Diabetes Prediction — 01 EDA

Goal: Explore the Pima Indians Diabetes dataset to understand feature distributions, missing values, class balance, and correlations.

Dataset path (relative to this notebook): `../data/diabetes.csv`

In [1]:
```
# ===============
# 0. Setup
# ===============
import os
import sys
import math
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

# Plot config
plt.rcParams['figure.figsize'] = (8, 5)
plt.rcParams['axes.grid'] = True

pd.set_option('display.max_columns', None)
pd.set_option('display.width', 120)

DATA_PATH = os.path.join('C:/Users/nazar/OneDrive/Documentos/machine learning/di
assert os.path.exists(DATA_PATH), f"Dataset not found at {DATA_PATH}. Please pla
```

In [13]:
```
# ===============
# 1. Load data
# ===============
df = pd.read_csv(DATA_PATH, sep=";")  # <--- agregamos sep=";" para separar corr
print("Shape:", df.shape)
print("Columns:", df.columns.tolist())
display(df.head())
```

```
Shape: (768, 9)
Columns: ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome']
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
0	6	148	72	35	0	33.6	
1	1	85	66	29	0	26.6	
2	8	183	64	0	0	23.3	
3	1	89	66	23	94	28.1	
4	0	137	40	35	168	43.1	

In [14]:
```
# ===============
# 2. Quick overview
# ===============
display(df.info())
display(df.describe().T)
```

```
<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
None
```

	count	mean	std	min	25%	50%	
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.

About "zeros" as missing values

In this dataset, certain features use **0** to represent missing measurements. Common columns:

- `Glucose`, `BloodPressure`, `SkinThickness`, `Insulin`, `BMI`

We'll convert 0 → NaN for these to correctly analyze missingness.

In [15]:
```
# Columns where 0 means 'missing'
zero_as_missing = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI'

df_clean = df.copy()
for col in zero_as_missing:
    if col in df_clean.columns:
        df_clean[col] = df_clean[col].replace(0, np.nan)

# Missing summary
```

```
missing_counts = df_clean.isna().sum().sort_values(ascending=False)
missing_ratio = (missing_counts / len(df_clean)).round(3)
missing_table = pd.DataFrame({'missing_count': missing_counts, 'missing_ratio':
display(missing_table[missing_table['missing_count'] > 0])
```

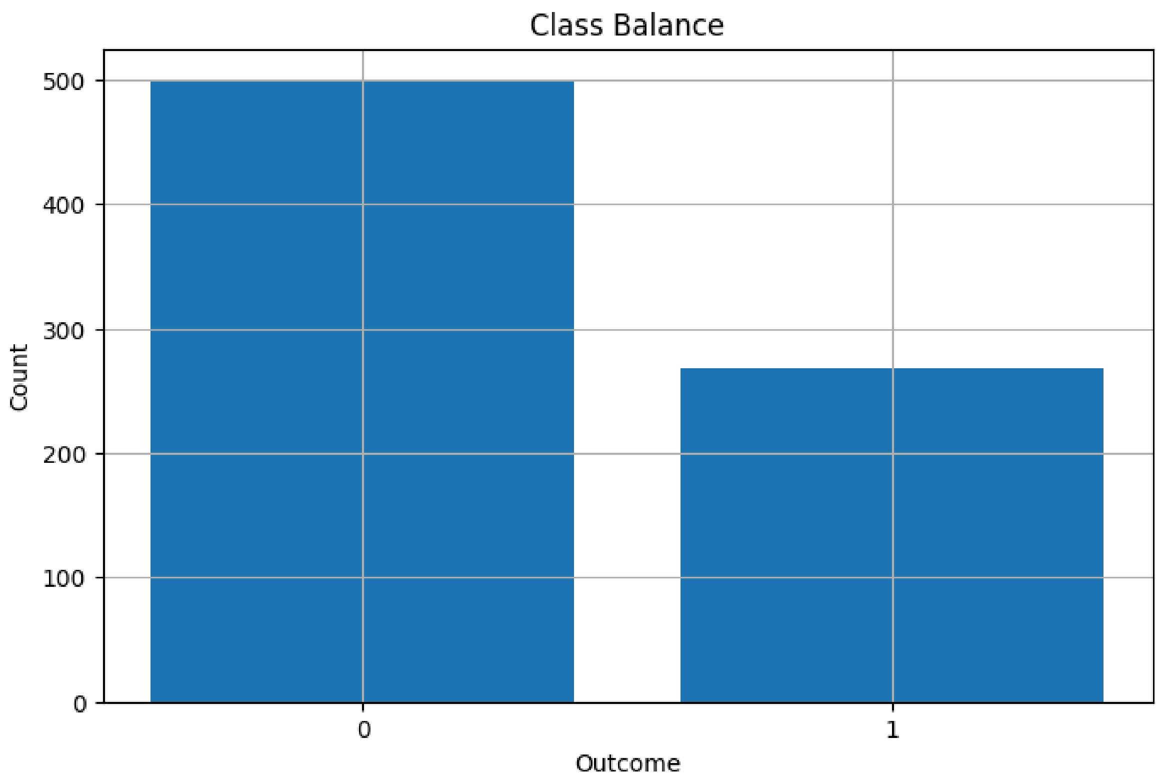
	missing_count	missing_ratio
Insulin	374	0.487
SkinThickness	227	0.296
BloodPressure	35	0.046
BMI	11	0.014
Glucose	5	0.007

Class balance

Check the distribution of the target variable `Outcome` (1 = Diabetes, 0 = No Diabetes).

In [16]:
```
target_col = 'Outcome'
class_counts = df_clean[target_col].value_counts(dropna=False).sort_index()
class_ratio = (class_counts / class_counts.sum()).round(3)
class_summary = pd.DataFrame({'count': class_counts, 'ratio': class_ratio})
display(class_summary)

