databricks
(https://databricks.com)
Patient Readmission Model (Python)

Import notebook

Import Libraries

```
# Pandas is a Python data analysis library used for analysing data
import pandas as pd

# Is a Python library used for numerical analysis/to perform mathematical calculations
import numpy as np
```

Data Ingestion

```
data_path = '/Workspace/Users/michaelarobyn01@gmail.com/Patient Readmission
Analysis/Expanded_Patient_Readmission_Data (1).csv'
```

```
# To read the data from a csv file to a pandas DataFrame
df=pd.read_csv(data_path)
```

df: pandas.core.frame.DataFrame = [Patient ID: int64, Age: int64 ... 8 more fields]

```
# Pandas function to help us to see the first 10 rows of the data
df.head(10)
```

	Patient ID	Age	Gender	Admission Type	Length of Stay	Number of Diagnoses	Blood Pressure	Blood Sugar Levels	Previous Admissions	Readmission
0	1	62	Female	Elective	4	5	110	130	1	No
1	2	65	Male	Emergency	19	2	157	81	4	No
2	3	82	Female	Emergency	18	4	74	84	0	No
3	4	85	Male	Emergency	2	4	106	85	4	No
4	5	85	Female	Elective	19	3	80	119	3	No
5	6	27	Male	Emergency	18	6	136	99	2	No
6	7	39	Male	Elective	21	3	116	74	0	Yes
7	8	54	Male	Emergency	3	4	136	68	3	No
8	9	88	Female	Elective	6	6	120	81	2	No
9	10	30	Male	Elective	6	8	139	106	3	No

EDA

Step 1: Understand the data structure

```
# To check number of rows and columns of the data
df.shape
```

```
(3000, 10)
```

```
df.columns
```

```
Index(['Patient ID', 'Age', 'Gender', 'Admission Type', 'Length of Stay',
       'Number of Diagnoses', 'Blood Pressure', 'Blood Sugar Levels',
       'Previous Admissions', 'Readmission'],
      dtype='object')
```

```
# Checking the Data Types
df.dtypes
```

```
Patient ID              int64
Age                     int64
Gender                 object
Admission Type         object
Length of Stay          int64
Number of Diagnoses     int64
Blood Pressure          int64
Blood Sugar Levels      int64
Previous Admissions     int64
```

;

```
Readmission            object
dtype: object
```

Observation

- Categorical columns in our data: Gender, Admission Type, Readmission are the
- The rest of the columns are numerical columns: Patient ID, Age, Length of Stay, Number of Diagnoses, Blood Pressure, Blood Sugar Levels, Previous Admissions

```
    # It helps us select categorical columns from our data using its data type
    print("Categorical Columns:", list(df.select_dtypes(include=['object']).columns))
```

```
Categorical Columns: ['Gender', 'Admission Type', 'Readmission']
```

```
    # It helps us select numerical columns from our data using its data type
    print("Numerical Columns:", list(df.select_dtypes(include=['int64']).columns))
```

```
Numerical Columns: ['Patient ID', 'Age', 'Length of Stay', 'Number of Diagnoses', 'Blood Pressure', 'Blood Sugar Level
s', 'Previous Admissions']
```

Step 2: Check the data quality

```
    # Counting the number of rows that are duplicated in data
    df.duplicated().sum()
```

```
np.int64(0)
```

```
    # Displays more detail of duplications. False means 0 duplications
    df.duplicated()
```

```
0       False
1       False
2       False
3       False
4       False
        ...  
2995    False
2996    False
2997    False
2998    False
2999    False
Length: 3000, dtype: bool
```

```
    # Checking the number os NULL values in dataset
    df.isnull().sum()
```

```
Patient ID             0
Age                    0
Gender                 0
Admission Type         0
Length of Stay         0
Number of Diagnoses    0
Blood Pressure         0
Blood Sugar Levels     0
Previous Admissions    0
Readmission            0
dtype: int64
```

```
    df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3000 entries, 0 to 2999
Data columns (total 10 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   Patient ID           3000 non-null   int64 
 1   Age                  3000 non-null   int64 
 2   Gender               3000 non-null   object
 3   Admission Type       3000 non-null   object
 4   Length of Stay       3000 non-null   int64 
 5   Number of Diagnoses  3000 non-null   int64 
 6   Blood Pressure       3000 non-null   int64 
 7   Blood Sugar Levels   3000 non-null   int64 
 8   Previous Admissions  3000 non-null   int64 
 9   Readmission          3000 non-null   object
dtypes: int64(7), object(3)
memory usage: 234.5+ KB
```

```
# Visual inspection for checking impossible values
display(df)
```

