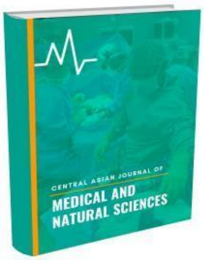

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Article

Early Diabetic Prediction System using Machine Learning

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Abstract: The goal of this project is to create a machine learning-based system that is inclusive and can predict many chronic illnesses, including diabetes, heart disease, and chronic kidney disease. To determine which machine learning classification technique is best for disease prediction, this study uses a variety of models, including K-Nearest Neighbours, Support Vector Machines, Decision Trees, Random Forests, and Logistic Regression. These models are tested using numerous disease-specific datasets to ensure accuracy, sensitivity, and specificity. It is important to identify chronic diseases early to improve patient outcomes and reduce mortality. The present work aims to develop predictive models to identify at-risk individuals for chronic conditions by analysing patient data, including medical history, demographics, and clinical measurements. The end product would be a web application that supports early diagnosis, better patient care, and the effective use of healthcare resources. This research helps in proving the capability of machine learning to diagnose chronic diseases at an early stage.

Keywords: Machine Learning, Chronic Disease Prediction, Early Detection, Healthcare Diagnostics, Classification Algorithms, Predictive Modelling, Data Mining, Algorithm Evaluation.

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1. Introduction

Numerous illnesses, such as diabetes, heart disease, and chronic renal disease, can be predicted because of this research [1]. The classification methods utilised for this are KNN, SVM, Random Forest, and Logistic Regression [6]. This task will detect viruses by classifying them and comparing their levels to the correct ones. We also collected a large number of records for each disease to improve the accuracy of the results [7]. Create web applications by integrating the best guesses for each virus [8]. The user can quickly guess the desired virus by entering the attribute (input) values appropriate to that feature [20]. Various data sets are used here; each is subject to a specific condition [9]. Cardiovascular examination using the Cleveland, Hungary, Switzerland and Long Beach V databases [47]. However, this study used 14 of 76 quality methods (including predictive features). The target is the patient's heart disease [48]. A value of 1 indicates infection, a value of 0 indicates no infection [2].

The data for chronic kidney disease used in this study were collected over 2 months in India and included 25 variables, such as white blood cell (WBC) count and red blood cell (RBC) count [21]. "ckd" and "notckd" are classifications of chronic kidney disease, about the purpose of the attack [22]. The collection contains 400 documents [10]. The patient's body mass index, insulin levels, age, number of previous pregnancies, and many other factors differ [23]. The file has 9 lines and 769 records [11]. The dataset is collected from various sources. We use label encoding and other information before the method [46]. To create models, we employ a variety of machine learning techniques, such as random forests, logistic regression, K-NN, decision trees, and support vector machines [24]. Classifier models are built using multiple algorithms for each disease. Each virus's training and test data are separated [25]. For every model, the training data is used [26]. After evaluating each model against the specific diseases in the test data, the accuracy of each is assessed by comparing it with other models, and the best model is chosen [3].

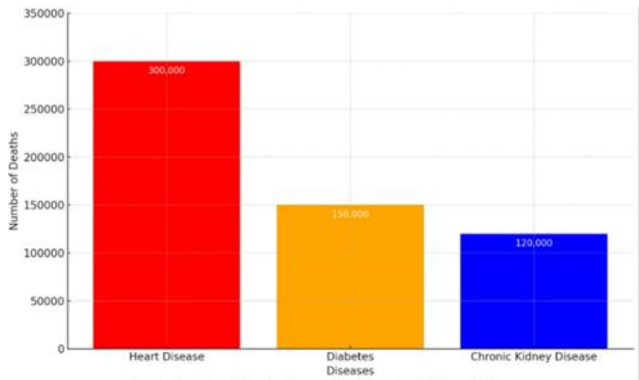

Fig 1 . Number of Deaths due to Late Diagnosis of Chronic Diseases.

Figure 1. Number of Deaths Due To Late Diagnosis of Chronic Diseases.

Figure 1 illustrates the devastating impact of late diagnosis for three chronic diseases [12]. Heart disease leads to the highest number of deaths at 300,000, underscoring the critical need for early detection [13]. Diabetes and chronic kidney disease also contribute significantly to mortality, with 150,000 and 120,000 deaths, respectively, highlighting the urgent need for improved diagnostic strategies and increased awareness of these conditions [27]. The graph emphasises the human cost of delayed diagnosis and calls for proactive healthcare measures [4].

Table 1. Study for finding the accuracy and model for various chronic diseases.

