Import installed libraries and than use it and also For clean output plots

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.feature_selection import VarianceThreshold
from scipy import stats
from scipy.stats import ttest_1samp, chi2_contingency
from scipy.integrate import odeint, solve_ivp
import warnings
warnings.filterwarnings("ignore")
```

Load Dataset for solving this assignment

```
data = pd.read_csv("patient_data.csv")

# Show first 5 rows
data.head()
```

```
   PatientID  Gender  Age  CholesterolLevel  BloodPressure Region
RiskCategory
0          1    Male   37             193.4          129.4   East
High
1          2  Female   45             210.7          107.1   West
Low
2          3    Male   63             244.3          103.9   West
Low
3          4    Male   53             184.5          127.2   West
High
4          5    Male   29             175.7          116.6  South
High
```

Handle Missing Values (if any)

```
# Check for missing values
print("Missing values:\n", data.isnull().sum())

# Fill missing CholesterolLevel with mean
data['CholesterolLevel'].fillna(data['CholesterolLevel'].mean(),
inplace=True)
```

```
Missing values:
 PatientID          0
Gender             0
Age                0
CholesterolLevel   0
BloodPressure      0
Region             0
```

```
RiskCategory       0
dtype: int64
```

Feature Selection with VarianceThreshold

```
# Apply VarianceThreshold to numeric columns
numeric_data = data.select_dtypes(include=np.number)
selector = VarianceThreshold()
data_var = selector.fit_transform(numeric_data)

# Print selected features
print("Remaining Features:",
      numeric_data.columns[selector.get_support()])
```

```
Remaining Features: Index(['PatientID', 'Age', 'CholesterolLevel',
'BloodPressure'], dtype='object')
```

Outlier Detection using Z-Score

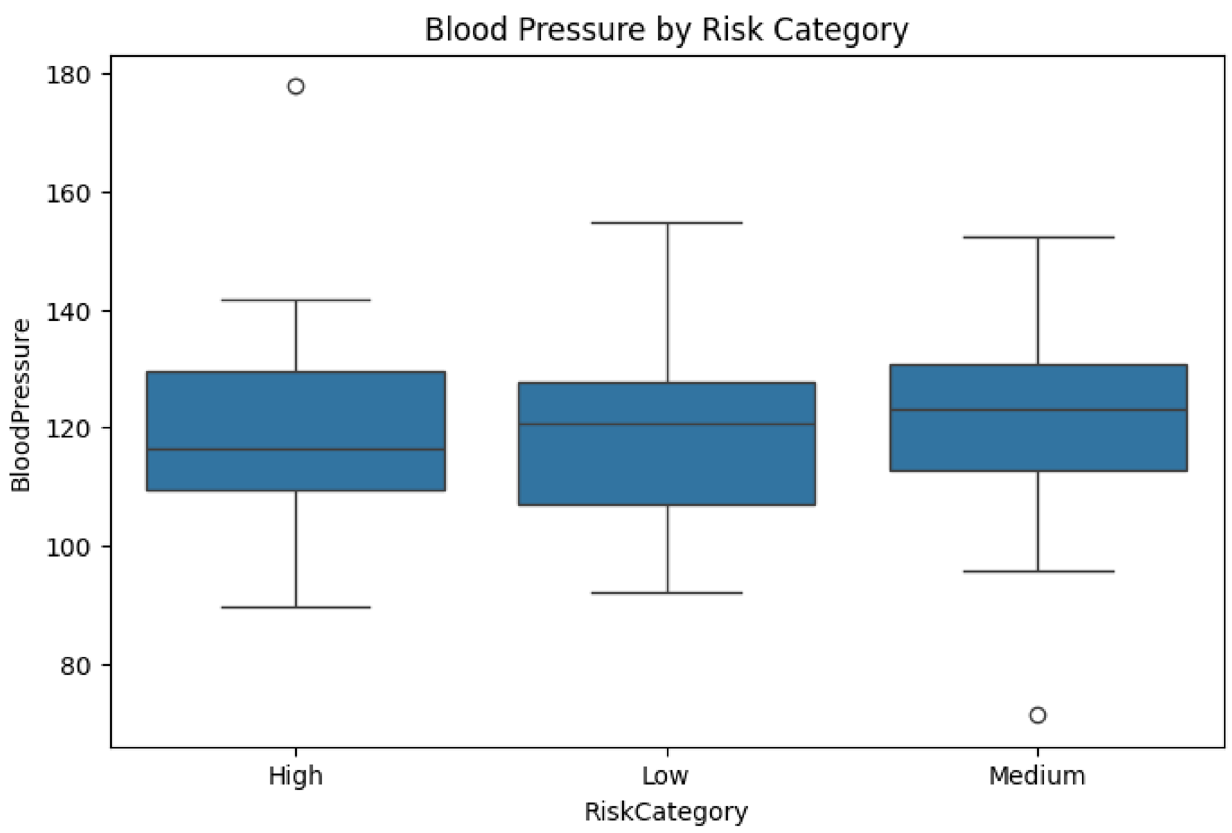
```
# Detect outliers in CholesterolLevel
z_scores = np.abs(stats.zscore(data['CholesterolLevel']))
data = data[(z_scores < 3)]

