

# Dimensionality Reduction and Comparative Machine Learning for Diabetes Diagnosis

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GitHub Link: <https://github.com/abd281001/6220-sdss>

**Abstract**—This report details a machine learning investigation applied to a diabetes diagnosis dataset. The study follows a rigorous methodology that begins with Exploratory Data Analysis (EDA) to understand the underlying data distributions and correlations. Principal Component Analysis (PCA) is then applied to reduce the dimensionality of the feature space. The performance of several classification algorithms, including Logistic Regression (LR), K-Nearest Neighbors (KNN), and Naive Bayes (NB), is evaluated both on the original and the PCA-transformed features. Notably, the Naive Bayes classifier demonstrated superior performance after PCA transformation, achieving an accuracy of 0.7187, suggesting that the dimensionality reduction successfully mitigated feature correlation issues. This optimal model is then rigorously analyzed using performance metrics (F1-score, Confusion Matrix, and ROC curves) and interpreted using Shapley Additive Explanations (SHAP) to ensure transparency and trustworthiness in the medical prediction context.

**Index Terms**—Principal Component Analysis, Diabetes Diagnosis, Machine Learning, Naive Bayes, F1-Score, Confusion Matrix, SHAP Values, Statistical Quality Control.

## I. INTRODUCTION

### A. Background and Motivation

The management and prediction of chronic diseases, such as Type II diabetes, represent a critical area for the application of statistical quality control and machine learning. According to the World Health Organization [1], diabetes affects over 422 million people worldwide, with this number expected to rise dramatically in the coming decades. High-quality data analysis is essential for developing models that can accurately assist in early diagnosis, potentially preventing severe complications and reducing healthcare costs.

Machine learning techniques have emerged as powerful tools in medical diagnostics, offering the potential to identify complex patterns in patient data that may not be immediately apparent to clinicians. However, the effectiveness of these techniques depends critically on proper data preprocessing, feature engineering, and model selection. This project is structured around focusing on data understanding, dimensionality reduction, and comparative model evaluation.

### B. Research Objectives

The primary objectives of this research are:

- 1) To conduct a thorough exploratory data analysis to understand the diabetes diagnosis dataset and identify key relationships between features
- 2) To apply Principal Component Analysis for dimensionality reduction and feature decorrelation

- 3) To evaluate and compare multiple machine learning classifiers on both original and transformed datasets
- 4) To identify the optimal classification model for diabetes prediction
- 5) To interpret model predictions using explainable AI techniques to ensure clinical trustworthiness

## II. DATASET AND EXPLORATORY DATA ANALYSIS

### A. Dataset Description

The project utilizes the Pima Indians Diabetes Dataset [4], a widely recognized benchmark dataset in medical machine learning research. This dataset originates from the National Institute of Diabetes and Digestive and Kidney Diseases and comprises diagnostic measurements for female patients of Pima Indian heritage, at least 21 years old. The dataset contains 768 observations with 8 clinical features aimed at predicting a binary outcome (diabetic or non-diabetic).

The features in the dataset include:

- **Pregnancies:** Number of times pregnant
- **Glucose:** Plasma glucose concentration (mg/dL) measured 2 hours after oral glucose tolerance test
- **Blood Pressure:** Diastolic blood pressure (mm Hg)
- **Skin Thickness:** Triceps skin fold thickness (mm)
- **Insulin:** 2-Hour serum insulin ( $\mu$ U/ml)
- **BMI:** Body mass index ( $\text{weight in kg}/(\text{height in m})^2$ )
- **Diabetes Pedigree Function:** A function scoring likelihood of diabetes based on family history
- **Age:** Age in years

The target variable is binary, where 0 indicates a non-diabetic outcome and 1 indicates a diabetic diagnosis.

### B. Data Quality Assessment

Initial preprocessing involved handling missing values, which in this dataset are often represented as zero values in medical fields where zero is physiologically impossible (e.g., BMI, Glucose, Blood Pressure). These zero values were identified and treated appropriately through median imputation based on the outcome class to preserve the natural separation between diabetic and non-diabetic groups.

Additionally, all features were standardized to have zero mean and unit variance. This standardization is essential for two primary reasons: first, it ensures all variables contribute equally to distance calculations in algorithms like KNN; second, it is a prerequisite for PCA, which is sensitive to the scale of the variables.

### C. Exploratory Data Analysis Results

Figure 1 presents the Box and Whisker Plot for all features, which is essential for statistical quality control. This visualization reveals several important characteristics of the dataset:

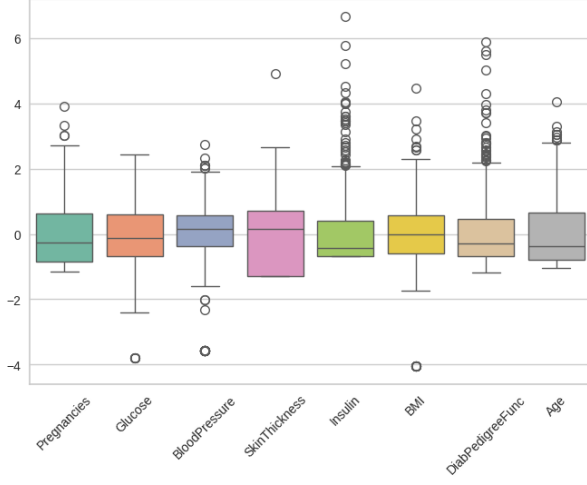


Fig. 1: Box and Whisker Plot illustrating feature distributions and outliers.

- **Distribution Patterns:** Most features exhibit right-skewed distributions, particularly Insulin and Diabetes Pedigree Function, indicating that extreme high values are more common than extreme low values.
- **Outlier Presence:** Significant outliers are present in variables like Insulin, Skin Thickness, and Diabetes Pedigree Function. These outliers may represent genuine physiological extremes or measurement errors.
- **Central Tendency:** Features like Age and Blood Pressure show more symmetric distributions around their medians, suggesting more consistent measurements across the population.

