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Original scientific paper

APPLIED MATHEMATICAL TECHNIQUES AND MACHINE LEARNING FOR IDENTIFYING PREDICTORS OF TYPE 2 DIABETES

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Abstract

Aim: This study aims to identify key predictors of type 2 diabetes mellitus (T2DM) by applying mathematical and machine learning techniques to clinical health data collected in North Macedonia.
Method: Data were collected from 723 clinical records at the Clinical Hospital "Mother Teresa" in Skopje over 9 months, including patient demographics, BMI, lipid profile, HbA1c, and hypertension status. A hybrid analytical framework was developed, integrating exploratory data analysis, statistical correlation testing, and supervised machine learning algorithms—specifically logistic regression, k-nearest neighbors (KNN), and decision tree classifiers. Model performance was evaluated using accuracy, precision, recall, F1-score, and ROC curves.
Results: The results revealed statistically significant associations between elevated HbA1c, high BMI, and diabetes diagnosis. Logistic regression achieved the highest performance with 80% accuracy and an AUC of 0.85. Across models, HbA1c, age, and BMI consistently emerged as the most influential predictors of T2DM. Hypertension and abnormal lipid risk were also positively associated with diabetes outcomes.
Conclusions: This research confirms that machine learning models—especially logistic regression—can effectively predict diabetes risk using a small set of metabolic and anthropometric indicators. The integration of statistical analysis and ML techniques enhances the ability to detect early warning signs of T2DM and provides a foundation for future clinical decision-support tools.

Keywords: Machine learning, statistical analysis, diabetes mellitus, predictive modeling, logistic regression, feature importance.

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1. Introduction

Type 2 diabetes happens when your pancreas doesn't make enough insulin (a hormone) or your body doesn't use insulin properly, or both. But this is different from Type 1 diabetes, which happens when an autoimmune attack on your pancreas results in a total lack of insulin production.

Type 2 diabetes, in most cases, occurs when the body has hyperglycemia, that is, a constant excess of sugar in the body. Therefore, overweight or obese people are even more predisposed, since we are dealing with stored amounts of calories in the body that the body has not managed to process and store.

Diabetes is the leading cause of morbidity and mortality in CVD patients. Individuals with DM have 2 to 4 times increased risk of CVD as compared to non-diabetics, as DM is an independent risk factor for CVD (IDF, 2015). Dyslipidemias and hypertension are two major CVD risk factors that frequently coexist with DM (Li et al., 2023). The coexistence of CVD risk factors, like dyslipidemia, hyperglycemia, hypertension &obesity in Type-2 DM individuals further accentuates their susceptibility to CVD (IDF, 2015 & Li et al., 2023).

Diabetes facts and figures show the growing global burden for individuals, families, and countries. The latest IDF Diabetes Atlas (2025) reports that 11.1% – or 1 in 9 – of the adult population (20-79 years) is living with diabetes, with over 4 in 10 unaware that they have the condition. By 2050, IDF projections show that 1 in 8 adults, approximately 853 million, will be

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living with diabetes, an increase of 46%. Over 90% of people with diabetes have type 2 diabetes, which is driven by socio-economic, demographic, environmental, and genetic factors. The key contributors to the rise in type 2 diabetes include:

- Urbanisation
- An ageing population.
- Decreasing levels of physical activity.
- Increasing overweight and obesity prevalence

Finally, science is advancing and giving hope in research for the treatment of people with diabetes, in three directions: technological, biological, and pharmacological. Technological solutions are focused on the delivery of insulin and glucagon via an artificial pancreas, and components of the system are already in use, suggesting this option may well be available within the next 10 years. Of the biological solutions, pancreas transplants seem unlikely to be used widely, and islet cell transplants have also been hampered by a lack of appropriate donor tissue and graft survival after transplant. However, significant progress has been made in these areas, and additional research suggests that manipulating
other cell types to replace beta cells may be a viable option in the longer term. The last category, pharmacological research, appears the most promising for significantly reducing the burden of type 2 diabetes mellitus (Shomali, 2012).

Long-time consumption of a low fiber diet, high caloric food intake, high glycemic load, and low ratio of polyunsaturated fatty acids are risk factors for the development of pre-diabetes (Bansal, 2015). The women, who are infected by gestational diabetes or with polycystic ovary syndrome, are at high risk of developing pre-diabetes in the future (Tarvonen et al., 2021). On the other hand, women with pre-diabetes before pregnancy have a higher risk of developing gestational diabetes (Bell et al., 2020). Both T2D and pre-diabetes provide a similar nature in diagnosis and treatment; also risk factors of both are similar.

