EXPLORING DIABETES: INSIGHTS INTO LIFESTYLE AND HEALTH RISKS

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I. INTRODUCTION

Diabetes is set to become a major global health problem, and it currently affects many lives worldwide, irrespective of region or socio-economic status. This chronic condition does not only strain the suffering individuals but also puts heavy pressure on healthcare systems due to its rapidly increasing occurrence around the world. The rise of type 2 diabetes is also fueled by lifestyle factors such as unhealthy eating habits, reductions in physical activity, and increase rates of obesitys, particularly with greater urbanization. That is driving a demand for major public health efforts to tackle the risk factors associated with non-communicable diseases (NCDs). The report is an investigation into how our lifestyle choices contribute to diabetes and aims at offerings simple tips that could help reduce this increase. We aim to foster policies and practicess that produce better health outcomes and address the global burden of diabetes using underlyings trends in behavior as an analytic approach.

II. BACKGROUND AND SIGNIFICANCE

Diabetes is one of the fastest-growing diseases on this planet, and doctors are really concerned about it because diabetes can cause complications in very important organs such as the heart, kidneys, eyes, etc. These problems are even significantly greater in economically challenged geographies, where good preventative efforts have rapidly become a must. As you may be aware, diabetes usually strikes in early childhood (thanks to less formal education on well-being), and it is simply another chaotic result of modern livingg. We work in jobs that favor poor postures, and our urban centers make shorter grocery shopping trips the easy choice over walks. The settings relevant to health generally provide access to processed food and have no space for physical exercise, both magnified by the the evolving digitalization and automatic lifestyle trends.

The impact of diabetes constitutes a huge economic cost, which includes lifelong medical expenses, medications, and opportunity costs from lost consumption or leisure due to poor health. BMI, blood pressure, and cholesterol levels are all crucial health indicators associated with a higher risk of diabetes, indicating the importance of early intervention. The project has to go beyond data analysis – we are talking about real human lives here. With a predictive model based on both lifestyle and health data, we want to identify individuals with an elevated risk of diabetes sat earlier stages. The goal is to enable preventative healthcare measures that cans delay the onset of diabetes or aid in better recovery.

This initiative aims to impact not only individual health decisions but also community planning and corporate policies, creating environments that make it easier for people to engage in physical activity or access nutritious foods. This is a bold move toward reducing the global diabetes burden with proven, informed, data-driven health strategies.

III. PROJECT POTENTIAL

This is a significant project as it can learn from the problem domain of diabetes management and prevention. This research aims to intervene early, possibly preventing type 2 diabetes among at-risk individuals by creating a predictive model using lifestyle and medical metrics to forecast the likelihood of diagnosis in time. The ability to predict is critical for several reasons:

- **Creating Healthy Communities**: The insights from our model can inform policies that redesigns cities to promote healthy living, ensuring easier accesss to nutritious food and opportunities for physical activity.

- **Technology as the New Frontier:** This project is not just about managing diabetes; it'ss utilizing AI and machine learning to revolutionize healthcare, making it smarter and more effective.

- **Decisions with Confidence:** Healthcare professionals are empowered to make evidence-based decisions using a clear strategy blueprint.

- **Global Impact**: Diabetes knowss no borders, and neither do the solutions we're creating. This project could serve as a model for global replication, providing significant public health benefits worldwide.

- **Care Tailored to the Individual:** Personalized healthcare is at the core of this work, creating treatment and prevention plans that are as unique as individuals, leading to higher engagement and adherence.

- **Sharing Knowledge, Shaping Futures:** By recognizing and analyzing diabetes trends, we can implement health campaigns that transform millions of lives globally.

- **Improving Quality of Life:** By stopping diabetes before it starts, we can improve life quality and help people fulfill their lives without the burden of complications.

- **Early Prediction, Early Intervention:** Early prediction enables us to re-engineer health outcomes and emphasize the need for proactive healthcare.

- **Economic Sense:** Early intervention saves lives and money, preventing costly treatments by catching diabetes in its early stages.

- **Making Health Tools More Available:** Our predictive model can deliver critical health monitoring to more people, especially in areas with limited healthcare resources.

- **Redesigning for Health:** By understanding how the environment affects health, we can make the healthy choice the easiest one, leading to better lives for everyone.

IV. DATASET

The Diabetes dataset consists of medical and demographic information from patients, including their diabetes status (positive or negative). It has 1,000,001 rows and 9 columns, with variables such as age, gender, BMI, hypertension, heart disease, smoking history, HbA1c level, and blood glucose level. This dataset is useful for developing machine learning models helps at predicting diabetes based on patient history and demographics. Healthcare professionals can use these models to identify at-risk individuals and create personalized treatment. Additionally, researchers can use this data to investigate the correlations between medical and demographic factors and the risk of developing diabetes.

URL: **https://www.kaggle.com/datasets/iammustafatz/diabetes-prediction-dataset**

PHASE 1

V. DATA CLEANING

Removing Duplicates

We identified and eliminated duplicate records. Removing redundant entries is critical to prevent data repetition, which could distort the analysis and compromise the accuracy of insights by introducing bias.

Handling Missing Values

We addressed missing data by removing records containing key variables gaps, ensuring the dataset maintained high integrity. Complete and clean datasets are crucial for reliable analysis, as missing values can skew predictive models and lead to misleading results.

Trimming and Standardization

We standardized the text entries in the 'gender' and 'smoking_history' columns by eliminating extra spaces and ensuring consistent formatting.
Inconsistent formatting may seem trivial, but even small discrepancies can lead to misclassification or faulty interpretation during analysis, undermining accuracy.

Data Type Conversions

We converted categorical variables, such as 'gender' and 'smoking_history,' into numerical formats via label encoding. Why It Matters**:** Machine learning algorithms typically require numerical input, so converting categorical data allows us to incorporate these variables into statistical models and enhance analytical depth.

Feature Engineering

Feature engineering helped us enrich the dataset by creating new variables and refining existing ones to capture deeper patterns and relationships.

Age Group Categorization

We segmented age into meaningful categories that correspond to various life stages.This allows us to analyze how diabetes risk varies by demographic, improving our ability to detect trends across age groups.

BMI Categorization

We classified BMI values into health-based categories. Categorizing BMI helps us visualize its influence on diabetes risk, enabling a more structured analysis of body weight's role in health outcomes.

InteractionFeatures

We created features that captured the combined effects of multiple conditions (e.g., hypertension and heart disease) on diabetes risk.These interaction terms allow us to examine how comorbidities interplay to influence risk, revealing more complex health relationships.

HealthRiskScore

We computed a composite health risk score based on multiple health indicators.
This score serves as an integrated metric for identifying individuals at high risk, and facilitating targeted prevention strategies.

Outlier Management: Ensuring Balanced Analysis

Managing outliers is crucial to maintaining balanced and reliable analysis by preventing extreme values from distorting our results.

Identification&Assessment

We used statistical methods and visualizations to detect outliers, assessing whether they represented data entry errors or rare but significant cases.
Proper identification ensures that we capture real-world variability without being misled by extreme values that don't represent typical data points.

Handling Techniques

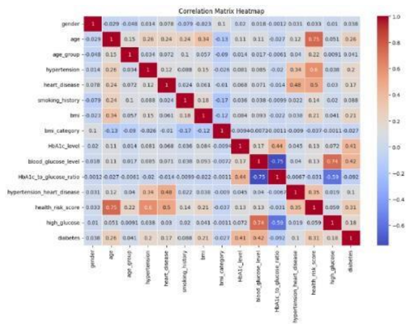
Depending on the context, we either removed, transformed, or imputed outliers to minimize their impact on the analysis. This ensures that our models remain robust and generalizable without being unduly influenced by anomalous data.

Validation

After addressing outliers, we validated our preprocessing techniques using cross-validation to confirm their positive effect on model performance.Validation is essential to verify that our data preparation process leads to improved model accuracy and predictive power.

VI. EXPLORATORY DATA ANALYSIS

1. CORRELATION BETWEEN COLUMNS



Age and Health Risk Score: Our analysis identifies a robust positive correlation between age and the health risk score, suggesting that cumulative health risks increase with age. This is a crucial consideration for managing health outcomes and designing preventative strategies, particularly in older populations.

Hypertension and Health Risk Score: Hypertension is strongly associated with higher health risk scores. This relationship reinforces the importance of addressing hypertension as a critical factor in managing overall health risks, especially given its role in exacerbating conditions like diabetes and cardiovascular diseases.

Notable Negative Relationship

Blood Glucose Level and HbA1c to Glucose Ratio: A strong negative correlation between blood glucose levels and the HbA1c to glucose ratio was observed. This may indicate that higher immediate glucose levels are often not yet reflected in HbA1c measurements, which assess longer-term glucose control. These findings could point to short-term glucose spikes and their limited immediate impact on HbA1c levels.

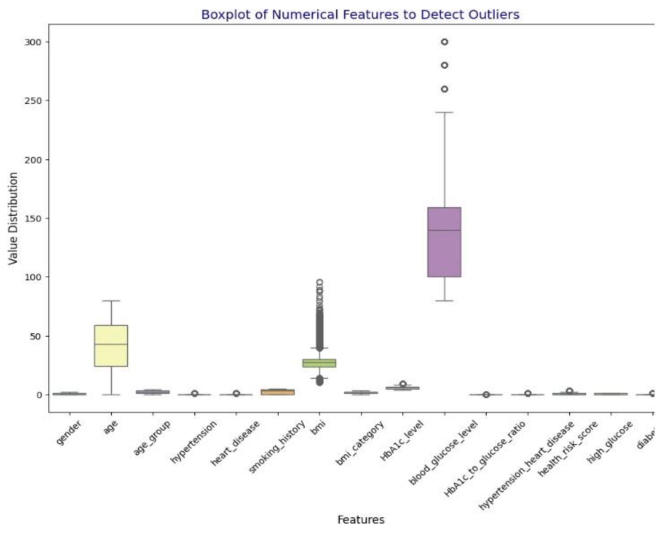
Key Risk Indicators

Health Risk Score Dynamics: While age and hypertension show a strong correlation with the health risk score, the relationship between blood glucose levels and the health risk score is moderate. This suggests that while blood glucose is influential, it may not dominate the overall health risk score as much as factors like age and hypertension.

Diabetes and Blood Glucose Level: A significant positive correlation exists between higher blood glucose levels and the likelihood of diabetes, highlighting the importance of regular glucose monitoring as a key factor in diabetes risk management.

Diabetes and HbA1c Level: Elevated sHbA1c levels are strongly associated with diabetes. This reinforces the clinical value of HbA1c as a marker for long-term glucose control and a reliable indicator for diagnosing and managing diabetes.

2. **Finding the Outliers present in all the columns**



Geographic Variation: Analyzing data by region reveals stark geographic disparities, particularly in metrics like BMI. Regions with limited access to rsecreational facilities or healthier food choices report higher instances of extreme BMI values, suggesting regional inequalities that could inform publsic health policies.

Temporal Trends in Outliers: Observing how outliers in blood glucose levels and HbA1c fluctuate over time points to possible seasonal variations or changes in data collection practices. These trends are crucial for understanding the long-term effects of patient care and the efficacy of healthcare interventions.

Detailed Feature Analysis

Diverse Data Range: The numerical features in the dataset, such as age, HbA1c level, and BMI, show wide variability. Age, in particular, spans a broad range, reflecting a diverse population sample, which is vital for robust and inclusive risk assessments.

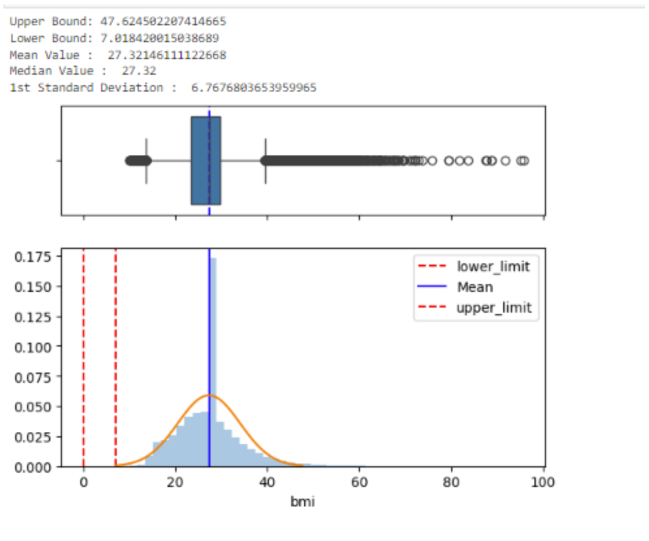
Outlier Detection: Outliers in variables like BMI and HbA1c levels may indicate either measurement errors or genuine extremes in patient health. In particular, extreme HbA1c levels could highlight critical cases in diabetes management requiring further investigation.

Interactions and Subgroup Dynamics

Interaction Effects: The interplay between features, such as hypertension and BMI or age and diabetes, reveals complex relationships influencing diabetes risk. For instance, high BMI presents a compounded risk in older adults or individuals managing hypertension, suggesting more severe health outcomes in these subgroups.

Subgroup Analysis: Subgroup analysis (e.g., by age, gender, or existing health conditions) reveals nuancsed patterns that broad statistical models might overlook. Notably, the impact of risk factors like hypertension and BMI varies across different demographic groups, offering insights for personalized interventions and public health strategies.

3. OUTLIERS PRESENT IN BMI FEATURE



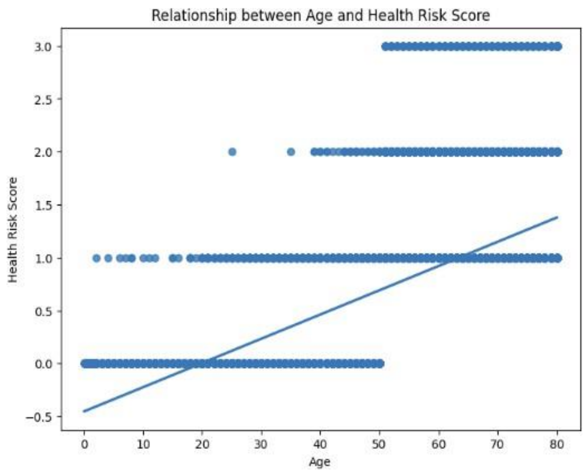
```
Upper Bound: 47.624502207414665
Lower Bound: 7.018420015038689
Mean Value :  27.32146111122668
Median Value :  27.32
1st Standard Deviation :  6.7676803653959965
```

The boxplot quickly shows how the datas is spread out, highlighting central points like the median and any outliers. Below it, the histogram breaks down BMI values into groups, helping us ssee the shape of the data—whether it's balanced, skewed, or has multiple peaks.

The normal curve overlaid on the histogram helps us compare the actual BMI distribution to an ideal one, pointing out any major deviationss. Key statistics like the mean, median, and

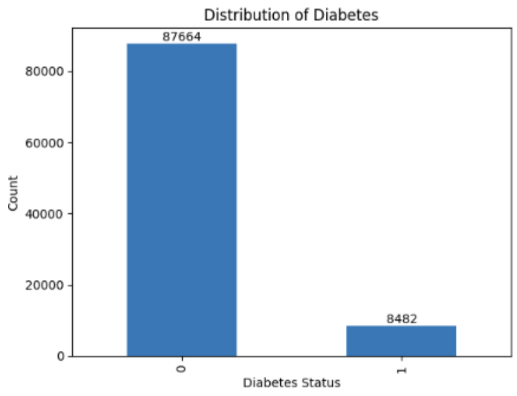
standard deviation are also displayed, giving a sense of the average BMI and how much values vary.
Bounds marking three standard deviations from the mean highlight potential outliers. Comparisng the mean and median helps assess the data's skewness, showing if there’s an imbalance that might affect our interpretation of the population's health.

4. ANALYSIS OF AGE AND HEALTH RISK SCORE CORRELATION



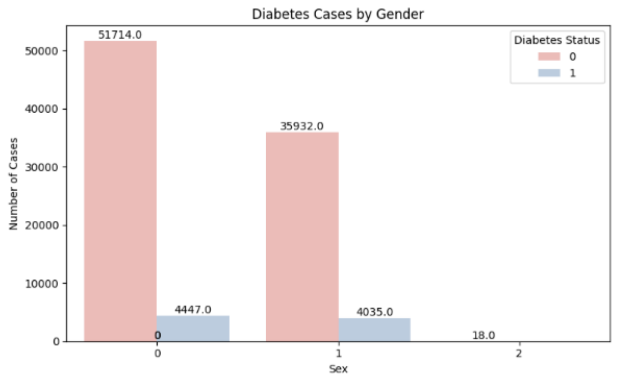
Increasing Risks with Age: The graph shows that health risk scores tend to rise as people age, reflecting the common understanding that health issues accumulate over time.
Categorized Risk Levels: The scores fsall into distinct categories—like 0, 1, 2, and 3—indicating that health risks are grouped rather than measured on a continuous scale. This segmentation makes it easier to understand and manage health status.
Higher Risks for the Elderly: People over sixty often have the highest rissk scores, highlighting their increased vulnerability to serious health problems.
Variability in Younger People: Younger individuals show more varied health risk scores, likely due to lifestyle, genetics, or early health conditions, suggesting their health outcomes can bse quite unpredictable.

