CLASSIFICATION OF PERSISTENCY AND NON-PERSISTENCY OF DRUGS

Problem Statement

- One of the challenge for all Pharmaceutical companies is to understand the persistency of drug as per the physician prescription.
- With an objective to gather insights on the factors that are impacting the persistency, build a classification for the given dataset.

Dataset Description

- The dataset folder contains the following files:
  Case Study Data scientist Challenge_dataset_Persistent_Non_Persistent (1).csv : (3425, 69)

Columns Provided in the Dataset

Group	Variable	Variable Description
Unique Row Id	Patient ID	Unique ID of each patient
Target Variable	Persistency_Flag	Flag indicating if a patient was persistent or not
Demographics	Age	Age of the patient during their therapy
Demographics	Race	Race of the patient from the patient table
Demographics	Region	Region of the patient from the patient table
Demographics	Ethnicity	Ethnicity of the patient from the patient table
Demographics	Gender	Gender of the patient from the patient table
Demographics	IDN Indicator	Flag indicating patients mapped to IDN
Provider Attributes	NTM - Physician Specialty	Specialty of the HCP that prescribed the NTM Rx
Clinical Factors	NTM - T-Score	T Score of the patient at the time of the NTM Rx (within 2 years prior from rxdate)
Clinical Factors	Change in T Score	Change in Tscore before starting with any therapy and after receiving therapy (Worsened, Remained Same, Improved, Unknown)
Clinical Factors	NTM - Risk Segment	Risk Segment of the patient at the time of the NTM Rx (within 2 years days prior from rxdate)
Clinical Factors	Change in Risk Segment	Change in Risk Segment before starting with any therapy and after receiving therapy (Worsened, Remained Same, Improved, Unknown)
Clinical Factors	NTM - Multiple Risk	Factors Flag indicating if patient falls under multiple risk category (having more than 1 risk) at the time of the NTM Rx (within 365 days prior from rxdate)
Clinical Factors	NTM - Dexa Scan Frequency	Number of DEXA scans taken prior to the first NTM Rx date (within 365 days prior from rxdate)
Clinical Factors	NTM - Dexa Scan Recency	Flag indicating the presence of Dexa Scan before the NTM Rx (within 2 years prior from rxdate or between their first Rx and Switched Rx; whichever is smaller and applicable)
Clinical Factors	Dexa During Therapy	Flag indicating if the patient had a Dexa Scan during their first continuous therapy
Clinical Factors	NTM - Fragility Fracture Recency	Flag indicating if the patient had a recent fragility fracture (within 365 days prior from rxdate)
Clinical Factors	Fragility Fracture During Therapy	Flag indicating if the patient had fragility fracture during their first continuous therapy
Clinical Factors	NTM - Glucocorticoid Recency	Flag indicating usage of Glucocorticoids (>=7.5mg strength) in the one year look-back from the first NTM Rx
Clinical Factors	Glucocorticoid Usage During Therapy	Flag indicating if the patient had a Glucocorticoid usage during the first continuous therapy
Disease/Treatment Factor	NTM - Injectable Experience	Flag indicating any injectable drug usage in the recent 12 months before the NTM OP Rx
Disease/Treatment Factor	NTM - Risk Factors	Risk Factors that the patient is falling into. For chronic Risk Factors complete lookback to be applied and for non-chronic Risk Factors, one year lookback from the date of first OP Rx
Disease/Treatment Factor	NTM - Comorbidity	Comorbidities are divided into two main categories - Acute and chronic, based on the ICD codes. For chronic disease we are taking complete look back from the first Rx date of NTM therapy and for acute diseases, time period before the NTM OP Rx with one year lookback has been applied
Disease/Treatment Factor	NTM - Concomitancy	Concomitant drugs recorded prior to starting with a therapy(within 365 days prior from first rxdate)
Disease/Treatment Factor	Adherence	Adherence for the therapies

In [1]:
```
from google.colab import drive
drive.mount('/content/drive')

import os

# Change the current directory to your desired directory path
required_directory = '/content/drive/MyDrive/Interview Related Documents/Trinity Life Science Assignment'
os.chdir(required_directory)
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).
```

In [2]:
```
# Importing Necessary Libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
pd.set_option('display.max_columns', None)
```

1. DATA INGESTION

- Collect data from various sources and prepare it for analysis. This step involves cleaning, organizing, and loading the data into a suitable format, like a DataFrame, to make it ready for exploration.
- Since, our data data is clean we don't need to perform cleaning

In [3]:
```
# Read csv file using pandas
file_name = 'Case Study Data scientist Challenge_dataset_Persistent_Non_Persistent (1).xlsx'
df = pd.read_excel(file_name, sheet_name = 'Dataset')
```

2. Exploratory Data Analysis (EDA)

- Explore the data visually and statistically to understand its patterns, distributions, and potential outliers. EDA helps in gaining initial insights into the dataset, which informs subsequent steps.

In [4]:
```
# Check for missing values in all the columnns of the dataset
df.isnull().sum().sum()
```

Out[4]:
```
0
```

In [5]:
```
#check shape of the dataset
df.shape
```

Out[5]: (3424, 69)

In [6]:
```
# check columns of dataset
df.columns
```

Out[6]:
```
Index(['Ptid', 'Persistency_Flag', 'Gender', 'Race', 'Ethnicity', 'Region',
       'Age_Bucket', 'Ntm_Speciality', 'Ntm_Specialist_Flag',
       'Ntm_Speciality_Bucket', 'Gluco_Record_Prior_Ntm',
       'Gluco_Record_During_Rx', 'Dexa_Freq_During_Rx', 'Dexa_During_Rx',
       'Frag_Frac_Prior_Ntm', 'Frag_Frac_During_Rx', 'Risk_Segment_Prior_Ntm',
       'Tscore_Bucket_Prior_Ntm', 'Risk_Segment_During_Rx',
       'Tscore_Bucket_During_Rx', 'Change_T_Score', 'Change_Risk_Segment',
       'Adherent_Flag', 'Idn_Indicator', 'Injectable_Experience_During_Rx',
       'Comorb_Encounter_For_Screening_For_Malignant_Neoplasms',
       'Comorb_Encounter_For_Immunization',
       'Comorb_Encntr_For_General_Exam_W_O_Complaint,_Susp_Or_Reprtd_Dx',
       'Comorb_Vitamin_D_Deficiency',
       'Comorb_Other_Joint_Disorder_Not_Elsewhere_Classified',
       'Comorb_Encntr_For_Oth_Sp_Exam_W_O_Complaint_Suspected_Or_Reprtd_Dx',
       'Comorb_Long_Term_Current_Drug_Therapy', 'Comorb_Dorsalgia',
       'Comorb_Personal_History_Of_Other_Diseases_And_Conditions',
       'Comorb_Other_Disorders_Of_Bone_Density_And_Structure',
       'Comorb_Disorders_of_lipoprotein_metabolism_and_other_lipidemias',
       'Comorb_Osteoporosis_without_current_pathological_fracture',
       'Comorb_Personal_history_of_malignant_neoplasm',
       'Comorb_Gastro_esophageal_reflux_disease',
       'Concom_Cholesterol_And_Triglyceride_Regulating_Preparations',
       'Concom_Narcotics', 'Concom_Systemic_Corticosteroids_Plain',
       'Concom_Anti_Depressants_And_Mood_Stabilisers',
       'Concom_Fluoroquinolones', 'Concom_Cephalosporins',
       'Concom_Macrolides_And_Similar_Types',
       'Concom_Broad_Spectrum_Penicillins', 'Concom_Anaesthetics_General',
       'Concom_Viral_Vaccines', 'Risk_Type_1_Insulin_Dependent_Diabetes',
       'Risk_Osteogenesis_Imperfecta', 'Risk_Rheumatoid_Arthritis',
       'Risk_Untreated_Chronic_Hyperthyroidism',
       'Risk_Untreated_Chronic_Hypogonadism', 'Risk_Untreated_Early_Menopause',
       'Risk_Patient_Parent_Fractured_Their_Hip', 'Risk_Smoking_Tobacco',
       'Risk_Chronic_Malnutrition_Or_Malabsorption',
       'Risk_Chronic_Liver_Disease', 'Risk_Family_History_Of_Osteoporosis',
       'Risk_Low_Calcium_Intake', 'Risk_Vitamin_D_Insufficiency',
       'Risk_Poor_Health_Frailty', 'Risk_Excessive_Thinness',
       'Risk_Hysterectomy_Oophorectomy', 'Risk_Estrogen_Deficiency',
       'Risk_Immobilization', 'Risk_Recurring_Falls', 'Count_Of_Risks'],
      dtype='object')
```

In [7]:
```
# Checking duplicates
df.duplicated().sum()
# drop Unnamed: 0, Address, Index from dataset
# df.drop(columns = ['Unnamed: 0', 'Address', 'Index'], inplace = True)
```

