AI BASED DIABETES PREDICTION SYSTEM

Phase 3: Development Part 1

Todo:

- Load the dataset
- Preprocess it
- Perform different analysis as needed
- Document all above steps

Step 1: Importing Libraries

We will start by importing all the necessary libraries needed.

```
# Importing necessary libraries

import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plt
import seaborn as sns
```

Step 2: Loading the Dataset

Next we will load the diabetes dataset from the provided Kaggle link into our Jupyter Notebook. This dataset contains relevant medical features and information about diabetes.

```
# Load the diabetes dataset from the URL

dataset_url = "/content/dataset/diabetes.csv"
data = pd.read_csv(dataset_url)
```

Step 3: Data Exploration

We'll conduct initial data exploration to understand the structure and characteristics of the dataset. This includes examining data types, summary statistics, and detecting missing values.

```
# Display the first few rows of the dataset
data.head()

# Get an overview of the dataset
```

```
data.info()

# Check for missing values
data.isnull().sum()

# Summary statistics
data.describe()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  -------                   --------------  ------
 0   Pregnancies               768 non-null    int64
 1   Glucose                   768 non-null    int64
 2   BloodPressure             768 non-null    int64
 3   SkinThickness             768 non-null    int64
 4   Insulin                   768 non-null    int64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB

       Pregnancies     Glucose  BloodPressure  SkinThickness
Insulin  \
count   768.000000  768.000000     768.000000     768.000000
768.000000
mean      3.845052  120.894531      69.105469      20.536458
79.799479
std       3.369578   31.972618      19.355807      15.952218
115.244002
min       0.000000    0.000000       0.000000       0.000000
0.000000
25%       1.000000   99.000000      62.000000       0.000000
0.000000
50%       3.000000  117.000000      72.000000      23.000000
30.500000
75%       6.000000  140.250000      80.000000      32.000000
127.250000
max      17.000000  199.000000     122.000000      99.000000
846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    31.992578                  0.471876   33.240885    0.348958
std      7.884160                  0.331329   11.760232    0.476951
min      0.000000                  0.078000   21.000000    0.000000
25%     27.300000                  0.243750   24.000000    0.000000
```

```
50%      32.000000                    0.372500   29.000000    0.000000
75%      36.600000                    0.626250   41.000000    1.000000
max      67.100000                    2.420000   81.000000    1.000000

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import numpy as np
from google.colab import autoviz

def histogram(df, colname, num_bins=20, figscale=1):
  from matplotlib import pyplot as plt
  df[colname].plot(kind='hist', bins=num_bins, title=colname,
figsize=(8*figscale, 4*figscale))
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = histogram(_df_0, *['Pregnancies'], **{})
chart

import numpy as np
from google.colab import autoviz

def histogram(df, colname, num_bins=20, figscale=1):
  from matplotlib import pyplot as plt
  df[colname].plot(kind='hist', bins=num_bins, title=colname,
figsize=(8*figscale, 4*figscale))
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = histogram(_df_1, *['Glucose'], **{})
chart

import numpy as np
from google.colab import autoviz

def histogram(df, colname, num_bins=20, figscale=1):
  from matplotlib import pyplot as plt
  df[colname].plot(kind='hist', bins=num_bins, title=colname,