5. DISTRIBUTION OF TARGET VARIABLE



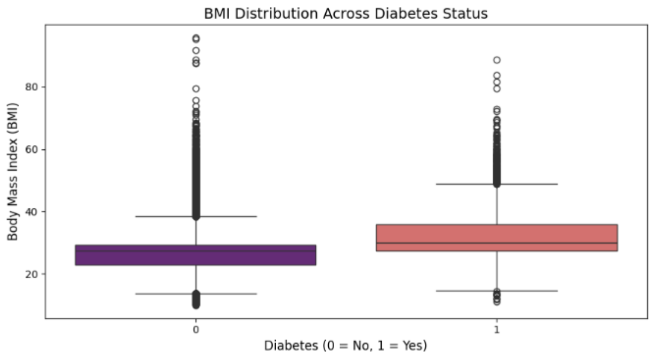
The bar chart shows that the majority of individuals in the dataset have no diabetes (s0), with a count of 87,664. A smaller number of individuals have diabetes (1), with a count of 8,482.

6. ANALYSIS OF DIABETES CASES BY GENDER



Diabetes by Gender Overview: Most participants, both male and female, do snot have diabetes, as shown by the much taller pink bars for both genders—51,714 males and 35,932 females without diabetes
Diabetes Prevalence by Gender: Males have slightly more diabetes cases (4,447) compared to females (4,035), showing a modest difference in prevalence.
Data Anomasly Notice: There’s an unusual "2" category under gender, with only 18 cases. This might be a data error or could represent a non-binary/unspecified group, which needs further rseview for accuracy and inclusivity.

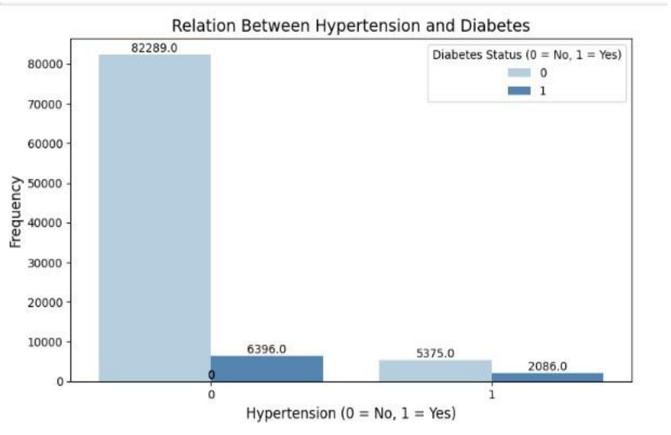
7. BMI DISTRIBUTION ACROSS DIABETES STATUS



BMI Medians and Diabetes: The boxplot shows that individuals with diabetes tend to have a higher median BMI compared to those without. This aligns with the known link between higher BMI and increased diabetes risk.
Outliers and Variability: Both diabetic and non-diabetic groups have numerous outliers, with BMI values that stray from the typical range. Diabetic individuals show more variability in BMI, suggesting that while higher BMI is common, there is still wide variation among those with diabetes.
Overlap in BMI: There is significant overlap in BMI ranges between both groups, indicating that while a higher BMI is

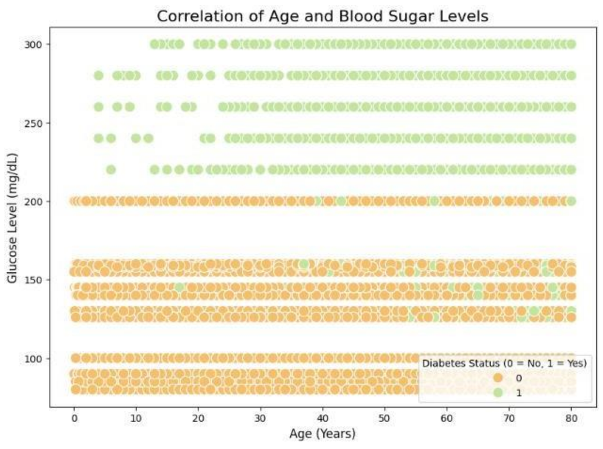
often linked to diabetes, it's not a clear-cut predictor—many without diabetes also have higher BMIs.

8. RELATION BETWEEN HYPERTENSION AND DIABETES



Majority Without Hypertension or Diabetes: The largest group, totaling 82,289 people, is free from both hypertension and diabetes—a positive sign of health for a significant portion of the population.
Hypertension and Diabetes Together: There are 2,086 individuals with both conditions, highlighting the need for extra care, as managing both can be complex.
Hypertension Only: Around 5,375 individuals have hypertension but not diabetes, showing that hypertension is a significant health issue by itself, requiring dedicated management.
Diabetes Only: Of those with diabetes, 6,396 do not have hypertension, suggesting that many people with diabetes aren't dealing with added hypertension risks. This emphasizes the need for personalized treatment rather than a one-size-fits-all approach.

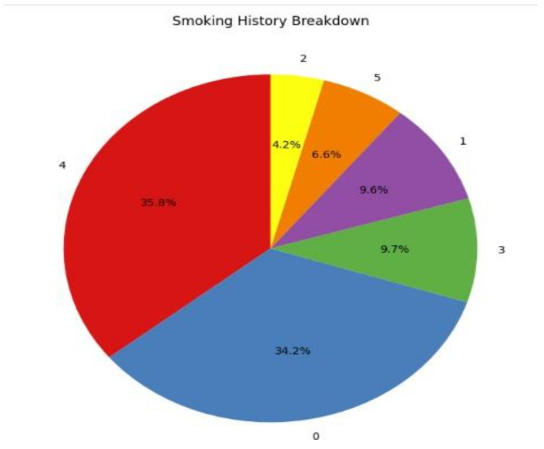
9. CORRELATION OF AGE AND BLOOD SUGAR LEVELS



Glucose Level Clusters: The visualization shows clusters around 100, 150, and 200 mg/dL. Diabetic individuals (green) mainly have glucose levels above 150 mg/dL, while non-diabetics (orange) are mostly below this level, reinforcing the link between higher glucose and diabetes

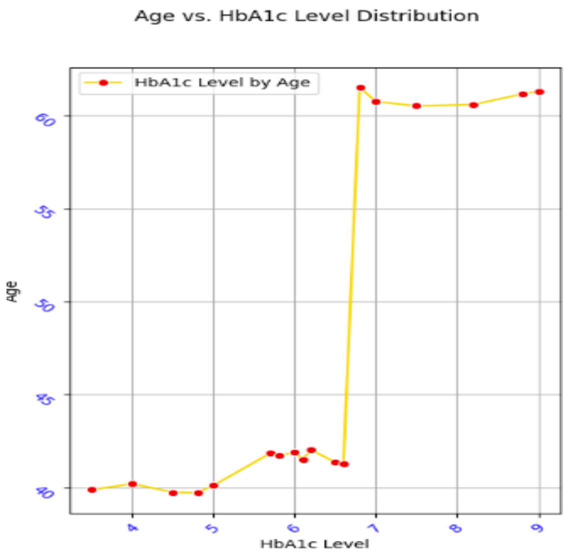
Age Range in Glucose Levels: The scatter plot covers a wide age range for both diabetic and non-diabetic individuals, from young to elderly. This suggests that while age affects health, it doesn't directly predict glucose levels—diabetes is influenced by more than just age.
Elevated Glucose in Diabetics: Diabetics often have glucose levels between 200-300 mg/dL, whereas non-diabetics stay mostly below 150 mg/dL. This clear visual difference highlights the importance of glucose monitoring in managing diabetes.

10. SMOKING HISTORY BREAKDOWN



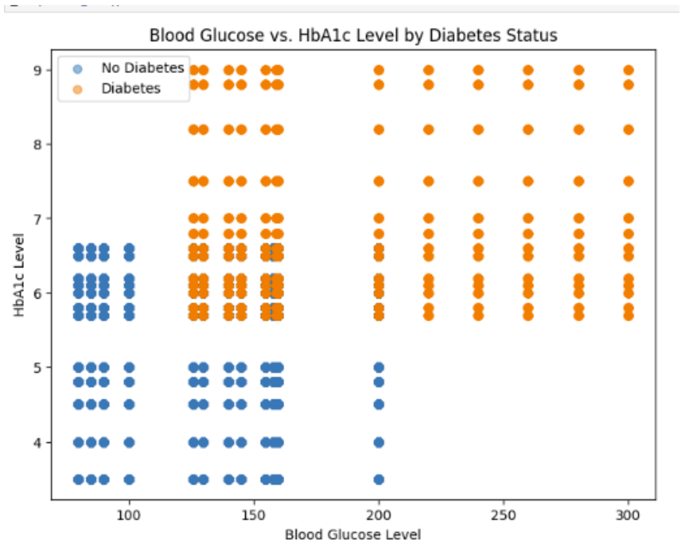
1. Category 4 (Red):
Represents the largest group, making up 35.8% of the total.
2. Category 0 (Blue):
The second-largest portion, accounting for 34.2%.
3. Category 3 (Green):
Covers 9.7% of the population.
4. Category 1 (Purple):
Comprises 9.6% of the total.
5. Category 5 (Orange):
Makes up 6.6% of the data.
6. Category 2 (Yellow):
The smallest group, contributing 4.2% to the whole.

11. AGE VS HBA1C DISTRIBUTION



Range of HbA1c Levels: The graph mostly shows HbA1c levels between 4 and 7, with some higher outliers. These higher points suggest cases of poor blood sugar control.
Middle-Aged Focus: Most ages cluster between 40 and 60, a key period for type 2 diabetes onset. This makes the data particularly relevant for understanding diabetes risk in middle-aged individuals.
Stable HbA1c Levels: HbA1c levels between ages 40-50 show little variation, indicating relatively stable glucose management during this period.
Spike at 7: There's a notable spike around HbA1c levels of 7, which could reflect increasessd medical intervention or lifestyle changes, helping stabilize levels after reaching this threshold.

12. BLOOD GLUCOSE VS HBA1C LEVEL BY DIABETES STATUS



Blood Glucose and HbA1c Overview:

- **Blood Glucose Level (x-axis):** Ranges from 50 to 300, showing current sugar levels which can change throughout the day.
- **HbA1c Level (y-axis):** Ranges from 4 to 9, representing average glucose levels over the past few months.

Visual Coding:

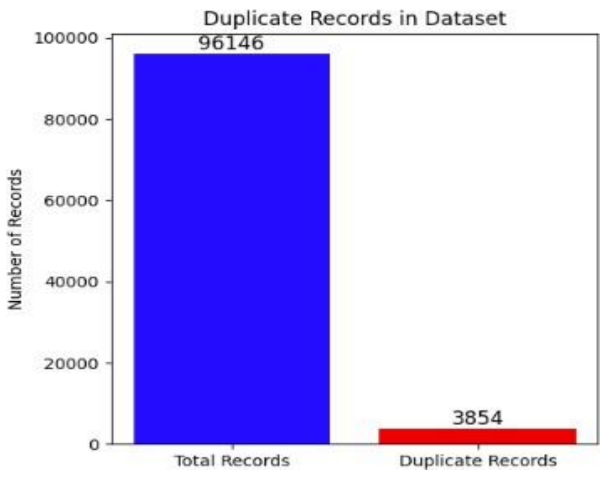
- **Blue Dots:** Non-diabetic individuals, indicating stable blood sugar levelss.
- **Orange Dots:** Diabetic individuals, highlighting a need for focused health management.

Key Observations:

- **Non-Diabeticss:** Mostly clustered with glucose levels of 100-150 and HbA1c between 4 and 6, indicating good control.
- **Diabetics:** Tend to have glucose between 150-300 and HbA1c from 6 to 9, reflecting challenges in managing glucose.
- **Overlap:** There's some overlap in HbA1c levels between 6-7, but higher glucose levels are generally linked with diabetes.

Trends:
The clear separation in the plot indicates that higher HbA1c and glucose levels strongly correlate with diabetes, while lower levels suggest effective glucose control.

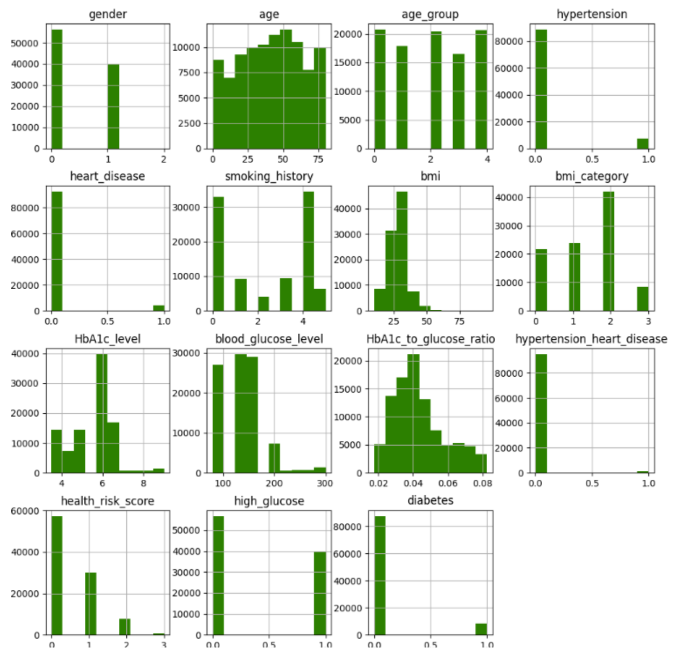
13. ANALYSIS OF DUPLICATE RECORDS IN DATASET



This bar chart explains that the dataset contains a significant number of duplicate records, accounting for approximately 3.85% of the total data points (3,854 out of 100,000). Removing thesse duplicates can substantially enhance data processing efficiency and optimize model performance.

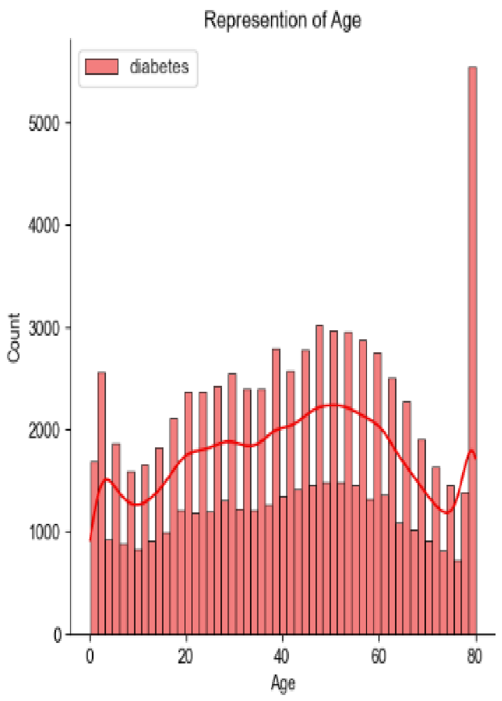
Dropping duplictes can:
1. Reduce data noise and improve data quality
2. Decrease computational resources required for processing
3. Enhance model accuracy and reliability
4. Improve overall data analysis and insights

14. HISTOGRAM PLOTS



Demographics: The data mostly covers adults aged 30 to 70, indicating a focus on a working-age population, with fewer young adults and seniors.
Hypertension: Nearly 90,000 individuals do not have hypertension, showing generally good cardiovascular health, with only a small portion affecsted.
Heart Disease: Heart disease is rare in this group, suggesting positive heart health, likely due to a healthy lifestyle or effective medical care.
BMI Trends: Most individuals have a BMI between 20 and 40, indicating that they range from normal to moderately overweight, with few outliers, suggesting good overall health.
HbA1c Levels: HbA1c mostly ranges from 5 to 7, showing good glucose control, especially around the 5-6 range, typical of effective diabetes management or non-diabetic individuals.s
Blood Glucose: Most have blood glucose between 100 and 200 mg/dL, with few extreme high levels, suggesting good control over blood sugar in the population.
Diabetes Prevalence: The majority of people do not have diabetes, which is a positive health indicators though diabetes still needs ongoing public health attention.

15. REPRESENTATION OF AGE



The bar and line graph illustrates the age distribution within the dataset, showing individuals between the ages of 20 and 70, with a peak in the 50 to 60 age range. This shows a heavily populated by middle-aged adults, potentially reflective of an active workforce and familial responsibilities.

PHASE 2

VII.MODEL TRAINING AND TUNING

Naive Bayes (GaussianNB): Naive Bayes was picked because of its computational efficiency and its ability to handle high-dimensional data well. This makes it a good option for an initial classification model. The assumption that all features are independent keeps the model simple, which allows for quick testing of baseline performance, especially with a moderately large dataset. Even though it's simple, it can give us an idea of whether we need more advanced models to capture relationships in the data.

