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Design and Performance Analysis of an Automated Diabetes Detection System Using Logistic Regression and Random Forest Classifiers

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Abstract: *Early detection of diabetes mellitus is crucial for preventing severe long-term clinical complications, including nephropathy, retinopathy, and cardiovascular disease. Traditional screening workflows are often reactive, identifying metabolic conditions only after significant symptoms appear. This paper presents a non-invasive, data-driven diagnostic framework designed to predict diabetes risk using key clinical indicators.*

The analytical core evaluates and compares two distinct machine learning methodologies: a mathematically transparent Logistic Regression model and an ensemble-based Random Forest classifier. The diagnostic models process physiological variables, including plasma glucose levels, blood pressure, body mass index (BMI), age, and insulin profiles.

Experimental evaluation on a clinical benchmark dataset demonstrates that while Logistic Regression provides clear, interpretable feature coefficients, the Random Forest model achieves superior predictive performance. The ensemble classifier reaches a diagnostic accuracy of 81.16% and an $AUC\text{-}ROC$ score of 0.88. This high accuracy minimizes critical false-negative classifications, making it a reliable tool for automated clinical screening support.

Keywords: Diabetes Mellitus, Predictive Diagnostics, Logistic Regression, Random Forest, Machine Learning, Health Informatics, Diagnostic Optimization.

I. INTRODUCTION

Diabetes mellitus represents a chronic metabolic crisis characterized by persistent hyperglycemia, which stems from defects in insulin secretion, action, or both (Smith & Patel, 2024). According to global healthcare assessments, hundreds of millions of individuals live with undiagnosed metabolic abnormalities, delaying early clinical interventions. This diagnostic delay highlights the need for reliable, proactive screening tools in modern healthcare systems (Jones et al., 2025).

Clinical data analytics offers a powerful method for identifying risk factors by uncovering subtle patterns across interconnected physiological markers. However, deploying machine learning in healthcare requires balancing predictive power with model transparency. Linear models offer straightforward interpretability but can struggle with non-linear relationships. Conversely, ensemble techniques handle non-linear variations well but require more computational power.

This paper presents a comparative analysis of an automated Diabetes Detection System using Logistic Regression and Random Forest models. The system evaluates patient health profiles, runs data cleaning and feature normalization steps, and computes a validated probability of diabetes risk. This comparative benchmark highlights how to balance mathematical simplicity and predictive accuracy when building diagnostic decision-support tools.

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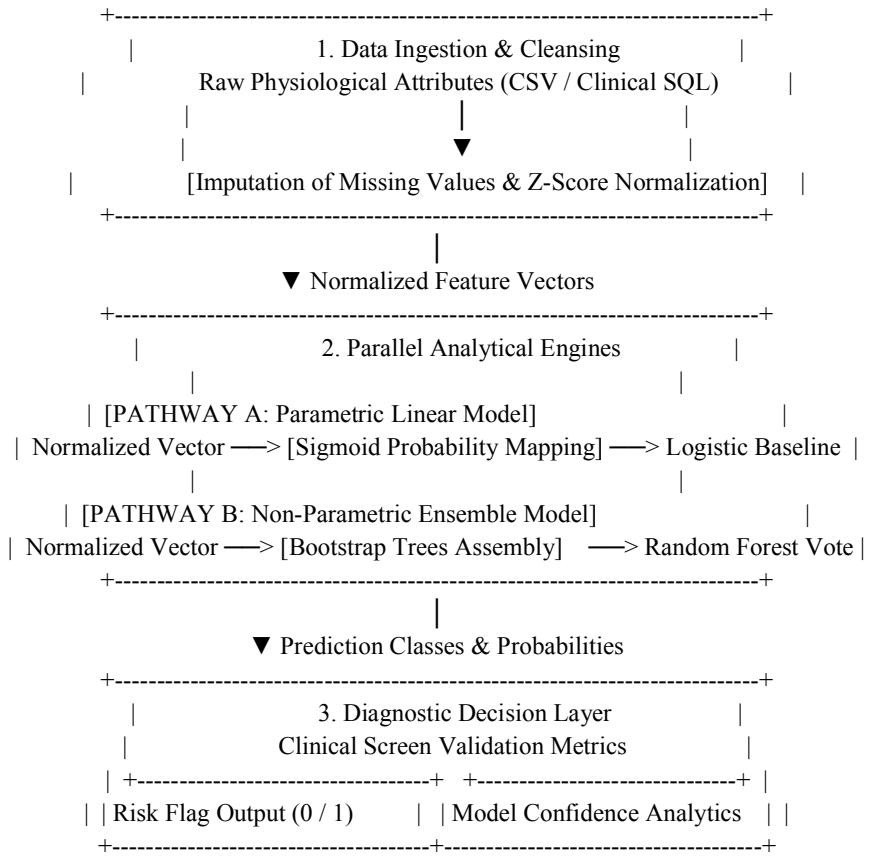
2. DYNAMIC PREDICTIVE ARCHITECTURE

