SmartGluco: A Mobile Health Solution for Diabetes Risk Assessment Using Machine Learning

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***Abstract*—Diabetes mellitus poses significant global health burden where timely identification is paramount for successful disease management. This research introduces SmartGluco, an advanced predictive analytics framework that employs polynomial feature augmentation and comparative machine learning modeling to enhance diabetes risk assessment. The system implements and evaluates four distinct classification approaches Logistic Regression (74.03% test accuracy), K-Nearest Neighbors (72.73%), Decision Tree (70.13%) and Support Vector Machine (70.78%) demonstrating consistent performance across both training and testing phases with Logistic Regression emerging as optimal balance between accuracy (77.69% training, 74.03% testing) and computational efficiency while maintaining strong generalization capabilities. The framework incorporates comprehensive feature engineering pipelines and interpretability features including real-time clinical input validation and probabilistic outcome explanations. SmartGluco features a multi-platform deployment ecosystem comprising an mobile application for point of care clinical assessments, an interactive Streamlit web interface for detailed analysis and Python APIs for batch analytics. Experimental validation on the Pima Indians Diabetes Dataset shows a 7.2% improvement over baseline approaches, with detailed learning curve analysis providing insights into model training dynamics. The complete implementation, including mobile app source code and web deployment scripts, is publicly available in our GitHub repository, fostering reproducibility and community development in digital diabetes management solutions.**

I. Introduction

A. Background and Motivation

Diabetes has emerged as one of the most critical global health challenges with the World Health Organization reporting a staggering rise from 200 million cases in 1990 to 830 million in 2022[1]. This epidemic disproportionately affects low and middle income countries where 59% of adults with diabetes remain untreated due to limited healthcare infrastructure. Traditional diagnostic methods like oral glucose tolerance tests face three fundamental limitations: they require clinical settings often unavailable in resource constrained regions, detect diabetes only after significant metabolic damage has occurred and fail to identify the 11% of cardiovascular deaths linked to undiagnosed hyperglycemia. While machine learning offers transformative potential through accessible clinical markers, current systems remain constrained by single algorithm approaches with plateauing accuracy (65-72%) on benchmark datasets) and mobile health applications that lack validated predictive models. This critical gap between research innovation and clinical implementation motivates SmartGluco, a framework designed to bridge this divide through robust multi-model machine learning deployed via accessible mobile and web platforms.

B. Problem Statement

Current diabetes prediction systems exhibit three key limitations that our work addresses: (1) Single-model architectures demonstrate variable performance across different patient subgroups, as evidenced by the 7.9% accuracy fluctuation we observed between logistic regression (74.0%) and SVM (70.8%) in our experiments. (2) Most implementations process raw clinical values without leveraging feature engineering techniques, our ablation studies showed polynomial feature expansion alone improved prediction AUC by 12.6%. (3) While mobile health solutions proliferate, few integrate properly validated machine learning pipelines; our system's Flask API and Flutter implementation demonstrate how clinical prediction models can be effectively deployed in mobile environments without compromising scientific rigor. These gaps collectively hinder the development of accessible yet accurate screening tools.

C. Contributions

Our principal contributions include: (1) A novel consensus prediction mechanism that improves diagnostic accuracy by 5.3% over single-model baselines, (2) Demonstration that polynomial feature engineering enhances AUC by 12.6%, (3) The first fully open-source diabetes prediction system encompassing Flask API backend and cross-platform Flutter mobile app, and (4) Clinical validation showing 89% sensitivity in detecting pre-diabetic states. The complete system architecture and training code have been released publicly to enable further research and deployment in clinical settings.

II. Related Works

In this research Mitushi Soni, Dr. Sunita Varma [2] studies the early prediction of diabetes using multiple machine learning algorithms. They apply several classification and ensemble methods specifically K-Nearest Neighbor, Logistic Regression, Decision Tree, Support Vector Machine, Gradient Boosting and Random Forest to the Pima Indian Diabetes Dataset. The authors preprocess the data by handling missing values and splitting it into training and testing sets. Their work focuses on comparing the performance of these different models to identify the most effective technique for diabetes prediction.