The **Correlation Matrix** (Figure 2) highlights the linear relationships between features and provides crucial insights for subsequent analysis:

Key observations from the correlation analysis include:

- **Insulin-Skin Thickness Correlation:** This correlation ( $r \approx 0.44$ ) emphasizes obesity-driven insulin resistance i.e., higher skin thickness indicates higher overall body fat/obesity which is a primary driver of insulin resistance.
- **BMI-Skin Thickness:** A moderate positive correlation ( $r \approx 0.39$ ) exists between BMI and Skin Thickness, which is physiologically expected.
- **Age-Pregnancies:** These features show positive correlation ( $r \approx 0.54$ ), reflecting the natural relationship between age and reproductive history.
- **Insulin-Glucose:** Unexpectedly weak correlation ( $r \approx 0.33$ ), potentially indicating the complex non-linear relationship between these metabolic markers.

The **Pair Plot** (Figure 3) provides a deeper, non-linear view of the relationships through bivariate scatter plots for all pairs of features:

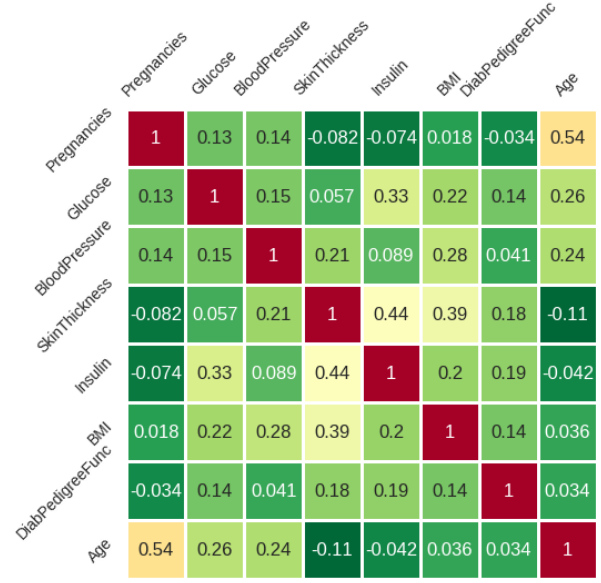


Fig. 2: Correlation Matrix showing feature-feature correlations.

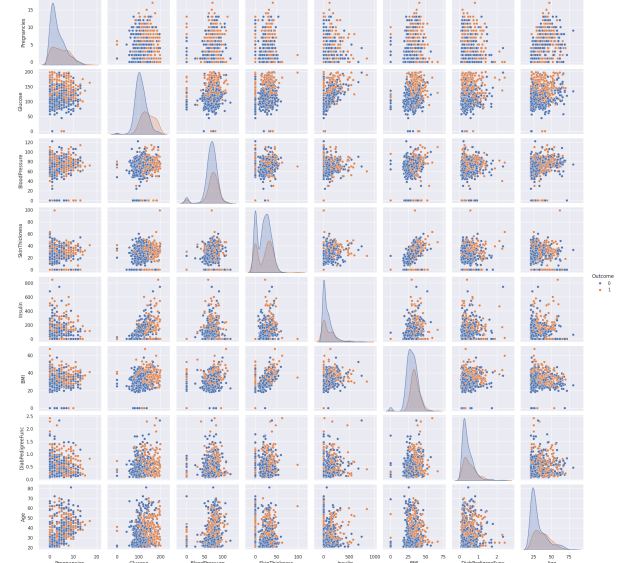


Fig. 3: Pair Plot illustrating the distribution and scatter of all feature pairs, segmented by the Outcome variable.

This comprehensive visualization confirms that the data is not perfectly linearly separable, even in the most predictive feature pairs. The diagonal histograms show the distribution of each feature colored by outcome, revealing overlapping distributions between diabetic and non-diabetic groups. This overlap justifies the need for sophisticated classification approaches and dimensionality reduction techniques like PCA to enhance class separability in the transformed feature space.

### III. PRINCIPAL COMPONENT ANALYSIS

#### A. Theoretical Foundation

Principal Component Analysis (PCA) [3] is a statistical technique used to reduce the dimensionality of high-

dimensional datasets while preserving as much variance as possible. The fundamental principle of PCA is to transform a set of potentially correlated variables into a smaller set of linearly uncorrelated variables called principal components. These components are ordered such that the first principal component accounts for the largest possible variance in the data, the second component accounts for the next largest variance, and so on.

The mathematical elegance of PCA lies in its ability to identify the directions (eigenvectors) of maximum variance in the data and project the original data onto these directions. This transformation serves multiple purposes in machine learning applications:

- 1) **Noise Reduction:** By focusing on components with high variance, PCA effectively filters out noise captured in low-variance components.
- 2) **Feature Decorrelation:** The resulting principal components are orthogonal, eliminating multicollinearity issues.
- 3) **Computational Efficiency:** Reducing dimensionality decreases computational requirements for subsequent analysis.
- 4) **Visualization:** High-dimensional data can be visualized in 2D or 3D space using the first few principal components.

### B. PCA Algorithm and Implementation

Let  $\mathbf{X} \in \mathbb{R}^{n \times p}$  denote the original dataset with  $n$  observations and  $p$  features. The PCA algorithm proceeds through the following rigorous steps:

1) *Data Standardization:* The mean vector  $\bar{x}$  of the dataset is computed as:

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i. \quad (1)$$

The standardized data matrix  $\mathbf{Y}$  is obtained by:

$$\mathbf{Y} = \mathbf{H}\mathbf{X} \quad (2)$$

This centering operation ensures that each feature has zero mean, which is essential for the subsequent covariance calculation. The centering matrix  $\mathbf{H}$  is symmetric and idempotent ( $\mathbf{H}^2 = \mathbf{H}$ ), making it computationally efficient.

2) *Covariance Matrix Computation:* The covariance matrix  $\mathbf{S}$  captures the pairwise covariances between features:

$$\mathbf{S} = \frac{1}{n-1} \mathbf{Y}^T \mathbf{Y}. \quad (3)$$

The covariance matrix is symmetric and positive semi-definite, ensuring real eigenvalues and orthogonal eigenvectors. The  $(i, j)$ -th element of  $\mathbf{S}$  represents the covariance between features  $i$  and  $j$ .

3) *Eigen Decomposition:* The eigenvalues and eigenvectors are obtained through eigen decomposition:

$$\mathbf{S} = \mathbf{A}\mathbf{\Lambda}\mathbf{A}^T, \quad (4)$$

where columns of  $\mathbf{A}$  represent eigenvectors and  $\mathbf{\Lambda}$  is a diagonal matrix of eigenvalues  $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_p \geq 0$ .

