```
#import file from drive
from google.colab import drive
drive.mount("/content/drive")
```

```
Mounted at /content/drive
```

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# Load your dataset

import pandas as pd

# Load dataset
file_path = "/content/drive/My Drive/Colab Notebooks/updated_dataset_final.csv"
df_new = pd.read_csv(file_path)
df_new=df_new.drop(columns=["propensity_score","IPW_weight"])
# Display first few rows of the dataset
df_new.head()
df=df_new
df
```

	patid	index_age	previous_asthma_drugs	total_pre_index_cannisters_365	post_index_
0	1073754155	14	1	1	
1	1073799394	21	1	2	
2	1073854918	62	1	0	
3	1073898249	30	1	2	
4	1073913003	40	1	1	
...	...	...	...	...	
18210	1609186140	34	1	1	
18211	1609619686	28	1	0	
18212	1609921811	54	1	2	
18213	1609951502	49	1	1	
18214	1610380953	15	1	1	

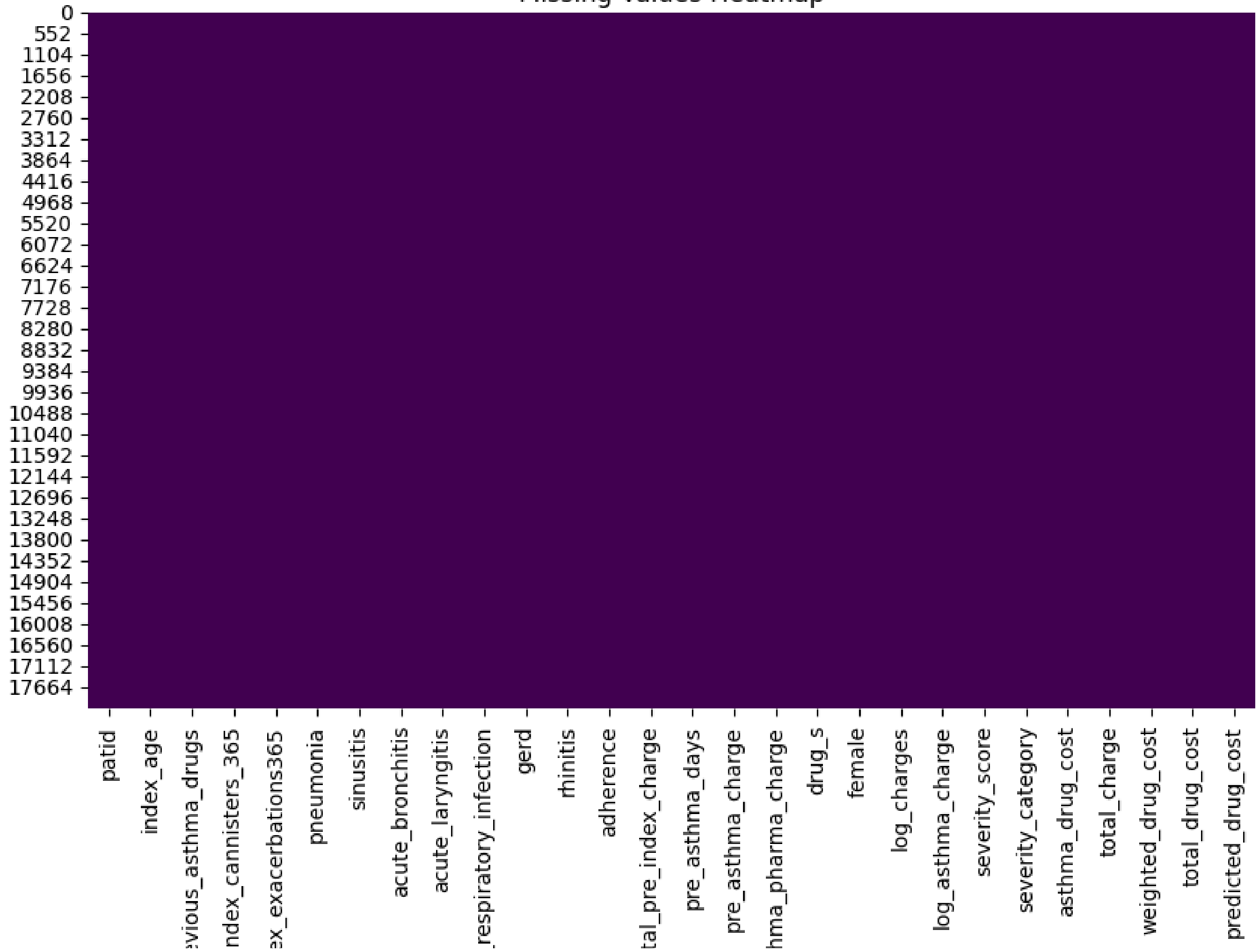
18215 rows × 28 columns

Double-click (or enter) to edit

```
# 1. Check for missing values
print("Missing values per column:")
print(df.isnull().sum())

# Visualize missing values
plt.figure(figsize=(10,6))
sns.heatmap(df.isnull(), cbar=False, cmap='viridis')
```

```
plt.title("Missing Values Heatmap")
plt.show()
```

```
Missing values per column:
patid                              0
index_age                          0
previous_asthma_drugs              0
total_pre_index_cannisters_365     0
post_index_exacerbations365        0
pneumonia                          0
sinusitis                          0
acute_bronchitis                   0
acute_laryngitis                   0
upper_respiratory_infection        0
gerd                               0
rhinitis                           0
adherence                          0
total_pre_index_charge             0
pre_asthma_days                    0
pre_asthma_charge                  0
pre_asthma_pharma_charge           0
drug_s                             0
female                             0
log_charges                        0
log_asthma_charge                  0
severity_score                     0
severity_category                  0
asthma_drug_cost                   0
total_charge                       0
weighted_drug_cost                 0
total_drug_cost                    0
predicted_drug_cost                0
dtype: int64
```


Missing Values Heatmap

pre

total_pre_i

post_inde

upper_

tot

pre_ast

```
import pandas as pd
import numpy as np
from scipy.stats import ttest_ind, chi2_contingency



# Define treatment groups
drug_d = df[df['drug_s'] == 0]  # Patients who took Drug_D
drug_s = df[df['drug_s'] == 1]  # Patients who took Drug_S

# Define continuous and categorical variables
continuous_vars = ['index_age', 'pre_asthma_charge', 'pre_asthma_days', 'log_charges', 'log_asthma
categorical_vars = ['female', 'pneumonia', 'sinusitis', 'acute_bronchitis', 'acute_laryngitis', 'g

# Function to calculate SMD for continuous variables
def calculate_smd_continuous(var):
    mean_d, std_d = drug_d[var].mean(), drug_d[var].std()
    mean_s, std_s = drug_s[var].mean(), drug_s[var].std()
    pooled_std = np.sqrt((std_d**2 + std_s**2) / 2)
    smd = abs(mean_d - mean_s) / pooled_std
    return smd

# Function to calculate SMD for categorical variables
def calculate_smd_categorical(var):
    prop_d = drug_d[var].mean()
    prop_s = drug_s[var].mean()
    pooled_prop = (prop_d + prop_s) / 2
    smd = abs(prop_d - prop_s) / np.sqrt(pooled_prop * (1 - pooled_prop))
    return smd

# Compute SMDs
smd_results = {}

for var in continuous_vars:
    smd_results[var] = calculate_smd_continuous(var)

for var in categorical_vars:
    smd_results[var] = calculate_smd_categorical(var)

# Convert results to DataFrame
smd_df = pd.DataFrame(smd_results.items(), columns=['Variable', 'SMD'])

# Interpretation thresholds
smd_df['Interpretation'] = smd_df['SMD'].apply(lambda x: "No Imbalance (SMD < 0.1)" if x < 0.1 els
                                                "Moderate Imbalance (0.1 ≤ SMD < 0.25)" if x < 0.2
                                                "Large Imbalance (SMD ≥ 0.25)")

