Data Preprocessing

Importing The Libraries

```
# Import required libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix, ConfusionMatrixDisplay

# For models
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB, MultinomialNB
```

Read The Dataset

```
# Load dataset
file_path = 'patient_data.csv'
df = pd.read_csv(file_path)

# Display first few rows to understand the data
print("First 5 rows of dataset:")
print(df.head())

# Check dataset info
print("\nDataset Info:")
print(df.info())

# Check for missing values
print("\nMissing Values:")
print(df.isnull().sum())
```

```
First 5 rows of dataset:
        C    Age History Patient TakeMedication Severity
BreathShortness  \
0    Male  18-34     Yes      No             No     Mild
No
1  Female  18-34     Yes      No             No     Mild
No
2    Male  35-50     Yes      No             No     Mild
No
3  Female  35-50     Yes      No             No     Mild
```

```
No
4    Male  51-64     Yes      No             No     Mild
No

  VisualChanges NoseBleeding Whendiagnoused   Systolic Diastolic  \
0            No          No        <1 Year  111 - 120   81 - 90
1            No          No        <1 Year  111 - 120   81 - 90
2            No          No        <1 Year  111 - 120   81 - 90
3            No          No        <1 Year  111 - 120   81 - 90
4            No          No        <1 Year  111 - 120   81 - 90

  ControlledDiet                  Stages
0             No  HYPERTENSION (Stage-1)
1             No  HYPERTENSION (Stage-1)
2             No  HYPERTENSION (Stage-1)
3             No  HYPERTENSION (Stage-1)
4             No  HYPERTENSION (Stage-1)

Dataset Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1825 entries, 0 to 1824
Data columns (total 14 columns):
 #   Column           Non-Null Count  Dtype
---  ------           --------------  -----
 0   C                1825 non-null   object
 1   Age              1825 non-null   object
 2   History          1825 non-null   object
 3   Patient          1825 non-null   object
 4   TakeMedication   1825 non-null   object
 5   Severity         1825 non-null   object
 6   BreathShortness  1825 non-null   object
 7   VisualChanges    1825 non-null   object
 8   NoseBleeding     1825 non-null   object
 9   Whendiagnoused   1825 non-null   object
 10  Systolic         1825 non-null   object
 11  Diastolic        1825 non-null   object
 12  ControlledDiet   1825 non-null   object
 13  Stages           1825 non-null   object
dtypes: object(14)
memory usage: 199.7+ KB
None

Missing Values:
C                  0
Age                0
History            0
Patient            0
TakeMedication     0
Severity           0
BreathShortness    0
```

```
VisualChanges      0
NoseBleeding       0
Whendiagnoused     0
Systolic           0
Diastolic          0
ControlledDiet     0
Stages             0
dtype: int64
```

Handling Missing Values

```python
# Fill missing numerical values with the mean
df.fillna(df.mean(numeric_only=True), inplace=True)

# For categorical columns, fill missing values with the mode
for col in df.select_dtypes(include='object').columns:
    df[col].fillna(df[col].mode()[0], inplace=True)

# Verify that missing values are handled
print("\nMissing Values After Handling:")
print(df.isnull().sum())
```

```
Missing Values After Handling:
C                  0
Age                0
History            0
Patient            0
TakeMedication     0
Severity           0
BreathShortness    0
VisualChanges      0
NoseBleeding       0
Whendiagnoused     0
Systolic           0
Diastolic          0
ControlledDiet     0
Stages             0
dtype: int64

/tmp/ipython-input-8-4103537396.py:6: FutureWarning: A value is trying
to be set on a copy of a DataFrame or Series through chained
assignment using an inplace method.
The behavior will change in pandas 3.0. This inplace method will never
work because the intermediate object on which we are setting values
always behaves as a copy.

For example, when doing 'df[col].method(value, inplace=True)', try
using 'df.method({col: value}, inplace=True)' or df[col] =
df[col].method(value) instead, to perform the operation inplace on the
```

```
original object.


  df[col].fillna(df[col].mode()[0], inplace=True)
```

Handling Categorical Values

```
from sklearn.preprocessing import LabelEncoder

# Encode categorical variables
label_encoders = {}
for col in df.columns:
    le = LabelEncoder()
    df[col] = le.fit_transform(df[col])
    label_encoders[col] = le

# Display the encoded dataset
print("\nEncoded Dataset:")
print(df.head())


Encoded Dataset:
   C  Age  History  Patient  TakeMedication  Severity  BreathShortness
\
0  1    0        1        0               0         0                0

1  0    0        1        0               0         0                0

2  1    1        1        0               0         0                0

3  0    1        1        0               0         0                0

4  1    2        1        0               0         0                0


   VisualChanges  NoseBleeding  Whendiagnoused  Systolic  Diastolic  \
0              0             1               1         1          3
1              0             1               1         1          3
2              0             1               1         1          3
3              0             1               1         1          3
4              0             1               1         1          3

   ControlledDiet  Stages
0               0       0
1               0       0
2               0       0
3               0       0
4               0       0
```

Label

```python
from collections import Counter
from sklearn.model_selection import train_test_split

# Split into features and target
X = df.drop('Stages', axis=1)
y = df['Stages']

# Remove rare classes (e.g., classes with fewer than 2 samples)
min_samples_per_class = 2
class_counts = Counter(y)
valid_indices = [i for i, label in enumerate(y) if class_counts[label]
>= min_samples_per_class]

# Filter the data using iloc and then reset the index
X_filtered = X.iloc[valid_indices].reset_index(drop=True)
y_filtered = y.iloc[valid_indices].reset_index(drop=True)

# Perform stratified train-test split
X_train, X_test, y_train, y_test = train_test_split(
    X_filtered, y_filtered, test_size=0.2, random_state=42,
stratify=y_filtered
)

# Print class distribution after filtering
print("\nClass Distribution After Filtering:")
print(Counter(y_filtered))
```

```
Class Distribution After Filtering:
Counter({'HYPERTENSION (Stage-1)': 648, 'HYPERTENSION (Stage-2)': 599,
'NORMAL': 336, 'HYPERTENSIVE CRISIS': 240})
```

Exploratory Data Analysis (EDA)

Descriptive Statistical Analysis

```python
# Import required libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

# Load dataset
file_path = 'patient_data.csv'
df = pd.read_csv(file_path)

# Display first few rows
print("First 5 rows of dataset:")
print(df.head())
```

```python
# Check dataset info
print("\nDataset Info:")
print(df.info())

# Summary statistics
print("\nSummary Statistics:")
print(df.describe())
```

```
First 5 rows of dataset:
        C    Age History Patient TakeMedication Severity
BreathShortness  \
0    Male  18-34     Yes      No             No     Mild
No
1  Female  18-34     Yes      No             No     Mild
No
2    Male  35-50     Yes      No             No     Mild
No
3  Female  35-50     Yes      No             No     Mild
No
4    Male  51-64     Yes      No             No     Mild
No

  VisualChanges NoseBleeding Whendiagnoused   Systolic Diastolic  \
0            No           No         <1 Year  111 - 120   81 - 90
1            No           No         <1 Year  111 - 120   81 - 90
2            No           No         <1 Year  111 - 120   81 - 90
3            No           No         <1 Year  111 - 120   81 - 90
4            No           No         <1 Year  111 - 120   81 - 90

  ControlledDiet                   Stages
0             No  HYPERTENSION (Stage-1)
1             No  HYPERTENSION (Stage-1)
2             No  HYPERTENSION (Stage-1)
3             No  HYPERTENSION (Stage-1)
4             No  HYPERTENSION (Stage-1)

Dataset Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1825 entries, 0 to 1824
Data columns (total 14 columns):
 #   Column           Non-Null Count  Dtype
---  ------           --------------  -----
 0   C                1825 non-null   object
 1   Age              1825 non-null   object
 2   History          1825 non-null   object
 3   Patient          1825 non-null   object
 4   TakeMedication   1825 non-null   object
 5   Severity         1825 non-null   object
 6   BreathShortness  1825 non-null   object
 7   VisualChanges    1825 non-null   object
```