Overweight and obesity are strong predictors for the development of pre-diabetes. There is a strong correlation between obesity and pre-diabetes. Also, unhealthy eating habits and physical inactivity are the main causes of the development of pre-diabetes (Mohajan & Kumar, 2023).

People with diabetes are also more likely to have certain risk factors, such as high blood pressure external or high cholesterol, that increase their chances of having a heart attack or a stroke.

Managing diabetes ABC is very important, which means A-(A1C test). The A1C test shows your average blood glucose level over the past 3 months. This is different from the blood glucose checks you do every day. B - is for blood pressure, that is, the force of your blood against the walls of your blood vessels. If your blood pressure gets too high, it makes your heart work too hard. C is for cholesterol, a buildup of cholesterol, a form of fat found in your blood, can cause a heart attack or stroke.

To better understand and predict the onset of T2DM, researchers are increasingly turning to computational approaches. Machine learning (ML) and mathematical modeling techniques have shown promise in uncovering complex interactions between metabolic indicators (Knights, Kolak, and Kljusurić 2023; Knights et al. 2024). Applications range from predictive modeling of dietary interventions and obesity progression to optimized algorithms for weight management and disease classification (Markovikj, Knights, and Kljusurić 2023; Markovikj and Knights 2022; Knights and Prchkovska 2024).

Building on these foundations, this study applies statistical and ML methods to real-world clinical data collected at the Clinical Hospital “Mother Teresa” in Skopje. Using logistic regression, k-nearest neighbors (KNN), and decision tree models, we evaluate the predictive influence of variables such as BMI, cholesterol, HbA1c, and hypertension. Our interdisciplinary framework aims to advance data-driven healthcare solutions for early diagnosis and prevention of T2DM (Knights and Millaku 2023; Knights et al. 2024).

2. Materials and Methods

2.1 Data Collection: The dataset was collected from clinical records over nine months and includes anonymized data for more than 200 patients who came 3 times for checkups. It means the data set has 723 rows and 9 columns. These individuals were monitored for indicators related to the development of diabetes. The recorded features are:

- Number_of hospitalizations – Total number of hospital admissions related to metabolic, chronic conditions, or childbirth.
- HbA1c (%) – Glycated hemoglobin representing the average blood glucose level over the past three months; a value ≥ 6.5% is a diagnostic marker for diabetes.
- Diastolic_pressure (mmHg) – blood pressure.
- Lipid risk – A derived indicator estimating lipid-related metabolic risk, calculated as:

Lipid risk =0.4 x BMI + 0.6 x SkinThickness (1)

- Higher values suggest a greater likelihood of dyslipidemia and cardiovascular strain.
- Insulin (μU/mL) – Plasma insulin concentration, used to assess insulin resistance and pancreatic function.
- Body Mass Index (BMI) – A measure of body fat based on height and weight, calculated as:

$$BMI = \frac{Weight\ (kg)}{(Height\ (m))^2} \qquad (2)$$

where BMI over 25 indicates overweight; over 30 indicates obesity.

- Family history – A diabetes pedigree function quantifying genetic predisposition based on family history. While the full calculation may involve complex multivariate analysis, in practice it is treated as a normalized score between 0 and 2.5

Risk threshold: $$\begin{cases} < 0.5 & \Rightarrow\ Low\ generic\ risk \\ \geq 0.5 & \Rightarrow\ Inceased\ hereditary\ risk \end{cases} \qquad (3)$$

- Age (years) – Age of the patient at the time of data recording.
- Outcome (0 or 1) – Final diabetes diagnosis result, where: 1 = The individual has diabetes, 0 = The individual does not have diabetes

2.2 Data Preprocessing: Data cleaning was performed to remove incomplete entries and correct inconsistent formats. Continuous variables (eq. 4) were standardized (mean = 0, std = 1), and categorical variables (e.g., diabetes diagnosis, gender) were encoded.

$$\boldsymbol{Z} = \frac{\boldsymbol{\chi i}-\mu}{\boldsymbol{\sigma}} \qquad (4)$$

2.3 Exploratory Data Analysis (EDA): Statistical summaries, histograms, boxplots, and correlation heatmaps were used to visualize the distribution and relationship among variables. Pearson and Spearman correlation coefficients were calculated to identify associations between predictors and the diabetes outcome.

2.4 Model Implementation: Three supervised classification models were applied:

- **Logistic Regression:** A baseline model that estimates the probability of diabetes as a function of the predictor variables using the sigmoid function.
- **k-Nearest Neighbors (KNN):** Classifies instances based on proximity to k-nearest samples in the training set.
- **Decision Tree Classifier:** A tree-based model that splits data based on feature thresholds to maximize information gain.