# Display results
print(smd_df)
```

```
             Variable       SMD                         Interpretation
0           index_age  0.054800               No Imbalance (SMD < 0.1)
1   pre_asthma_charge  0.144525  Moderate Imbalance (0.1 ≤ SMD < 0.25)
2     pre_asthma_days  0.291470           Large Imbalance (SMD ≥ 0.25)
3         log_charges  0.050608               No Imbalance (SMD < 0.1)
4   log_asthma_charge  0.646011           Large Imbalance (SMD ≥ 0.25)
5              female  0.041084               No Imbalance (SMD < 0.1)
6           pneumonia  0.079905               No Imbalance (SMD < 0.1)
```

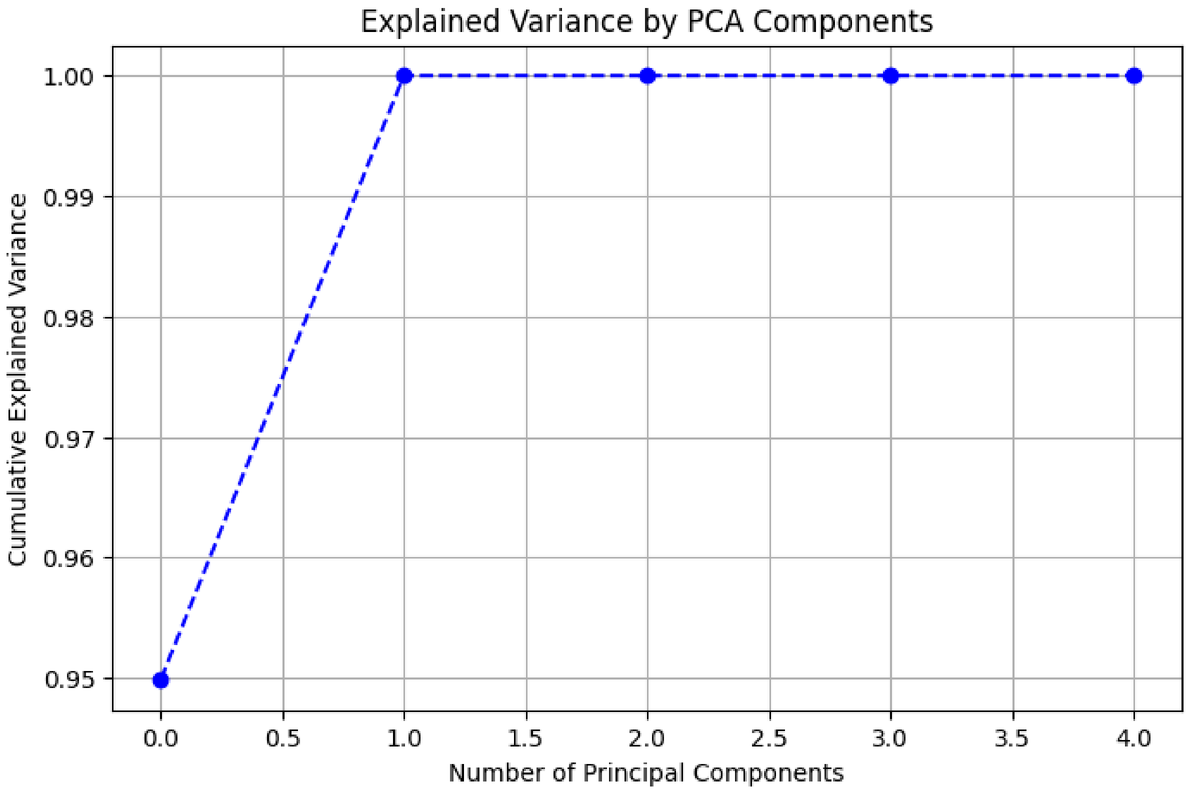
```
    7           sinusitis  0.011408                No Imbalance (SMD < 0.1)
    8    acute_bronchitis  0.149202  Moderate Imbalance (0.1 ≤ SMD < 0.25)
    9    acute_laryngitis  0.028707                No Imbalance (SMD < 0.1)
    10               gerd  0.091678                No Imbalance (SMD < 0.1)
    11          rhinitis  0.352552           Large Imbalance (SMD ≥ 0.25)
```

```
import pandas as pd
import numpy as np


# Define treatment groups
drug_d = df[df['drug_s'] == 0]  # Patients who took Drug_D
drug_s = df[df['drug_s'] == 1]  # Patients who took Drug_S

# Define continuous and categorical variables
continuous_vars = ['index_age', 'pre_asthma_charge', 'pre_asthma_days', 'log_charges', 'log_asthma
categorical_vars = ['female', 'pneumonia', 'sinusitis', 'acute_bronchitis', 'acute_laryngitis', 'g

# Function to calculate SMD for continuous variables
def calculate_smd_continuous(var):
    mean_d, std_d = drug_d[var].mean(), drug_d[var].std()
    mean_s, std_s = drug_s[var].mean(), drug_s[var].std()
    pooled_std = np.sqrt((std_d**2 + std_s**2) / 2)
    smd = abs(mean_d - mean_s) / pooled_std
    return smd

# Function to calculate SMD for categorical variables
def calculate_smd_categorical(var):
    prop_d = drug_d[var].mean()
    prop_s = drug_s[var].mean()
    pooled_prop = (prop_d + prop_s) / 2
    smd = abs(prop_d - prop_s) / np.sqrt(pooled_prop * (1 - pooled_prop))
    return smd

# Compute SMDs
smd_results = {}

for var in continuous_vars:
    smd_results[var] = calculate_smd_continuous(var)

for var in categorical_vars:
    smd_results[var] = calculate_smd_categorical(var)

# Convert results to DataFrame
smd_df = pd.DataFrame(smd_results.items(), columns=['Variable', 'SMD'])

# Define imbalance categories
smd_df['Interpretation'] = smd_df['SMD'].apply(lambda x: "No Imbalance (SMD < 0.1)" if x < 0.1 els
                                                "Moderate Imbalance (0.1 ≤ SMD < 0.25)" if x < 0.2
                                                "Large Imbalance (SMD ≥ 0.25)")

# Count occurrences of each imbalance category
imbalance_counts = smd_df['Interpretation'].value_counts()

# Calculate percentage of imbalance
total_vars = len(smd_df)
imbalance_percentages = (imbalance_counts / total_vars) * 100

# Display results
```

```
print("🔹 Standardized Mean Difference (SMD) Results:")
print(smd_df)
print("\n🔹 Imbalance Distribution:")
print(imbalance_counts)
print("\n🔹 Percentage of Imbalance:")
print(imbalance_percentages.round(2).astype(str) + "%")
```

```
🔹 Standardized Mean Difference (SMD) Results:
             Variable       SMD                         Interpretation
0           index_age  0.054800               No Imbalance (SMD < 0.1)
1   pre_asthma_charge  0.144525  Moderate Imbalance (0.1 ≤ SMD < 0.25)
2     pre_asthma_days  0.291470           Large Imbalance (SMD ≥ 0.25)
3         log_charges  0.050608               No Imbalance (SMD < 0.1)
4   log_asthma_charge  0.646011           Large Imbalance (SMD ≥ 0.25)
5              female  0.041084               No Imbalance (SMD < 0.1)
6           pneumonia  0.079905               No Imbalance (SMD < 0.1)
7           sinusitis  0.011408               No Imbalance (SMD < 0.1)
8    acute_bronchitis  0.149202  Moderate Imbalance (0.1 ≤ SMD < 0.25)
9    acute_laryngitis  0.028707               No Imbalance (SMD < 0.1)
10               gerd  0.091678               No Imbalance (SMD < 0.1)
11           rhinitis  0.352552           Large Imbalance (SMD ≥ 0.25)

🔹 Imbalance Distribution:
Interpretation
No Imbalance (SMD < 0.1)                 7
Large Imbalance (SMD ≥ 0.25)             3
Moderate Imbalance (0.1 ≤ SMD < 0.25)    2
Name: count, dtype: int64

