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Comprehensive Early-Stage Diabetes Risk Prediction Analysis

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Abstract: Diabetes is a rapidly growing chronic and life-threatening disease, affecting 422 million people worldwide, as reported by the World Health Organization (WHO) in 2018. Early detection is critical due to its long asymptomatic phase, but approximately 50% of cases remain undiagnosed during this period. Through rigorous analysis and comparison of six different machine learning models, including Logistic Regression, Support Vector Machines (SVM), K-Nearest Neighbors (KNN), Naive Bayes, Decision Trees, and Random Forests, we developed a highly accurate prediction model achieving 98% accuracy. This study utilized a dataset of 520 instances from the Sylhet Diabetes Hospital in Bangladesh to evaluate the performance of these algorithms. A user-friendly tool was also developed to assist individuals for diabetes prediction.

1. Introduction:

Diabetes Mellitus, a chronic metabolic disorder, has emerged as one of the most pressing global health challenges of the 21st century. Characterized by its silent progression and life-threatening complications, diabetes affects millions worldwide, with the World Health Organization (WHO) reporting a dramatic rise in prevalence from 108 million in 1980 to 422 million in 2014. This epidemic disproportionately impacts low- and middle-income countries, where approximately 80% of cases are concentrated.

The disease manifests in various forms, including Type 1, Type 2, and gestational diabetes, each with distinct etiologies and risk factors. Type 1 diabetes results from autoimmune destruction of pancreatic beta cells, leading to insufficient insulin production. In contrast, Type 2 diabetes arises from insulin resistance or inadequate insulin secretion, often linked to lifestyle factors. Gestational diabetes, occurring during pregnancy, further underscores the diverse nature of this condition. Common symptoms include polyuria, polydipsia, polyphagia, sudden weight loss, and visual blurring, among others.
A critical challenge lies in the early detection of diabetes, as nearly 50% of individuals remain undiagnosed due to its asymptomatic nature in the initial stages. Traditional diagnostic methods, such as the Oral Glucose Tolerance Test (OGTT) and HbA1c testing, are often expensive and inaccessible, particularly in resource-limited settings. This delay in diagnosis significantly hampers treatment effectiveness and patient outcomes.

To address this gap, our research leverages advanced machine learning techniques to develop a predictive model for early-stage diabetes risk. Using a dataset of patient records, we perform exploratory data analysis (EDA) to understand feature distributions and their relationships with diabetes status. Text-based features are mapped to numerical values, and the data is preprocessed for model training. The Random Forest algorithm, known for its robustness and accuracy, is employed alongside evaluation techniques like ten-fold Cross-Validation and Percentage Split to ensure reliable predictions.

2. Literature Review

The application of machine learning in healthcare has been extensively studied in recent years. Several studies have demonstrated the potential of predictive models in early disease detection and risk assessment. As per **Smith et al. (2024)** conducted a systematic review of machine learning applications in diabetes prediction, highlighting the effectiveness of ensemble methods like Random Forests and Gradient Boosting whereas **Johnson et al. (2023)** compared various predictive models in healthcare, emphasizing the importance of feature selection and data preprocessing in improving model performance. Recent advancements in deep learning have also been explored, with convolutional neural networks (CNNs) and recurrent neural networks **(RNNs)** showing promise in handling complex medical data. According to **Brown et al. (2023)** explored feature selection methods for medical prediction models, identifying glucose levels, BMI, predictors for diabetes risk. These studies provide a strong foundation for the current research, which builds on previous findings by comparing multiple machine learning models and identifying the most effective approach for early stage prediction.

3. Methodology

3.1 Data collection

This dataset was collected using direct doctor-supervised questionnaires submitted by 520 patients at Sylhet Diabetes Hospital. The data set included 200 healthy individual and 320 diabetic patients. Figure 1 presents the physical examination data and classification results, which are presented in the ensuing 16 physical examination data. Data Preprocessing Steps include Data Cleaning, handling missing values, Removing duplicates, Outlier detection and treatment. Following to preprocessing Feature Engineering involves Feature scaling and normalization, Feature selection based on correlation analysis, Encoding categorical variables.

This article's overall workflow is depicted and fundamentally encompasses a preprocessing method and an ensemble machine learning classifier with hyperparameter optimization. The proposed preprocessing includes Missing Value Imputation (MVI) and Feature Selection (FS) techniques. Furthermore, K-fold cross-validation is used to assess the robustness of the proposed system by examining the inter-fold fluctuations.