# Check updated shape
print("Shape after removing outliers:", data.shape)
```

```
Shape after removing outliers: (100, 7)
```

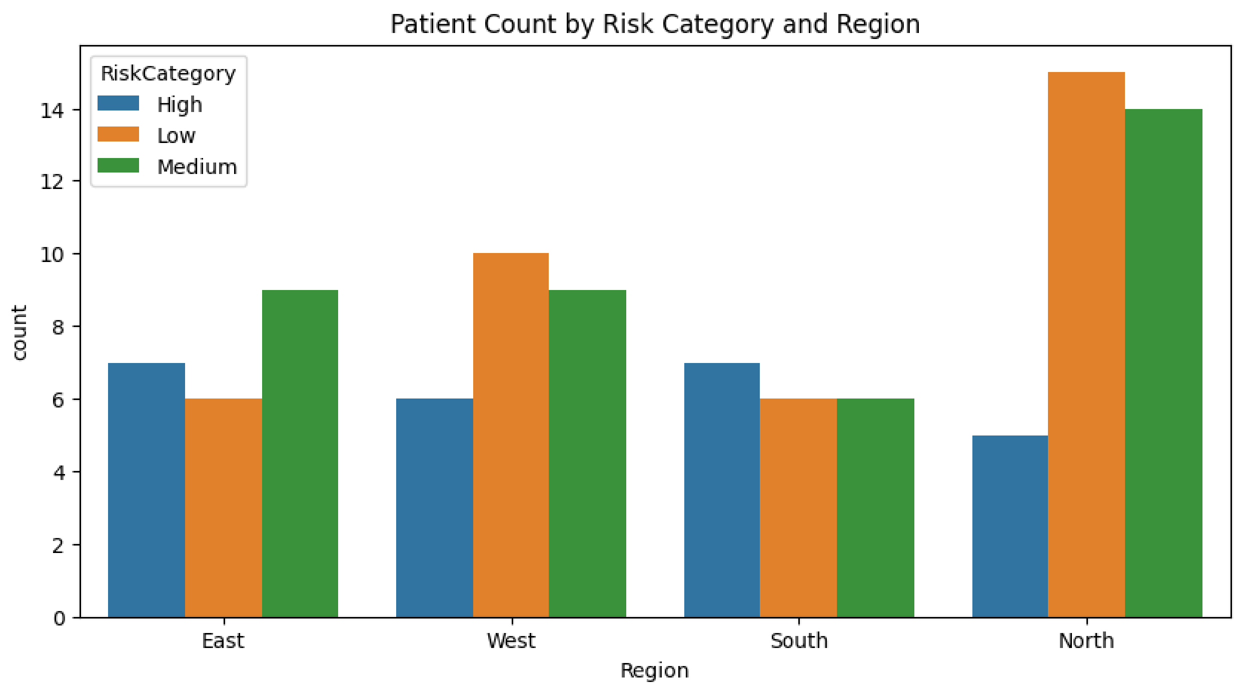
Boxplot of Blood Pressure by Risk Category

```
plt.figure(figsize=(8, 5))
sns.boxplot(x='RiskCategory', y='BloodPressure', data=data)
plt.title("Blood Pressure by Risk Category")
plt.show()
```



Countplot by Region and RiskCategory

```
plt.figure(figsize=(10, 5))
sns.countplot(x='Region', hue='RiskCategory', data=data)
plt.title("Patient Count by Risk Category and Region")
plt.show()
```



One-Sample T-Test (Cholesterol vs 200)

```python
# One-Sample T-Test
sample = data['CholesterolLevel'].sample(20)
t_stat, p_val = ttest_1samp(sample, 200)

print(f"T-statistic: {t_stat:.3f}, p-value: {p_val:.3f}")
print("Null Hypothesis: μ = 200")
print("Alternative Hypothesis: μ ≠ 200")

if p_val < 0.05:
    print("Reject H0: The average CholesterolLevel is significantly
different from 200 mg/dL.")
else:
    print("Fail to Reject H0: No significant difference from 200
mg/dL.")
```

```
T-statistic: 0.423, p-value: 0.677
Null Hypothesis: μ = 200
Alternative Hypothesis: μ ≠ 200
Fail to Reject H0: No significant difference from 200 mg/dL.
```

Chi-Square Test (Region vs RiskCategory)

```python
# Chi-square test
contingency_table = pd.crosstab(data['Region'], data['RiskCategory'])
chi2, p, dof, expected = chi2_contingency(contingency_table)

print(f"Chi2: {chi2:.3f}, p-value: {p:.3f}")
print("Null Hypothesis: Region and RiskCategory are independent.")
print("Alternative Hypothesis: Region and RiskCategory are
dependent.")