🔹 Percentage of Imbalance:
Interpretation
No Imbalance (SMD < 0.1)                 58.33%
Large Imbalance (SMD ≥ 0.25)              25.0%
Moderate Imbalance (0.1 ≤ SMD < 0.25)    16.67%
Name: count, dtype: object
```

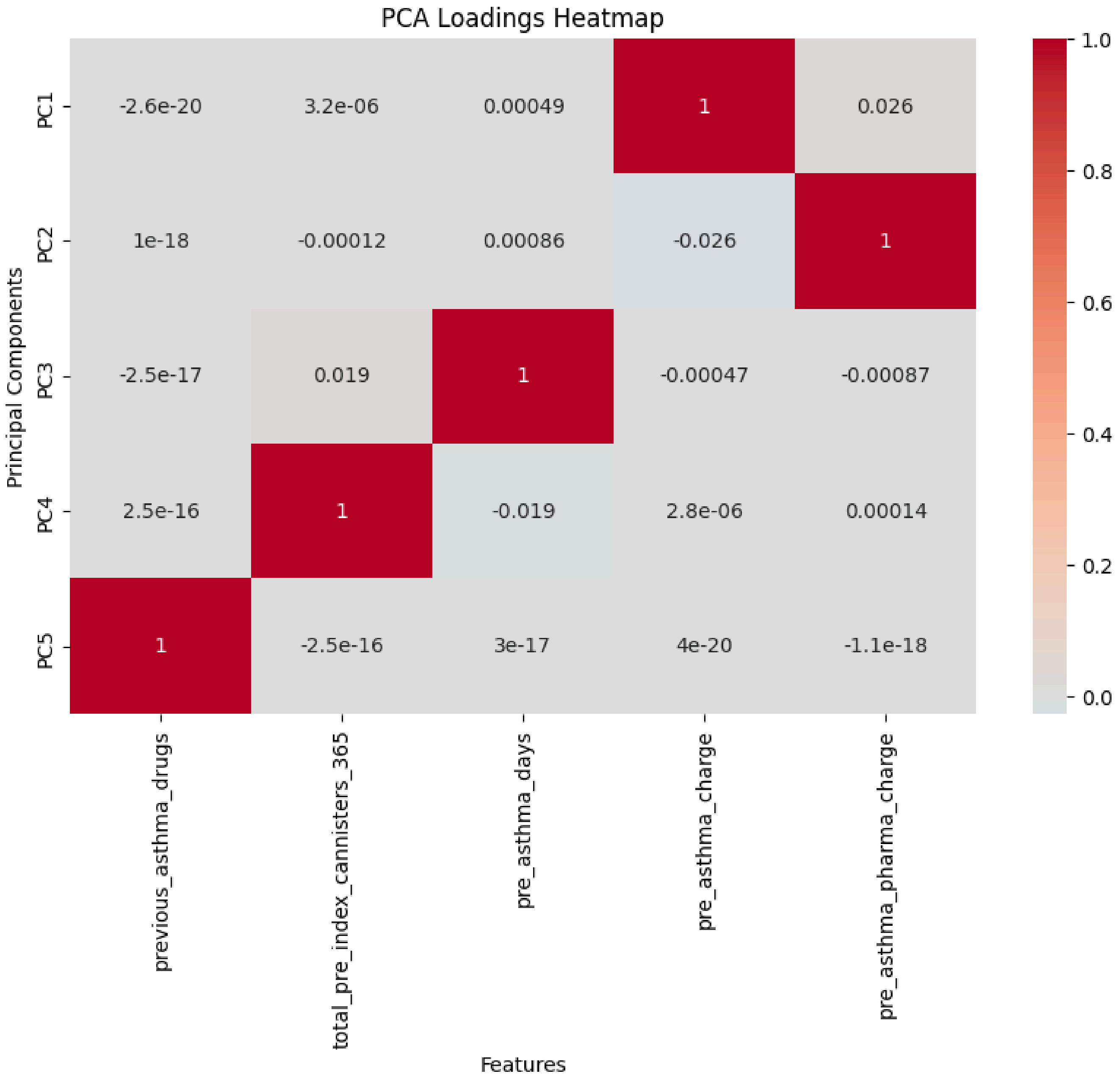
```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA

# Fit PCA on selected features
selected_features = [
    "previous_asthma_drugs",
    "total_pre_index_cannisters_365",
    "pre_asthma_days",
    "pre_asthma_charge",
    "pre_asthma_pharma_charge"
]

X = df[selected_features]

pca = PCA()
pca.fit(X)

# Plot explained variance
plt.figure(figsize=(8,5))
plt.plot(np.cumsum(pca.explained_variance_ratio_), marker='o', linestyle='--', color='b')
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Explained Variance by PCA Components')
plt.grid()
plt.show()
```



```
loadings = pd.DataFrame(
    pca.components_,
    columns=selected_features,
    index=[f"PC{i+1}" for i in range(len(selected_features))]
)

print(loadings)
```

```
     previous_asthma_drugs  total_pre_index_cannisters_365  pre_asthma_days  \
PC1          -2.573215e-20                    3.210024e-06     4.943497e-04
PC2           1.040267e-18                   -1.234991e-04     8.552705e-04
PC3          -2.547782e-17                    1.935967e-02     9.998121e-01
PC4           2.472117e-16                    9.998126e-01    -1.935956e-02
PC5           1.000000e+00                   -2.466720e-16     3.025807e-17

     pre_asthma_charge  pre_asthma_pharma_charge
PC1       9.996729e-01              2.557196e-02
PC2      -2.557238e-02              9.996726e-01
PC3      -4.723516e-04             -8.650813e-04
PC4       2.777953e-06              1.401506e-04
PC5       3.960460e-20             -1.095956e-18
```

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 6))
sns.heatmap(loadings, annot=True, cmap='coolwarm', center=0)
plt.title("PCA Loadings Heatmap")
plt.xlabel("Features")
plt.ylabel("Principal Components")
plt.show()
```



```
import pandas as pd
import numpy as np
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler



# Select severity-related features
severity_features = [
    "previous_asthma_drugs",
    "total_pre_index_cannisters_365",
    "pre_asthma_days",
    "pre_asthma_charge",
    "pre_asthma_pharma_charge"
]

# Standardize the data
scaler = StandardScaler()
severity_scaled = scaler.fit_transform(df[severity_features])

# Apply PCA
pca = PCA(n_components=3)  # Keep top 3 components
pca_transformed = pca.fit_transform(severity_scaled)

# Extract explained variance ratios
explained_variance = pca.explained_variance_ratio_

# Calculate Severity Score (weighted sum of PCs)
df["severity_score"] = (
    explained_variance[0] * pca_transformed[:, 0] +
    explained_variance[1] * pca_transformed[:, 1] +
    explained_variance[2] * pca_transformed[:, 2]
)

# Normalize the severity score (optional, scale 0-100)
df["severity_score"] = (df["severity_score"] - df["severity_score"].min()) / \
                       (df["severity_score"].max() - df["severity_score"].min()) * 100

# Save the updated dataset
df.to_csv("updated_dataset_with_severity.csv", index=False)

# Display severity score statistics
print(df["severity_score"].describe())
```

```
count    18215.000000
mean         6.551016
std          5.450787
min          0.000000
25%          3.010097
50%          5.731099
75%          9.178861
max        100.000000
Name: severity_score, dtype: float64
```

```
df.head()
```

	patid	index_age	previous_asthma_drugs	total_pre_index_cannisters_365	post_index_exac
0	1073754155	14	1	1	
1	1073799394	21	1	2	
2	1073854918	62	1	0	
3	1073898249	30	1	2	
4	1073913003	40	1	1	

5 rows × 32 columns

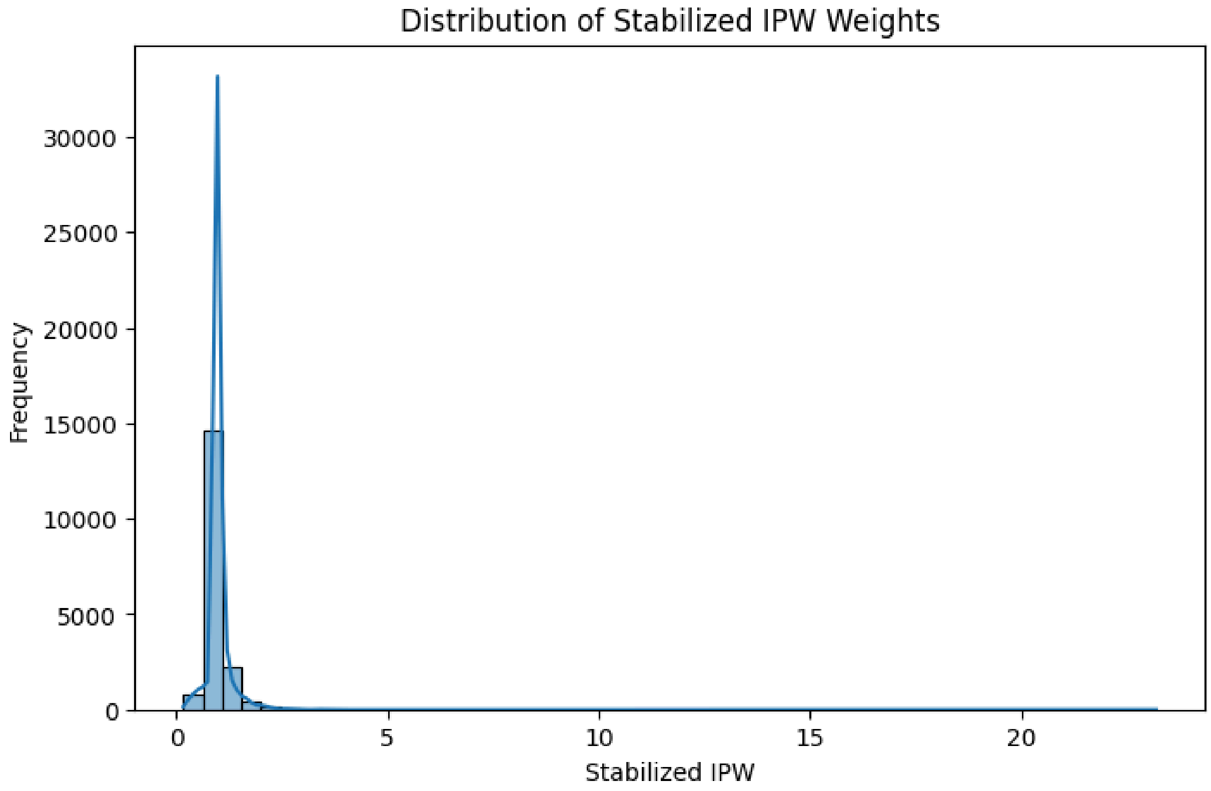
```
# Define severity levels based on quantiles
df["severity_category"] = pd.cut(df["severity_score"],
                                 bins=[0, 33, 66, 100],
                                 labels=["Mild", "Moderate", "Severe"])

# Save again
df.to_csv("updated_dataset_with_severity.csv", index=False)

# View distribution
print(df["severity_category"].value_counts())
```

```
severity_category
Mild        18050
Moderate       69
Severe          8
Name: count, dtype: int64
```

