Data Science Intern at Data Glacier

Project: Healthcare - Persistency of a drug

Week 10: Deliverables

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Date: 9 November 2022

Submitted to: Data Glacier

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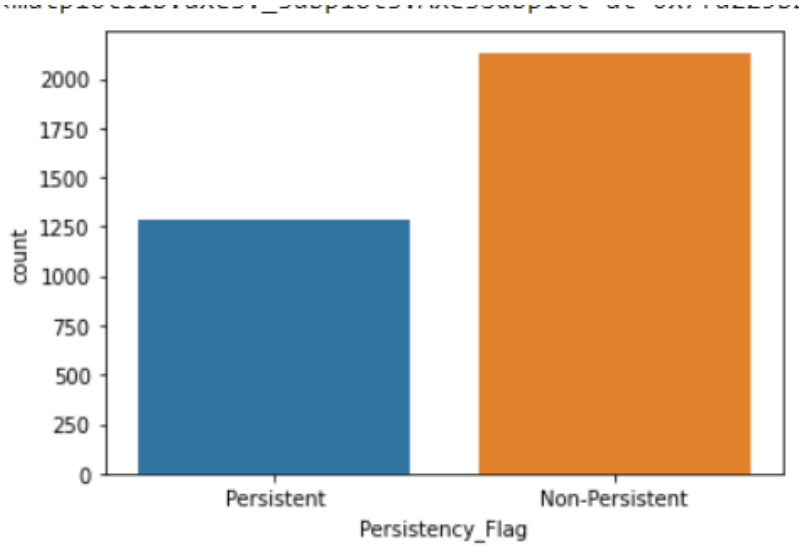
1. Problem Description

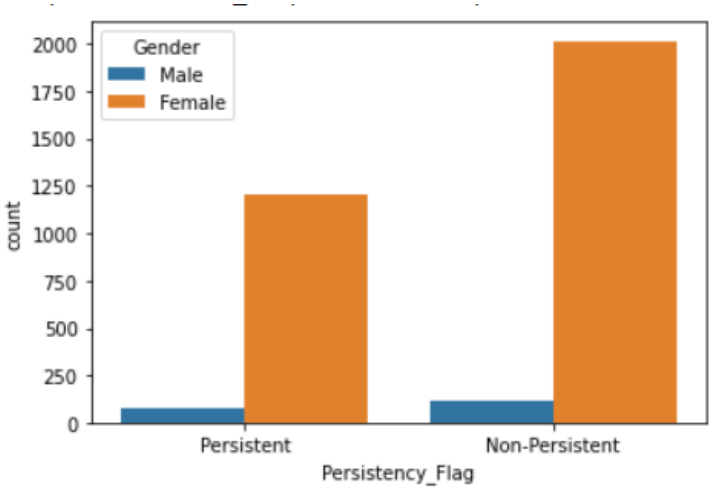
Persistence represents the time (e.g., days, months, years) over which a patient continues the treatment. For practical reasons, it might be assessed according to the time taken for a patient to fill their prescription and can capture both the timeliness and frequency of refilling. In reality, as defined by the adherence taxonomy, adherence is a dynamic behavior, consisting of initiation, implementation and discontinuation phases of treatment that vary over time, resulting in periods of persistence and non-persistence. Therefore, rather than measuring the specific components of adherence, we could measure persistence, which captures the chronology of adherence and enables us to examine and understand patterns of medication-taking behavior.
For that this project aims to build an automated classifier that predict whether a patient was persistent or not.

2. Exploratory data analysis

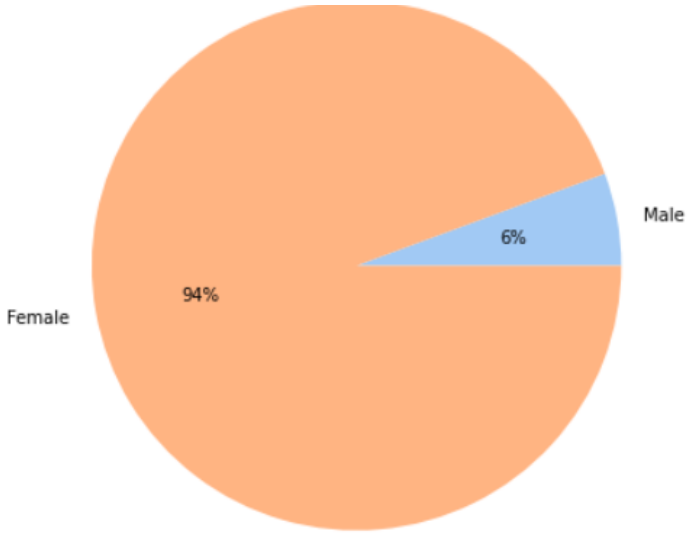
First let's start by visualizing the target variable: Persistency flag