Table

	Patient ID	Age	Gender	Admission Type	Length of Stay	Number of Diagnoses
1	1	62	Female	Elective	4	
2	2	65	Male	Emergency	19	
3	3	82	Female	Emergency	18	
4	4	85	Male	Emergency	2	
5	5	85	Female	Elective	19	
6	6	27	Male	Emergency	18	
7	7	39	Male	Elective	21	
8	8	54	Male	Emergency	3	
9	9	88	Female	Elective	6	
10	10	30	Male	Elective	6	
11	11	76	Female	Emergency	13	
12	12	83	Male	Emergency	13	
13	13	57	Female	Emergency	22	
14	14	64	Male	Elective	3	
15						

3,000 rows

Step 3: Describe Each Column

Describe our numerical columns

```
df.describe()
```

	Patient ID	Age	Length of Stay	Number of Diagnoses	Blood Pressure	Blood Sugar Levels	Previous Admissions
count	3000.000000	3000.000000	3000.000000	3000.000000	3000.000000	3000.000000	3000.000000
mean	1500.500000	53.453000	15.226333	4.956667	119.058000	133.536000	1.958333
std	866.169729	20.892996	8.264858	2.575073	34.089265	37.626311	1.401637
min	1.000000	18.000000	1.000000	1.000000	60.000000	51.000000	0.000000
25%	750.750000	35.000000	8.000000	3.000000	89.750000	101.000000	1.000000
50%	1500.500000	53.000000	15.000000	5.000000	119.000000	133.000000	2.000000
75%	2250.250000	72.000000	22.000000	7.000000	147.250000	167.000000	3.000000
max	3000.000000	89.000000	29.000000	9.000000	179.000000	199.000000	4.000000

Describe Categorical Columns

```
# Checking the unique values in the 'Readmission', 'Gender' and 'Admission Type' columns
print(df['Readmission'].unique())
print(df['Gender'].unique())
print(df['Admission Type'].unique())
```

```
['No' 'Yes']
['Female' 'Male']
['Elective' 'Emergency']
```

```
# Gives us the number(count) of the number of different values in the 'Readmission''Gender' and 'Admission Type' col
print(df['Readmission'].nunique())
print(df['Gender'].nunique())
print(df['Admission Type'].nunique())
```

```
2
2
2
```

```
# Shows you the unique values in the 'Readmission' column and the number of times they appear
df['Readmission'].value_counts()
```

```
Readmission
No     2134
Yes     866
Name: count, dtype: int64
```

```
# Shows you the unique values in the 'Gender' column and the number of times they appear
df['Gender'].value_counts()
```

```
Gender
Male      1555
Female    1445
Name: count, dtype: int64
```

```
# Shows you the unique values in the 'Admission Type' column and the number of times they appear
df['Admission Type'].value_counts()
```

```
Admission Type
Elective     1563
Emergency    1437
Name: count, dtype: int64
```

Step 4: Visualize Single Variables

Univariate Analysis

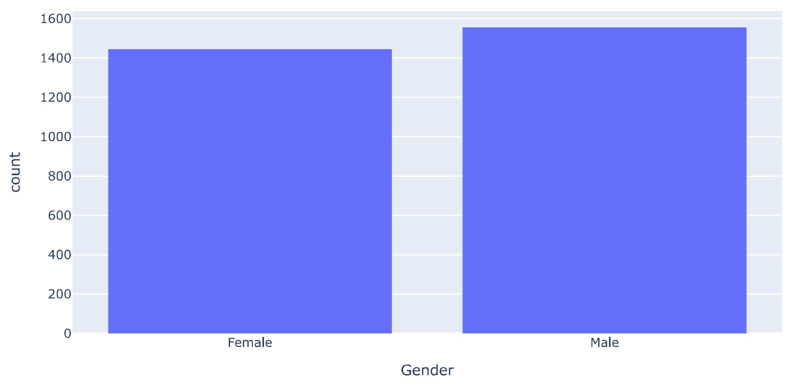
```
# Import plotting libraries
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
```

```
df.head(3)
```

	Patient ID	Age	Gender	Admission Type	Length of Stay	Number of Diagnoses	Blood Pressure	Blood Sugar Levels	Previous Admissions	Readmission
0	1	62	Female	Elective	4	5	110	130	1	No
1	2	65	Male	Emergency	19	2	157	81	4	No
2	3	82	Female	Emergency	18	4	74	84	0	No

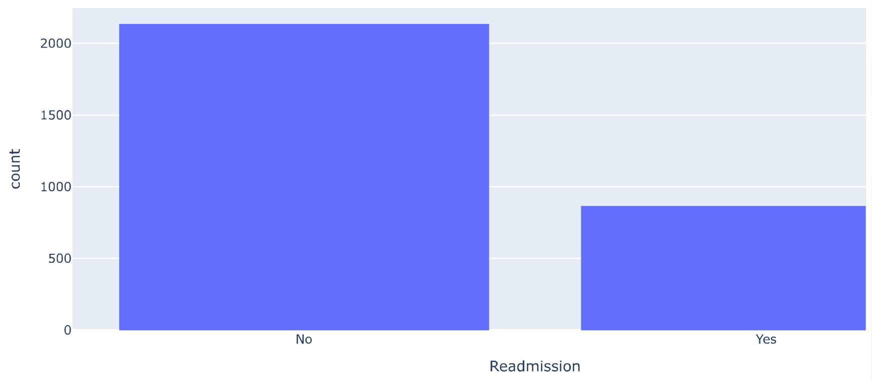
34

```
fig = px.histogram(df, x="Gender")
fig.show()
```