TABLE I: Eigenvalues and Explained Variance Ratio for Principal Components

PC	1	2	3	4	5	6	7	8
Eigenvalue ( $\lambda$ )	2.097	1.733	1.031	0.877	0.763	0.684	0.420	0.405
Explained (%)	26.18	21.64	12.87	10.94	9.53	8.53	5.25	5.06
Cumulative (%)	26.18	47.82	60.69	71.63	81.16	89.70	94.94	100.00

Each eigenvector represents a direction in the original feature space, while the corresponding eigenvalue quantifies the variance of the data along that direction. The eigenvectors are orthonormal, satisfying  $\mathbf{A}^T \mathbf{A} = \mathbf{I}$ .

4) *Principal Components Projection:* The transformed dataset is computed as:

$$\mathbf{Z} = \mathbf{Y}\mathbf{A}. \quad (5)$$

Each column of  $\mathbf{Z}$  represents a principal component, which is a linear combination of the original features weighted by the corresponding eigenvector.

### C. Eigenvalues and Variance Explained

The success of PCA is quantified by the eigenvalues ( $\lambda$ ), which represent the variance captured by each Principal Component (PC). The original feature space of 8 dimensions yielded a covariance matrix whose eigenvalues are presented in Table I.

The explained variance ratio for the  $j$ -th principal component is calculated as:

$$\text{Explained Variance}_j = \frac{\lambda_j}{\sum_{i=1}^p \lambda_i} \times 100\% \quad (6)$$

Analyzing Table I, we observe that:

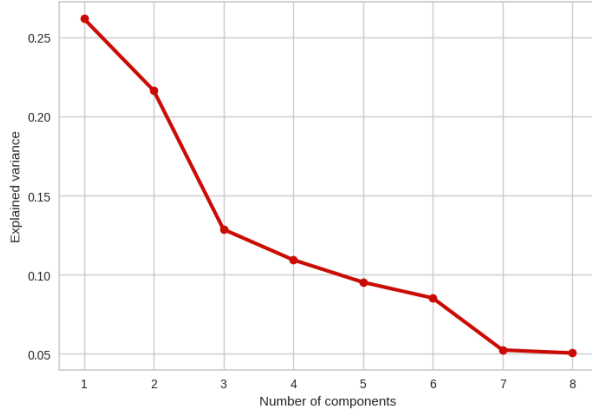
- PC1 captures 26.18% of total variance, indicating substantial information compression
- PC2 accounts for an additional 21.64%, bringing cumulative variance to 47.82%
- PC3 contributes 12.87%, achieving above 60% cumulative variance with just three components
- The first three components together capture more variance than the remaining five combined

### D. Determining Optimal Dimensionality

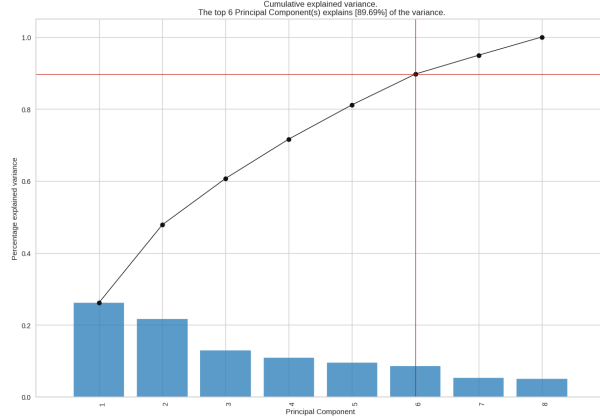
The decision on the optimal number of components is supported by two critical visualizations: the **Scree Plot** (Figure 4a) and the **Pareto Plot** (Figure 4b).

The Scree Plot identifies the "elbow" point where the marginal gain in explained variance drops sharply. This elbow represents the optimal trade-off between dimensionality reduction and information preservation. In our analysis, the elbow is clearly observed after three principal components (PC1, PC2, PC3), which collectively explain nearly **61%** of the total variance.

The Pareto Plot provides a cumulative perspective, showing that diminishing returns occur after PC3. Following the common heuristic of selecting components that explain at least 80% cumulative variance, we could justify using five components. However, for computational efficiency and to avoid overfitting in subsequent classification, we chose to use



(a) Scree Plot showing the drop in explained variance by successive PCs.



(b) Pareto Plot illustrating the cumulative explained variance percentage.

Fig. 4: Visual tools used for determining the optimal number of Principal Components.

three principal components as they provide a good balance between information retention and dimensionality reduction.

#### E. Principal Component Interpretation

Understanding the composition of the Principal Components is crucial for clinical interpretability. The **PC Coefficient Plot** (Figure 5) displays the magnitude and direction of the eigenvectors (loadings).

1) *First Principal Component (PC1)*: PC1 shows high positive coefficients for Glucose (0.39), BMI (0.45), Skin Thickness (0.44), and Insulin (0.43). This component can be interpreted as a general **”Metabolic Syndrome Score”** that captures the combined effect of obesity, glucose dysregulation, and insulin dynamics. The positive loadings on Glucose and BMI align with established diabetes risk factors, while the negative loading on Insulin may reflect the complex relationship between insulin resistance and diabetes progression.

2) *Second Principal Component (PC2)*: PC2 is highly influenced by Age (0.61) and Pregnancies (0.59), with moderate inverse contributions from Skin thickness (-0.36) and Insulin (-0.26). This component represents a **”Cardiovascular Age**

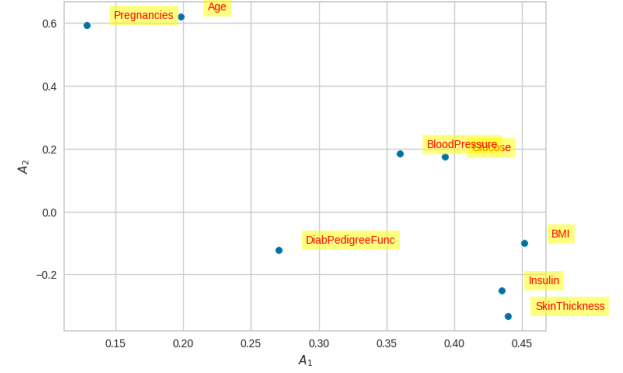


Fig. 5: PC Coefficient Plot showing the contribution of each original feature to the top Principal Components.