Out[7]: 0

In [8]:
```
# Check which columns are having categorical, numerical or boolean values
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3424 entries, 0 to 3423
Data columns (total 69 columns):
 #   Column                                                              Non-Null Count  Dtype 
---  ------                                                              --------------  ----- 
 0   Ptid                                                                3424 non-null   object
 1   Persistency_Flag                                                    3424 non-null   object
 2   Gender                                                              3424 non-null   object
 3   Race                                                                3424 non-null   object
 4   Ethnicity                                                           3424 non-null   object
 5   Region                                                              3424 non-null   object
 6   Age_Bucket                                                          3424 non-null   object
 7   Ntm_Speciality                                                      3424 non-null   object
 8   Ntm_Specialist_Flag                                                 3424 non-null   object
 9   Ntm_Speciality_Bucket                                               3424 non-null   object
 10  Gluco_Record_Prior_Ntm                                              3424 non-null   object
 11  Gluco_Record_During_Rx                                              3424 non-null   object
 12  Dexa_Freq_During_Rx                                                 3424 non-null   int64 
 13  Dexa_During_Rx                                                      3424 non-null   object
 14  Frag_Frac_Prior_Ntm                                                 3424 non-null   object
 15  Frag_Frac_During_Rx                                                 3424 non-null   object
 16  Risk_Segment_Prior_Ntm                                              3424 non-null   object
 17  Tscore_Bucket_Prior_Ntm                                             3424 non-null   object
 18  Risk_Segment_During_Rx                                              3424 non-null   object
 19  Tscore_Bucket_During_Rx                                             3424 non-null   object
 20  Change_T_Score                                                      3424 non-null   object
 21  Change_Risk_Segment                                                 3424 non-null   object
 22  Adherent_Flag                                                       3424 non-null   object
 23  Idn_Indicator                                                       3424 non-null   object
 24  Injectable_Experience_During_Rx                                     3424 non-null   object
 25  Comorb_Encounter_For_Screening_For_Malignant_Neoplasms              3424 non-null   object
 26  Comorb_Encounter_For_Immunization                                   3424 non-null   object
 27  Comorb_Encntr_For_General_Exam_W_O_Complaint,_Susp_Or_Reprtd_Dx     3424 non-null   object
 28  Comorb_Vitamin_D_Deficiency                                         3424 non-null   object
 29  Comorb_Other_Joint_Disorder_Not_Elsewhere_Classified                3424 non-null   object
 30  Comorb_Encntr_For_Oth_Sp_Exam_W_O_Complaint_Suspected_Or_Reprtd_Dx  3424 non-null   object
 31  Comorb_Long_Term_Current_Drug_Therapy                               3424 non-null   object
 32  Comorb_Dorsalgia                                                    3424 non-null   object
 33  Comorb_Personal_History_Of_Other_Diseases_And_Conditions            3424 non-null   object
 34  Comorb_Other_Disorders_Of_Bone_Density_And_Structure                3424 non-null   object
 35  Comorb_Disorders_of_lipoprotein_metabolism_and_other_lipidemias     3424 non-null   object
 36  Comorb_Osteoporosis_without_current_pathological_fracture           3424 non-null   object
 37  Comorb_Personal_history_of_malignant_neoplasm                       3424 non-null   object
 38  Comorb_Gastro_esophageal_reflux_disease                             3424 non-null   object
 39  Concom_Cholesterol_And_Triglyceride_Regulating_Preparations         3424 non-null   object
 40  Concom_Narcotics                                                    3424 non-null   object
 41  Concom_Systemic_Corticosteroids_Plain                               3424 non-null   object
 42  Concom_Anti_Depressants_And_Mood_Stabilisers                        3424 non-null   object
 43  Concom_Fluoroquinolones                                             3424 non-null   object
 44  Concom_Cephalosporins                                               3424 non-null   object
 45  Concom_Macrolides_And_Similar_Types                                 3424 non-null   object
 46  Concom_Broad_Spectrum_Penicillins                                   3424 non-null   object
 47  Concom_Anaesthetics_General                                         3424 non-null   object
 48  Concom_Viral_Vaccines                                               3424 non-null   object
 49  Risk_Type_1_Insulin_Dependent_Diabetes                              3424 non-null   object
 50  Risk_Osteogenesis_Imperfecta                                        3424 non-null   object
 51  Risk_Rheumatoid_Arthritis                                           3424 non-null   object
 52  Risk_Untreated_Chronic_Hyperthyroidism                              3424 non-null   object
 53  Risk_Untreated_Chronic_Hypogonadism                                 3424 non-null   object
 54  Risk_Untreated_Early_Menopause                                      3424 non-null   object
 55  Risk_Patient_Parent_Fractured_Their_Hip                             3424 non-null   object
 56  Risk_Smoking_Tobacco                                                3424 non-null   object
 57  Risk_Chronic_Malnutrition_Or_Malabsorption                          3424 non-null   object
 58  Risk_Chronic_Liver_Disease                                          3424 non-null   object
 59  Risk_Family_History_Of_Osteoporosis                                 3424 non-null   object
 60  Risk_Low_Calcium_Intake                                             3424 non-null   object
 61  Risk_Vitamin_D_Insufficiency                                        3424 non-null   object
 62  Risk_Poor_Health_Frailty                                            3424 non-null   object
 63  Risk_Excessive_Thinness                                             3424 non-null   object
 64  Risk_Hysterectomy_Oophorectomy                                      3424 non-null   object
 65  Risk_Estrogen_Deficiency                                            3424 non-null   object
 66  Risk_Immobilization                                                 3424 non-null   object
 67  Risk_Recurring_Falls                                                3424 non-null   object
 68  Count_Of_Risks                                                      3424 non-null   int64 
dtypes: int64(2), object(67)
memory usage: 1.8+ MB
```

In [9]:
```python
# For more information on the dataset like the total count in all the columns of the data
# min, max values and more information of the respective columns
#  This will only show the numeric values distribution
df.describe().T
```

Out[9]:

	count	mean	std	min	25%	50%	75%	max
Dexa_Freq_During_Rx	3424.0	3.016063	8.136545	0.0	0.0	0.0	3.0	146.0
Count_Of_Risks	3424.0	1.239486	1.094914	0.0	0.0	1.0	2.0	7.0

In [10]:
```python
# check length of dataset
print(f" dataset length : {len(df)}")
```

```
 dataset length : 3424
```

In [11]:
```python
# Loop through datatset to find count of unique values of each column
for col in df.columns:
  print(f" {col} : {len(df[col].value_counts())}")
```

```
Ptid : 3424
Persistency_Flag : 2
Gender : 2
Race : 4
Ethnicity : 3
Region : 5
Age_Bucket : 4
Ntm_Speciality : 36
Ntm_Specialist_Flag : 2
Ntm_Speciality_Bucket : 3
Gluco_Record_Prior_Ntm : 2
Gluco_Record_During_Rx : 2
Dexa_Freq_During_Rx : 58
Dexa_During_Rx : 2
Frag_Frac_Prior_Ntm : 2
Frag_Frac_During_Rx : 2
Risk_Segment_Prior_Ntm : 2
Tscore_Bucket_Prior_Ntm : 2
Risk_Segment_During_Rx : 3
Tscore_Bucket_During_Rx : 3
Change_T_Score : 4
Change_Risk_Segment : 4
Adherent_Flag : 2
Idn_Indicator : 2
Injectable_Experience_During_Rx : 2
Comorb_Encounter_For_Screening_For_Malignant_Neoplasms : 2
Comorb_Encounter_For_Immunization : 2
Comorb_Encntr_For_General_Exam_W_O_Complaint,_Susp_Or_Reprtd_Dx : 2
Comorb_Vitamin_D_Deficiency : 2
Comorb_Other_Joint_Disorder_Not_Elsewhere_Classified : 2
Comorb_Encntr_For_Oth_Sp_Exam_W_O_Complaint_Suspected_Or_Reprtd_Dx : 2
Comorb_Long_Term_Current_Drug_Therapy : 2
Comorb_Dorsalgia : 2
Comorb_Personal_History_Of_Other_Diseases_And_Conditions : 2
Comorb_Other_Disorders_Of_Bone_Density_And_Structure : 2
Comorb_Disorders_of_lipoprotein_metabolism_and_other_lipidemias : 2
Comorb_Osteoporosis_without_current_pathological_fracture : 2
Comorb_Personal_history_of_malignant_neoplasm : 2
Comorb_Gastro_esophageal_reflux_disease : 2
Concom_Cholesterol_And_Triglyceride_Regulating_Preparations : 2
Concom_Narcotics : 2
Concom_Systemic_Corticosteroids_Plain : 2
Concom_Anti_Depressants_And_Mood_Stabilisers : 2
Concom_Fluoroquinolones : 2
Concom_Cephalosporins : 2
Concom_Macrolides_And_Similar_Types : 2
Concom_Broad_Spectrum_Penicillins : 2
Concom_Anaesthetics_General : 2
Concom_Viral_Vaccines : 2
Risk_Type_1_Insulin_Dependent_Diabetes : 2
Risk_Osteogenesis_Imperfecta : 2
Risk_Rheumatoid_Arthritis : 2
Risk_Untreated_Chronic_Hyperthyroidism : 2
Risk_Untreated_Chronic_Hypogonadism : 2
Risk_Untreated_Early_Menopause : 2
Risk_Patient_Parent_Fractured_Their_Hip : 2
Risk_Smoking_Tobacco : 2
Risk_Chronic_Malnutrition_Or_Malabsorption : 2
Risk_Chronic_Liver_Disease : 2
Risk_Family_History_Of_Osteoporosis : 2
Risk_Low_Calcium_Intake : 2
Risk_Vitamin_D_Insufficiency : 2
Risk_Poor_Health_Frailty : 2
Risk_Excessive_Thinness : 2
Risk_Hysterectomy_Oophorectomy : 2
Risk_Estrogen_Deficiency : 2
Risk_Immobilization : 2
Risk_Recurring_Falls : 2
Count_Of_Risks : 8
```

In [12]:
```
df['Gender'].value_counts(normalize = True)*100
# Observation: Majority of the population are female
```

Out[12]:
```
Female    94.334112
Male       5.665888
Name: Gender, dtype: float64
```

In [13]:
```
df['Age_Bucket'].value_counts(normalize = True)*100
# Observation: Majority of the population are senior citizen
```

Out[13]:
```
>75      42.026869
65-75    31.717290
55-65    21.407710
<55       4.848131
Name: Age_Bucket, dtype: float64
```

Correlation Matrix

Why?

- A correlation matrix is a table showing correlation coefficients between variables

There are three broad reasons for computing a correlation matrix:

1. To summarize a large amount of data where the goal is to see patterns. In our example above, the observable pattern is that all the variables highly correlate with each other.
2. To input into other analyses. For example, people commonly use correlation matrixes as inputs for exploratory factor analysis, confirmatory factor analysis, structural equation models, and linear regression when excluding missing values pairwise.
3. As a diagnostic when checking other analyses. For example, with linear regression, a high amount of correlations suggests that the linear regression estimates will be unreliable.

In [14]:
```
# Using pandas
df.corr().style.background_gradient(cmap='coolwarm')
```

```
<ipython-input-14-529453c119e0>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of numeric_only to silence this warning.
  df.corr().style.background_gradient(cmap='coolwarm')
```

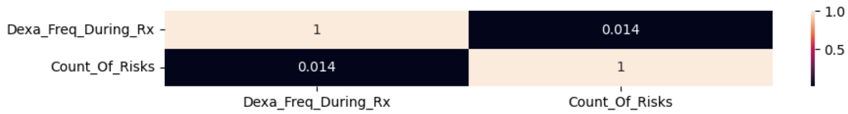
Out[14]:

	Dexa_Freq_During_Rx	Count_Of_Risks
Dexa_Freq_During_Rx	1.000000	0.013964
Count_Of_Risks	0.013964	1.000000

In [15]:
```
 #Using seaborn
plt.figure(figsize = (10,1))
sns.heatmap(df.corr(), annot = True)
```

```
<ipython-input-15-288ac2be8c21>:3: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of numeric_only to silence this warning.
  sns.heatmap(df.corr(), annot = True)
<Axes: >
```

Out[15]:



Observation:

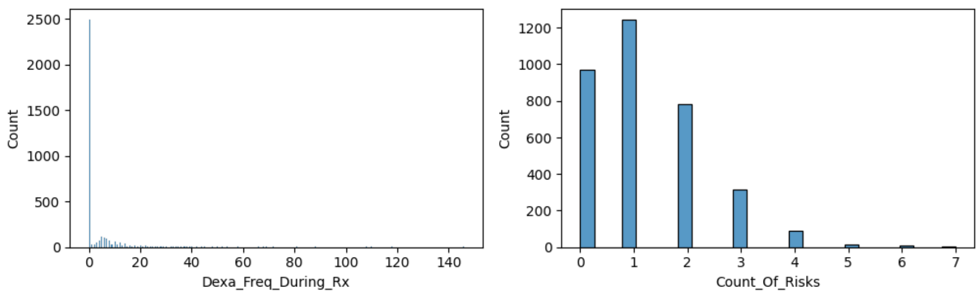
- Correlation is low between the two features. No need to remove any one of them.

CHECKING IF DATASET IS SKEWED OR NOT

Histogram

1. A histogram is an approximate representation of the distribution of numerical data.
2. To construct a histogram, the first step is to "bin" (or "bucket") the range of values—that is, divide the entire range of values into a series of intervals—and then count how many values fall into each interval.
3. The words used to describe the patterns in a histogram are: "symmetric", "skewed left" or "right", "unimodal", "bimodal" or "multimodal".