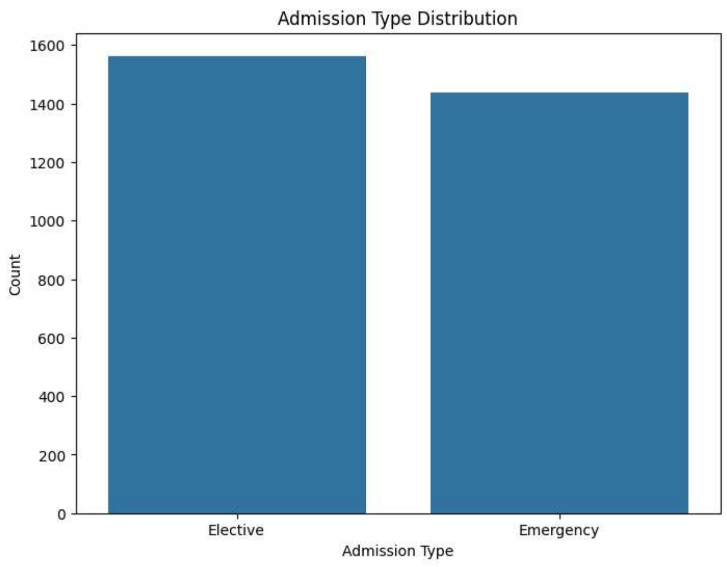


35

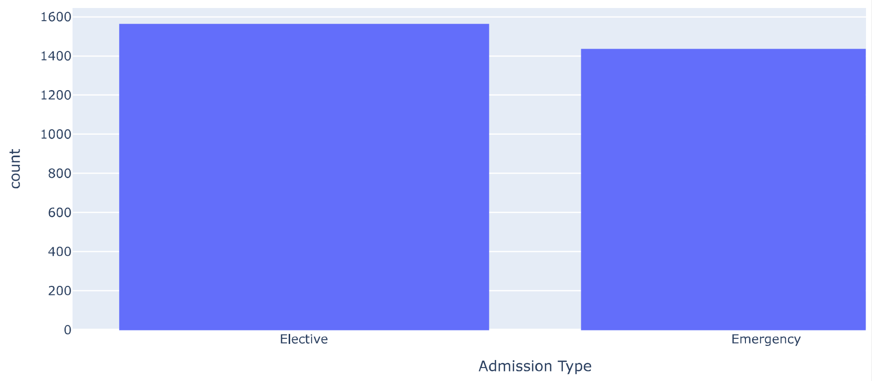
```
fig = px.histogram(df, x="Readmission")
fig.show()
```



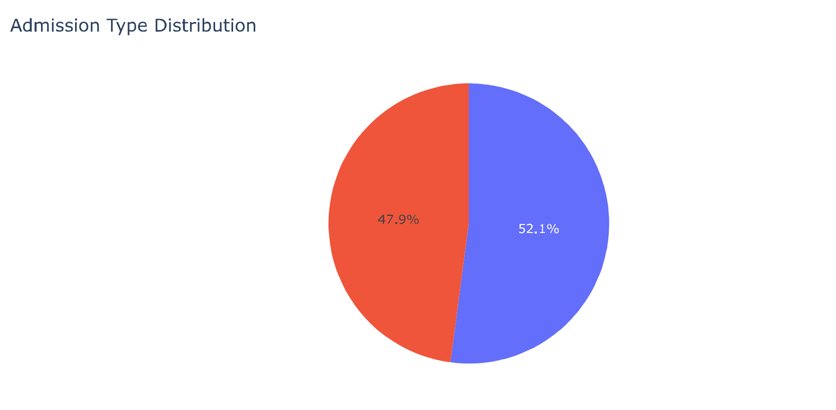
```
plt.figure(figsize=(8, 6))
sns.countplot(data=df, x="Admission Type")
plt.title("Admission Type Distribution")
plt.xlabel("Admission Type")
plt.ylabel("Count")
plt.show()
```