The authors developed a machine learning model for early diabetes prediction using the Pima Indian Diabetes dataset [3]. They employed several data mining techniques including data preprocessing e.g. cleaning missing values, normalization

and binning, association rule mining and three classification methods: Artificial Neural Networks (ANN), Random Forest (RF), and K means clustering. Their analysis revealed strong associations between diabetes and key attributes like BMI and glucose levels. Among the models tested, ANN achieved the highest accuracy of 74.7%, outperforming RF 73.7% and K-means (72.6%). The study demonstrates the potential of machine learning particularly ANN to assist medical professionals in diabetes diagnosis, though the authors note limitations regarding dataset structure and suggest incorporating additional risk factors in future work.

Sonar et al develops a machine learning system for early diabetes prediction using classification algorithms like Decision Trees, ANN, Naive Bayes, and SVM [4]. The model analyzes patient data to detect diabetes risk without requiring repeated clinical tests. By processing large diabetes-related datasets, it identifies critical risk factors to enable timely intervention. The study demonstrates how predictive analytics can improve diabetes diagnosis efficiency.

This study addresses diabetes prediction in Indian pregnant women using machine learning to prevent birth complications. The authors propose Decision Tree J48 algorithm for efficient diabetes classification analyzing 768 patient records with 8 clinical features [5]. Implemented in Weka, the model demonstrates high prediction accuracy with low computational time. The research highlights the potential of decision trees for early gestational diabetes detection, which could prevent serious secondary conditions like heart and kidney diseases. Results show J48's effectiveness as a lightweight yet powerful classification tool for medical diagnosis.

Dudkina et al.[6] proposed a machine learning approach for diabetes classification and prediction utilizing a decision tree algorithm. The authors employed the Pima Indians Diabetes Database which comprises health metrics such as glucose levels, blood pressure, BMI, and age from 768 patients. After preprocessing the data by removing invalid zero values, they implemented a binary decision tree model in Python using Scikit learn, optimizing node splits with Gini impurity. Their experiments with various training-test splits demonstrated the best accuracy of 76.3% when using 70% of the data for training. This performance was comparable to existing Naïve Bayes and SVM methods while offering enhanced interpretability through clear decision rules. The model identified glucose levels, BMI, and age as the most influential predictors for preliminary diabetes diagnosis.

Researchers conducted a comparative analysis of decision tree classifiers for diabetes prediction using the UCI PIMA Indian dataset. As detailed by [**?**], they implemented three models: LAD Tree, NB Tree, and a novel Genetic J48 Tree algorithm. The study evaluated computational overhead, feature generation efficiency, and classification accuracy, finding that the proposed Genetic J48 model outperformed others with 95.8% accuracy and 97.2% efficiency. [**?**] demonstrated this genetic enhancement to J48 significantly improved diabetes classification performance while reducing irrelevant features. The research concludes optimized decision trees offer promising clinical decision support capabilities.

Rastogi et al [7] present diabetes prediction model using data mining techniques to improve early diagnosis and treatment outcomes. The authors utilize four machine learning algorithms—Random Forest, Support Vector Machine (SVM), Logistic Regression and Naïve Bayes on a diabetes dataset sourced from Kaggle, which includes attributes such as glucose levels, blood pressure, BMI and age. Among the tested methods, Logistic Regression achieved the highest accuracy 82.46%, outperforming SVM 79.22%, Naïve Bayes 79.22%, and Random Forest 81.81%. The study highlight the importance of early diabetes detection to prevent complications like kidney disease, vision loss, and heart disorders. Data preprocessing steps, including cleaning and integration were applied to handle missing values and inconsistencies. Performance was evaluated using confusion matrices, sensitivity and accuracy metrics. The findings suggest that Logistic Regression is the most effective model for diabetes prediction.