In [16]:
```
# Histogram using pandas
fig, ax = plt.subplots(ncols=2, nrows=1, figsize=(10,3))
index = 0
ax = ax.flatten()
for col, value in df.items():
  if df[col].dtypes != 'O':
    sns.histplot(value, ax=ax[index])
    index += 1
plt.tight_layout(pad=0.5, w_pad=0.7, h_pad=5.0)
```



Skewness

- The skew method returns a scalar value representing the skewness of the distribution. A positive value indicates a positive skew (i.e., the tail on the right side of the distribution is longer), a negative value indicates a negative skew (i.e., the tail on the left side of the distribution is longer), and a value of 0 indicates that the distribution is symmetrical

In [17]:
```
# check skewness of dataset
df.skew(axis = 0, skipna = True)
```

```
<ipython-input-17-77a6948006c4>:2: FutureWarning: The default value of numeric_only in DataFrame.skew is deprecated. In a future version, it will default to False. In addition, specifying 'nume
ric_only=None' is deprecated. Select only valid columns or specify the value of numeric_only to silence this warning.
  df.skew(axis = 0, skipna = True)
```

Out[17]:
```
Dexa_Freq_During_Rx    6.808730
Count_Of_Risks         0.879791
dtype: float64
```

CHECKING IF DATASET IS BALANCED OR NOT

In [18]:
```
# check total number of fraudulent and non-fraudulent instances
df['Persistency_Flag'].value_counts()
```

Out[18]:
```
Non-Persistent    2135
Persistent        1289
Name: Persistency_Flag, dtype: int64
```

In [19]:
```
# find Percentage of non-persistent flag
print(f"% of non-persistent flag : {round(df['Persistency_Flag'].value_counts(normalize = True)[0]*100,0)}%")
```

```
% of non-persistent flag : 62.0%
```

In [20]:
```
# find Percentage of persistent flag
print(f"% of persistent flag : {round(df['Persistency_Flag'].value_counts(normalize = True)[1]*100,0)}%")
```

```
% of persistent flag : 38.0%
```

- Observation: This dataset is balanced data. No need to do balancing of the data.

In [21]:
```
# display value_counts in categorical columns
for col in df.columns:
  if df[col].dtypes == 'O':
    print(df[col].value_counts())
```

```
P1       1
P2275    1
P2277    1
P2278    1
P2279    1
        ..
P1145    1
P1146    1
P1147    1
P1148    1
P3424    1
Name: Ptid, Length: 3424, dtype: int64
Non-Persistent    2135
Persistent        1289
Name: Persistency_Flag, dtype: int64
Female    3230
Male       194
Name: Gender, dtype: int64
Caucasian           3148
Other/Unknown         97
African American      95
Asian                 84
Name: Race, dtype: int64
Not Hispanic    3235
Hispanic          98
Unknown           91
Name: Ethnicity, dtype: int64
Midwest          1383
South            1247
West              502
Northeast         232
Other/Unknown      60
Name: Region, dtype: int64
>75      1439
65-75    1086
55-65     733
<55       166
Name: Age_Bucket, dtype: int64
GENERAL PRACTITIONER                                                1535
RHEUMATOLOGY                                                         604
ENDOCRINOLOGY                                                        458
Unknown                                                              310
ONCOLOGY                                                             225
OBSTETRICS AND GYNECOLOGY                                             90
UROLOGY                                                               33
ORTHOPEDIC SURGERY                                                    30
CARDIOLOGY                                                            22
PATHOLOGY                                                             16
HEMATOLOGY & ONCOLOGY                                                 14
OTOLARYNGOLOGY                                                        14
PEDIATRICS                                                            13
PHYSICAL MEDICINE AND REHABILITATION                                  11
PULMONARY MEDICINE                                                     8
SURGERY AND SURGICAL SPECIALTIES                                       8
PSYCHIATRY AND NEUROLOGY                                               4
NEPHROLOGY                                                             3
ORTHOPEDICS                                                            3
PLASTIC SURGERY                                                        2
VASCULAR SURGERY                                                       2
HOSPICE AND PALLIATIVE MEDICINE                                        2
GERIATRIC MEDICINE                                                     2
GASTROENTEROLOGY                                                       2
TRANSPLANT SURGERY                                                     2
CLINICAL NURSE SPECIALIST                                              1
OCCUPATIONAL MEDICINE                                                  1
HOSPITAL MEDICINE                                                      1
OPHTHALMOLOGY                                                          1
PODIATRY                                                               1
EMERGENCY MEDICINE                                                     1
RADIOLOGY                                                              1
OBSTETRICS & OBSTETRICS & GYNECOLOGY & OBSTETRICS & GYNECOLOGY         1
NEUROLOGY                                                              1
PAIN MEDICINE                                                          1
NUCLEAR MEDICINE                                                       1
Name: Ntm_Speciality, dtype: int64
Others        2013
Specialist    1411
Name: Ntm_Specialist_Flag, dtype: int64
OB/GYN/Others/PCP/Unknown    2104
Endo/Onc/Uro                  716
Rheum                         604
Name: Ntm_Speciality_Bucket, dtype: int64
N    2619
Y     805
Name: Gluco_Record_Prior_Ntm, dtype: int64
N    2522
Y     902
Name: Gluco_Record_During_Rx, dtype: int64
N    2488
Y     936
Name: Dexa_During_Rx, dtype: int64
N    2872
Y     552
Name: Frag_Frac_Prior_Ntm, dtype: int64
N    3007
Y     417
Name: Frag_Frac_During_Rx, dtype: int64
VLR_LR    1931
HR_VHR    1493
Name: Risk_Segment_Prior_Ntm, dtype: int64
>-2.5     1951
<=-2.5    1473
Name: Tscore_Bucket_Prior_Ntm, dtype: int64
Unknown    1497
HR_VHR      965
VLR_LR      962
Name: Risk_Segment_During_Rx, dtype: int64
Unknown    1497
<=-2.5     1017
>-2.5       910
Name: Tscore_Bucket_During_Rx, dtype: int64
No change    1660
Unknown      1497
Worsened      173
Improved       94
Name: Change_T_Score, dtype: int64
Unknown      2229
No change    1052
Worsened      121
Improved       22
Name: Change_Risk_Segment, dtype: int64
Adherent        3251
Non-Adherent     173
```

```
Name: Adherent_Flag, dtype: int64
Y    2557
N     867
Name: Idn_Indicator, dtype: int64
Y    3056
N     368
Name: Injectable_Experience_During_Rx, dtype: int64
N    1891
Y    1533
Name: Comorb_Encounter_For_Screening_For_Malignant_Neoplasms, dtype: int64
N    1911
Y    1513
Name: Comorb_Encounter_For_Immunization, dtype: int64
N    2072
Y    1352
Name: Comorb_Encntr_For_General_Exam_W_O_Complaint,_Susp_Or_Reprtd_Dx, dtype: int64
N    2331
Y    1093
Name: Comorb_Vitamin_D_Deficiency, dtype: int64
N    2425
Y     999
Name: Comorb_Other_Joint_Disorder_Not_Elsewhere_Classified, dtype: int64
N    2633
Y     791
Name: Comorb_Encntr_For_Oth_Sp_Exam_W_O_Complaint_Suspected_Or_Reprtd_Dx, dtype: int64
N    2607
Y     817
Name: Comorb_Long_Term_Current_Drug_Therapy, dtype: int64
N    2645
Y     779
Name: Comorb_Dorsalgia, dtype: int64
N    2747
Y     677
Name: Comorb_Personal_History_Of_Other_Diseases_And_Conditions, dtype: int64
N    2906
Y     518
Name: Comorb_Other_Disorders_Of_Bone_Density_And_Structure, dtype: int64
Y    1765
N    1659
Name: Comorb_Disorders_of_lipoprotein_metabolism_and_other_lipidemias, dtype: int64
N    2507
Y     917
Name: Comorb_Osteoporosis_without_current_pathological_fracture, dtype: int64
N    2775
Y     649
Name: Comorb_Personal_history_of_malignant_neoplasm, dtype: int64
N    2794
Y     630
Name: Comorb_Gastro_esophageal_reflux_disease, dtype: int64
N    2242
Y    1182
Name: Concom_Cholesterol_And_Triglyceride_Regulating_Preparations, dtype: int64
N    2191
Y    1233
Name: Concom_Narcotics, dtype: int64
N    2451
Y     973
Name: Concom_Systemic_Corticosteroids_Plain, dtype: int64
N    2465
Y     959
Name: Concom_Anti_Depressants_And_Mood_Stabilisers, dtype: int64
N    2787
Y     637
Name: Concom_Fluoroquinolones, dtype: int64
N    2821
Y     603
Name: Concom_Cephalosporins, dtype: int64
N    2853
Y     571
Name: Concom_Macrolides_And_Similar_Types, dtype: int64
N    2985
Y     439
Name: Concom_Broad_Spectrum_Penicillins, dtype: int64
N    2927
Y     497
Name: Concom_Anaesthetics_General, dtype: int64
N    3071
Y     353
Name: Concom_Viral_Vaccines, dtype: int64
N    3285
Y     139
Name: Risk_Type_1_Insulin_Dependent_Diabetes, dtype: int64
N    3421
Y       3
Name: Risk_Osteogenesis_Imperfecta, dtype: int64
N    3294
Y     130
Name: Risk_Rheumatoid_Arthritis, dtype: int64
N    3422
Y       2
Name: Risk_Untreated_Chronic_Hyperthyroidism, dtype: int64
N    3297
Y     127
Name: Risk_Untreated_Chronic_Hypogonadism, dtype: int64
N    3412
Y      12
Name: Risk_Untreated_Early_Menopause, dtype: int64
N    3168
Y     256
Name: Risk_Patient_Parent_Fractured_Their_Hip, dtype: int64
N    2780
Y     644
Name: Risk_Smoking_Tobacco, dtype: int64
N    2954
Y     470
Name: Risk_Chronic_Malnutrition_Or_Malabsorption, dtype: int64
N    3406
Y      18
Name: Risk_Chronic_Liver_Disease, dtype: int64
N    3066
Y     358
Name: Risk_Family_History_Of_Osteoporosis, dtype: int64
N    3382
Y      42
Name: Risk_Low_Calcium_Intake, dtype: int64
N    1788
Y    1636
Name: Risk_Vitamin_D_Insufficiency, dtype: int64
N    3232
Y     192
Name: Risk_Poor_Health_Frailty, dtype: int64
N    3357
Y      67
```

```
Name: Risk_Excessive_Thinness, dtype: int64
N    3370
Y      54
Name: Risk_Hysterectomy_Oophorectomy, dtype: int64
N    3413
Y      11
Name: Risk_Estrogen_Deficiency, dtype: int64
N    3410
Y      14
Name: Risk_Immobilization, dtype: int64
N    3355
Y      69
Name: Risk_Recurring_Falls, dtype: int64
```