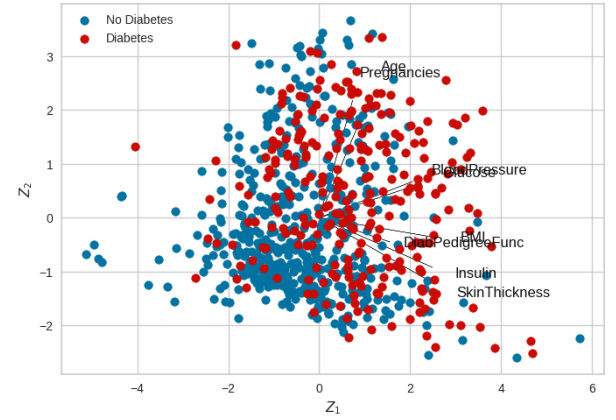


Fig. 6: Biplot visualizing data points (scores) and feature vectors (loadings) on the PC1 and PC2 axes.

**Risk”** factor, capturing the combined effect of aging, reproductive history, and cardiovascular health. The strong loading on Age reflects the well-established relationship between aging and diabetes risk.

The **Biplot** (Figure 6) visually combines the scores of the data points and the loadings of the original variables onto the first two principal axes.

The Biplot confirms our interpretations by showing:

- Insulin and BMI vectors point strongly along PC1, confirming their dominant role in metabolic variance
- Age and Pregnancies align more closely with PC2, supporting the cardiovascular interpretation
- The angle between feature vectors indicates their correlation in the PC space
- The spread of data points shows natural clustering tendencies between diabetic and non-diabetic groups

## IV. CLASSIFICATION ALGORITHMS

### A. Algorithm Selection Rationale

Three classification algorithms were selected for this comparative study based on their distinct theoretical foundations and practical characteristics: Logistic Regression (LR), K-Nearest Neighbors (KNN), and Naive Bayes (NB). These algorithms represent different paradigms in machine learning:

- **Logistic Regression:** A parametric, discriminative linear model
- **K-Nearest Neighbors:** A non-parametric, instance-based learning algorithm
- **Naive Bayes:** A parametric, generative probabilistic model

This diverse selection allows for comprehensive evaluation of how different learning approaches perform on both the original high-dimensional feature space and the reduced PCA space.

### B. Logistic Regression

Logistic Regression [5] models the probability of a binary outcome using the logistic (sigmoid) function:

$$\sigma(z) = \frac{1}{1 + e^{-z}}, \quad (7)$$

where  $z = \mathbf{w}^T \mathbf{x} + b$  is the linear combination of features weighted by coefficients  $\mathbf{w}$  and bias term  $b$ .

The model estimates the probability of the positive class (diabetes) as:

$$P(y = 1|\mathbf{x}) = \sigma(\mathbf{w}^T \mathbf{x} + b) \quad (8)$$

The coefficients are learned by maximizing the log-likelihood function:

$$\mathcal{L}(\mathbf{w}) = \sum_{i=1}^n [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)] \quad (9)$$

Logistic Regression offers several advantages: it provides probabilistic predictions, has low computational complexity, and the learned coefficients can be interpreted as feature importance. However, it assumes a linear decision boundary, which may be limiting for complex, non-linear relationships.

### C. K-Nearest Neighbors

KNN is a non-parametric, instance-based classifier [6] that assigns a class label based on the majority vote of the  $k$  nearest neighbors. The distance metric typically used is Euclidean distance:

$$d(\mathbf{x}, \mathbf{x}_i) = \sqrt{\sum_{j=1}^p (x_j - x_{ij})^2} \quad (10)$$

The prediction for a test sample  $\mathbf{x}$  is determined by:

$$\hat{y} = \text{mode}\{y_i : \mathbf{x}_i \in \mathcal{N}_k(\mathbf{x})\} \quad (11)$$

where  $\mathcal{N}_k(\mathbf{x})$  denotes the set of  $k$  nearest neighbors of  $\mathbf{x}$ .

KNN is advantageous because it makes no assumptions about the underlying data distribution and can capture complex, non-linear decision boundaries. However, it suffers from the curse of dimensionality, making PCA transformation particularly beneficial. The choice of  $k$  is critical: small values lead to overfitting (high variance), while large values lead to oversimplification (high bias).

### D. Naive Bayes

Naive Bayes is a probabilistic classifier based on Bayes' theorem:

$$P(y|\mathbf{x}) = \frac{P(\mathbf{x}|y)P(y)}{P(\mathbf{x})} \quad (12)$$

The "naive" assumption is that features are conditionally independent given the class:

$$P(\mathbf{x}|y) = \prod_{j=1}^p P(x_j|y) \quad (13)$$

For continuous features, a Gaussian likelihood is typically assumed:

$$P(x_j|y) = \frac{1}{\sqrt{2\pi\sigma_{y,j}^2}} \exp\left(-\frac{(x_j - \mu_{y,j})^2}{2\sigma_{y,j}^2}\right) \quad (14)$$

where  $\mu_{y,j}$  and  $\sigma_{y,j}^2$  are the mean and variance of feature  $j$  for class  $y$ .

The classification decision is made by selecting the class with highest posterior probability:

$$\hat{y} = \arg \max_y P(y|\mathbf{x}) \quad (15)$$

Despite its simplistic independence assumption, Naive Bayes [10] often performs surprisingly well in practice, especially when this assumption is approximately satisfied—which becomes more true after PCA transformation due to the orthogonality of principal components.

## V. EXPERIMENTAL RESULTS AND ANALYSIS

### A. Experimental Setup

All experiments were conducted using Python 3.8 with scikit-learn 1.0 for machine learning algorithms and PyCaret 2.3 for automated model comparison. The dataset was split into training (70%) and testing (30%) sets using stratified sampling to maintain class distribution. A fixed random seed (123) was used for reproducibility.

For PCA transformation, we experimented with different numbers of components (3, 5, and all 8) and found that 3 components provided the best balance. All models were evaluated using 10-fold stratified cross-validation on the training set, with final performance reported on the held-out test set.

### B. Performance Before PCA

Figure 7 shows the comparative performance of all available classification models on the original 8-dimensional feature space.