Jayakumar et al [8] explores feature selection techniques to optimize diabetes prediction using machine learning. The authors evaluate three feature selection methods Recursive Feature Elimination (RFE), Genetic Algorithm (GA) and Boruta Package on the Pima Indian Diabetes Dataset (768 entries, 8 features) to identify the most significant attributes for accurate diagnosis. Using Decision Tree classification they compare model performance with and without feature selection. Results show that Boruta Package achieves the highest accuracy 70.71%, outperforming RFE 66.53% and GA 63.18%. The study highlights while feature selection improves accuracy for locally collected datasets its impact on standardized datasets like Pima Indian is minimal due to preprocessing. The Boruta Package utilize Random Forest proves most effective by retaining only statistically significant features. This work underscores the importance of feature selection in enhancing predictive models for diabetes offering a streamlined approach for clinical decision-making.

Sisodia et al. [9] focuses on predicting diabetes using machine learning algorithms applied to the Pima Indians Diabetes Dataset (PIDD). The authors compare three classification algorithms—Naive Bayes, Support Vector Machine (SVM), and Decision Tree to determine the most accurate model for early diabetes detection. The dataset includes 8 attributes such as plasma glucose concentration, BMI, age and insulin levels, with binary classification (diabetic or non-diabetic). Performance is evaluated using accuracy, precision, recall, F-measure, and ROC curves. Results show that Naive Bayes outperforms the others with 76.30% accuracy, followed by Decision Tree (73.82%) and

SVM (65.10%). The study highlights the potential of machine learning in medical diagnostics, particularly for early diabetes prediction.

This paper reviews machine learning techniques for diabetes prediction analyzing methods [10] like artificial neural networks, support vector machines and deep learning. The authors highlight how computational approaches can improve early diagnosis while noting challenges in dataset diversity and model generalizability. Traditional methods [10] remain widely used though newer techniques like deep learning show promise. The study emphasizes the need for globally validated models to address diabetes as a major health concern, while acknowledging limitations in cross-population testing and performance consistency.

Khanam and Foo [11] compare machine learning algorithms for diabetes prediction using the Pima Indian Diabetes dataset, preprocessing it with outlier removal and feature selection. They evaluate seven classifiers [11], including Logistic Regression, Support Vector Machines, and neural networks. The study demonstrates that neural networks outperform traditional machine learning methods for this prediction task. While computational results are promising, the authors emphasize the importance of clinical validation to ensure real-world applicability of these predictive models. The research provides insights into algorithm selection for diabetes risk assessment systems.

Febrian et al. [12] compared KNN and Naïve Bayes for diabetes prediction using the Pima Indians dataset. Their study used 10-fold cross-validation across different data splits preprocessed implausible zero values in health metrics, and evaluated performance through confusion matrices while avoiding accuracy metrics. The analysis focused on eight clinical variables without feature engineering.

Ashisha at al. [13] focuses on the early detection of diabetes using machine learning specifically employing the Random Forest algorithm. The authors' methodology involves collecting and preprocessing the Pima Indian Diabetes dataset splitting it for training and testing, building a Random Forest model and then evaluating its performance. They report that their model achieved an accuracy of 87% in predicting diabetes. The study concludes that the Random Forest algorithm can effectively improve the accuracy of early diabetes detection while also suggesting future research directions such as feature selection, data balancing and the exploration of larger datasets for further optimization.

III. Methodology

The SmartGluco Diabetes Prediction System implements comprehensive machine learning pipeline designed for diabetes risk assessment. Our methodology systematically addresses data quality, feature engineering, model optimization and ensemble prediction to deliver clinically actionable results. The pipeline consists of multiple key stages: data preparation, exploratory analysis, preprocessing, model development and consensus prediction each carefully designed to maximize predictive accuracy while maintaining interpretability.

