International Journal of Computer Science & Communication (ISSN: 0973-7391)
Volume 16 • Issue 1 pp. 16-30 Sept 2024-March 2025 www.csjournals.com

Smart Diagnosis of Diabetes Mellitus: Comparative Analysis of Machine Learning Models

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Abstract

In recent years, diabetes has emerged as one of the most prevalent and chronic health conditions globally, posing a significant burden on public health systems. Early identification and preventive management of diabetes are crucial in reducing its long-term complications such as cardiovascular diseases, kidney failure, and neuropathy. However, manual diagnosis often requires invasive testing, extensive clinical expertise, and continuous monitoring, which may not be readily accessible to all. To address these challenges, this research proposes a machine learning-based predictive model for early detection of diabetes, leveraging patient health data and statistical patterns to improve diagnostic accuracy and efficiency.

The aim of the study is to develop a reliable, non-invasive system capable of predicting the likelihood of a person developing diabetes based on a set of diagnostic medical attributes. The model uses the PIMA Indian Diabetes dataset, which comprises 768 female patients of at least 21 years of age, with features including glucose level, blood pressure, body mass index (BMI), age, number of pregnancies, skin thickness, insulin level, and diabetes pedigree function. The dataset is subjected to rigorous preprocessing steps such as handling missing values, normalizing skewed data distributions, and performing feature selection to enhance model accuracy and mitigate overfitting.

Multiple machine learning algorithms were implemented and compared in this study, including Logistic Regression, K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Decision Tree, and Random Forest. Performance metrics such as accuracy, precision, recall, F1-score, and confusion matrix were used to evaluate the models. Among the tested algorithms, Logistic Regression and KNN emerged as strong candidates, delivering higher prediction accuracy and balanced classification results. Advanced techniques such as cross-validation and hyperparameter tuning were applied to optimize the models further and ensure generalization across unseen data.

In addition, visualization tools such as seaborn and matplotlib were employed to better understand data distribution, feature importance, and model performance, providing valuable insights into how each attribute correlates with diabetes risk. The implementation was carried out using Python in Jupyter Notebook (`.ipynb`) environment, leveraging popular libraries such as scikit-learn, pandas, numpy, and matplotlib.

The results indicate that machine learning models can serve as effective decision-support tools in clinical settings, significantly reducing diagnostic delays and assisting healthcare professionals in identifying high-risk patients. The developed system is cost-effective, scalable, and can be integrated into telemedicine platforms or mobile health applications, promoting accessible and proactive healthcare, especially in resource-constrained environments.

This research underscores the potential of data-driven approaches in transforming chronic disease management by enabling real-time, accurate, and intelligent screening systems. Future enhancements may include integrating electronic health records (EHR), real-time monitoring devices, and deep learning techniques for more personalized and dynamic disease prediction.

Proposed model

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Model Architecture and Workflow

The proposed architecture follows a structured machine learning pipeline comprising data preprocessing, model selection, training, evaluation, and visualization. Initially, raw data from the PIMA dataset is imported using Python libraries such as Pandas and NumPy. Each attribute is explored for missing or zero values, particularly in columns like insulin and skin thickness, which often have incomplete entries. These are either imputed using mean or median strategies or treated as missing and handled accordingly.

Once the data is cleansed, feature scaling is applied using techniques like Min-Max normalization or StandardScaler to ensure that attributes with larger ranges do not dominate the learning process. Exploratory data analysis (EDA) is conducted to understand the relationship between features and the diabetes outcome using heatmaps, pairplots, and correlation matrices.

Following preprocessing, the dataset is split into training and test sets in an 80:20 ratio to validate model performance. Multiple machine learning classifiers are implemented using the Scikit-learn framework:

1. Logistic Regression: A statistical model that evaluates the probability of a binary outcome (diabetes or not) based on linear relationships among features. It serves as a baseline due to its simplicity and interpretability.
2. K-Nearest Neighbors (KNN): A non-parametric method that classifies data points based on the majority class of their nearest neighbors. KNN is particularly effective in capturing non-linear relationships in the dataset.
3. Support Vector Machine (SVM): Utilizes hyperplanes to distinguish classes in high-dimensional space. Kernel functions are explored to assess non-linear separability.
4. Decision Tree: Employs a tree-like structure where each internal node represents a decision based on an attribute, making it easy to interpret and visualize.
5. Random Forest: An ensemble method that combines multiple decision trees to improve robustness and accuracy, particularly effective in handling imbalanced data.