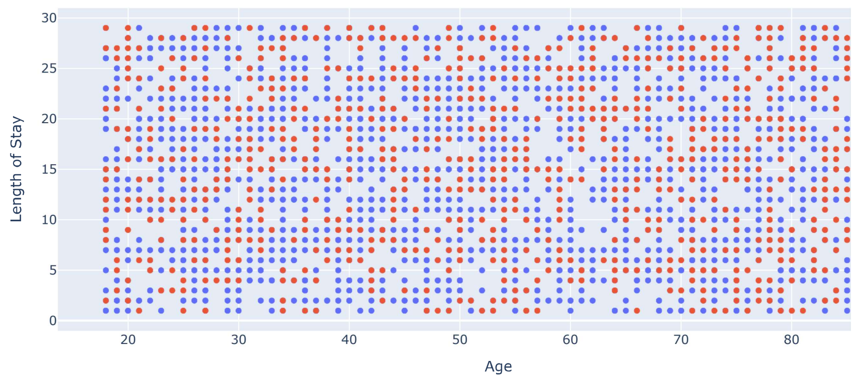
```
fig = px.histogram(df, x="Admission Type")
fig.show()
```



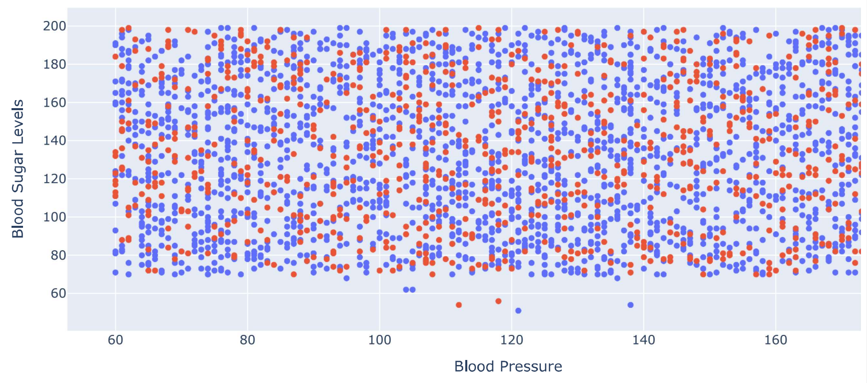
```
fig = px.pie(df, names="Admission Type", title="Admission Type Distribution")
fig.show()
```



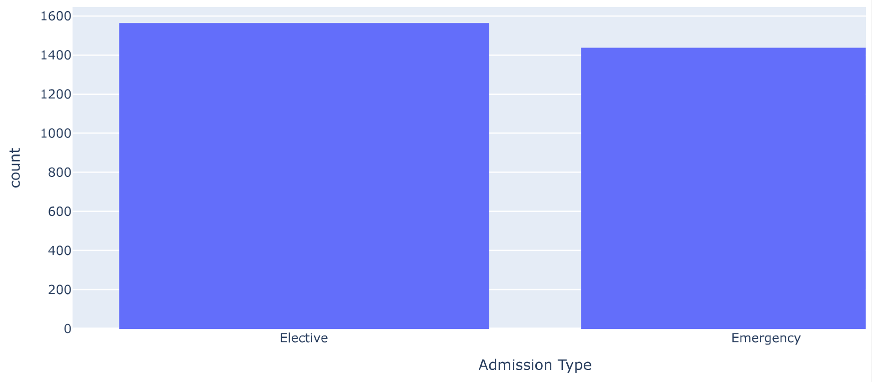
```
import plotly.express as px

fig = px.scatter(
    df, x = 'Age',
    y = 'Length of Stay',
    color = 'Readmission')
fig.show()
```



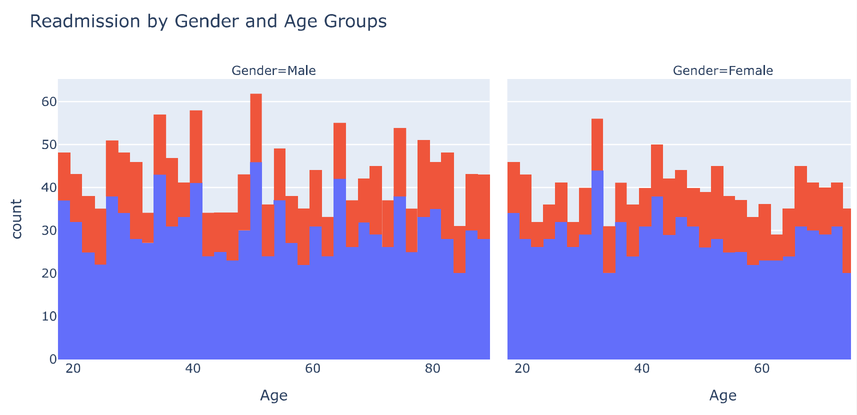
```
import plotly.express as px

fig = px.scatter(
    df, x = 'Blood Pressure',
    y = 'Blood Sugar Levels',
    color = 'Readmission',
    hover_name = 'Patient ID')
fig.show()
```