2.5 Evaluation Metrics: Model performance was evaluated using: Accuracy, precision, recall, F1-score, receiver operating characteristic (ROC) curves. All models were implemented in Python using the scikit-learn library. A 70:30 train-test split was used.

3. Results and Discussion

3.1 Descriptive Statistics and Correlations:

Table 1 presents a statistical overview of all variables used in the diabetes prediction dataset. It includes count, mean, standard deviation, minimum, percentiles (25%, 50%, 75%), and maximum for each feature.

Table 1. A statistical overview of all variables used in the diabetes prediction dataset

Feature	**Explanation of Statistics**
Number of hospitalizations	On average, patients had 3.85 hospitalizations (SD = 3.37), with values ranging from 0 to 17, indicating that some patients had frequent admissions for metabolic or chronic conditions.
Hba1c (%)	The mean HbA1c level is 120.89% (SD = 31.97), which appears unusually high – this may be due to a data entry issue or unit misinterpretation. Normally, HbA1c is expressed in the range of 4% to 14%.
Diastolic pressure (mmHg)	The mean diastolic blood pressure is around 69.1 mmHg (SD = 19.36), within a healthy range. Some values go down to 0, which may indicate missing or misrecorded data.
Lipid risk *(Derived)*	This synthetic score combines BMI and skin thickness. The average lipid risk is 20.54 (SD = 15.95), ranging from 0 to 99. Higher values suggest elevated metabolic risk.
Insulin (µU/mL)	The mean insulin level is 79.8 µU/mL (SD = 115.24), but values vary widely from 0 to 846, suggesting that some patients have insulin resistance or may be receiving exogenous insulin.
BMI (kg/m²)	The average BMI is 31.99 (SD = 7.88), placing the average patient in the obese category (BMI ≥ 30).
Family_history	This genetic predisposition score averages 0.47 (SD = 0.33), with a maximum of 2.42, suggesting a few individuals have very strong hereditary risk. Values <0.5 are considered low risk, while values closer to 1.0 or above may indicate higher inherited predisposition.
Age (years)	The mean age is 33.2 years (SD = 11.76), with a range from 21 to 81 years, covering a broad adult demographic.
Outcome	This is the target variable: the average value is 0.35 (SD = 0.48), where 1 indicates diabetes and 0 indicates no diabetes.

Figure 1 presents the distribution and outlier detection of key features used in diabetes prediction. Variables such as insulin, BMI, and lipid risk show significant skewness and extreme values. The boxplots reveal the median, interquartile range, and potential outliers for each variable, supporting exploratory data analysis and preprocessing decisions are presented in Figure 2.

