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Original Article

Early Phase, Multi Diseases Detection, Using AI & Intelligent Hybrid Supervised Machine Learning Classifier Model

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Abstract *- The healthcare industry generates vast amounts of data processed using specific techniques. Data mining is key to the healthcare industry's illness prediction process. The patient should be required to undergo a number of tests in order to diagnose the condition. The two main organ diseases that affect humans are kidney and liver diseases. Regardless, the two well-known conditions affecting people nowadays are Chronic Kidney Disease (CKD) and Chronic Liver Disease (CLD). A small number of people pass away these days due to chronic liver and kidney diseases. These are the most common illnesses on the earth and are real infections. In addition, the progressive degeneration of the kidney and liver is referred to as chronic kidney disease and chronic liver disease, respectively. A promising technique that aids in early disease identification and may support medical practitioners in their decision-making is machine learning. This study examines data mining techniques that can be applied to forecast conditions such as liver and kidney disorders. Using a dataset for training and testing, we compute the precision of machine learning calculations for predicting kidney and liver infection. We found that the proposed hybrid classifier model, K-Nearest Neighbor, Naïve Bayesian, and Decision Tree methods all had superior accuracy. This research aims to develop a framework to more accurately forecast a patient's risk of developing kidney and liver problems. The suggested methodology yielded higher results than other methods under consideration, scoring 99.24% and 99.96 for CKD and CLD, respectively. Furthermore, data pick-up and other attribute evaluators have been included to show the framework's tall execution with the fewest possible features.*

Keywords *- Chronic Kidney Disease, Chronic Liver Disease, Classification, Prediction, Hybrid classifier model, K-Nearest Neighbor, Decision Tree, Bayesian classifier, Machine Learning and AI techniques.*

1. Introduction

These days, the healthcare sector provides a number of advantages, such as enhanced patient consideration, improved client-clinician relationships, clinical offices that are affordable for patients to access, evidence of more intelligent treatment philosophies, development of practical medical care strategies, successful emergency clinic asset the board, and clinic disease control. The infection location is just another one of the many topics covered by medical study.

The most well-known illness in the world is kidney disease. Diabetes and hypertension play a major role in kidney damage. These diseases have the potential to damage the kidney's supporting structures. An identical material level can be maintained in the human body, and side effects can be removed from the blood by a healthy kidney, also known as an ordinary kidney. The CKD unique dataset can be used in this work to identify the disease.

The progressive loss of liver tissue over time is a hallmark of chronic liver disease. This group of liver illnesses includes:

- Cirrhosis
- Fibrosis of the liver

1.1. Cirrhosis of the Liver

Cirrhosis is the 12th largest cause of death in the United States, according to the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK).

Because of persistent hepatic damage:

- As normal liver tissue is lost, the liver's ability to process nutrients, hormones, drugs, and poisons and produce proteins and other substances is compromised.
- Scar tissue gradually replaces normal functioning liver tissue. It also gradually reduces blood flow through the liver.

1.2. Fibrosis of the Liver

The expansion of scar tissue brought on by an infection, inflammation, trauma, or even recovery is known as fibrosis. Almost every organ might have an overabundance of scar tissue. Liver fibrosis can make it difficult for the organ to operate normally. Cirrhosis is typically the cause of liver fibrosis.

One kind of data analysis is classification, which involves extracting models that define pertinent data classes.

- K-Nearest Neighbour (K-NN): This straightforward tactic uses regression and classification techniques. This approach produces different results depending on whether k-NN is used for regression or classification.
- Decision Tree (DT): An information base choice tree is a tree-like information design. It is utilized in task exploration and AI to pursue choices that will prompt a significant end and in information mining to characterize information and recover information.
- Bayesian Classifier: It may be applied to medical diagnosis in a logical manner and is based on the probability theorem. It is particularly useful in automated medical diagnosis decision support systems. It can handle an infinite number of categorical and continuous independent variables.

There are multiple sections in this document. Section 2 discusses the research studies that are pertinent to this investigation. Section 3 presented an outline of the research objectives. Section 4 displays the results of all methods. The research is concluded in Section 5, and its future directions are covered in Section 6.

2. Literature Survey

AI calculations have been utilized for quite some time to settle difficulties in the clinical field. This has been endeavoured by various scientists. Different procedures and techniques have been utilized to order and expect the patient's disease status. They fostered a choice emotionally supportive network that utilizes characterization calculations to analyse and foresee ongoing renal disappointment.

2.1. Chronic Kidney Disease

Saurabh Pal has employed three different types of chronic renal illness [1]. The original CKD pattern used the machine learning classifiers Support Vector Machine, Random Forest, and Artificial Neural Network, together with the categorical features bp, sg, al, su, rbc, pc, pcc, ba, htn, dm, cad, appet, pe, and ane. Second, employ attributes that are not categorical, like id, age, bgr, bu, sc, sod, pot, hemo, pcv, wc, and rc. Next, machine learning classifiers such as Support Vector Machines, Random Forests, and Artificial Neural Networks are utilized to achieve the aim variable, which is classification. In the last experiment, the performance of the classifiers on the combined dataset is tested to determine which Random Forest classifier performs best in terms of accuracy, precision, recall, F-score, and ROC-AUC. The results show that the classifiers perform 0.92, 0.63, 0.55, 0.60, and 0.76, respectively.

