43
5	96.92
6	93.13
7	97.10
8	92.33
9	97.85
10	91.11

Table 2 contains the accuracy for the logistic regression classifier with N = 10. The Naive Bayes classifier input is taken from the dataset and it gives an output accuracy of 90.83%.

Table 2

Naive Bayes Accuracy and Loss for N = 10. The accuracy of predicting kidney disease using Naive Bayes (90.83%) is obtained.

Iterations	Accuracy(%)
1	90.83
2	85.20
3	91.23
4	82.12
5	92.10
6	78.23
7	93.30
8	73.64
9	93.78
10	69.12

From Table 3 the statistical analysis of Novel Decision Tree and Naive Bayes Mean accuracy value and Standard deviation are observed that the DT algorithm performed better than the NB algorithm.

Table 3

Group Statistics results (Mean of Novel Decision Tree Algorithm is 96.66% is more compared to Naive Bayes Algorithm 90.83%) and got the highest accuracy and the least error. Standard deviation and Standard Error Mean were also calculated.

	Group	N	Mean	Std. Deviation	Std. Error Mean
Accuracy	Novel Decision Tree	10	95.1430	2.31026	.73057
	Naive Bayes	10	84.9550	8.84786	2.79794

In Table 4 it is observed that the Novel Decision Tree has better significance than Naive Bayes with the value of p = 0.001.

Table 5 shows the accuracy values for both the Novel Decision Tree and Logistic regression algorithm. The DT algorithm obtained 2.31 standard deviations with 8.84 standard error while the NB algorithm obtained.730 standard deviations with 2.79 standard error.

Accuracy for both the algorithms is presented in a bar graph in Fig. 1. From Table 5 it is observed that the Novel Decision Tree proved with better and higher accuracy (96.66%) than Naive Bayes (90.83%).

Figure 1 has the mean accuracy of the two algorithms has been shown and compared the mean error and the graph shows that Novel Decision tree is better than the NB algorithm

The Novel DT model obtained 96.66% and the NB algorithm already predicted 90.83%. performance value. Finally, we compared the mean error of DT and

Table 4

Independent Sample Test for significance and standard error determination. P-value is 0.001 (less than 0.005) considered to be statistically significant and 95% confidence interval was considered.

		Levene's test for equality of variances		T-test for equality means with 95% confidence interval						
		f	Sig.	t	df	Sig. (2-tailed)	Mean difference	Std.Error difference	Lower	Upper
Accuracy	Equal variances assumed	14.977	.001	3.523	18	.001	10.18800	2.89174	4.11267	16.26333
	Equal Variances not assumed			3.523	10.222	.001	10.18800	2.89174	3.76367	16.612333