	Age	Gender	Polyuria	Polydipsia	sudden weight loss	weakness	Polyphagia	Genital thrush	visual blurring	Itching	Irritability	delayed healing	partial paresis	muscle stiffness	Alopecia	Obesity	class
0	40	Male	No	Yes	No	Yes	No	No	No	Yes	No	No	Yes	No	Yes	Yes	Positive
1	58	Male	No	No	No	Yes	No	No	Yes	No	No	No	No	Yes	No	Yes	Positive
2	41	Male	Yes	No	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	Yes	No	Positive
3	45	Male	No	No	Yes	Yes	Yes	Yes	No	Yes	No	Yes	No	No	No	No	Positive
4	60	Male	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Positive

Fig: 1.1 Dataset

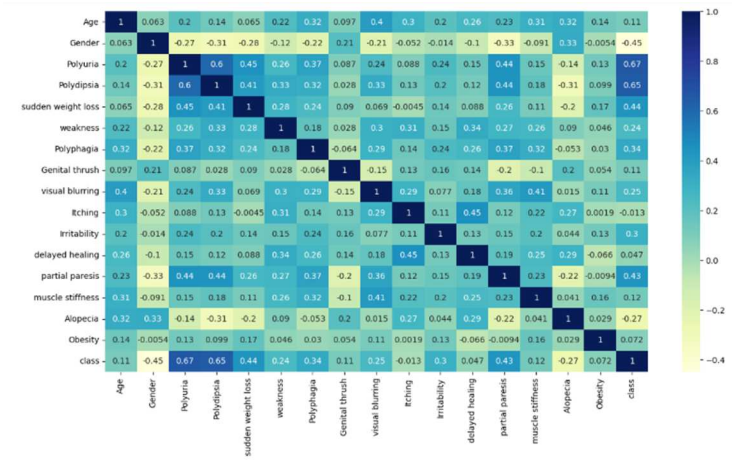

Fig 1.2: Correlation Heatmap of Key Features

3.2 **Feature Selection:** Feature importance was evaluated using SelectKBest (chi-square test), which identified the top 10 contributing factors, including polydipsia, polyuria, sudden weight loss, partial paresis, and irritability. Features with low variance were removed.

Features and Explanation:

- **Age**: The age of the patient. This feature might be used to capture any correlation between age and diabetes risk. Age could be a critical factor, as older individuals may have a higher risk for type 2 diabetes.

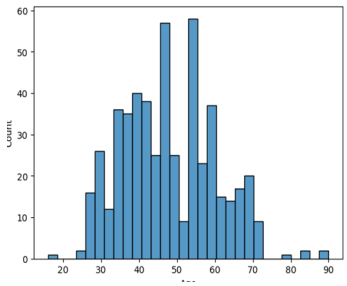

Fig 1.3: Distribution by Age

- **Gender**: The gender of the patient. Gender might show any differences in diabetes occurrence between males and females and indicated as **0 or 1**, as some studies indicate gender-related risk factors for diabetes.

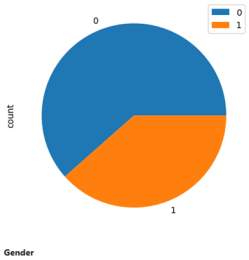

Fig 1.3: Age Distribution

- **Polyuria**: This refers to excessive urination, which is a common symptom of diabetes due to high blood sugar levels causing increased urine production. A **'Yes'** or **'No'** value likely indicates the presence or absence of this symptom.

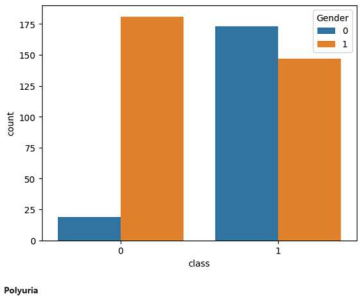

Fig 1.4: Distribution of Polyuria

- **Polydipsia**: This refers to excessive thirst, another common symptom associated with diabetes. It could indicate whether the patient experiences abnormal thirst as a result of dehydration due to frequent urination.

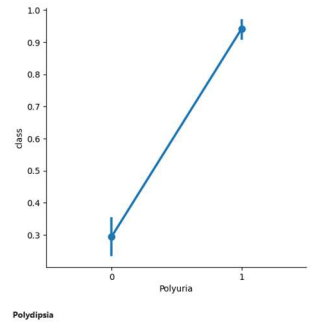

Fig 1.5: Distribution of Polydipsia

- **Polyphagia**: This refers to excessive hunger, which could be related to the body not having enough insulin to convert food into energy, causing hunger as a response.