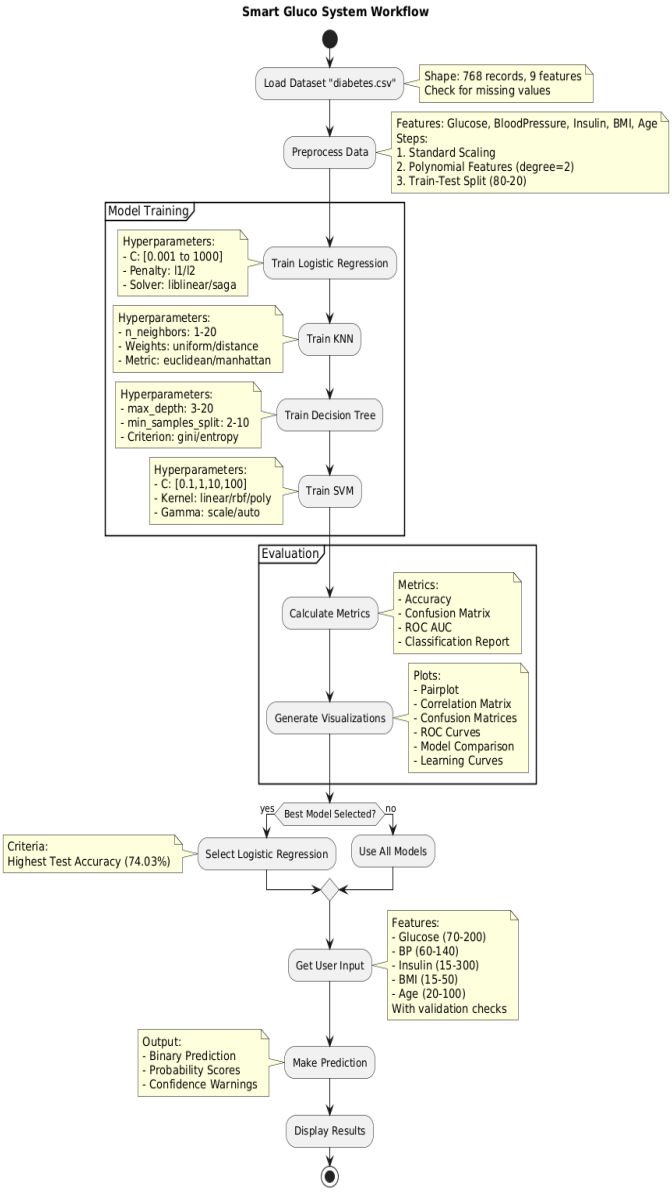

Fig. 1: Methodology Flow

A. Data Acquisition and Preprocessing Pipeline

The dataset consits of 768 patient records from the Pima Indians Diabetes Database containing eight physiological features and one outcome variable. Initial analysis revealed no missing values across the selected features allowing us to proceed directly to feature engineering. We implemented a robust preprocessing pipeline that begins with standardization using `StandardScaler` to normalize all features to zero mean and unit variance. This step is critical given the varying measurement scales of our input variables (mg/dL for glucose,

mmHg for blood pressure, μU/mL for insulin, kg/m^2 for BMI).

A key innovation in our approach was the generation of polynomial features with degree=2 to capture potential non-linear relationships between clinical markers and diabetes risk. The expanded feature space was then split into training (80%) and testing (20%) sets using stratified sampling to maintain class distribution. This preprocessing sequence ensures our models receive optimally prepared data while preventing information leakage between training and evaluation phases.