In [22]:

```
#Check frequency distribution of categorical variables
for col in df.columns:
  if df[col].dtypes == 'O':
    print(f"{round(df[col].value_counts(normalize = True)*100,1)}")
```

```
P1       0.0
P2275    0.0
P2277    0.0
P2278    0.0
P2279    0.0
        ...
P1145    0.0
P1146    0.0
P1147    0.0
P1148    0.0
P3424    0.0
Name: Ptid, Length: 3424, dtype: float64
Non-Persistent    62.4
Persistent        37.6
Name: Persistency_Flag, dtype: float64
Female    94.3
Male       5.7
Name: Gender, dtype: float64
Caucasian           91.9
Other/Unknown        2.8
African American     2.8
Asian                2.5
Name: Race, dtype: float64
Not Hispanic    94.5
Hispanic         2.9
Unknown          2.7
Name: Ethnicity, dtype: float64
Midwest          40.4
South            36.4
West             14.7
Northeast         6.8
Other/Unknown     1.8
Name: Region, dtype: float64
>75      42.0
65-75    31.7
55-65    21.4
<55       4.8
Name: Age_Bucket, dtype: float64
GENERAL PRACTITIONER                                              44.8
RHEUMATOLOGY                                                      17.6
ENDOCRINOLOGY                                                     13.4
Unknown                                                            9.1
ONCOLOGY                                                           6.6
OBSTETRICS AND GYNECOLOGY                                          2.6
UROLOGY                                                            1.0
ORTHOPEDIC SURGERY                                                 0.9
CARDIOLOGY                                                         0.6
PATHOLOGY                                                          0.5
HEMATOLOGY & ONCOLOGY                                              0.4
OTOLARYNGOLOGY                                                     0.4
PEDIATRICS                                                         0.4
PHYSICAL MEDICINE AND REHABILITATION                               0.3
PULMONARY MEDICINE                                                 0.2
SURGERY AND SURGICAL SPECIALTIES                                   0.2
PSYCHIATRY AND NEUROLOGY                                           0.1
NEPHROLOGY                                                         0.1
ORTHOPEDICS                                                        0.1
PLASTIC SURGERY                                                    0.1
VASCULAR SURGERY                                                   0.1
HOSPICE AND PALLIATIVE MEDICINE                                    0.1
GERIATRIC MEDICINE                                                 0.1
GASTROENTEROLOGY                                                   0.1
TRANSPLANT SURGERY                                                 0.1
CLINICAL NURSE SPECIALIST                                          0.0
OCCUPATIONAL MEDICINE                                              0.0
HOSPITAL MEDICINE                                                  0.0
OPHTHALMOLOGY                                                      0.0
PODIATRY                                                           0.0
EMERGENCY MEDICINE                                                 0.0
RADIOLOGY                                                          0.0
OBSTETRICS & OBSTETRICS & GYNECOLOGY & OBSTETRICS & GYNECOLOGY     0.0
NEUROLOGY                                                          0.0
PAIN MEDICINE                                                      0.0
NUCLEAR MEDICINE                                                   0.0
Name: Ntm_Speciality, dtype: float64
Others        58.8
Specialist    41.2
Name: Ntm_Specialist_Flag, dtype: float64
OB/GYN/Others/PCP/Unknown    61.4
Endo/Onc/Uro                 20.9
Rheum                        17.6
Name: Ntm_Speciality_Bucket, dtype: float64
N    76.5
Y    23.5
Name: Gluco_Record_Prior_Ntm, dtype: float64
N    73.7
Y    26.3
Name: Gluco_Record_During_Rx, dtype: float64
N    72.7
Y    27.3
Name: Dexa_During_Rx, dtype: float64
N    83.9
Y    16.1
Name: Frag_Frac_Prior_Ntm, dtype: float64
N    87.8
Y    12.2
Name: Frag_Frac_During_Rx, dtype: float64
VLR_LR    56.4
HR_VHR    43.6
Name: Risk_Segment_Prior_Ntm, dtype: float64
>-2.5     57.0
<=-2.5    43.0
Name: Tscore_Bucket_Prior_Ntm, dtype: float64
Unknown    43.7
HR_VHR     28.2
VLR_LR     28.1
Name: Risk_Segment_During_Rx, dtype: float64
Unknown    43.7
<=-2.5     29.7
>-2.5      26.6
Name: Tscore_Bucket_During_Rx, dtype: float64
No change    48.5
Unknown      43.7
Worsened      5.1
Improved      2.7
Name: Change_T_Score, dtype: float64
Unknown      65.1
No change    30.7
Worsened      3.5
Improved      0.6
Name: Change_Risk_Segment, dtype: float64
Adherent        94.9
Non-Adherent     5.1
```

```
Name: Adherent_Flag, dtype: float64
Y    74.7
N    25.3
Name: Idn_Indicator, dtype: float64
Y    89.3
N    10.7
Name: Injectable_Experience_During_Rx, dtype: float64
N    55.2
Y    44.8
Name: Comorb_Encounter_For_Screening_For_Malignant_Neoplasms, dtype: float64
N    55.8
Y    44.2
Name: Comorb_Encounter_For_Immunization, dtype: float64
N    60.5
Y    39.5
Name: Comorb_Encntr_For_General_Exam_W_O_Complaint,_Susp_Or_Reprtd_Dx, dtype: float64
N    68.1
Y    31.9
Name: Comorb_Vitamin_D_Deficiency, dtype: float64
N    70.8
Y    29.2
Name: Comorb_Other_Joint_Disorder_Not_Elsewhere_Classified, dtype: float64
N    76.9
Y    23.1
Name: Comorb_Encntr_For_Oth_Sp_Exam_W_O_Complaint_Suspected_Or_Reprtd_Dx, dtype: float64
N    76.1
Y    23.9
Name: Comorb_Long_Term_Current_Drug_Therapy, dtype: float64
N    77.2
Y    22.8
Name: Comorb_Dorsalgia, dtype: float64
N    80.2
Y    19.8
Name: Comorb_Personal_History_Of_Other_Diseases_And_Conditions, dtype: float64
N    84.9
Y    15.1
Name: Comorb_Other_Disorders_Of_Bone_Density_And_Structure, dtype: float64
Y    51.5
N    48.5
Name: Comorb_Disorders_of_lipoprotein_metabolism_and_other_lipidemias, dtype: float64
N    73.2
Y    26.8
Name: Comorb_Osteoporosis_without_current_pathological_fracture, dtype: float64
N    81.0
Y    19.0
Name: Comorb_Personal_history_of_malignant_neoplasm, dtype: float64
N    81.6
Y    18.4
Name: Comorb_Gastro_esophageal_reflux_disease, dtype: float64
N    65.5
Y    34.5
Name: Concom_Cholesterol_And_Triglyceride_Regulating_Preparations, dtype: float64
N    64.0
Y    36.0
Name: Concom_Narcotics, dtype: float64
N    71.6
Y    28.4
Name: Concom_Systemic_Corticosteroids_Plain, dtype: float64
N    72.0
Y    28.0
Name: Concom_Anti_Depressants_And_Mood_Stabilisers, dtype: float64
N    81.4
Y    18.6
Name: Concom_Fluoroquinolones, dtype: float64
N    82.4
Y    17.6
Name: Concom_Cephalosporins, dtype: float64
N    83.3
Y    16.7
Name: Concom_Macrolides_And_Similar_Types, dtype: float64
N    87.2
Y    12.8
Name: Concom_Broad_Spectrum_Penicillins, dtype: float64
N    85.5
Y    14.5
Name: Concom_Anaesthetics_General, dtype: float64
N    89.7
Y    10.3
Name: Concom_Viral_Vaccines, dtype: float64
N    95.9
Y     4.1
Name: Risk_Type_1_Insulin_Dependent_Diabetes, dtype: float64
N    99.9
Y     0.1
Name: Risk_Osteogenesis_Imperfecta, dtype: float64
N    96.2
Y     3.8
Name: Risk_Rheumatoid_Arthritis, dtype: float64
N    99.9
Y     0.1
Name: Risk_Untreated_Chronic_Hyperthyroidism, dtype: float64
N    96.3
Y     3.7
Name: Risk_Untreated_Chronic_Hypogonadism, dtype: float64
N    99.6
Y     0.4
Name: Risk_Untreated_Early_Menopause, dtype: float64
N    92.5
Y     7.5
Name: Risk_Patient_Parent_Fractured_Their_Hip, dtype: float64
N    81.2
Y    18.8
Name: Risk_Smoking_Tobacco, dtype: float64
N    86.3
Y    13.7
Name: Risk_Chronic_Malnutrition_Or_Malabsorption, dtype: float64
N    99.5
Y     0.5
Name: Risk_Chronic_Liver_Disease, dtype: float64
N    89.5
Y    10.5
Name: Risk_Family_History_Of_Osteoporosis, dtype: float64
N    98.8
Y     1.2
Name: Risk_Low_Calcium_Intake, dtype: float64
N    52.2
Y    47.8
Name: Risk_Vitamin_D_Insufficiency, dtype: float64
N    94.4
Y     5.6
Name: Risk_Poor_Health_Frailty, dtype: float64
N    98.0
Y     2.0
```

```
Name: Risk_Excessive_Thinness, dtype: float64
N    98.4
Y     1.6
Name: Risk_Hysterectomy_Oophorectomy, dtype: float64
N    99.7
Y     0.3
Name: Risk_Estrogen_Deficiency, dtype: float64
N    99.6
Y     0.4
Name: Risk_Immobilization, dtype: float64
N    98.0
Y     2.0
Name: Risk_Recurring_Falls, dtype: float64
```

Observation:

1. We'll remove variables that have an uneven distribution. If variables have a distribution of 96:4 or higher, we'll drop them, as they tend to cause more misclassification and errors. This decision is based on the distribution of the 'persistancy_flag' which is distributed in a ratio of 62:38.
2. The 'Ntm_Speciality' variable has numerous levels with an imbalanced distribution. So, we'll combine levels with less than 1% frequency into a single level called 'others'.

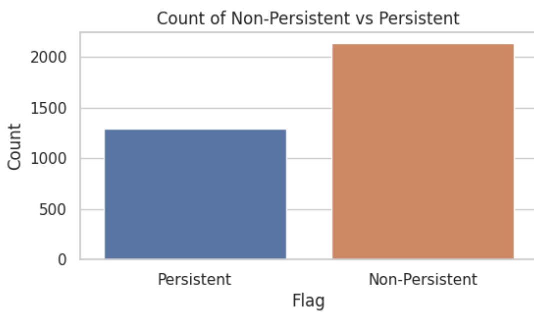
Uni-Variate Analysis

In [23]:

```
df["Persistency_Flag"].value_counts()
# Create the countplot using Seaborn
plt.figure(figsize=(6, 3))
sns.set(style="whitegrid")
sns.countplot(data=df, x='Persistency_Flag')
# Add labels and title
plt.xlabel('Flag')
plt.ylabel('Count')
plt.title('Count of Non-Persistent vs Persistent')
```

Out[23]:

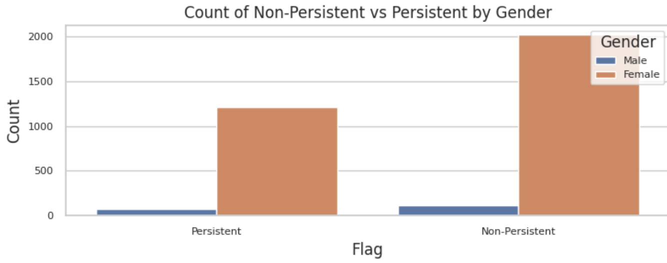
```
Text(0.5, 1.0, 'Count of Non-Persistent vs Persistent')
```

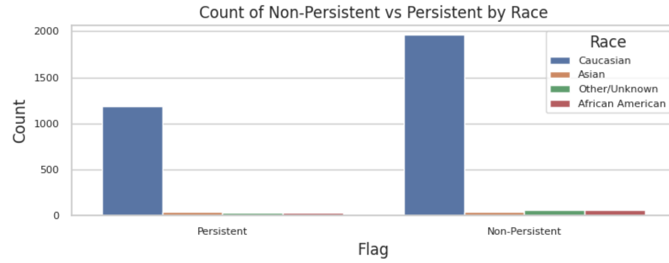


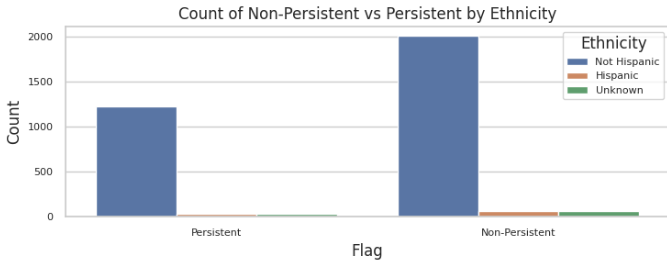
Bi-Variate Analysis

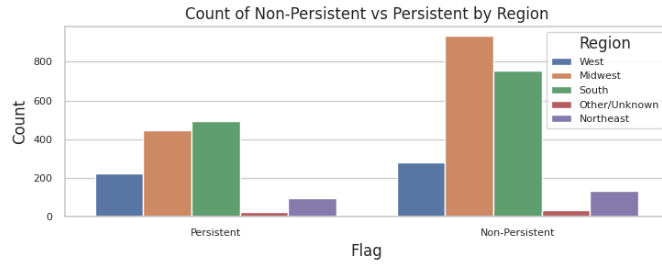
In [24]:

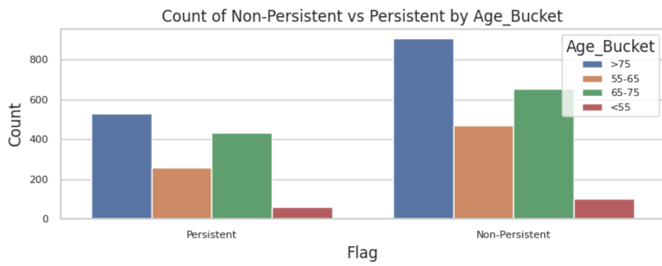
```
import matplotlib.pyplot as plt
import seaborn as sns

# List of columns for hue
hue_columns = ['Gender', 'Race', 'Ethnicity', 'Region', 'Age_Bucket']  # You can add more columns as needed

# Create subplots based on the number of hue columns
num_hue_columns = len(hue_columns)
num_columns_per_row = 2
num_rows = (num_hue_columns + num_columns_per_row - 1) // num_columns_per_row  # Calculate number of rows

plt.figure(figsize=(15, 3 * num_rows))  # Adjust the figure size
sns.set(style="whitegrid")

# Loop through each hue column and create countplots
for index, hue_column in enumerate(hue_columns, start=1):
    plt.subplot(num_rows, num_columns_per_row, index)
    sns.countplot(data=df, x='Persistency_Flag', hue=hue_column)
    plt.xlabel('Flag')
    plt.ylabel('Count')
    plt.title(f'Count of Non-Persistent vs Persistent by {hue_column}')
    plt.xticks(fontsize=8, rotation=0)  # Adjust font size for x-axis tick labels and rotate
    plt.yticks(fontsize=8)  # Adjust font size for y-axis tick labels
    plt.legend(title=hue_column, loc='upper right', fontsize=8, ncol=1)  # Adjust legend font size and position

# Adjust layout with space between charts and show plots
plt.tight_layout()
plt.show()
```











Observation:

1. Almost every group has one major class and rest is minor.

3. DATA PREPROCESSING

- Prepare the data for modeling by addressing missing values, scaling numerical features, and encoding categorical variables. Feature engineering might involve creating new features that capture relevant information for better model performance.

In [25]:
```
# Deleting the "Ptid" column because it doesn't have any significance
df.drop(columns=['Ptid'], inplace=True)
```

In [26]:
```
# Calculate frequency distribution of categorical variables
columns_to_drop = []  # To store columns to be dropped

for col in df.columns:
    if df[col].dtypes == 'O':  # Check if the column is categorical
        distribution_percentage = df[col].value_counts(normalize=True).max() * 100
        if distribution_percentage > 96:
            columns_to_drop.append(col)

print(f"Before dropping column:{len(df.columns)})")
# Drop columns with distribution greater than 96.4%
df.drop(columns=columns_to_drop, inplace=True)
print(f"Columns dropped:{columns_to_drop} and number of dropped columns: {len(columns_to_drop)}")
print(f"After dropping column:{len(df.columns)})")
```

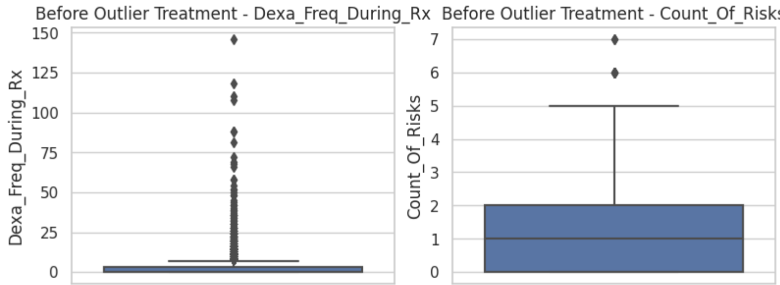
```
Before dropping column:68)
Columns dropped:['Risk_Osteogenesis_Imperfecta', 'Risk_Rheumatoid_Arthritis', 'Risk_Untreated_Chronic_Hyperthyroidism', 'Risk_Untreated_Chronic_Hypogonadism', 'Risk_Untreated_Early_Menopause', 'Risk_Chronic_Liver_Disease', 'Risk_Low_Calcium_Intake', 'Risk_Excessive_Thinness', 'Risk_Hysterectomy_Oophorectomy', 'Risk_Estrogen_Deficiency', 'Risk_Immobilization', 'Risk_Recurring_Falls']
and number of dropped columns: 12
After dropping column:56)
```

In [27]:
```
# Calculate value counts as a percentage
value_counts_percent = df['Ntm_Speciality'].value_counts(normalize=True) * 100
# Identify values with distribution less than 1%
values_to_tag_as_other = value_counts_percent[value_counts_percent < 1].index
# Replace these values with 'Other'
df.loc[df['Ntm_Speciality'].isin(values_to_tag_as_other), 'Ntm_Speciality'] = 'Other'
```

Box plot

- A boxplot is a standardized way of displaying the dataset based on a five-number summary:
  1. Minimum (Q0 or 0th percentile): the lowest data point excluding any outliers.
  2. Maximum (Q4 or 100th percentile): the largest data point excluding any outliers.
  3. Median (Q2 or 50th percentile): the middle value of the dataset.
  4. First quartile (Q1 or 25th percentile): also known as the lower quartile qn(0.25), is the median of the lower half of the dataset.
  5. Third quartile (Q3 or 75th percentile): also known as the upper quartile qn(0.75), is the median of the upper half of the dataset

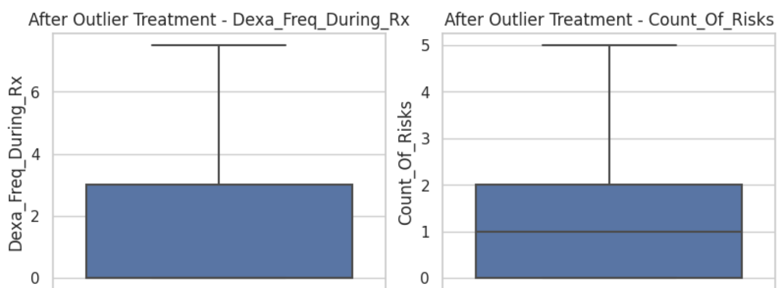
In [28]:
```
# Box plot for numeric columns with chart titles
fig, ax = plt.subplots(ncols=2, nrows=1, figsize=(8, 3))
index = 0
ax = ax.flatten()
for col, value in df.items():
    if df[col].dtypes != 'O':
        sns.boxplot(y=col, data=df, ax=ax[index])
        ax[index].set_title("Before Outlier Treatment - " + col)
        index += 1
plt.tight_layout(pad=0.5, w_pad=0.7, h_pad=5.0)
plt.show()
```



- Outliers are present. Outliers treatment is required.

In [29]:
```
def outlier_imputation(df, column):
    q75, q25 = np.percentile(df[column], [75, 25])
    intr_qr = q75 - q25
    max_val = q75 + (1.5 * intr_qr)
    min_val = q25 - (1.5 * intr_qr)
    df.loc[df[column] < min_val, column] = min_val
    df.loc[df[column] > max_val, column] = max_val
    return df
# Apply outlier_imputation function to specific columns
columns_to_impute = ['Dexa_Freq_During_Rx', 'Count_Of_Risks']
for column in columns_to_impute:
    df = outlier_imputation(df, column)
```

In [30]:
```
# Box plot for numeric columns with chart titles
fig, ax = plt.subplots(ncols=2, nrows=1, figsize=(8, 3))
index = 0
ax = ax.flatten()
for col, value in df.items():
    if df[col].dtypes != 'O':
        sns.boxplot(y=col, data=df, ax=ax[index])
        ax[index].set_title("After Outlier Treatment - " + col)
        index += 1
plt.tight_layout(pad=0.5, w_pad=0.7, h_pad=5.0)
plt.show()
```



Segregating the Independent and Dependent features

In [31]:
```
## Split the labels and the target
X= df.drop(columns='Persistency_Flag')
y = df['Persistency_Flag']

#check the shape
print(X.shape)
print(y.shape)
```

```
(3424, 55)
(3424,)
```

Encoding

In [32]:
```
from sklearn.preprocessing import LabelEncoder

def label_encode_categorical(data):
    label_encoder = LabelEncoder()
    encoded_data = data.copy()
    if isinstance(data, pd.DataFrame):
        for column in data.columns:
            if data[column].dtype == 'object':
                encoded_data[column] = label_encoder.fit_transform(data[column])
    elif isinstance(data, pd.Series):
        if data.dtype == 'object':
            encoded_data = label_encoder.fit_transform(data)
    return encoded_data

# Assuming X is a DataFrame and y is a Series
X = label_encode_categorical(X)
y = label_encode_categorical(y)
```

Train-Test Split

In [33]:
```
# import train test split
from sklearn.model_selection import train_test_split
# Split into training (80%) and testing set (20%)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=1)
# check the shape of train and test
print(X_train.shape)
print(X_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(2739, 55)
(685, 55)
(2739,)
(685,)
```

Note: To handle Imbalnce data, we can use the below method though our dataset is not imbalanced so we don't need to work on it

- SMOTE stands for Synthetic Minority Oversampling Technique. This is a statistical technique for increasing the number of cases in your dataset in a balanced way. The module works by generating new instances from existing minority cases that you supply as input.
- SMOTE - https://www.geeksforgeeks.org/ml-handling-imbalanced-data-with-smote-and-near-miss-algorithm-in-python/

In [34]:
```
# from imblearn.over_sampling import SMOTE

# # Instantiate the SMOTE class
# sm = SMOTE(sampling_strategy='minority')

# # Fit and transform the training data using SMOTE
# X_train, y_train = sm.fit_resample(X_train, y_train)

# # Print the shape of X_train after oversampling
# print("Shape of X_train after oversampling:", X_train.shape)

# # Print the shape of y_train after oversampling
# print("Shape of y_train after oversampling:", y_train.shape)
```

4. MODEL BUILDING AND SELECTION

- Select and train machine learning models suited for the task, based on the problem type. This step involves dividing the data into training and testing sets and fine-tuning model parameters.