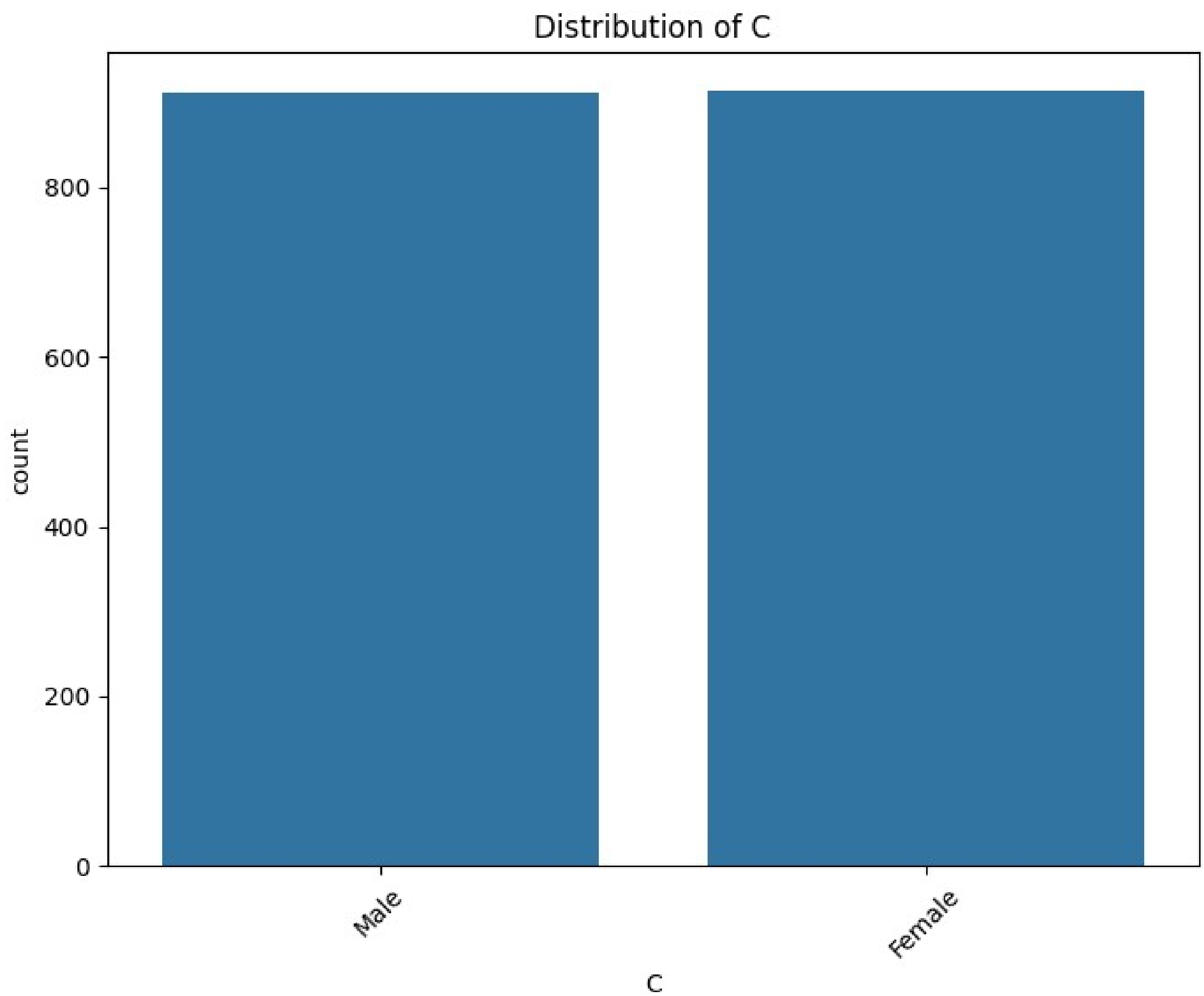
```
 8   NoseBleeding     1825 non-null   object
 9   Whendiagnoused   1825 non-null   object
 10  Systolic         1825 non-null   object
 11  Diastolic        1825 non-null   object
 12  ControlledDiet   1825 non-null   object
 13  Stages           1825 non-null   object
dtypes: object(14)
memory usage: 199.7+ KB
None

Summary Statistics:
             C    Age History Patient TakeMedication  Severity  \
count     1825   1825    1825    1825           1825      1825
unique       2      4       2       2              3         3
top     Female  51-64     Yes      No             No  Moderate
freq       913    475    1657     984            744       697

       BreathShortness VisualChanges NoseBleeding Whendiagnoused
Systolic  \
count             1825          1825         1825           1825
1825
unique               2             2            3              3
5
top                 No            No           No        <1 Year  111
- 120
freq               976           940          984            625
1008

       Diastolic ControlledDiet                  Stages
count       1825           1825                    1825
unique         5              2                       6
top      81 - 90             No  HYPERTENSION (Stage-1)
freq         708            984                     648
```