# Bar plot (matplotlib only, no styles)
fig, ax = plt.subplots()
ax.bar(class_summary.index.astype(str), class_summary['count'])
ax.set_xlabel('Outcome')
ax.set_ylabel('Count')
ax.set_title('Class Balance')
plt.show()
```

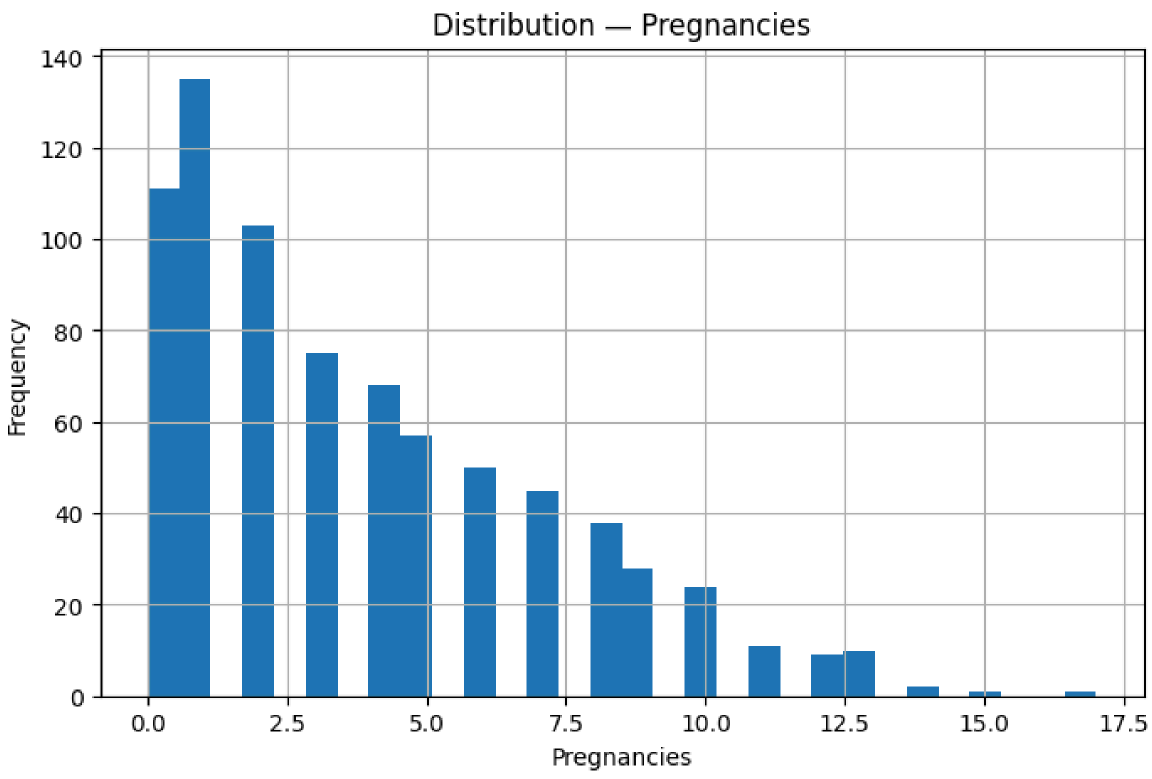
	count	ratio
Outcome		
0	500	0.651
1	268	0.349