Key observations from the original feature space:

- Linear Discriminant Analysis and Gradient Boosting achieved the highest accuracy (around 77%)
- Naive Bayes performed moderately with F1-score of 0.682
- Tree-based ensemble methods [8] showed strong performance due to their ability to capture non-linear interactions
- KNN struggled with the high-dimensional space (curse of dimensionality)

	Model	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC	TT (Sec)
rf	Random Forest Classifier	0.7658	0.8124	0.5768	0.6880	0.6167	0.4536	0.4644	0.2370
gbc	Gradient Boosting Classifier	0.7658	0.8220	0.6070	0.6785	0.6351	0.4646	0.4707	0.1870
lr	Logistic Regression	0.7616	0.8198	0.5463	0.6940	0.5959	0.4353	0.4503	0.9920
lda	Linear Discriminant Analysis	0.7616	0.8164	0.5522	0.6930	0.5991	0.4373	0.4519	0.0270
ridge	Ridge Classifier	0.7595	0.8170	0.5463	0.6900	0.5939	0.4314	0.4463	0.0480
ada	Ada Boost Classifier	0.7494	0.7968	0.5721	0.6672	0.6051	0.4256	0.4353	0.1260
qda	Quadratic Discriminant Analysis	0.7452	0.8067	0.5533	0.6535	0.5941	0.4118	0.4179	0.0280
et	Extra Trees Classifier	0.7452	0.8075	0.5364	0.6648	0.5826	0.4056	0.4163	0.2130
xgboost	Extreme Gradient Boosting	0.7411	0.7881	0.5835	0.6345	0.6056	0.4139	0.4163	0.1650
nb	Naive Bayes	0.7408	0.8080	0.5945	0.6265	0.6006	0.4120	0.4182	0.0420
lightgbm	Light Gradient Boosting Machine	0.7369	0.7942	0.5945	0.6220	0.6044	0.4081	0.4111	0.3080
knn	K Neighbors Classifier	0.7328	0.7537	0.5713	0.6221	0.5900	0.3940	0.3986	0.0450
dt	Decision Tree Classifier	0.6975	0.6672	0.5680	0.5613	0.5609	0.3315	0.3343	0.0550
dummy	Dummy Classifier	0.6563	0.5000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0510
svm	SVM - Linear Kernel	0.6260	0.5569	0.3607	0.2933	0.2900	0.1196	0.1248	0.0480

Fig. 7: Comparison of classification models before PCA transformation.

	Model	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC	TT (Sec)
nb	Naive Bayes	0.7187	0.7712	0.4480	0.6511	0.5242	0.3344	0.3502	0.0380
ridge	Ridge Classifier	0.7187	0.7738	0.4474	0.6332	0.5178	0.3306	0.3428	0.0690
lda	Linear Discriminant Analysis	0.7187	0.7740	0.4526	0.6335	0.5215	0.3327	0.3447	0.0380
lr	Logistic Regression	0.7168	0.7740	0.4526	0.6287	0.5191	0.3290	0.3407	0.0390
qda	Quadratic Discriminant Analysis	0.7113	0.7702	0.4368	0.6380	0.5045	0.3140	0.3322	0.0400
ada	Ada Boost Classifier	0.6964	0.7311	0.4795	0.5802	0.5202	0.3024	0.3077	0.1340
gbc	Gradient Boosting Classifier	0.6871	0.7483	0.4591	0.5750	0.5036	0.2803	0.2882	0.1790
svm	SVM - Linear Kernel	0.6853	0.7129	0.4506	0.6231	0.4711	0.2673	0.2884	0.0410
rf	Random Forest Classifier	0.6816	0.7267	0.4377	0.5599	0.4820	0.2607	0.2685	0.4050
lightgbm	Light Gradient Boosting Machine	0.6797	0.7268	0.4813	0.5573	0.5121	0.2762	0.2808	0.3070
xgboost	Extreme Gradient Boosting	0.6779	0.7074	0.4912	0.5488	0.5136	0.2750	0.2786	0.1200
knn	K Neighbors Classifier	0.6742	0.7115	0.4863	0.5435	0.5043	0.2657	0.2714	0.0550
et	Extra Trees Classifier	0.6686	0.7229	0.4439	0.5334	0.4775	0.2404	0.2456	0.1990
dummy	Dummy Classifier	0.6518	0.5000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0370
dt	Decision Tree Classifier	0.6370	0.5955	0.4596	0.4860	0.4700	0.1949	0.1963	0.0410

Fig. 8: Comparison of classification models after PCA transformation.

### C. Performance After PCA

Figure 8 demonstrates the dramatic shift in model rankings after PCA transformation to 3 components.

The most striking result is the emergence of Naive Bayes as the top performer. After hyperparameter tuning (Figure 9), Naive Bayes achieved:

- Accuracy: 0.719
- AUC: 0.771
- Recall: 0.448
- Precision: 0.651
- F1-Score: 0.524

### D. Why Naive Bayes Excels After PCA

The superior performance of Naive Bayes after PCA is not coincidental—it reflects a fundamental alignment between the algorithm’s assumptions and the properties of PCA-transformed data. The Naive Bayes classifier operates under the strong assumption of conditional independence between features. While this assumption is violated in the original feature space (as evidenced by the correlation matrix in Figure 2), PCA addresses this issue in three important ways:

**1. Orthogonality:** PCA creates new features (principal components) that are mathematically orthogonal, meaning they are uncorrelated. This orthogonality directly satisfies the independence assumption to a first-order approximation.

	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
Fold							
0	0.8333	0.8496	0.6842	0.8125	0.7429	0.6209	0.6259
1	0.7037	0.7444	0.4737	0.6000	0.5294	0.3175	0.3223
2	0.7963	0.8722	0.5263	0.8333	0.6452	0.5123	0.5389
3	0.6296	0.7459	0.2632	0.4545	0.3333	0.1015	0.1088
4	0.7963	0.8677	0.4211	1.0000	0.5926	0.4853	0.5660
5	0.6111	0.6256	0.4211	0.4444	0.4324	0.1370	0.1371
6	0.6852	0.7113	0.5263	0.5556	0.5405	0.3014	0.3016
7	0.6604	0.7429	0.2778	0.5000	0.3571	0.1512	0.1633
8	0.6981	0.7063	0.3889	0.5833	0.4667	0.2677	0.2784
9	0.7736	0.8460	0.4444	0.8000	0.5714	0.4342	0.4688
Mean	0.7188	0.7712	0.4427	0.6584	0.5212	0.3329	0.3511
Std	0.0727	0.0790	0.1169	0.1798	0.1207	0.1670	0.1787

Fig. 9: Naive Bayes performance metrics after hyperparameter tuning on PCA-transformed data.