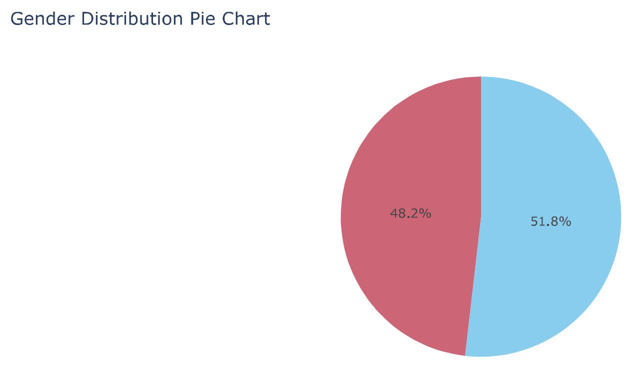
```
import plotly.express as px

fig = px.histogram(df, x="Admission Type")
fig.show()
```



```
import plotly.express as px

fig = px.histogram(
    df,
    x='Age',
    color='Readmission',
    facet_col='Gender',
    category_orders={"Gender": ["Male", "Female"]},
    title="Readmission by Gender and Age Groups"
)
fig.show()
```



```
import plotly.express as px

fig = px.pie(
    df,
    names="Gender",
    title="Gender Distribution Pie Chart",
    color_discrete_sequence=px.colors.qualitative.Safe
)
display(fig)
```



Step 5: Explore Relationships Between Variables

(Bivariate/Multivariate Analysis)

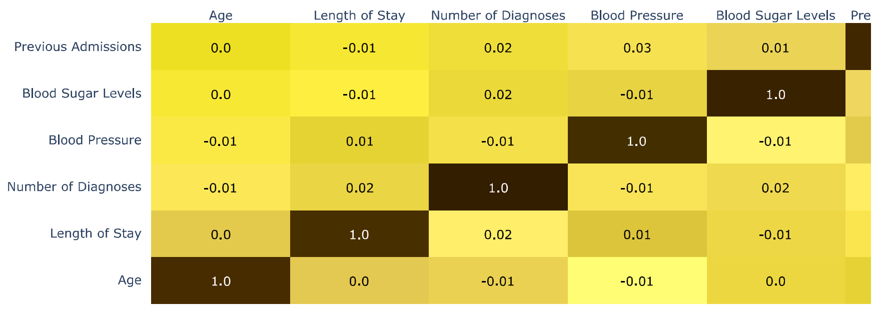
```
df.head(3)
```

	Patient ID	Age	Gender	Admission Type	Length of Stay	Number of Diagnoses	Blood Pressure	Blood Sugar Levels	Previous Admissions	Readmission
0	1	62	Female	Elective	4	5	110	130	1	No
1	2	65	Male	Emergency	19	2	157	81	4	No
2	3	82	Female	Emergency	18	4	74	84	0	No

```
import plotly.figure_factory as ff

cols = [
    "Age",
    "Length of Stay",
    "Number of Diagnoses",
    "Blood Pressure",
    "Blood Sugar Levels",
    "Previous Admissions"
]

corr_matrix = df[cols].corr().round(2)
fig = ff.create_annotated_heatmap(
    z=corr_matrix.values,
    x=cols,
    y=cols,
    annotation_text=corr_matrix.values.astype(str),
    colorscale='Viridis',
    showscale=True,
    reversescale=True
)
fig.update_layout(title="Correlation Matrix of Selected Features")
fig.show()
```

```
› corr_matrix:  pandas.core.frame.DataFrame = [Age: float64, Length of Stay: float64 ... 4 more fields]
```

Correlation Matrix of Selected Features



Observation:

The correlation matrix above displays the pairwise relationships between our selected numerical features: Age, Length of Stay, Number of Diagnoses, Blood Pressure, Blood Sugar Levels, and Previous Admissions. Each cell in the matrix shows the correlation coefficient between two features, ranging from -1 (perfect negative correlation) to +1 (perfect positive correlation), with 0 indicating no linear relationship.

Interpreting the matrix:

- High positive values (close to +1) indicate that as one feature increases, the other tends to increase as well.
- High negative values (close to -1) suggest that as one feature increases, the other tends to decrease.
- Values near 0 imply little to no linear relationship between the features.

This analysis helps identify which features are strongly related and may provide insights for further modeling or feature selection.

import plotly.express as px

fig = px.scatter(

df,

x="Blood Pressure",

y="Blood Sugar Levels",

color="Readmission",

hover_name="Patient ID",x

size_max=60,

)

fig.show()