The Pearson correlation feature selection method was utilized by Hira Khalid et al. [2] and applied to a machine learning classifier. The base classifiers for the stacking algorithm include GB, GNB, decision trees, and random forests. These are implemented using cross-validation based on accuracy score. They used the same dataset to assess various algorithms in this study. Additionally, they have used the 400 instances and 14 attributes of the CKD dataset from the UCI directory. Based on these characteristics, the suggested stacking model may determine a person's status as a CKD patient with 92% accuracy.

Zahid Ullah et al. [3] use machine learning approaches to create prediction models for CKD diagnosis based on main traits, with the goal of diagnosing chronic illness. Furthermore, fewer required tests that are adequate to diagnose Chronic Kidney Disease (CKD) can be carried out to help reduce the clinical costs spent by patients who are prescribed several identical tests. The dataset has undergone a number of preparation operations, including feature selection, normalization, and imputation of missing values. The processed dataset was trained with various prediction models, including bagging, KNN, SVM, and RF. According to estimates of accuracy, sensitivity, F-measure, specificity, and AUC score, the models' performance demonstrated higher dependability and significance. KNN demonstrated the model's effectiveness in utilizing it as a decision-making system for identifying and diagnosing CKD in its early stages by outperforming the state-of-the-art techniques currently employed in the literature.

A variety of machine learning techniques, including RF, SVM, ANN, and others, were given by Md. Ariful Islam et al. [4] in an effort to diagnose CKD sooner. The original CKD dataset was pre-processed to validate the machine learning-based detection algorithms. Subsequently, PCA was used to determine which traits were most prevalent, which allowed for the detection of CKD. The models constructed from CKD patients are trained and validated using the previously described input parameters. SVM's 95% rate surpassed the accuracy rate of other algorithms.

Dibaba Adeba Debal and colleagues [5] examined two feature selection techniques and three machine learning models: RF, SV, and DT. The suggested models were constructed using RFECV and UFS. Tenfold cross-validation was used for model evaluation. Originally, datasets containing all 19 features were subjected to the four machine learning methods. Using RF, SVM, and XGBoost, we achieved the maximum accuracy when applying the models to the original dataset. For the binary class, the accuracy was 94.8%, and for

the five-class, it was 82.56%. DT performed the worst when contrasted with RF. Furthermore, the highest f1_score values were produced by RF. SVM and RF combined with RFECV produced the best accuracy of 95.8% for the binary class. XGBoost achieves the highest accuracy of 82.56% on five-class datasets.

2.2. Chronic Liver Disease

Venugopal Reddy Modhugu et al. [6] use a Kaggle dataset with 20,000 training records and roughly 1,000 test records to examine the Support Vector Machine (SVM), Logistic Regression, and Decision Tree algorithms for liver disease prediction. Accuracy, precision, recall, and F1-score are among the performance criteria used by the research to assess the algorithms. With an accuracy of 85%, SVM was the most successful model; Logistic Regression came in second with 82%, and Decision Tree came in third with 79%.

The results emphasize the value of algorithm selection in healthcare applications and show how SVM may be used to identify and treat liver disease patients early on, improving patient outcomes and healthcare administration. Subsequent research endeavors will center on optimizing the algorithms and verifying the outcomes using more extensive and varied datasets to further augment predicted precision and resilience.

In an effort to support medical practitioners in the early detection of liver cirrhosis, Ahmet Ercan Topcu et al. [7] introduce an Artificial Intelligence (AI) system powered by cutting-edge Machine Learning (ML) techniques. The main goal of the machine learning algorithms now in research is to forecast the probability of liver cirrhosis infection. Seven unique models have been developed as a result of this research, utilizing a variety of parameters and various machine learning algorithms, including AdaBoost, k-Nearest Neighbors (KNN), Random Forest (RF), Multi-layer Perceptron (MLP), Linear Discriminant Analysis (LDA), Logistic Regression (LR), and Random Forest (RF). Out of all of them, the RF algorithm was the most accurate, showing an astounding accuracy rate of about 98 percent.

Mandakini Priyadarshani Behera et al. [8] combined the modified particle swarm optimization model with the Support Vector Machine (SVM) technique to produce a hybrid model for diagnosing heart and liver disorders. The data is collected from the machine learning repository at UCI. Classification accuracy, error, correctness, recall, and F1 score determine the results. Comparing the results with SVM, hybrid PSO Support Vector Machine algorithm (PSOSVM), and hybrid Crazy PSO Support Vector Machine algorithm (CPSOSVM) yields different results. After conducting a thorough experimental analysis, it is possible to conclude that the intended CCPSOSVM produces better classification results, with the highest classification rate and lowest error rate for the prediction of liver and heart illness, with accuracy levels of 92.57% and 96.41%, respectively.