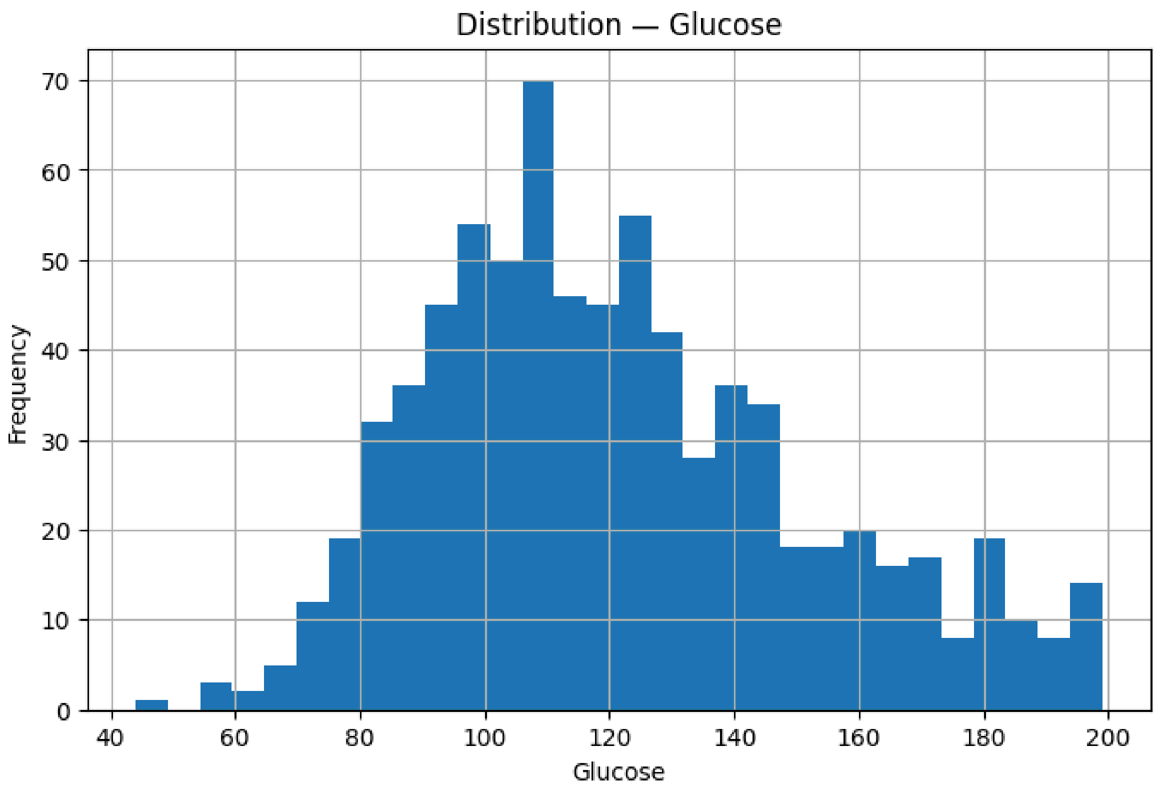


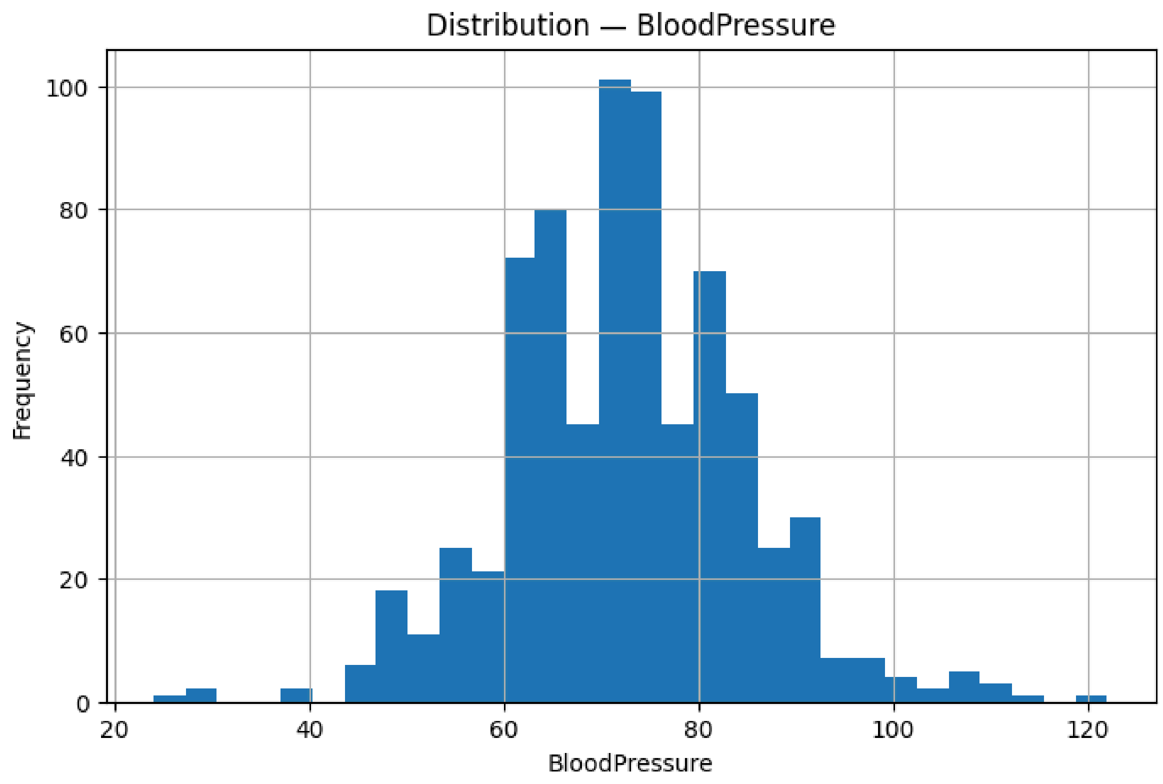
Distributions

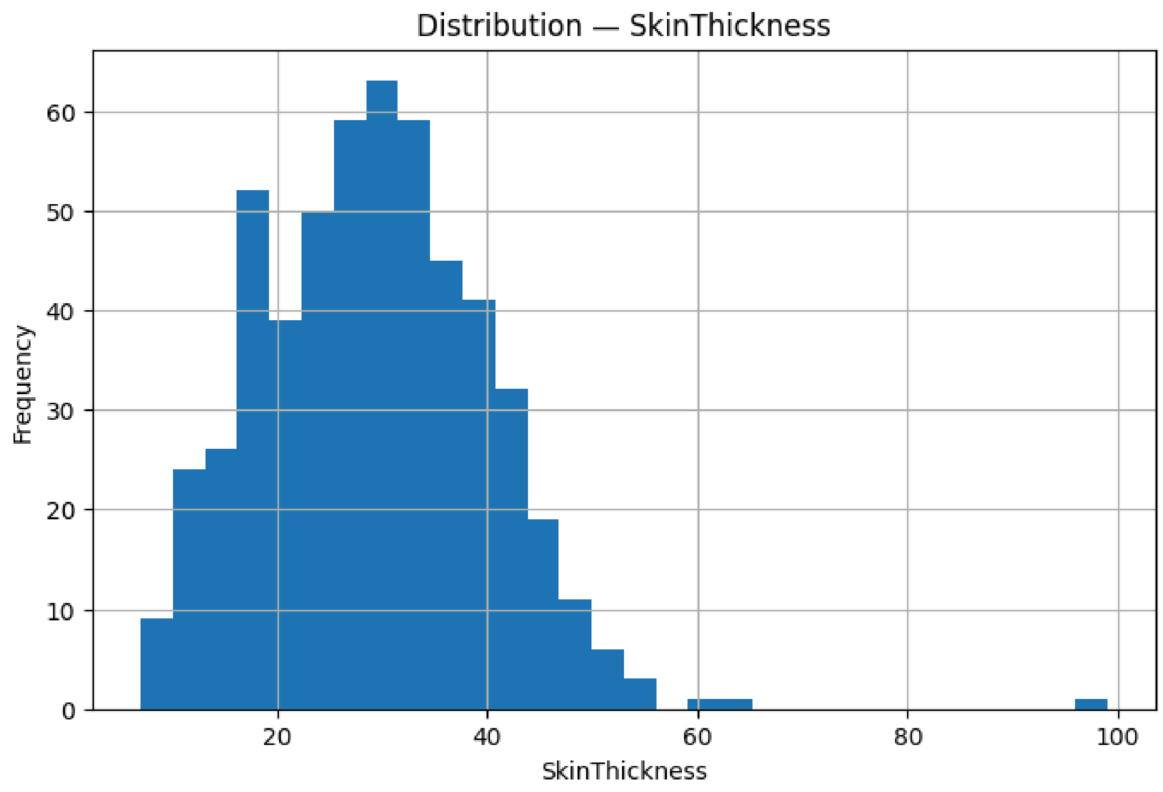
Look at feature distributions to spot skew, outliers, and ranges.

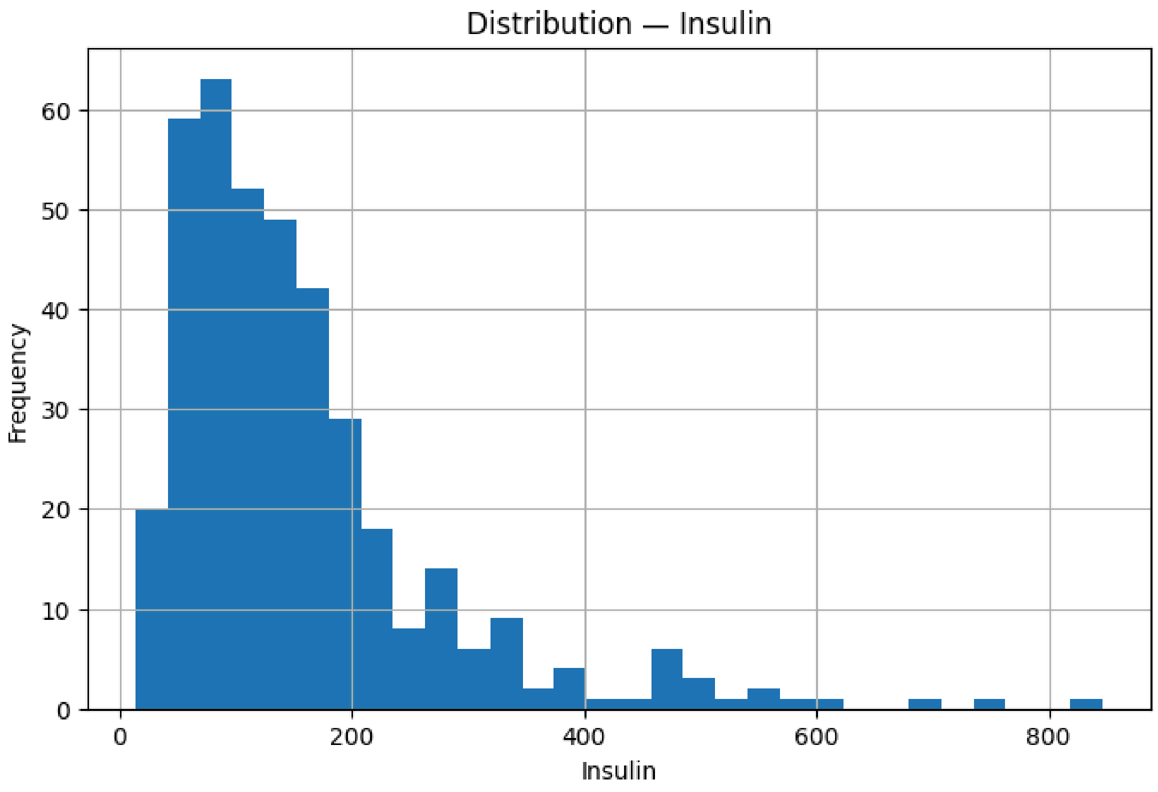
In [17]:
```
feature_cols = [c for c in df_clean.columns if c != target_col]