Feature Engineering

Encoding our categorical columns

```
from sklearn.preprocessing import OneHotEncoder
import pandas as pd

target_col = 'Readmission'
y = df[target_col]
X_raw = df.drop(columns=[target_col])

categorical_cols = X_raw.select_dtypes(include='object').columns
numeric_cols = X_raw.columns.difference(categorical_cols)

ohe = OneHotEncoder(
    handle_unknown='ignore',
    sparse_output=False  # Ensures output is a dense array
)

encoded_array = ohe.fit_transform(X_raw[categorical_cols])
encoded_feature_names = ohe.get_feature_names_out(categorical_cols)

encoded_df = pd.DataFrame(
    encoded_array,
    columns=encoded_feature_names,
    index=df.index
)

numeric_df = X_raw[numeric_cols]

X = pd.concat([numeric_df, encoded_df], axis=1)

display(X.head())
display(y.head())
```

```
> encoded_df:  pandas.core.frame.DataFrame = [Gender_Female: float64, Gender_Male: float64 ... 2 more fields]
> numeric_df:  pandas.core.frame.DataFrame = [Age: int64, Blood Pressure: int64 ... 5 more fields]
> X:  pandas.core.frame.DataFrame = [Age: int64, Blood Pressure: int64 ... 9 more fields]
> X_raw:  pandas.core.frame.DataFrame = [Patient ID: int64, Age: int64 ... 7 more fields]
```

Table

```
0    No
1    No
2    No
3    No
4    No
Name: Readmission, dtype: object
```

```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(
    X,
    y,
    test_size=0.2,      # 20% test, 80% train
    random_state=42,    # for reproducibility
    stratify=y          # optional but good for classification
)

print(X_train.shape, X_test.shape)
print(y_train.shape, y_test.shape)
```

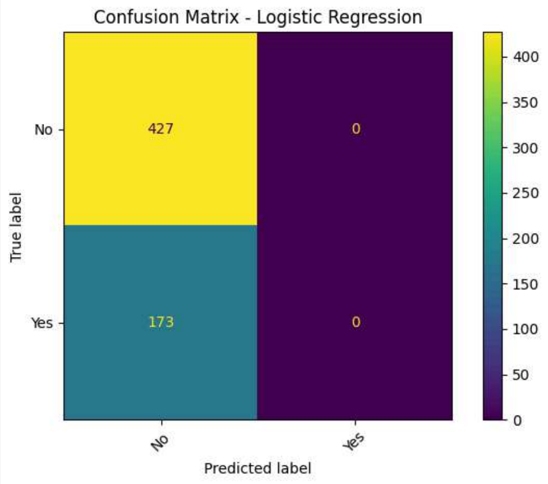
```
> X_test:  pandas.core.frame.DataFrame = [Age: int64, Blood Pressure: int64 ... 9 more fields]
> X_train:  pandas.core.frame.DataFrame = [Age: int64, Blood Pressure: int64 ... 9 more fields]
(2400, 11) (600, 11)
(2400,) (600,)
```

Model Training

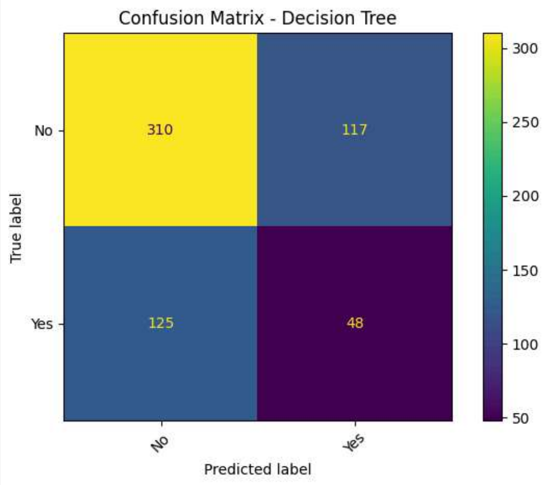
```python
from sklearn.metrics import (
    accuracy_score, precision_score, recall_score, f1_score,
    classification_report, confusion_matrix, ConfusionMatrixDisplay
)

# Algorithms
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier

# import matplotlib.pyplot as plt
# import numpy as np

# -------------------------------
# Define classification models
# -------------------------------
models = {
    'Logistic Regression': LogisticRegression(max_iter=1000),
    'Decision Tree': DecisionTreeClassifier(random_state=42),
    'Random Forest': RandomForestClassifier(random_state=42, n_jobs=-1),
    'Support Vector Classifier': SVC(),
    'K-Nearest Neighbors': KNeighborsClassifier(),
    'Naive Bayes': GaussianNB(),
    'Gradient Boosting': GradientBoostingClassifier(random_state=42)
}

# -------------------------------
# Define evaluation metrics
# -------------------------------
metrics = {
    'Accuracy': accuracy_score,
    'Precision': lambda y_true, y_pred: precision_score(
        y_true, y_pred, average='weighted', zero_division=0
    ),
    'Recall': lambda y_true, y_pred: recall_score(
        y_true, y_pred, average='weighted', zero_division=0
    ),
    'F1 Score': lambda y_true, y_pred: f1_score(
        y_true, y_pred, average='weighted', zero_division=0
    ),
}

# -------------------------------
# Train and evaluate models
# -------------------------------
evaluation_results = {}
confusion_matrices = {}

# Get class labels (for nicer axis names in plots)
class_labels = np.unique(y_test)

for name, model in models.items():
    print("=" * 70)
    print(f"Training {name}:\n")

    # Fit model
    model.fit(X_train, y_train)

    # Predict on test set
    y_pred = model.predict(X_test)

    # Store metrics
    evaluation_results[name] = {
        metric_name: metric_func(y_test, y_pred)
        for metric_name, metric_func in metrics.items()
    }

    # Compute and store confusion matrix
    cm = confusion_matrix(y_test, y_pred, labels=class_labels)
    confusion_matrices[name] = cm

    # Print detailed classification report
    print(f"Classification Report for {name}:")
    print(classification_report(y_test, y_pred, zero_division=0))
    print("Confusion Matrix (raw values):")
    print(cm)
    print("-" * 50)

    # -------------------------------
    # Plot confusion matrix for this model
    # -------------------------------
    disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=class_labels)
    disp.plot()
    plt.title(f"Confusion Matrix - {name}")
    plt.xticks(rotation=45)
    plt.tight_layout()
    plt.show()

# -------------------------------
# Print summary table
```

```
    # -------------------------------
    print("\nOverall Evaluation Results:")
    for name, scores in evaluation_results.items():
        print(f"\n{name}")
        for metric_name, score in scores.items():
            print(f"  {metric_name}: {score:.4f}")
```

```
STOP: TOTAL NO. OF ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html (https://scikit-learn.org/stable/modules/preprocessin
g.html)
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression (https://scikit-learn.org/stable/mo
dules/linear_model.html#logistic-regression)

Classification Report for Logistic Regression:
              precision    recall  f1-score   support

          No       0.71      1.00      0.83       427
         Yes       0.00      0.00      0.00       173

    accuracy                           0.71       600
   macro avg       0.36      0.50      0.42       600
weighted avg       0.51      0.71      0.59       600

Confusion Matrix (raw values):
[[427   0]
```

