Exploratory Data Analysis

The point of this project is to cover statistical principles supporting the data analytics life cycle. I compute and interpret measures of central tendency, correlations, and variation. I introduce hypothesis testing, focusing on application for parametric tests, and addresses communication skills and tools to explain an analyst's findings to others within an organization.

Competencies

Data Interpretation

Interprets central tendency, correlations, and variation to inform organizational decisions.

Conduct Parametric Testing

Conducts parametric hypothesis testing.

Write Up

Research Question

Does the complication risk influence patient re-admission?

Benefit of Analysis

Readmission of patients is an important issue to assess due to the penalties that come with excessive readmissions. Stakeholders will benefit from this analysis by focusing on the relationship between the complication risk of patients and the risk of readmission. If found significant, we can then focus on the care provided to those with higher complication risks to prevent readmission in the future. If not found significant, we can eliminate this potential cause for readmission and readjust our focus to other factors.

Code

```
In []: # Import necessary packages
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as stats

In []: # Import medical CSV file
medical_data = pd.read_csv("C:/Users/Makayla Avendano/Desktop/medical_clean.csv")

In []: # Looking at medical data information
medical_data.info()
```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 10000 entries, 0 to 9999
Data columns (total 50 columns):

Column # Non-Null Count Dtype _____ _____ _ _ _ _ _ 0 CaseOrder 10000 non-null int64 1 Customer id 10000 non-null object 2 Interaction 10000 non-null object 3 UID 10000 non-null object 4 City 10000 non-null object 5 State 10000 non-null object 6 County 10000 non-null object 7 10000 non-null int64 Zip 8 float64 Lat 10000 non-null 9 Lng 10000 non-null float64 10 Population 10000 non-null int64 11 10000 non-null Area object 12 TimeZone 10000 non-null object 13 Job 10000 non-null object 14 Children 10000 non-null int64 15 Age 10000 non-null int64 10000 non-null float64 16 Income 17 Marital 10000 non-null object 18 Gender 10000 non-null object 19 ReAdmis 10000 non-null object 20 VitD levels 10000 non-null float64 21 Doc visits 10000 non-null int64 22 Full meals eaten 10000 non-null int64 23 vitD supp 10000 non-null int64 Soft drink 10000 non-null object 25 Initial admin 10000 non-null object HighBlood 10000 non-null object 26 27 Stroke 10000 non-null object 28 Complication risk 10000 non-null object 29 Overweight 10000 non-null object 30 Arthritis 10000 non-null object 31 Diabetes 10000 non-null object 32 Hyperlipidemia 10000 non-null object BackPain 10000 non-null object 33 34 Anxiety 10000 non-null object 35 Allergic rhinitis 10000 non-null object Reflux esophagitis 36 10000 non-null object 37 Asthma 10000 non-null object 38 Services 10000 non-null object 39 Initial_days 10000 non-null float64 40 TotalCharge 10000 non-null float64 41 Additional charges 10000 non-null float64 42 Item1 10000 non-null int64 43 Item2 10000 non-null int64 44 Item3 10000 non-null int64 45 Item4 10000 non-null int64 46 10000 non-null Item5 int64 47 Item6 10000 non-null int64 48 Item7 10000 non-null int64 49 Item8 10000 non-null int64 dtypes: float64(7), int64(16), object(27) memory usage: 3.8+ MB

In []: medical_data_cat = medical_data[['ReAdmis','Complication_risk']]

```
medical_data_cat.info()
In [ ]:
        <class 'pandas.core.frame.DataFrame'>
        RangeIndex: 10000 entries, 0 to 9999
        Data columns (total 2 columns):
             Column
                                 Non-Null Count Dtype
             -----
                                 -----
                                 10000 non-null object
         0
             ReAdmis
             Complication_risk 10000 non-null object
        dtypes: object(2)
        memory usage: 156.4+ KB
        # Creating contingency table
In [ ]:
        med_cont = pd.crosstab(medical_data_cat.ReAdmis, medical_data_cat.Complication_risk, medical_data_cat.Complication_risk)
        print(med cont)
        Complication_risk High
                                   Low Medium
                                                  A11
        ReAdmis
        No
                            2135 1343
                                          2853
                                                 6331
        Yes
                            1223
                                  782
                                          1664
                                                 3669
        A11
                            3358
                                  2125
                                          4517
                                                10000
        # Looking at Chi-square test
In [ ]:
         stats.chi2 contingency(observed = med cont)
        Chi2ContingencyResult(statistic=0.15902193516217972, pvalue=0.9999210625319999, dof=
Out[ ]:
        6, expected_freq=array([[ 2125.9498, 1345.3375, 2859.7127, 6331.
                [ 1232.0502, 779.6625, 1657.2873, 3669.
                                                                1,
                              2125.
                                       , 4517.
                                                   , 10000.
                [ 3358.
                                                                ]]))
        # Interpreting the results
In [ ]:
        pvalue=0.9999210625319999
        alpha = 0.05
         if pvalue < alpha:</pre>
             print("There is a significant association between variables.")
         else:
            print("There is no significant association between variables.")
```

There is no significant association between variables.