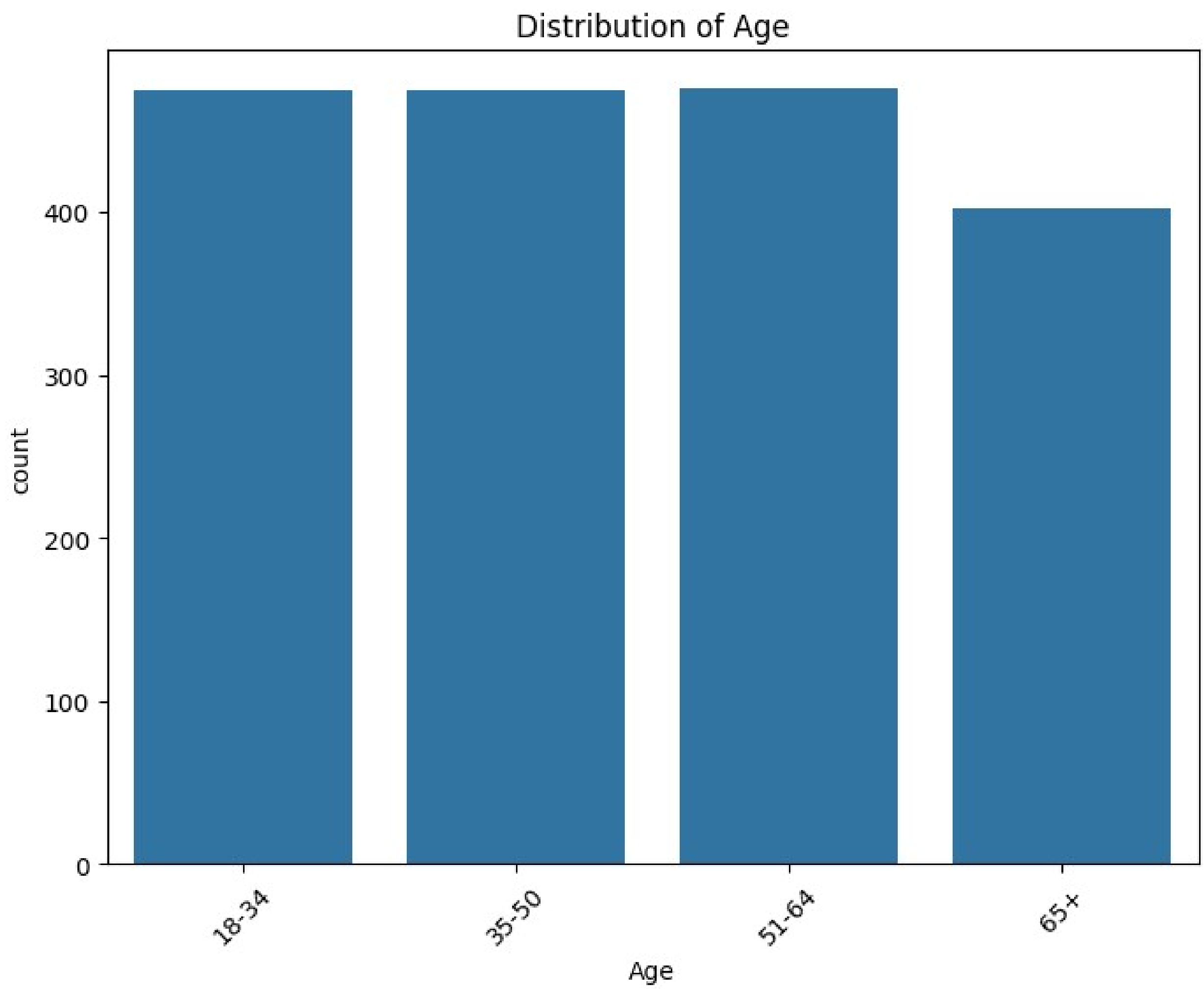
Visual Analysis

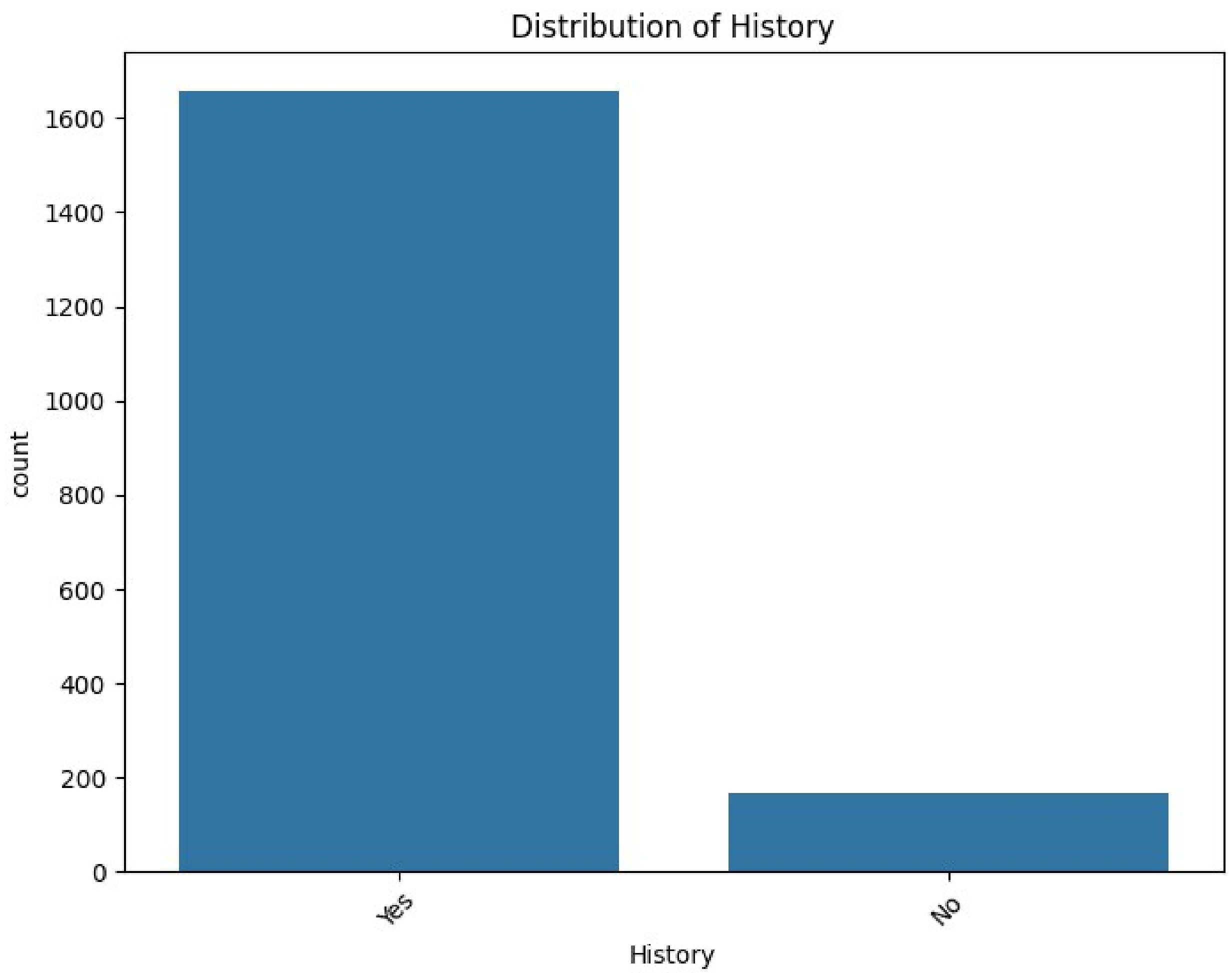
Univariate Analysis

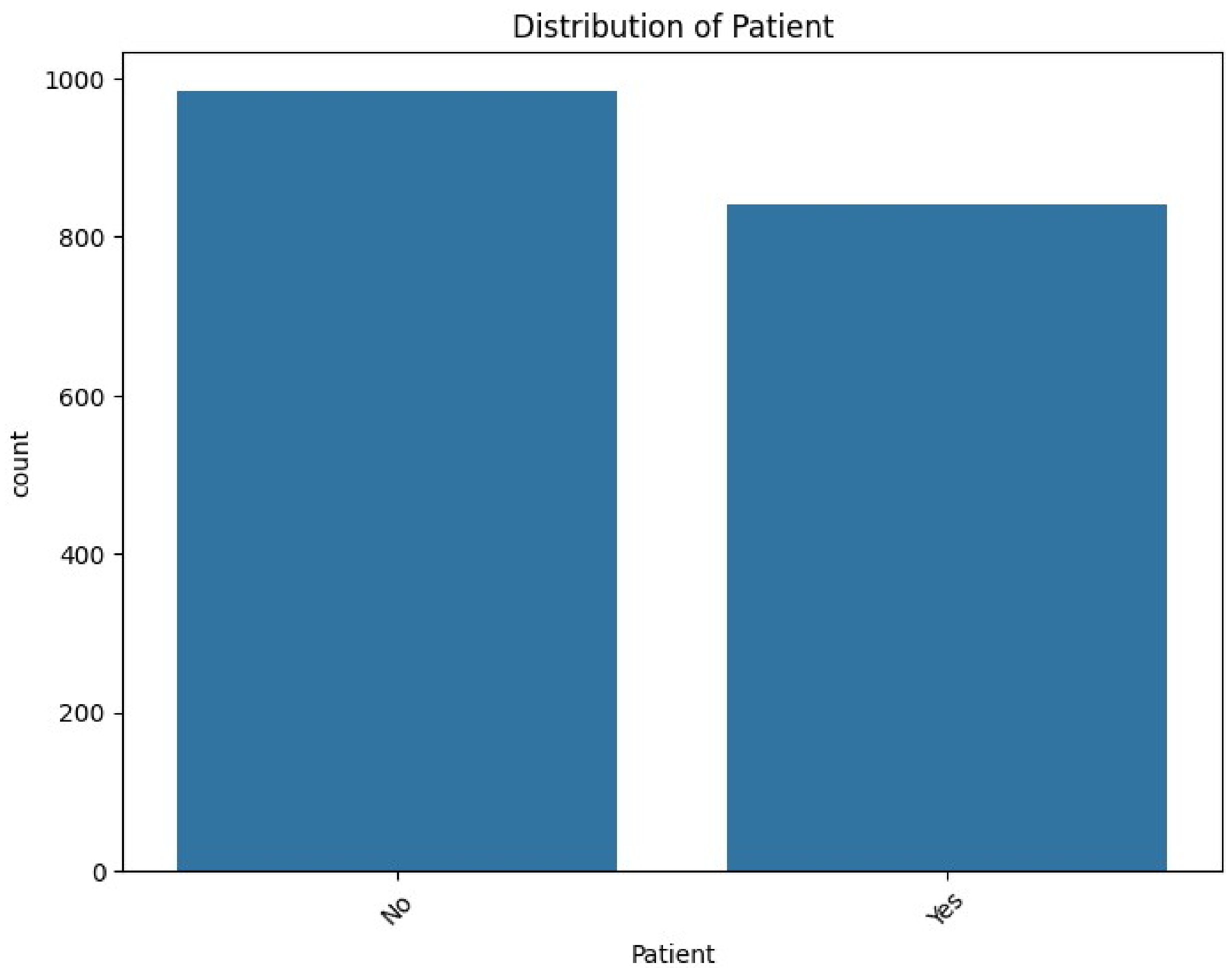
```python
# Univariate analysis for categorical variables
categorical_cols = df.select_dtypes(include=['object']).columns
for col in categorical_cols:
    plt.figure(figsize=(8, 6))
    sns.countplot(x=col, data=df)
    plt.title(f'Distribution of {col}')
    plt.xticks(rotation=45)
    plt.show()

# Univariate analysis for numerical variables
numerical_cols = df.select_dtypes(include=['number']).columns
```

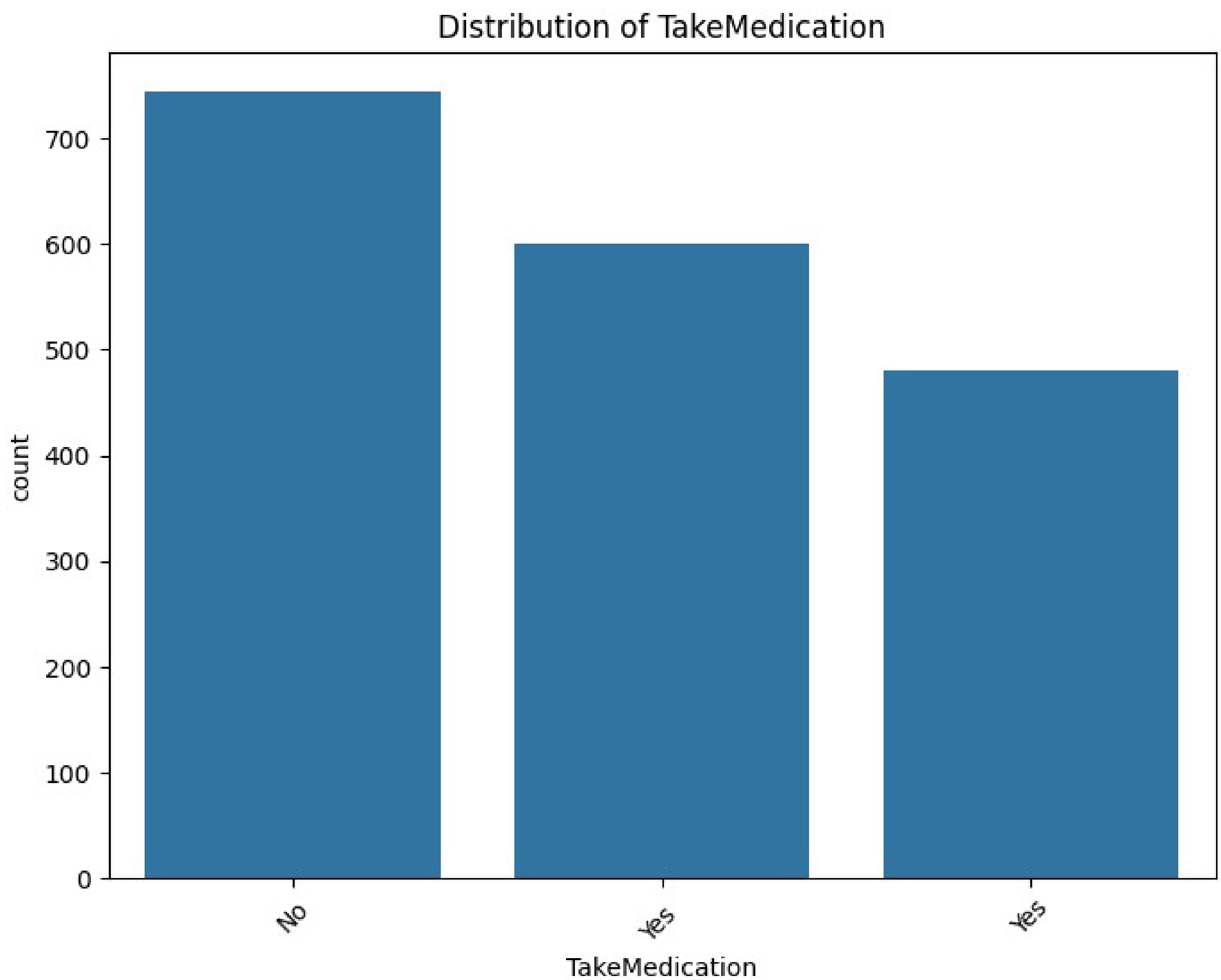
```
for col in numerical_cols:
    plt.figure(figsize=(8, 6))
    sns.histplot(data=df, x=col, kde=True)
    plt.title(f'Distribution of {col}')
    plt.show()
```