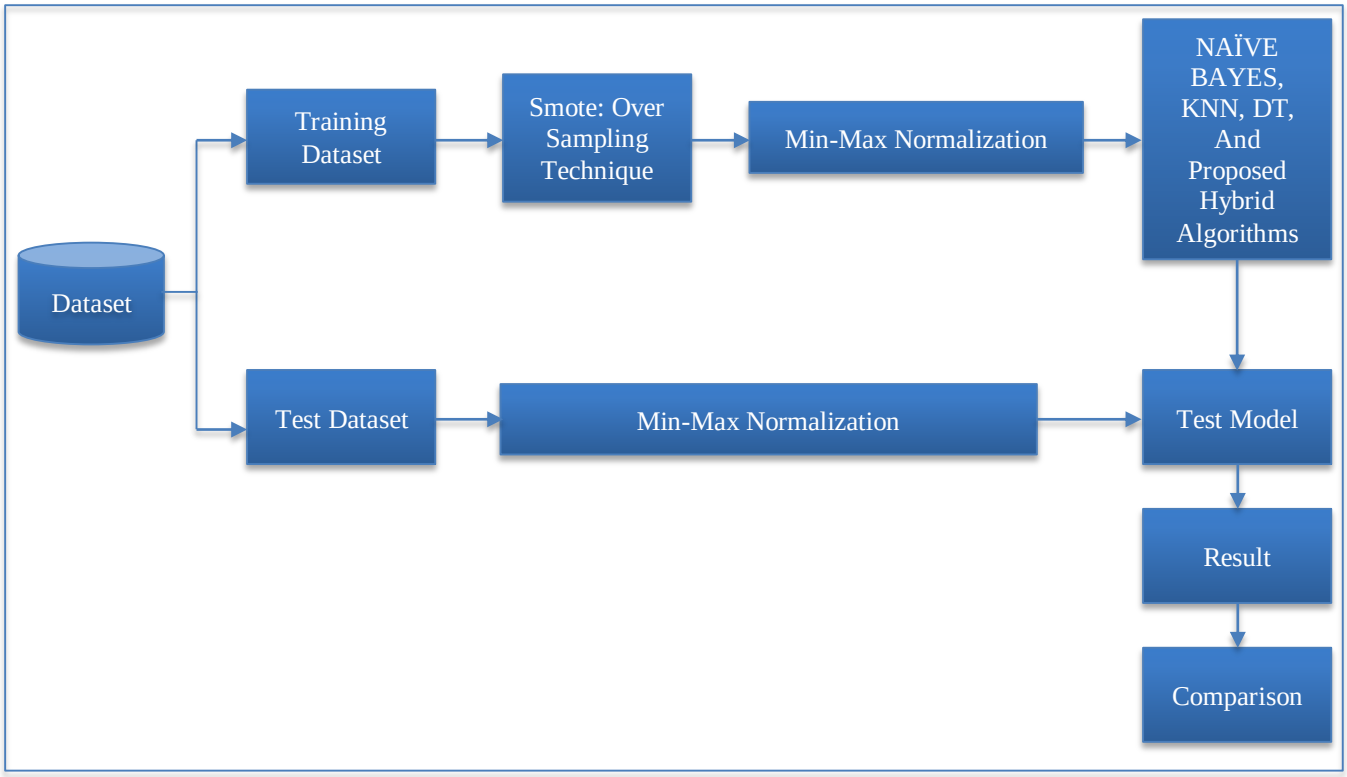


Fig. 1 Proposed architecture

A comparison of the performance of the ensemble models utilized by Abdul Quadir Md et al. [9] for diagnosing liver disease has been made. The best testing accuracy of 91.82% was obtained by the suggested model, which employs an upgraded preprocessing strategy with an additional tree classifier. The random forest model came in second with 86.06% testing accuracy. When classifying liver illness, our suggested models performed better than a number of machine-learning techniques found in the literature. The ILPD dataset was used for this study.

By utilizing dimensionality reduction strategies, including PCA, FA, and LDA, Ruhul Amin et al. [10] have investigated enhanced feature extraction systems for liver patient classification through statistical machine learning techniques. By considering the maximum variation in the data, the covariance between the observed variables, and a linear combination of the observed variables that optimize the class separation, the system could extract an enhanced feature space. Additionally, data balancing was done to prevent bias and overfitting, and various robust statistical methods were applied to manage missing values and outliers. Additionally, we ran simulation research to replicate the outcome with the suggested methodology, and the ensemble classification algorithm produced an average accuracy of 91.40%.

3. Proposed Architecture and Dataset

3.1. Proposed Architecture

This flow provides instructions on creating the suggested system depicted in Figure 1 and encapsulates the steps outlined in the design.

3.1.1. Load Dataset

- Input: A dataset is loaded, which contains the data to be used for training and testing.
- Output: The training dataset and the test dataset are the two subsets that make up the dataset.