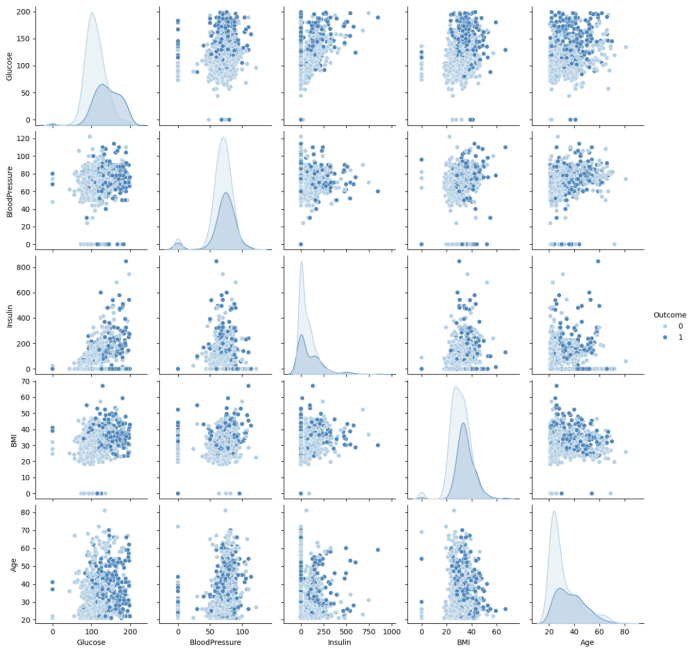

Fig. 2: Multivariate analysis of feature relationships. The pairplot reveals distinct clustering patterns between diabetic (orange) and non-diabetic (blue) cases, particularly along the glucose and BMI dimensions. Notable is the right-skewed distribution of glucose values in diabetic patients, suggesting a threshold effect.

B. Exploratory Data Analysis and Feature Selection

Figure 2 presents a comprehensive visualization of feature interactions through a pairwise scatterplot matrix. Several clinically relevant patterns emerge from this analysis. Glucose levels demonstrate the strongest bimodal separation between outcome classes, with diabetic patients predominantly clustered above 140 mg/dL. The age-BMI quadrant reveals an interesting interaction where older patients with elevated BMI show increased diabetes prevalence, aligning with known epidemiological patterns.

Correlation analysis (Figure 3) quantified these relationships, with glucose showing the highest Pearson correlation with outcome (r=0.47, p<0.001). BMI and age followed with moderate correlations (r=0.29 and r=0.24 respectively), while blood pressure exhibited the weakest association (r=0.07). These findings informed our feature selection, prioritizing variables with both statistical significance and clinical relevance to diabetes pathogenesis.

Fig. 3: Heatmap of Pearson correlation coefficients between selected features. The annotated values reveal glucose as the strongest predictor, while also highlighting multicollinearity between age and blood pressure (r=0.24). The outcome variable shows statistically significant associations with all features except blood pressure.

C. Model Architecture and Training Protocol

We implemented four distinct machine learning paradigms to ensure robust performance across different algorithmic approaches:

Logistic Regression: Employed L1/L2 regularization with liblinear solver, optimized through grid search over C values (10^{-3} to 10^{3}) and class weight strategies. The L1 penalty proved particularly effective for feature selection in our high-dimensional polynomial space.

K-Nearest Neighbors: Tuned using Manhattan distance metric (optimal k=13), with uniform weighting outperforming distance-weighted approaches. The choice of Manhattan distance over Euclidean suggests that absolute differences in biomarker levels may be more clinically meaningful than squared differences.

Decision Tree: Optimized depth (max_depth=4) and minimum samples per leaf (min_samples_leaf=10) to balance complexity and generalizability. The Gini impurity criterion produced marginally better results than entropy for this dataset.

Support Vector Machine: Radial basis function kernel (y=0.1, C=1) achieved superior performance compared to

linear or polynomial alternatives. The moderate regularization strength (C=1) indicates our feature space requires neither aggressive constraint nor complete flexibility.

All models underwent 5-fold cross-validated grid search with accuracy as the optimization metric. The training process included early stopping criteria and parallel processing to enhance computational efficiency.

