# The Comparison of Diabetes Risk Prediction Accuracy Across Different Models

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Abstract: The integration of machine learning technologies, particularly deep learning models, has significantly advanced disease prediction within the healthcare industry. People have begun leveraging large-scale medical data for research, combining various models aimed at enhancing the accuracy of medical disease prediction. This study focuses on diabetes, a severe disease, and employs four different machine learning algorithms: logistic regression, multilayer perceptron, support vector machine, and random forest. The author utilizes a dataset obtained through direct questionnaire surveys of patients at the Sirhaj Diabetic Hospital in Bangladesh, and conducts systematic data processing and visualization using the Python language to compare the strengths, weaknesses, and effectiveness of these four models in disease prediction. This research aims to provide more accurate and reliable tools for predicting the risk of diabetes in the healthcare field. Not only can this help doctors better understand the health status of patients, but it can also provide crucial reference for personalized treatment plans and preventive measures, thereby improving the cure rate of various major diseases.

## **1 INTRODUCTION**

The healthcare sector has consistently been a frontier for the remarkable success of deep learning technology. The potent capabilities of deep learning in pattern recognition and data analysis have positioned it as a robust tool for addressing medical challenges and enhancing patient care. In the realm of healthcare, early prediction of severe diseases holds paramount significance. Firstly, forecasting the future progression of diseases aids in the timely identification and preemptive intervention for patients, thereby augmenting the chances of recovery. Secondly, predictive models assist healthcare teams in tailoring more precise and personalized medical interventions, maximizing the efficacy of treatments.

Over the past few years, the area of disease prediction has seen notable developments, with numerous researchers achieving noteworthy breakthroughs. In their investigation, Hosseininian and colleagues (2024) employed a feature selection approach grounded in ANOVA, or analysis of variance to pinpoint the most pertinent features

concerning the prediction of Parkinson's illness by means of using voice-based characteristics. Subsequently, the Echo State Network (ESN) is evaluated as a predictive model for this purpose. Multiple models, encompassing the Echo State Network, Decision trees, Support Vector Classifiers, Random Forests, K-Nearest Neighbors, and Extreme Gradient Boosting, were meticulously evaluated and compared within the framework of the study. The analysis of results highlights the exceptional performance of the Echo State Network (ESN) among the employed models (Hosseininian et al, 2024). Niu et al. introduced an adaptive algorithm that improved upon the conventional Grey Wolf Optimization (GWO) with a sigmoid function, resulting in an enhanced version of the Grey Wolf Optimization algorithm for heart disease prediction (Niu et al, 2024). Wang et al. (2024) introduced an innovative approach termed Hybrid Ordinal Prototype Embedding (HOPE) in their research, aiming to delineate the sequential advancement of Alzheimer's disease for the prediction of mild cognitive impairment progression. Mary studied supervised

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machine learning algorithms for predicting heart disease (Kanchan 2016). Frasca and colleagues (2023) conducted an investigation utilizing the dataset from the "Parkinson's Progression Markers Initiative." Their study involved the development of a deep learning model dedicated to discerning the various stages of progression in Parkinson's disease. The conclusive 3DCNN + LSTM model, trained and assessed on MRI images, demonstrated exceptional performance in accurately classifying the four distinct levels of Parkinson's disease progression according to the Hoehn and Yahr scale. This state-of-the-art model achieved a macro-averaged One-Versus-Rest Area Under the Curve (OVR AUC) of 91.90%.

However, the domain of disease prediction confronts several difficulties and challenges. Issues such as limited sample sizes for rare diseases leading to reduced prediction accuracy, the complexity and uncertainty inherent in disease prediction data, and the inability of existing models to provide robust predictions for unknown diseases pose significant hurdles. Scholars have undertaken targeted research efforts to address these challenges. The use of bioinspired optimization methods, such as the Genetic Algorithm, Particle Swarm Optimization, and Whale Optimization Algorithm, was examined by Dyoub et al, for the purpose of selecting relevant features in predicting chronic diseases. The primary aim of their study was to improve the models' ability to anticipate outcomes, simplify dimension of the data, and make the resulting predictions more comprehensible and applicable in a practical context (Dyoub and Letteri, 2023). Saba et al. (2024) introduced a novel Continual Learning (CEL) model based on domain adaptation and Elastic Weight Consolidation (EWC), aiming to alleviate errors caused by catastrophic forgetting in deep neural networks, such as LSTM, in the context of incremental domain settings. In their 2019 study, Uddin and colleagues delved into the predominant trends characterizing diverse categories of supervised machine learning algorithms, elucidating both their performance metrics and practical applications in the realm of disease risk prediction. Conclusions were drawn through a comparative analysis. Dahiwade et al. (2019) discovered that, in this general disease prediction, considering individuals' lifestyle habits and examination information enables accurate forecasting. Patro et al. (2021) introduced an innovative framework for predicting heart disease, focusing on key risk factors and employing a variety of classifiers, including Naïve Bayes (NB), Bayesian Optimized Support Vector Machine (BO-SVM), K-Nearest Neighbors (KNN), and Salp Swarm