3.1.2. Apply SMOTE (Synthetic Minority Over-Sampling Technique)

- Input: The training dataset.
- Process: To address the class imbalance, apply the SMOTE approach to the training dataset and create synthetic samples for the minority class.
- Output: An oversampled training dataset.

3.1.3. Normalize Data Using Min-Max Normalization (for Training Dataset)

- Input: The oversampled training dataset.
- Process: To scale the training dataset's features to a certain range (usually [0, 1]), apply Min-Max normalization.
- Output: A normalized training dataset.

3.1.4. Train Models with Various Algorithms

- Input: The normalized training dataset.
- Process: Train models using the following algorithms:
  - Naïve Bayes
  - K-Nearest Neighbors (KNN)
  - Decision Tree (DT)
  - Proposed hybrid algorithms
  - Output: Trained models for each algorithm.

3.1.5. Apply Min-Max Normalization to Normalize Data (for Test Dataset)

- Input: The dataset for testing.
- Process: Using the same scaling settings obtained from the training dataset, apply Min-Max normalization to the test dataset.
- Output: A normalized test dataset.

3.1.6. Test Models on the Test Dataset

- Input: The normalized test dataset.
- Process: Use the trained models to make predictions on the test dataset.
- Output: Predicted results for each algorithm.

3.1.7. Obtain Results

- Input: The predicted results from each model.
- Process: Evaluate the models' performance using pertinent metrics (e.g., accuracy, precision, recall, F1-score).
- Output: Performance results of each algorithm.

3.1.8. Compare Results

- Input: The performance results of all models.
- Process: To determine which model performs best, compare the outcomes of Naïve Bayes, KNN, Decision Tree, and the suggested hybrid algorithms.
- Output: A comparison study of the algorithms, which helps choose the best-performing model.

3.2. Dataset

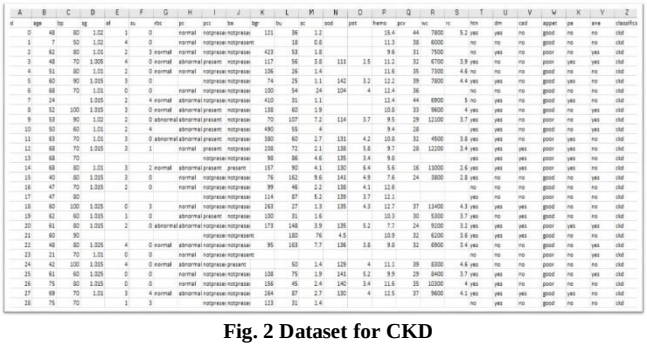
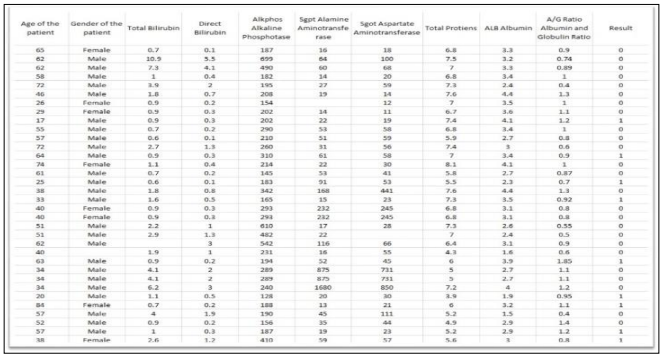


Fig. 2 Dataset for CKD

The dataset in Figure 2 was collected in India over a two-month period. It has 400 rows and 25 traits, including sugar, edema in the pedal region, and red blood cells. The goal is to determine whether or not a patient has chronic renal disease. The categorization is predicated on a characteristic called

"classification," which can be either "notckd" or "ckd" (chronic kidney disease). I've cleaned up the dataset by translating the language to numbers and making a few additional adjustments. After cleaning, I divided the dataset into training and testing sets, ran the models on each set, and did some exploratory data analysis. It has been noted that the initial classification findings are not very satisfying. Hence, I've used the lambda function to replace the rows with Nan values with the mode for each column rather than removing the rows with such values. The dataset was then divided into training and testing sets once more, and models were run on them. The better results this time show that the suggested hybrid model is the best performer, with an accuracy of 99.24%. The classification performance is measured by printing the classification report, the confusion matrix, and accuracy.