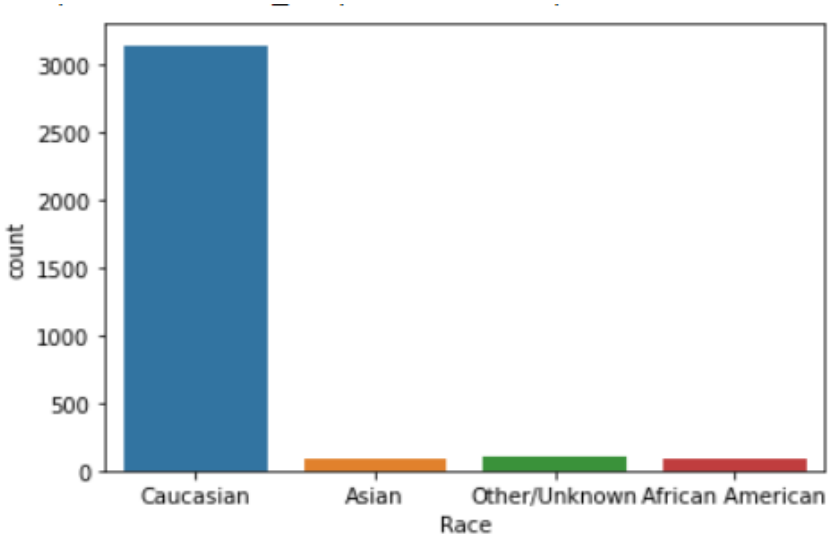
We notice that most of the patient are non-persistent in terms of data we can say that our classes are not balanced thing that should be handled in order to get good outcomes.
Now lets filter our target visualization by gender:



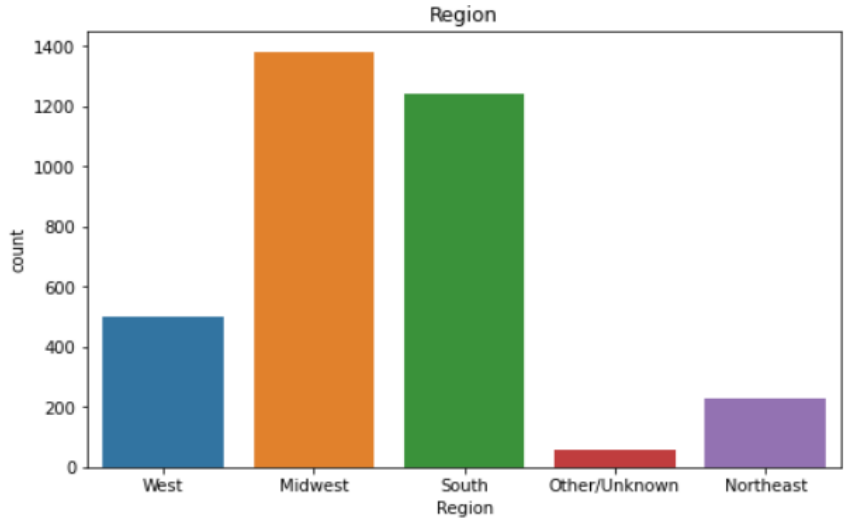
Here we see that the dominated gender in our data is female with a percentage of 94% from the totality of the data when males are presenting only 6% of data.