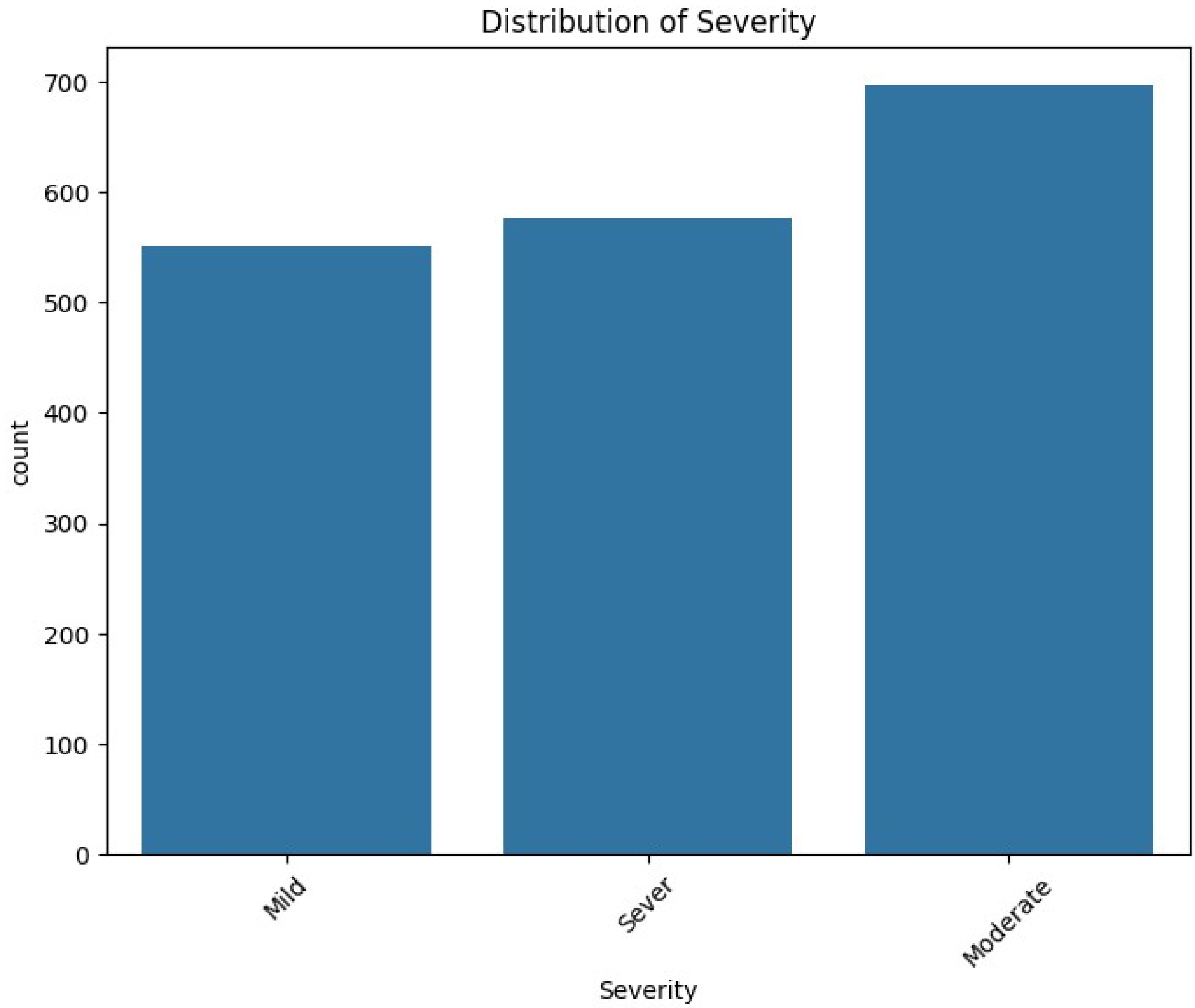



Distribution of Age
count
0
100
200
300
400
18-34
35-50
51-64
65+
Age

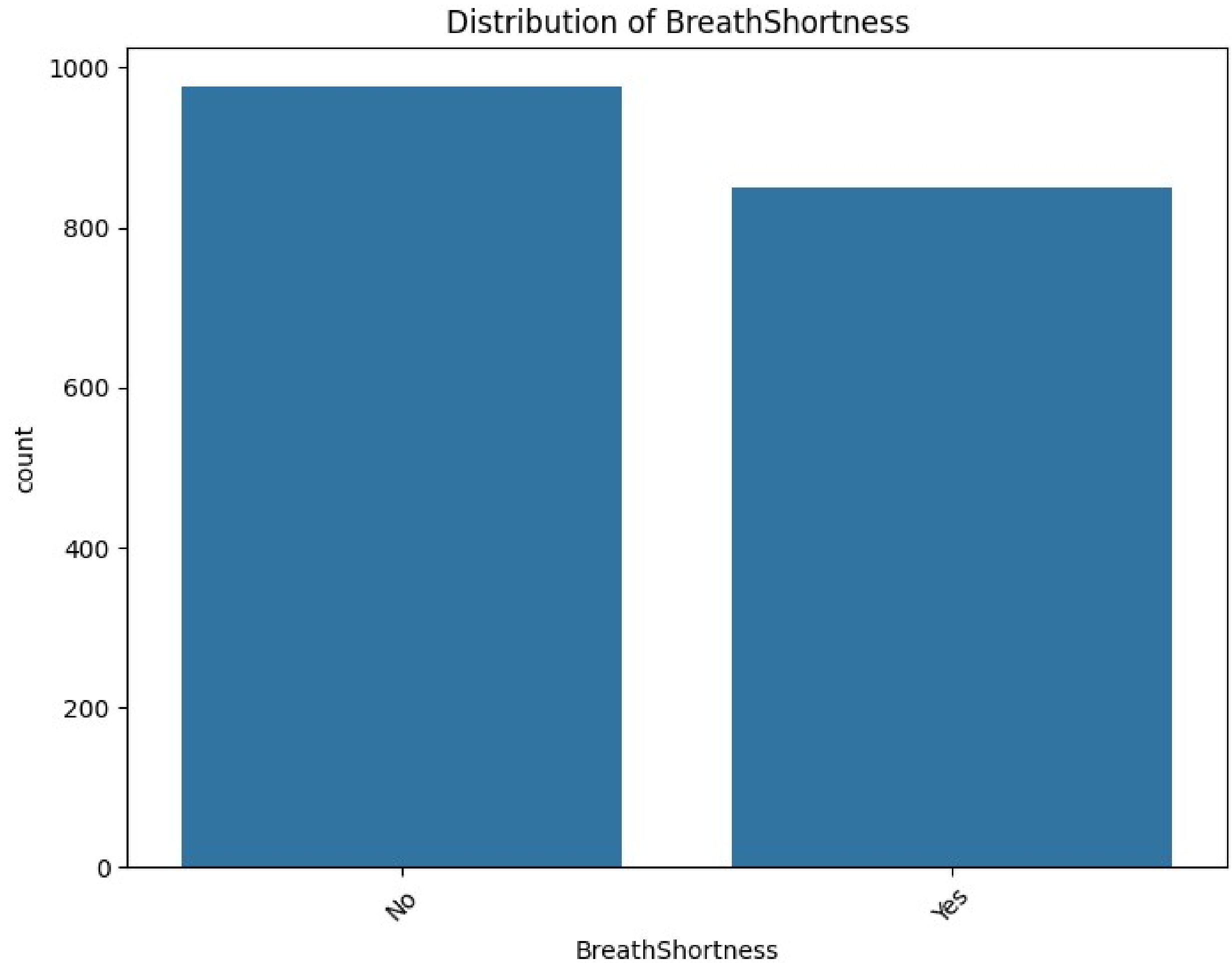

Distribution of History
count
1600
1400
1200
1000
800
600
400
200
0
Yes
No
History