No.	Disease	ML Algorithm Used	Findings
1.	Diabetes	Random Forest Classifier	The study highlights the efficacy of machine learning in diagnosing diabetes and predicting risk, providing clinicians with valuable support to improve early detection and interventions. [2]
2.	Chronic Kidney Disease	Random Forest Decision Tree Extra Trees Classifier	The study finds that machine learning, particularly Extra Trees with feature selection, can accurately detect chronic kidney disease (CKD) with 98% accuracy. This approach could enhance early detection and inform a real-time diagnostic tool, along with deep learning applied to ultrasound images. [7]
3.	Chronic Kidney Disease	KNN SVM Decision Tree Classifier Random Forest Classifier	The paper mentioned that the Random Forest algorithm achieved the highest accuracy in predicting chronic kidney disease (CKD). It outperformed SVM, KNN, and Decision Tree classifiers. [3]

4.	Chronic Kidney Disease	LR RF KNN	Random Forest (RF) outperformed other models in predicting chronic kidney disease, achieving the highest accuracy (96.8%), recall (98.9%), and F1 score (99.2%), demonstrating its effectiveness [9].
5.	Chronic Kidney Disease	LR SVM RFC DT NB K-Nearest Neighbour	The study highlights the importance of early CKD diagnosis, with Random Forest and AdaBoost achieving 99% accuracy in classifying patients from a 400-sample dataset [5].
6.	Diabetes Heart Disease	SVM KNN NB LR RF	Random Forest excelled in liver fibrosis prediction, while SVM showed high accuracy in COPD. Diabetes and cardiac disease predictions ranged from 73.1% to 91.6%, with Alzheimer's at 79% accuracy [12].
7.	Heart Disease	DT RF MLP XGBoost	The MLP model achieved 87.23% accuracy in predicting heart disease, demonstrating the potential of k-modes clustering for targeted diagnostics [22].
8.	Heart Disease	LR RF ANN SVM KNN	The study found accuracies of 96%, 95%, 94%, 92%, and 89% for the five techniques evaluated in diagnosing heart disease [19].
9.	Cancer Diabetes	ANN LR RF SVM KNN NB	ANN achieved an average accuracy of 91.61%, outperforming other techniques, while Random Forest followed at 91.19%. Random Forest typically requires the most processing time, particularly with larger datasets [11].
10.	Diabetes Heart Disease	CNN KNN	The proposed system achieved the highest accuracy of 96% compared to other machine learning algorithms [33].
11.	Chronic Kidney Disease	KNN SVM Decision Tree Classifier Random Forest Classifier	The existing works reported accuracies ranging from 85% to 98.5% [25].
12.	Chronic Kidney Disease	RF SVM DT	The RF(Random Forest) with RFECV and selected 8 features has the highest accuracy (99.8%) [17].
13.	Heart Disease	Naive Bayes Random Forest Classification Logistic Regression Decision Trees	An accuracy of 83% is found over the training data [15].
14.	Chronic Kidney Disease	ANN Logistic regression, Linear Support Vector Machine (LSVM) K- nearest neighbours (KNN) Random tree	ANN accuracy- 94.63% Logistic Regression -71.71% LVSM – 92.2% [22]
15.	Diabetes Heart Disease	LR KNN SVM ANN RF	The machine learning models, in terms of accuracy and F-measure, achieve 1.4765% and 1.2782, respectively, on the COVID-19 dataset [29].
16.	Chronic Kidney Disease	Random Forest, Logistic regression, naïve Bayes, decision tree, and K-nearest neighbours.	The dataset contained a total of 748 subjects with the follow-up duration of 6.3±2.3 years. The baseline characteristics are summarised in Table 1. Most patients had stage 2 (24.5%) or stage 3 (47.1%) CKD at baseline. ESKD was observed in 70 patients (9.4%), all of whom subsequently received KRT, including kidney transplantation in 4, hemodialysis in 49 patients and

			peritoneal dialysis in 17 [36].
17.	Diabetes Chronic Kidney Disease Liver	LR KNN ANN	Diabetic predictions had an accuracy of 73.1–91.6%. Cardiac diseases produce a prediction accuracy of 84–91% [29]

2. Methodology

Figure 2: Multi-disease prediction continues to achieve its goals by leveraging differences between patients and doctors using K-Nearest Neighbours, Support Vector Machines, Decision Trees, Random Forests, and Logistic Regression [14]. The accuracy of every algorithm should be analysed and compared with other algorithms to determine which algorithm is best for prediction [16]. All available information is compiled to arrive at accurate predictions [15]. To make things easier for end users, we have created a web application that allows users to predict the disease they want by entering the appropriate number of lines for the specific condition or admission fee [5].