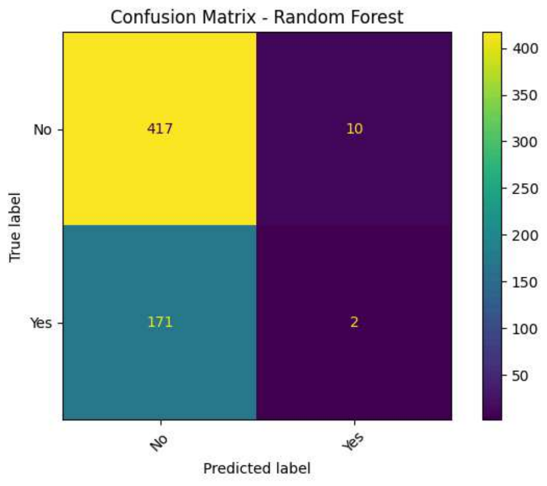


```
======================================================================
Training Decision Tree:

Classification Report for Decision Tree:
              precision    recall  f1-score   support

          No       0.71      0.73      0.72       427
         Yes       0.29      0.28      0.28       173

    accuracy                           0.60       600
   macro avg       0.50      0.50      0.50       600
weighted avg       0.59      0.60      0.59       600

Confusion Matrix (raw values):
[[310 117]
 [125  48]]
--------------------------------------------------
```

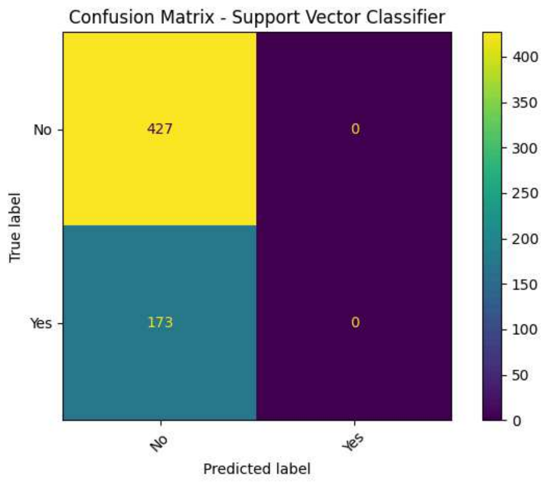


```
======================================================================
Training Random Forest:
```

```
Classification Report for Random Forest:
              precision    recall  f1-score   support

          No       0.71      0.98      0.82       427
         Yes       0.17      0.01      0.02       173

    accuracy                           0.70       600
   macro avg       0.44      0.49      0.42       600
weighted avg       0.55      0.70      0.59       600

Confusion Matrix (raw values):
[[417  10]
 [171   2]]
--------------------------------------------------
```