Distribution of Patient
count
1000
800
600
400
200
0
No
Yes
Patient

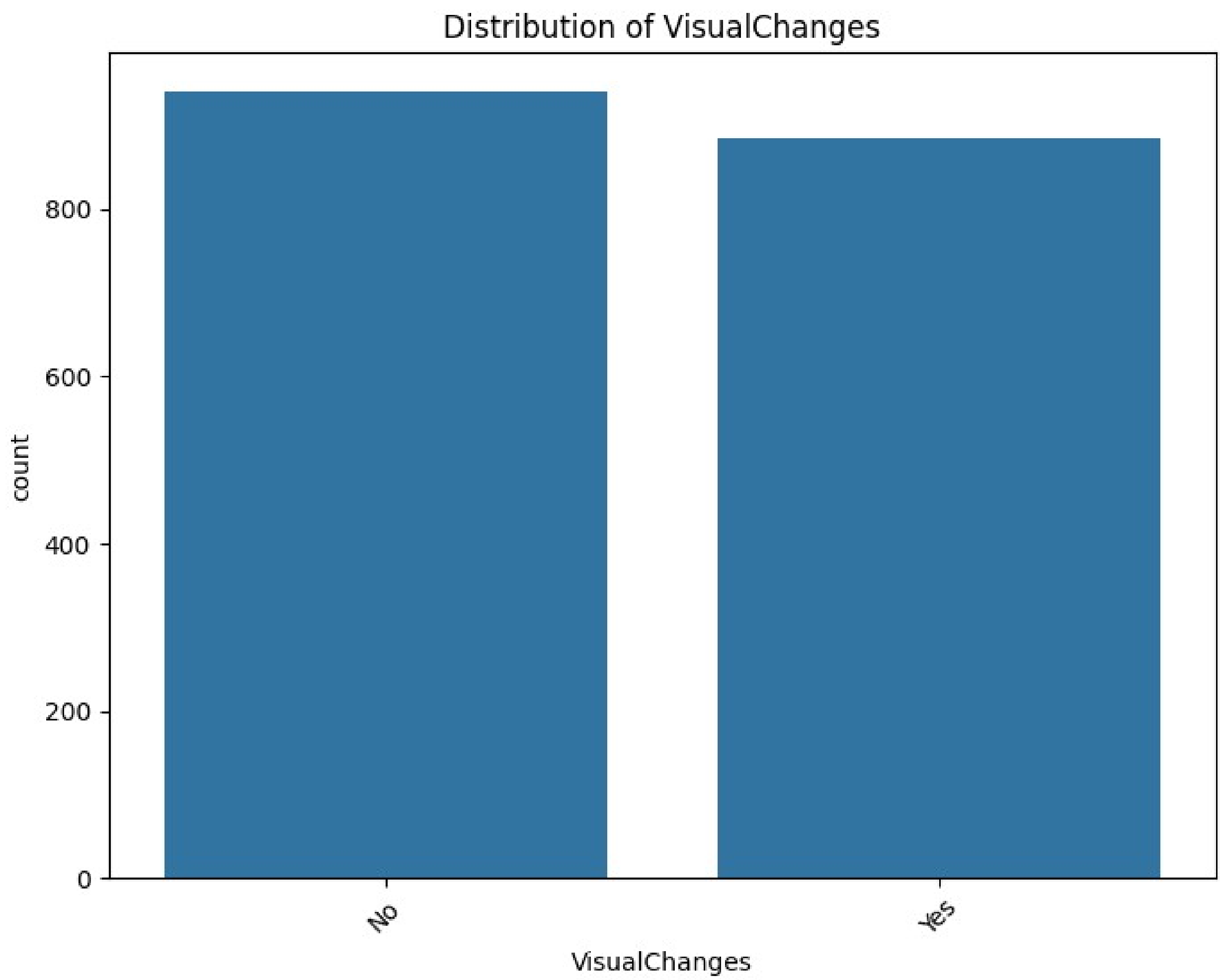

Distribution of TakeMedication
count
0
100
200
300
400
500
600
700
No
Yes
Yes
TakeMedication



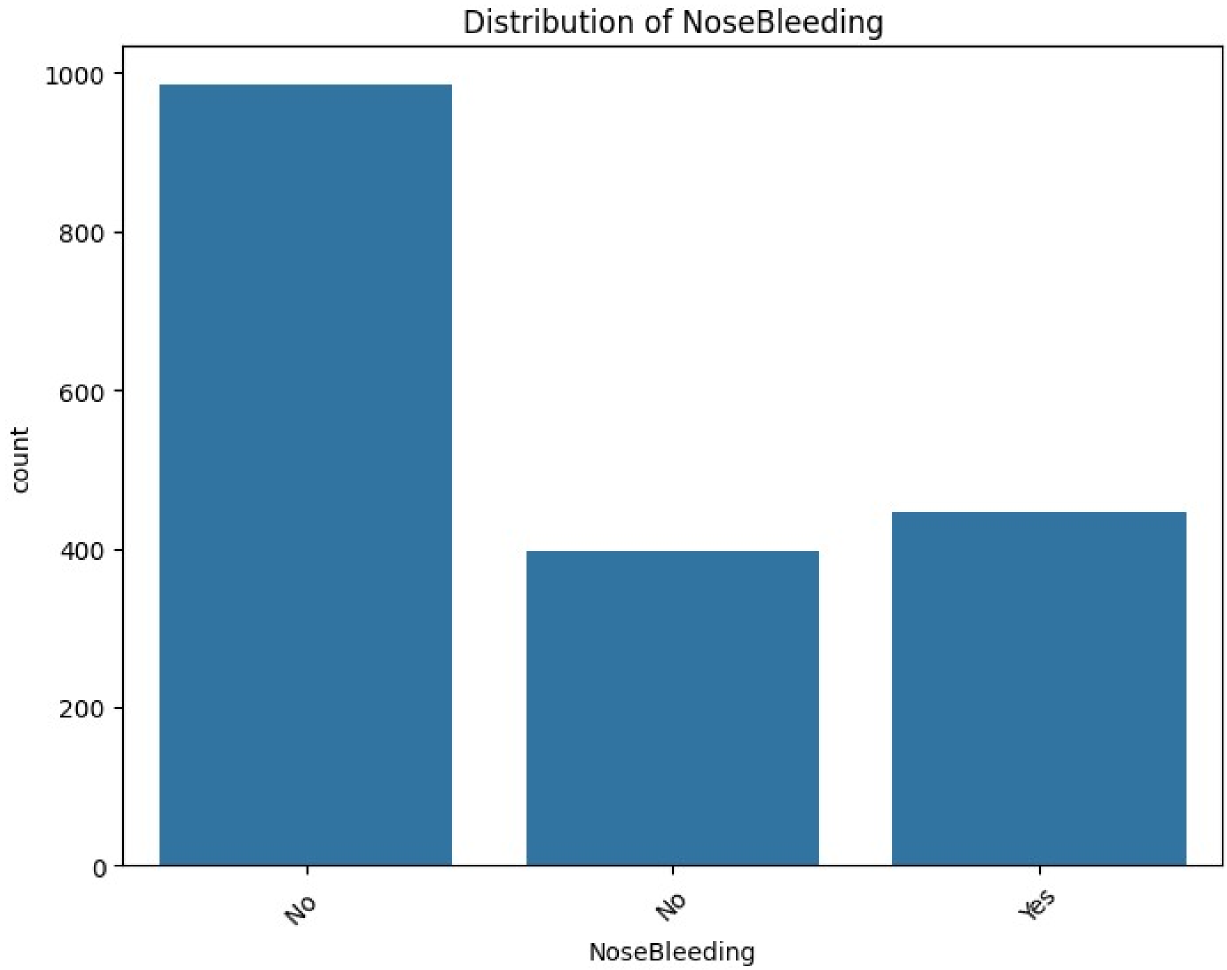
Distribution of Severity
700
600
500
400
300
200
100
0
count
Mild
Sever
Moderate
Severity

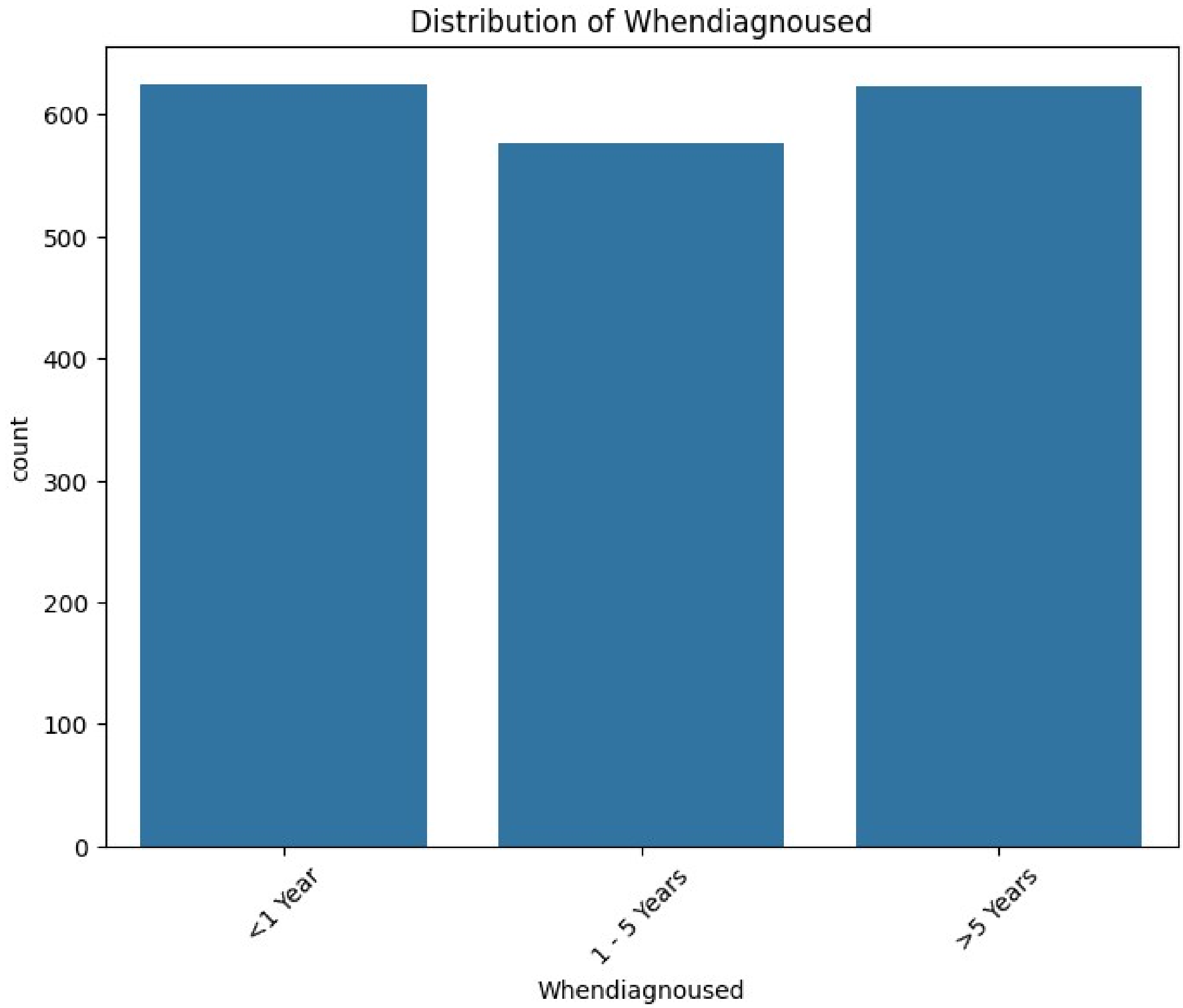


Distribution of BreathShortness
count
1000
800
600
400
200
0
No
Yes
BreathShortness