# Histograms
for col in feature_cols:
    fig, ax = plt.subplots()
    ax.hist(df_clean[col].dropna(), bins=30)
    ax.set_title(f'Distribution — {col}')
    ax.set_xlabel(col)
    ax.set_ylabel('Frequency')
    plt.show()
```

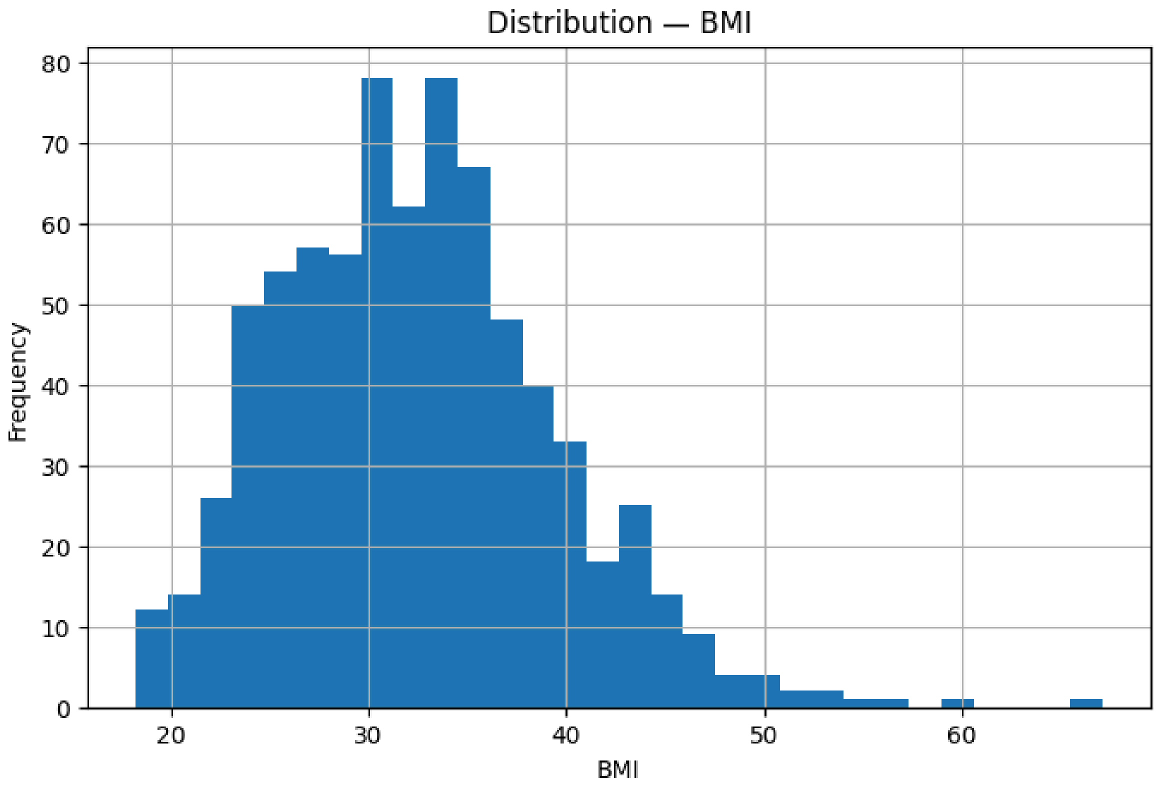

Distribution — Pregnancies
Frequency
Pregnancies
0
20
40
60
80
100
120
140
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5

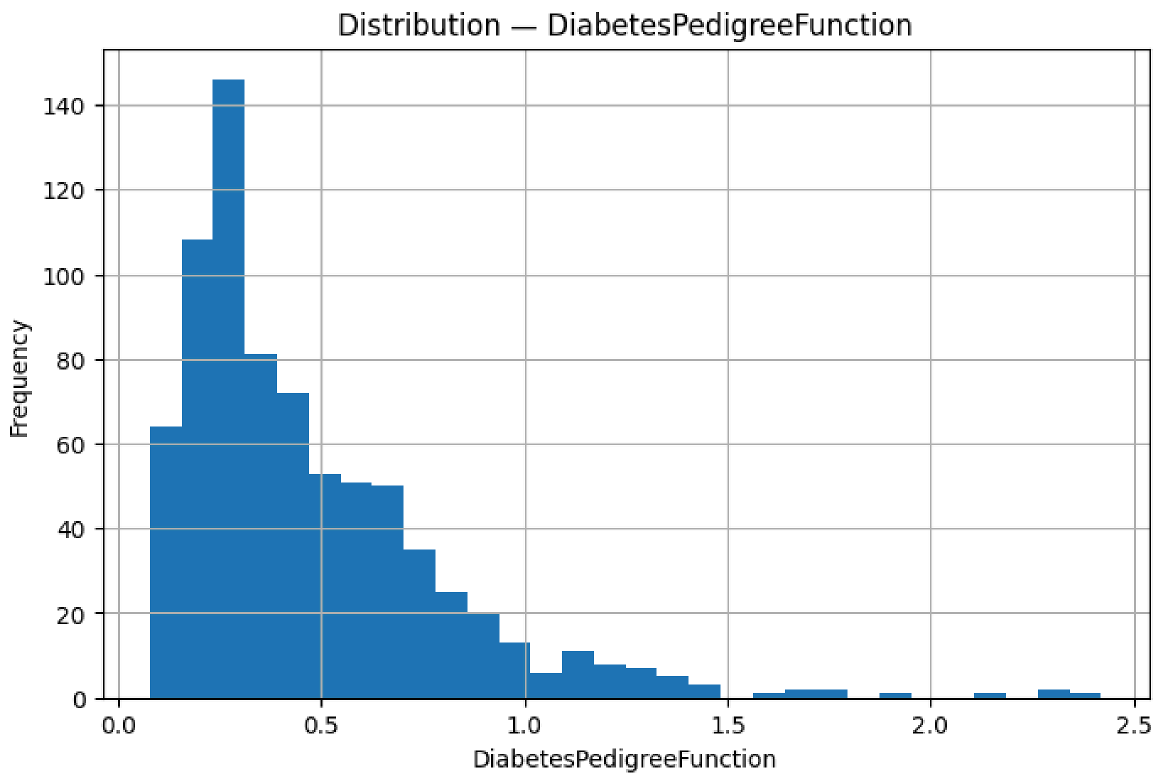

Distribution — Glucose
Frequency
Glucose
0
10
20
30
40
50
60
70
40
60
80
100
120
140
160
180
200

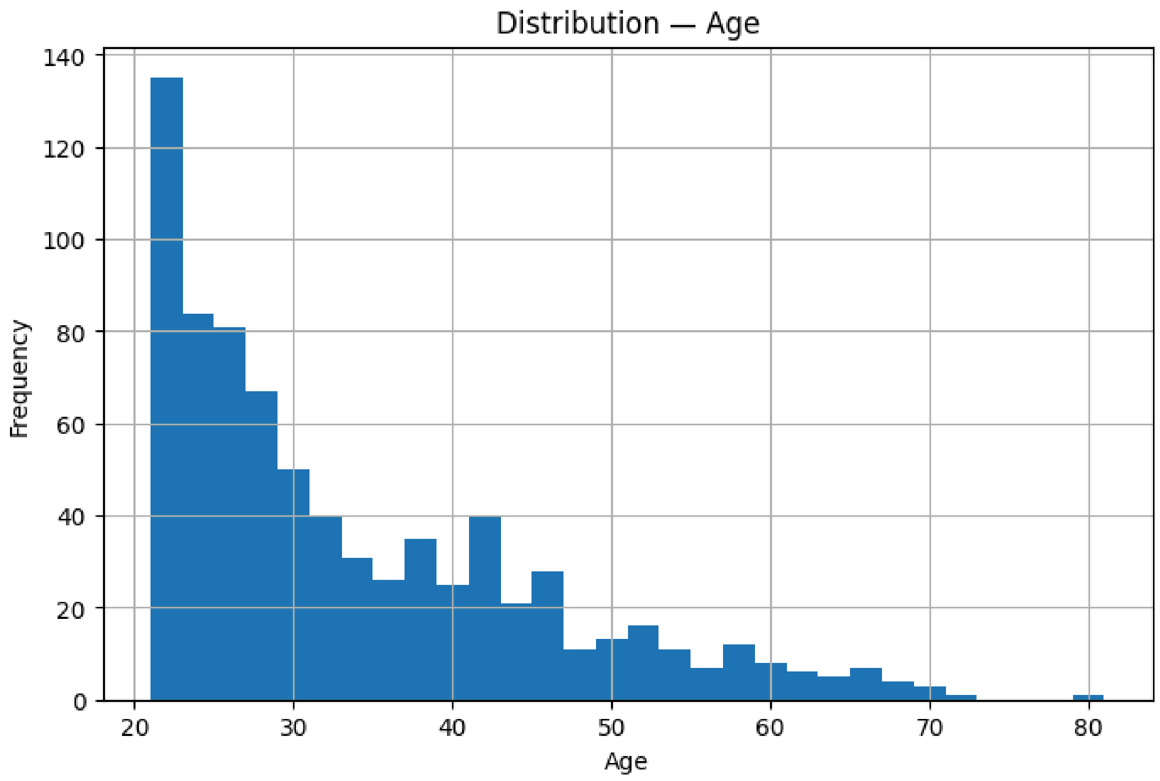

Distribution — BloodPressure
Frequency
BloodPressure
0
20
40
60
80
100
20
40
60
80
100
120


Distribution — SkinThickness
Frequency
SkinThickness
0
10
20
30
40
50
60
20
40
60
80
100


Distribution — Insulin
Frequency
Insulin
0
10
20
30
40
50
60
200
400
600
800


Distribution — BMI
Frequency
BMI
0
10
20
30
40
50
60
70
80
20
30
40
50
60



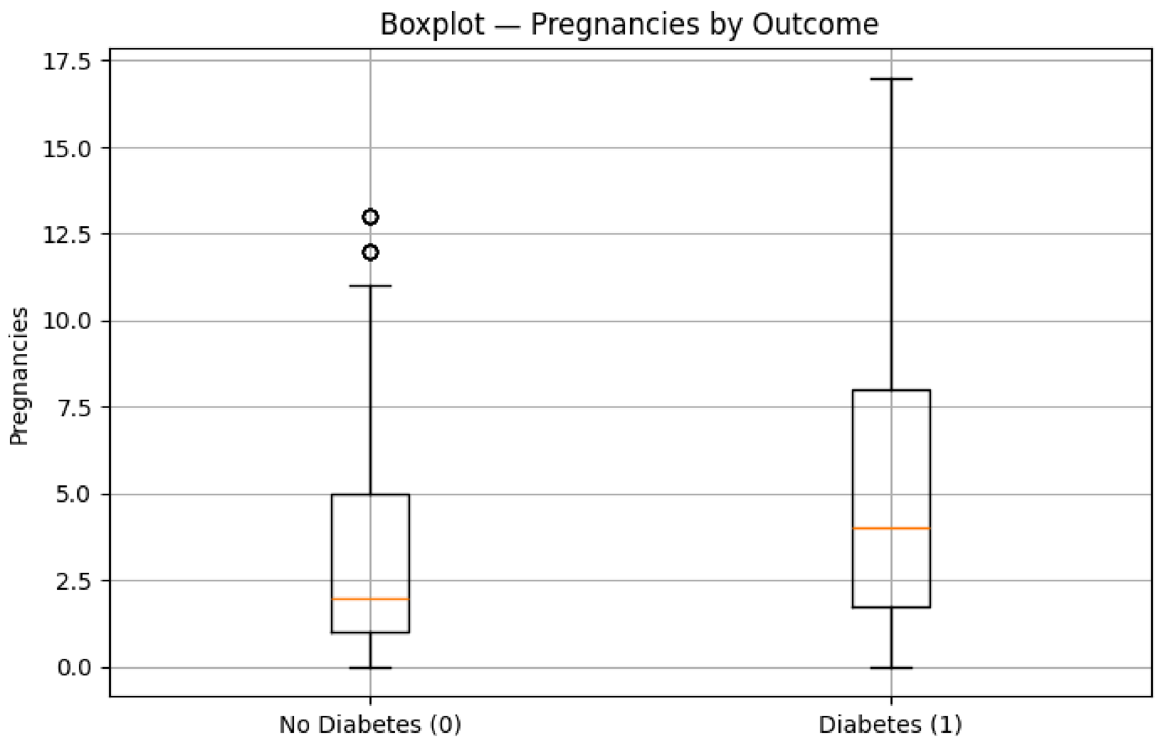


Boxplots by class

Visualize differences in distributions between Outcome classes.

In [18]:
```
for col in feature_cols:
    fig, ax = plt.subplots()
    # Create two arrays for each class
    data0 = df_clean.loc[df_clean[target_col] == 0, col].dropna()
    data1 = df_clean.loc[df_clean[target_col] == 1, col].dropna()
    ax.boxplot([data0, data1], labels=['No Diabetes (0)', 'Diabetes (1)'], showf
    ax.set_title(f'Boxplot — {col} by Outcome')
    ax.set_ylabel(col)
    plt.show()
```