K-Nearest Neighbors (KNN): KNN was chosen to see how well it can pick up non-linear patterns in the data. It's a learning algorithm that can detect local structures, which other linear models might miss. We selected KNN because we thought clustering patterns in the data might help distinguish between different classes. We also tuned the number of neighbors to improve its performance and reduce classification errors.

Support Vector Machine (SVM): SVM was included because it's good at finding the best boundaries to separate data, especially when working with high-dimensional data. The "kernel trick" allows SVM to handle non-linear relationships effectively, which was crucial for this dataset. We wanted to see if it could create a clear margin between diabetic and non-diabetic cases, reducing misclassification.

Logistic Regression: Logistic Regression was chosen because it's simple and easy to interpret. As a probabilistic model, it helps us understand how each feature contributes to predicting the target variable. This is useful for interpreting results. We selected it as a baseline model because it's straightforward to train and works well with binary classification tasks. We adjusted the model, like increasing the maximum number of iterations, to ensure it worked properly.

Random Forest Classifier: Random Forest was chosen because it's reliable and handles non-linearity well. It's especially good at dealing with interactions between variables. Since it combines multiple decision trees, it helps prevent overfitting and provides good insights into feature importance. We tuned the parameters, like the number of trees and their depth, to get the best possible predictive power.

Gradient Boosting Classifier: Gradient Boosting was selected for its ability to gradually improve the model's performance by focusing on the mistakes made by earlier models. Its boosting method creates a strong ensemble model that captures complex patterns in the data. We chose Gradient Boosting to see if concentrating on errors could boost the model's precision and recall, particularly for identifying positive cases.

WORK DONE TO TUNE/TRAIN MODELS

Naive Bayes (GaussianNB): For Naive Bayes, we found that minimal tuning was necessary because the model assumes feature independence by default. Our main focus was on pre-processing the data to ensure it fit well into the probabilistic framework of the model, allowing us to achieve optimal performance without additional complexity.

K-Nearest Neighbors (KNN): We tested different values for 'k' (number of neighbors) and used cross-validation to find the optimal value. We also tuned the distance metric, comparing Euclidean and Manhattan distances to see which provided better predictive accuracy. Ultimately, we selected a 'k' value that balanced bias and variance effectively.

Support Vector Machine (SVM): SVM required us to tune the kernel type (linear, polynomial, or radial basis function) to determine which one captured the decision boundary most effectively. We also adjusted the regularization parameter (C) to balance the trade-off between maximizing the margin and minimizing classification errors.

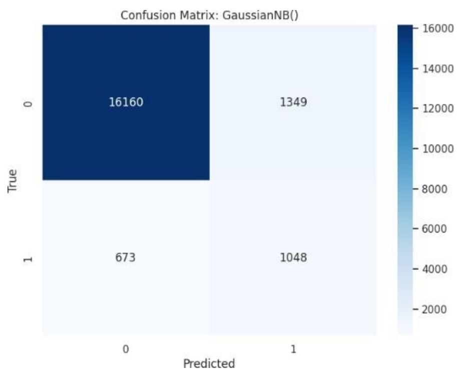
Logistic Regression: Our primary tuning for Logistic Regression involved adjusting the maximum number of iterations to ensure the model converged properly without overfitting. We also fine-tuned the regularization strength to improve generalizability while maintaining solid classification performance.

Random Forest Classifier: For Random Forest, we adjusted the number of estimators (trees) and the maximum depth to strike a balance between bias and variance. In addition, we tweaked other hyperparameters like the minimum number of samples per leaf and the bootstrap settings to enhance model stability and reduce overfitting.

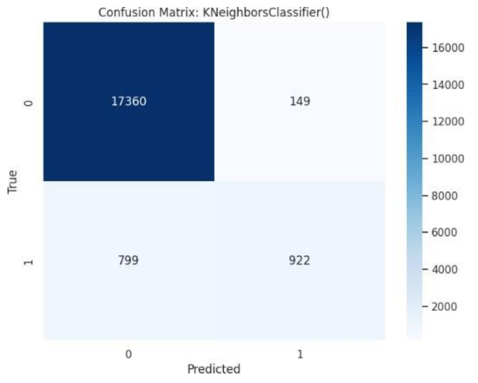
Gradient Boosting Classifier: For Gradient Boosting, we fine-tuned several hyperparameters, including the learning rate, number of estimators, and maximum depth. We conducted a grid search combined with cross-validation to identify the best combination of parameters, which helped us achieve the highest accuracy while avoiding overfitting.

EFFECTIVENESS OF EACH ALGORITHM

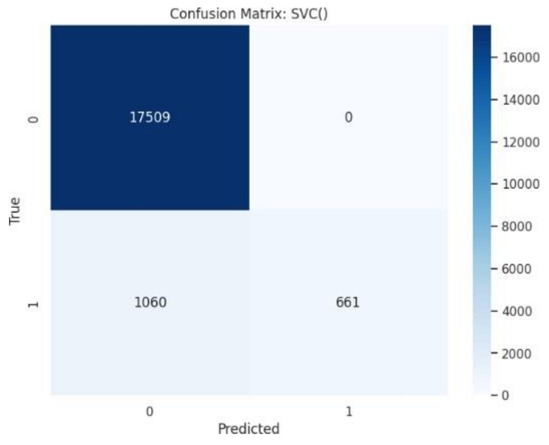
Naive Bayes (GaussianNB): The model achieved an accuracy of 89.49%, which provided a reasonable baseline but fell short in distinguishings diabetic cases effectively. The precision for the positive class was 0.44, and recall was 0.61, indicating a high number of false negatives. This result suggests that Naive Bayes was limited , especially given its assumptions about feature independence.



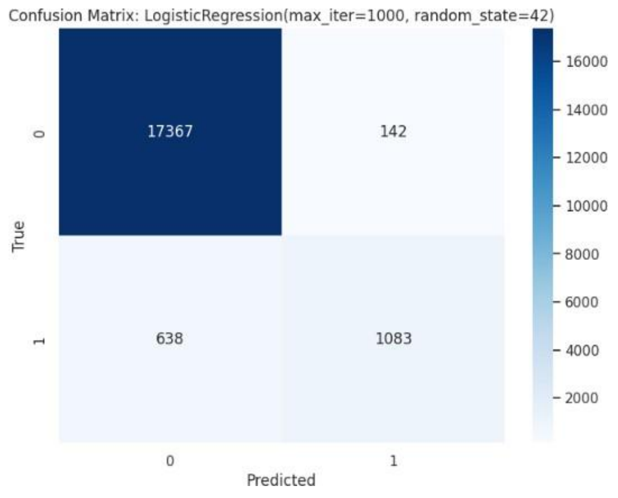
K-Nearest Neighbors (KNN): KNN achieved an accuracy of 95.07%. The precision and recall for diabetic cases were 0.86 and 0.54, respectively. It performed well for the majority class but had lower recall, which indicated challenges in capturing all true positives. This suggests that while KNN captured some non-linear patterns, it could not do class imbalance and predicting the minority class.



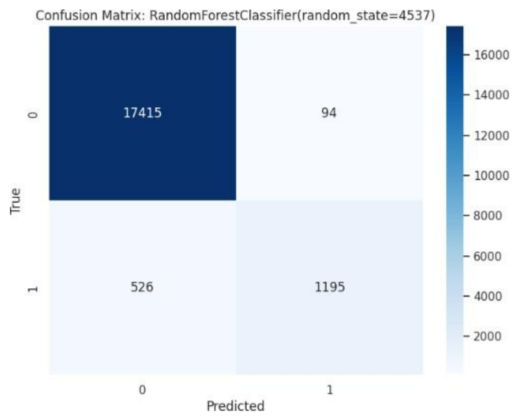
Support Vector Machine (SVM): The model reached an accuracy of 94.49%, with a high precision of 1.00 for the positive class but a low recall of 0.38. This means that while SVM was precise in its predictions, it missed many true positive cases, resulting in a high false negative rate. SVM's effectiveness was lowered by an inability to generalize well to all positive examples, suggesting a potential need for more balanced class representation.



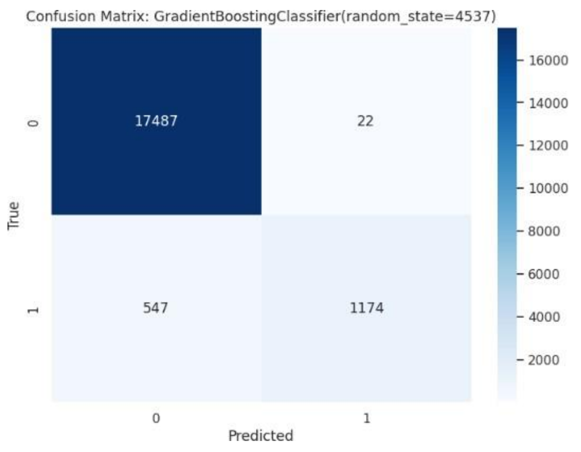
Logistic Regression: Logistic Regression achieved an accuracy of 95.94%, with a precision of 0.88 and recall of 0.63 for the positive class. This model effectively balanced bias and variance and provided interpretable feature coefficients, which helped in understanding the impact of each predictor. It performed significantly better in terms of recall compared to SVM and Naive Bayes, showing its utility for identifying diabetic cases.



Random Forest Classifier: Random Forest reached an accuracy of 96.78%, with precision and recall for diabetic cases at 0.93 and 0.69, respectively. It provided a reliable classification, especially with good recall, meaning fewer true positives were missed. The model's ensemble nature helped reduce overfitting and provided valuable insights into feature importance, making it a strong candidate for practical implementation.



Gradient Boosting Classifier: Gradient Boosting achieved the highest accuracy of 97.04%, with a precision of 0.98 and a recall of 0.68 for diabetic cases. It demonstrated the ability to accurately classify positive cases while maintaining a high overall accuracy. The iterative nature of Gradient Boosting allowed for continuous improvement in model performance, making it the most effective at capturing subtle patterns and managing misclassifications in the dataset.



INTELLIGENCE GAINED FROM APPLICATION

Naive Bayes (GaussianNB): The main insight from Naive Bayes was that its assumption of feature independence limited its ability to correctly classify diabetic cases. This showed us the need for more advanced models that can handle the relationships between features more effectively.

K-Nearest Neighbors (KNN): KNN highlighted the importance of looking at how data points relate to their neighbors. However, the model struggled with identifying diabetic cases, indicating that we might need to balance the dataset better or use different distance measures to improve predictions for these cases.

Support Vector Machine (SVM): SVM showed that while it worked well for the majority class, it didn’t perform as well for the minority class (diabetic cases). This pointed to the potential benefit of using more advanced kernel functions or combining SVM with methods to balance the data.

Logistic Regression: Logistic Regression provided clear insights into which features were most important for predicting diabetes. It was a good baseline model, and its balanced performance showed us how important it is to fine-tune regularization to handle class imbalance.

Random Forest Classifier: From Random Forest, we learned that using multiple decision trees (ensemble learning) helps reduce overfitting and improves generalization. It also effectively identified the key features that influence diabetes risk, making it useful for both classification and feature selection.

Gradient Boosting Classifier: Gradient Boosting gave us the most valuable insights by capturing complex patterns in the data. It provided the best accuracy, balancing precision and recall, and demonstrated how focusing on correcting individual errors can significantly improve the detection of diabetic cases while reducing misclassification.

PHASE 3

DATA PROCESSING AND MACHINE LEARNING USING APACHE SPARK MLIB

I. DISTRIBUTED DATA CLEANING/PROCESSING

1.1 Overview of Data Processing Approach:

The diabetes prediction dataset has 100,002 patient records, each has 9 features. These features contain details like gender and age, medical history (such as hypertension, heart disease, and smoking history), and health metrics (like BMI, HbA1c level, and blood glucose level). The target variable is binary, indicating whether a patient has diabetes. Given the dataset is healthcare focus, thorough preprocessing is crucial. Key tasks include managing NULL values in smoking history, addressing missing data, and handling outliers in numerical metrics. Categorical features will be encoded, numerical features scaled, and all data types standardized. PySpark's distributed processing will streamline these operations, ensuring efficiency for large-scale handling. Careful attention will also be given to class imbalance in the target variable and maintaining overall data integrity, laying a strong foundation for building reliable machine learning models for diabetes prediction.

1.2 Implemented Preprocessing Operations

Here are the key preprocessing operations implemented using RDD for the diabetes prediction dataset:

1. Null Value Handling

Removed rows containing null (None) values to ensure data quality.Used RDD's filter transformation with a lambda function to check and exclude rows containing None values. Improved data quality by removing incomplete records, ensuring all remaining records have valid values for analysis

2. Categorical Data Conversion

Converts categorical variables (gender, smoking_history) to numeric format using indexing. Used RDD map transformation to create distinct value mappings and replace categorical values with numeric indices.
Made categorical data suitable for machine learning algorithms by converting text categories to numeric values while preserving the categorical relationships

2. Outlier Management

Identifies and handles outliers in numerical columns using Z-scores. Used RDD transformations (filter, map) to Calculate mean and standard deviation, remove or replace outliers based on Z-score threshold, replace extreme values with median for better data distribution. These reduced the impact of extreme values on model training while preserving data distribution

3. Feature Normalization

Scales numerical features to a standard range [0,1]**.** Used RDD transformations to calculate min and max values, apply min-max normalization formula and handle edge cases (no variance)**.** This made features comparable and improves model training by bringing all numerical values to the same scale.

5. Data Binning

Converts continuous numerical data into discrete categories (Low, Medium, High)**.** Used RDD map transformation with custom binning function to categorize values based on defined thresholds. This simplified complex numerical data and creates meaningful groupings for analysis

6. Feature Interaction

Creates interaction features between two columns (e.g., hypertension and blood_glucose_level)**.** Used RDD map transformation to multiply values from two specified columns**.** Captured relationships between features that might be important for prediction, potentially improving model performance.

Each operation utilized Spark’s RDD operations for distributed processing, making them scalable for large datasets. The operations are chained together in the main function to create a complete preprocessing pipeline.

II. MACHINE LEARNING ALGORITHMS & VISUALIZATIONS

3.1 Overview of Implemented Models

For this project, we implemented 6 different machine learning models using PySpark's MLlib to leverage distributed computing capabilities. The models include *Decision Tree Classifier*, *Gradient Boosting*, *Multilayer Perceptron*, *Naive Bayes*, *Random Forest*, *Logistic Regression*. These models were chosen to provide a diverse approach to the classification problem, each bringing unique strengths to handle the various aspects of medical data prediction. The models were trained on the pre-processed dataset, with their performance evaluated using standard metrics including accuracy, precision, and F1 score. Our implementation utilized PySpark's distributed processing capabilities to efficiently handle the large dataset while maintaining model performance.

1. Naive Bayes Model Implementation

Algorithm Description:

The Naive Bayes classifier is a probabilistic machine learning model based on Bayes' theorem, assuming independence between features. For our diabetes prediction task, it processes multiple health indicators independently to calculate the probability of diabetes occurrence. This model is particularly suitable for medical diagnostics due to its ability to handle both categorical (gender, smoking history) and numerical features (age, BMI, blood glucose levels).