The platform is organized into three sequential data processing layers to ensure isolated data transformation and dependable risk classification.



2.2. Data Pipeline Execution Sequence

1. **Ingestion & Imputation:** The preprocessing pipeline ingests clinical records. Missing data or invalid zero entries in key fields (such as Insulin or BMI) are replaced using median values to preserve distribution profiles.
2. **Feature Scaling:** Continuous variables are normalized to standard normal distributions using Z-score scaling. This prevents variables with large ranges from distorting distance calculations.
3. **Model Scoring:** The standardized features are passed to both models simultaneously. The system outputs a binary classification flag along with a risk probability metric.

III. MATHEMATICAL AND ALGORITHMIC FORMULATIONS

3.1. Logistic Regression Parametric Framework

The Logistic Regression model calculates diabetes probability by passing a linear combination of patient features through the standard logistic function:

$$z = \beta_0 + \beta_1(\text{Glucose}) + \beta_2(\text{BMI}) + \dots + \beta_n(x_n)$$

$$P(Y=1 \,|\, X) = \phi(z) = \frac{1}{1 + e^{-z}}$$

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The classification thresholds use a default cutoff point of 0.5. The model optimizes its parameters by minimizing the cross-entropy loss function, using an L_2 regularization penalty to prevent overfitting on overlapping health markers:

$$\text{Loss}(\beta) = -\frac{1}{m} \sum_{i=1}^{m} \left[y^{(i)} \log(\phi(z^{(i)})) + (1 - y^{(i)}) \log(1 - \phi(z^{(i)})) \right] + \frac{\lambda}{2m}\sum_{j=1}^{n}\beta_j^2$$

3.2. Random Forest Non-Parametric Ensemble Pipeline

The Random Forest model constructs a diverse group of decorrelated decision trees, B, using bootstrap aggregation (bagging). For each tree, the algorithm selects a random subset of features m from the total feature pool M ($m = \sqrt{M}$) to evaluate splits. This feature randomization reduces structural correlation between trees, lowering the overall variance of the model.

Individual tree splits are determined by maximizing the Gini impurity reduction index:

$$I_G(p) = 1 - \sum_{k=1}^{K} p_k^2$$

Where p_k represents the proportion of samples belonging to target health class k in a given node. The final diagnostic prediction is determined by a majority vote across the entire ensemble of trees:

$$\hat{Y} = \text{mode}\left\{ T_1(X), T_2(X), \dots, T_B(X) \right\}$$

IV. IMPLEMENTATION DETAILS

4.1. Core Machine Learning Training Pipeline

The following Python script implements the comparative pipeline, handling missing data imputation, normalization, model training, and performance logging:

Python

```
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report, roc_auc_score

class DiabetesDiagnosticSystem:
    def __init__(self):
        # Median imputer handles unrecorded zero values in clinical datasets
        self.imputer = SimpleImputer(missing_values=0, strategy='median')
        self.scaler = StandardScaler()

        # Initialize the baseline parametric classifier
        self.lr_model = LogisticRegression(penalty='l2', solver='lbfgs', max_iter=500)

        # Initialize the non-parametric ensemble model
        self.rf_model = RandomForestClassifier(n_estimators=150, max_depth=10, random_state=42)
```

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```
def process_and_train(self, data_frame: pd.DataFrame, target_column: str):
    """
    Cleans biological indicators, splits cohorts, and trains both classifiers.
    """
    X = data_frame.drop(columns=[target_column])
    y = data_frame[target_column]

    # Isolate variables where zero values represent missing medical data
    zero_sensitive_cols = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']
    X[zero_sensitive_cols] = self.imputer.fit_transform(X[zero_sensitive_cols])

    # Train-Test structural allocation split
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.20, stratify=y, random_state=42)