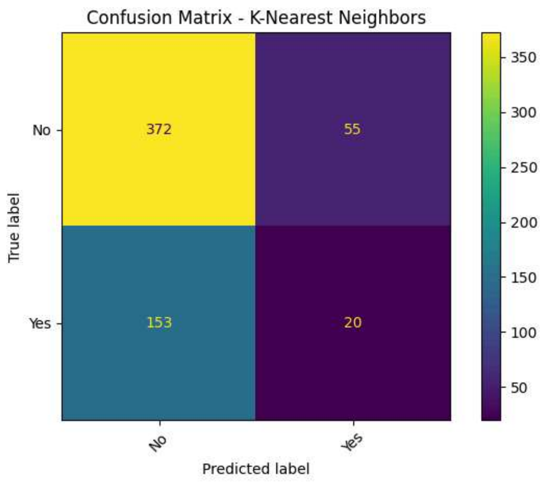


```
======================================================================
Training Support Vector Classifier:

Classification Report for Support Vector Classifier:
              precision    recall  f1-score   support

          No       0.71      1.00      0.83       427
         Yes       0.00      0.00      0.00       173

    accuracy                           0.71       600
   macro avg       0.36      0.50      0.42       600
weighted avg       0.51      0.71      0.59       600

Confusion Matrix (raw values):
[[427   0]
 [173   0]]
--------------------------------------------------
```

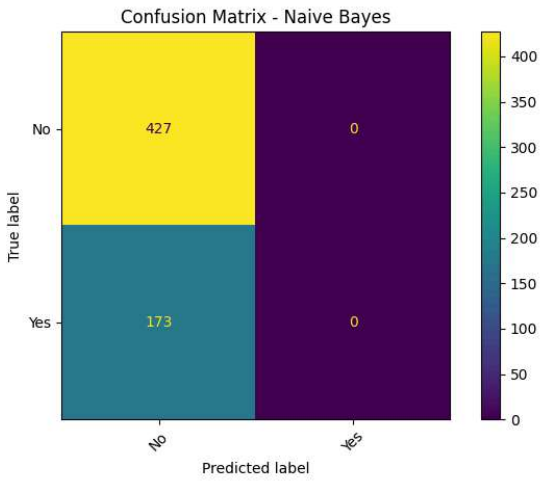


```
======================================================================
Training K-Nearest Neighbors:

Classification Report for K-Nearest Neighbors:
              precision    recall  f1-score   support

          No       0.71      0.87      0.78       427
         Yes       0.27      0.12      0.16       173

    accuracy                           0.65       600
   macro avg       0.49      0.49      0.47       600
weighted avg       0.58      0.65      0.60       600

Confusion Matrix (raw values):
[[372  55]
```

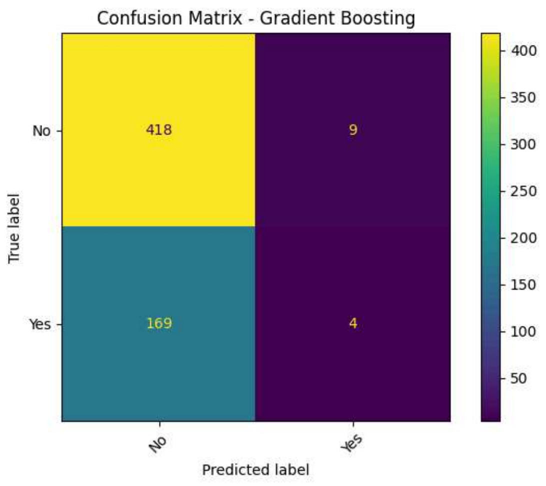
```
 [153  20]]
--------------------------------------------------
```



```
======================================================================
Training Naive Bayes:

Classification Report for Naive Bayes:
              precision    recall  f1-score   support

          No       0.71      1.00      0.83       427
         Yes       0.00      0.00      0.00       173

    accuracy                           0.71       600
   macro avg       0.36      0.50      0.42       600
weighted avg       0.51      0.71      0.59       600

Confusion Matrix (raw values):
[[427   0]
 [173   0]]
--------------------------------------------------
```



```
======================================================================
Training Gradient Boosting:

Classification Report for Gradient Boosting:
              precision    recall  f1-score   support

          No       0.71      0.98      0.82       427
         Yes       0.31      0.02      0.04       173

    accuracy                           0.70       600
   macro avg       0.51      0.50      0.43       600
weighted avg       0.60      0.70      0.60       600

Confusion Matrix (raw values):
[[418   9]
 [169   4]]
--------------------------------------------------
```



```
  Precision: 0.5065
  Recall: 0.7117
  F1 Score: 0.5918

K-Nearest Neighbors
  Accuracy: 0.6533
  Precision: 0.5812
  Recall: 0.6533
  F1 Score: 0.6027

Naive Bayes
  Accuracy: 0.7117
  Precision: 0.5065
  Recall: 0.7117
  F1 Score: 0.5918

Gradient Boosting
  Accuracy: 0.7033
  Precision: 0.5955
  Recall: 0.7033
  F1 Score: 0.5991
```