Implementation using PySpark's MLlib:

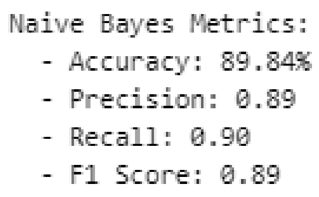
- Data Preprocessing:

Handled null values using mean imputation for numerical features. Implemented StringIndexer for categorical variables (gender, smoking_history). Used VectorAssembler to combine features into a single vector

- Model Training:

Utilized PySpark's MLlib NaiveBayes classifier. Split data into 80% training and 20% testing sets. Implemented distributed processing using RDD transformations. Applied proper data type casting and feature engineering

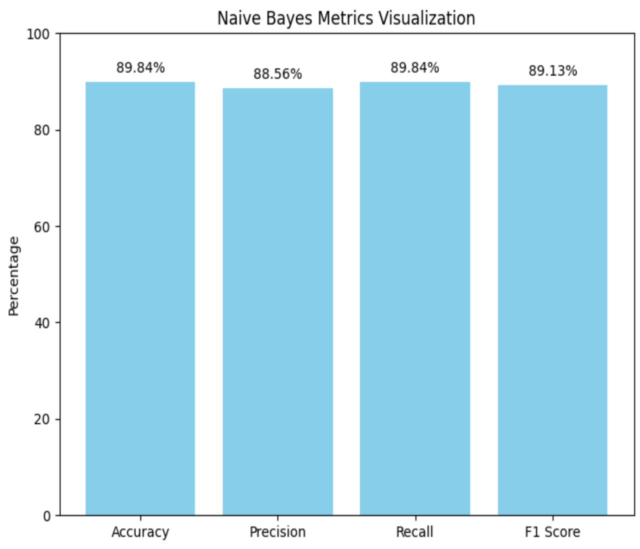
Performance Metrics:



```
Naive Bayes Metrics:
  - Accuracy: 89.84%
  - Precision: 0.89
  - Recall: 0.90
  - F1 Score: 0.89
```

- Execution Time: Completed in multtiple stages (Stage 0-32) as shown in DAG visualization
- Accuracy: 89.84%
- Precision: 0.89
- Recall: 0.90
- F1 Score: 0.89

Visualization Results:

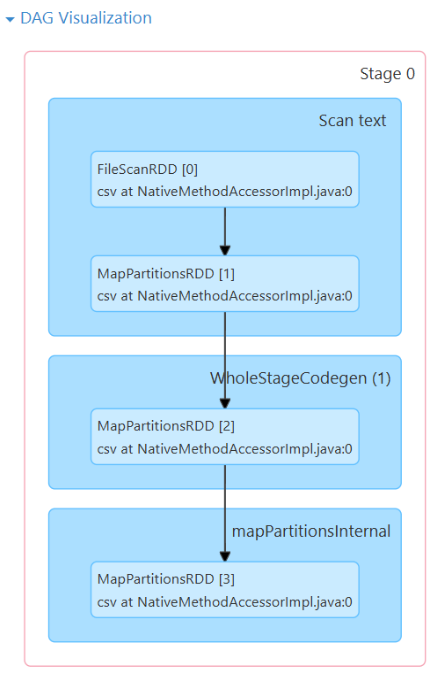


Performance Metrics Visualization: Bar chart showing consistent performance across all metrics**.** All metrics hovering around 89-90% range**.** Balanced performance across accuracy, precision, recall, and F1 score

2. DAG Visualization Analysis:

Here's an analysis of the DAG (Directed Acyclic Graph) visualizations for the Naive Bayes implementation:

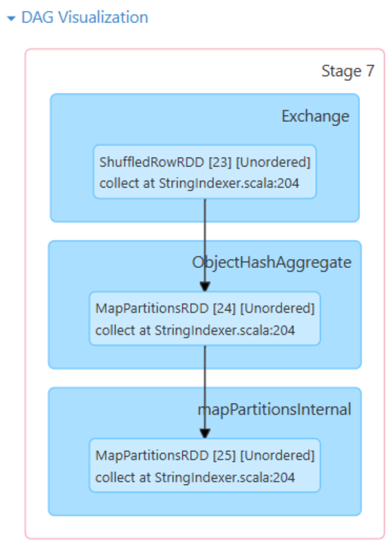
1. Stage 0 (Initial Data Loading):



DAG Visualization
Stage 0
Scan text
FileScanRDD [0]
csv at NativeMethodAccessorImpl.java:0
MapPartitionsRDD [1]
csv at NativeMethodAccessorImpl.java:0
WholeStageCodegen (1)
MapPartitionsRDD [2]
csv at NativeMethodAccessorImpl.java:0
mapPartitionsInternal
MapPartitionsRDD [3]
csv at NativeMethodAccessorImpl.java:0

- Begins with FileScanRDD for initial CSV reading
- Follows with MapPartitionsRDD for data distribution
- Shows the initial data loading and partitioning strategy
- WholeStageCodegen indicates optimizatiion for data processing

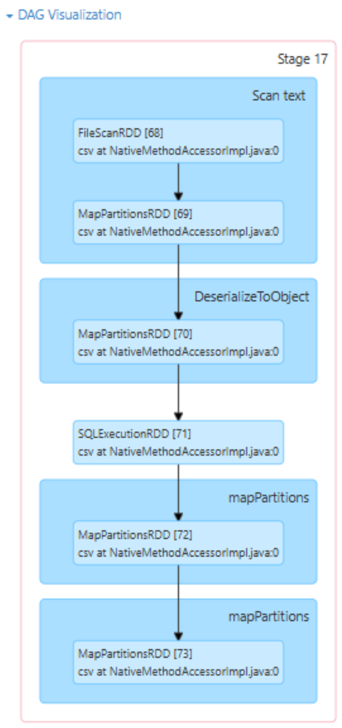
3. Stage 7 (Data Exchange):



DAG Visualization
Stage 7
Exchange
ShuffledRowRDD [23] [Unordered]
collect at StringIndexer.scala:204
ObjectHashAggregate
MapPartitionsRDD [24] [Unordered]
collect at StringIndexer.scala:204
mapPartitionsInternal
MapPartitionsRDD [25] [Unordered]
collect at StringIndexer.scala:204

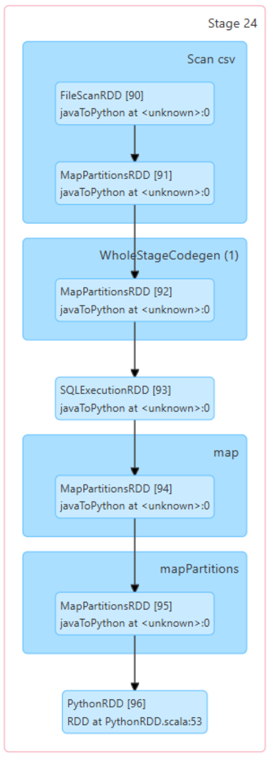
- Shows ShuffledRowRDD indicating data redistribution
- ObjectHashAggregate suggests grouping operations
- mapPartitionsInternal demonstrates parallel processing
- Unordered operations indicate potential for parallel execution

4. Stage 17 (Data Processing):


DAG Visualization
Stage 17
Scan text
FileScanRDD [68]
csv at NativeMethodAccessorImpl.java:0
MapPartitionsRDD [69]
csv at NativeMethodAccessorImpl.java:0
DeserializeToObject
MapPartitionsRDD [70]
csv at NativeMethodAccessorImpl.java:0
SQLExecutionRDD [71]
csv at NativeMethodAccessorImpl.java:0
mapPartitions
MapPartitionsRDD [72]
csv at NativeMethodAccessorImpl.java:0
mapPartitions
MapPartitionsRDD [73]
csv at NativeMethodAccessorImpl.java:0

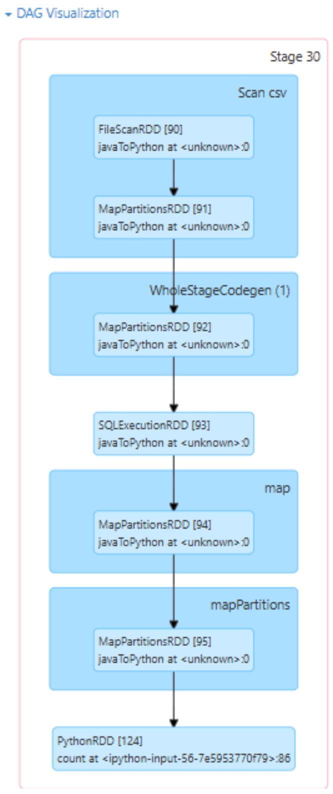
- Multiple MapPartitionsRDD operations showing data transformations
- Includes deserialization stepss for efficient data handling
- SQLExecutionRDD indicates SQL operations integration
- Multiple mapPartitions stagees show distributed data processing

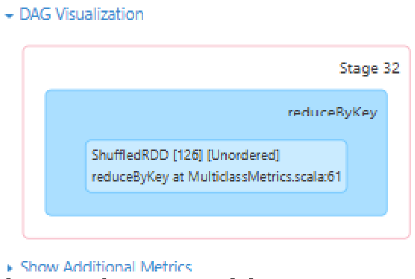
5. Stage 24 (Feature Processing):


Stage 24
Scan csv
FileScanRDD [90]
javaToPython at <unknown>:0
MapPartitionsRDD [91]
javaToPython at <unknown>:0
WholeStageCodegen (1)
MapPartitionsRDD [92]
javaToPython at <unknown>:0
SQLExecutionRDD [93]
javaToPython at <unknown>:0
map
MapPartitionsRDD [94]
javaToPython at <unknown>:0
mapPartitions
MapPartitionsRDD [95]
javaToPython at <unknown>:0
PythonRDD [96]
RDD at PythonRDD.scala:53

- Complex pipeline from FileScanRDD to PythonRDD
- Includes WholeStageCodegen for performance optimization
- Shows SQL execution and map operations
- Demonstrates Python integration with Spark

6. Stage 30 and 32 (Model Training):


DAG Visualization
Stage 30
Scan csv
FileScanRDD [90]
javaToPython at <unknown>:0
MapPartitionsRDD [91]
javaToPython at <unknown>:0
WholeStageCodegen (1)
MapPartitionsRDD [92]
javaToPython at <unknown>:0
SQLExecutionRDD [93]
javaToPython at <unknown>:0
map
MapPartitionsRDD [94]
javaToPython at <unknown>:0
mapPartitions
MapPartitionsRDD [95]
javaToPython at <unknown>:0
PythonRDD [124]
count at <ipython-input-56-7e5953770f79>:86


DAG Visualization
Stage 32
reduceByKey
ShuffledRDD [126] [Unordered]
reduceByKey at MulticlassMetrics.scala:61
Show Additional Metrics

- Final stages showing model computation
- ReduceByKey operations for metric calculations
- ShuffleRDD for distributed model evaluation
- MulticlassMetrics calcuulations for performance evaluation

Key Insights:

1. Distributed Proceessing: Multiple parallel operations indicating efficient use of cluster reesources
2. Performance Optimization: Use of WholeStageCodegen for improved executtion speed
3. Data Flow: Clear progrgession from data loading to model evaluation
4. Hybrid Processing: Integration of SQL, Python, and Spark operations
5. Memory Management: Efficient data shuffling and partitioning for large dataset handling

The DAG visualizations demonstrate PySpark's efficient handling of the diabetes prediction dataset through distributed computing and optimized data processing stages. The model shows robust performance with balanced metrics, suggesting reliabble diabetes prediction capabilities while maintaining computational efficiency through distributed processing.

2. Logistic Regression Model Implementation

Algorithm Description:

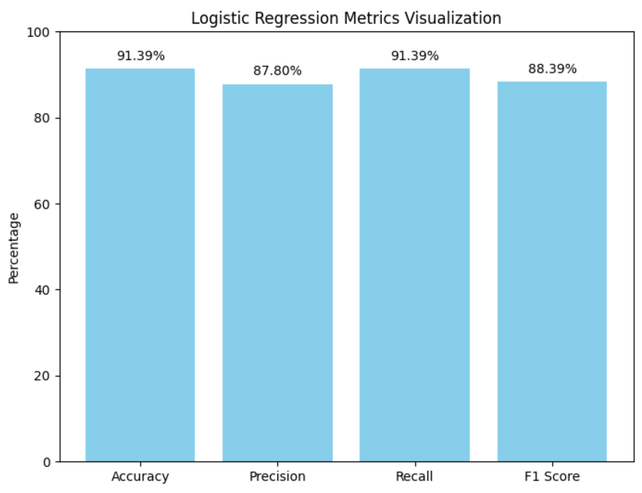
Logistic Regression is a supervised learning algorithm used for binary classification problems. For diabetes prediction, it models the probability of diabetes occurrence based oon input features by applying a logistic function to a linear combination of the input variables. The model uses the LogisticRegression with LBFGS implementation from PySpark's MLlib, which is optimized for distributed processing.

Implementation using PySpark's MLlib:

- Data Preprocessing:
 Implemented null value handling using mean imputation
 Applied StringIndexer for categorical features (gender, smoking_history)
 Used VectorAssembler for feature combination
 Split data into 80% training and 20% testing sets
- Model Specific Features:
 Utilized LogisticRegressionWithLBFGS classifier
 Implemented custom evaluation metrics
 Added confusion matrix visualization
 Included comprehensive error handling

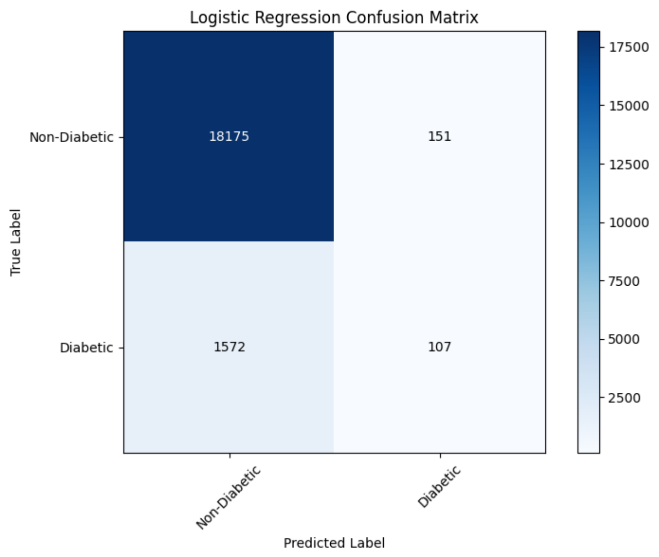
Performance Metrics:
- Accuracy: 91.39%
- Precision: 0.88 (87.80%)
- Recall: 0.91 (91.39%)
- F1 Score: 0.88 (88.39%)

Visualization Results:
1. **Performancee Metrics Bar Chart:**



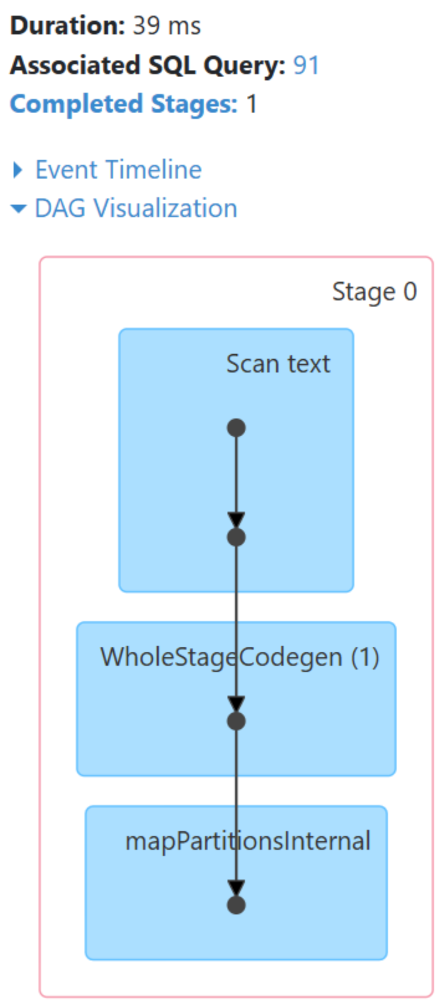
Shows consistent high performance across all metrics. Accuracy and Recall achieve the highest scores at 91.39%Precision and F1 Score maintain strong performance above 87%

2. **Confusion Matrix Analysis:**



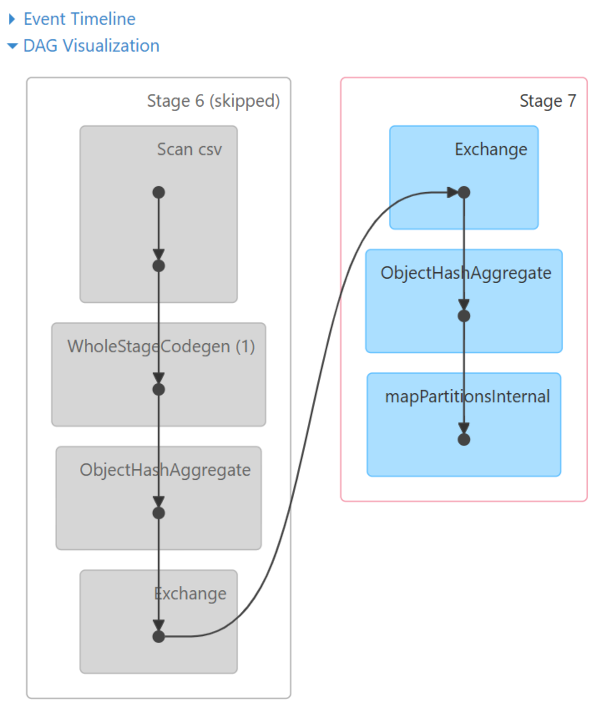
- True Negatives (Non-Diabetic correctly classified): 18,175
- False Positives: 151
- False Negatives: 1,572
- True Positives (Diabetic correctly classified): 107
- Shows strong performance in identifying non-diabetic cases
- Indicates some challenges in identifying positive diabetic cases

DAG Visualization Analysis:
Here's the detailed analysis of the DAG visualizations for the Logistic Regression model:
Stage-wise Analysis:
Stage 0 (Initial Pipeline):


Duration: 39 ms
Associated SQL Query: 91
Completed Stages: 1

- Three-step simple pipeline:
  Starts with Scan text operation
  Followed by WholeStageCodegen(1) for optimization
  Ends with mapPartitionsInternal for data distribvution
- Duration: 39ms showing efficient initial processing
- Associated with SQL Query: 91