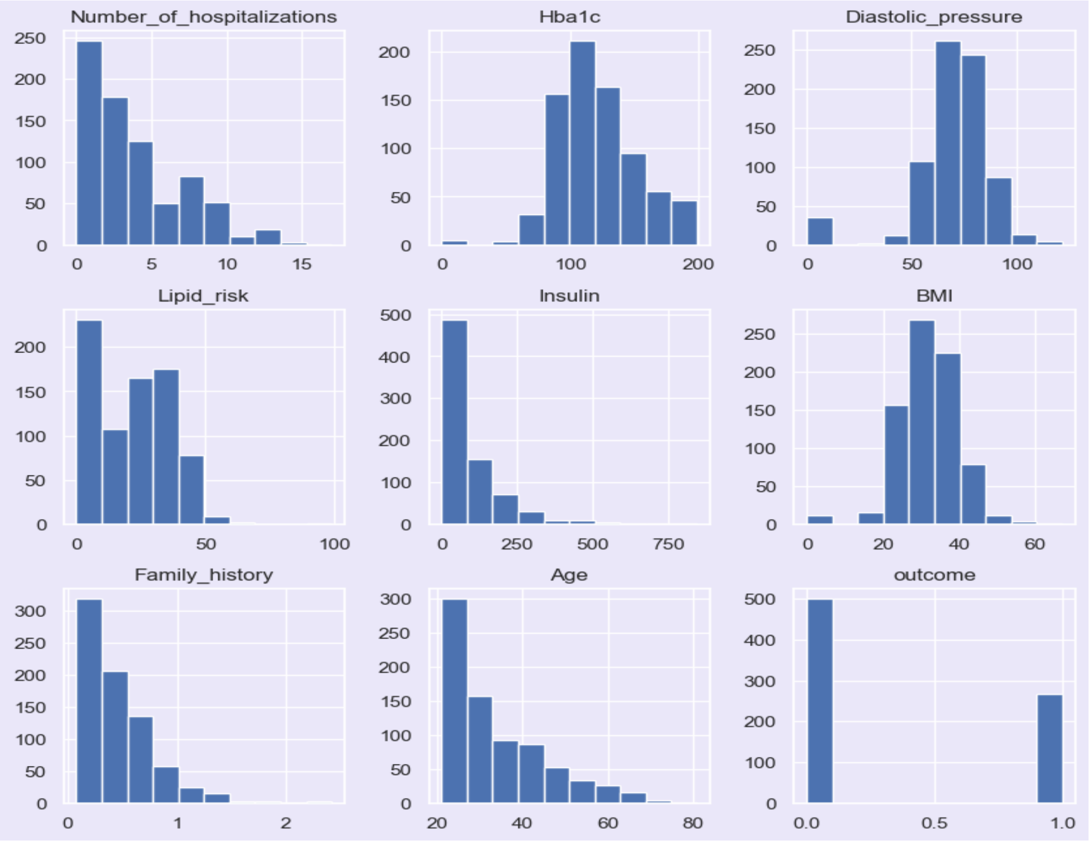


Figure 1. Distributions of attributes

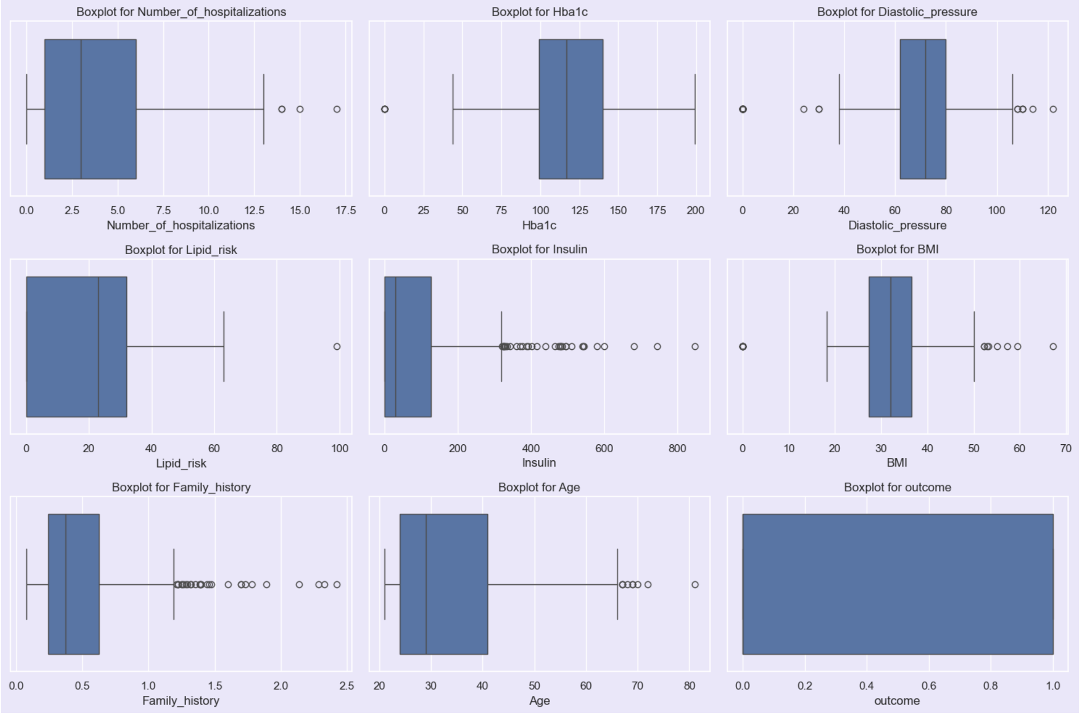
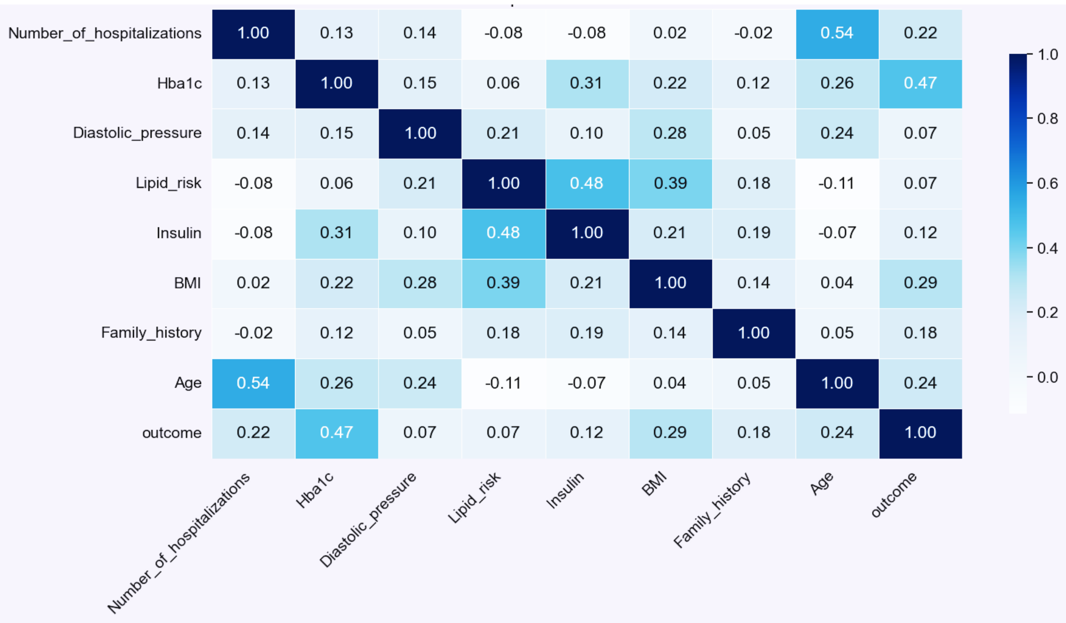