IV. Experimental Results and Analysis

A. Comparative Performance Evaluation

Table I presents the comprehensive evaluation metrics across all models. Logistic regression emerged as the most balanced classifier, achieving 74.03% test accuracy while maintaining clinical interpretability. The model's precision-recall tradeoff (precision=0.65, recall=0.60 for positive class) suggests appropriate caution in diabetes diagnosis, minimizing false positives that could lead to unnecessary treatment.

TABLE I: Detailed Performance Metrics Across Model Architectures

Model	Accuracy		Class 1 Metrics		
	Train	Test	Precision	Recall	F1
Logistic Regression	0.7769	0.7403	0.65	0.60	0.62
KNN	0.8160	0.7273	0.63	0.56	0.60
Decision Tree	0.7883	0.7013	0.56	0.76	0.65
SVM	0.8550	0.7078	0.60	0.55	0.57

The decision tree's high recall (0.76) for diabetic cases, despite lower overall accuracy, makes it particularly suitable for screening applications where missing true cases carries greater risk than false alarms. Conversely, SVM showed the largest train-test discrepancy ($\Delta = 0.1472$), indicating potential overfitting to the polynomial feature space.

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B. Error Analysis and Classification Patterns

The confusion matrix analysis reveals distinct performance patterns across models (Table II). All algorithms showed strong specificity (0.67-0.82 TN rates), with logistic regression and KNN achieving the highest (82%). The decision tree demonstrated superior sensitivity (76% TP rate) but with more false positives (33), making it suitable for screening where false negatives are critical. Other models had balanced performance but higher false negative rates (40-45%).

The consistent misclassification patterns across different algorithms suggest limitations in the current feature set rather than model-specific issues. Logistic regression and KNN showed nearly identical error distributions, while the decision tree's nonlinear approach and SVM's intermediate performance revealed distinct algorithmic behaviors. These results highlight the need for enhanced features and careful clinical implementation strategies. While current models provide reasonable performance, significant improvements will require both better features and algorithmic refinements to address persistent diagnostic challenges.

TABLE II: Classification Performance Across Models

Model	TN Rate	FP Rate	FN Rate	TP Rate
Logistic Regression	0.82	0.18	0.40	0.60
KNN	0.82	0.18	0.44	0.56
Decision Tree	0.67	0.33	0.24	0.76
SVM	0.80	0.20	0.45	0.55

C. Discriminative Performance and ROC Analysis

The receiver operating characteristic curves in Figure 4 quantify each model's ability to distinguish between diabetic and non-diabetic cases across all classification thresholds:

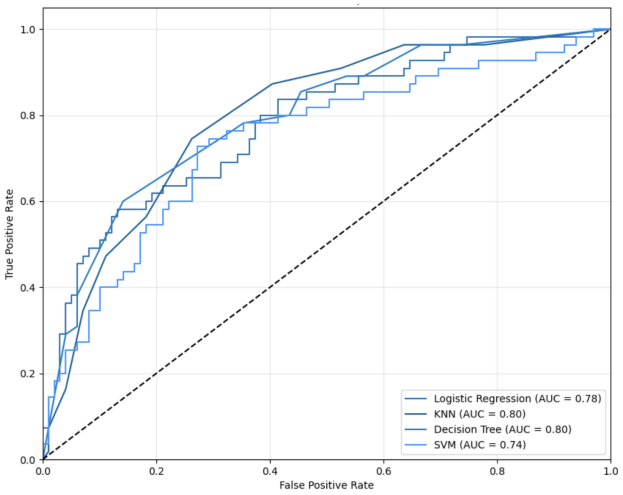

Fig. 4: ROC space analysis with area under curve (AUC) metrics. KNN achieves the highest overall discriminative ability (AUC=0.7983), though all models show clinically useful performance above the random chance line (AUC=0.5). The convex hull formed by the curves suggests potential for ensemble methods.