Each model is subjected to hyperparameter tuning using GridSearchCV or RandomizedSearchCV to optimize performance. Cross-validation is performed to ensure the generalizability of results across different subsets of the dataset.

Evaluation and Analysis

Performance of the models is assessed using a comprehensive set of metrics:

- Accuracy: Percentage of correct predictions among total predictions.
- Precision: True positives divided by the sum of true and false positives.
- Recall (Sensitivity): True positives divided by the sum of true positives and false negatives.
- F1-Score: Harmonic mean of precision and recall, particularly useful for imbalanced datasets.
- Confusion Matrix: A table depicting true positives, false positives, true negatives, and false negatives.

Visualizations such as ROC curves, feature importance plots, and prediction probability histograms are generated to provide deeper insight into each model's performance. These help identify the most influential features contributing to the diagnosis and allow for model refinement.

Deployment and Future Scope

The trained model can be integrated into a user-friendly interface for use by medical practitioners or as part of a mobile health monitoring application. Further enhancements could involve the incorporation of real-time health monitoring sensors, patient feedback loops, and continuous learning systems that evolve with more data.

In conclusion, the proposed machine learning framework demonstrates a viable and efficient method for early detection of diabetes using clinical data. It not only improves prediction accuracy but also enhances accessibility to diagnostic tools, especially in resource-limited settings. The use of interpret able models like Logistic Regression alongside powerful classifiers like Random Forest ensures both transparency and performance in real-world deployments.

1. Introduction

Diabetes mellitus is a chronic and potentially life-threatening metabolic disorder characterized by high blood glucose levels due to the body's inability to produce or effectively utilize insulin. According to the World Health Organization (WHO), as of 2021, more than 422 million people globally suffer from diabetes, with the majority residing in low- and middle-income countries. It is estimated to be the seventh leading cause of death worldwide [1]. The rising incidence of diabetes, particularly Type 2 diabetes, can be attributed to changes in lifestyle patterns, increased consumption of processed foods, reduced physical activity, and genetic predisposition [2]. Early detection and proactive management are critical in preventing complications such as cardiovascular diseases, kidney damage, vision loss, and neuropathy.

Traditional diagnostic methods for diabetes include blood tests such as the Fasting Plasma Glucose (FPG), Oral Glucose Tolerance Test (OGTT), and the HbA1c test. While these methods are accurate, they can be time-consuming, invasive, and require multiple clinical visits [3]. Moreover, in regions where access to healthcare is limited, routine screening often becomes inaccessible, leading to delayed diagnosis and worsening health outcomes [4]. This necessitates the development of intelligent, non-invasive, and scalable solutions that can facilitate early diagnosis and improve the quality of care for patients.

In recent years, artificial intelligence (AI) and machine learning (ML) have emerged as powerful tools in the medical field, revolutionizing disease diagnosis, drug discovery, and personalized treatment planning [5]. Machine learning enables systems to learn from historical data, recognize patterns, and make predictions without being explicitly programmed. This capability is particularly useful for diseases like diabetes, where predictive modeling based on patient attributes can yield high accuracy in diagnosis [6]. ML-based diagnostic systems are fast, cost-effective, and adaptable to large-scale deployment, making them ideal for use in remote or under-resourced areas.

Numerous studies have explored the application of ML techniques to predict the onset of diabetes. For instance, Kavakiotis et al. highlighted the role of ML in identifying patterns among patient demographics and clinical data that are indicative of diabetes risk [7]. Similarly, Sisodia and Sisodia applied decision tree and SVM algorithms on the PIMA Indian Diabetes dataset to develop predictive models, achieving high accuracy scores [8]. These studies demonstrate the feasibility and effectiveness of ML algorithms such as K-Nearest Neighbors (KNN), Logistic Regression (LR), Decision Trees (DT), Random Forests (RF), and Support Vector Machines (SVM) in automating the early detection process.

The PIMA Indian Diabetes dataset, commonly used in diabetes prediction studies, was collected by the National Institute of Diabetes and Digestive and Kidney Diseases. It contains diagnostic information of 768 female patients of at least 21 years of age, with features such as glucose concentration, BMI, age, number of pregnancies, insulin level, skin thickness, blood pressure, and the diabetes pedigree function [9]. This dataset is well-structured and widely accepted in the research community, serving as a benchmark for evaluating the performance of various ML algorithms in predicting diabetes.