Age of the patient	Gender of the patient	Total Bilirubin	Direct Bilirubin	Alkphos Alkaline Phosphotase	Sgot Alamine Aminotransferase	Sgot Aspartate Aminotransferase	Total Protiens	ALB Albumin	A/G Ratio Albumin and Globulin Ratio	Result
65	Female	0.7	0.1	187	16	18	6.8	3.3	0.9	0
62	Male	10.9	5.5	699	64	100	7.5	3.2	0.74	0
62	Male	7.3	4.1	490	60	68	7	3.3	0.89	0
58	Male	1	0.4	182	14	20	6.8	3.4	1	0
72	Male	3.9	2	195	27	59	7.3	2.4	0.4	0
46	Male	1.8	0.7	208	19	14	7.6	4.4	1.3	0
26	Female	0.9	0.2	154		12	7	3.5	1	0
29	Female	0.9	0.3	202	14	11	6.7	3.6	1.1	0
17	Male	0.9	0.3	202	22	19	7.4	4.1	1.2	1
55	Male	0.7	0.2	290	53	58	6.8	3.4	1	0
57	Male	0.6	0.1	210	51	59	5.9	2.7	0.8	0
72	Male	2.7	1.3	260	31	56	7.4	3	0.6	0
64	Male	0.9	0.3	310	61	58	7	3.4	0.9	1
74	Female	1.1	0.4	214	22	30	8.1	4.1	1	0
61	Male	0.7	0.2	145	53	41	5.8	2.7	0.87	0
25	Male	0.6	0.1	183	91	53	5.5	2.3	0.7	1
38	Male	1.8	0.8	342	168	441	7.6	4.4	1.3	0
33	Male	1.6	0.5	165	15	23	7.3	3.5	0.92	1
40	Female	0.9	0.3	293	232	245	6.8	3.1	0.8	0
40	Female	0.9	0.3	293	232	245	6.8	3.1	0.8	0
51	Male	2.2	1	610	17	28	7.3	2.6	0.55	0
51	Male	2.9	1.3	482	22		7	2.4	0.5	0
62	Male		3	542	116	66	6.4	3.1	0.9	0
40	Male	1.9	1	231	16	55	4.3	1.6	0.6	0
63	Male	0.9	0.2	194	52	45	6	3.9	1.85	1
34	Male	4.1	2	289	875	731	5	2.7	1.1	0
34	Male	4.1	2	289	875	731	5	2.7	1.1	0
34	Male	6.2	3	240	1680	850	7.2	4	1.2	0
20	Male	1.1	0.5	128	20	30	3.9	1.9	0.95	1
84	Female	0.7	0.2	188	13	21	6	3.2	1.1	1
57	Male	4	1.9	190	45	111	5.2	1.5	0.4	0
52	Male	0.9	0.2	156	35	44	4.9	2.9	1.4	0
57	Male	1	0.3	187	19	23	5.2	2.9	1.2	1
58	Female	2.6	1.2	410	59	57	5.6	3	0.8	1

Fig. 3 Dataset for CLD

There is more to the dataset displayed in Figure 3 than just rows and columns. Provide a description of how you obtained the data and the time period it reflects to make it easier for others to get started.

The ten variables in this data collection are age, gender, albumin, total proteins, total and direct bilirubin, A/G ratio, SGPT, SGOT, and alkphos.

- Information about Attributes:
- Age of the patient
- Gender of the patient
- Total Bilirubin
- Direct Bilirubin
- Alkaline Phosphotase
- Alamine Aminotransferase
- Aspartate Aminotransferase
- Total Proteins
- Albumin
- Albumin and Globulin Ratio

A selector field (labeled by experts) was utilized to divide the data into two sets. Two non-liver patients and one liver patient

The better results this time show that the suggested hybrid model is the best performer, with an accuracy of 99.96%. The classification performance is measured by printing the classification report, the confusion matrix, and accuracy.

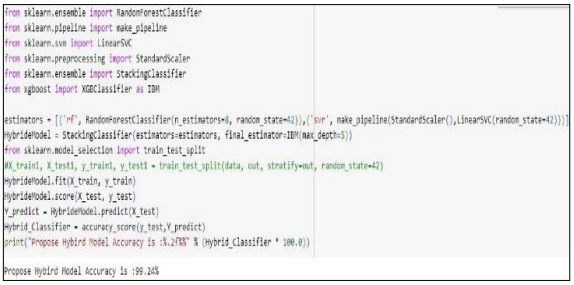
The essential objective of this study is to exhibit the worth of information mining in surveying life-related messes. It is tried to audit the writing piece whose examination action is centered on the two specialists and patients. The fundamental focuses (disease, technique, discoveries, precision) of the different review studies and the use of instruments or strategies will be featured. At last, the objective is to recognize what locales request additional consideration from information mining and AI devices.

The examination objectives are to sort material per conduct informatics and group information to dissect information designs. By surveying demonstrative data with regulated and solo AI calculations, we desire to work on the symptomatic execution of present indicative methodologies for infection forecast. To survey the proposed approach's presentation utilizing models, for example, accuracy, review, F-measure, and precision with characterization rate. Analyze the exhibition of various classifiers and bunching calculations on various datasets.