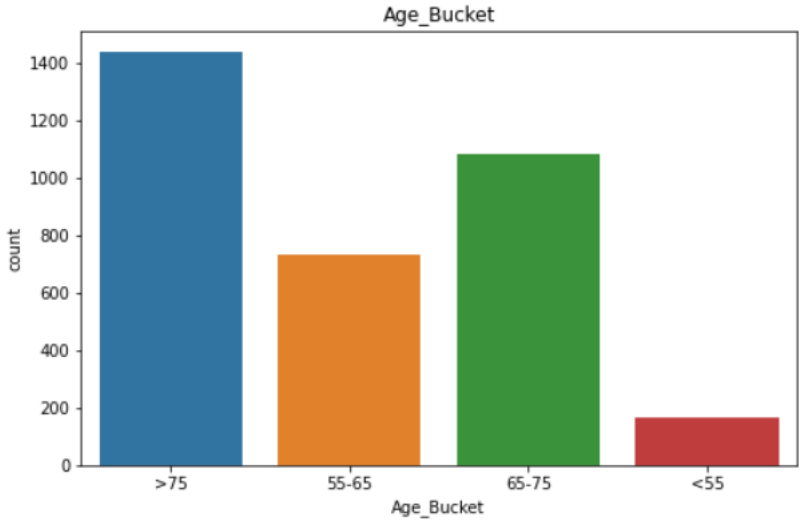
Now let's have an idea about the different patient's race:



The majority of patients have a Caucasian race. Then let's plot the different regions available in our data:



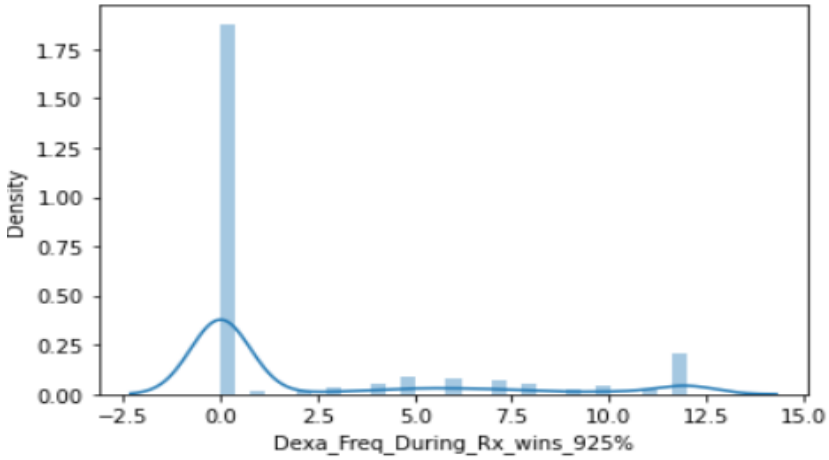
Here we can see the diversity of regions where Midwest and south region are the most Presented.



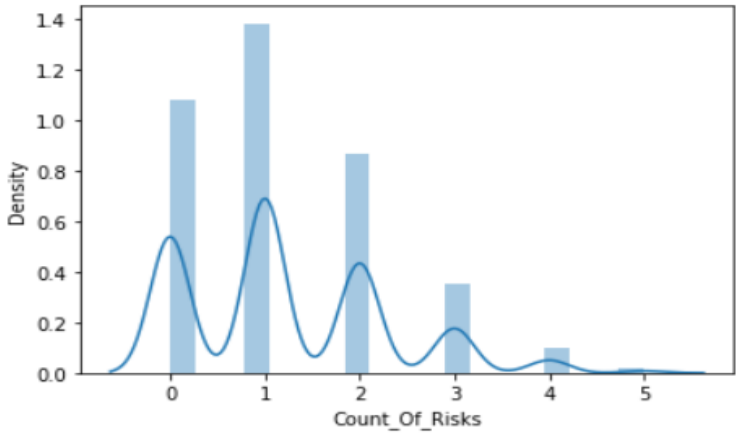
We constate from the plot above that the dataset is more focused on people who have more Than 55 which is normal related to the data topic.

The rest of categorical variables involve only two values which are N (no) and Y(yes) where N value occur more than Y .

Now let's move to continuous attributes where only two variables exist :



We notice that most of the values are presenting 0, this is due to winsorization technique that we've applied in order to handle the large number of outliers that we had at the beginning.



Here we see that we have 5 values where 1, 0 and 2 are the most presented. And the distribution doesn't seem to be normal and it's positively skewed.