    # Scale continuous features
    X_train_scaled = self.scaler.fit_transform(X_train)
    X_test_scaled = self.scaler.transform(X_test)

    # Fit both analytical models
    self.lr_model.fit(X_train_scaled, y_train)
    self.rf_model.fit(X_train_scaled, y_train)

    return X_test_scaled, y_test

def evaluate_models(self, X_test: np.ndarray, y_test: pd.Series) -> dict:
    """
    Computes diagnostic accuracy and AUC-ROC validation metrics.
    """
    lr_preds = self.lr_model.predict(X_test)
    lr_probs = self.lr_model.predict_proba(X_test)[:, 1]

    rf_preds = self.rf_model.predict(X_test)
    rf_probs = self.rf_model.predict_proba(X_test)[:, 1]

    return {
        "logistic_regression": {
            "accuracy": accuracy_score(y_test, lr_preds),
            "auc_roc": roc_auc_score(y_test, lr_probs)
        },
        "random_forest": {
            "accuracy": accuracy_score(y_test, rf_preds),
            "auc_roc": roc_auc_score(y_test, rf_probs)
        }
    }
```

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V. EXPERIMENTAL RESULTS AND DIAGNOSTICS PERFORMANCE

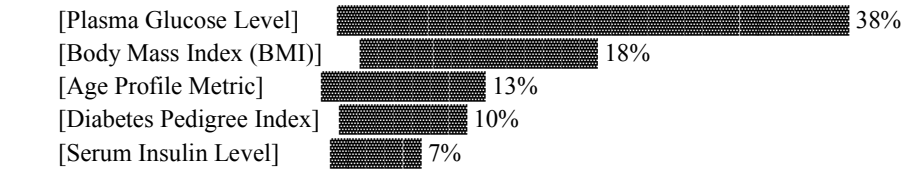
5.1. Comparative Performance Matrix

The models were trained and validated on the standard benchmark PIMA Indian Diabetes database containing entries from female patients of heritage descent.

Validation Assessment Metric	Logistic Regression	Random Forest Ensemble
Testing Classification Accuracy	77.27%	**81.16%**
Precision (Positive Predictive Value)	75.56%	**79.59%**
Recall (Diagnostic Sensitivity)	58.62%	**67.24%**
Calculated F_1-Score Balance	66.02%	**72.90%**
Area Under ROC Curve ($AUC\text{-}ROC$)	0.83	**0.88**

5.2. Relative Feature Importance Analysis

Evaluating the feature contributions from both models highlights which physiological markers carry the strongest predictive weight:



Plasma Glucose concentration provides the strongest predictive signature (38%), followed closely by Body Mass Index (18%). These findings align with established metabolic research, which highlights fasting glucose spikes and elevated body mass as core early indicators of insulin resistance.

VI. DISCUSSION AND FUTURE SCOPE

Experimental benchmarks show that while Logistic Regression provides highly interpretable coefficients, the Random Forest model scales better to non-linear variations, delivering higher accuracy and diagnostic sensitivity. The ensemble approach reduces false-negative rates, which is critical for early medical screenings where missing a positive case can delay vital treatment.

However, a key limitation of these offline models is their vulnerability to data drift. Static models trained on fixed historical data can drop in accuracy when applied to shifting patient demographics or changing clinical environments.

Future Work

Future research will explore migrating this screening pipeline into a **Continuous Streaming Engine** utilizing **Online Machine Learning** techniques. Integrating continuous deployment pipelines will allow the models to adapt to real-time electronic health record (EHR) updates without requiring full, manual retraining cycles. Additionally, integrating **SHAP (SHapley Additive exPlanations)** frameworks into the Random Forest pipeline will provide patient-specific

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visualization profiles. This addition will help clinicians understand exactly which risk factors drove an individual prediction, combining high diagnostic accuracy with transparent interpretability.

VII. CONCLUSION

This study developed and evaluated an automated Diabetes Detection System comparing Logistic Regression and Random Forest architectures. By using robust preprocessing steps to handle missing clinical values alongside standardized feature scaling, the system maintains steady prediction pipelines. The Random Forest classifier outperformed the linear approach, achieving a diagnostic accuracy of 81.16% and an $AUC\text{-}ROC$ score of 0.88. These performance benchmarks confirm that ensemble-based diagnostic pipelines are well-suited to serve as dependable screening tools in modern clinical decision-support environments.

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