```
C:\Users\nazar\AppData\Local\Temp\ipykernel_7608\787247708.py:6: MatplotlibDeprec
ationWarning: The 'labels' parameter of boxplot() has been renamed 'tick_labels'
since Matplotlib 3.9; support for the old name will be dropped in 3.11.
  ax.boxplot([data0, data1], labels=['No Diabetes (0)', 'Diabetes (1)'], showflie
rs=True)
```



```
C:\Users\nazar\AppData\Local\Temp\ipykernel_7608\787247708.py:6: MatplotlibDeprec
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since Matplotlib 3.9; support for the old name will be dropped in 3.11.
  ax.boxplot([data0, data1], labels=['No Diabetes (0)', 'Diabetes (1)'], showflie
rs=True)
```

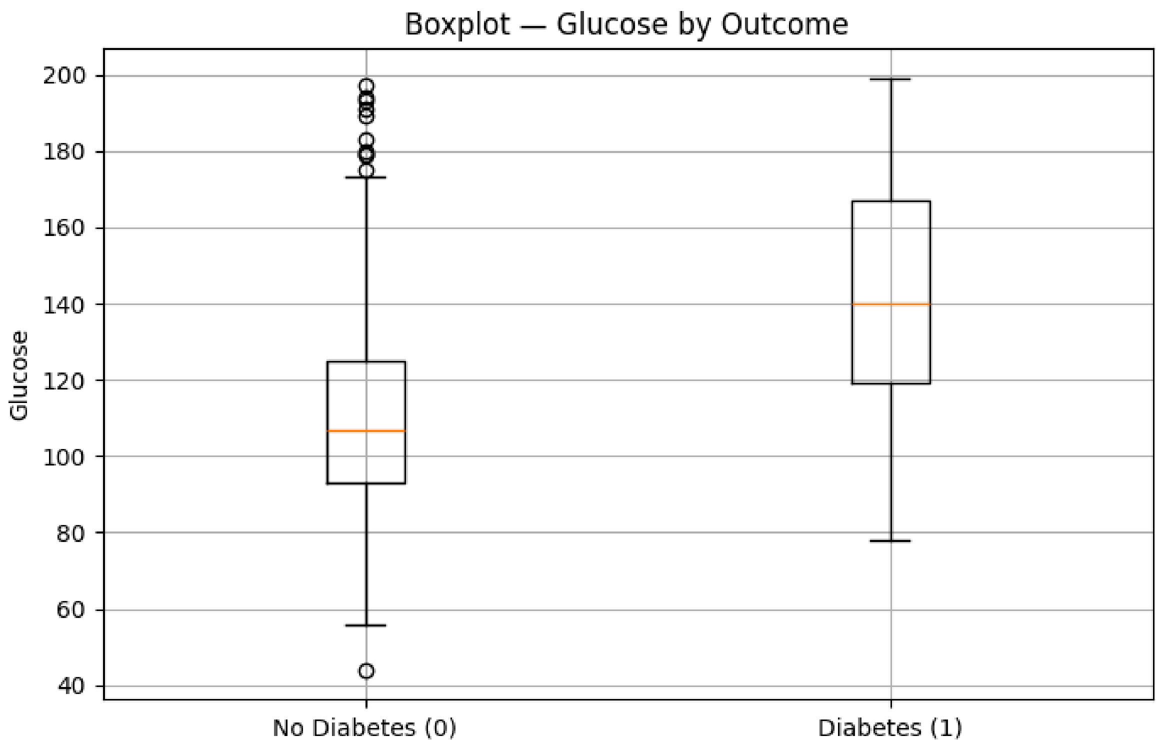