In [35]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from imblearn.pipeline import Pipeline
from sklearn.linear_model import SGDClassifier
from sklearn.ensemble import AdaBoostClassifier
from sklearn.svm import SVC
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import RandomizedSearchCV
from sklearn.model_selection import GridSearchCV
# Evaluation Metrics
from sklearn.metrics import accuracy_score,roc_auc_score, classification_report, precision_score, recall_score, f1_score, confusion_matrix, roc_curve
# Plots
from sklearn import tree
```

In [36]:
```
# Function for calculating all the relevant metrics
"""Function to calculate all evaluation metrics"""
def evaluation(y_test,y_pred):
    Accuracy = accuracy_score(y_test, y_pred)
    conf_mat = confusion_matrix(y_test, y_pred)
    true_positive = conf_mat[0][0]
    false_positive = conf_mat[0][1]
    false_negative = conf_mat[1][0]
    true_negative = conf_mat[1][1]
    Precision = true_positive /(true_positive + false_positive)
    Recall = true_positive/(true_positive + false_negative)
    F1_Score = 2*(Recall * Precision) / (Recall + Precision)
    AUC = roc_auc_score(y_test, y_pred)
    return Accuracy,Precision,Recall,F1_Score,AUC
```

In [37]:
```
'''All Models'''
models = {
    1: LogisticRegression(),
    2: SGDClassifier(),
    3: GaussianNB(),
    4: DecisionTreeClassifier(),
    5: RandomForestClassifier(),
    6: GradientBoostingClassifier(),
    7: AdaBoostClassifier()
}

map_keys = list(models.keys())
```

In [38]:
```
# Get model name using id from linear_model_collection
def get_model_building_technique_name(num):
  if num == 1:
    return 'LogisticRegression'
  if num == 2:
    return 'SGDClassifier_Hinge_Loss'
  if num == 3:
    return 'NaiveBayes'
  if num == 4:
    return 'DecisionTreeClassifier'
  if num == 5:
    return 'RandomForestClassifier'
  if num == 6:
    return 'GradientBoostingClassifier'
  if num == 7:
    return 'AdaBoostClassifier'
  return ''
```

In [39]:
```
results = [];
for key_index in range(len(map_keys)):
  key = map_keys[key_index]
  try:
    # if key in [3,4,5,6,7,8]:
    model = models[key]
    print(key)
    model.fit(X_train, y_train)


    y_pred_train = model.predict(X_train)
    y_pred_test = model.predict(X_test)

    '''Test Accuracy'''
    Accuracy_Test, Precision_Test, Recall_Test, F1_Score_Test, AUC_Test =  evaluation(y_test, y_pred_test)

    '''Train Accuracy'''
    y_pred_train = model.predict(X_train)

    Accuracy_Train, Precision_Train, Recall_Train, F1_Score_Train, AUC_Train =  evaluation(y_train, y_pred_train)

    results.append({
        'Model Name' : get_model_building_technique_name(key),
        'Trained Model' : model,
        'Accuracy_Test' : Accuracy_Test,
        'Precision_Test' : Precision_Test,
        'Recall_Test' : Recall_Test,
        'F1_Score_Test' : F1_Score_Test,
        'AUC_Test' : AUC_Test,
        'Accuracy_Train' : Accuracy_Train,
        'Precision_Train' : Precision_Train,
        'Recall_Train' : Recall_Train,
        'F1_Score_Train' : F1_Score_Train,
```

```
        'AUC_Train' : AUC_Train
        })

  except Exception as e:
    print(e)
```

```
1
2
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge (status=1):
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
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
3
4
5
6
7
```

In [40]:

```
pd.DataFrame(results)
```

Out[40]:

	Model Name	Trained Model	Accuracy_Test	Precision_Test	Recall_Test	F1_Score_Test	AUC_Test	Accuracy_Train	Precision_Train	Recall_Train	F1_Score_Train	AUC_Train
0	LogisticRegression	LogisticRegression()	0.842336	0.890995	0.858447	0.874419	0.827627	0.815626	0.892586	0.826486	0.858266	0.789860
1	SGDClassifier_Hinge_Loss	SGDClassifier()	0.835036	0.909953	0.836601	0.871737	0.812391	0.810880	0.909515	0.811036	0.857457	0.777857
2	NaiveBayes	GaussianNB()	0.789781	0.767773	0.875676	0.818182	0.796434	0.789704	0.802102	0.852886	0.826715	0.785554
3	DecisionTreeClassifier	DecisionTreeClassifier()	0.712409	0.751185	0.775061	0.762936	0.700687	1.000000	1.000000	1.000000	1.000000	1.000000
4	RandomForestClassifier	(DecisionTreeClassifier(max_features='sqrt', r...	0.833577	0.883886	0.851598	0.867442	0.818369	1.000000	1.000000	1.000000	1.000000	1.000000
5	GradientBoostingClassifier	([DecisionTreeRegressor(criterion='friedman_ms...	0.839416	0.883886	0.859447	0.871495	0.825974	0.863454	0.934618	0.859367	0.895414	0.839629
6	AdaBoostClassifier	(DecisionTreeClassifier(max_depth=1, random_st...	0.827737	0.886256	0.842342	0.863741	0.810048	0.821468	0.899591	0.829386	0.863064	0.795312

In [40]:

Observation:

- The difference in how well the models perform on the training and testing data is small, usually less than 5%. However, the DecisionTreeClassifier and RandomForestClassifier show higher differences. To improve their performance, we'll adjust the hyperparameters and re-evaluate the models. We'll then choose the best model based on these evaluations.

Hyper parameter tunning

- A hyperparameter is a parameter whose value is set before the learning process begins
- Hyperparameters tuning is crucial as they control the overall behavior of a machine learning model
- Every machine learning models will have different hyperparameters that can be set

Note: We will try to build more robust model

In [41]:

```
'''Hyperparameters of Logistics Regression'''
LR_parameters = {
    'C': np.random.uniform(0.001,1,5),
    'tol':np.random.uniform(0.0001,0.1,5)
    }

'''Hyperparameters of SGD Classifier With Hinge Loss'''
SGD_parameters = {
    'penalty': ['l1','l2'],
    'alpha':np.random.uniform(0.0001,0.1,9)
    }

'''Hyperparameters of Naive Bayes'''
NB_parameters = {
    'var_smoothing': np.random.uniform(1e-16,1e-14,100)
    }

# Hyperparameters of Decision Tree Classifier
DTC_parameters = {
    'criterion': ['gini', 'entropy'],        # Testing both Gini impurity and entropy criteria
    'max_depth': [None, 10, 15, 20, 25],     # Testing a range of max_depth values
    'min_samples_split': [2, 5, 10],         # Testing different values for min_samples_split
    'min_samples_leaf': [1, 2, 4]            # Testing different values for min_samples_leaf
}

# Hyperparameters of Random Forest Classifier
RF_parameters = {
    'n_estimators': [300, 500, 600, 650, 700],  # Testing different numbers of trees
    'criterion': ['gini', 'entropy'],            # Testing both Gini and entropy criteria
    'max_depth': [None, 80, 110, 125, 135],      # Testing a range of max_depth values
    'min_samples_split': [2, 5, 10],             # Testing different values for min_samples_split
    'min_samples_leaf': [1, 2, 4]                # Testing different values for min_samples_leaf
}

# Hyperparameters of Gradient Boosted Decision Trees
# Hyperparameters of Gradient Boosted Decision Trees
GBDT_parameters = {
    'n_estimators': [100, 250, 350, 500],       # Testing different numbers of trees
    'criterion': ['friedman_mse'],              # Using 'friedman_mse' criterion
    'max_depth': [3, 4, 5],                      # Testing different values for max_depth
    'learning_rate': [0.01, 0.1, 0.2],           # Testing different learning rates
    'subsample': [0.8, 0.9, 1.0]                 # Testing different subsample ratios
}


'''Hyperparameters of AdaBoost Classifier'''
AB_parameters = {
    'n_estimators':[ 400 , 600 , 650 , 700 , 750 , 800 ]
    }

'''All Models'''
models = {
1 : RandomizedSearchCV(estimator = LogisticRegression(), param_distributions = LR_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5),
2 : RandomizedSearchCV(estimator = SGDClassifier(), param_distributions = SGD_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5),
3 : RandomizedSearchCV(estimator = GaussianNB(), param_distributions = NB_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5),
4 : RandomizedSearchCV(estimator = DecisionTreeClassifier(), param_distributions = DTC_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5),
5 : RandomizedSearchCV(estimator = RandomForestClassifier(), param_distributions = RF_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5),
6 : RandomizedSearchCV(estimator = GradientBoostingClassifier(), param_distributions = GBDT_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5),
7 : RandomizedSearchCV(estimator = AdaBoostClassifier(), param_distributions = AB_parameters, scoring= 'f1',verbose=2, n_jobs = -1, cv=5)

}

map_keys = list(models.keys())
```

In [42]:
```python
# Get model name using id from linear_model_collection
def get_model_building_technique_name(num):
  if num == 1:
    return 'LogisticRegression_Tuned'
  if num == 2:
    return 'SGDClassifier_Hinge_Loss_Tuned'
  if num == 3:
    return 'NaiveBayes_Tune'
  if num == 4:
    return 'DecisionTreeClassifier_Tuned'
  if num == 5:
    return 'RandomForestClassifier_Tuned'
  if num == 6:
    return 'GradientBoostingClassifier_Tuned'
  if num == 7:
    return 'AdaBoostClassifier_Tuned'
  return ''
```

In [43]:
```python
results_tuned = []
for key_index in range(len(map_keys)):
  key = map_keys[key_index]
  try:
    # if key in [3,4,5,6,7,8]:
    model = models[key]
    print(key)
    model.fit(X_train, y_train)


    y_pred_train = model.predict(X_train)
    y_pred_test = model.predict(X_test)

    '''Test Accuracy'''
    Accuracy_Test, Precision_Test, Recall_Test, F1_Score_Test, AUC_Test =  evaluation(y_test, y_pred_test)

    '''Train Accuracy'''
    y_pred_train = model.predict(X_train)

    Accuracy_Train, Precision_Train, Recall_Train, F1_Score_Train, AUC_Train =  evaluation(y_train, y_pred_train)

    results_tuned.append({
        'Model Name' : get_model_building_technique_name(key),
        'Trained Model' : model,
        'Accuracy_Test' : Accuracy_Test,
        'Precision_Test' : Precision_Test,
        'Recall_Test' : Recall_Test,
        'F1_Score_Test' : F1_Score_Test,
        'AUC_Test' : AUC_Test,
        'Accuracy_Train' : Accuracy_Train,
        'Precision_Train' : Precision_Train,
        'Recall_Train' : Recall_Train,
        'F1_Score_Train' : F1_Score_Train,
        'AUC_Train' : AUC_Train
        })