Univariate Statistics

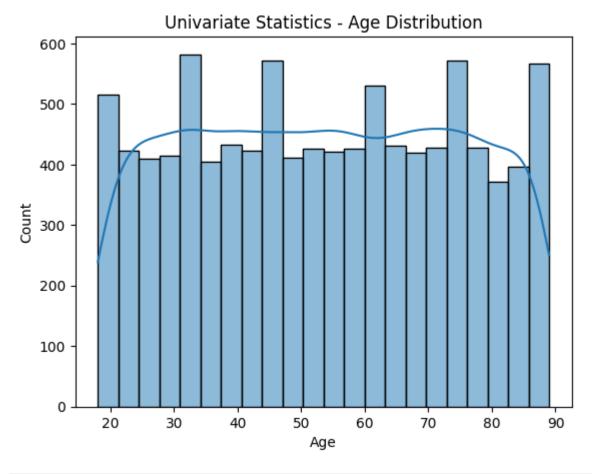
Two continuous variables: Age and Income

Two categorical variables: Initial admin and Complication risk

```
# Univariate Statistics
In [ ]:
        # Continuous variables - Age
        medical_data['Age'].describe()
                  10000.000000
        count
Out[]:
        mean
                    53.511700
        std
                    20.638538
                    18.000000
        min
        25%
                    36.000000
                    53.000000
        50%
        75%
                    71.000000
                    89.000000
        Name: Age, dtype: float64
```

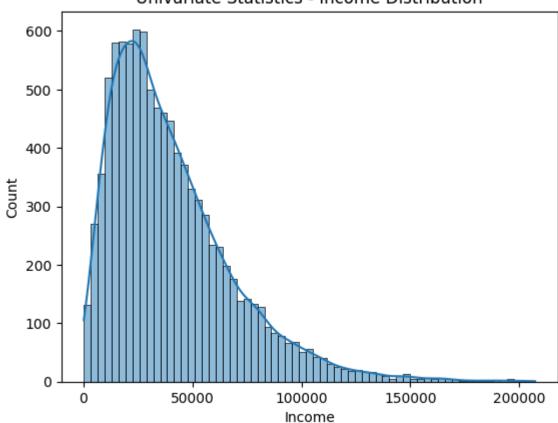
```
In [ ]: #Age - Histogram
    sns.histplot(medical_data.Age,kde=True)
    plt.title("Univariate Statistics - Age Distribution")
```

Out[]: Text(0.5, 1.0, 'Univariate Statistics - Age Distribution')

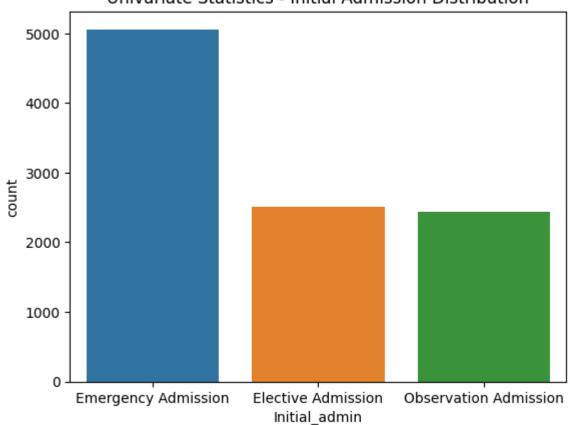


```
# Continuous variables - Income
        medical_data['Income'].describe()
        count
                   10000.000000
Out[]:
        mean
                   40490.495160
                   28521.153293
        std
        min
                     154.080000
        25%
                   19598.775000
        50%
                   33768.420000
        75%
                   54296.402500
                  207249.100000
        Name: Income, dtype: float64
In [ ]: #Income - Histogram
         sns.histplot(medical data.Income,kde=True)
         plt.title("Univariate Statistics - Income Distribution")
        Text(0.5, 1.0, 'Univariate Statistics - Income Distribution')
Out[ ]:
```