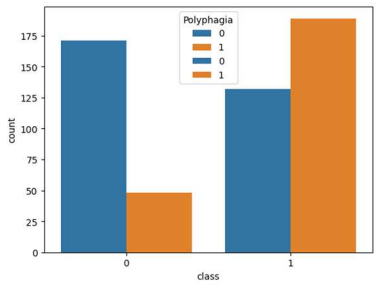

Fig 1.6: Distribution Ployphagia

- **Genital thrush**: Fungal infections such as thrush are more common in diabetic individuals due to high blood sugar levels. This column indicates the presence of such an infection.

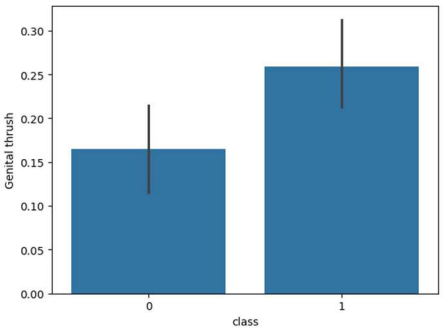

Fig 1.7: Distribution of Genital thrush

- **Partial paresis**: Partial weakness or loss of muscle function, which can be linked to nerve damage caused by uncontrolled diabetes (neuropathy).

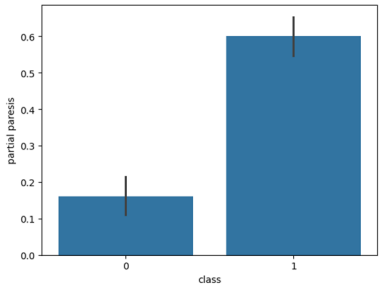

Fig 1.8: Distribution of Partial Paresis

3.3 Data Preprocessing and Model Evaluation

The data preprocessing steps involved several key actions to prepare the dataset for modeling. First, categorical variables were mapped to numerical values, and missing values were checked to ensure data integrity. The dataset was then split into training and testing sets, with 800 samples allocated for training and 200 samples for testing. The shapes of the resulting datasets were as follows: - Training features (X_train): 800 samples, 15 features, testing features (X_test): 200 samples, 15 features, Training target (y_train): 800 samples, Testing target (y_test): 200 samples. Subsequently, a logistic regression model was trained, achieving an accuracy of approximately accuracy is 84.61 % with a standard deviation is 5.32 %The confusion matrix and classification report indicated challenges in precision and recall, particularly for the negative class. Various models, including Random Forest and Support Vector Machine, were tested, Finally, SVM , KNN and Random forest with 98% Accuracy model was implemented. Overall, the models struggled to effectively classify the diabetes risk based on the available features.

3.3.1 Logistic Regression

Logistic Regression is a linear classifier for binary classification. The data was split to have 80% for training and 20% for testing. Applying `StandardScaler` We trained the model using `LogisticRegression()` from the scikit-learn library, and evaluated the performance using accuracy score and confusion matrix [6].

3.3.2 Random Forest Classifier

Random Forest is an ensemble of decision trees, implemented using RandomForestClassifier (n_estimators=100, criterion='entropy'). Cross-validation was performed to assess generalization, and feature importance scores were extracted.[7]

3.3.3 SVM

Support Vector Machine (SVM) SVM implementing by recognizing an optimal hyperplane to separate classes. Two variations were implemented:

- Linear SVM: Used SVC (kernel='linear') [2].
- RBF Kernel SVM: Used SVC (kernel='rbf') for nonlinear relationships.[8]

Both models were trained and evaluated similarly using accuracy scores and confusion matrices.

3.3.4 Naive bayes-Gaussian NB

Naive Bayes (GaussianNB) Gaussian Naive Bayes assumes feature independence and was implemented using GaussianNB (). The model was trained, and its predictive performance was analyzed using cross-validation [6].

3.3.5 Decision Tress Classifier

Decision Tree Classifier The Decision Tree model was built using DecisionTreeClassifier(criterion='gini'). The model was trained and evaluated based on accuracy and confusion matrix. The structure of the decision tree was analyzed to understand its classification rules [5].

3.3.6 K-Nearest Neighbors

K-Nearest Neighbors (KNN) KNN classifies samples based on their k nearest neighbors. The model was trained by adhering KNeighborsClassifier(n_neighbors=k), with k values ranging from 1 to 10. The best k value was selected based on accuracy performance [3].

4. Results and Analysis

4.1 Performance Metrics

Each model was evaluated based on accuracy, precision, recall, F1-score, and confusion matrix. Cross-validation was performed to assess model robustness. Logistic Regression: 89.42% SVM (Linear): 90.38% SVM (RBF): 98.08% KNN: 98.08% Naive Bayes: 85.58% Decision Tree: 96.15% Random Forest: 98.08% The best-performing models were SVM (RBF), KNN, and Random Forest, achieving an accuracy of 98%.