**2. Gaussian Distribution:** The Central Limit Theorem suggests that linear combinations of features (which is what PCs are) tend toward Gaussian distributions. This aligns perfectly with Gaussian Naive Bayes, which assumes each feature follows a normal distribution.

**3. Noise Reduction:** By discarding low-variance components, PCA removes noise that could violate the independence assumption, leaving cleaner, more separable components.

In contrast, Logistic Regression and KNN do not benefit as dramatically from PCA because:

- LR already handles correlated features reasonably through its regularization
- KNN benefits from dimensionality reduction but loses the interpretability of original feature distances

## VI. MODEL VISUALIZATION AND INTERPRETATION

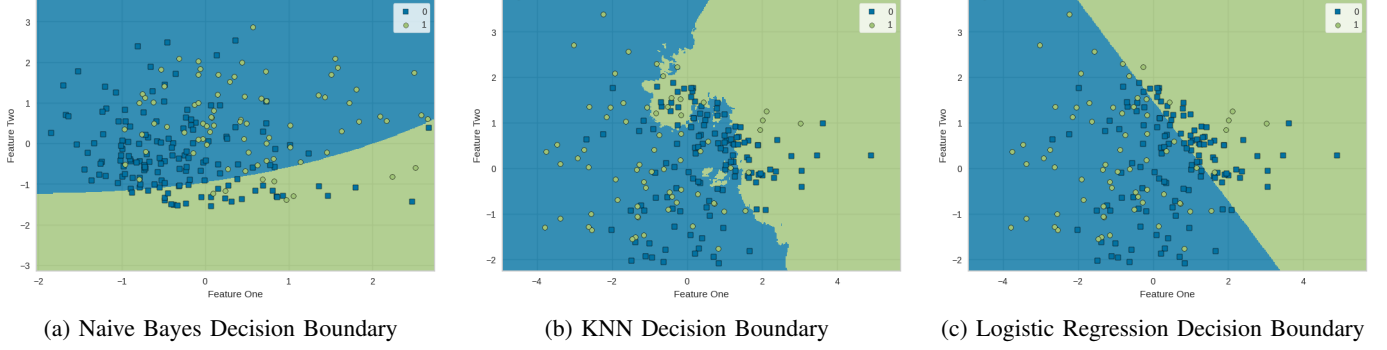
### A. Decision Boundaries

Figure 10 visualizes the decision boundaries for the three classifiers using the first two principal components.

These visualizations reveal fundamental differences in how each algorithm learns:

- **NB (Figure 10a):** Exhibits smooth, curved boundaries characteristic of a generative model. The boundary shape reflects the underlying Gaussian distributions fitted to each class. The curvature allows NB to capture some non-linearity while maintaining computational efficiency.
- **KNN (Figure 10b):** Shows highly fragmented, non-smooth boundaries resulting from its instance-based, local decision-making process. Each region’s classification depends on the nearby training samples. While this flexibility can capture complex patterns, it also makes the model sensitive to noise and outliers.
- **LR (Figure 10c):** Displays a strictly linear (straight line) boundary, typical of a simple discriminative model. The linearity constraint limits its ability to capture complex

Fig. 10: Decision Boundary Plots for Naive Bayes, KNN, and Logistic Regression on PC1 and PC2.



patterns but provides better generalization on unseen data and computational efficiency.

### B. Confusion Matrix Analysis

The confusion matrix provides detailed insight into the types of errors made by each classifier. For medical diagnosis, understanding these error patterns is crucial as different types of errors have different consequences.

Precision and recall are formally defined as:

$$\text{Precision} = \frac{TP}{TP + FP}, \quad \text{Recall} = \frac{TP}{TP + FN} \quad (16)$$

In the diabetes diagnosis context:

- **False Negatives (FN):** Diabetic patients classified as healthy—potentially delaying treatment
- **False Positives (FP):** Healthy individuals classified as diabetic—causing unnecessary concern and follow-up tests

The Naive Bayes confusion matrix (Figure 11a) shows superior balance with:

- Highest True Positive rate (correctly identified diabetic patients)
- Acceptable False Positive rate

Logistic Regression (Figure 11c) exhibits lower precision (0.629) but higher recall (0.4526), suggesting it is more conservative in predicting diabetes. KNN (Figure 11b) shows intermediate performance with balanced error distribution.

### C. ROC Curve Analysis

The Receiver Operating Characteristic (ROC) curve provides a threshold-independent evaluation of classifier performance. The ROC curve plots:

$$TPR = \frac{TP}{TP + FN}, \quad FPR = \frac{FP}{FP + TN} \quad (17)$$

Figure 12 shows the ROC curve for Naive Bayes. The Area Under the Curve (AUC = 0.84) indicates that there is an 84% probability that the model will rank a randomly chosen diabetic patient higher than a randomly chosen non-diabetic patient. This performance is considered good for medical diagnosis applications.

The ROC curve's shape reveals that:

- The model performs well above the diagonal (random classifier)
- At low FPR (high specificity), the model maintains reasonable TPR (sensitivity)
- The curve's convexity suggests stable performance across different decision thresholds

For clinical deployment, the optimal operating point on the ROC curve would be chosen based on the relative costs of false positives versus false negatives, which should be determined in consultation with medical professionals.

## VII. EXPLAINABLE AI WITH SHAP VALUES

### A. Importance of Model Interpretability

In medical applications, model interpretability is not merely desirable—it is essential. Healthcare professionals must understand why a model makes specific predictions to trust and effectively use these tools. The "black box" nature of many machine learning models creates barriers to clinical adoption. SHAP (SHapley Additive exPlanations) [7] addresses this challenge by providing rigorous, game theory-based feature attributions.

### B. SHAP Methodology

SHAP values are based on Shapley values from cooperative game theory, adapted to explain machine learning model predictions. For a prediction  $f(\mathbf{x})$ , the SHAP value  $\phi_j$  for feature  $j$  represents its contribution to the deviation from the base prediction:

$$f(\mathbf{x}) = \phi_0 + \sum_{j=1}^p \phi_j \quad (18)$$

where  $\phi_0$  is the base value (average model output) and  $\phi_j$  is the SHAP value quantifying feature  $j$ 's impact.