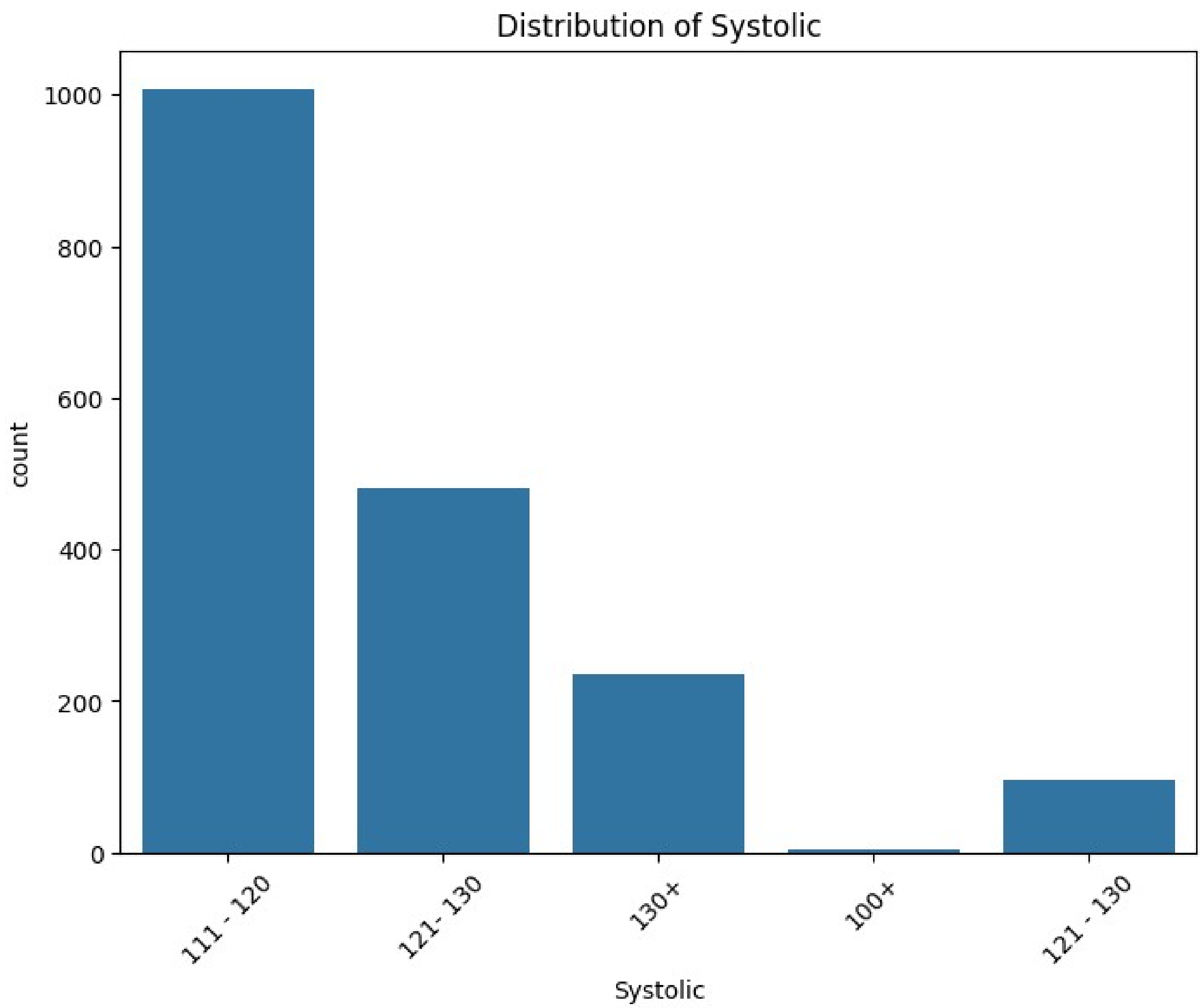


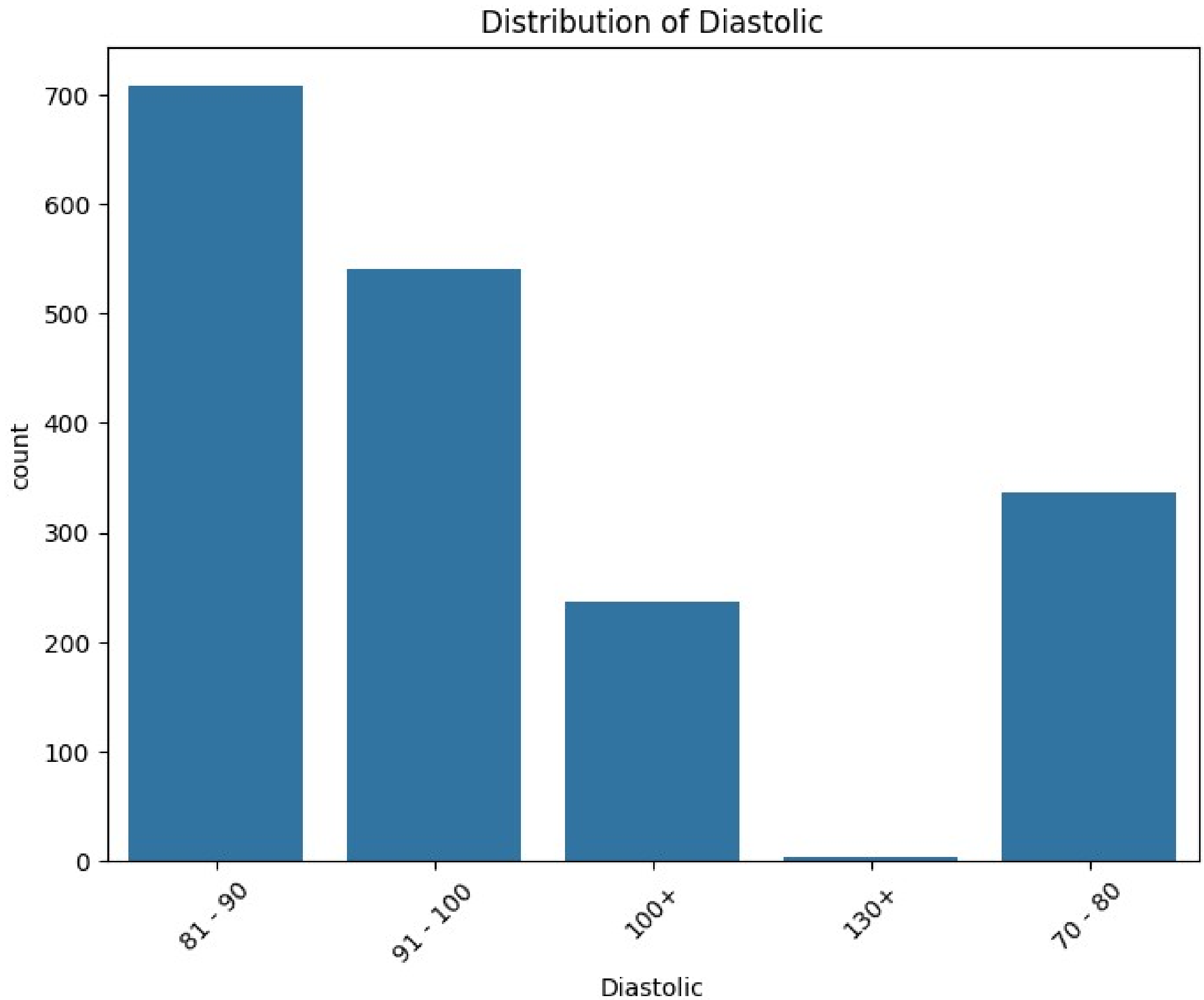
Distribution of VisualChanges
count
0
200
400
600
800
No
Yes
VisualChanges