figsize=(8*figscale, 4*figscale))
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = histogram(_df_2, *['BloodPressure'], **{})
chart

import numpy as np
from google.colab import autoviz
```

```
def histogram(df, colname, num_bins=20, figscale=1):
  from matplotlib import pyplot as plt
  df[colname].plot(kind='hist', bins=num_bins, title=colname,
figsize=(8*figscale, 4*figscale))
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = histogram(_df_3, *['SkinThickness'], **{})
chart

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import numpy as np
from google.colab import autoviz

def scatter_plot(df, x_colname, y_colname, figscale=1, alpha=.8):
  from matplotlib import pyplot as plt
  plt.figure(figsize=(6 * figscale, 6 * figscale))
  df.plot(kind='scatter', x=x_colname, y=y_colname, s=(32 * figscale),
alpha=alpha)
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = scatter_plot(_df_4, *['Pregnancies', 'Glucose'], **{})
chart

import numpy as np
from google.colab import autoviz

def scatter_plot(df, x_colname, y_colname, figscale=1, alpha=.8):
  from matplotlib import pyplot as plt
  plt.figure(figsize=(6 * figscale, 6 * figscale))
  df.plot(kind='scatter', x=x_colname, y=y_colname, s=(32 * figscale),
alpha=alpha)
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = scatter_plot(_df_5, *['Glucose', 'BloodPressure'], **{})
chart

import numpy as np
from google.colab import autoviz

def scatter_plot(df, x_colname, y_colname, figscale=1, alpha=.8):
  from matplotlib import pyplot as plt
  plt.figure(figsize=(6 * figscale, 6 * figscale))
  df.plot(kind='scatter', x=x_colname, y=y_colname, s=(32 * figscale),
alpha=alpha)
```

```
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = scatter_plot(_df_6, *['BloodPressure', 'SkinThickness'], **{})
chart

import numpy as np
from google.colab import autoviz

def scatter_plot(df, x_colname, y_colname, figscale=1, alpha=.8):
  from matplotlib import pyplot as plt
  plt.figure(figsize=(6 * figscale, 6 * figscale))
  df.plot(kind='scatter', x=x_colname, y=y_colname, s=(32 * figscale),
alpha=alpha)
  plt.gca().spines[['top', 'right',]].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = scatter_plot(_df_7, *['SkinThickness', 'Insulin'], **{})
chart

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import numpy as np
from google.colab import autoviz

def value_plot(df, y, figscale=1):
  from matplotlib import pyplot as plt
  df[y].plot(kind='line', figsize=(8 * figscale, 4 * figscale),
title=y)
  plt.gca().spines[['top', 'right']].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = value_plot(_df_8, *['Pregnancies'], **{})
chart

import numpy as np
from google.colab import autoviz

def value_plot(df, y, figscale=1):
  from matplotlib import pyplot as plt
  df[y].plot(kind='line', figsize=(8 * figscale, 4 * figscale),
title=y)
  plt.gca().spines[['top', 'right']].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = value_plot(_df_9, *['Glucose'], **{})
chart
```

```
import numpy as np
from google.colab import autoviz

def value_plot(df, y, figscale=1):
  from matplotlib import pyplot as plt
  df[y].plot(kind='line', figsize=(8 * figscale, 4 * figscale),
title=y)
  plt.gca().spines[['top', 'right']].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = value_plot(_df_10, *['BloodPressure'], **{})
chart

import numpy as np
from google.colab import autoviz

def value_plot(df, y, figscale=1):
  from matplotlib import pyplot as plt
  df[y].plot(kind='line', figsize=(8 * figscale, 4 * figscale),
title=y)
  plt.gca().spines[['top', 'right']].set_visible(False)
  plt.tight_layout()
  return autoviz.MplChart.from_current_mpl_state()

chart = value_plot(_df_11, *['SkinThickness'], **{})
chart
```