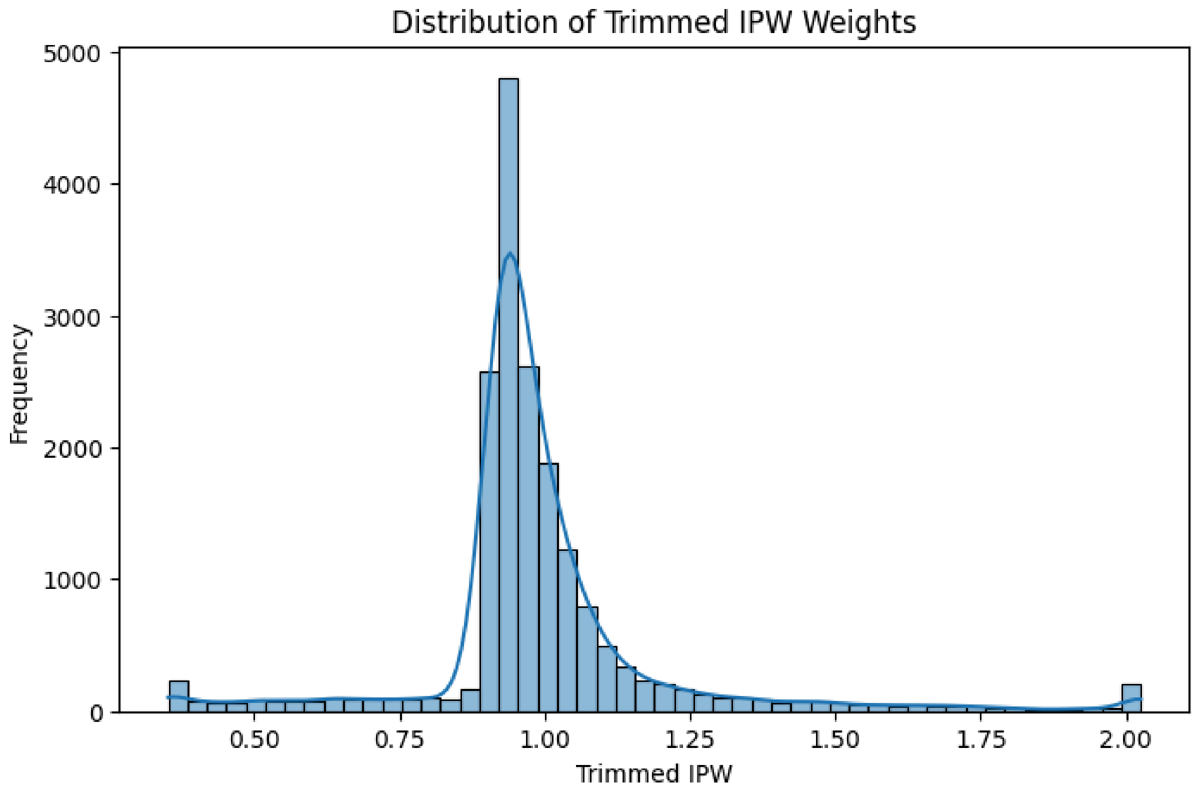
```
import pandas as pd
import numpy as np
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler

# Define independent variables (features affecting treatment assignment)
features = ['index_age', 'total_pre_index_cannisters_365',
            'pneumonia', 'sinusitis', 'acute_bronchitis', 'acute_laryngitis',
            'upper_respiratory_infection', 'gerd', 'rhinitis', 'female','severity_score','severity

X = df[features]  # Features used for treatment assignment
y = df['drug_s']  # Treatment indicator (1 for Drug_S, 0 for Drug_D)

# Scale features for better logistic regression performance
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Train a logistic regression model to estimate propensity scores
propensity_model = LogisticRegression()
propensity_model.fit(X_scaled, y)

# Predict probabilities of receiving Drug_S
df['propensity_score'] = propensity_model.predict_proba(X_scaled)[:, 1]

# Compute **Raw IPW weights**
df['IPW_weight'] = np.where(df['drug_s'] == 1,
                            1 / df['propensity_score'],
                            1 / (1 - df['propensity_score']))

# Compute **Stabilized IPW weights** to reduce skewness
p_treated = df['drug_s'].mean()  # Marginal probability of treatment
df['stabilized_IPW'] = np.where(df['drug_s'] == 1,
                                p_treated / df['propensity_score'],
                                (1 - p_treated) / (1 - df['propensity_score']))

# Check weights distribution
print(df[['drug_s', 'propensity_score', 'IPW_weight', 'stabilized_IPW']].head())

# Plot the distribution of stabilized weights to check for skewness
import matplotlib.pyplot as plt
import seaborn as sns

plt.figure(figsize=(8,5))
```

```
sns.histplot(df['stabilized_IPW'], bins=50, kde=True)
plt.title('Distribution of Stabilized IPW Weights')
plt.xlabel('Stabilized IPW')
plt.ylabel('Frequency')
plt.show()
```

```
   drug_s  propensity_score  IPW_weight  stabilized_IPW
0       0          0.089396    1.098172        0.920921
1       0          0.102478    1.114179        0.934344
2       0          0.209079    1.264349        1.060276
3       0          0.060085    1.063926        0.892203
4       0          0.215834    1.275240        1.069410
```



```
# Trim extreme weights (Common threshold: 99th percentile)
upper_limit = np.percentile(df['stabilized_IPW'], 99)  # 99th percentile
lower_limit = np.percentile(df['stabilized_IPW'], 1)   # 1st percentile

df['trimmed_IPW'] = np.clip(df['stabilized_IPW'], lower_limit, upper_limit)

# Plot the trimmed distribution
plt.figure(figsize=(8,5))
sns.histplot(df['trimmed_IPW'], bins=50, kde=True)
plt.title('Distribution of Trimmed IPW Weights')
plt.xlabel('Trimmed IPW')
plt.ylabel('Frequency')
plt.show()
```