Optimized Neural Network (SSA-NN). In their investigation, the Convolutional Neural Network (CNN) demonstrated a superior accuracy of 84.5% in general disease prediction compared to the performance of the KNN algorithm, or K-Nearest Neighbors. The proposed optimization algorithm in this framework aims to establish an effective healthcare monitoring system for the early detection of heart disease. This paper employs four algorithms - Random Forest, Support Vector Machine (SVM), Multilayer Perceptron (MLP), and logistic regression-to foresee the likelihood of an individual developing a specific illness. The accuracy of these four algorithms will be compared to explore ways to enhance the prediction capabilities for severe diseases, consequently elevating the potential for early detection and intervention. This introduction sets the stage for a comprehensive exploration of disease prediction methodologies and their potential impact on healthcare outcomes.

## 2 METHODS

### 2.1 Data Source

These data are sourced from the UC Irvine Machine Learning Repository. The data collection involved direct questionnaire surveys with patients from Sylhet Diabetes Hospital in Bangladesh, and it has received approval from a doctor.

#### 2.2 Indicator Selection and Description

Table 1 displays various symptoms and health characteristics related to diabetes in the dataset used for the study.

Symptom	Introduction
Gender	1=Male, 0=Female
Polyuria	1=Yes, 0=No
Polydipsia	1=Yes, 0=No
Sudden Weight Loss	1=Yes, 0=No
Weakness	1=Yes, 0=No
Polyphagia	1=Yes, 0=No
Genital Thrush	1=Yes, 0=No
Visual Blurrin	1=Yes, 0=No
Itching	1=Yes, 0=No
Irritability	1=Yes, 0=No
Delayed Healing	1=Yes, 0=No
Partial Paresis	1=Yes, 0=No
Muscle Stiffness	1=Yes, 0=No
Obesity	1=Yes, 0=No

Table 1: Variable information.

### 2.3 Method Introduction

#### 2.3.1 Data Processing

In this experiment, Python is used to systematically process the data, employing the Pandas library to read the dataset related to diabetes. The initial step involves feature encoding, where the Label Encoder is utilized to convert binary categorical features (such as gender, presence of polyuria, etc.) into numerical representations. For multi-categorical features, the One Hot Encoder is used for independent encoding. Subsequently, label encoding is performed using the Label Encoder to convert categorical labels into numerical format.

After that, the data set is separated into a training and a test set, typically with an 80-20 ratio. Finally, data standardization is conducted to normalize the features, ensuring consistent scales across different features, and enhancing the stability of the model during training. This standardization is achieved using the Standard Scaler function.

#### 2.3.2 Support Vector Machine Model

Support Vector Machine is a supervised learning algorithm suitable for binary classification problems. Its main idea is to find an optimal hyperplane that separates data points belonging to different types. And then a linear kernel function is used to map the data into a high-dimensional space, making it easier to separate in the new space.

In the SVM model, the data was initially divided into feature variables (X) and target variables (y). Categorical features were processed using one-hot encoding, while Label Encoder was employed to convert the target variable into numerical form. The data was divided into test and training sets in a two to eight ratio. An SVM model was constructed with a linear kernel function and a regularization parameter C=1. Model performance was verified using 5-fold cross-validation. The learning\_curve function was utilized to visualize the accuracy trends of the model with different numbers of training samples.

### 2.3.3 Random Forest Model

The quarterly differential autoregressive moving equilibrium model (SARIMA model) is an improvement on the (ARIMA model), which is used to transform non-smooth time series into smooth periodic series. The model achieves the difference and autoregressive moving average of the time series by regression of the current and lagging values of the dependent variable, as well as taking into account the random error term. This transformation makes the time series smoother and better able to capture periodic features.

In the random forest model, categorical variables were initially mapped to numerical representations. Subsequently, the dataset was partitioned into feature variables (X) and target variables (Y), and a random forest classifier was employed for binary classification. Model performance was assessed through 5-fold cross-validation, followed by an analysis of learning curves to examine the model's ability at various training set sizes. The accuracy from cross-validation was ultimately derived, and the swerve of the model's training and validation performance with increasing training data was visualized using learning curve plots.

### 2.3.4 Multilayer Perceptron Model

A Multilayer Perceptron model is an artificial neural network composed of multiple layers of neurons, such as input, hidden and an output layer. Every neuron has a connection with all neurons in the preceding layer and is associated with weights and biases. MLP captures complex relationships between input features by learning these weights and biases.