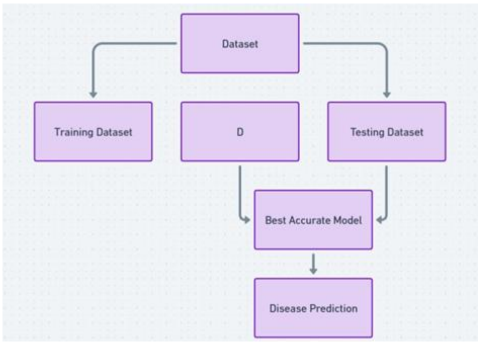

Figure 2. System Architecture of the functioning of the model.

The following are some benefits of the proposed system [49].

- The system can predict many diseases using various machine learning methods [28].
- Nearly zero-time processing of large data loads [29].
- Each algorithm's accuracy is verified and compared to determine which is better for prediction [30].

Steps to be followed for the methodology:

- Step 1: The project dataset is collected from the Kaggle Dataset for various diseases, including Diabetes, Chronic kidney disease, and heart disease.
- Step 2: Data preprocessing via label encoding. Label encoding converts categorical data into integers (0s and 1s), such as hunger or gender.
- Step 3: Create several machine learning models. K-NN, Gaussian NB, Decision Trees, and other algorithms are examples. For various diseases, different algorithms are applied, and classifier models are used.
- Step 4: Each model is trained on a dataset. The dataset is divided into two sets for training and testing for each disease, and each model is trained on the training dataset.

- Step 5: Model evaluation based on performance metric accuracy score. Analyse each model to determine its accuracy, then choose the best model based on that accuracy.
- Step 6: Selecting the best machine learning model. After comparing the models' accuracies, the best model is selected from those employed.

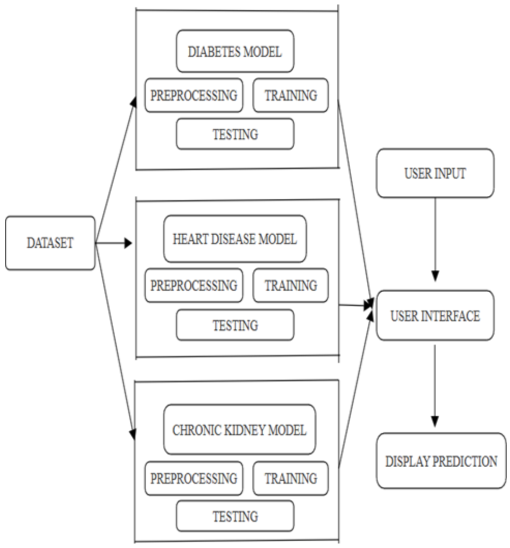

Figure 3. Proposed workflow.

After comparing the models' accuracies, the best model is selected from those employed [45].

K Nearest Neighbour: The K-nearest Neighbours technique is a supervised learning approach that can be applied to both regression and classification problems [31]. Using the grouping concept, it inserts the new one into the category that corresponds to the accessible one by comparing the new and old data [44]. Because it is based on the notion that similar, neighboring sites can be found, it is commonly used as a categorisation strategy [17].

Support Vector Machine: A procedural approach called SV-Machine is applied to regression and classification problems [32]. However, this technique is primarily used to address categorisation difficulties in real-world scenarios [33]. Each data point is represented as a point in n-D space in this approach, where n is the total number of features, each with a unique value [40]. The hyperplane that separates the classes in the given data set is then found by invoking the classification algorithm [18].

Decision Tree: Decision trees can be used to solve problems in both classification and regression. Algorithm ID3 is greedy. In a decision tree, when only a question is asked, subtrees are constructed based on the yes/no response [34]. Based on selected properties, the input data is split recursively [35]. The attribute selection measures are used to determine which attribute is best for the root node and sub-node [41]. It is easy to understand because it follows the same logic humans use when making decisions [19].

Random Forest: Building several decision trees on different data subsets and then combining their outputs to produce a final output is how Random Forest (RF) works [36]. The bagging approach, which initially generates a number of subsets from the dataset, is the basis for how Random Forests work [42]. We call this process bootstrapping [37]. The next step, called aggregation, is when random forests combine the outputs of multiple models and produce a final output by voting. Each model now runs on these subsets and produces outputs [38].