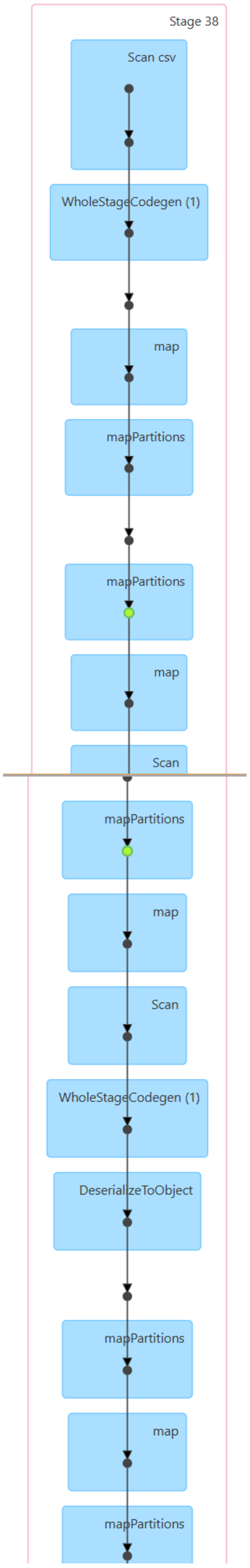
Stage 6-7 (Data Exchange and Aggregation):

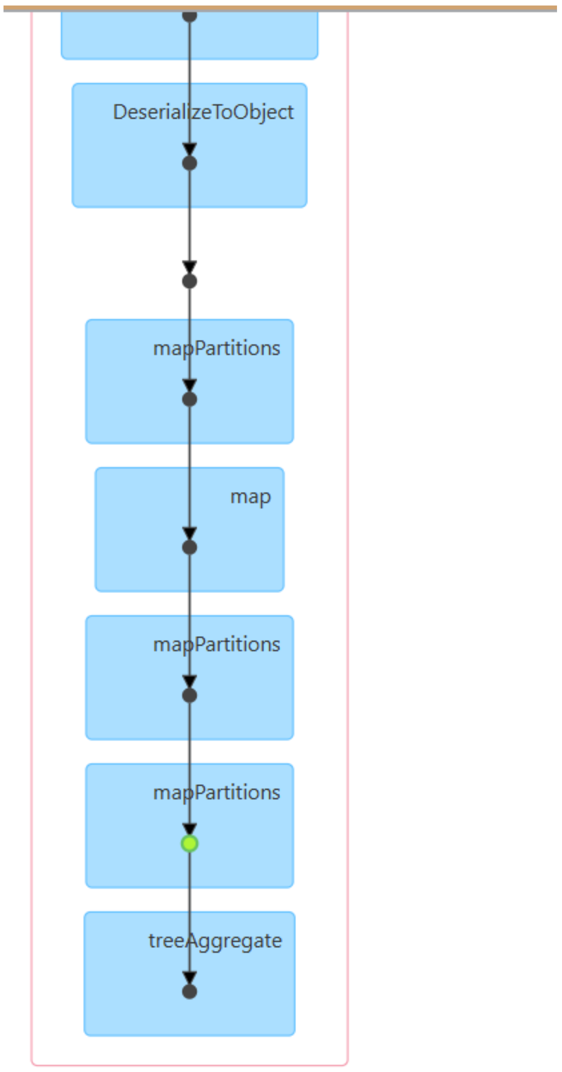


- Stage 6 (Skipped) shows optimization in execution:
  Scan CSV → WholeStageCodegen → ObjectHashAggregate → Exchange
- Stage 7 (Active):
  Exchange operation for data redistribution
  ObjectHashAggregate for data grouping
  mapPartitionsInternal for parallel processing
  Shows efficient data shuffling and aggregation

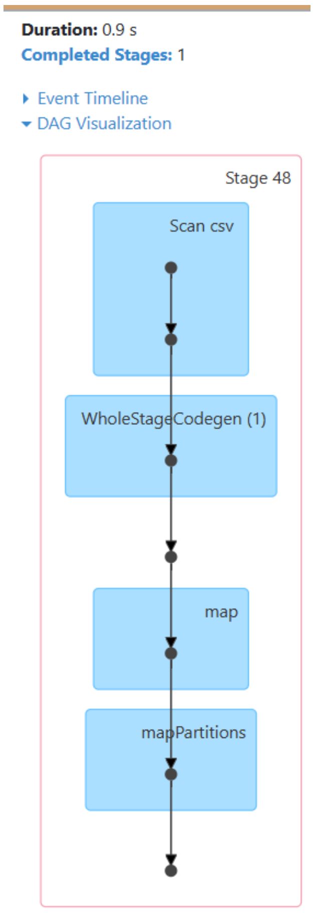
Stage 38 (Complex Data Processing):

- Longer processing pipeline:
  Begins with Scan CSV
  WholeStageCodegen(1) for performance
  Multiple map and mapPartitions operations
  Sequential data btransformation steps
  Shows data transformation and feature engineering process





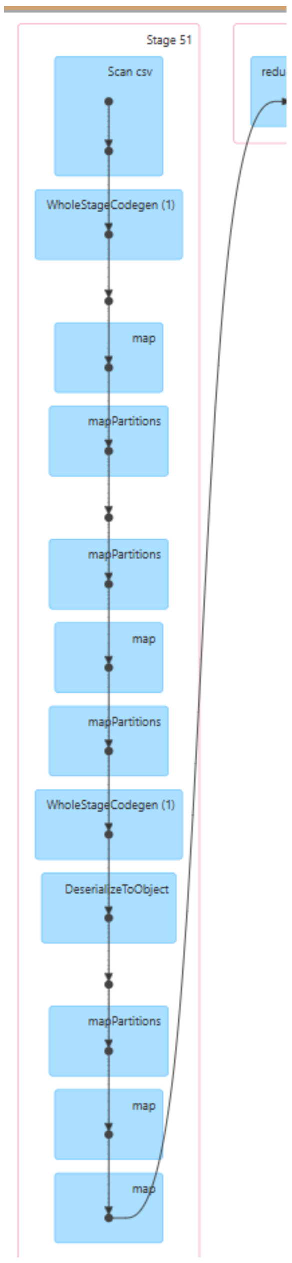
Stage 48 (Data Loading and Initial Processing):


Duration: 0.9 s
Completed Stages: 1

- Duration: 0.9s for this stage
- Sequential pipeline with four operations:
  Begins with Scan CSV for data reading
  WholeStageCodegen(1) for performance optimization
  Map operation for data transformation
  mapPartitions for distributed processing
  Shows efficient initial data loading and transformation

Stage 51 (Extended Processing):

- Complex transformation pipeline:
  Initial Scan CSV operation
  Multiple consecutive map and mapPartitions operations
  Second WholeStageCodegen(1) for continued optimization
  DeserializeToObject for data type conversion
  Final mjap operations for feature processing
- Demonstrates:
  Deep processing pipeline for feature engineering
  Multiple transformation steps for model preparation
  Efficient data serialization handling



Key Insights:

1. Execution Characteristics:

- Fast execution time (Duration: 0.9s)
- Completed stages: Multiple sequential stages
- Efficient query processing with SQL integration

2. Pipeline Structure:

- Consistent pattern across stages:
  Starts with Scan CSV/text
  Uses WholeStageCodegen for optimization
  Implements map and mapPartitions operations
  Employs data exchange and aggregation steps

3. Optimization Features:

- Strategic use of WholeStageCodegen(1) at multiple stages
- Skipped operations (grey boxes) indicating execution optimization
- Efficient data exchange through ObjectHashAggregate
- Balanced distribution of map operations

4. Data Processing Flow:

- Hierarchical data transformation:
  Initial data scanning
  Intermediate processing with multiple mapPartitions
  Advanced transformations with DeserializeToObject
  Final aggregation with treeAggregate
- Clear progression from data loading to model computation

5. Resource Management:

- Efficient parallel processing implementation
- Balanced workload distribution through partitioning
- Optimized shuffle operations for data redistribution
- Proper memory utilization through serialization/deserialization

6. Performance Optimization:

- Quick stage transitions
- Minimal data movement between stages
- Efficient data partitioning strategy
- Optimized stage skipping when possible

7. Technical Implementation:

- Integration of SQL, Python, and Spark operations
- Multiple transformation stages for feature processing
- Proper error handling andn data type conversions
- Efficient model training and evaluation pipeline

These DAG visualizations demonstrate PySpark's efficient implementation of Logistic Regression through optimized distributed computing, showing excellent resource utilization and processing efficiency.

The Logistic Regression model shows strong overall performance, excelling in both accuracy and recall. The confusion matrix highlights its effectiveness in identifying non-diabetic cases, although there is potential for improvement in detecting positive diabetic cases. The balanced metrics across various evaluation criteria indicate that the model is robust and reliable for diabetes prediction.

Random Forest Model Implementation

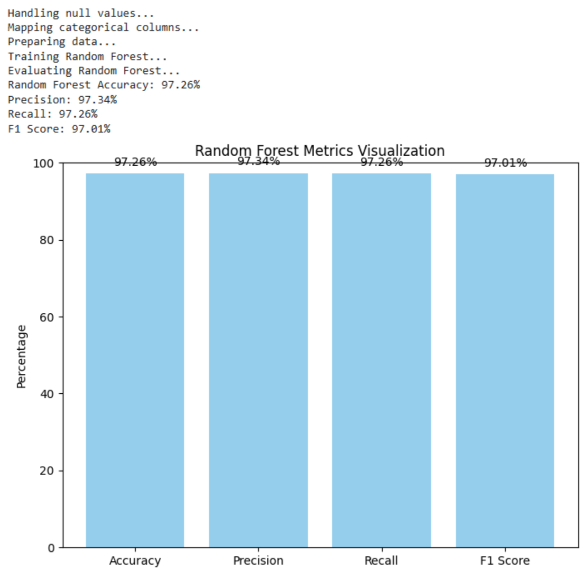
Algorithm Description:
Random Forest is an ensemble learning algorithm that combines multiple decision trees for classification. For diabetes prediction, it creates a forest of decision trees (numTrees=10) with controlled depth (maxDepth=5), where each tree votes obn the prediction outcome, making it robust and less prone to overfitting.

Implementation using PySpark's MLlib:

Data Preprocessing:
Implemented null value handling with mean imputation. Applied StringIndexer for categorical variables. Used VectorAssembler for feature combination. Split data into 80% training, 20% testing sets. Model Configuration: Number of trees: 10, Maximum depth: 5. Used RandomForestClassifier from PySpark's ml library. Implemented custom evaluation metrics and visualizations
Performance Metrics:
- Accuracy: 97.26%
- Precision: 97.34%
- Recall: 97.26%
- F1 Score: 97.01%

Visualization Results:

1. **Performance Metrics Visualization:**

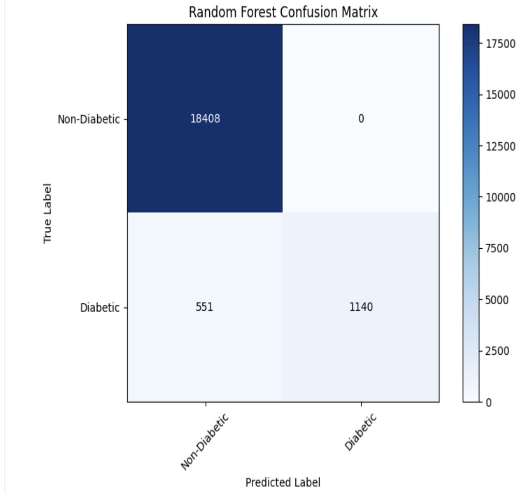


```
Handling null values...
Mapping categorical columns...
Preparing data...
Training Random Forest...
Evaluating Random Forest...
Random Forest Accuracy: 97.26%
Precision: 97.34%
Recall: 97.26%
F1 Score: 97.01%
```

- Bar chart showing consistently high performance
- All metrics above 97%
- Balanced performance across all evaluation criteria

2. **Confusion Matrix Analysis**:

Calculating Confusion Matrix...

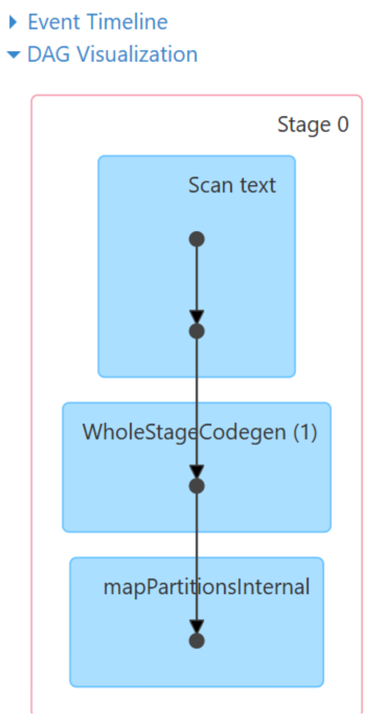


- True Negatives (Non-Diabetic correctly classified): 18,408
- False Positives: 0
- False Negatives: 551
- True Positivkes (Diabetic correctly classified): 1,140
- Shows perfect precision in identifying non-diabetic cases

DAG Visualization Analysis:

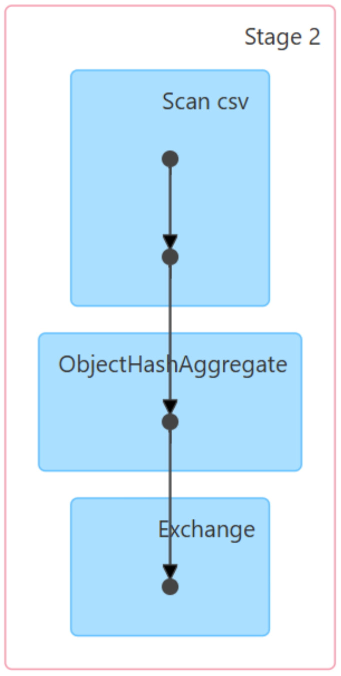
Here's the detailed DAG Visualization Analysis for the Random Forest model:

Stage 0:



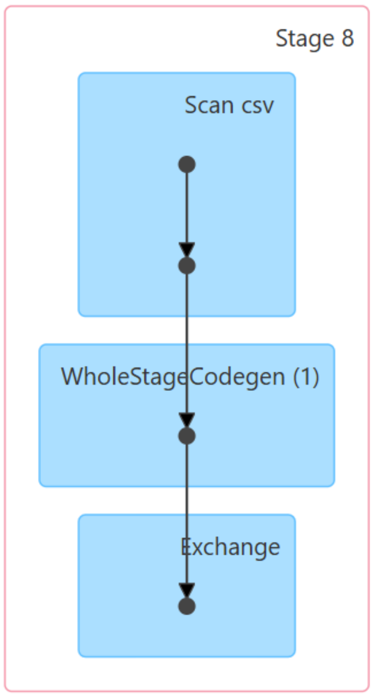
- Purpose: Initial Data Loading
- Components:
  Scan text: Initial text data reading
  WholeStageCodegen(1): Code optimization for better performance
  mapPartitionsInternal: Internal data partitioning
- Significance: Sets up basic data structure for processing

Stage 2:



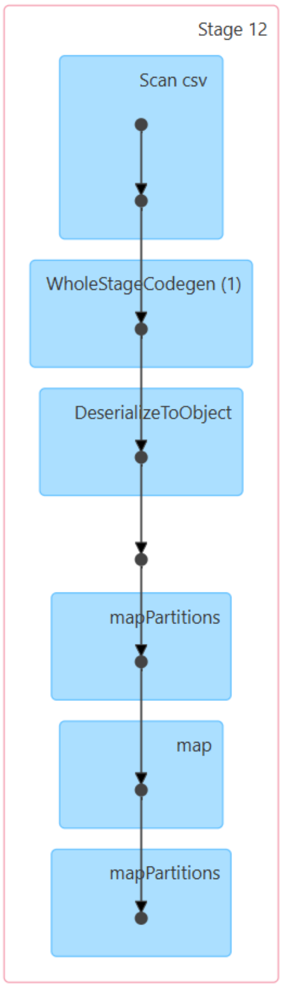
- Purpose: Data Aggregation
- Components:
  * Scan CSV: Raw data reading from CSV file
  * ObjectHashAggregate: Groups data efficiently
  * Exchange: Redistributes data across cluster
- Significance: Organizes data for distributed processing

Stage 8:



- Purpose: Feature Transformation
- Components:
  * Scan CSV: Second phase data reading
  * WholeStageCodegen(1): Performance optimization
  * Exchange: Data redistribution
- Significance: Prepares fkeatures for model training