```
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rs=True)
```

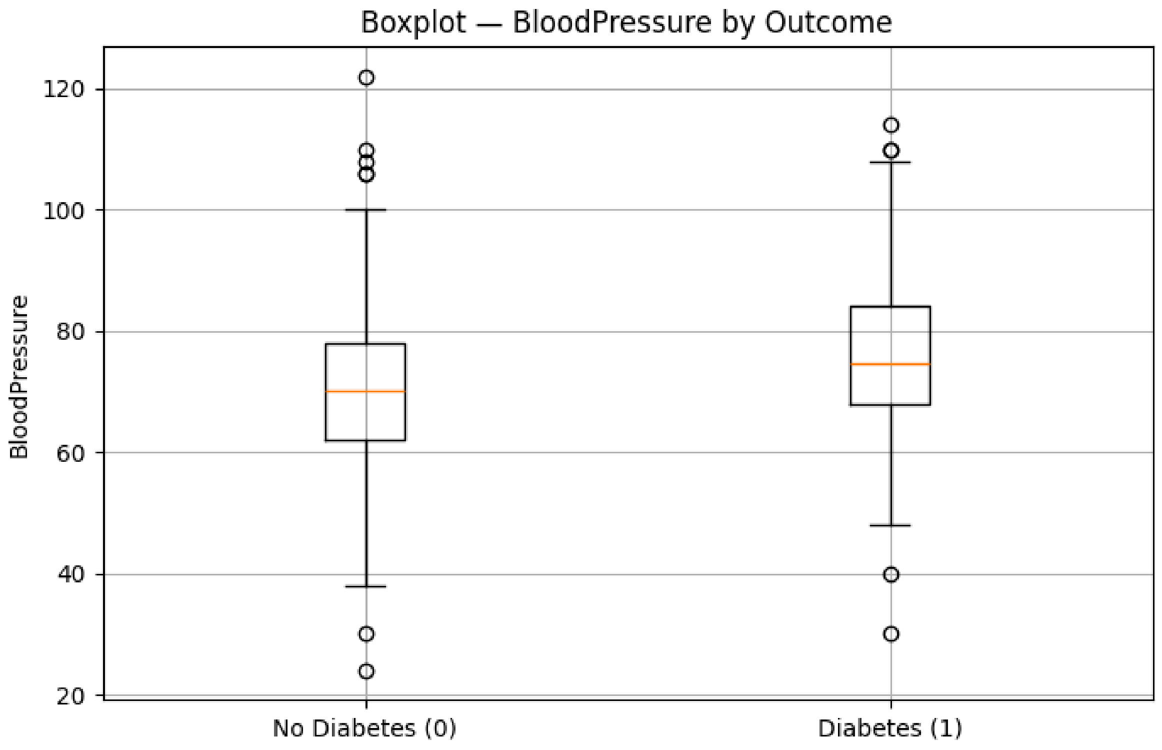

```
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  ax.boxplot([data0, data1], labels=['No Diabetes (0)', 'Diabetes (1)'], showflie
rs=True)
```

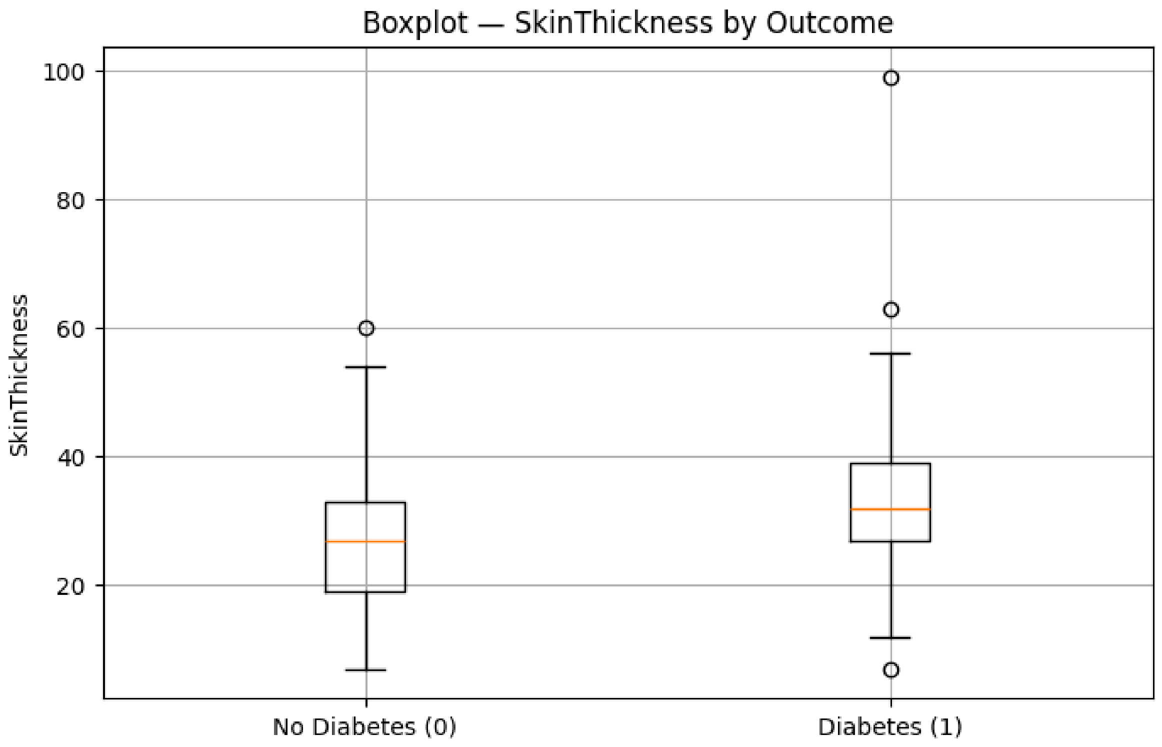

```
C:\Users\nazar\AppData\Local\Temp\ipykernel_7608\787247708.py:6: MatplotlibDeprec
ationWarning: The 'labels' parameter of boxplot() has been renamed 'tick_labels'
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rs=True)
```

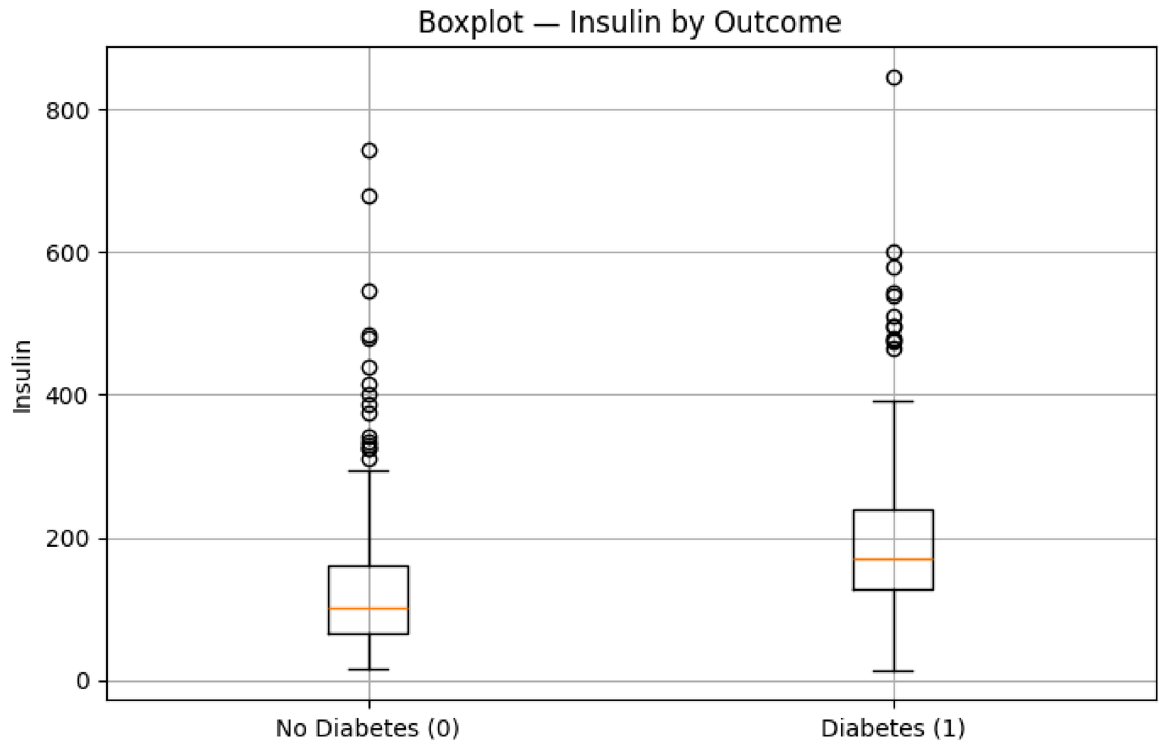