4. Results

4.1. For Chronic Kidney Disease

The accuracy report for the suggested hybrid model using the CKD dataset from kaggle.com is displayed in Figure 4.



```
from sklearn.ensemble import RandomForestClassifier
from sklearn.pipeline import make_pipeline
from sklearn.svm import LinearSVC
from sklearn.preprocessing import StandardScaler
from sklearn.ensemble import StackingClassifier
from xgboost import XGBClassifier as IBM

estimators = [('rf', RandomForestClassifier(n_estimators=8, random_state=42)),('svr', make_pipeline(StandardScaler(),LinearSVC(random_state=42)))]
HybrideModel = StackingClassifier(estimators=estimators, final_estimator=IBM(max_depth=5))
from sklearn.model_selection import train_test_split
#X_train1, X_test1, y_train1, y_test1 = train_test_split(data, out, stratify=out, random_state=42)
HybrideModel.fit(X_train, y_train)
HybrideModel.score(X_test, y_test)
Y_predict = HybrideModel.predict(X_test)
Hybrid_Classifier = accuracy_score(y_test,Y_predict)
print("Propose Hybird Model Accuracy is :%.2f%%" % (Hybrid_Classifier * 100.0))

Propose Hybird Model Accuracy is :99.24%
```

Fig. 4 Accuracy report of hybrid model for CKD

Figure 5 shows the precision (0.98), recall (0.99), F1 (0.99), and support scores for the recommended model in the classification report.

```
from sklearn.metrics import classification_report
HybrideModel_Pred=HybrideModel.predict(X_test)
Hybridreport = classification_report(y_test, HybrideModel_Pred)
print(Hybridreport)
```

	precision	recall	f1-score	support
0	1.00	0.99	0.99	84
1	0.98	1.00	0.99	48
accuracy			0.99	132
macro avg	0.99	0.99	0.99	132
weighted avg	0.99	0.99	0.99	132

Fig. 5 Classification report of hybrid model for CKD (precision, recall, F1-score)

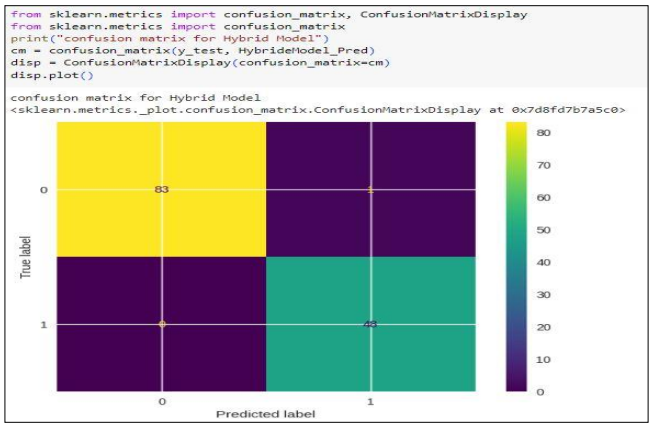


Fig. 6 Classification report of hybrid model for CKD (precision, recall, F1-score)

Accuracy suggests a classifier's ability to do whatever it takes not to name a negative event as certain. Not entirely settled as to the extent of authentic up-sides of how many certifiable up-sides and deceiving up-sides for each class. It's generally called positive assumption precision.

The constraint of a classifier to observe every one of the specific cases is known as review. Still up in the air as the extent of certifiable empowering focuses on how many veritable sides and misdirecting negatives for each class. It decides the degree of really perceived upsides.

The F1 score is the weighted consonant mean of survey and precision, with 1.0 denoting the most significant and 0.0 the least essential. Since exactness and survey are considered in addition to the computation, they are less meticulous than accuracy assessments. Use the weighted ordinary of F1 instead of overall accuracy when analyzing classifier models.

The amount of genuine class occasions in the given dataset is known as help. Support doesn't shift between models but dissects the evaluation connection.

As explained in the disorganized layout of the proposed hybrid model in Figure 6, there are four ways to decide which of the gauges is accurate.

- True Negative (TN): a negative outcome was consistently predicted for the case.
- True Positive (TP): The situation was and ought to be favorable.
- False Negative (FN): although the case was favorable, a negative result was anticipated.
- False Positive (FP): Although it was predicted to be positive at this point, the case was really negative.

The confusion matrix displays not only the accuracy of a predictive model but also the classes that are badly forecasted, those that are accurately expected, and the types of errors occurring.