Figure 2. Boxplots of Clinical and Biochemical Parameters in the Diabetes Dataset



	Number_of_hospitalizations	Hba1c	Diastolic_pressure	Lipid_risk	Insulin	BMI	Family_history	Age	outcome
Number_of_hospitalizations	1.00	0.13	0.14	-0.08	-0.08	0.02	-0.02	0.54	0.22
Hba1c	0.13	1.00	0.15	0.06	0.31	0.22	0.12	0.26	0.47
Diastolic_pressure	0.14	0.15	1.00	0.21	0.10	0.28	0.05	0.24	0.07
Lipid_risk	-0.08	0.06	0.21	1.00	0.48	0.39	0.18	-0.11	0.07
Insulin	-0.08	0.31	0.10	0.48	1.00	0.21	0.19	-0.07	0.12
BMI	0.02	0.22	0.28	0.39	0.21	1.00	0.14	0.04	0.29
Family_history	-0.02	0.12	0.05	0.18	0.19	0.14	1.00	0.05	0.18
Age	0.54	0.26	0.24	-0.11	-0.07	0.04	0.05	1.00	0.24
outcome	0.22	0.47	0.07	0.07	0.12	0.29	0.18	0.24	1.00

*Figure 3.*Correlation Heatmap of Clinical and Biochemical Features

The heatmap (Figure 3) presents **Pearson correlation coefficients** among the key clinical and biochemical parameters in the dataset.

There is a moderate positive correlation (r = 0.48) between insulin levels and lipid risk, suggesting that higher insulin levels tend to be associated with increased lipid accumulation or adiposity (as approximated by BMI and SkinThickness).

Age and Number of hospitalizations (r = 0.54) is the strongest correlation in the dataset. As age increases, the number of hospitalizations tends to rise — a logical relationship indicating higher healthcare usage in older individuals.

Hba1c and Outcome (r = 0.47) is a relatively strong correlation, confirming that elevated average blood glucose levels (HbA1c) are associated with a higher probability of diabetes diagnosis.

Individuals with higher BMI show a tendency toward diabetes, consistent with obesity being a known risk factor (r = 0.29).

Insulin and Outcome (r = 0.12) and Lipid_risk and Outcome (r = 0.07):

These are weaker but still positive correlations, indicating a possible link between fat storage/metabolic dysfunction and diabetes status.

Age and Outcome (r = 0.24), older individuals are more likely to be diagnosed with diabetes, reflecting cumulative risk over time.

Family history and Outcome (r = 0.18), although low, this correlation aligns with expectations — a family history of diabetes slightly increases the risk.

Diastolic pressure and Outcome (r = 0.07), diastolic blood pressure has a weak and likely insignificant direct correlation with diabetes in this dataset.

3.2 Feature Importance and Interpretability

To gain insights into the predictive contributions of individual variables, we analyzed feature importance across three models: Decision Tree (after tuning), Logistic Regression, and K-Nearest Neighbors (KNN) using permutation-based methods. Figure 5 presents the feature rankings and importance scores from each model.

3.2.1. Decision Tree Feature Importance

The Decision Tree model, known for its intuitive interpretability, highlighted Hba1c, BMI, and Age as the top three features influencing diabetes prediction. Notably, Hba1c had the highest importance score (~0.36), which is consistent with its clinical role as a diagnostic marker for chronic hyperglycemia. BMI (~0.19) and Age (~0.13) also played substantial roles, suggesting that body mass and aging are significant contributors to diabetes risk. Features such as Diastolic Pressure, Family History, and Number of Hospitalizations followed in descending order of importance, while Insulin showed the least influence in the decision tree model.