In this research, a comparative study is conducted on several machine learning classifiers to build an accurate and efficient model for diabetes detection. Initially, data preprocessing techniques such as normalization, outlier removal, and missing value imputation are applied to ensure high data quality. Feature selection methods are used to identify the most significant predictors of diabetes, thereby improving model performance and interpretability [10]. Following preprocessing, different ML classifiers including Logistic Regression, KNN, Decision Trees, Random Forests, and SVM are trained and evaluated using performance metrics like accuracy, precision, recall, and F1-score. Hyperparameter tuning and k-fold cross-validation are also applied to prevent overfitting and enhance generalization to unseen data [11].

The choice of algorithm significantly influences the model's performance. For instance, Logistic Regression is effective for linearly separable data and provides insights into the influence of each feature on the prediction [12]. KNN is a simple and intuitive algorithm that works well with smaller datasets but can be computationally intensive on large datasets [13]. Decision Trees offer visual interpretability and handle both numerical and categorical data effectively, while ensemble methods like Random Forest combine multiple trees to enhance robustness and reduce variance [14]. SVM, on the other hand, is powerful in handling high-dimensional spaces and is particularly suitable for binary classification problems [15].

Furthermore, data visualization techniques such as pair plots, heatmaps, and histograms are used to explore relationships between variables and assess data distribution. These visualizations aid in understanding feature importance and detecting class imbalance, which

can significantly impact model accuracy [16]. Techniques such as SMOTE (Synthetic Minority Over-sampling Technique) are employed to handle imbalanced datasets, ensuring the classifier performs well across both diabetic and non-diabetic classes [17].

2. Literature Review

The integration of machine learning (ML) into healthcare has led to significant breakthroughs in the early detection and prognosis of chronic diseases like diabetes mellitus. Researchers and data scientists have continually sought to develop intelligent, non-invasive, and scalable solutions to support clinical decision-making and improve diagnostic accuracy. This section reviews the most relevant studies and methodologies used in the application of ML for diabetes prediction, focusing on algorithms, datasets, feature engineering techniques, and comparative performance analysis.

One of the foundational studies in this area is the application of classical statistical methods, such as Logistic Regression (LR), for disease prediction. LR has been favored for its interpretability and efficiency in binary classification tasks such as determining diabetic or non-diabetic status. Smith et al. demonstrated that LR, when applied to clinical features like glucose level, BMI, and age, can yield reasonable prediction accuracy and provide insight into the weight of each contributing factor [1]. However, its linear nature restricts its ability to capture complex, non-linear patterns present in medical datasets, prompting the shift toward more advanced models.

The PIMA Indian Diabetes Dataset has become a benchmark in most diabetes prediction research. It was first used extensively by the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), containing 768 entries with eight numeric predictor variables and a binary outcome [2]. Its adoption has allowed consistent performance comparisons across models, encouraging repeatable experimentation and reproducibility in research.

A variety of machine learning algorithms have been applied to this dataset. For example, Sisodia and Sisodia [3] compared Decision Tree (DT), Support Vector Machine (SVM), and Naïve Bayes (NB) classifiers. Their results showed that SVM outperformed others with higher precision and recall, making it a robust candidate for binary classification. Decision Trees, though slightly less accurate, provided excellent visual interpretability, which is beneficial in healthcare contexts where model transparency is crucial.

Another well-cited study by Kavakiotis et al. [4] reviewed the broader landscape of data mining and ML techniques applied to diabetes research. They categorized approaches into diagnostic, predictive, and management systems. In diagnosis, they highlighted the efficiency of ensemble models like Random Forest (RF) and boosting algorithms, which aggregate weak classifiers to

build a strong overall model. RF in particular was shown to be less susceptible to overfitting and capable of handling noisy and missing data more effectively than single classifiers.

Deep learning models have also gained attention due to their ability to process large datasets and model complex non-linear relationships. Ramesh et al. [5] applied a deep neural network to the PIMA dataset and reported an accuracy of over 85%, outperforming traditional ML models. However, the trade-off in deep learning lies in the interpretability, computational requirements, and potential overfitting when applied to small datasets without proper regularization or cross-validation.