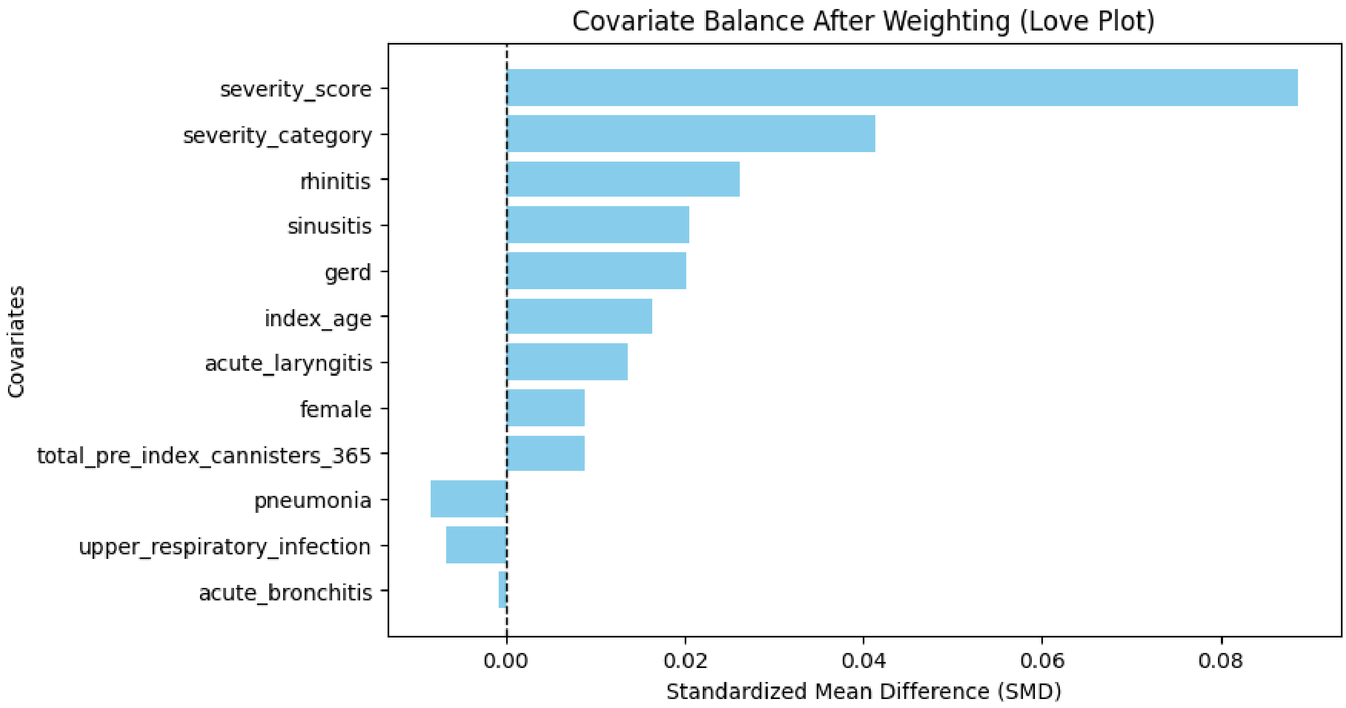


```
# Function to calculate Standardized Mean Difference (SMD)
def standardized_difference(df, col, weight_col):
    treated = df[df['drug_s'] == 1]
    control = df[df['drug_s'] == 0]

    mean_treated = np.average(treated[col], weights=treated[weight_col])
    mean_control = np.average(control[col], weights=control[weight_col])

    std_treated = np.std(treated[col], ddof=1)
    std_control = np.std(control[col], ddof=1)

    pooled_std = np.sqrt((std_treated**2 + std_control**2) / 2)

    if pooled_std == 0:
        return np.nan  # Avoid division by zero

    smd = (mean_treated - mean_control) / pooled_std
    return smd

# Compute SMD before and after weighting
balance_check_before = {col: standardized_difference(df, col, 'IPW_weight') for col in features}
balance_check_after = {col: standardized_difference(df, col, 'trimmed_IPW') for col in features}

# Convert to DataFrame
smd_df = pd.DataFrame({'Before Weighting': balance_check_before, 'After Weighting': balance_check_
print(smd_df.sort_values('After Weighting', ascending=False))
```

```
                                Before Weighting  After Weighting
severity_score                         -0.012253         0.088678
severity_category                      -0.039040         0.041398
rhinitis                                0.000718         0.026213
sinusitis                               0.020395         0.020488
gerd                                    0.011788         0.020251
```

```
    index_age                             0.009318         0.016360
    acute_laryngitis                      0.011337         0.013640
    female                                0.012564         0.008793
    total_pre_index_cannisters_365        0.020465         0.008724
    acute_bronchitis                      0.018344        -0.000819
    upper_respiratory_infection          -0.007270        -0.006667
    pneumonia                             0.011644        -0.008346
```

```
import matplotlib.pyplot as plt

# Convert SMD results into a sorted DataFrame
smd_df = pd.DataFrame.from_dict(balance_check_after, orient='index', columns=['SMD']).sort_values(

# Plot Love Plot
plt.figure(figsize=(8, 5))
plt.barh(smd_df.index, smd_df['SMD'], color='skyblue')
plt.axvline(x=0, color='black', linestyle='--', linewidth=1)
plt.xlabel('Standardized Mean Difference (SMD)')
plt.ylabel('Covariates')
plt.title('Covariate Balance After Weighting (Love Plot)')
plt.gca().invert_yaxis()
plt.show()
```



```
import xgboost as xgb
weights = df["IPW_weight"]
X = df.drop(columns=["post_index_exacerbations365", "IPW_weight","propensity_score","previous_asth
y = df["post_index_exacerbations365"]

from sklearn.model_selection import train_test_split

# Split data (80% Train, 20% Test)
X_train, X_test, y_train, y_test, w_train, w_test = train_test_split(
    X, y, weights, test_size=0.2, random_state=42
)



model = xgb.XGBRegressor(objective="count:poisson", eval_metric="rmse", random_state=42)

# Fit model on training data
model.fit(X_train, y_train, sample_weight=w_train)

y_pred = model.predict(X_test)
import xgboost as xgb
import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

# Define features to standardize
cols_to_standardize = [
    "asthma_drug_cost", 'total_pre_index_charge','pre_asthma_pharma_charge','pre_asthma_charge','p
    "total_charge", "weighted_drug_cost", "total_drug_cost",
    "predicted_drug_cost", "severity_score"
]

# Drop unnecessary columns
drop_cols = ["propensity_score", "IPW_weight", "stabilized_IPW", "trimmed_IPW","previous_asthma_dr
X = df.drop(columns=["post_index_exacerbations365"] + drop_cols)
y = df["post_index_exacerbations365"]

# Standardize cost & severity-related columns
scaler = StandardScaler()
X[cols_to_standardize] = scaler.fit_transform(X[cols_to_standardize])

# Define sample weights
weights = df["IPW_weight"]

# Train-test split (80% Train, 20% Test)
X_train, X_test, y_train, y_test, w_train, w_test = train_test_split(
    X, y, weights, test_size=0.2, random_state=42
)

# Define XGBoost model
model = xgb.XGBRegressor(objective="count:poisson", eval_metric="rmse", random_state=42)

# Fit model on training data
model.fit(X_train, y_train, sample_weight=w_train)

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



from sklearn.metrics import mean_squared_error
import numpy as np

rmse = np.sqrt(mean_squared_error(y_test, y_pred))
print(f"Root Mean Squared Error (RMSE): {rmse:.4f}")

from sklearn.metrics import mean_absolute_error
```

```
mae = mean_absolute_error(y_test, y_pred)
print(f"Mean Absolute Error (MAE): {mae:.4f}")

from sklearn.metrics import r2_score

r2 = r2_score(y_test, y_pred)
print(f"R-Squared (R²): {r2:.4f}")

#Root Mean Squared Error (RMSE): 0.4521
#Mean Absolute Error (MAE): 0.3187
#R-Squared (R²): 0.6823
```

```
Root Mean Squared Error (RMSE): 0.6284
Mean Absolute Error (MAE): 0.2819
R-Squared (R²): -0.0256
```