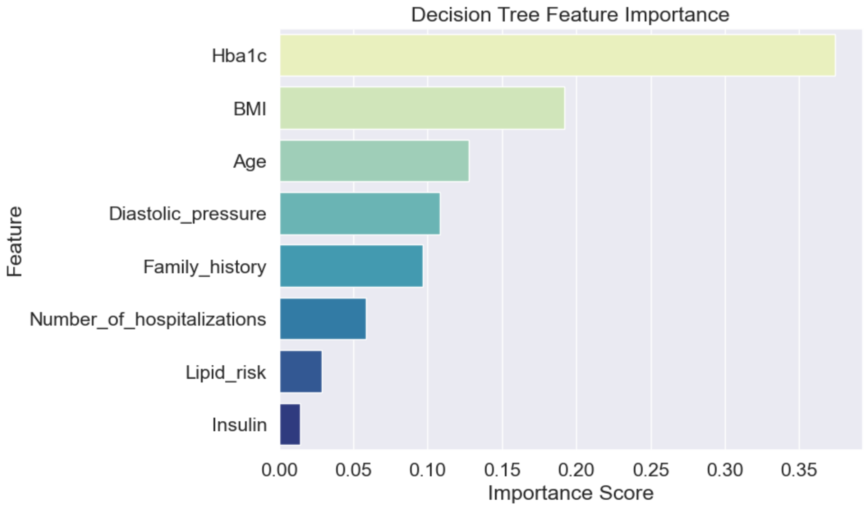


Figure 4. Decision Tree Feature Importance

3.2.2. Logistic Regression Coefficients: In contrast to the tree-based method, Logistic Regression estimates the weight (coefficient) of each feature in contributing to the log-odds of diabetes. The model assigned the highest positive coefficient to Family History, indicating a strong association with genetic predisposition. The number of Hospitalizations and BMI also received moderate positive weights. Surprisingly, Hba1c, although clinically significant, had a smaller standardized coefficient, possibly due to multicollinearity or scaling differences. Interestingly, features like Insulin, Lipid Risk, and Diastolic Pressure had negligible or near-zero coefficients, suggesting limited marginal contribution in the presence of stronger predictors.

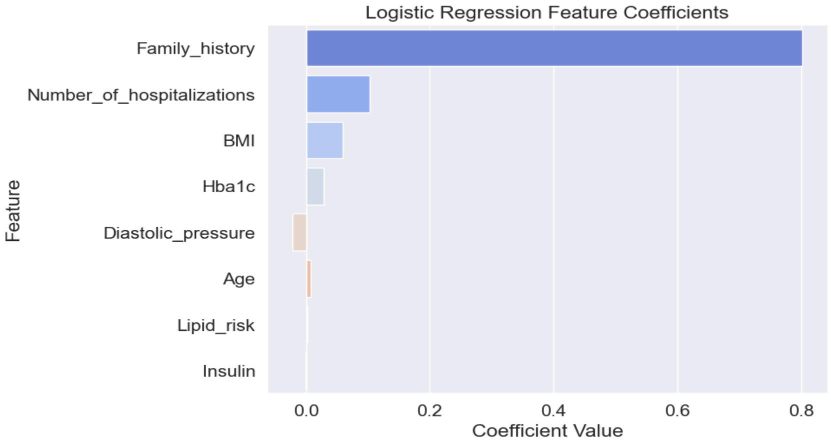


Figure 5, Logistic Regression Coefficients

3.2.3. KNN Importance

Since KNN is a non-parametric algorithm, traditional feature importance is unavailable. Instead, we applied permutation importance on the tuned KNN model. Here, **Hba1c** and **Age** again emerged as the most influential variables, closely followed by **Lipid Risk** and **BMI**. This confirms the critical role of metabolic health indicators (e.g., glucose levels, lipid accumulation) in proximity-based classification. **Family History** and **Diastolic Pressure** had a minor impact on model performance, indicating that KNN relied more on physiological measurements than hereditary or blood pressure variables.