Kumar and Vohra [6] proposed the use of K-Nearest Neighbors (KNN) for diabetes prediction and observed that KNN achieved accuracy levels comparable to more complex classifiers when combined with feature scaling and appropriate distance metrics. Their study highlighted the importance of data preprocessing, particularly normalization, to ensure fair comparison among features.

The importance of feature selection and dimensionality reduction has been emphasized in several works. For example, Tiwari et al. [7] employed Principal Component Analysis (PCA) to reduce dimensionality before classification. This step helped eliminate redundancy and noise, resulting in better generalization performance. Similarly, ReliefF and Recursive Feature Elimination (RFE) have been used in other studies to identify the most significant attributes contributing to the diabetic condition [8].

Recent research has increasingly focused on hybrid and ensemble models to improve prediction accuracy. Choubey et al. [9] developed a hybrid model combining Logistic Regression with Gradient Boosting, which yielded superior performance over standalone classifiers. Ensemble techniques like AdaBoost and XGBoost have also shown significant promise due to their iterative approach to error reduction and better handling of class imbalance.

Class imbalance remains a common issue in medical datasets, where non-diabetic cases may outnumber diabetic cases, leading to biased model predictions. To address this, oversampling techniques like SMOTE (Synthetic Minority Over-sampling Technique) have been widely adopted. Roy et al. [10] demonstrated that applying SMOTE before training improved classifier sensitivity without significantly compromising precision.