```
C:\Users\nazar\AppData\Local\Temp\ipykernel_7608\787247708.py:6: MatplotlibDeprec
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  ax.boxplot([data0, data1], labels=['No Diabetes (0)', 'Diabetes (1)'], showflie
rs=True)
```

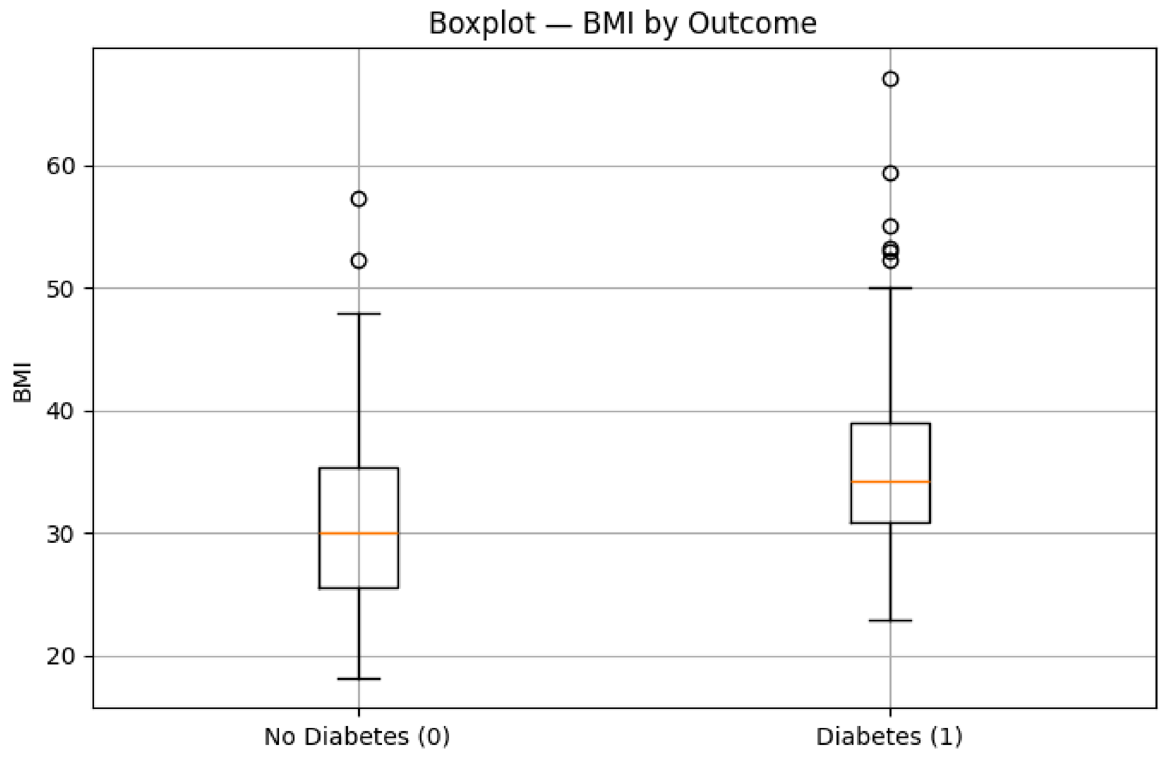

```
C:\Users\nazar\AppData\Local\Temp\ipykernel_7608\787247708.py:6: MatplotlibDeprec
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rs=True)
```

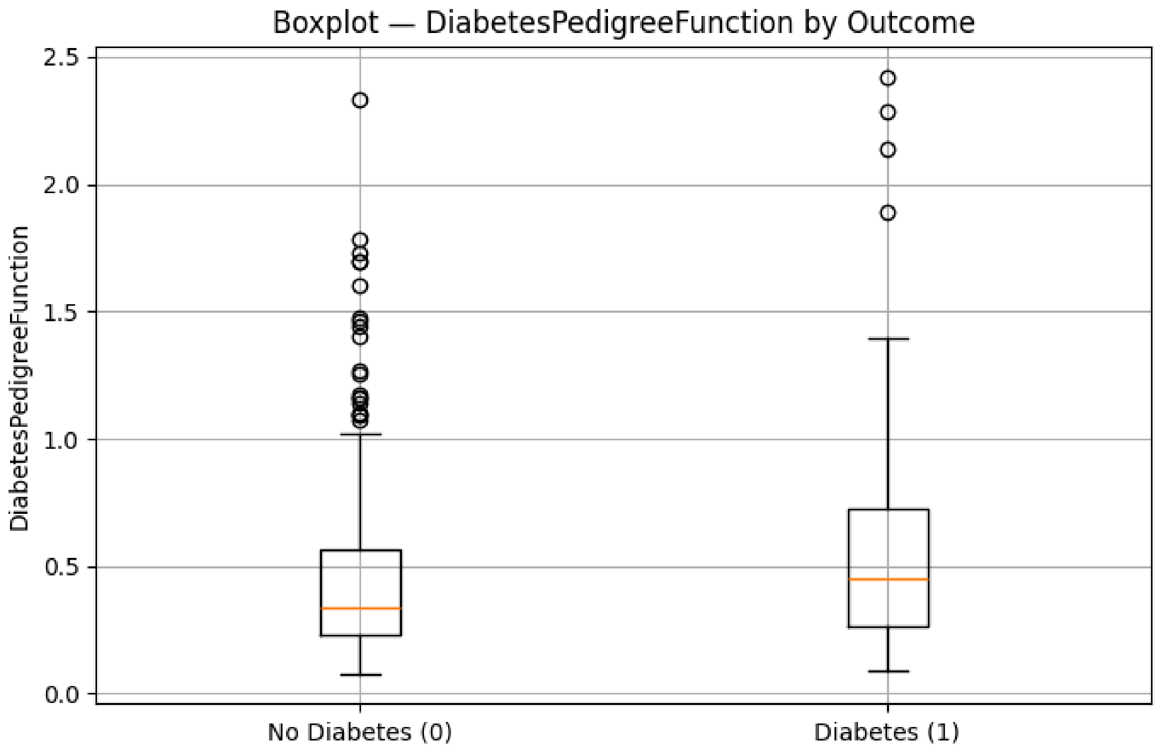