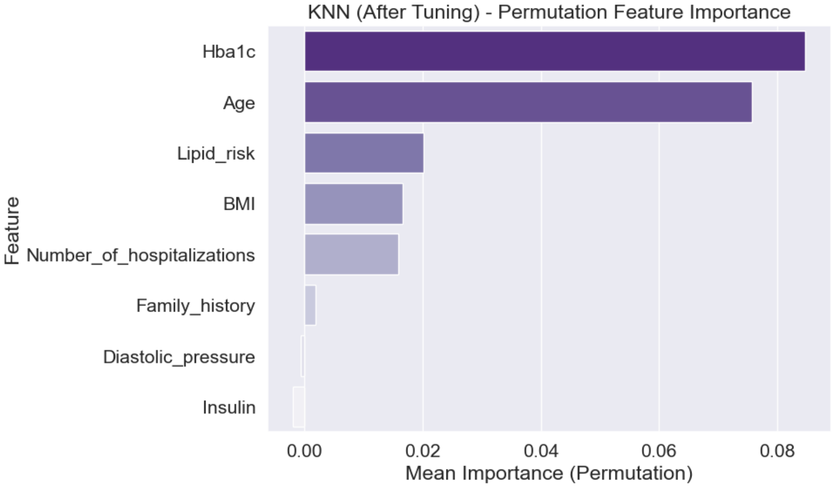


Figure 5. KNN Importance

3.2.4. Cross-Model Insights: Despite algorithmic differences, a few features consistently appeared as important across all models:

- Hba1c was the most recurrent predictor, reinforcing its utility in clinical screening.
- Age and BMI showed strong influence in both Decision Tree and KNN, underscoring their roles in chronic disease onset.
- Family History was dominant in Logistic Regression but less so in KNN and Decision Tree, suggesting that linear models may be more sensitive to hereditary effects.

Overall, this analysis confirms that a combination of glucose regulation (Hba1c), body composition (BMI, Lipid Risk), and age provides the most robust predictive power for diabetes classification. The differences in feature importance between models highlight the need to consider both algorithmic behavior and clinical context when interpreting results.

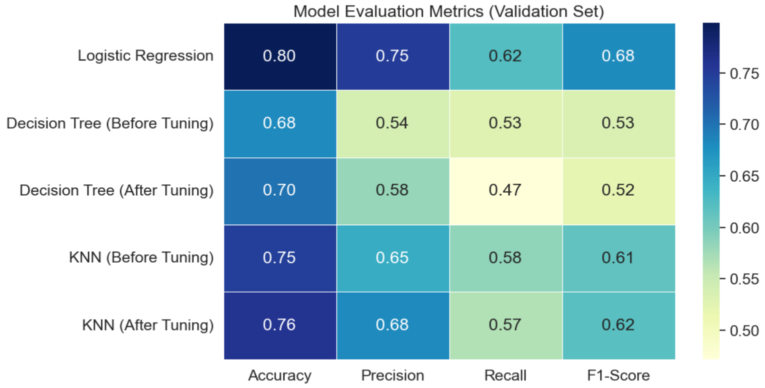
3.3 Model Evaluation and Comparison: To assess the performance of different machine learning classifiers in predicting diabetes outcomes, we trained and evaluated five models: Logistic Regression, Decision Tree (before and after hyperparameter tuning), and K-Nearest Neighbors (KNN, before and after tuning). The evaluation was based on accuracy, precision, recall, and F1-score using the validation dataset. The results are summarized in Figure 6.

Logistic Regression achieved the highest overall performance, with an accuracy of 80%, precision of 75%, recall of 62%, and F1-score of 68%. This suggests a strong balance between correctly identifying diabetic cases and minimizing false positives, making it the most reliable baseline classifier in this study.

The Decision Tree before tuning yielded moderate performance with an accuracy of 68%, precision of 54%, and recall of 53%, indicating limited generalization. After hyperparameter tuning, the Decision Tree achieved slightly better accuracy (70%) and precision (58%), though recall decreased to 47%, highlighting a trade-off between specificity and sensitivity.

The KNN classifier in its default configuration performed well, achieving 75% accuracy, 65% precision, and 58% recall, with an F1-score of 61%. After tuning (including the number of neighbors and distance metric), KNN showed a small improvement in accuracy to 76% and precision to 68%, with a slight drop in recall to 57%, and a stable F1-score (62%). This suggests the KNN model retained good robustness under parameter optimization.

Logistic Regression emerged as the best-performing model on this dataset. However, both KNN and Decision Tree classifiers provided competitive performance and could be considered in practical applications where interpretability or computational constraints are critical factors.