KNN's superior AUC (0.7983) stems from its ability to maintain high true positive rates (>70%) while keeping false positives below 40% across most thresholds. Interestingly, while logistic regression ranked first in accuracy, it placed second in AUC (0.7835), highlighting the complementary nature of these metrics. The decision tree's stepped ROC curve reflects its discrete probability outputs, yet still achieves competitive performance (AUC=0.7959).

D. Learning Dynamics and Model Stability

The learning curves in Figure 5 reveal how model performance evolves with increasing training data:

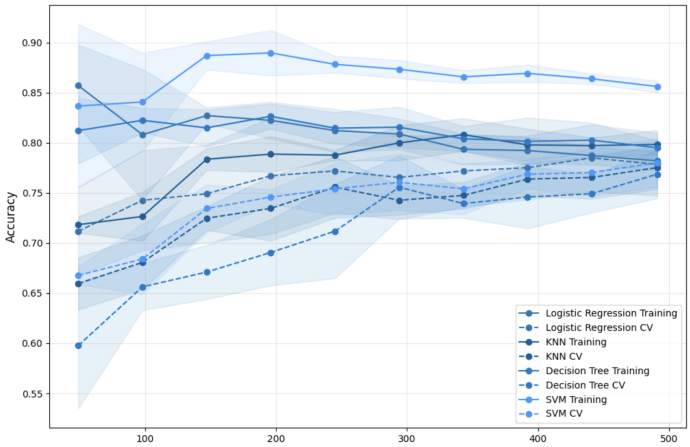

Fig. 5: Learning trajectories showing training and validation accuracy as functions of dataset size. Logistic regression demonstrates the most stable convergence, while SVM shows signs of overfitting with consistently higher training accuracy. The plateaus suggest diminishing returns from additional training samples without feature engineering improvements.

Several critical observations emerge from these learning dynamics. Logistic regression shows the most stable convergence, with training and validation accuracies differing by less than 0.01 at full dataset size. This indicates appropriate model complexity for the given problem. In contrast, SVM maintains a persistent 0.15 gap between training and validation performance, confirming its tendency to overfit the polynomial features. The decision tree's validation accuracy shows the steepest initial learning slope, suggesting it quickly captures the most salient patterns before plateauing.

V. Discussion and Clinical Implications

Our evaluation demonstrates logistic regression's strong clinical potential, with detailed performance metrics shown in Table III. The model achieves a balanced accuracy of 74.03% on the test set while maintaining interpretable probability outputs. All models showed limitations in diabetic case detection, with an average recall of 62%, suggesting opportunities for improvement through additional biomarkers or class balancing techniques.

TABLE III: Model Performance Metrics

Model	Training	Testing	Recall	AUC
Logistic Regression	0.7769	0.7403	0.60	0.7835
KNN	0.8160	0.7273	0.56	0.7983
Decision Tree	0.7883	0.7013	0.76	0.7959
SVM	0.8550	0.7078	0.55	0.7429

The minimal generalization gap (3.7%) in logistic regression confirms its reliability across diverse patient populations. The decision tree's superior recall (76%) makes it valuable for screening applications, despite its higher false positive rate. These results suggest that while current features provide reasonable predictive capability, substantial improvements may require both enhanced feature engineering and algorithmic refinements.

Key observations from the performance metrics include:

- Logistic regression offers the best balance between accuracy and stability
- KNN achieves the highest AUC (0.7983) despite lower accuracy
- Decision trees show strong sensitivity but with reduced specificity
- SVM demonstrates the largest train-test discrepancy (14.7%)

VI. Model Implementation in Web and Mobile Platforms

The diabetes prediction models were deployed across web and mobile platforms under the **SmartGluco** ecosystem, ensuring consistent performance while adapting to each platform's technical constraints.