In the MLP model, categorical variables were initially converted into numerical representations using Label Encoder. Subsequently, feature variables (X) and target variables (y) were extracted. Following this, Standard Scaler was applied to standardize the features, ensuring uniform scales. The MLP model was defined, comprising two hidden layers with 100 and 50 neurons, respectively, and a maximum iteration limit set to 500. 5-fold cross-validation was performed using Stratified K Fold, recording training, and testing accuracies, as well as losses for each fold. Finally, charts depicting the variation of training loss and training/testing accuracies with the number of iterations were generated to analyze the model's performance.

### 2.3.5 Measurement

The Logistic Regression is a linear model which is the main tool to solve binary classification problems. It achieves the result by passing the weighted sum of input features through a sigmoid function, mapping the input to a probability range between 0 and 1, facilitating classification.

In the logistic model, the data was initially preprocessed and features were standardized. Subsequently, the data was split into a training and a testing set. This model was defined as a logistic regression model with a linear layer, a Sigmoid activation function, BCELoss loss function, and trained for 500 epochs using the SGD optimizer. Learning curves were employed to illustrate the trends in training and testing accuracies. Ultimately, the data of the model accuracy on the testing set was reported.

### **3 RESULTS AND DISCUSSION**

### 3.1 Analysis of Results

This study utilizes the pre-defined training set and employs the Python language for visualizing the output.

#### 3.1.1 SVM Model Results

From Figure 1, with the increase in the number of training samples, the Training Accuracy initially experiences a slight decline before stabilizing. The initial decrease may be attributed to overfitting noise or local features when training on a small amount of data. As the dataset grows, the model generalizes better to overall features.

Test Accuracy exhibits fluctuations, but the overall trend is a slow increase. The initial fluctuations may arise from suboptimal performance on specific validation sets during cross-validation with a small dataset. With an increase in data, the model's performance averages across different validation sets, leading to a gradual rise in Test Accuracy.

The trend of accuracy shows that the SVM has a good performance on the training set without significant overfitting. The gradual increase in Cross-Validation Accuracy suggests that with more data, the model performs better over a larger range and is likely to generalize to unseen data. The model might benefit from additional data to further enhance performance, as the current sample size results in relatively high fluctuations in Test Accuracy.

### 3.1.2 Random Forest Model Results

From Figure 2, Random Forest demonstrates strong fitting capability, easily achieving perfect accuracy on smaller training sets, resulting in a Training Accuracy that remains stable at 1. The Test Accuracy stabilizes initially, then rapidly increases with an increase in training samples, eventually levelling off at 97.3%. This suggests that the model starts generalizing on larger samples and performs well on the test set.

The strength of Random Forest lies in its fitting ability to the data, but it is also prone to overfitting on small datasets. Therefore, when using Random Forest for predictive classification tasks, efforts should be made to avoid overfitting, ensuring the model maintains stable generalization on unseen data.



Figure 1: Support Vector Machine.



Figure 3: Multilayer Perceptron.

### 3.1.3 Multilayer Perceptron Model

From Figure 3, the training loss curve of the MLP rapidly decreases during the initial stages of training iterations before stabilizing, indicating that the model has known the features of the data successfully. Both training accuracy and test accuracy gradually increase with an increase in the number of model iterations. The test accuracy is a little lower than the training's, suggesting that the MLP performs well on both two sets without exhibiting overfitting. The final model achieves a test accuracy of 99.2%.

#### 3.1.4 Logistic Regression Model Result

From Figure 4, the test accuracy figure is a little lower than the trainings, and their accuracy curves exhibit a similar upward trend with the number increase of training epochs, eventually converging around a stable value. This indicates that with an increase of the model iterations, the accuracy of predicting disease status significantly improves, ultimately reaching 83.7%.



Figure 4: Logistic Regression.

### 3.2 The Comparison of Results

Table 2 shows the results of the four models.

Table 2: The Comparison of results.

Types of Models	Test Accuracy
Support Vector Machine	0.911
Random Forest	0.973
Multilayer Perceptron	0.992
Logistic Regression	0.837

Through comparing the performance of multiple models, it was found that the Multilayer Perceptron (MLP) excelled in this task, achieving an impressive accuracy of 99.2%.

### 4 CONCLUSION

This study delved into the early diabetes prediction domain, comparing the performance of various models. It was observed that the Multilayer Perceptron (MLP) exhibited outstanding performance in this task, achieving 99.2% as the accuracy. Future research could consider expanding the dataset to validate the model's ability on a larger scale or explore more sophisticated feature engineering to improve the model's sensitivity to early diabetes indicators or experiment with combinations of different algorithms, potentially further improving model performance.

## AUTHORS CONTRIBUTION

All the authors contributed equally and their names were listed in alphabetical order.

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