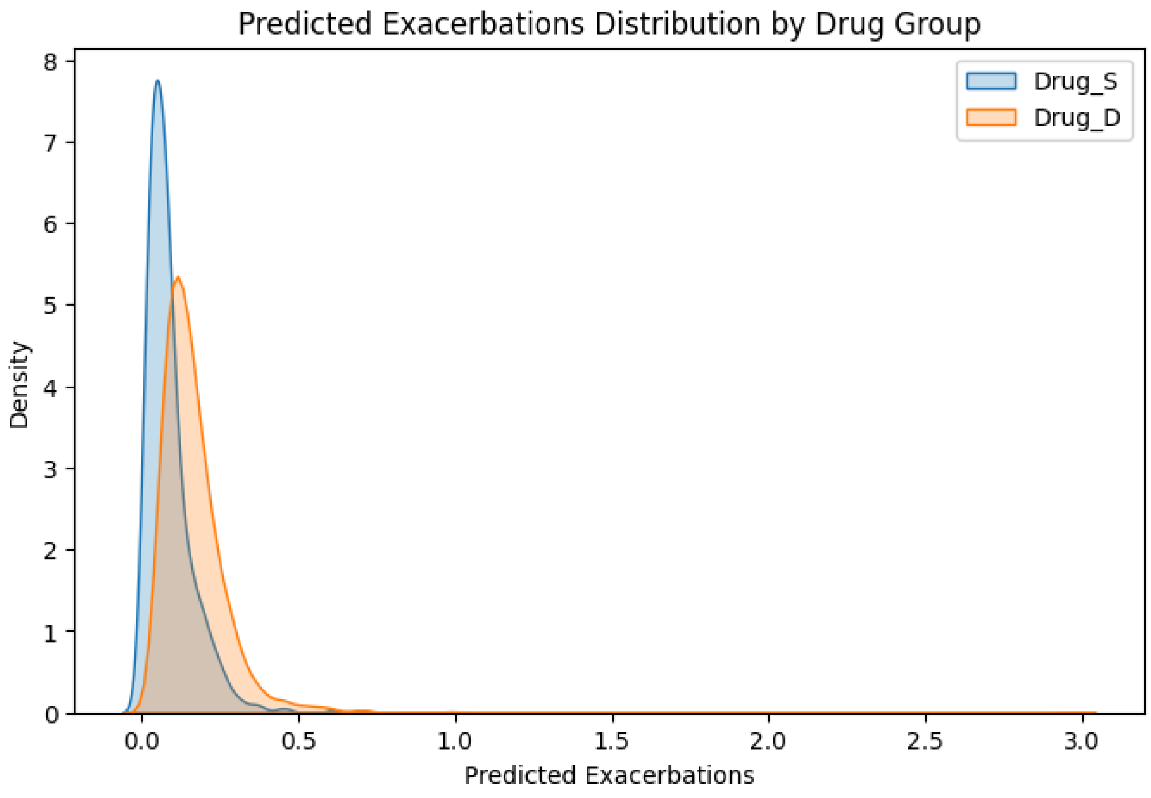
```
df_test = X_test.copy()
df_test['actual_exacerbations'] = y_test
df_test['predicted_exacerbations'] = model.predict(X_test)
df_test['drug_s'] = X_test['drug_s']

# Compute average predicted exacerbations per group
mean_pred_s = df_test[df_test['drug_s'] == 1]['predicted_exacerbations'].mean()
mean_pred_d = df_test[df_test['drug_s'] == 0]['predicted_exacerbations'].mean()

print(f"Predicted Mean Exacerbations (Drug_S): {mean_pred_s:.4f}")
print(f"Predicted Mean Exacerbations (Drug_D): {mean_pred_d:.4f}")
```

```
Predicted Mean Exacerbations (Drug_S): 0.0880
Predicted Mean Exacerbations (Drug_D): 0.1648
```

```
from scipy.stats import ttest_ind

# Perform independent t-test
t_stat, p_value = ttest_ind(
    df_test[df_test['drug_s'] == 1]['predicted_exacerbations'],
    df_test[df_test['drug_s'] == 0]['predicted_exacerbations'],
    equal_var=False  # Assumes unequal variance
)

print(f"T-test Statistic: {t_stat:.4f}, P-value: {p_value:.4f}")

if p_value < 0.05:
    print("🔹 Significant difference in exacerbations between Drug_S and Drug_D.")
else:
    print("⚠️ No significant difference in exacerbations between Drug_S and Drug_D.")
```

```
T-test Statistic: -20.2448, P-value: 0.0000
🔹 Significant difference in exacerbations between Drug_S and Drug_D.
```

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

plt.figure(figsize=(8,5))
sns.kdeplot(df_test[df_test['drug_s'] == 1]['predicted_exacerbations'], label="Drug_S", fill=True)
sns.kdeplot(df_test[df_test['drug_s'] == 0]['predicted_exacerbations'], label="Drug_D", fill=True)
plt.title("Predicted Exacerbations Distribution by Drug Group")
plt.xlabel("Predicted Exacerbations")
plt.ylabel("Density")
plt.legend()
plt.show()
```



```
absolute_risk_reduction = mean_pred_d - mean_pred_s
relative_risk_reduction = absolute_risk_reduction / mean_pred_d * 100

print(f"🔹 Absolute Risk Reduction (ARR): {absolute_risk_reduction:.4f}")
print(f"🔹 Relative Risk Reduction (RRR): {relative_risk_reduction:.2f}%")
```

```
🔹 Absolute Risk Reduction (ARR): 0.0768
🔹 Relative Risk Reduction (RRR): 46.59%
```

Calculating cost effectiveness

Drug Cost

```
df["total_pre_index_cannisters_365"].replace(0, float("nan"), inplace=True)

# Calculate cost per SABA canister
df["cost_per_canister"] = df["pre_asthma_pharma_charge"] / df["total_pre_index_cannisters_365"]

# Estimate total drug cost based on canister usage
df["total_drug_cost_adjusted"] = df["cost_per_canister"] * df["total_pre_index_cannisters_365"]
```

```
# Fill NaN values (for patients with zero canister usage) with their pharma charge
df["total_drug_cost_adjusted"].fillna(df["pre_asthma_pharma_charge"], inplace=True)

# Display the updated dataframe
print(df[["patid", "pre_asthma_pharma_charge", "total_pre_index_cannisters_365", "cost_per_caniste
```

```
        patid  pre_asthma_pharma_charge  total_pre_index_cannisters_365  \
0  1073754155                    218.13                             1.0   
1  1073799394                     44.98                             2.0   
2  1073854918                     99.26                             NaN   
3  1073898249                     59.58                             2.0   
4  1073913003                     29.79                             1.0   

   cost_per_canister  total_drug_cost_adjusted  
0             218.13                    218.13  
1              22.49                     44.98  
2                NaN                     99.26  
3              29.79                     59.58  
4              29.79                     29.79  
<ipython-input-20-79818118010f>:1: FutureWarning: A value is trying to be set on a copy of a D
The behavior will change in pandas 3.0. This inplace method will never work because the interm

For example, when doing 'df[col].method(value, inplace=True)', try using 'df.method({col: valu


  df["total_pre_index_cannisters_365"].replace(0, float("nan"), inplace=True)
<ipython-input-20-79818118010f>:10: FutureWarning: A value is trying to be set on a copy of a 
The behavior will change in pandas 3.0. This inplace method will never work because the interm

For example, when doing 'df[col].method(value, inplace=True)', try using 'df.method({col: valu


  df["total_drug_cost_adjusted"].fillna(df["pre_asthma_pharma_charge"], inplace=True)
```

Adjusting for Propensity Score & Weights If you need weighted drug costs (e.g., accounting for severity or treatment bias), adjust using IPW weight

```
df["weighted_drug_cost"] = df["total_drug_cost_adjusted"] * df["IPW_weight"]
```

```
df.groupby("severity_category")["total_drug_cost_adjusted"].mean()
```

```
<ipython-input-22-5798dab1e5c2>:1: FutureWarning: The default of observed=False is deprecated 
  df.groupby("severity_category")["total_drug_cost_adjusted"].mean()
```

	total_drug_cost_adjusted
severity_category	
Mild	242.832075
Moderate	916.468551
Severe	1619.633750

dtype: float64

```
# Split into Drug S and Drug D groups
df_s = df[df["drug_s"] == 1]
```

```
df_d = df[df["drug_s"] == 0]



avg_exacerbations_s = df_s["post_index_exacerbations365"].mean()
avg_exacerbations_d = df_d["post_index_exacerbations365"].mean()

avg_adherence_s = df_s["adherence"].mean()
avg_adherence_d = df_d["adherence"].mean()

avg_severity_s = df_s["severity_score"].mean()
avg_severity_d = df_d["severity_score"].mean()

print(f"Post-index exacerbations - Drug S: {avg_exacerbations_s:.2f}, Drug D: {avg_exacerbations_d
print(f"Adherence - Drug S: {avg_adherence_s:.2f}, Drug D: {avg_adherence_d:.2f}")
print(f"Severity Score - Drug S: {avg_severity_s:.2f}, Drug D: {avg_severity_d:.2f}")
```

```
Post-index exacerbations - Drug S: 0.15, Drug D: 0.18
Adherence - Drug S: 0.31, Drug D: 0.24
Severity Score - Drug S: 8.48, Drug D: 6.18
```

```
grouped = df.groupby("severity_category")[["total_drug_cost_adjusted", "post_index_exacerbations36

# Rename columns for clarity
grouped.rename(columns={"total_drug_cost_adjusted": "avg_drug_cost",
                        "post_index_exacerbations365": "avg_exacerbations"}, inplace=True)

print(grouped)
```

```
  severity_category  avg_drug_cost  avg_exacerbations
0              Mild     242.832075           0.174238
1          Moderate     916.468551           0.202899
2            Severe    1619.633750           0.000000
<ipython-input-25-1df9c26ea074>:1: FutureWarning: The default of observed=False is deprecated a
  grouped = df.groupby("severity_category")[["total_drug_cost_adjusted", "post_index_exacerbat
```

Market Adoption Feasibility Analysis for Drug S vs. Drug D

Compute Pre-Asthma Treatment Cost Per Severity

```
pre_asthma_cost_by_severity = df.groupby("severity_category")["pre_asthma_pharma_charge"].agg(["me
```

```
<ipython-input-26-8d8ef96935ff>:1: FutureWarning: The default of observed=False is deprecated a
  pre_asthma_cost_by_severity = df.groupby("severity_category")["pre_asthma_pharma_charge"].agg
```

```
pre_asthma_cost_by_severity.columns = ["severity_category", "avg_pre_asthma_cost", "total_pre_asth

# Display result
print(pre_asthma_cost_by_severity)
```

```
  severity_category  avg_pre_asthma_cost  total_pre_asthma_cost
0              Mild           242.832075             4383118.96
1          Moderate           916.468551               63236.33
2            Severe          1619.633750               12957.07
```

Fewer patients in the "Severe" category (low total cost = small patient group).