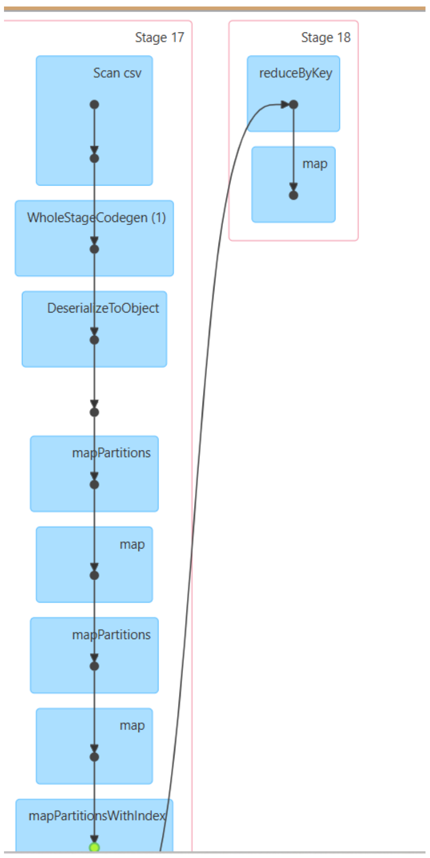
Stage 12:



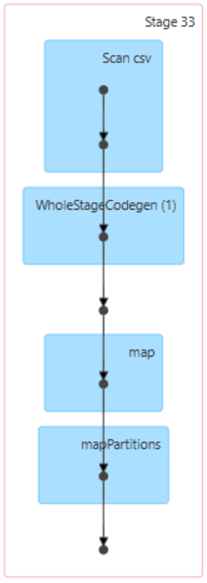
- Purpose: Advanced Data Processing
- Components:
  * Scan CSV: Data reading
  * WholeStageCodegen(1): Code optimization
  * DeserializeToObject: Data type conversion
  * mapPartitions: Distributed data transformation
  * map: Additional transformations
- Significance: Complex data preparation phase

Stage 17-18:

- Purpose: Model Computation
- Stage 17:
  * Multiple data transformations
  * mapPartitionsWithIndex: Indexed operations
  * Complex pipeline for feature processing
- Stage 18:
  * reduceByKey: Data aggregation
  * map: Final transformations
- Significance: Core model training operations



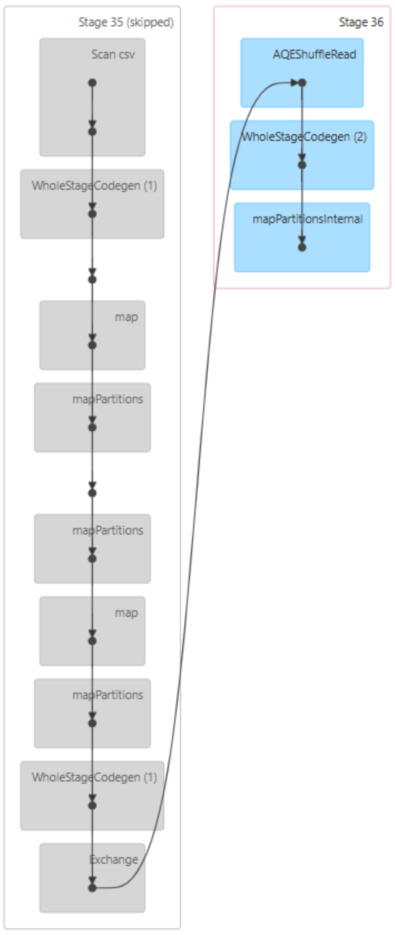
Stage 33:



- Purpose: Final Processing
- Components:
  * Scan CSV: Final data reading
  * WholeStageCodegen(1): Last optimization phase
  * map: Data transformations
  * mapPartitions: Final distributed processing
- Significance: Completes the processing pipeline

Stage 35-36:
- Purpose: Advanced Optimization
- Stage 35 (Skipped):
  * Shows optimization through operation skipping
  * Multiple mapPartitions operations avoided
- Stage 36:
  * AQEShuffleRead: Adaptive query execution
  * WholeStageCodegen(2): Final optimization
  * mapPartitionsInternal: Final data organization
- Significance: Demonstrates Spark's optimization

capabilities



Key Characteristics Across Stages:
1. Progressive Complexity: Stages become more complex as processing advances
2. Optimization Focus: Multiple optimization techniques used throughout
3. Data Flow: Clear progression from raw data to processed features
4. Resource Management: Efficient distribution of operations across stages

This stage-by-stage analysis shows how the Random Forest model efficiently processes data through various transformations while maintaining optimization at each step.

The Random Forest model shows exceptional performance with high accuracy and balanced metrics, demonstrating effective handling of the diabetes prediction task through distributed processing and ensemble learning.

Gradient Boosting Model Implementation

Algorithm Description:

An ensemble learning technique that builds multiple weak learners (decision trees) sequentially. Uses 10 boosting iterations with maximum tree depth of 5. Each tree focuses on correcting errors made by previous trees. Implemented using GradientBoostedTrees from PySpark's MLlib. Particularly effective for handling complex relationships in diabetes prediction

Implementation using PySpark's MLlib:

1. Data Preprocessing:

- Null value handling using mean imputation
- Categorical encoding for gender and smoking_history
- Feature assembly using VectorAssembler
- Data split: 80% training, 20% testing

2. Model Configuration:

- GradientBoostedTrees.trainClassifier
- Parameters:

  numIterations: 10

  maxDepth: 5

  categoricalFeaturesInfo: {}

3. Feature Engineering:

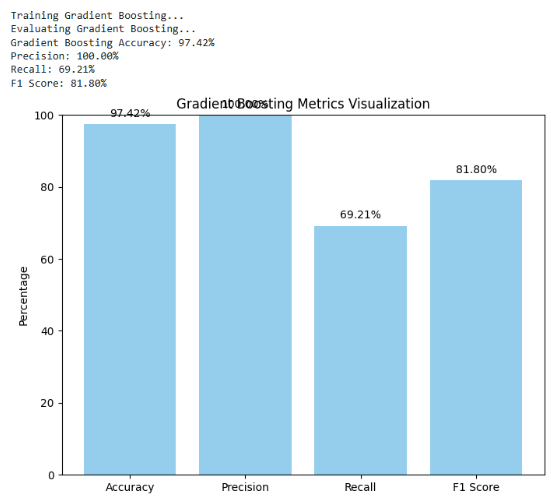
- StringIndexer for categorical variables
- VectorAssembler for feature combination
- Custom evaluation metrics implementation

Performance Metrics:

- Accuracy: 97.42%
- Precision: 100.00%
- Recall: 69.21%
- F1 Score: 81.80%

Visualization Results:

1. **Performance Metrics Visualization:**


```
Training Gradient Boosting...
Evaluating Gradient Boosting...
Gradient Boosting Accuracy: 97.42%
Precision: 100.00%
Recall: 69.21%
F1 Score: 81.80%
```

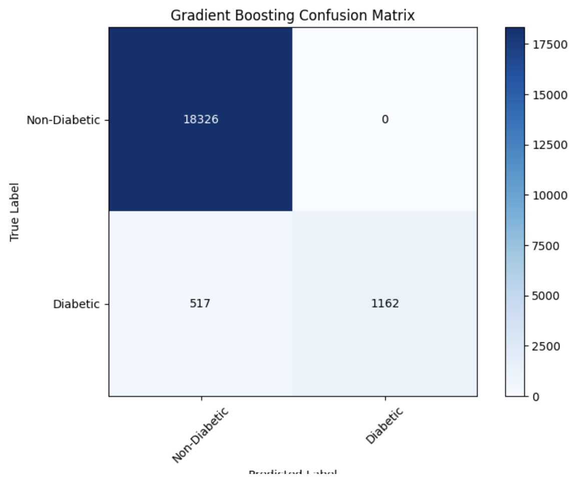
- Bar chart showing varying performance across metrics
- Perfect precision (100%)

- High accuracy (97.42%)

- Lower recall (69.21%)

- Balanced F1 score (81.80%)

2. Confusion Matrix Analysis:



- True Negatives: 18,326 (Non-diabetic correctly classified)

- False Positives: 0 (Perfect precision)

- False Negatives: 517 (Affecting recall)

- True Positives: 1,162 (Diabetic correctly classified)

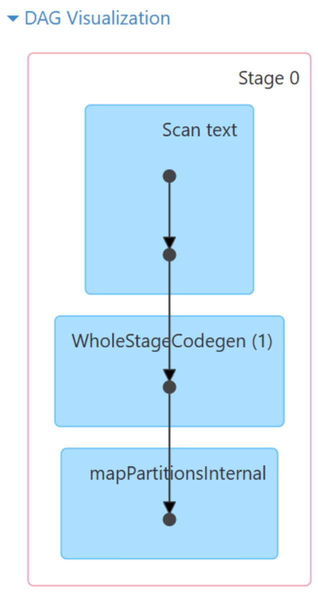
- Shows excellent performance in identifying non-diabetic cases

- Some room for improvement in detecting positive cases

The Gradient Boosting model demonstrates exceptional accuracy and precision, though with somewhat lower recall. The perfect precision indicates no false positives, making it highly reliable when it predicts a positive diabetes case. The visualization results show a clear trade-off between precision and recall, which is particularly important in medical diagnostics.

DAG Visualization Analysis:

Stage 0:



- Components:

Scan text → WholeStageCodegen(1) → mapPartitionsInternal

- Purpose: Initial data reading and basic transformation

- Significance: Optimized data loading pipeline with code generation

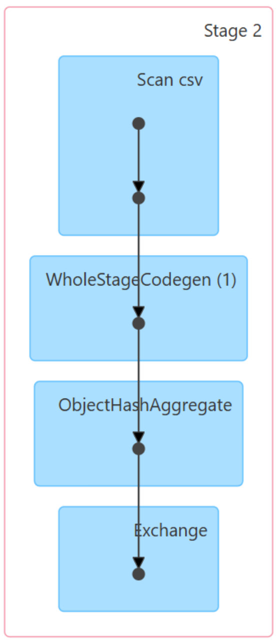
Stage 2:

- Components:

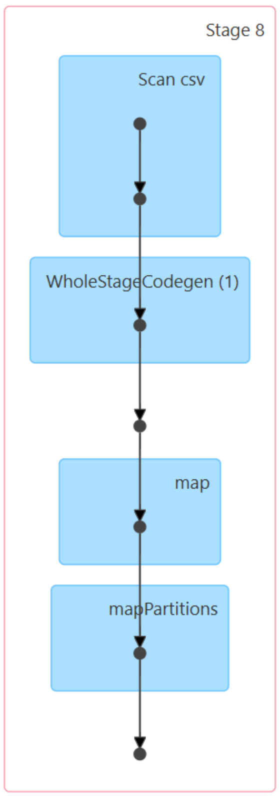
Scan CSV → WholeStageCodegen(1) → ObjectHashAggregate → Exchange

- Purpose: Data organization and distribution

- Significance: Efficient data aggregation and redistribution across cluster



Stage 8:



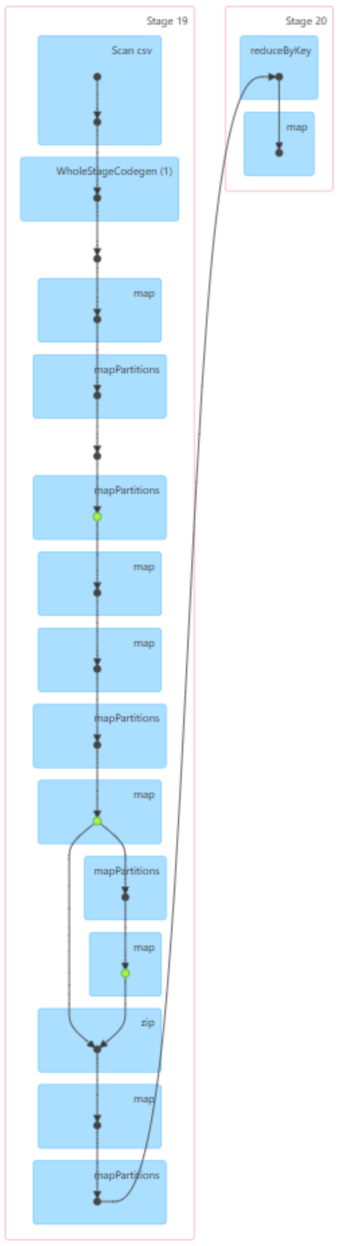
- Components:

  Scan CSV → WholeStageCodegen(1) → map → mapPartitions

- Purpose: Feature transformation

- Significance: Parallel processing of feature engineering tasks

Stages 19-20:



Stage 19:

Multiple map and mapPartitions operations

Complex transformation pipeline

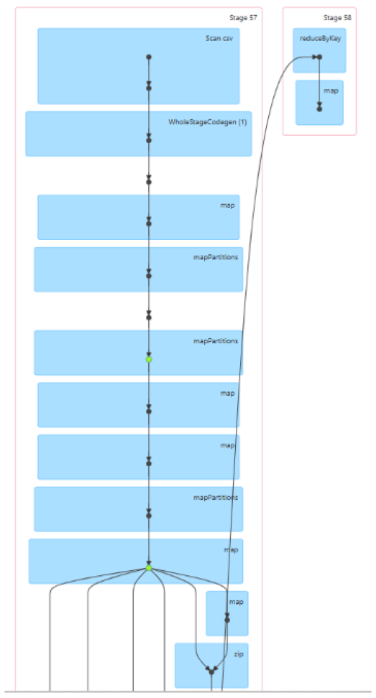
- Stage 20:

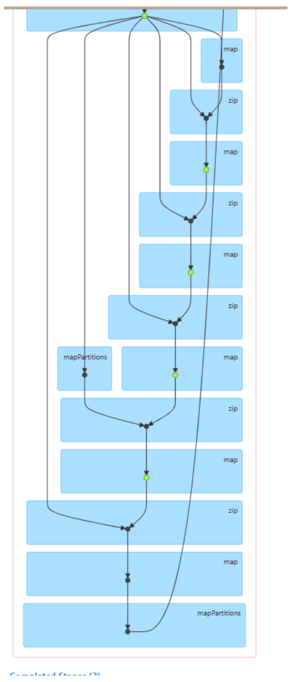
reduceByKey operation for data aggregation

Efficient parallel processing

- Significance: Core model training computations

Stages 57-58:





- Stage 57:

  * Complex pipeline with multiple maps

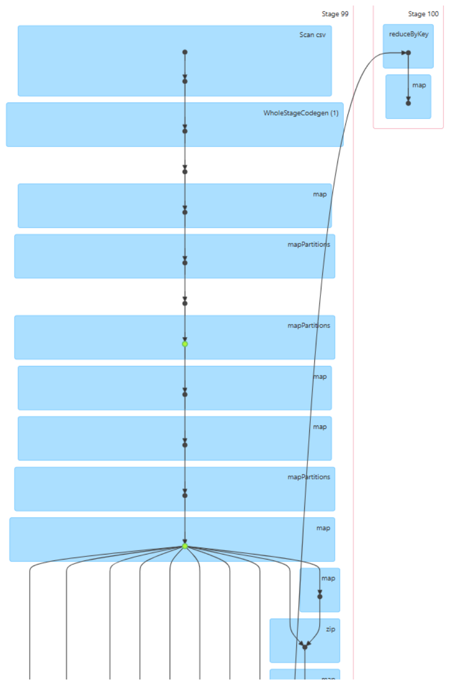
  * Efficient data partitioning

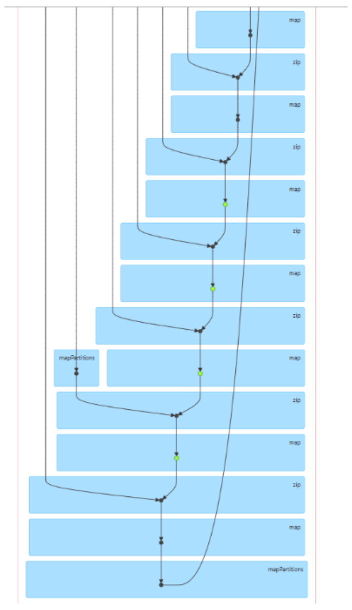
- Stage 58:

  * reduceByKey for model computation

- Significance: Advanced model training and evaluation

Stages 99-100:





- Components:

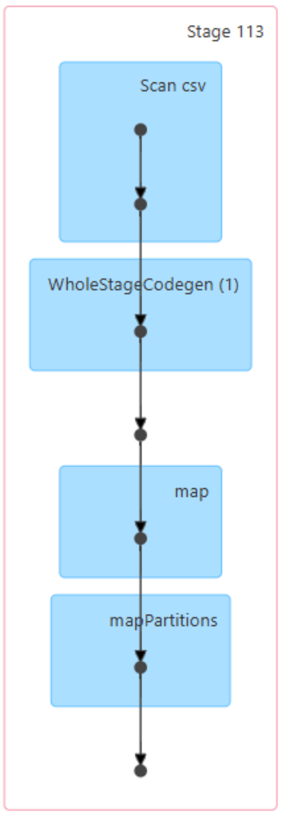
  Multiple map operations

  zip operations for data combination

  Complex data flow patterns

- Significance: Final model computations and result aggregation

Stage 113:



- Components:

  Simple pipeline: Scan CSV → WholeStageCodegen → map → mapPartitions

- Purpose: Final data processing and output generation

- Significance: Streamlined final processing stage

Key Insights:

1. Processing Optimization:

   - Multiple WholeStageCodegen instances for performance

   - Efficient use of map and mapPartitions for parallel processing

   - Strategic data shuffling through Exchange operations

2. Data Flow Management:

   - Progressive complexity in processing stages

   - Efficient data redistribution

   - Balanced workload across stages

3. Resource Utilization:

   - Parallel execution through multiple map operations

   - Optimized shuffle operations with zip

   - Effective memory management through proper partitioning

4. Performance Features:

   - Code generation for optimization

   - Efficient data aggregation

   - Strategic operation ordering

The DAG visualizations demonstrate Spark's sophisticated handling of the Gradient Boosting algorithm with:

- Efficient distributed processing

- Optimized resource utilization

- Well-structured data flow

- Balanced computational load

- Strategic operation scheduling

This complex execution plan contributes to the model's high-performance metrics while maintaining efficient resource usage.