if p < 0.05:
    print("Reject H0: There is a significant relationship.")
else:
    print("Fail to Reject H0: No significant relationship.")
```

```
Chi2: 4.538, p-value: 0.604
Null Hypothesis: Region and RiskCategory are independent.
Alternative Hypothesis: Region and RiskCategory are dependent.
Fail to Reject H0: No significant relationship.
```

ODE Model using odeint

```
# Medication level model using odeint
def model(C, t):
    k = 0.1
    D = 100
    dCdt = k * (D - C)
    return dCdt

t = np.linspace(0, 50, 100)
C0 = 0
C_odeint = odeint(model, C0, t)
```

ODE Model using solve_ivp

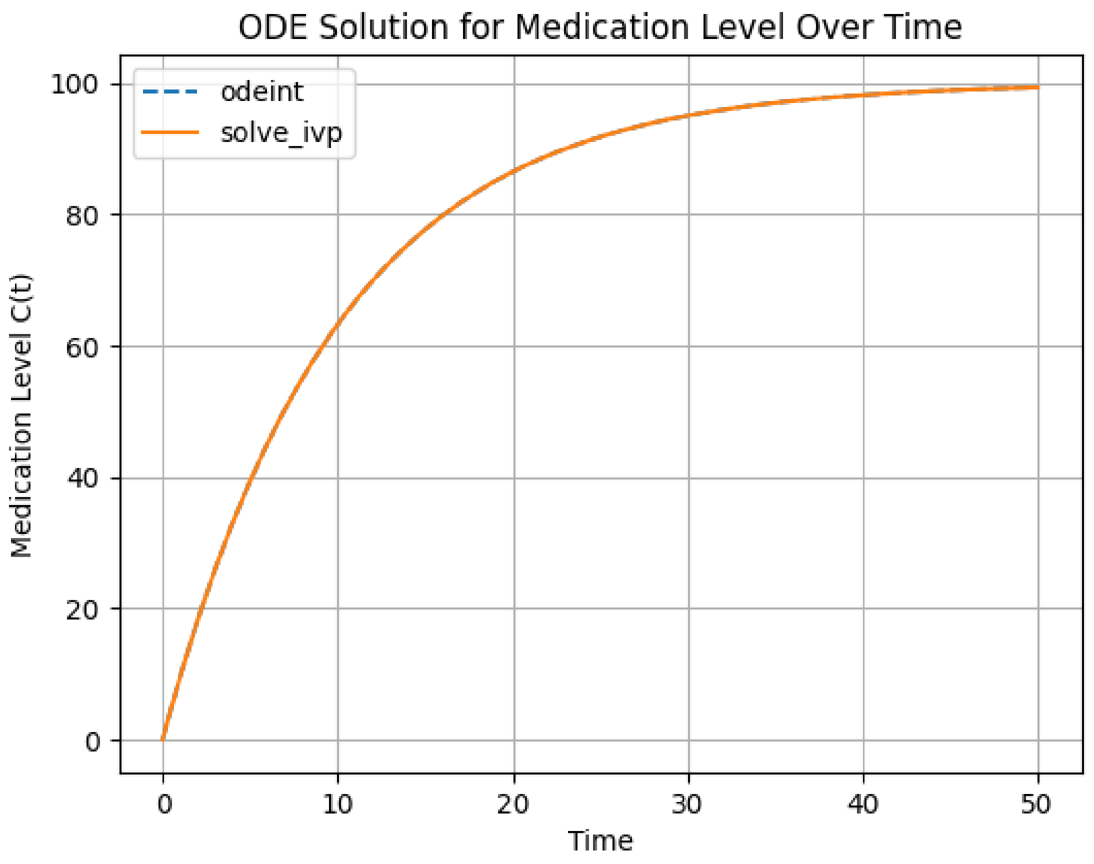
```
# Medication level model using solve_ivp
def model_ivp(t, C):
    k = 0.1
    D = 100
    return k * (D - C)

sol = solve_ivp(model_ivp, [0, 50], [0], t_eval=t)
```

Plot and Compare Both ODE Solutions

```
plt.plot(t, C_odeint, label='odeint', linestyle='--')
plt.plot(sol.t, sol.y[0], label='solve_ivp', linestyle='-')
plt.title("ODE Solution for Medication Level Over Time")
plt.xlabel("Time")
plt.ylabel("Medication Level C(t)")
plt.legend()
plt.grid(True)
plt.show()

print("Both methods give similar results; solve_ivp provides more
flexibility and is modern.")
```



```
Both methods give similar results; solve_ivp provides more flexibility
and is modern.
```

Save Your Cleaned Data

```python
data.to_csv("cleaned_patient_data.csv", index=False)
```