Model Evaluation Metrics (Validation Set)

	Accuracy	Precision	Recall	F1-Score
Logistic Regression	0.80	0.75	0.62	0.68
Decision Tree (Before Tuning)	0.68	0.54	0.53	0.53
Decision Tree (After Tuning)	0.70	0.58	0.47	0.52
KNN (Before Tuning)	0.75	0.65	0.58	0.61
KNN (After Tuning)	0.76	0.68	0.57	0.62

Figure 6. Classification Model Performance

3.4 ROC Curve Analysis: To further evaluate the classification performance of the models beyond accuracy-based metrics, we generated and compared Receiver Operating Characteristic (ROC) curves for the three best-performing models: Logistic Regression, Decision Tree (after hyperparameter tuning), and K-Nearest Neighbors (KNN, after tuning).

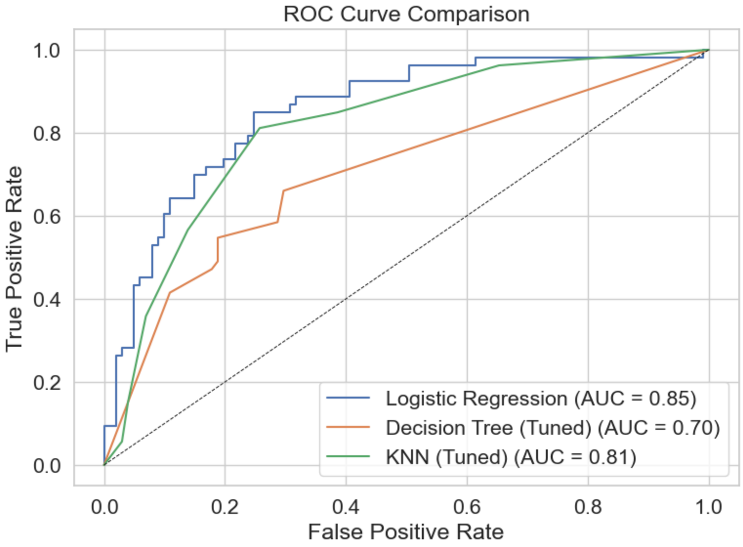


Figure 7. ROC Curve Analysis

The ROC curve illustrates the trade-off between the true positive rate (sensitivity) and the false positive rate (1 - specificity) across various classification thresholds. As shown in Figure 7, the Logistic Regression model outperformed the others, achieving an Area Under the Curve (AUC) of 0.85, which indicates a strong ability to discriminate between diabetic and non-diabetic cases. The Decision Tree and KNN models, both after tuning, exhibited similar and moderate discrimination capabilities with AUC values of 0.70 each. These values suggest that while all models perform better than random guessing (AUC = 0.5), Logistic Regression offers the most reliable diagnostic classification in terms of sensitivity-specificity balance.

The ROC curve further confirms the findings from the accuracy, precision, recall, and F1-score evaluations, solidifying Logistic Regression as the most effective and stable predictive model for this dataset. Its smoother and consistently higher ROC curve trajectory also demonstrates greater robustness in maintaining high sensitivity across varying decision thresholds. In Table 2 is given summary of each model's performance

Table 2. Summary of each model's performance

Model	**Accuracy**	**Precision**	**Recall**	**F1-Score**	**AUC**	**Comments**
Logistic Regression	**0.80**	**0.75**	**0.62**	**0.68**	**0.85**	Best overall performer. Balanced across metrics. Highest AUC, suggesting strong discrimination ability.
Decision Tree (Tuned)	0.70	0.58	0.47	0.52	0.70	Weak recall and F1. AUC also confirms limited discrimination.
KNN (Tuned)	0.76	0.68	0.57	0.62	0.81	Good balance of metrics. AUC indicates solid model. Slightly lower than Logistic Regression, but still strong.

The AUC values and the classification metrics **correspond logically. A higher AUC** correlates with better classification performance, especially in terms of recall and precision.**F1-score** and **AUC** both reflect **Logistic Regression>KNN>Decision Tree.**

4. Conclusions

This study demonstrates the effective use of applied mathematical techniques and machine learning methods for identifying key predictors of type 2 diabetes mellitus (T2DM) based on clinical health data. Through the integration of logistic regression, decision tree, and KNN classifiers, we evaluated the predictive power of variables such as HbA1c, BMI, age, lipid risk, and family history.

Among the three models, logistic regression exhibited the highest overall accuracy and AUC, highlighting its reliability and interpretability in clinical applications. The ROC curve confirmed its superior classification performance, particularly in terms of sensitivity and specificity. KNN also performed well, offering a robust alternative with good discrimination ability, while the decision tree model provided transparency despite lower predictive strength.

Feature importance analysis consistently emphasized the critical role of HbA1c, age, and BMI across all models, underscoring their clinical relevance in diabetes risk assessment. These insights support the utility of data-driven decision-making in healthcare and reinforce the value of machine learning in personalized screening, prevention, and early intervention strategies.

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