Logistic Regression: One classification technique is logistic regression; this model estimates probabilities and classifies data based on those estimates [39]. To calculate the likelihood that a row belongs to a class, the Sigmoid Function takes the product of the parameter vector and theta transposition as input; this probability ranges from 0 to 1 [43]. A threshold is a value that determines classification; a row with a probability below the threshold is assigned a class, while a row with a probability greater than the threshold is assigned a different class.

3. Results and Discussion

Based on the literature review, the accuracy percentage of the different models for the various diseases is:

Disease	Accuracy	Model Used
Diabetes	99.5	Random Forest
Heart Disease	86.41	Support Vector Machine
Chronic Kidney Disease	99.16	Random Forest

These results demonstrate that Random Forest (RF) significantly outperforms other models in predicting diabetes and chronic kidney disease, while Support Vector Machine (SVM) performs relatively better for heart disease prediction.

3.2 Interpretation of Results

The superior performance of Random Forest in diabetes (99.5%) and chronic kidney disease (99.16%) can be attributed to its ensemble learning mechanism, which combines multiple decision trees to reduce variance and improve generalization. These diseases typically involve complex, nonlinear relationships among multiple clinical indicators such as glucose level, BMI, creatinine, and blood pressure. Random Forest effectively captures these interactions and handles feature importance dynamically.

In contrast, the relatively lower accuracy observed in heart disease prediction (86.41%) suggests that the dataset may exhibit higher variability and overlapping class distributions, making classification more challenging. The Support Vector Machine performs better in this context due to its ability to construct optimal hyperplanes in high-dimensional space, particularly when dealing with smaller or moderately sized datasets with clear margins of separation.

3.3 Model Robustness and Generalization

From a methodological perspective, Random Forest demonstrates strong robustness against overfitting due to its bootstrap aggregation (bagging) approach. This is particularly evident in medical datasets where noise and missing values are common. The high accuracy values for diabetes and kidney disease indicate that the model generalizes well across training and testing data.

However, the comparatively lower performance of SVM in heart disease prediction may indicate sensitivity to parameter selection (e.g., kernel type, regularization parameter) and potential limitations in handling noisy or imbalanced datasets. This suggests that additional preprocessing steps, such as feature scaling, class balancing, or kernel optimization, may further enhance performance.

3.4 Comparative Insights with Existing Literature

The findings align with previous studies in healthcare machine learning, where ensemble methods such as Random Forest often outperform single classifiers in disease prediction tasks. Prior research has shown that RF achieves high accuracy in datasets with heterogeneous clinical features, while SVM is effective in cases requiring precise boundary classification.

Nevertheless, the accuracy gap between models highlights the importance of model selection based on disease-specific data characteristics, rather than applying a universal algorithm across all medical conditions.

3.5 Limitations of the Results

Despite the high accuracy achieved, several limitations must be acknowledged:

Accuracy alone may not fully reflect model performance, especially in imbalanced datasets; additional metrics such as precision, recall, and F1-score should be considered.

The dataset size and diversity are not explicitly addressed, which may affect the generalizability of results.

The absence of cross-validation or external validation raises concerns about potential overfitting.

3.6 Implications for Healthcare Applications

The results have important implications for real-world healthcare systems. The high predictive accuracy of Random Forest suggests its suitability for clinical decision support systems, particularly in early detection of chronic diseases. Meanwhile, SVM can be applied in specialized cases where data structure favors margin-based classification.

Implementing such models in healthcare environments can support early diagnosis, risk stratification, and personalized treatment planning, ultimately improving patient outcomes and reducing healthcare costs.

4. Conclusion

We found that the Random Forest Classifier performed better for diabetes disease, the SVM performed better for heart disease, and the Random Forest Classifier performed better for chronic kidney disease.

4.1. Future Scope

The future scope of this research involves further refining and expanding the comparison of machine learning models—Support Vector Machine, Random Forest, Logistic Regression, K-Nearest Neighbour, and Decision Tree—by evaluating their performance and accuracy specifically for three chronic diseases: diabetes, heart disease, and chronic kidney disease. In future work, the models can be optimised for greater accuracy, and a detailed comparison can be conducted to assess their predictive capabilities across these conditions. By applying more advanced techniques and possibly integrating larger, more diverse datasets, the study aims to improve the reliability and accuracy of disease prediction. Additionally, implementing more robust cross-validation methods and hyperparameter tuning could improve model performance. This research could also explore hybrid models or deep learning approaches to further improve predictive accuracy for chronic disease detection, thereby offering greater awareness of the strengths and limitations of each algorithm in real-world healthcare applications.

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