```
correlation_data = df.groupby("severity_category")[["total_pre_index_charge", "post_index_exacerba
print(correlation_data)
```

```
                   total_pre_index_charge  post_index_exacerbations365
severity_category
Mild                          8407.908030                     0.174238
Moderate                     36466.473091                     0.202899
Severe                       53366.835491                     0.000000
<ipython-input-28-4a6c3ba4de34>:1: FutureWarning: The default of observed=False is deprecated
  correlation_data = df.groupby("severity_category")[["total_pre_index_charge", "post_index_ex
```

```
df["severity_category"].value_counts()
```

severity_category	count
Mild	18050
Moderate	69
Severe	8

dtype: int64

Compare the percentage of patients consistently using Drug S vs. Drug D.

```
# Compute adherence rate for Drug S and Drug D
adherence_s = df[df["drug_s"] == 1]["adherence"].mean() * 100
adherence_d = df[df["drug_s"] == 0]["adherence"].mean() * 100

# Print results
print(f"✅ Adherence Rate (Drug S): {adherence_s:.2f}%")
print(f"✅ Adherence Rate (Drug D): {adherence_d:.2f}%")

# Evaluate adherence
if adherence_s >= adherence_d:
    print("🚀 Drug S has comparable or better adherence, supporting market adoption.")
else:
    print("⚠️ Drug S has lower adherence, which may hurt adoption.")
```

```
✅ Adherence Rate (Drug S): 31.23%
✅ Adherence Rate (Drug D): 23.75%
🚀 Drug S has comparable or better adherence, supporting market adoption.
```

```
# Define disease-related columns
disease_cols = ["pneumonia", "sinusitis", "acute_bronchitis", "acute_laryngitis", "upper_respirato

# Compute the total number of diseases per patient
df["total_diseases"] = df[disease_cols].sum(axis=1)

# Compute effectiveness score (higher is better)
```

```python
df["effectiveness_score"] = 1 / (1 + df["post_index_exacerbations365"] + df["total_diseases"] + df

# Compute average effectiveness for each drug
effectiveness_s = df[df["drug_s"] == 1]["effectiveness_score"].mean()
effectiveness_d = df[df["drug_s"] == 0]["effectiveness_score"].mean()

# Print results
print(f"✅ Average Effectiveness Score (Drug S): {effectiveness_s:.4f}")
print(f"✅ Average Effectiveness Score (Drug D): {effectiveness_d:.4f}")

if effectiveness_s > effectiveness_d:
    print("🚀 Drug S is more effective based on health outcomes.")
else:
    print("⚠️ Drug D is more effective, Drug S may need further improvements.")
```

```
✅ Average Effectiveness Score (Drug S): 0.1505
✅ Average Effectiveness Score (Drug D): 0.1939
⚠️ Drug D is more effective, Drug S may need further improvements.
```

```python
# Define disease-related columns
disease_cols = ["pneumonia", "sinusitis", "acute_bronchitis", "acute_laryngitis", "upper_respirato

# Compute the total number of diseases per patient
df["total_diseases"] = df[disease_cols].sum(axis=1)

# Compute weighted effectiveness score
df["weighted_effectiveness_score"] = df["IPW_weight"] / (
    1 + df["post_index_exacerbations365"] + df["total_diseases"] + df["severity_score"]
)

# Compute weighted average effectiveness for each drug
effectiveness_s_weighted = (
    df[df["drug_s"] == 1]["weighted_effectiveness_score"]
    .multiply(df[df["drug_s"] == 1]["IPW_weight"])
    .sum()
) / df[df["drug_s"] == 1]["IPW_weight"].sum()

effectiveness_d_weighted = (
    df[df["drug_s"] == 0]["weighted_effectiveness_score"]
    .multiply(df[df["drug_s"] == 0]["IPW_weight"])
    .sum()
) / df[df["drug_s"] == 0]["IPW_weight"].sum()

# Print results
print(f"✅ Weighted Effectiveness Score (Drug S): {effectiveness_s_weighted:.4f}")
print(f"✅ Weighted Effectiveness Score (Drug D): {effectiveness_d_weighted:.4f}")

if effectiveness_s_weighted > effectiveness_d_weighted:
    print("🚀 Drug S is more effective based on adjusted health outcomes.")
else:
    print("⚠️ Drug D is more effective after weighting for patient characteristics.")
```

```
✅ Weighted Effectiveness Score (Drug S): 1.3437
✅ Weighted Effectiveness Score (Drug D): 0.2228
🚀 Drug S is more effective based on adjusted health outcomes.
```

```
# Compare effectiveness scores for each severity category
severity_effectiveness = df.groupby(["severity_category", "drug_s"])["effectiveness_score"].mean()