Now let's move to correlation analysis and run some statistical tests in order to figure out the most important variables that have an impact on the target variable.
If we start by analyzing categorical variables versus categorical variable(target) we have to run a chi squared test since both of the variables are categorical

Null hypothesis: there is no relationship between the categorical variables.
Alternative hypothesis: there is a relationship between categorical variables.

```
y = df['Persistency_Flag']
important_var = []
for i in cat_list:

  contingency_table = pd.crosstab(df[i], y)
  print(contingency_table,"\n\n\n")
  chi2_stat,p_val,dof,ex = stats.chi2_contingency(contingency_table)
  print("CHI-SQUARE TEST VALUES")
  print("Chi Square Value : ",chi2_stat)
  print("Degree of Freedom : ",dof)
  print("P Value : ", p_val, "\n")
  if (p_val <= 0.05) :
    important_var.append(i)
    print(i, " has an impact on persistency flag \n\n")
  else:
    print(i, " doesn't affect persistency flag \n\n")
```

```
Persistency_Flag  Non-Persistent  Persistent
Gender
Female                      2015        1208
Male                         116          77


CHI-SQUARE TEST VALUES
Chi Square Value :  0.35575982921459065
Degree of Freedom :  1
P Value :  0.5508706006957192

Gender  doesn't affect persistency flag
```

After selecting all the categorical variables and gathering them in a list, I ran the chi squared test that will enable us to select only the variables correlated to the target variable.

```
#variables that have an impact on the target variable
important_var
```

```
['Region',
 'Ntm_Speciality',
 'Ntm_Specialist_Flag',
 'Ntm_Speciality_Bucket',
 'Gluco_Record_During_Rx',
 'Dexa_During_Rx',
 'Frag_Frac_During_Rx',
 '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',
```

```
#from 65 variables we get only 46 which are dependent of target variable
len(important_var)
```

```
46
```

For Continuous vs categorical variables since N > 30 and we have only 2 classes (persistent and non persistent) we will run a Z test, it assesses whether the average of two groups are statistically different from each other.

Null Hypothesis: There is no statistically difference between our variable(continuous) values for Various Class

Alternate Hypothesis: There is difference between Observed values for Various Class

```
num_var = df.select_dtypes(include = "int").columns
num_var = num_var.tolist()
num_var
```

```
['Dexa_Freq_During_Rx', 'Count_Of_Risks']
```

```
from statsmodels.stats import weightstats as stests

y = df['Persistency_Flag']
important_var_num = []

for i in num_var:
  ztest, pval = stests.ztest(y, df[i], alternative='two-sided')
  print("Z Test Value is ",ztest)
  print("P Value is ",pval)
  if (pval <= 0.05):
    important_var_num.append(i)
    print(i, " can be a good predictor to persistency flag \n\n")
  else:
    print(i, " doesn't affect persistency flag \n\n")
```

```
Z Test Value is  -26.189732657966882
P Value is  3.478806353132994e-151
Dexa_Freq_During_Rx  can be a good predictor to persistency flag


Z Test Value is  -42.41495396358258
P Value is  0.0
Count_Of_Risks  can be a good predictor to persistency flag
```

Based on the Z score results we get that both of the continuous variables have an impact on the persistency flag.

3. Recommendations

Based on this analysis I can recommend the elimination of some attributes that don't have any effect on the persistency flag which are:

['Region',
'Ntm_Speciality',
'Ntm_Specialist_Flag',
'Ntm_Speciality_Bucket',
'Gluco_Record_During_Rx',
'Dexa_During_Rx',
'Frag_Frac_During_Rx',
'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_Rheumatoid_Arthritis',
'Risk_Untreated_Chronic_Hypogonadism',
'Risk_Smoking_Tobacco',
'Risk_Chronic_Malnutrition_Or_Malabsorption',
'Risk_Vitamin_D_Insufficiency',
'Risk_Poor_Health_Frailty',
'Risk_Excessive_Thinness',
'Risk_Immobilization',
'Dexa_Freq_During_Rx',
'Count_Of_Risks']

In total we keep only 49 independent variables instead of 67:

```
df_new = df[selected_var]
df_new.shape
```

```
(3416, 48)
```