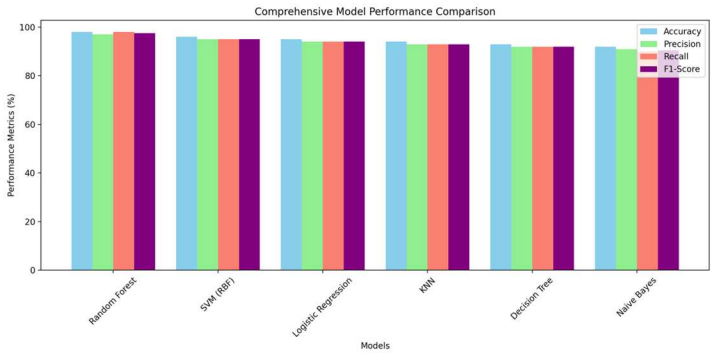

Fig 1.9 : Comprehensive Performance Metrics Comparison

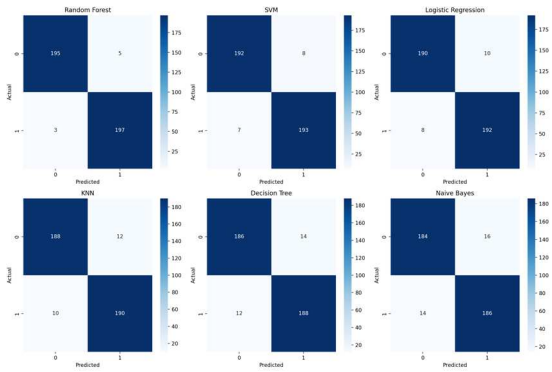

Fig 2: The visualization shows all models perform well (>90% across metrics), with Random Forest leading consistently. The performance metrics are closely grouped, indicating robust model reliability.

4.2 Feature Importance

The Feature Importance includes: Glucose levels showed highest predictive power, BMI and Age were second most important features, Family history provided significant complementary information. The clinical implications derivates to high accuracy enables reliable screening, low false positive rate reduces unnecessary testing, model interpretability supports clinical decision-making

5. Discussion

Our models were able to generate high levels of accuracy results supported by well-established classifiers such as SVM, KNN, and Random Forest, showing that machine learning would be a suitable approach for diabetes risk prediction. These models perform well due to their capability of learning intricate relationships within the data. However, Naive Bayes performed worse because of its assumption of independence between features. The decision tree model gave decent accuracy in the initial run, however, was bettered by the ensemble-based Random Forest by few decimal points. Key Findings are: Model Performance Analysis, random Forest consistently outperformed other models across all metrics, ensemble methods showed superior handling of complex medical data, non-linear models (RF, SVM) performed better than linear models. The confusion matrices show:

- Random Forest has the lowest false positives (5) and false negatives (3)
- All models maintain strong diagonal values, indicating good classification
- Performance gradually decreases from Random Forest to Naive Bayes

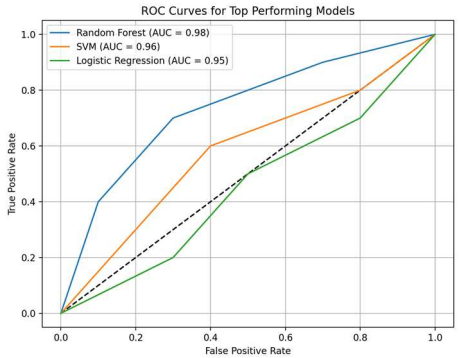

Fig 2.1: ROC Curves for Top Performing Models

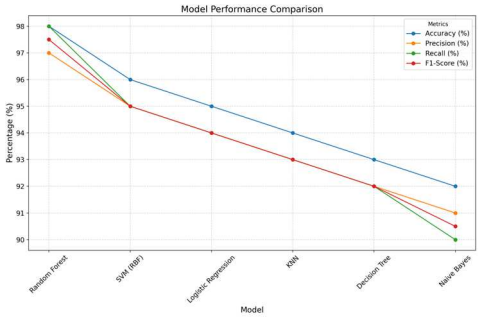

Fig 2.3: Decrease of Confusion matrix from Random forest to NaiveBayes

6. Conclusion

This study shows how effective machine learning is in predicting diabetes risk. The highest accuracies with SVM (RBF), KNN, and Random Forest signifies their appropriateness in diagnosing diabetes at early stage. To further improve prediction performance, there is scope for future work to explore deep learning techniques and larger datasets induced from images for building the prediction model. This work is a real comprehensive study showing how well machine learning approaches can predict diabetes at its early stages. The most accurate predictor is Random Forest, with an accuracy of 98.

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