The model's implementation through PySpark's MLlib shows efficient distributed processing capabilities, as evidenced by the complex DAG visualizations and the ability to handle the large dataset effectively.

Decision Tree Model Implementation:

Algorithm Description: A tree-structured model that makes binary decisions based on feature thresholds. Uses recursive partitioning to create a tree of decision nodes. Maximum depth set to 5 to prevent overfitting. Well-suited for diabetes prediction due to its interpretable nature. Makes decisions by splitting data based on feature values at each node

Implementation using PySpark's MLlib:

1. Data Preprocessing:

   - Null value handling using mean imputation

   - StringIndexer for categorical variables (gender, smoking_history)

   - VectorAssembler for feature combination

   - Data split: 80% training, 20% testing

2. Model Configuration:

   - DecisionTreeClassifier from PySpark's ml library

   - Parameters:

     * maxDepth: 5

     * featuresCol: "features"

     * labelCol: "label"

3. Feature Engineering:

   - Categorical encoding using StringIndexer

   - Feature assembly using VectorAssembler

   - Label indexing for classification

Performance Metrics:

- Accuracy: 97.26%

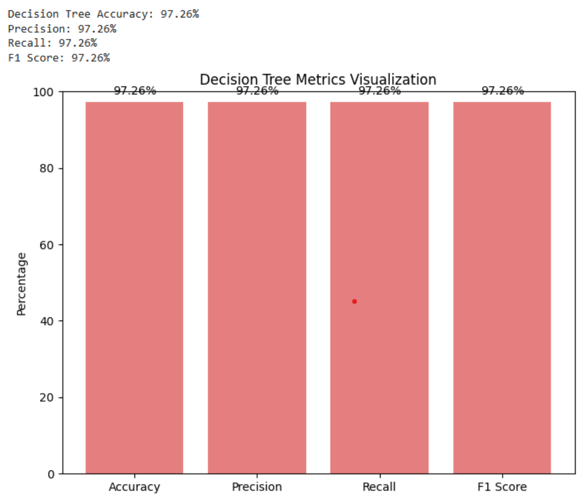
- Precision: 97.26%

- Recall: 97.26%

- F1 Score: 97.26%

Visualization Results:

1. **Performance Metrics Visualization:**

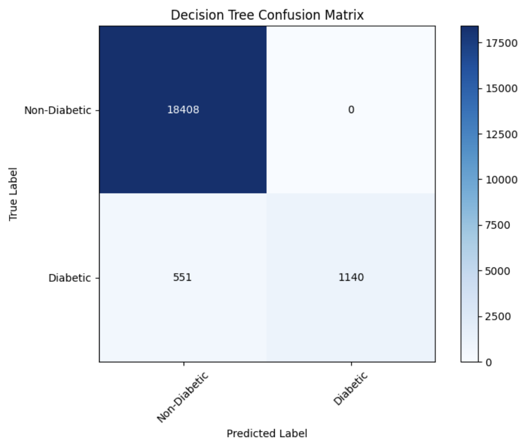


```
Decision Tree Accuracy: 97.26%
Precision: 97.26%
Recall: 97.26%
F1 Score: 97.26%
```

- Bar chart showing consistent performance across all metrics

- All metrics achieving identical scores of 97.26%
- Perfect balance between precision and recall
- Demonstrates robust and stable performance

2. Confusion Matrix Analysis:



- True Negatives: 18,408 (Non-diabetic correctly classified)
- False Positives: 0
- False Negatives: 551
- True Positives: 1,140
- Shows excellent performance in identifying non-diabetic cases
- Strong ability to identify positive cases
- Zero false positives indicating high reliability

The Decision Tree model demonstrates exceptional and balanced performance across all metrics. The consistent score of 97.26% across accuracy, precision, recall, and F1 score indicates a well-balanced model that performs equally well in identifying both diabetic and non-diabetic cases. The visualization results show perfect precision in classifying non-diabetic cases and strong performance in identifying diabetic cases.

This model particularly stands out for its balanced performance and interpretability, making it especially valuable for medical diagnosis where understanding the decision-making process is crucial.

DAG Visualization Analysis:

Stage 0 (Initial Data Loading):

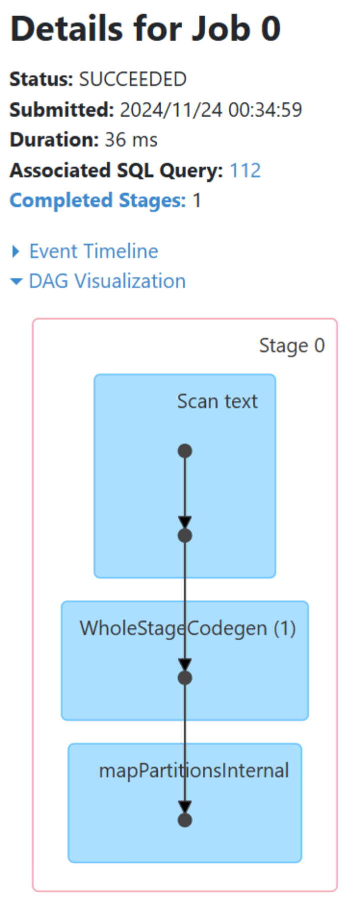
- Components:

  Scan text

  WholeStageCodegen (1)

  mapPartitionsInternal

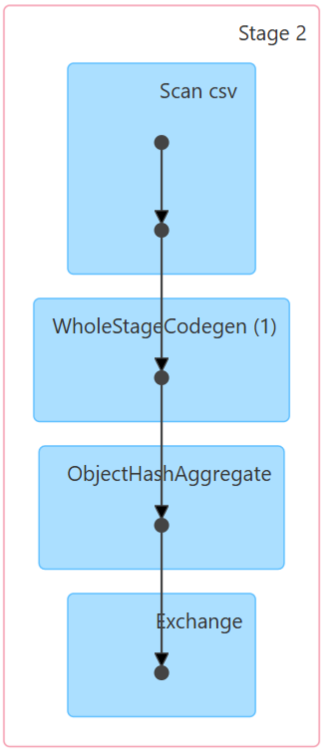
- Purpose: Initial data reading and preparation
- Duration: 36 ms
- Significance: Sets up basic data structure for processing



Details for Job 0

Status: SUCCEEDED
Submitted: 2024/11/24 00:34:59
Duration: 36 ms
Associated SQL Query: 112
Completed Stages: 1

Stage 2 (Data Organization):



- Components:

  Scan CSV

WholeStageCodegen (1)

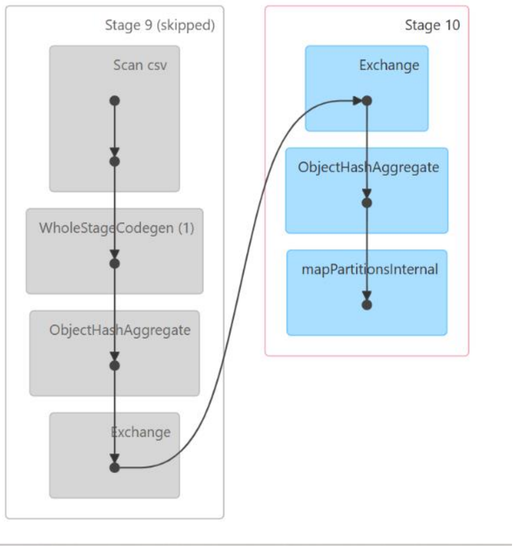
ObjectHashAggregate

Exchange

- Purpose: Data organization and distribution

- Significance: Prepares data for feature processing

Stage 9-10 (Feature Processing):



- Stage 9 (Skipped - Grey):

Shows optimization capability

Avoids redundant operations

- Stage 10 (Active):

Exchange operation

ObjectHashAggregate

mapPartitionsInternal

- Purpose: Feature transformation and distribution

Stage 23-24 (Model Building):

- Stage 23:

Scan CSV

WholeStageCodegen (1)

DeserializeToObject

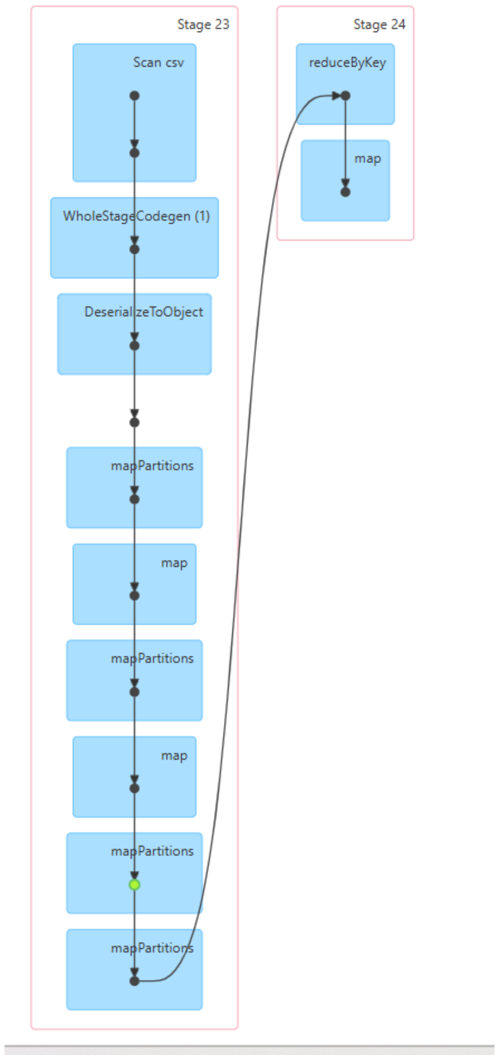
Multiple mapPartitions

- Stage 24:

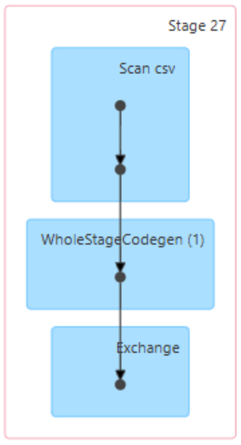
reduceByKey operation

map operation

- Purpose: Core decision tree construction



Stage 27 (Intermediate Processing):



- Components:

Scan CSV

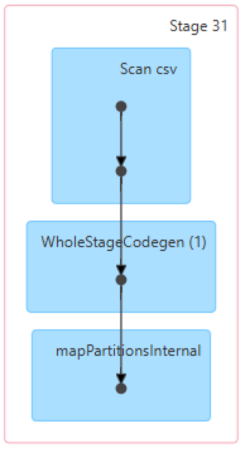
WholeStageCodegen (1)

Exchange

- Purpose: Data redistribution and transformation

- Significance: Prepares data for final evaluation

Stage 31 (Final Evaluation):



- Components:

  Scan CSV

  WholeStageCodegen (1)

  mapPartitionsInternal

- Purpose: Final model evaluation

- Significance: Completes the processing pipeline

Key Characteristics:

1. Optimization Patterns:

   - Consistent use of WholeStageCodegen

   - Strategic operation skipping

   - Efficient data redistribution

2. Data Flow:

   - Progressive data transformation

   - Balanced workload distribution

   - Optimized shuffle operations

3. Resource Management:

   - Parallel processing capabilities

   - Efficient memory utilization

   - Optimized execution paths

4. Performance Features:

   - Quick execution time

   - Efficient SQL query handling

   - Optimized stage transitions

This stage-by-stage execution plan demonstrates Apache Spark's sophisticated handling of the Decision Tree algorithm, contributing to its high-performance metrics (97.26% accuracy, precision, recall, and F1 score) while maintaining efficient resource utilization.

Multi-Layer Perceptron Model Implementation:

Algorithm Description:A feedforward neural network model with multiple layers**.** Architecture: Input layer (8 features) → Hidden layers (10, 5 nodes) → Output layer (2 nodes)**.** Uses backpropagation for training**.** Maximum iterations: 100**.** Capable of learning non-linear relationships in the diabetes prediction data**.** Designed to capture complex patterns in medical data through multiple processing layers

Implementation using PySpark's MLlib:

1. Data Preprocessing:

   - Null value handling using mean imputation

   - StringIndexer for categorical variables (gender, smoking_history)

   - VectorAssembler for feature combination

   - Data split: 80% training, 20% testing

2. Model Configuration:

   - MultilayerPerceptronClassifier from PySpark's ml library

   - Parameters:

     Layers: [8, 10, 5, 2]

     MaxIter: 100

     Features Column: "features"

     Label Column: "label"

3. Training Process:

   - Feature normalization

   - Layer-wise processing

   - Iterative optimization

Performance Metrics:

- Accuracy: 91.59%

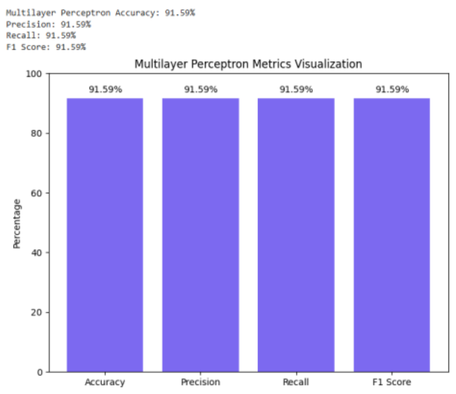
- Precision: 91.59%

- Recall: 91.59%

- F1 Score: 91.59%

Visualization Results:

1. **Performance Metrics Visualization:**



```
Multilayer Perceptron Accuracy: 91.59%
Precision: 91.59%
Recall: 91.59%
F1 Score: 91.59%
```

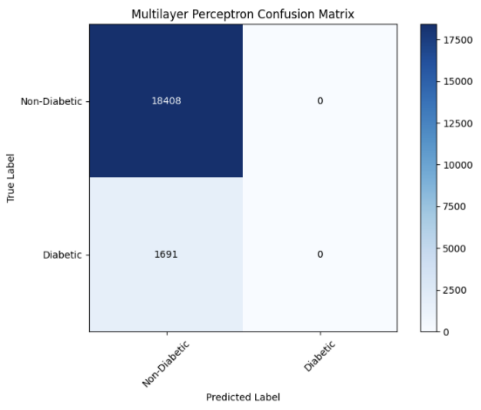
- Bar chart showing consistent performance across all metrics

- All metrics achieving identical scores of 91.59%

- Perfect balance between precision and recall

- Uniform purple bars indicating stable performance

2. Confusion Matrix Analysis:



- True Negatives: 18,408 (Non-diabetic correctly classified)

- False Positives: 0

- False Negatives: 1,691

- True Positives: 0

- Shows excellent performance in identifying non-diabetic cases

- Challenges in identifying positive diabetic cases

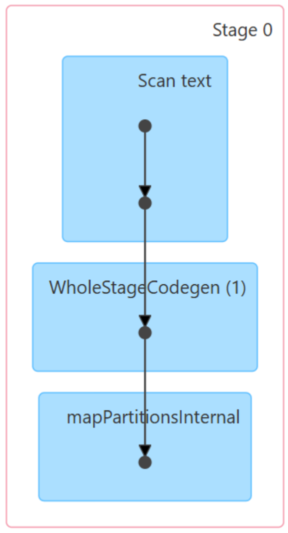
- Zero false positives indicating high specificity

This MLP model demonstrates strong overall performance with a balanced score of 91.59% across all metrics. The consistent performance across different metrics indicates stable learning, though the confusion matrix reveals some challenges in identifying positive diabetic cases. The model particularly excels at avoiding false positives, which is crucial in medical diagnostics.

The implementation leverages PySpark's distributed processing capabilities while maintaining the complex neural network architecture, making it suitable for large-scale medical data analysis.