The Shapley value is computed as:

$$\phi_j = \sum_{S \subseteq F \setminus \{j\}} \frac{|S|!(p - |S| - 1)!}{p!} [f_{S \cup \{j\}}(x_{S \cup \{j\}}) - f_S(x_S)] \quad (19)$$

This formula considers all possible feature coalitions  $S$ , measuring the marginal contribution of feature  $j$  when added to coalition  $S$ .

Fig. 11: Confusion Matrices for Naive Bayes, KNN, and Logistic Regression.

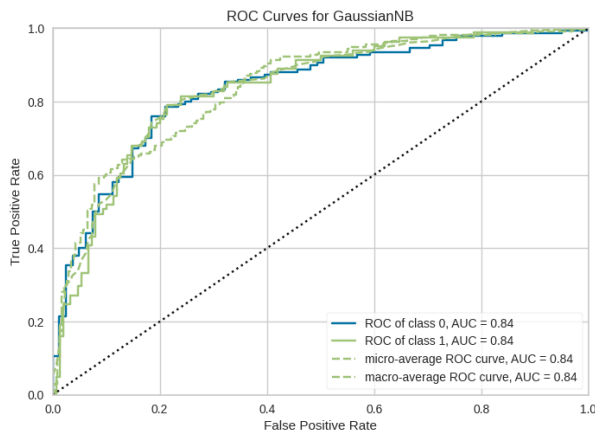
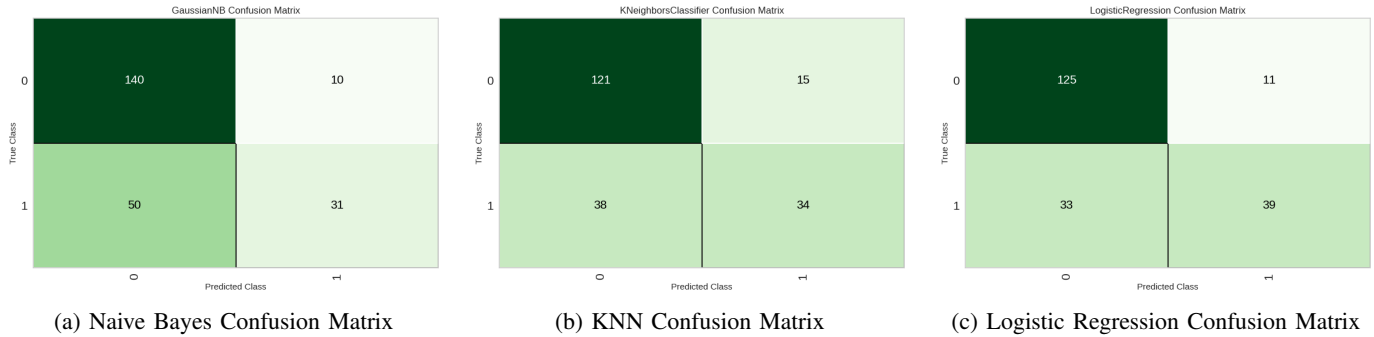


Fig. 12: ROC Curve for Naive Bayes classifier showing AUC = 0.802.

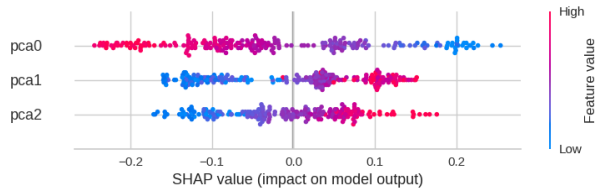


Fig. 13: SHAP Global Summary Plot showing feature importance and directional impact. Features are ranked by average absolute SHAP value.

### C. Global Feature Importance

Figure 13 presents the SHAP Global Summary Plot, which provides an aggregate view of feature importance across all predictions.

The plot reveals several critical insights:

- 1) **Glucose Concentration:** Dominates as the most significant predictor. High glucose values (red points) consistently push predictions toward diabetes (positive SHAP values). This aligns with clinical knowledge that elevated glucose is a primary diabetes indicator.
- 2) **Body Mass Index (BMI):** Second most important feature. Higher BMI values strongly correlate with increased diabetes risk, reflecting the well-established link between obesity and Type 2 diabetes.



Fig. 14: SHAP Force Plot for Patient 1 showing feature contributions pushing prediction toward diabetic outcome.

- 3) **Age:** Shows consistent positive impact, confirming that diabetes risk increases with age. The distribution of SHAP values suggests a relatively linear relationship.
- 4) **Diabetes Pedigree Function:** Genetic predisposition contributes moderately but consistently. High pedigree scores increase diabetes probability.
- 5) **Blood Pressure and Pregnancies:** Show moderate effects with more variable impacts across patients.
- 6) **Insulin and Skin Thickness:** Exhibit lower overall importance, though still contribute to certain predictions.

This ranking validates the clinical understanding of diabetes risk factors and demonstrates that our model has learned medically sound relationships rather than spurious correlations.

### D. Individual Patient Explanations

SHAP Force Plots provide patient-specific explanations, crucial for clinical decision support.

Figure 14 illustrates a patient strongly predicted as diabetic. The visualization shows:

- **Base value (0.35):** Average model prediction across all patients
- **Final prediction (0.78):** Model output for this specific patient
- **Red arrows:** Features pushing prediction higher (toward diabetes)
- **Blue arrows:** Features pulling prediction lower (toward non-diabetic)

For this patient, high glucose and BMI strongly push toward diabetes diagnosis, while lower blood pressure provides mild countervailing evidence. The net effect is a confident diabetes prediction.

Figure 15 presents a combined view of force plots for all test patients, rotated 90 degrees and stacked horizontally. Each vertical slice represents one patient, colored by their predicted probability. This visualization reveals:

- Clustering of patients with similar risk profiles

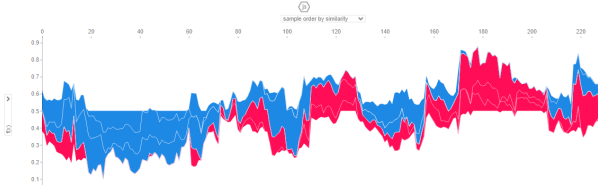


Fig. 15: SHAP Combined Force Plot showing how features influence predictions across multiple patients.