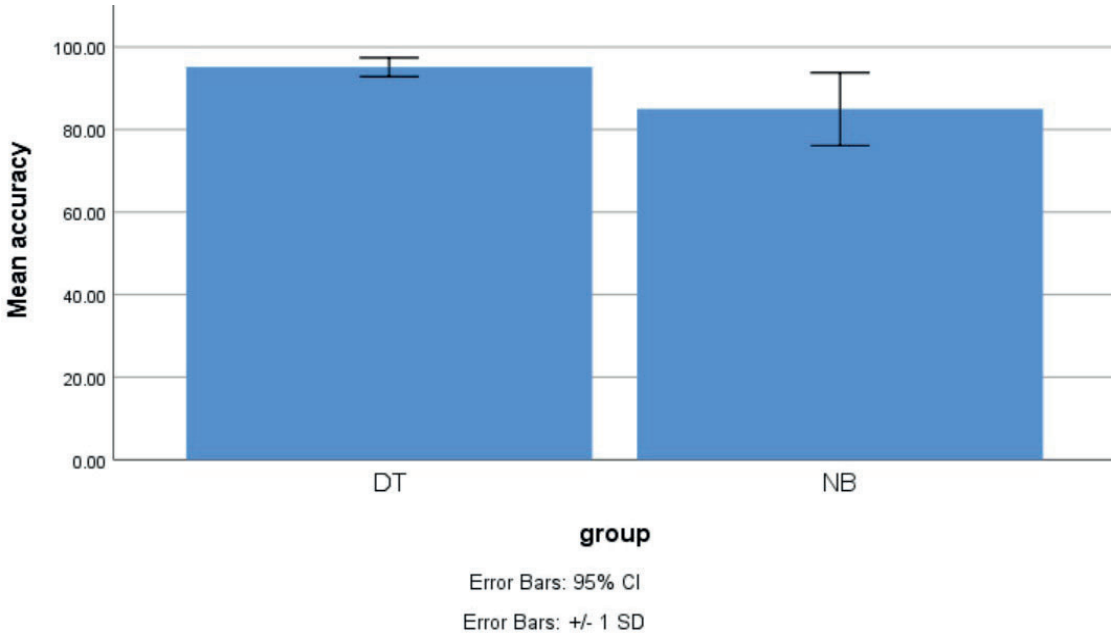


Fig. 1. Bar Chart representing the comparison of Mean Accuracy of Novel Decision Tree Algorithm and Naive Bayes algorithms. Mean accuracy of the Novel Decision Tree Algorithm appears to be better than Naive Bayes algorithm. The X-axis represents Novel Novel Decision Tree Algorithm and Naive Bayes algorithms and Y-axis represents the mean accuracy ± 1 SD.

Table 5

Comparison of the Decision Tree Algorithm and Logistic Regression Algorithm with their accuracy

CLASSIFIER	ACCURACY(%)
Decision Tree	96.66%
Naive Bayes	90.83%

NB algorithms as shown in Fig. 1. Therefore the Novel DT is significantly better than the NB algorithm.

DISCUSSION

Novel Decision Tree appears to be significantly better than Naive Bayes with improved accuracy. The Novel Decision Tree classifier shows a significant difference in terms of accuracy score, speed, and performance when compared to the Naive Bayes classifier.

This finding is similar to (Rashed-Al-Mahfuz et al. 2021) who have found that the Novel Decision Tree classifier performs better than the logistic regression classifier. Similar studies that have been made by others such as (Bradley et al. 2019) also have similar findings where Novel Decision Tree is better than Naive Bayes and so it can be implemented in real-time detection of CKD. (Amiri et al. 2021) presents a methodology to control the disease using a suitable diet plan. In this research, classifiers are constructed using different algorithms like Multiclass Decision Jungle, Multiclass Decision Forest, Multiclass Neural Network, and Naive Bayes. (Shih et al. 2021) The classification and regression tree, i.e. RPART model, showed considerably good results. It uses the ratio of information gain for the splitting criterion, where the optimal split would decrease the impurity of resulting subsets. The performance of four kernel-based ELM, namely RBF-ELM, Linear-ELM, Polynomial-ELM, Wavelet-ELM is compared with the performance of standard ELM. The above methodologies were compared on metrics of sensitivity and specificity. Radial Basis Function – Extreme Learning Machine (RBF-ELM) showed higher prediction rates (Bellocchio et al. 2021).

Most of the previous work done is based on the data from the specific dataset. In the proposed work the lack of accuracy in predicting chronic kidney disease is improved by machine learning algorithms (Lee et al. 2022). In the future, this work can be extended to find how likely nondiabetic people can have kidney failure in the next few years (Lee et al. 2022; Shih et al. 2021). Artificial intelligence can also be used in the future to predict the severity of kidney failure. Even more, data can be accumulated over the existing data, and also datasets of feature set selection can be used (Singh, Asari, and Rajasekaran 2022). Deep Neural networks can be used for those datasets which will have a significant difference in terms of accuracy and real-world implementation.

CONCLUSION

In this research, Chronic kidney disease prediction is performed using the kidney disease symptoms dataset for Novel Decision Tree and Naive Bayes. The accuracy value of the Novel Decision Tree classifier is 96.66% whereas the accuracy value of the Naive Bayes Algorithm is 90.83%. The quality of Chronic kidney disease prediction and accuracy using Novel Decision Tree appears to be better than Naive Bayes.

DECLARATION

Conflicts of Interests

No conflict of interest in this manuscript.

Authors Contributions

Author RJ was involved in data collection, data analysis, and manuscript writing. Author RJ was involved in conceptualization, data validation, and critical review of the manuscripts.

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