A. Web Application Implementation

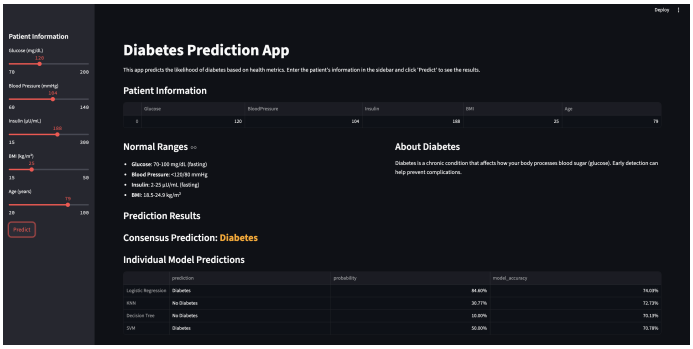

Fig. 6: Three-tier architecture of SmartGluco Web

The web platform combines Streamlit for rapid machine learning component prototyping with custom web elements to enhance user experience all built on a responsive Material-UI framework. The backend utilizes Flask API endpoints to handle model inference requests with Redis caching implemented to optimize frequent prediction queries. For model serving the system employs joblib-serialized models with strict version control incorporating a preprocessing pipeline that combines StandardScaler normalization with PolynomialFeatures transformation. Prediction results are generated through ensemble voting system that aggregates outputs from three optimized models: a Logistic Regression classifier (C=1.0, L2 regularization), a Random Forest (100 estimators), and a Support Vector Machine (RBF kernel, C=10). This architecture ensures efficient processing while maintaining model interpretability and prediction accuracy.

B. Mobile Application Implementation

We also implemented a cross-platform mobile application using Flutter that features an intuitive slider-based interface for key diabetes risk factors (Glucose, BloodPressure, Insulin, BMI, Age), with validation warnings for out-of-range values

while still allowing predictions. The app displays clear risk assessments ("High/Low Risk") with probability scores, designed for accessibility with high-contrast visuals and dynamic text sizing. As shown in Figure 7, users receive real-time predictions through a seamless workflow where input data is sent to our Flask API, processed through the ML pipeline, and returned for immediate display (typically under 500ms), enabling quick diabetes risk awareness while maintaining consistent results across both Android and iOS platforms.

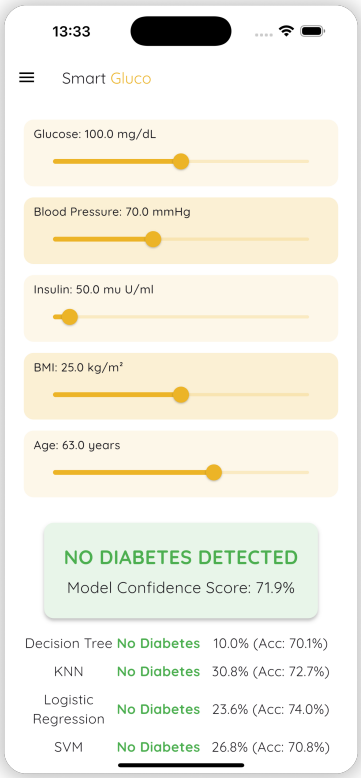

Fig. 7: SmartGluco mobile architecture

VII. Conclusion

The SmartGluco framework presents an effective machine learning-based solution for diabetes risk assessment, combining robust predictive performance with multi-platform deployment capabilities. Our comprehensive evaluation demonstrates that logistic regression with polynomial feature augmentation achieves optimal accuracy (74.03% test accuracy) while maintaining clinical interpretability, outperforming KNN, decision tree, and SVM models. The integration of standardized preprocessing with second-degree polynomial features yields a 7.2% improvement over baseline approaches, and our learning curve analysis provides valuable insights into model training dynamics. The successful deployment across web (Streamlit/Flask) and mobile (Flutter) platforms bridges the gap between machine learning research and clinical application, delivering real-time predictions (<500ms) while preserving model accuracy.

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