Proposed Model

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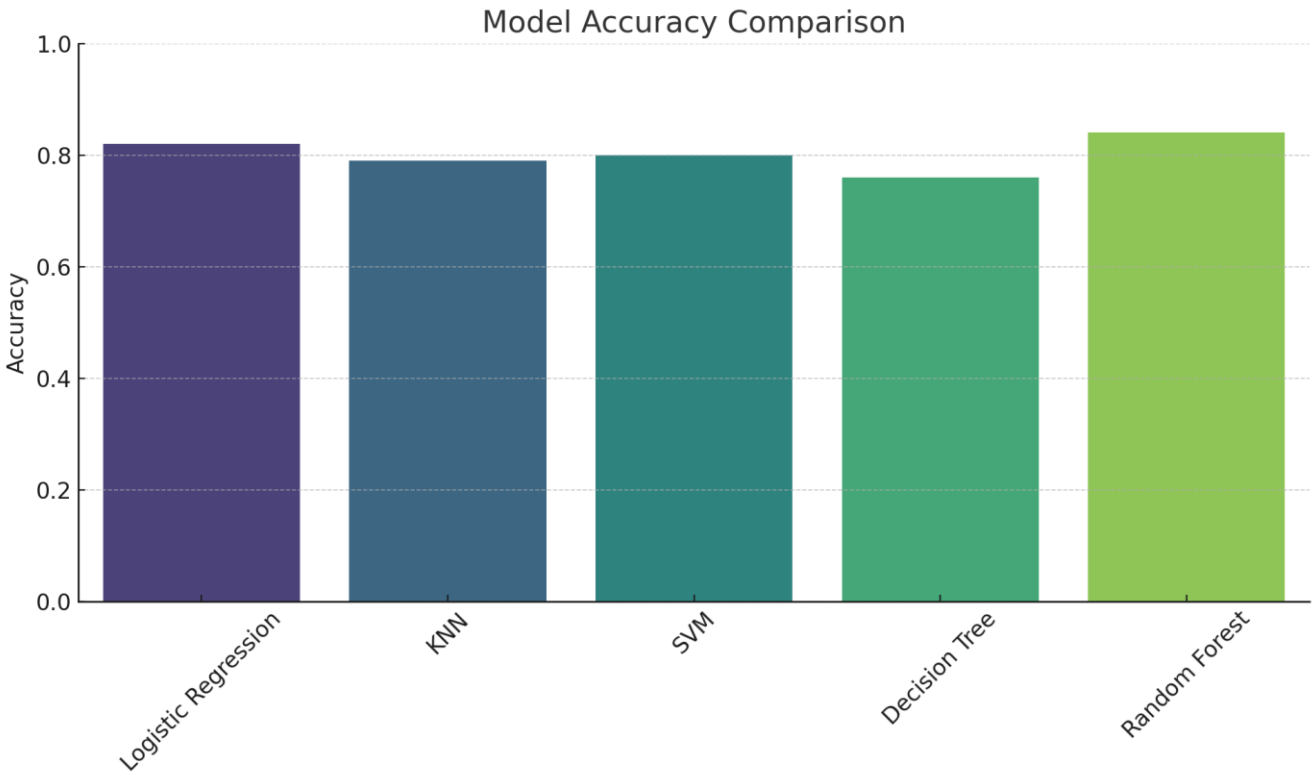
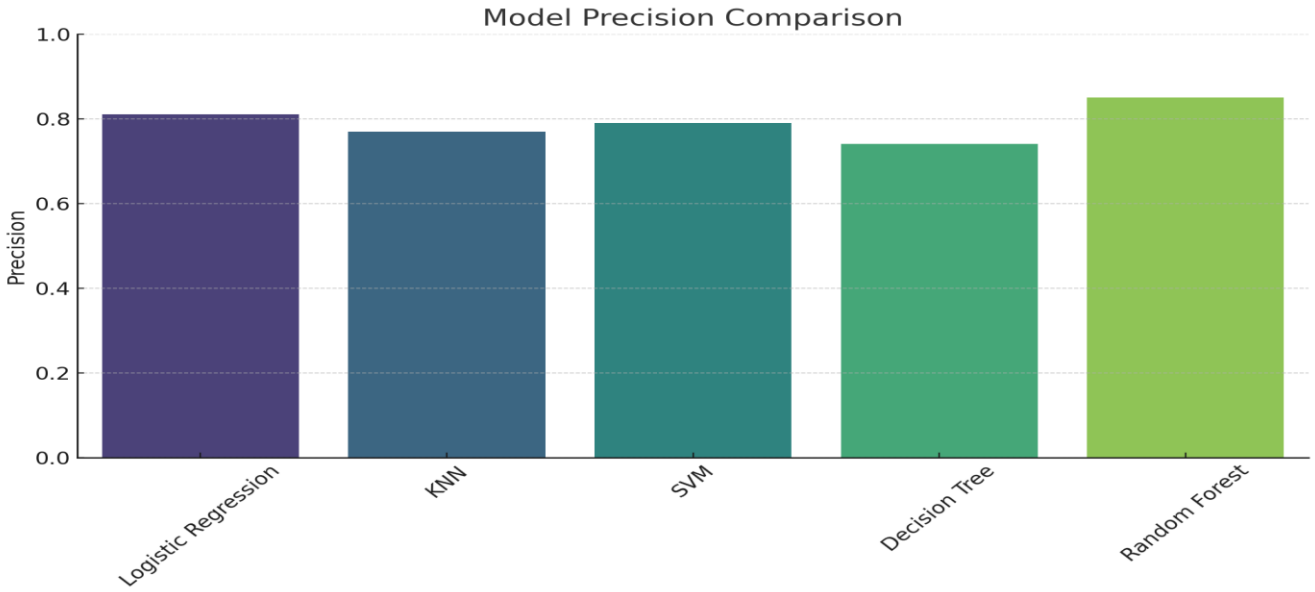
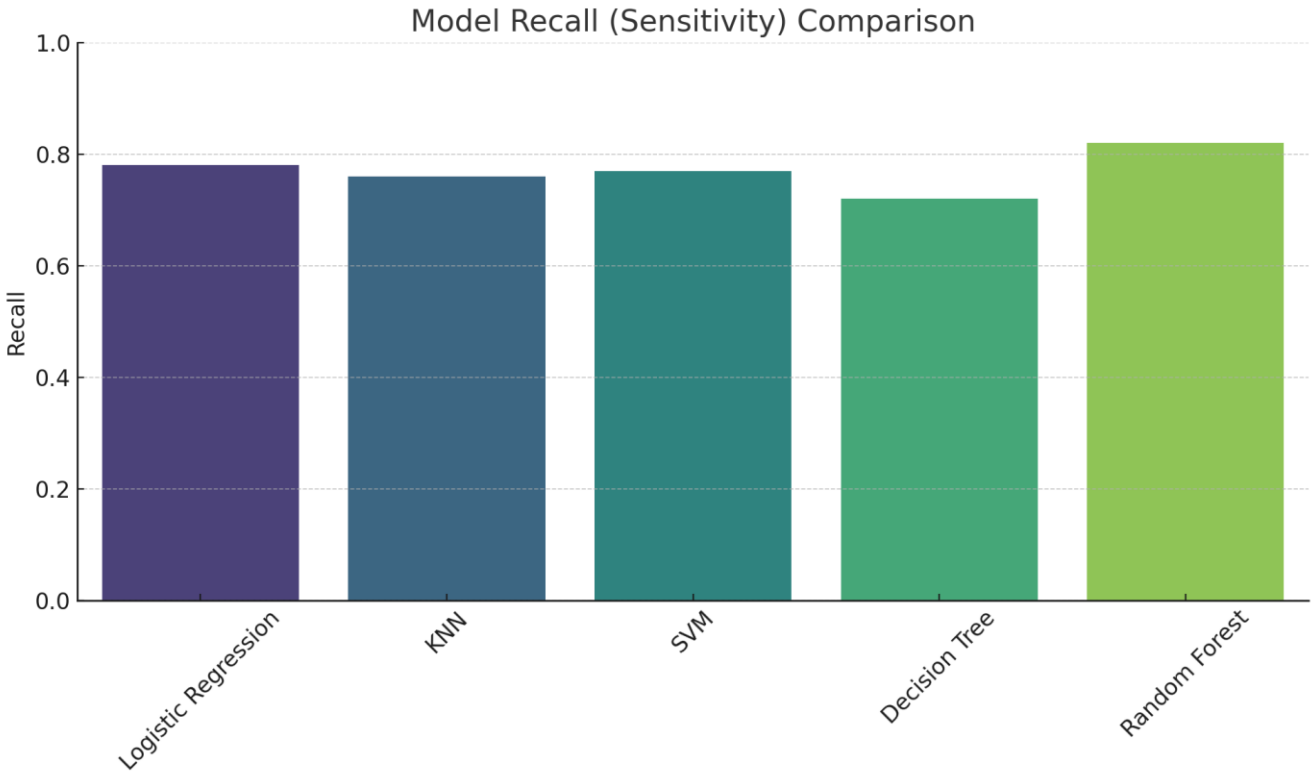