  except Exception as e:
    print(e)
```

```
1
Fitting 5 folds for each of 10 candidates, totalling 50 fits
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge (status=1):
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
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
2
Fitting 5 folds for each of 10 candidates, totalling 50 fits
3
Fitting 5 folds for each of 10 candidates, totalling 50 fits
4
Fitting 5 folds for each of 10 candidates, totalling 50 fits
5
Fitting 5 folds for each of 10 candidates, totalling 50 fits
6
Fitting 5 folds for each of 10 candidates, totalling 50 fits
7
Fitting 5 folds for each of 6 candidates, totalling 30 fits
/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_search.py:305: UserWarning: The total space of parameters 6 is smaller than n_iter=10. Running 6 iterations. For exhaustive sear
ches, use GridSearchCV.
  warnings.warn(
```

In [44]:
```python
pd.DataFrame(results_tuned)
```

Out[44]:

	Model Name	Trained Model	Accuracy_Test	Precision_Test	Recall_Test	F1_Score_Test	AUC_Test	Accuracy_Train	Precision_Train	Recall_Train	F1_Score_Train	AUC_Train
0	LogisticRegression_Tuned	RandomizedSearchCV(cv=5, estimator=LogisticReg...	0.842336	0.890995	0.858447	0.874419	0.827627	0.815261	0.892586	0.826040	0.858025	0.789373
1	SGDClassifier_Hinge_Loss_Tuned	RandomizedSearchCV(cv=5, estimator=SGDClassifi...	0.824818	0.933649	0.810700	0.867841	0.791920	0.804673	0.940455	0.788160	0.857599	0.759214
2	NaiveBayes_Tune	RandomizedSearchCV(cv=5, estimator=GaussianNB(...	0.789781	0.767773	0.875676	0.818182	0.796434	0.789704	0.802102	0.852886	0.826715	0.785554
3	DecisionTreeClassifier_Tuned	RandomizedSearchCV(cv=5, estimator=DecisionTre...	0.762044	0.819905	0.799076	0.809357	0.744553	0.891201	0.950379	0.884302	0.916151	0.871389
4	RandomForestClassifier_Tuned	RandomizedSearchCV(cv=5, estimator=RandomFores...	0.836496	0.890995	0.850679	0.870370	0.820022	0.933552	0.972563	0.925042	0.948207	0.920492
5	GradientBoostingClassifier_Tuned	RandomizedSearchCV(cv=5, estimator=GradientBoo...	0.826277	0.862559	0.856471	0.859504	0.815310	0.964951	0.993579	0.952434	0.972571	0.955366
6	AdaBoostClassifier_Tuned	RandomizedSearchCV(cv=5, estimator=AdaBoostCla...	0.836496	0.886256	0.853881	0.869767	0.821455	0.824754	0.896089	0.835602	0.864789	0.800871

Observation:

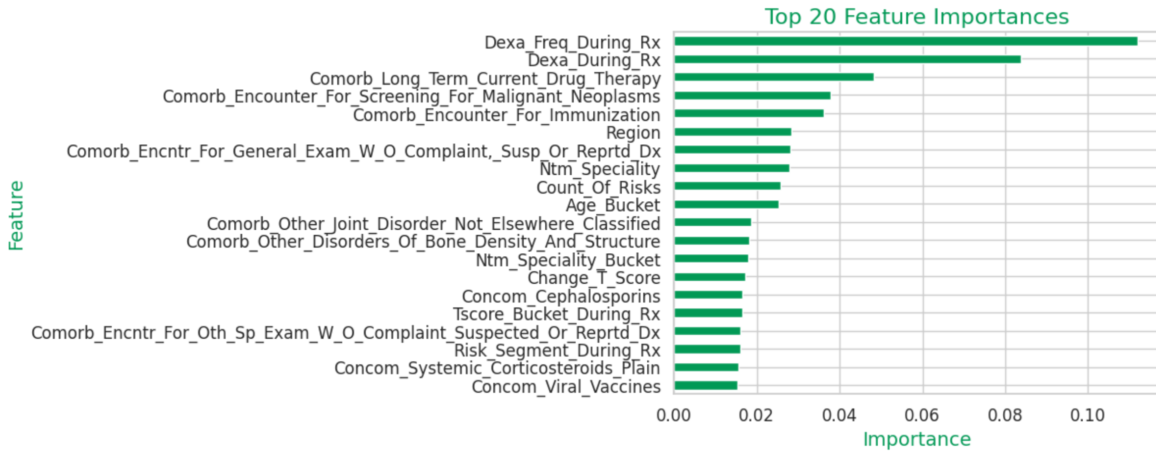
- We noticed that the models named DecisionTreeClassifier_Tuned and RandomForestClassifier_Tuned are fitting too closely to the training data. To make them better, we'll work on the model before training, by picking the most important features and making sure the data is scaled properly.

Data Pre-Processing for model improvement

In [45]:
```python
# Checking feature importance
# Fit a random forest classifier to get feature importances
rf_classifier = RandomForestClassifier()
rf_classifier.fit(X, y)

# Checking feature importance
feature_importance_ = pd.DataFrame({'Importance': rf_classifier.feature_importances_}, index=X.columns)
top_features = feature_importance_.sort_values(by='Importance', ascending=False)[:20]

# Plotting the top feature importances in a horizontally spread chart
plt.figure(figsize=(10, 8))
```

```
top_features.sort_values(by='Importance', ascending=True).plot(kind='barh', color='#019955')
plt.xlabel("Importance", color="#019955", fontsize=14)
plt.ylabel("Feature", color="#019955", fontsize=14)
plt.title("Top 20 Feature Importances", color="#019955", fontsize=16)
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)
plt.legend().set_visible(False)
plt.tight_layout()
plt.show()
```

```
<ipython-input-45-9227fe3ff4c5>:19: UserWarning: Tight layout not applied. The left and right margins cannot be made large enough to accommodate all axes decorations.
  plt.tight_layout()
<Figure size 1000x800 with 0 Axes>
```



Observation:

- We're choosing the most important 20 features from our dataset. We have 68 columns in our data, so we didn't set a specific limit to remove columns. Instead, we're focusing on the top 20 features that matter the most.

In [46]:
```
X_train_New = X_train[top_features.index]
X_test_New = X_test[top_features.index]
```

In [47]:
```
# Get model name using id from linear_model_collection
def get_model_building_technique_name(num):
  if num == 1:
    return 'LogisticRegression_Tuned2'
  if num == 2:
    return 'SGDClassifier_Hinge_Loss_Tuned2'
  if num == 3:
    return 'NaiveBayes_Tuned2'
  if num == 4:
    return 'DecisionTreeClassifier_Tuned2'
  if num == 5:
    return 'RandomForestClassifier_Tuned2'
  if num == 6:
    return 'GradientBoostingClassifier_Tuned2'
  if num == 7:
    return 'AdaBoostClassifier_Tuned2'
  return ''
```

In [48]:
```
results_tuned2 = []
for key_index in range(len(map_keys)):
  key = map_keys[key_index]
  try:
    # if key in [3,4,5,6,7,8]:
    model = models[key]
    print(key)
    model.fit(X_train_New, y_train)


    y_pred_train = model.predict(X_train_New)
    y_pred_test = model.predict(X_test_New)

    '''Test Accuracy'''
    Accuracy_Test, Precision_Test, Recall_Test, F1_Score_Test, AUC_Test =  evaluation(y_test, y_pred_test)

    '''Train Accuracy'''
    y_pred_train = model.predict(X_train_New)

    Accuracy_Train, Precision_Train, Recall_Train, F1_Score_Train, AUC_Train =  evaluation(y_train, y_pred_train)

    results_tuned2.append({
        'Model Name' : get_model_building_technique_name(key),
        'Trained Model' : model,
        'Accuracy_Test' : Accuracy_Test,
        'Precision_Test' : Precision_Test,
        'Recall_Test' : Recall_Test,
        'F1_Score_Test' : F1_Score_Test,
        'AUC_Test' : AUC_Test,
        'Accuracy_Train' : Accuracy_Train,
        'Precision_Train' : Precision_Train,
        'Recall_Train' : Recall_Train,
        'F1_Score_Train' : F1_Score_Train,
        'AUC_Train' : AUC_Train
        })

  except Exception as e:
    print(e)
```

```
1
Fitting 5 folds for each of 10 candidates, totalling 50 fits
2
Fitting 5 folds for each of 10 candidates, totalling 50 fits
3
Fitting 5 folds for each of 10 candidates, totalling 50 fits
4
Fitting 5 folds for each of 10 candidates, totalling 50 fits
5
Fitting 5 folds for each of 10 candidates, totalling 50 fits
6
Fitting 5 folds for each of 10 candidates, totalling 50 fits
7
Fitting 5 folds for each of 6 candidates, totalling 30 fits
/usr/local/lib/python3.10/dist-packages/sklearn/model_selection/_search.py:305: UserWarning: The total space of parameters 6 is smaller than n_iter=10. Running 6 iterations. For exhaustive sear
ches, use GridSearchCV.
  warnings.warn(
```

In [49]:
```
results_tuned2_df = pd.DataFrame(results_tuned2)
results_tuned2_df
```

Out[49]:

	Model Name	Trained Model	Accuracy_Test	Precision_Test	Recall_Test	F1_Score_Test	AUC_Test	Accuracy_Train	Precision_Train	Recall_Train	F1_Score_Train	AUC_Train
0	LogisticRegression_Tuned2	RandomizedSearchCV(cv=5, estimator=LogisticReg...	0.824818	0.883886	0.840090	0.861432	0.806962	0.806864	0.896089	0.813892	0.853015	0.776992
1	SGDClassifier_Hinge_Loss_Tuned2	RandomizedSearchCV(cv=5, estimator=SGDClassifi...	0.818978	0.789100	0.904891	0.843038	0.828010	0.787514	0.785756	0.862268	0.822236	0.788102
2	NaiveBayes_Tuned2	RandomizedSearchCV(cv=5, estimator=GaussianNB(...	0.817518	0.824645	0.872180	0.847747	0.815364	0.787514	0.823117	0.834813	0.828924	0.775594
3	DecisionTreeClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=DecisionTre...	0.781022	0.848341	0.806306	0.826790	0.760673	0.902519	0.946877	0.902113	0.923953	0.887668
4	RandomForestClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=RandomFores...	0.829197	0.895735	0.838137	0.865979	0.809084	0.864184	0.942207	0.855326	0.896667	0.838062
5	GradientBoostingClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=GradientBoo...	0.824818	0.860190	0.856132	0.858156	0.814125	0.863454	0.932283	0.860916	0.895179	0.840410
6	AdaBoostClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=AdaBoostCla...	0.837956	0.898104	0.847875	0.872267	0.819775	0.814531	0.900175	0.820649	0.858575	0.785858

5. MODEL EVALUATION AND INTERPRETATION

- Evaluate the trained models using appropriate metrics to assess their performance. Interpret the model results to understand which factors influence predictions and whether the model aligns with real-world expectations.

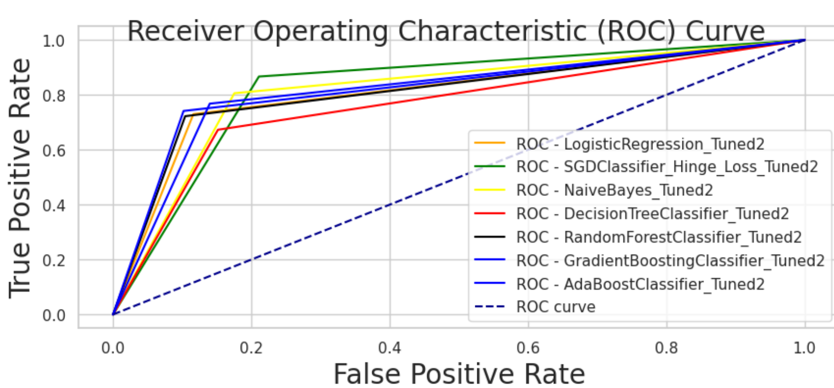
ROC Curve

- The overall performance of a classifier, summarized over all possible thresholds, is given by the Receiver Operating Characteristics (ROC) curve. The name "ROC" is historical and comes from communications theory. ROC Curves are used to see how well your classifier can separate positive and negative examples and to identify the best threshold for separating them.
- To be able to use the ROC curve, your classifier should be able to rank examples such that the ones with higher rank are more likely to be positive (fraudulent)
- ROC Curves summarize the trade-off between the true positive rate and false positive rate for a predictive model using different probability thresholds.

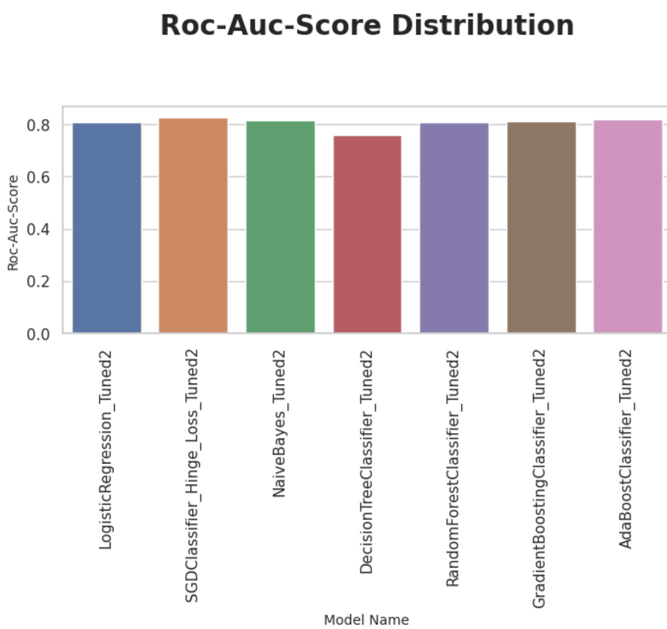
AUC (Area Under the Curve)

- The model performance is determined by looking at the area under the ROC curve (or AUC). An excellent model has AUC near to the 1.0, which means it has a good measure of separability

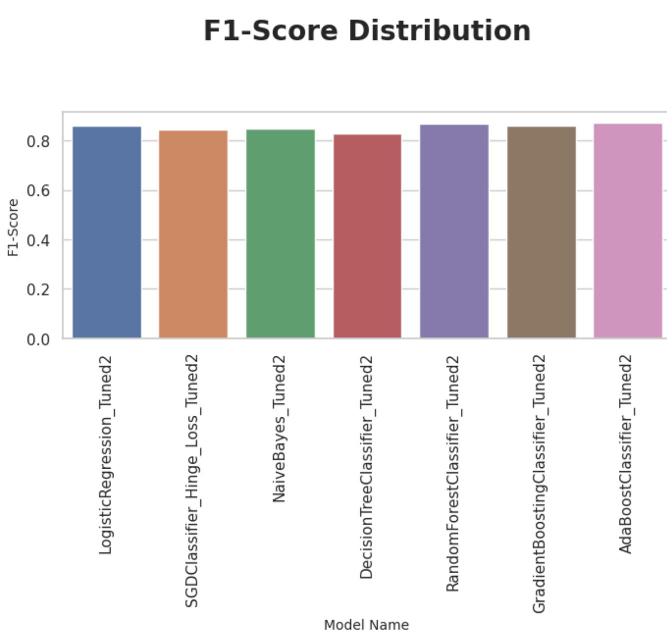
In [50]:
```
fpr_dict = {}
tpr_dict = {}
for i in range(len(map_keys)):