Step 4: Data Preprocessing

Data preprocessing is crucial to ensure the dataset is suitable for model development. Steps will include:

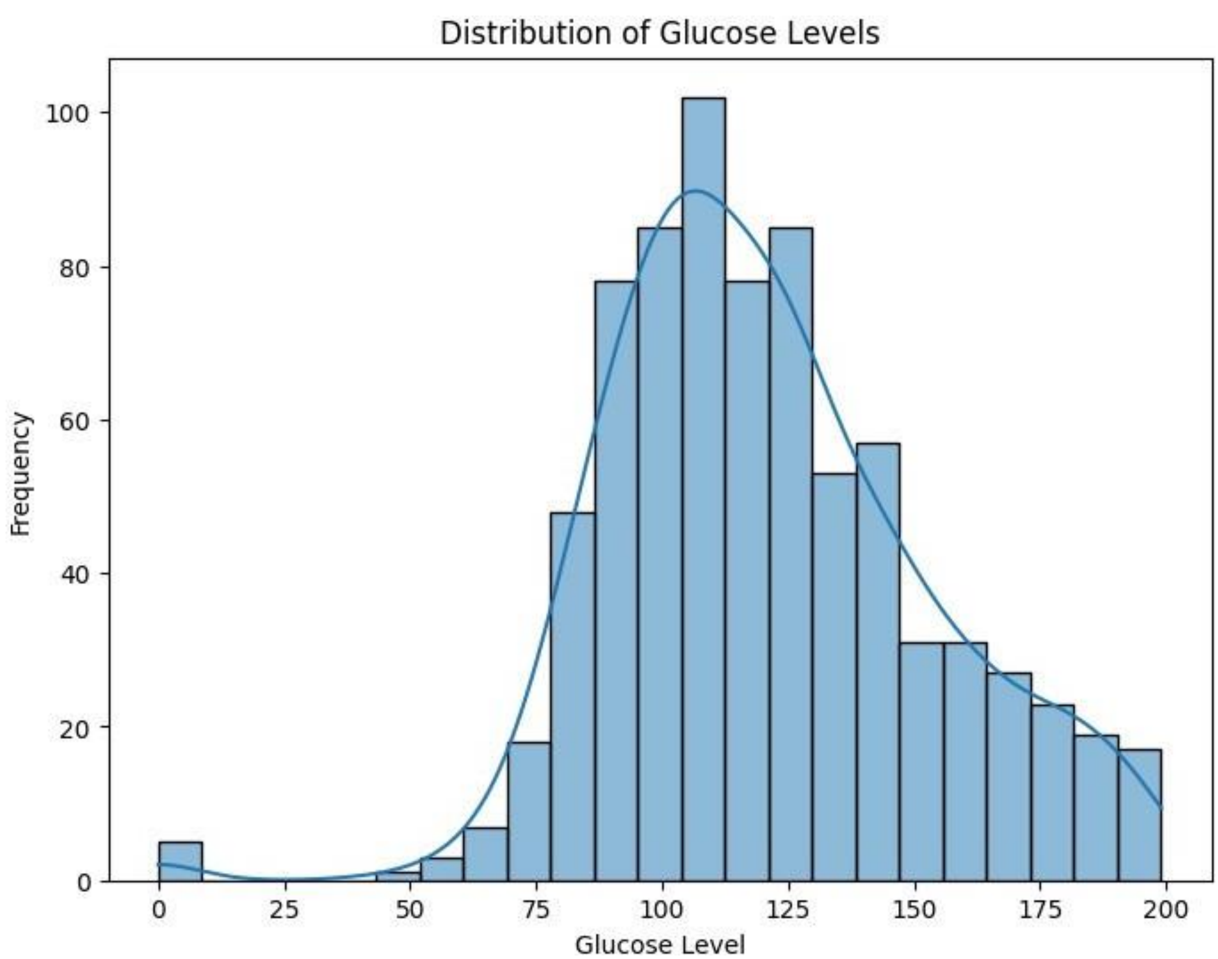
- *Handling missing data through imputation.*
- *Normalizing and scaling numerical features.*
- *Encoding categorical variables.*
- *Balancing class distribution, as diabetes prediction datasets are often imbalanced.*