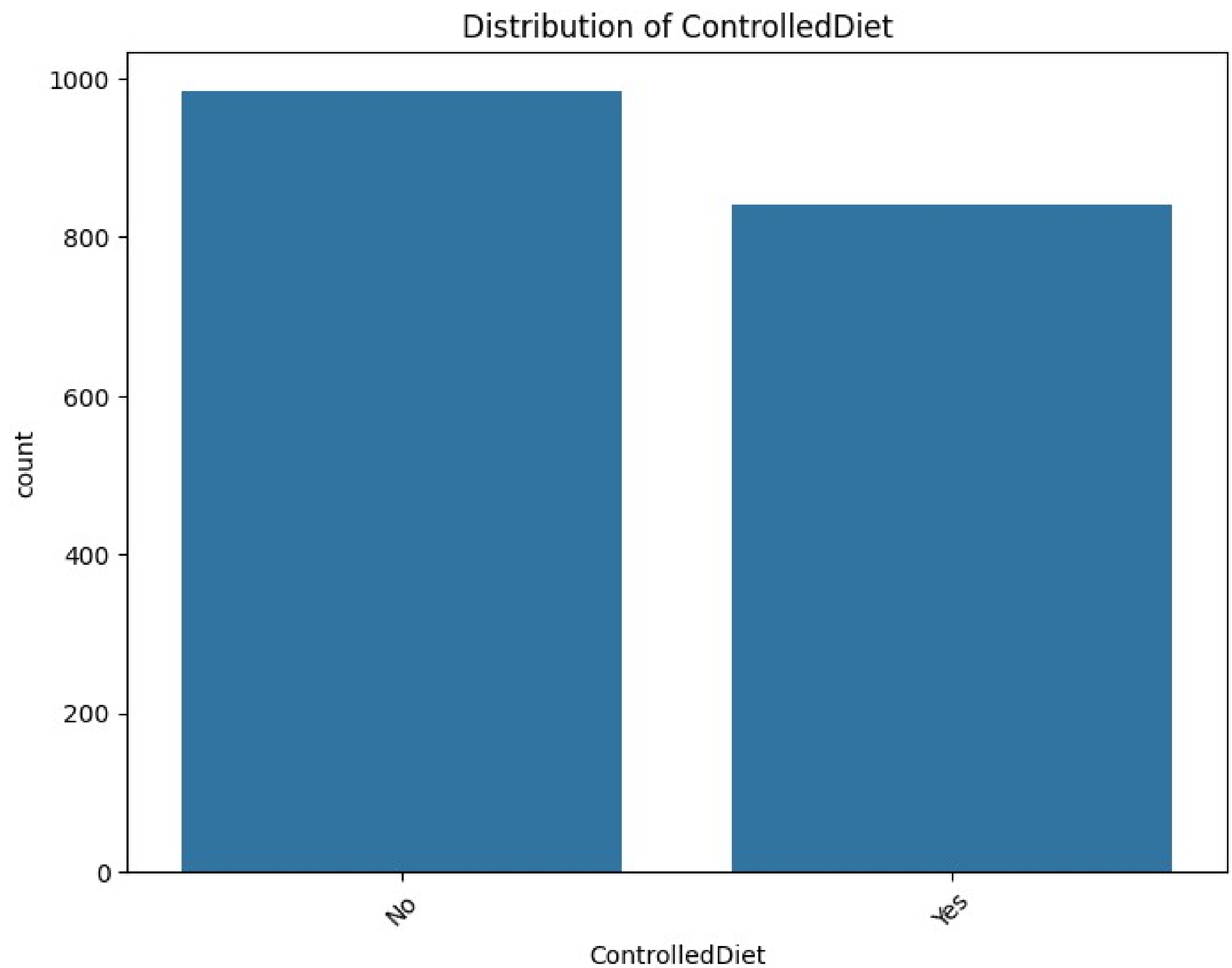

Distribution of NoseBleeding
1000
800
600
400
200
0
count
No
No
Yes
NoseBleeding



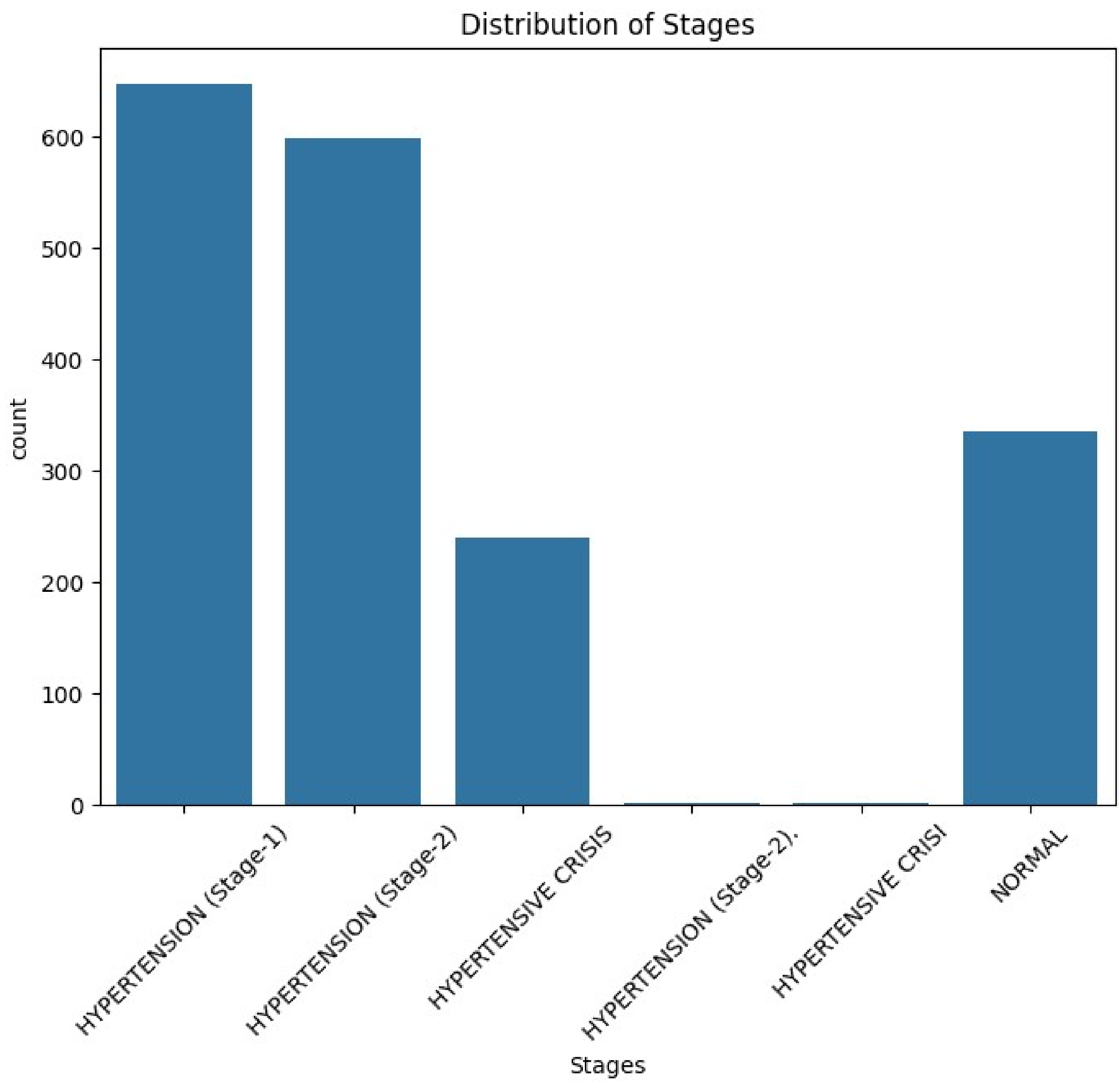
Distribution of Whendiagnoused
count
600
500
400
300
200
100
0
<1 Year
1 - 5 Years
>5 Years
Whendiagnoused


Distribution of Systolic
count
1000
800
600
400
200
0
111 - 120
121- 130
130+
100+
121 - 130
Systolic


Distribution of Diastolic
count
0
100
200
300
400
500
600
700
81 - 90
91 - 100
100+
130+
70 - 80
Diastolic



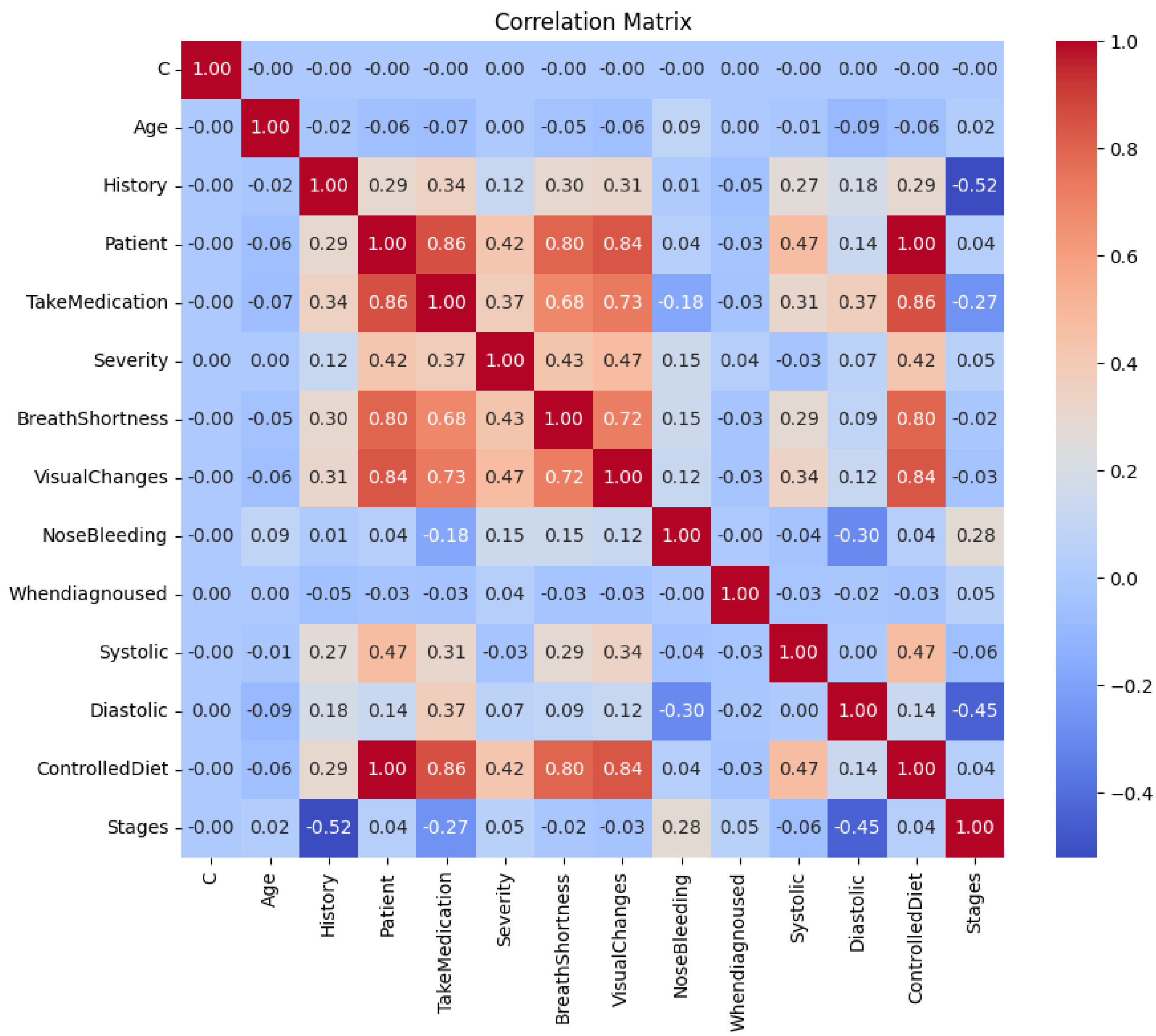
Distribution of ControlledDiet
1000
800
600
400
200
0
count
No
Yes
ControlledDiet