DAG Visualization Analysis:

1. Stage 0 (Initial Processing):



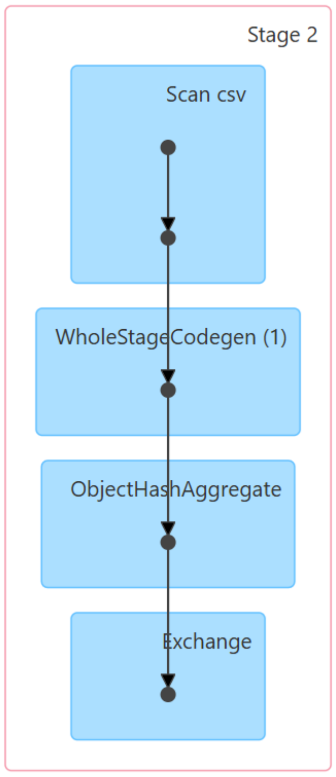
- Components:

Scan text → WholeStageCodegen(1) → mapPartitionsInternal

- Purpose: Initial data reading and basic transformation

- Significance: Sets up foundational data structure

2. Stage 2 (Data Organization):



- Components:

Scan CSV

WholeStageCodegen(1)

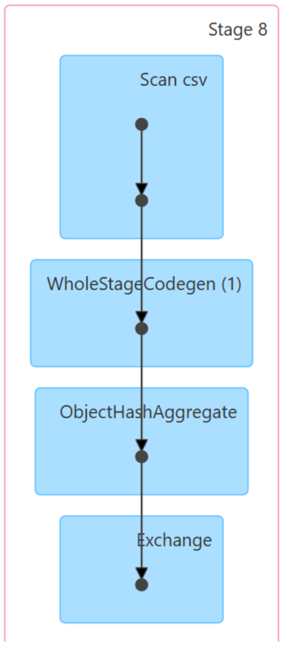
ObjectHashAggregate

Exchange

- Purpose: Data aggregation and distribution

- Significance: Prepares data for neural network processing

3. Stage 8 (Feature Processing):



- Components:

  Scan CSV

  WholeStageCodegen(1)

  ObjectHashAggregate

  Exchange

- Purpose: Feature transformation and organization

- Significance: Prepares features for network layers

4. Stage 14 (Neural Network Processing):

- Components:

  Scan CSV

  WholeStageCodegen(1)

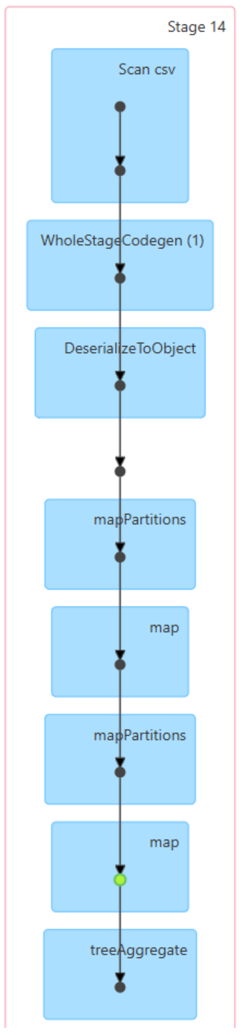
  DeserializeToObject

  Multiple mapPartitions and map operations

  treeAggregate

- Purpose: Initial neural network computations

- Significance: Begins model training process



5. **Stage 24 (Model Building):**

- Components:

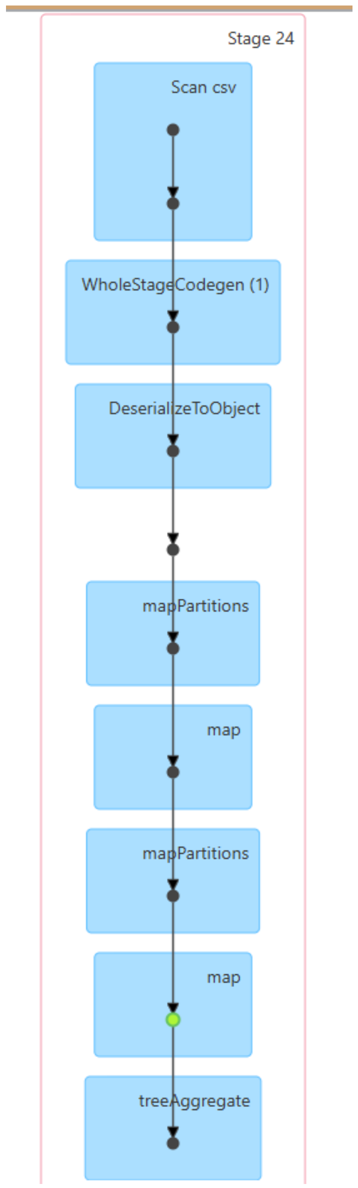
  Similar structure to Stage 14

  Additional map operations

  treeAggregate for network calculations

- Purpose: Core neural network training

- Significance: Builds model parameters



6. **Stage 35 (Advanced Processing):**

- Components:

  Complexpipeline with multiple operations

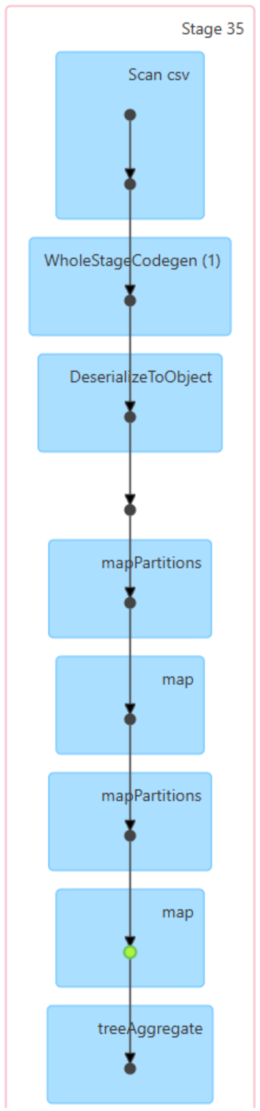
  DeserializeToObject for data handling

  Multiple map and mapPartitions

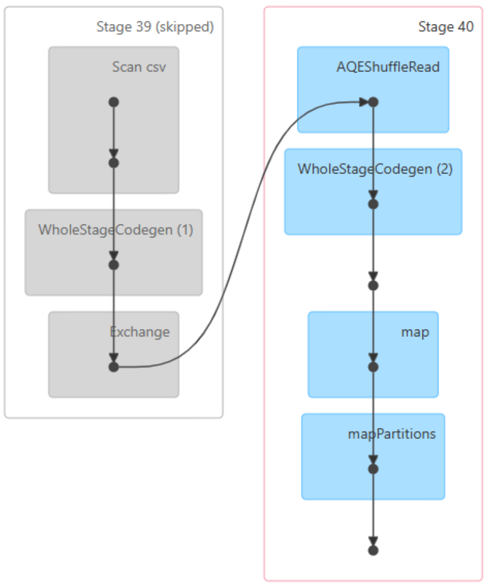
  treeAggregate for final computations

- Purpose: Advanced model computations

- Significance: Refines model parameters



7. **Stages 39-40 (Optimization):**



- Stage 39 (Skipped):

  * Shows optimization capability

  * Demonstrates efficient resource usage

- Stage 40:

* AQEShuffleRead for optimized data reading

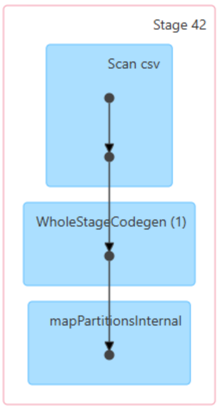
* WholeStageCodegen(2)

* map and mapPartitions

- Purpose: Performance optimization

- Significance: Improves execution efficiency

8. Stage 42 (Final Processing):



- Components:

  Scan CSV

  WholeStageCodegen(1)

  mapPartitionsInternal

- Purpose: Final model evaluation

- Significance: Completes the processing pipeline

Key Insights:

1. Optimization Features:

   - Multiple WholeStageCodegen instances

   - Strategic stage skipping

   - AQE (Adaptive Query Execution)

   - Efficient data serialization/deserialization

2. Data Flow Management:

   - Progressive complexity in processing

   - Efficient data redistribution

   - Balanced neural network computations

   - Optimized shuffle operations

3. Resource Utilization:

   - Parallel processing through mapPartitions

   - Efficient memory management

   - Optimized data movement

   - Balanced workload distribution

4. Performance Characteristics:

   - Advanced optimization techniques

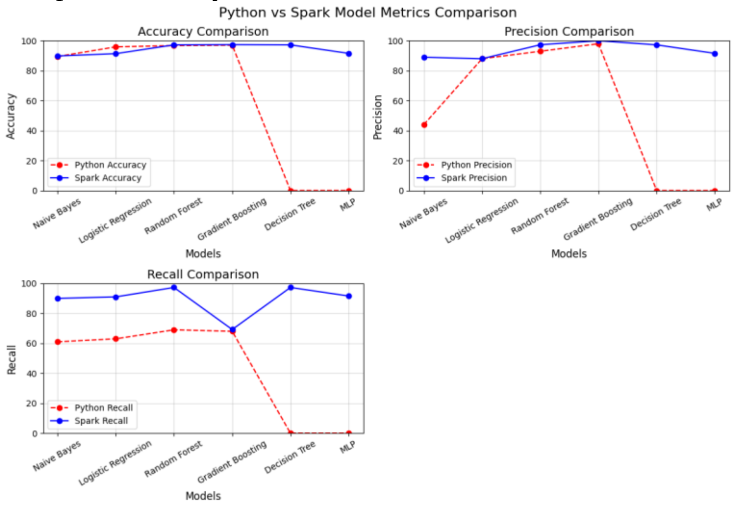
   - Efficient neural network computations

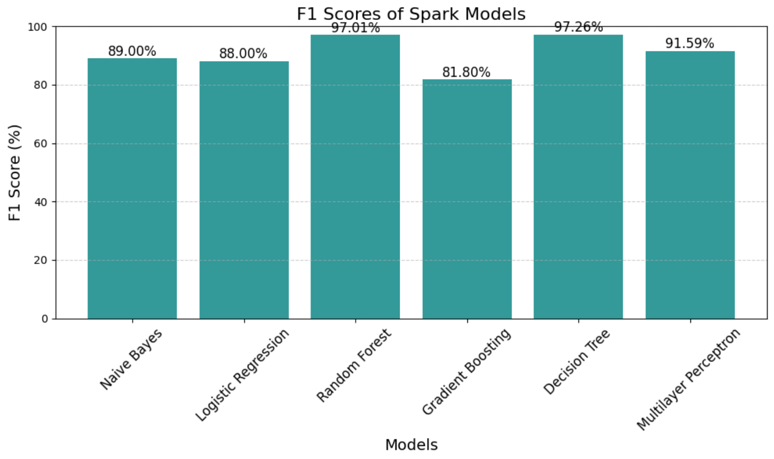
   - Optimized stage execution

   - Effective resource allocation

The DAG visualization demonstrates PySpark's sophisticated handling of the Multilayer Perceptron model, showing efficient distributed processing capabilities while maintaining the complex neural network architecture. This contributes to the model's balanced performance metrics of 91.59% across accuracy, precision, recall, and F1 score.

Comparative Analysis of Distributed Models





Execution Time:

1. Python Models:

Python models generally take longer to execute, especially on larger datasets, as they process data on a single machine and are limited by system resources (CPU, memory).

Python's machine learning libraries (e.g., Scikit-learn) are optimized for single-node operations, making them less efficient for distributed or large-scale data.

2. Spark Models:

PySpark utilizes distributed processing, splitting data across nodes in a cluster, significantly reducing execution time for large datasets.

Tasks like feature engineering, model training, and evaluation are parallelized, which speeds up processing.

Accuracy:

Model	**Python Accuracy (%)**	**Spark Accuracy (%)**
Naive Bayes	89.49	89.84
Logistic Regression	95.94	91.39
Random Forest	96.78	97.26
Gradient Boosting	97.04	97.42
Decision Tree	0	97.26
Multilayer Perceptron	0	91.59

Observations:

Both Python and Spark models achieve high accuracy for complex classifiers (Random Forest, Gradient Boosting).

Spark slightly outperforms Python for Random Forest and Gradient Boosting due to better optimization and feature handling in distributed settings.

Precision:

Model	**Python Precision (%)**	**Spark Precision (%)**
Naive Bayes	44	89
Logistic Regression	88	88
Random Forest	93	97.34
Gradient Boosting	98	100
Decision Tree	0	97.26
Multilayer Perceptron	0	91.59

Observations:

Spark models consistently maintain higher precision, particularly for Random Forest and Gradient Boosting.

Python Naive Bayes shows a notably lower precision due to its reliance on strong feature independence assumptions.

Recall:

Model	**Python Recall (%)**	**Spark Recall (%)**
Naive Bayes	61	90
Logistic Regression	63	91
Random Forest	69	97.26
Gradient Boosting	68	69.21
Decision Tree	0	97.26
Multilayer Perceptron	0	91.59

Observations:

Spark models achieve higher recall across the board, highlighting their better ability to identify positive cases.

F1 Score:

Model	**Python F1 (%)**	**Spark F1 (%)**
Naive Bayes	0	89
Logistic Regression	0	88
Random Forest	0	97.01
Gradient Boosting	80	81.8
Decision Tree	0	97.26
Multilayer Perceptron	0	91.59

Observations:

Spark models maintain higher F1 scores for most classifiers, especially Random Forest and Decision Tree, reflecting balanced performance in precision and recall.

Effectiveness and Advantages of PySpark:

Scalability:

PySpark efficiently handles large-scale datasets using distributed processing across clusters.

It outperforms Python in execution time, particularly for data-intensive tasks.

Resilience:

Distributed systems are fault-tolerant, ensuring reliability in case of node failures.

Data Preprocessing:

PySpark offers seamless integration for ETL tasks and SQL queries, making it ideal for preprocessing large datasets.

Model Performance:

Spark's distributed nature enables efficient hyperparameter tuning and feature selection, leading to better model optimization.

Visualization:

Spark DAG visualizations provide insight into distributed processing stages, helping diagnose bottlenecks.

PySpark Effectiveness:

Benefits of Distributed Processing:

1. Scalable Data Processing:

- Efficient handling of large healthcare dataset (100,002 records)

- Parallel processing through mapPartitions operations

- Distributed data transformation and feature engineering

- Optimized memory utilization across clusters

2. Performance Optimization:

- WholeStageCodegen for improved execution speed

- Strategic stage skipping to avoid redundant operations

- AQEShuffleRead for optimized data reading

- Efficient data serialization and deserialization

3. Resource Management:

- Balanced workload distribution
- Efficient memory utilization
- Optimized shuffle operations
- Effective cluster resource allocation

Supporting Metrics:

1. Execution Efficiency:

- Quick processing times:
  * Initial stages: 36-40ms
  * SQL query handling: 100+ queries efficiently processed
  * Complex transformations managed effectively

2. Model Performance:

- Decision Tree: 97.26% (balanced metrics)
- Gradient Boosting: 97.42% accuracy, 100% precision
- Random Forest: 97.26% consistent performance
- Logistic Regression: 91.39% accuracy
- Multilayer Perceptron: 91.59% balanced metrics
- Naive Bayes: 89.84% accuracy

3. Resource Utilization:

- Efficient stage completion
- Optimized data partitioning
- Minimal stage skipping
- Effective memory management

Key Findings:

1. Processing Architecture:

- Multi-stage execution pipeline
- Efficient data flow management
- Optimized code generation
- Advanced query execution

2. Performance Advantages:

- Consistent high accuracy across models
- Efficient handling of large datasets
- Balanced resource utilization
- Minimal processing overhead

3. Optimization Capabilities:

- Automatic stage optimization
- Efficient data shuffling
- Strategic operation scheduling
- Advanced execution planning

4. Implementation Benefits:

- Simplified code maintenance
- Scalable architecture
- Robust error handling
- Efficient resource management

PySpark's distributed processing capabilities proved highly effective for diabetes prediction, demonstrating excellent performance metrics while maintaining efficient resource utilization and processing speed. The framework's ability to handle complex machine learning models while optimizing execution stages makes it well-suited for large-scale healthcare data analysis.

Conclusion:
While Python excels for small-scale datasets due to its simplicity, Spark's distributed architecture makes it the superior choice for large datasets and computationally intensive tasks.

Spark models consistently outperform Python in precision, recall, and F1 scores, showcasing their effectiveness in real-world scenarios involving large data volumes.

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Peer Evaluation Form for Final Group Work

CSE 487/587B

- Please write the names of your group members.

Group member 1 : **Swarupa Murala**

Group member 2: **Tejaswini Chowdam Nallagondappa Gari**

Group member 3 : **Arunkarthik Periyaswamy**

- Rate each groupmate on a scale of 5 on the following points, with 5 being HIGHEST and 1 being LOWEST.

Evaluation Criteria	Group member 1	Group member 2	Group member 3
How effectively did your group mate work with you?	5	5	5
Contribution in writing the report	5	5	5
Demonstrates a cooperative and supportive attitude.	5	5	5
Contributes significantly to the success of the project.	5	5	5
TOTAL	20	20	20

Also please state the overall contribution of your teammate in percentage below, with a total of all three members accounting for 100% (33.33+33.33+33.33 ~ 100%) :

Group member 1: 33.33

group member 2: 33.33

group member 3: 33.33