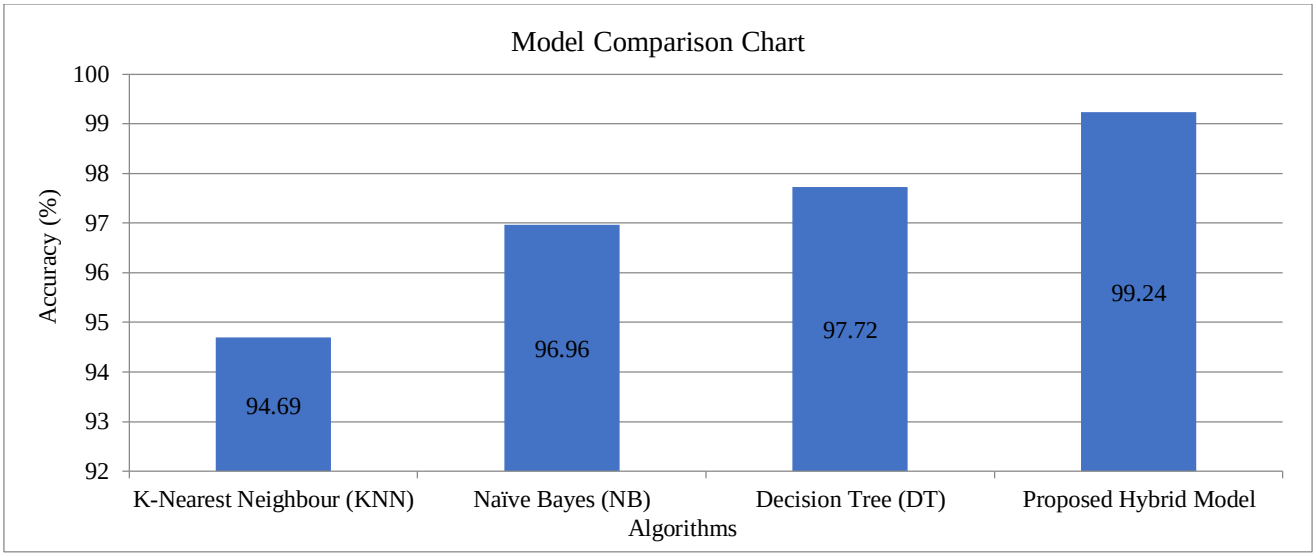


Fig. 7 Accuracy chart of Machine Learning algorithms for CKD

We usually imply accuracy at this stage when we use the word precision. The proportion is the amount of correct expectations divided by the total number of information tests.

Figure 7 displays the precision of each of the three calculations used in this estimation, including k-NN, Naïve Bayes, DT, and the proposed hybrid model for CKD.

In the wake of ascertaining the presentation of proposed models and looking at them all, the best classifier to anticipate Chronic Kidney Disease was picked. As per the exploratory information, the Proposed Hybrid Model has the greatest exactness of 99.24%, contrasted with 94.69%, 96.96%, and 97.72% for the k-NN, Naïve Bayes and DT calculations, individually. The outcomes are displayed in Table 1.

Table 1. Comparison of algorithms for CKD

Algorithms	Accuracy (%)
K-Nearest Neighbour (KNN)	94.69
Naïve Bayes (NB)	96.96
Decision Tree (DT)	97.72
Proposed Hybrid Model	99.24

4.2. For Chronic Liver Disease

Fig. 8 Accuracy report of hybrid model for CLD

Figure 8 shows the accuracy report for the proposed Hybrid model with the CLD dataset taken from kaggle.com

```
from sklearn.metrics import classification_report
STK_Pred=STK.predict(X_test)
STKreport = classification_report(Y_test, STK_Pred)
print(STKreport)
```

	precision	recall	f1-score	support
0	1.00	1.00	1.00	3561
1	1.00	1.00	1.00	3489
accuracy			1.00	7050
macro avg	1.00	1.00	1.00	7050
weighted avg	1.00	1.00	1.00	7050

Fig. 9 Classification report of hybrid model for CLD (precision, recall, F1-score)

Figure 9 shows the precision (1.00), recall (1.00), F1 (1.00), and support scores for the recommended model in the classification report. As explained in the disorganized layout of the proposed hybrid model in Figure 10, there are four ways to decide which of the gauges is accurate.

- True Negative (TN): a negative outcome was consistently predicted for the case.
- True Positive (TP): The situation was and ought to be favorable.
- False Negative (FN): although the case was favorable, a negative result was anticipated.
- False Positive (FP): Although it was predicted to be positive at this point, the case was really negative.

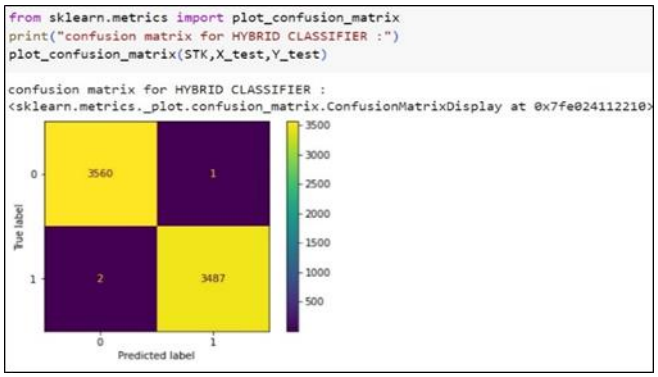


Fig. 10 Classification report of hybrid model for CLD (precision, recall, F1-score)

The confusion matrix displays not only the accuracy of a predictive model but also the classes that are badly forecasted, those that are accurately expected, and the types of errors occurring. We usually imply accuracy at this stage when we use the word precision.

The proportion is the amount of correct expectations divided by the total number of information tests. Figure 11 displays the precision of each of the three calculations used in this estimation, including k-NN, Naïve Bayes, DT, and the proposed hybrid model for CLD.