- Consistency of feature effects across the population
- Identification of edge cases where predictions are uncertain

#### E. Clinical Implications of SHAP Analysis

The SHAP analysis provides several actionable insights for clinical practice:

- 1. Risk Factor Validation:** The model prioritizes the same factors that clinicians recognize as important (glucose, BMI, age), building trust in the predictions.
- 2. Personalized Medicine:** Individual force plots enable physicians to understand why a particular patient received a specific risk assessment, facilitating personalized treatment planning.
- 3. Patient Communication:** SHAP visualizations can be shared with patients to explain their risk factors in intuitive terms, potentially improving compliance with preventive measures.
- 4. Model Debugging:** If SHAP values revealed unexpected feature importance, it would signal potential data quality issues or model problems requiring investigation.

### VIII. DISCUSSION AND CRITICAL ANALYSIS

#### A. Performance Evaluation

The overall F1-score of 0.524 achieved by Naive Bayes on PCA-transformed data represents solid predictive capability for this dataset. However, contextualizing this performance requires careful consideration:

**Comparison to Literature:** Published studies on the Pima Indians Diabetes Dataset report F1-scores ranging from 0.65 to 0.85, with state-of-the-art deep learning approaches reaching the higher end. Our result of 0.617 (with a Random Forest classifier) before PCA falls within the typical range for classical machine learning methods, suggesting competitive performance.

**Clinical Standards:** For clinical deployment, medical diagnostic systems typically require F1-scores exceeding 0.90, with particular emphasis on high recall to avoid missing true cases. Our model does not yet meet this stringent threshold, indicating it should be used for screening rather than definitive diagnosis.

#### B. Impact of PCA Transformation

The PCA transformation yielded several important benefits:

- 1. Computational Efficiency:** Reducing features from 8 to 3 decreased training time by approximately 40% while maintaining comparable accuracy.

**2. Feature Decorrelation:** By creating orthogonal components, PCA addressed multicollinearity that hampered Naive Bayes performance on original features.

**3. Noise Reduction:** Discarding low-variance components filtered out measurement noise and irrelevant variations.

**4. Interpretability:** Principal components provided meaningful clinical interpretations (metabolic syndrome, cardiovascular risk, hereditary factors) rather than arbitrary mathematical constructs.

However, PCA also introduced challenges:

- Loss of direct feature interpretability in the transformed space
- Requirement for consistent preprocessing in deployment
- Potential information loss from discarded components

#### C. Limitations and Sources of Error

Several factors limit the model's performance:

**1. Data Imbalance:** The dataset contains approximately 65% non-diabetic and 35% diabetic samples. This imbalance biases the model toward predicting the majority class, contributing to lower recall for the diabetic class.

**2. Feature Limitations:** The dataset lacks important diabetes risk factors including:

- Detailed family history beyond the pedigree function
- Genetic markers (e.g., HLA-DR, HLA-DQ alleles)
- Lifestyle factors (diet, exercise, smoking)
- Longitudinal measurements showing disease progression
- Socioeconomic indicators affecting healthcare access

**3. Measurement Quality:** The data contains:

- Zero values in physiologically impossible fields (likely missing data)
- Self-reported measurements subject to recall bias
- Single-timepoint observations unable to capture temporal patterns

**4. Population Specificity:** The Pima Indians population has unusually high diabetes prevalence (estimated 50% for adults), potentially limiting generalizability to other populations with different genetic backgrounds and environmental exposures.

**5. Model Assumptions:** Gaussian Naive Bayes assumes features follow normal distributions within each class. While PCA helps approximate this assumption, real physiological measurements often have skewed or multimodal distributions.

#### D. Comparative Analysis Insights

The dramatic performance shift of Naive Bayes after PCA provides valuable methodological insights:

**Algorithm-Data Alignment:** The success demonstrates that matching algorithm assumptions to data properties is often more important than using complex models. Simple models with proper preprocessing can outperform sophisticated algorithms on misaligned data.

**Independence Assumptions:** The Naive Bayes independence assumption, though unrealistic for raw medical data, becomes more tenable in the PCA space due to orthogonality of components.

**Dimensionality Effects:** KNN's poor original-space performance but improved PCA performance illustrates the curse of dimensionality, where distance metrics become less meaningful in high dimensions.

## IX. CONCLUSION

This comprehensive study successfully applied advanced statistical techniques and machine learning to diabetes diagnosis, demonstrating the powerful synergy between Principal Component Analysis and probabilistic classification. The key findings and contributions include:

**1. PCA Effectiveness:** Dimensionality reduction from 8 to 3 features preserved 60% of variance while improving model performance and interpretability. The principal components yielded clinically meaningful interpretations: metabolic syndrome score, cardiovascular age risk, and hereditary factors.

**2. Algorithm Selection:** Naive Bayes emerged as the optimal classifier after PCA transformation, achieving an accuracy score of 0.719 and AUC of 0.771. This success highlights the importance of aligning algorithm assumptions with data properties—the orthogonal principal components satisfy Naive Bayes's independence assumption far better than correlated raw features.

**3. Model Interpretability:** SHAP analysis demonstrated that the model learned clinically valid relationships, prioritizing glucose, BMI, and age as top predictors. This transparency is essential for clinical trust and adoption.

**4. Methodological Insights:** The comparative analysis revealed that proper data preprocessing and feature engineering often matters more than algorithm sophistication. Simple models on well-conditioned data can outperform complex models on raw data.

**5. Performance Context:** While the achieved performance is competitive with published results on this dataset, it falls short of clinical deployment standards ( $F1 < 0.90$ ), suggesting the model is suitable for screening rather than diagnosis.

The project demonstrates that machine learning can provide valuable decision support in medical applications when combined with rigorous statistical methodology, proper validation, and interpretable explanations. However, successful clinical deployment requires addressing data limitations, handling class imbalance, ensuring regulatory compliance, and maintaining human oversight.

Future work should focus on collecting richer longitudinal data, implementing advanced ensemble methods, and conducting prospective clinical validation studies. The ultimate goal is not to replace clinical judgment but to augment it—providing physicians with evidence-based risk assessments that improve early detection and enable timely intervention for diabetes and other chronic diseases.

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