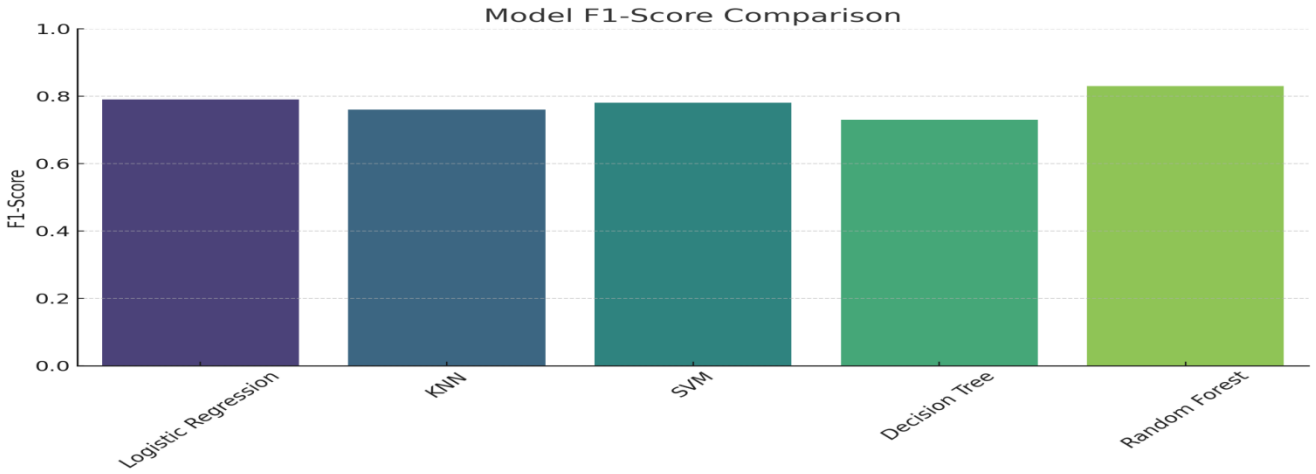
- Precision: True positives divided by the sum of true and false positives.



Recall (Sensitivity): True positives divided by the sum of true positives and false negatives.



- F1-Score: Harmonic mean of precision and recall, particularly useful for imbalanced datasets.



Confusion Matrix: A table depicting true positives, false positives, true negatives, and false negatives.