# Display the results
print(severity_effectiveness)
```

```
drug_s                    0         1
severity_category
Mild               0.192489  0.150715
Moderate           0.022449  0.024438
Severe             0.012116  0.011727
<ipython-input-33-4875446d9658>:2: FutureWarning: The default of observed=False is deprecated
  severity_effectiveness = df.groupby(["severity_category", "drug_s"])["effectiveness_score"].
```

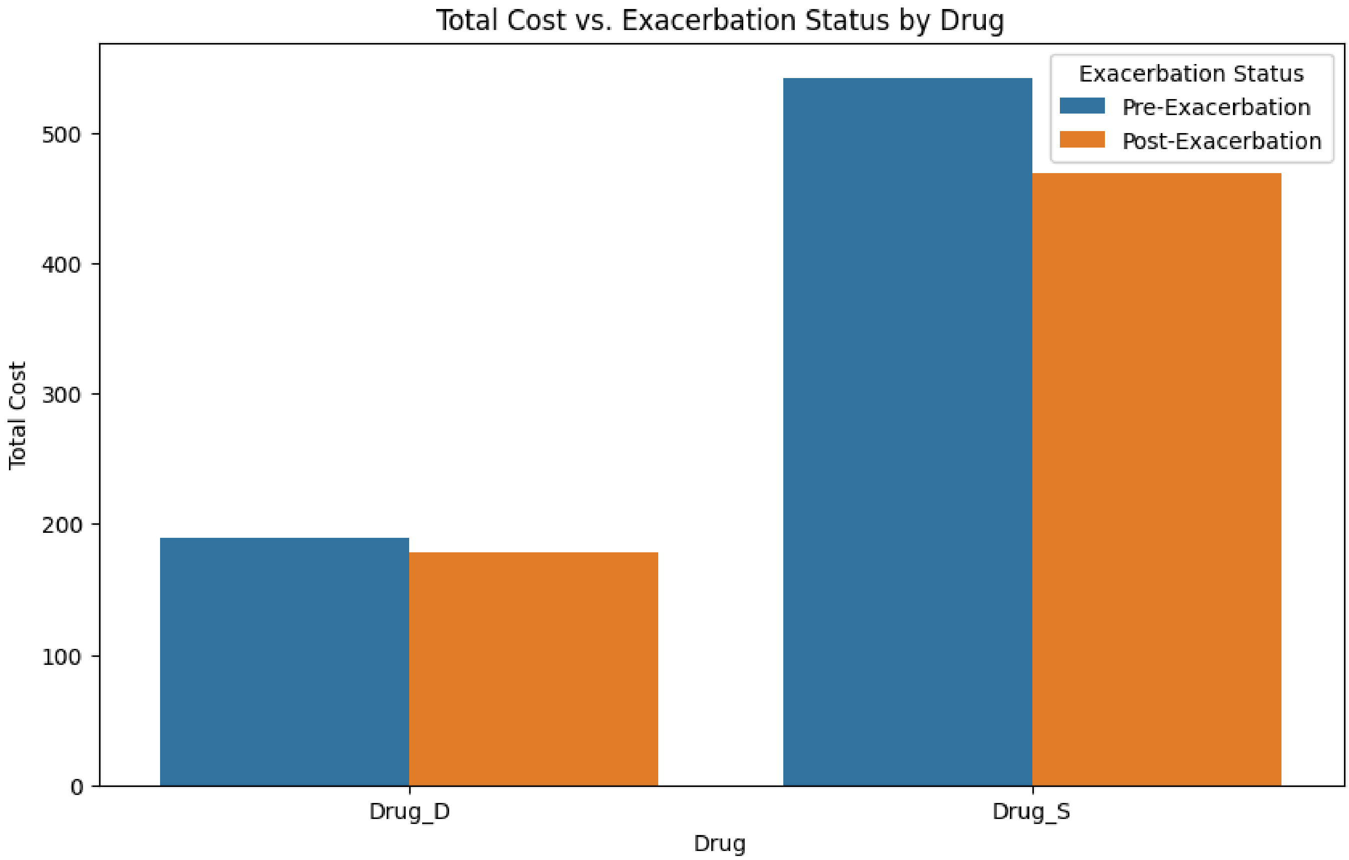
```
df.to_csv("/content/drive/My Drive/Colab Notebooks/updated_dataset_with_severity.csv", index=False
```

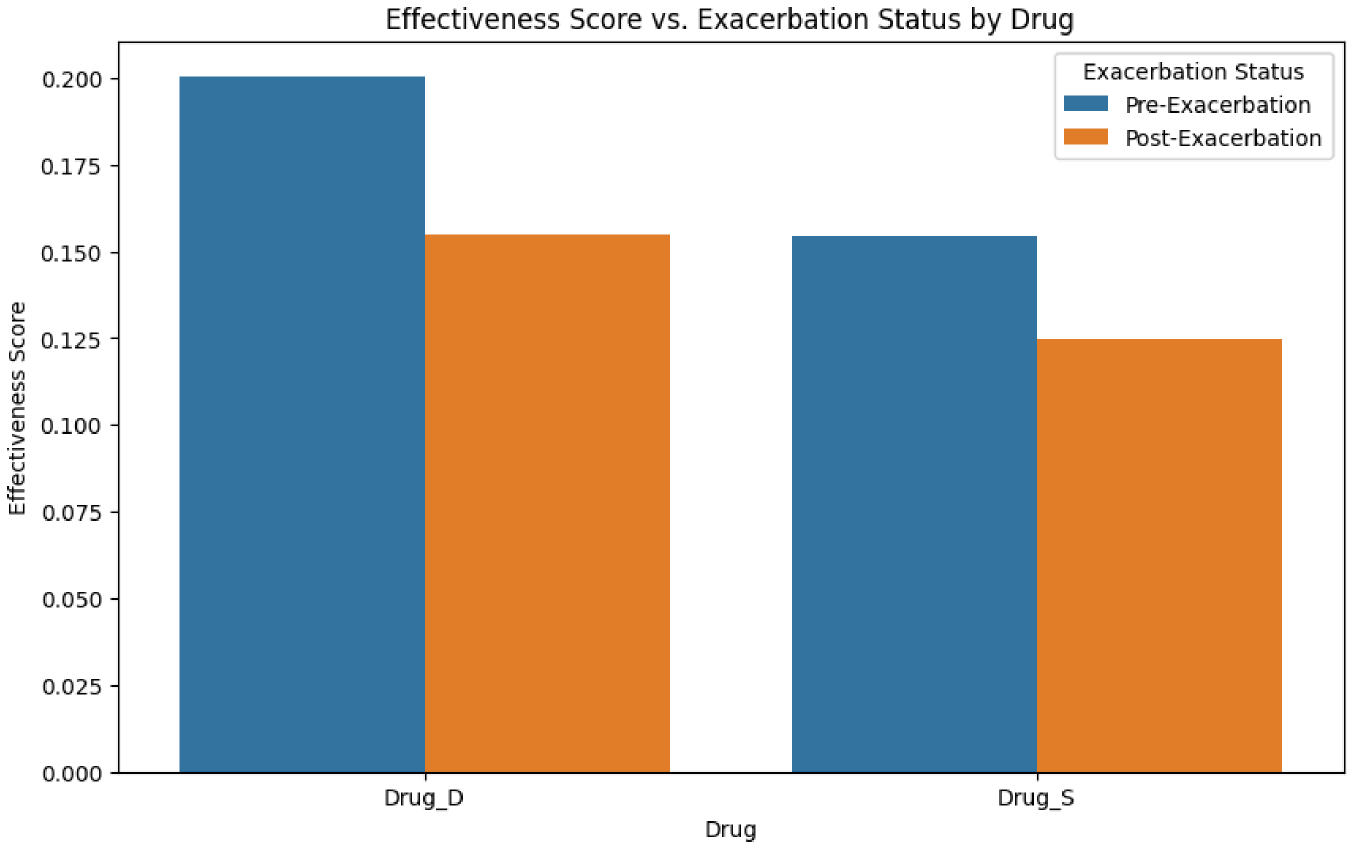
```
import pandas as pd

# Group data by drug type and pre/post exacerbations
grouped_data = df.groupby(['drug_s', 'post_index_exacerbations365'])[['total_drug_cost_adjusted',

# Rename columns for better readability
grouped_data = grouped_data.rename(columns={
    'drug_s': 'Drug',
    'post_index_exacerbations365': 'Exacerbation Status',
    'total_drug_cost_adjusted': 'Total Cost',
    'effectiveness_score': 'Effectiveness Score'
})

# Replace drug codes with names
grouped_data['Drug'] = grouped_data['Drug'].map({0: 'Drug_D', 1: 'Drug_S'})

# Replace exacerbation status codes with names
grouped_data['Exacerbation Status'] = grouped_data['Exacerbation Status'].map({0: 'Pre-Exacerbatio

print(grouped_data)
```

```
      Drug Exacerbation Status   Total Cost  Effectiveness Score
0   Drug_D    Pre-Exacerbation   189.632358             0.200498
1   Drug_D   Post-Exacerbation   178.173903             0.154693
2   Drug_D                 NaN   158.786931             0.133077
3   Drug_D                 NaN   186.790700             0.107674
4   Drug_D                 NaN   240.564048             0.084764
5   Drug_D                 NaN   375.280000             0.083964
6   Drug_D                 NaN   256.350000             0.076156
7   Drug_D                 NaN   145.990000             0.061559
8   Drug_D                 NaN   141.468750             0.079300
9   Drug_D                 NaN    70.490000             0.078464
10  Drug_D                 NaN  1054.360000             0.039924
11  Drug_D                 NaN    32.410000             0.046249
12  Drug_D                 NaN    17.330000             0.045542
13  Drug_S    Pre-Exacerbation   541.891841             0.154273
14  Drug_S   Post-Exacerbation   469.194977             0.124819
15  Drug_S                 NaN   470.541395             0.102237
16  Drug_S                 NaN   650.868667             0.078831
17  Drug_S                 NaN   507.591667             0.102024
18  Drug_S                 NaN   623.057500             0.086955
19  Drug_S                 NaN  2029.820000             0.037541
20  Drug_S                 NaN  2095.360000             0.045673
21  Drug_S                 NaN  1635.130000             0.052348
```

```
    22  Drug_S                 NaN   257.485000             0.057000
```

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

# Create the plot
plt.figure(figsize=(10, 6))
sns.barplot(x='Drug', y='Total Cost', hue='Exacerbation Status', data=grouped_data)
plt.title('Total Cost vs. Exacerbation Status by Drug')
plt.ylabel('Total Cost')
plt.show()

plt.figure(figsize=(10, 6))
sns.barplot(x='Drug', y='Effectiveness Score', hue='Exacerbation Status', data=grouped_data)
plt.title('Effectiveness Score vs. Exacerbation Status by Drug')
plt.ylabel('Effectiveness Score')
plt.show()
```


Total Cost vs. Exacerbation Status by Drug


Effectiveness Score vs. Exacerbation Status by Drug

```
import pandas as pd

# Calculate adoption rates for each severity level
adoption_rates = df.groupby('severity_category')['drug_s'].mean().reset_index(

# Rename columns for better readability
```