Bivariate Analysis

```
from sklearn.preprocessing import LabelEncoder

# Encode categorical columns
label_encoders = {}
for col in df.columns:
    if df[col].dtype == 'object':  # Check if column is categorical
        le = LabelEncoder()
        df[col] = le.fit_transform(df[col])
        label_encoders[col] = le

# Now compute correlation matrix
correlation_matrix = df.corr()
```

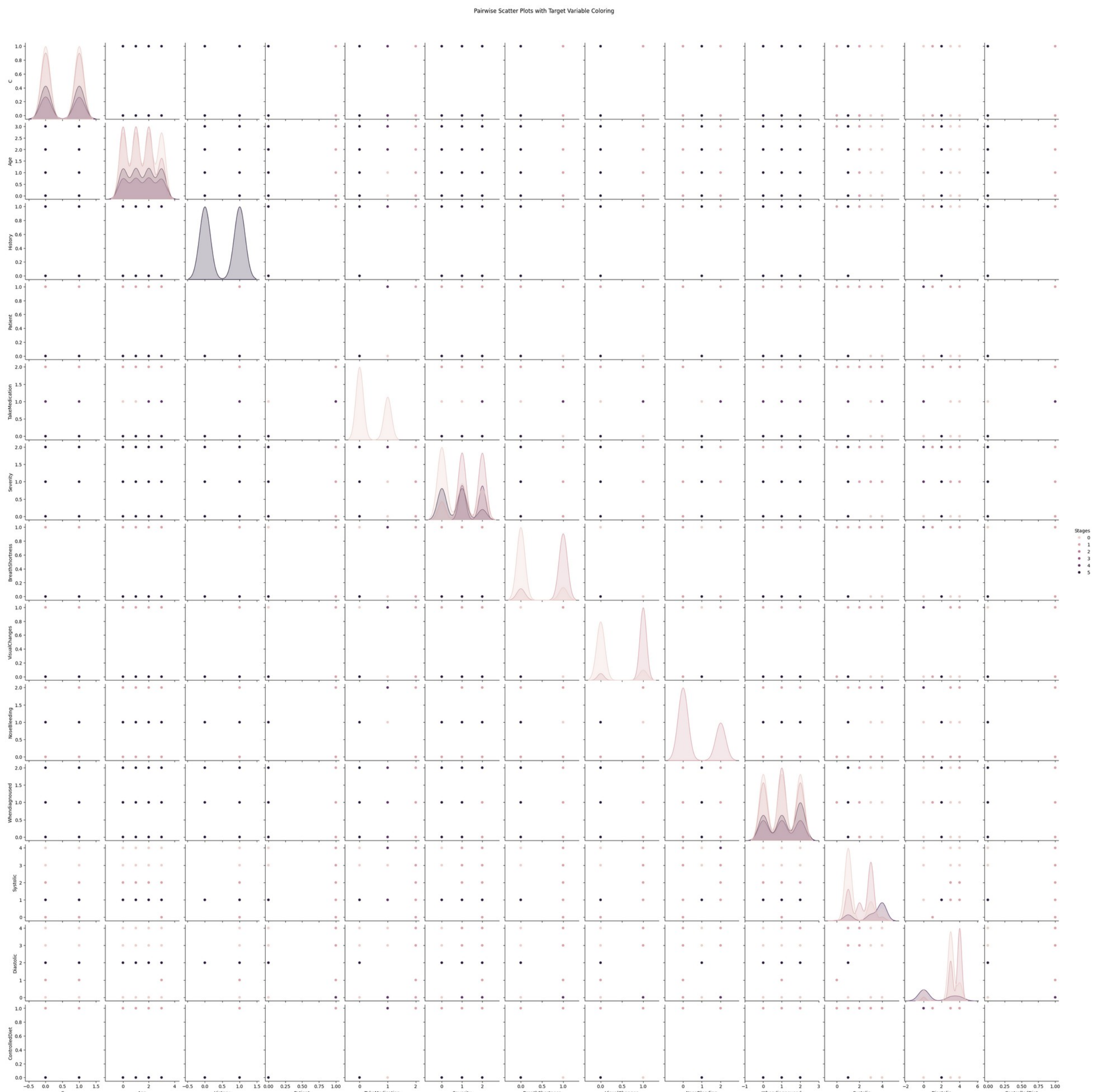
```python
# Plot heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm',
fmt=".2f")
plt.title('Correlation Matrix')
plt.show()
```



Multivariate analysis

```python
import seaborn as sns
import matplotlib.pyplot as plt

# Select only numeric columns for pairwise scatter plots
numeric_df = df.select_dtypes(include=['number'])
```

```python
# Pairplot to visualize pairwise relationships
sns.pairplot(numeric_df, hue='Stages', diag_kind='kde')  # Use 'hue' if you have a target variable
plt.suptitle('Pairwise Scatter Plots with Target Variable Coloring', y=1.02)
plt.show()
```



Model Building

```python
# Import required libraries
import pandas as pd
import numpy as np
```

```python
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestRegressor
from sklearn.naive_bayes import GaussianNB, MultinomialNB
from sklearn.metrics import accuracy_score, classification_report

# Load dataset
file_path = 'patient_data.csv'
df = pd.read_csv(file_path)

# Encode categorical variables
label_encoders = {}
for col in df.columns:
    le = LabelEncoder()
    df[col] = le.fit_transform(df[col])
    label_encoders[col] = le

# Split into features and target
X = df.drop('Stages', axis=1)
y = df['Stages']

# Remove rare classes (if any)
min_samples_per_class = 2
class_counts = Counter(y)
valid_indices = [i for i, label in enumerate(y) if class_counts[label]
>= min_samples_per_class]

X_filtered = X.iloc[valid_indices].reset_index(drop=True)
y_filtered = y.iloc[valid_indices].reset_index(drop=True)

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X_filtered,
y_filtered, test_size=0.2, random_state=42, stratify=y_filtered)

# Define models
models = {
    "Logistic Regression": LogisticRegression(random_state=42),
    "Random Forest Regressor": RandomForestRegressor(random_state=42),
    "Decision Tree": DecisionTreeClassifier(random_state=42),
    "Gaussian Naïve Bayes": GaussianNB(),
    "Multinomial Naïve Bayes": MultinomialNB()
}

# Train and evaluate each model
results = {}

for name, model in models.items():
    print(f"\nTraining {name}...")
```

```python
    # Handle MultinomialNB: Ensure all features are non-negative
    if name == "Multinomial Naïve Bayes":
        # MultinomialNB requires non-negative features
        X_train_non_negative = X_train.clip(lower=0)
        X_test_non_negative = X_test.clip(lower=0)

        model.fit(X_train_non_negative, y_train)
        y_pred = model.predict(X_test_non_negative)
    else:
        model.fit(X_train, y_train)
        y_pred = model.predict(X_test)

    acc = accuracy_score(y_test, y_pred)
    results[name] = {"model": model, "accuracy": acc}

    print(f"{name} Accuracy: {acc:.4f}")
    print(classification_report(y_test, y_pred))
    print("-" * 60)

# Select best model
best_model_name = max(results, key=lambda k: results[k]['accuracy'])
best_model = results[best_model_name]['model']
print(f"\n Best Model: {best_model_name} with Accuracy:
{results[best_model_name]['accuracy']:.4f}")

# Save best model
import joblib
joblib.dump(best_model, 'best_model.pkl')
print("\nModel saved as 'best_model.pkl'")
```

```
Training Logistic Regression...
Logistic Regression Accuracy: 0.9753
              precision    recall  f1-score   support

           0       0.96      0.97      0.97       130
           1       1.00      1.00      1.00       120
           4       1.00      1.00      1.00        48
           5       0.94      0.93      0.93        67

    accuracy                           0.98       365
   macro avg       0.98      0.97      0.97       365
weighted avg       0.98      0.98      0.98       365

------------------------------------------------------------

Training Random Forest Regressor...
Random Forest Regressor Accuracy: 1.0000
              precision    recall  f1-score   support
```

```
           0       1.00      1.00      1.00       130
           1       1.00      1.00      1.00       120
           4       1.00      1.00      1.00        48
           5       1.00      1.00      1.00        67

    accuracy                           1.00       365
   macro avg       1.00      1.00      1.00       365
weighted avg       1.00      1.00      1.00       365

------------------------------------------------------------

Training Decision Tree...
Decision Tree Accuracy: 1.0000
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       130
           1       1.00      1.00      1.00       120
           4       1.00      1.00      1.00        48
           5       1.00      1.00      1.00        67

    accuracy                           1.00       365
   macro avg       1.00      1.00      1.00       365
weighted avg       1.00      1.00      1.00       365

------------------------------------------------------------

Training Gaussian Naïve Bayes...
Gaussian Naïve Bayes Accuracy: 1.0000
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       130
           1       1.00      1.00      1.00       120
           4       1.00      1.00      1.00        48
           5       1.00      1.00      1.00        67

    accuracy                           1.00       365
   macro avg       1.00      1.00      1.00       365
weighted avg       1.00      1.00      1.00       365

------------------------------------------------------------

Training Multinomial Naïve Bayes...
Multinomial Naïve Bayes Accuracy: 0.8219
              precision    recall  f1-score   support

           0       0.81      0.94      0.87       130
           1       0.84      0.94      0.89       120
           4       0.79      0.56      0.66        48
           5       0.84      0.57      0.68        67
```

```
    accuracy                           0.82       365
   macro avg       0.82      0.75      0.77       365
weighted avg       0.82      0.82      0.81       365

------------------------------------------------------------

□ Best Model: Random Forest Regressor with Accuracy: 1.0000

Model saved as 'best_model.pkl'
```