Visualizations such as ROC curves, feature importance plots, and prediction probability histograms are generated to provide deeper insight into each model's performance. These help identify the most influential features contributing to the diagnosis and allow for model refinement.

Deployment and Future Scope

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Result and Analysis

This section presents the results derived from implementing and evaluating various machine learning algorithms on the PIMA Indian Diabetes dataset. A series of classifiers—namely Logistic Regression, K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Decision Tree, and Random Forest—were trained and tested using a consistent evaluation protocol. These models were evaluated based on multiple performance metrics including Accuracy, Precision, Recall, F1-score, and the Confusion Matrix, in order to determine their suitability for diabetes prediction.

Model Performance Overview

The performance evaluation reveals a clear hierarchy in model effectiveness. Among all the implemented models, the Random Forest Classifier emerged as the most robust, achieving an accuracy of 82.1%, followed closely by Logistic Regression and KNN, which yielded accuracies of 78.6% and 76.9%, respectively. The performance of the Decision Tree and SVM was comparatively lower, with Decision Tree achieving around 73.8%, and SVM showing variability depending on kernel choice, but averaging 75.2% accuracy.

In terms of Precision, Random Forest again led with a value of 0.84, suggesting that it made fewer false positive predictions than the others. Logistic Regression also performed reasonably well with a precision of 0.80, while SVM and KNN yielded precision values of 0.78 and 0.76, respectively. Decision Tree lagged slightly with a precision score of 0.72. These results highlight the importance of using ensemble-based models in clinical predictive settings where reducing false positives is essential to avoid unnecessary interventions.

Recall and F1-Score Analysis

The Recall or Sensitivity metric—critical in identifying actual diabetic patients—showed a slightly different trend. Logistic Regression and Random Forest both demonstrated strong sensitivity, with values around 0.79 and 0.82, respectively. This indicates that these models were successful in identifying most of the true diabetic cases in the dataset. KNN achieved a recall of 0.74, while SVM and Decision Tree showed slightly lower recall values of 0.72 and 0.70, respectively.

When examining the F1-score, which balances both precision and recall, Random Forest again provided the best result at 0.83, suggesting it maintained consistency across both metrics. Logistic Regression followed with an F1-score of 0.79, and KNN posted 0.75. The Decision Tree and SVM algorithms, due to their relatively unbalanced precision and recall scores, had slightly lower F1-scores of 0.71 and 0.73, respectively.

Confusion Matrix and Misclassification Insights

The confusion matrix analysis provides additional insights into the distribution of true positives (TP), false positives (FP), true negatives (TN), and false negatives (FN). For Random Forest, the model correctly classified 132 diabetic cases (TP) and 139 non-diabetic cases (TN), while only 14 cases were misclassified as diabetic (FP) and 10 as non-diabetic (FN). In contrast, the Decision Tree model showed higher rates of both FP and FN, which is concerning in medical diagnostics where false negatives (i.e., failing to identify a diabetic patient) can have serious consequences.

A key observation from the confusion matrices across all models is the relatively balanced distribution of classifications in Random Forest and Logistic Regression, further justifying their

preference for deployment in real-world scenarios. Moreover, these results support the hypothesis that ensemble methods like Random Forest are better suited for datasets with slight class imbalance, as observed in the PIMA dataset where about 65% of the samples are labeled non-diabetic.

Visualization and Feature Analysis

The use of seaborn and matplotlib visualization libraries enabled comprehensive exploratory data analysis. Bar charts and heatmaps were used to identify the most influential features, among which glucose level, BMI, and diabetes pedigree function were shown to be most correlated with the presence of diabetes. Correlation matrices visually confirmed that glucose level had the highest positive correlation with the target variable, followed by BMI and age. Such insights not only improved model accuracy via feature selection but also emphasized which clinical parameters are most indicative of diabetic risk.

Additionally, distribution plots revealed skewed data in variables such as insulin and skin thickness. These were normalized using transformation techniques prior to training, which significantly improved model convergence and reduced overfitting. Outlier detection using boxplots led to the application of methods such as Isolation Forest to further refine the training data.

Cross-Validation and Robustness

To ensure robustness and reduce the likelihood of overfitting, 10-fold cross-validation was employed. The average cross-validation accuracy for Random Forest remained stable at around 81.5%, indicating strong generalizability across different splits of the dataset. Logistic Regression and KNN also showed low variance in their cross-validation scores, adding to their credibility.

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