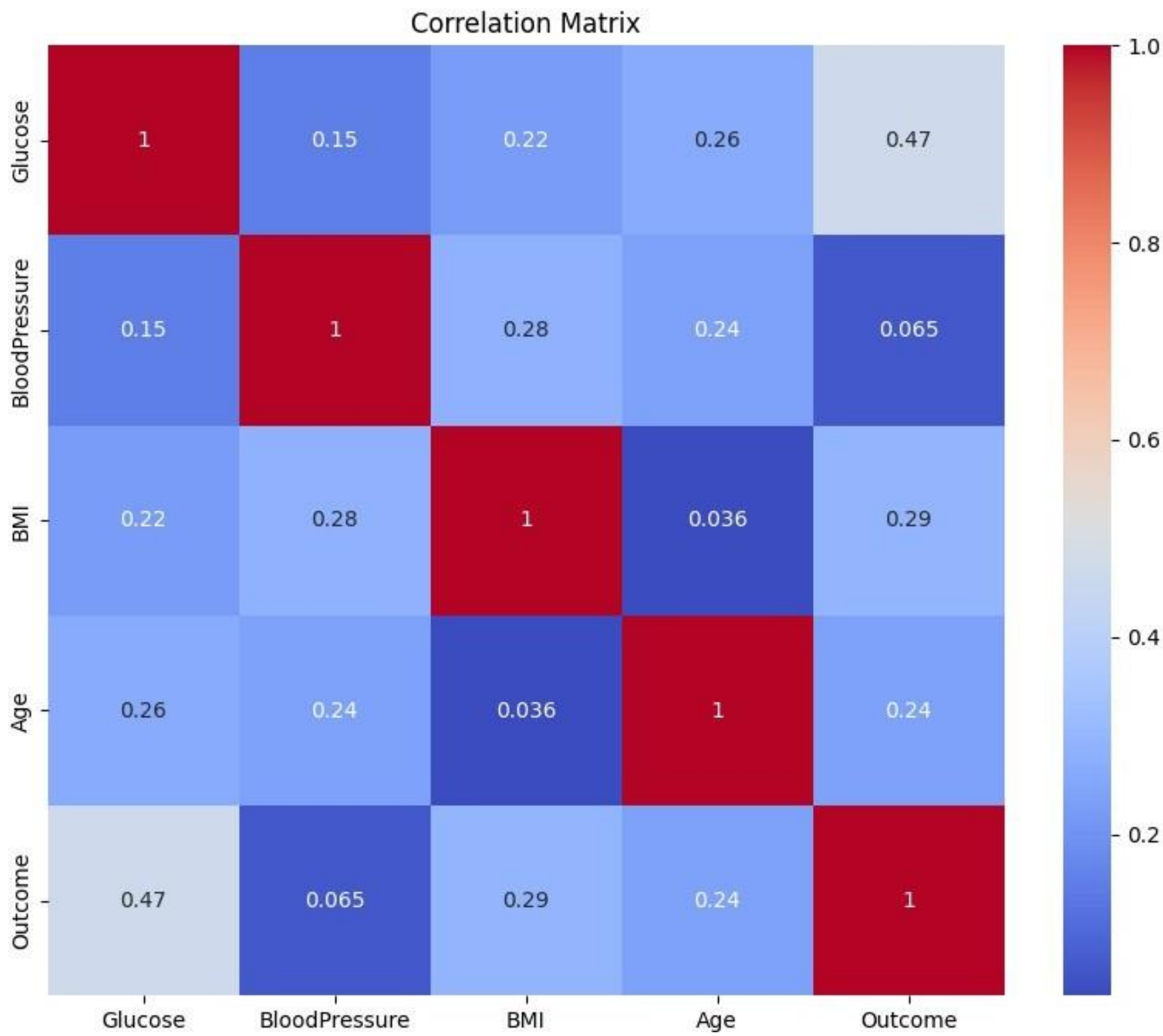
```
# Handle missing values (if any)
# Example: Replace missing values in a specific column (e.g., Glucose)
with the mean of that column
data['Glucose'].fillna(data['Glucose'].mean(), inplace=True)

# Feature selection: Choose relevant features based on domain
knowledge and data analysis
# Example: Select relevant columns
selected_features = ['Glucose', 'BloodPressure', 'BMI', 'Age',
'Outcome']
data = data[selected_features]
```

Step 5: Data Visualization

We'll create data visualizations to gain insights into the relationships between features and the distribution of diabetes cases. This will help us understand feature importance.

```
# Visualize the distribution of glucose levels
plt.figure(figsize=(8, 6))
sns.histplot(data['Glucose'], kde=True)
plt.title('Distribution of Glucose Levels')
plt.xlabel('Glucose Level')
plt.ylabel('Frequency')
plt.show()

# Correlation matrix to see feature relationships
correlation_matrix = data.corr()
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm')
plt.title('Correlation Matrix')
plt.show()
```





Step 6: Feature Engineering

We may perform feature engineering to create new features or transform existing ones based on domain knowledge and insights from data visualization.

```
# Example: Creating a new feature for BMI categories
def categorize_bmi(bmi):
    if bmi < 18.5:
        return 'Underweight'
    elif 18.5 <= bmi < 24.9:
        return 'Normal'
    elif 25 <= bmi < 29.9:
        return 'Overweight'
    else:
        return 'Obese'
```

```
data['BMI Category'] = data['BMI'].apply(categorize_bmi)
```

Step 7: Data Splitting

We will split the dataset into training and testing subsets to prepare for model development and evaluation.

```
from sklearn.model_selection import train_test_split

# Define the features (X) and target (y)
X = data.drop('Outcome', axis=1)
y = data['Outcome']

# Split the data into training and testing sets (e.g., 80% train, 20% test)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Check the shapes of the resulting sets
print("X_train shape:", X_train.shape)
print("X_test shape:", X_test.shape)
```

```
X_train shape: (614, 5)
X_test shape: (154, 5)
```

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