    model_pred = results_tuned2_df['Trained Model'][i].predict(X_test_New)
    fpr, tpr, thresholds = roc_curve(y_test, model_pred)
    fpr_dict[i] = fpr
    tpr_dict[i] = tpr

plt.figure(figsize=(10,4))
plt.suptitle('\nReceiver Operating Characteristic (ROC) Curve', fontsize=20)
plt.plot(fpr_dict[0], tpr_dict[0], color='orange', label=f"ROC - {results_tuned2_df['Model Name'][0]}")
plt.plot(fpr_dict[1], tpr_dict[1], color='green', label=f"ROC - {results_tuned2_df['Model Name'][1]}")
plt.plot(fpr_dict[2], tpr_dict[2], color='yellow', label=f"ROC - {results_tuned2_df['Model Name'][2]}")
plt.plot(fpr_dict[3], tpr_dict[3], color='red', label=f"ROC - {results_tuned2_df['Model Name'][3]}")
plt.plot(fpr_dict[4], tpr_dict[4], color='black', label=f"ROC - {results_tuned2_df['Model Name'][4]}")
plt.plot(fpr_dict[5], tpr_dict[5], color='blue', label=f"ROC - {results_tuned2_df['Model Name'][5]}")
plt.plot(fpr_dict[6], tpr_dict[6], color='blue', label=f"ROC - {results_tuned2_df['Model Name'][6]}")

plt.plot([0, 1], [0, 1], color='darkblue', linestyle='--',label='ROC curve')
plt.xlabel('False Positive Rate',fontdict={'fontsize': 20})
plt.ylabel('True Positive Rate',fontdict={'fontsize': 20})
plt.legend()
plt.show()
```



In [51]:
```
plt.figure(figsize=(8,3))
plt.title('\nRoc-Auc-Score Distribution\n\n', fontsize=20, fontweight='bold')
sns.barplot(data=results_tuned2_df, x='Model Name', y='AUC_Test')
plt.xlabel('Model Name',fontdict={'fontsize': 10})
plt.ylabel('Roc-Auc-Score',fontdict={'fontsize': 10})
plt.xticks(rotation=90)
plt.show()
```



In [52]:
```
plt.figure(figsize=(8,3))
plt.title('\nF1-Score Distribution\n\n', fontsize=20, fontweight='bold')
sns.barplot(data=results_tuned2_df, x='Model Name', y='F1_Score_Test')
plt.xlabel('Model Name',fontdict={'fontsize': 10})
plt.ylabel('F1-Score',fontdict={'fontsize': 10})
plt.xticks(rotation=90)
plt.show()
```



In [53]:
```
Best_Model_Name = results_tuned2_df['Trained Model'][results_tuned2_df[results_tuned2_df['F1_Score_Test'] == max(results_tuned2_df['F1_Score_Test'])]['Trained Model'].index[0]]
Best_Model_Index = results_tuned2_df['Trained Model'][results_tuned2_df[results_tuned2_df['F1_Score_Test'] == max(results_tuned2_df['F1_Score_Test'])]['Trained Model'].index].index[0]
Best_Model_Name
```

Out[53]:
```
▸ RandomizedSearchCV
▸ estimator: AdaBoostClassifier
  ▸ AdaBoostClassifier
```

In [54]:
```
results_tuned2_df
```

Out[54]:

	Model Name	Trained Model	Accuracy_Test	Precision_Test	Recall_Test	F1_Score_Test	AUC_Test	Accuracy_Train	Precision_Train	Recall_Train	F1_Score_Train	AUC_Train
0	LogisticRegression_Tuned2	RandomizedSearchCV(cv=5, estimator=LogisticReg...	0.824818	0.883886	0.840090	0.861432	0.806962	0.806864	0.896089	0.813892	0.853015	0.776992
1	SGDClassifier_Hinge_Loss_Tuned2	RandomizedSearchCV(cv=5, estimator=SGDClassifi...	0.818978	0.789100	0.904891	0.843038	0.828010	0.787514	0.785756	0.862268	0.822236	0.788102
2	NaiveBayes_Tuned2	RandomizedSearchCV(cv=5, estimator=GaussianNB(...	0.817518	0.824645	0.872180	0.847747	0.815364	0.787514	0.823117	0.834813	0.828924	0.775594
3	DecisionTreeClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=DecisionTre...	0.781022	0.848341	0.806306	0.826790	0.760673	0.902519	0.946877	0.902113	0.923953	0.887668
4	RandomForestClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=RandomFores...	0.829197	0.895735	0.838137	0.865979	0.809084	0.864184	0.942207	0.855326	0.896667	0.838062
5	GradientBoostingClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=GradientBoo...	0.824818	0.860190	0.856132	0.858156	0.814125	0.863454	0.932283	0.860916	0.895179	0.840410
6	AdaBoostClassifier_Tuned2	RandomizedSearchCV(cv=5, estimator=AdaBoostCla...	0.837956	0.898104	0.847875	0.872267	0.819775	0.814531	0.900175	0.820649	0.858575	0.785858

Saving Best Model Model and Pre-Processed dataset

In [56]:

```
import pickle

# Save the best model using pickle
with open('PERSISTENT_NON_PERSISTENT_CLASSIFICATION.sav', 'wb') as best_model_pickle:
    pickle.dump(Best_Model_Name, best_model_pickle)

# Convert NumPy arrays to DataFrames
X_train_New_df = pd.DataFrame(X_train_New)
y_train_df = pd.DataFrame(y_train)
X_test_New_df = pd.DataFrame(X_test_New)
y_test_df = pd.DataFrame(y_test)

# Concatenate DataFrames
train_preprocessed_1 = pd.concat([X_train, y_train_df], axis=1)
test_preprocessed_1 = pd.concat([X_test, y_test_df], axis=1)
train_preprocessed_2 = pd.concat([X_train_New_df, y_train_df], axis=1)
test_preprocessed_2 = pd.concat([X_test_New_df, y_test_df], axis=1)

# Save train_preprocessed_1 dataframe
train_preprocessed_1.to_csv('train_preprocessed_1.csv', index=False)
# Save test_preprocessed_1 dataframe
test_preprocessed_1.to_csv('test_preprocessed_1.csv', index=False)
# Save train_preprocessed_2 dataframe
train_preprocessed_2.to_csv('train_preprocessed_2.csv', index=False)
# Save test_preprocessed_2 dataframe
test_preprocessed_2.to_csv('test_preprocessed_2.csv', index=False)
```

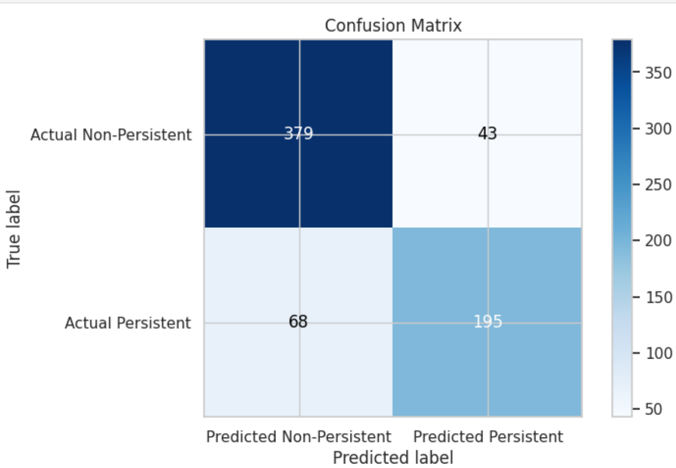
BEST MODEL VALIDATION

In [58]:

```
# Load the pickled model
with open('PERSISTENT_NON_PERSISTENT_CLASSIFICATION.sav', 'rb') as model_pickle:
    loaded_model = pickle.load(model_pickle)

# Predict on new data (X_test_New)
predictions = loaded_model.predict(X_test_New)
'''Test Accuracy'''
Accuracy_Test, Precision_Test, Recall_Test, F1_Score_Test, AUC_Test =  evaluation(y_test, predictions)
```

In [59]:

```
# Confusion Matrix
cm = confusion_matrix(y_test, predictions)
fig, ax = plt.subplots(figsize=(8, 5))
im = ax.imshow(cm, interpolation='nearest', cmap=plt.cm.Blues)
ax.figure.colorbar(im, ax=ax)
ax.set(xticks=np.arange(cm.shape[1]),
       yticks=np.arange(cm.shape[0]),
       xticklabels=['Predicted Non-Persistent', 'Predicted Persistent'],
       yticklabels=['Actual Non-Persistent', 'Actual Persistent'],
       title='Confusion Matrix',
       ylabel='True label',
       xlabel='Predicted label')

# Annotate the confusion matrix cells with counts
thresh = cm.max() / 2.
for i in range(cm.shape[0]):
    for j in range(cm.shape[1]):
        ax.text(j, i, format(cm[i, j], 'd'),
                ha="center", va="center",
                color="white" if cm[i, j] > thresh else "black")

plt.show()
```



In [60]:

```
#Classification Report
print(classification_report(y_test, predictions))
```

```
              precision    recall  f1-score   support

           0       0.85      0.90      0.87       422
           1       0.82      0.74      0.78       263

    accuracy                           0.84       685
   macro avg       0.83      0.82      0.83       685
weighted avg       0.84      0.84      0.84       685
```

Conclusion

- After training and predicting with various models, we have chosen the AdaBoostClassifier as our final model due to its superior performance among the options.
- Throughout the process, we conducted Exploratory Data Analysis (EDA), preprocessing, built multiple models, visualized the significance of features, fine-tuned hyperparameters, and made predictions.
- To enhance the model's robustness, we utilized the RandomForestClassifier for feature importance assessment and standardized the data using the StandardScaler, followed by hyperparameter tuning. We have incorporated evaluation metrics, preprocessed dataset and the analysis tab into the Project Report spreadsheet.

THE END