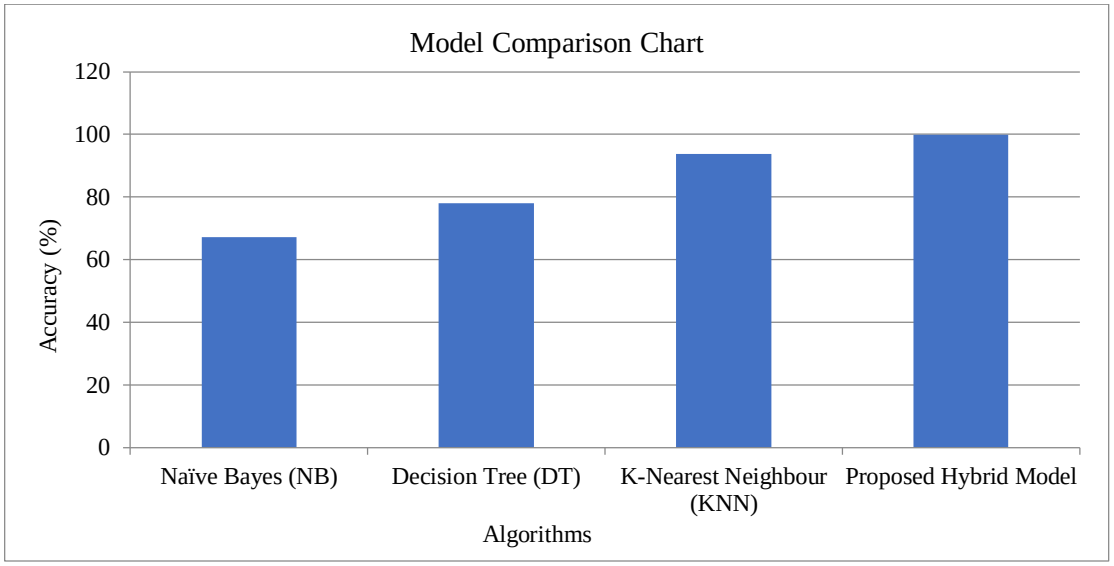


Fig. 11 Accuracy chart of Machine Learning algorithms for CLD

After determining how the suggested models were presented and examining each one, the most effective classifier for predicting chronic liver disease was selected. According to the preliminary data, the proposed hybrid model has the highest accuracy at 99.96%, while the k-NN, Naïve Bayes, and DT computations, taken separately, have the highest accuracy at 67.25%, 78.00% and 93.83%. The results are shown in Table 2.

Table 2. Comparison of algorithms for CLD

Algorithms	Accuracy (%)
Naïve Bayes (NB)	67.25
Decision Tree (DT)	78.00
K-Nearest Neighbour (KNN)	93.83
Proposed Hybrid Model	99.96

5. Conclusion

The reason for this review is to foster an original structure in light of bunching and order information-digging methods for foreseeing and diagnosing these problems in the medical services region utilizing genomic data sets.

Here is the Model Performance across the taken Datasets:

In relation to Chronic Kidney Disease (CKD):

- The K-Nearest Neighbor (KNN) algorithm's accuracy was 94.69%.
- At 96.96% accuracy, Naïve Bayes (NB) outperformed the other algorithm by a small margin.
- Decision Tree (DT) further improved with an accuracy of 97.72%.
- The Proposed Hybrid Model significantly outperformed all other models, achieving an accuracy of 99.24%.

For Chronic Liver Disease (CLD):

- With an accuracy of 67.25%, Naïve Bayes (NB) had the poorest performance.
- Decision Tree (DT) showed improvement with an accuracy of 78.00%.
- K-Nearest Neighbor (KNN) further enhanced the performance with an accuracy of 93.83%.
- The Proposed Hybrid Model demonstrated the highest accuracy, reaching 99.96%.

Proposed Hybrid Model Superiority

The proposed hybrid model consistently outperforms the traditional machine learning algorithms (KNN, NB, DT) across both datasets. This suggests that combining different approaches or algorithms into a hybrid model provides superior accuracy and reliability for predicting and diagnosing chronic kidney and liver diseases.

Significance of Hybrid Approaches

The proposed hybrid model's dramatic accuracy improvement underscores the potential benefits of integrating multiple algorithms or techniques. Such hybrid models may better capture complex patterns in the data that individual algorithms might miss.

Recommendation for Clinical Application

Given the high accuracy of the proposed hybrid model, especially its near-perfect performance on the chronic liver disease dataset, this model shows promise for clinical applications. It could potentially be used for more reliable and accurate early diagnosis and chronic kidney and liver disease prediction, leading to better patient outcomes.

Overall, the results indicate that while traditional algorithms like KNN, NB, and DT can perform well, hybrid models offer a substantial advantage in terms of accuracy and should be considered for deployment in real-world healthcare settings.

Future Direction

A review of multiple literature studies suggests that the suggested approach would also be applicable to other disease classification issues, including datasets of the same kind as those used in this study. To fully realize their potential and utility, however, research on fuzzy rule-based sickness diagnosis algorithms, noise reduction, and clustering needs to be done extensively. More focus will be needed in the future on the datasets used for disease classification and prediction using incremental machine learning techniques. Therefore, in order to prove this method's effectiveness in terms of large data computation time, it must be tested on more datasets, especially huge datasets. The study also investigates how the suggested technology might be modified to function with other kinds of medical datasets.

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