```
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since Matplotlib 3.9; support for the old name will be dropped in 3.11.
  ax.boxplot([data0, data1], labels=['No Diabetes (0)', 'Diabetes (1)'], showflie
rs=True)
```
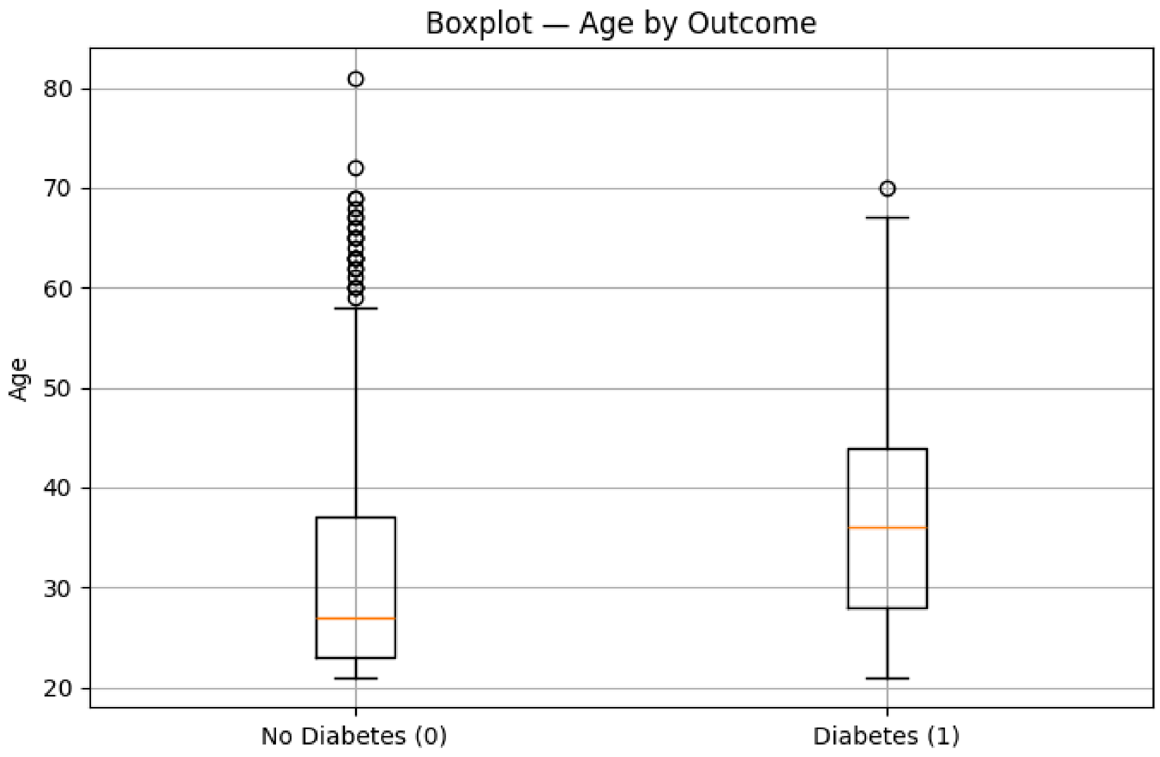
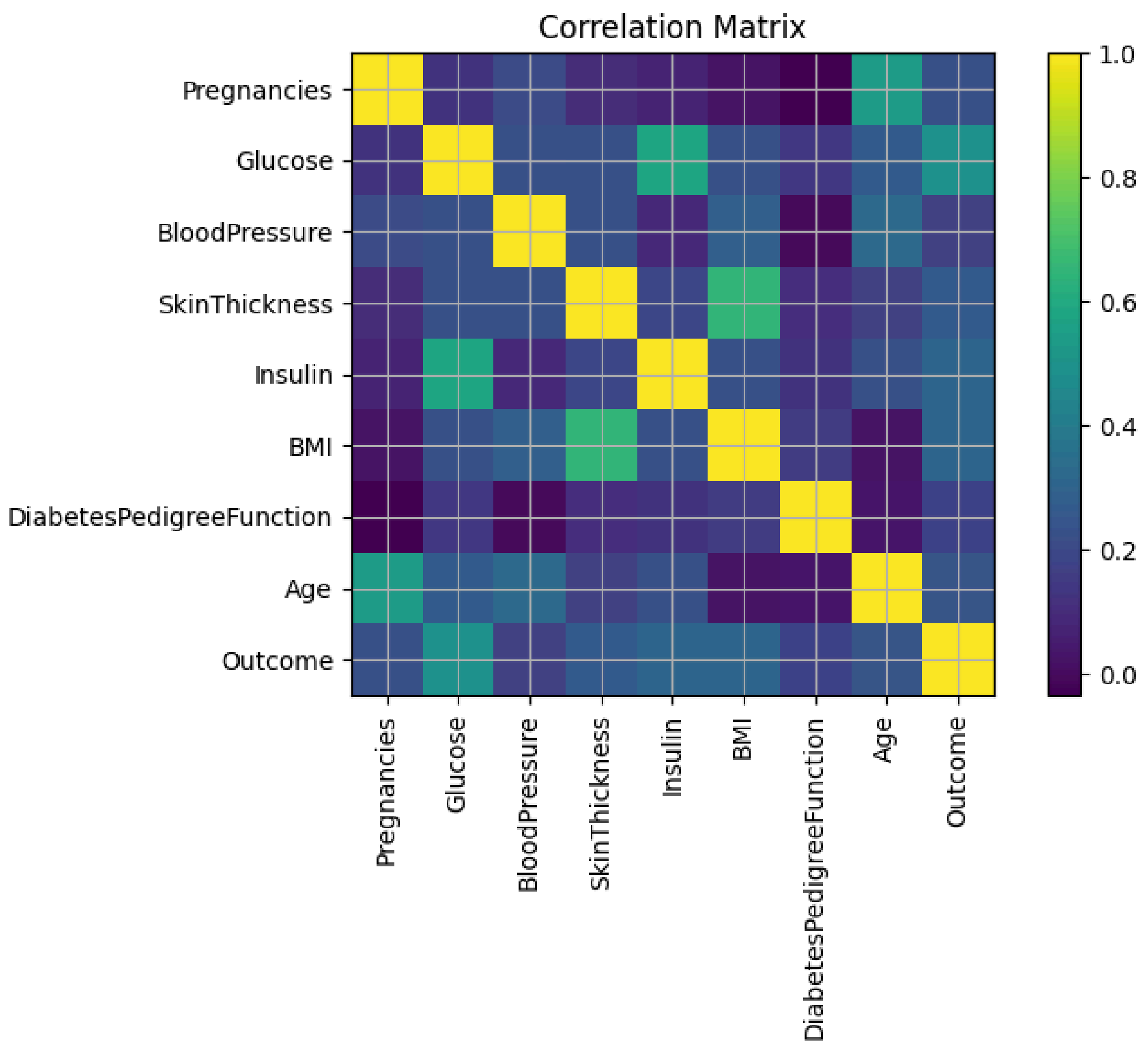



Correlation analysis

Compute Pearson correlation for numeric variables and visualize a simple correlation matrix.

In [19]:
```python
numeric_df = df_clean.select_dtypes(include=[np.number])
corr = numeric_df.corr(numeric_only=True)

display(corr.style.background_gradient(axis=None, cmap='Greys'))  # rendered as

# Also show a plain matplotlib image for correlation matrix values
fig, ax = plt.subplots(figsize=(8, 6))
cax = ax.imshow(corr, interpolation='nearest')
ax.set_title('Correlation Matrix')
ax.set_xticks(range(len(corr.columns)))
ax.set_yticks(range(len(corr.columns)))
ax.set_xticklabels(corr.columns, rotation=90)
ax.set_yticklabels(corr.columns)
fig.colorbar(cax)
plt.tight_layout()
plt.show()
```

	Pregnancies	**Glucose**	**BloodPressure**	**SkinThickness**	**Insulin**
Pregnancies	1.000000	0.128135	0.214178	0.100239	0.082171
Glucose	0.128135	1.000000	0.223192	0.228043	0.581186
BloodPressure	0.214178	0.223192	1.000000	0.226839	0.098272
SkinThickness	0.100239	0.228043	0.226839	1.000000	0.184888
Insulin	0.082171	0.581186	0.098272	0.184888	1.000000
BMI	0.021719	0.232771	0.289230	0.648214	0.228050
DiabetesPedigreeFunction	-0.033523	0.137246	-0.002805	0.115016	0.130395
Age	0.544341	0.267136	0.330107	0.166816	0.220261
Outcome	0.221898	0.494650	0.170589	0.259491	0.303454



Notes & Findings

Use this section to write observations:

- Which features differ the most between classes?
- Are there missing patterns worth addressing?
- Any strong correlations or multicollinearity?
- Potential feature engineering ideas.

Optional: simple imputation for later modeling

We won't model here, but you can prepare a processed dataset with median imputation for numeric columns.

In [24]:
```
import os

# Ruta completa al archivo CSV
out_path = os.path.join('C:/Users/nazar/OneDrive/Documentos/machine learning',
                        'diabetes_processed.csv')

# Crear carpeta si no existe
```

```python
os.makedirs(os.path.dirname(out_path), exist_ok=True)

# Guardar dataset procesado
processed.to_csv(out_path, index=False)
print(f'Processed dataset saved to: {out_path}')
```

```
Processed dataset saved to: C:/Users/nazar/OneDrive/Documentos/machine learning\d
iabetes_processed.csv
```