Univariate Statistics - Income Distribution

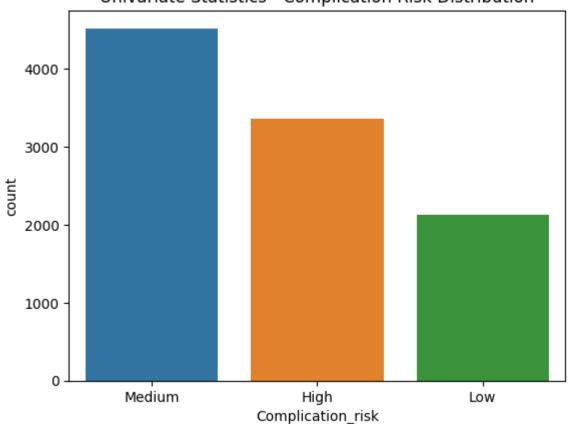


Univariate Statistics - Initial Admission Distribution



```
medical_data['Complication_risk'].describe()
In [ ]:
                    10000
        count
Out[]:
        unique
                        3
        top
                  Medium
        freq
                     4517
        Name: Complication_risk, dtype: object
        sns.countplot(data=medical data, x='Complication risk')
         plt.title("Univariate Statistics - Complication Risk Distribution")
        Text(0.5, 1.0, 'Univariate Statistics - Complication Risk Distribution')
Out[ ]:
```

Univariate Statistics - Complication Risk Distribution



Bivariate Statistics

```
In [ ]: # Bivariate Statistics
# Continuous vs Continuous - TotalCharge vs Initial_days (stats)
medical_data[['TotalCharge', 'Initial_days']].describe()
```

Out[]:		TotalCharge	Initial_days
	count	10000.000000	10000.000000
	mean	5312.172769	34.455299
	std	2180.393838	26.309341
	min	1938.312067	1.001981
	25%	3179.374015	7.896215
	50%	5213.952000	35.836244
	75%	7459.699750	61.161020
	max	9180.728000	71.981490

```
In [ ]: # Continuous vs Continuous - TotalCharge vs Initial_days (stats)
medical_data[['TotalCharge', 'Initial_days']].corr()
```

```
        TotalCharge
        Initial_days

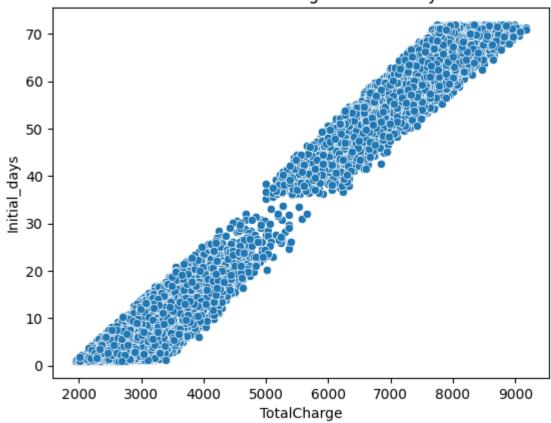
        1.00000
        0.98764

        Initial_days
        0.98764
        1.00000
```

```
In [ ]: # Continuous vs Continuous - TotalCharge vs Initial_days (plot)
    sns.scatterplot(data=medical_data, x='TotalCharge', y='Initial_days')
    plt.title("Bivariate Statistics - Total Charge vs Inital Days Distribution")
```

Out[]: Text(0.5, 1.0, 'Bivariate Statistics - Total Charge vs Inital Days Distribution')

Bivariate Statistics - Total Charge vs Inital Days Distribution

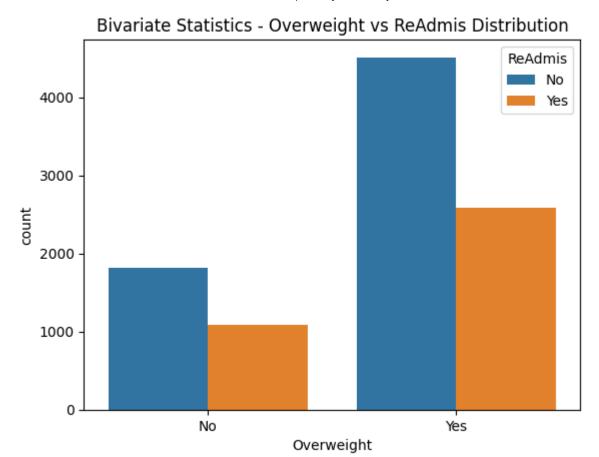


```
In [ ]: # Categorical - Bivariate Statistics (Overweight and ReAdmis - values)
pd.crosstab(medical_data.ReAdmis, medical_data.Overweight, margins=True)
```

```
Out[ ]:
         Overweight
                                     ΑII
                             Yes
            ReAdmis
                            4510
                 No
                      1821
                                   6331
                      1085
                            2584
                                   3669
                 Yes
                  ΑII
                      2906 7094
                                  10000
```

```
In [ ]: # Categorical vs Categorical - Bivariate Statistics (Overweight and ReAdmis - plot)
    sns.countplot(data=medical_data,x='Overweight', hue='ReAdmis')
    plt.title("Bivariate Statistics - Overweight vs ReAdmis Distribution")
```

Out[]: Text(0.5, 1.0, 'Bivariate Statistics - Overweight vs ReAdmis Distribution')



Analysis

The results of the Chi-square test indicate that there is no relationship between readmission and complication risk. The p value was approximately 0.99 which is significantly higher than the alpha 0.05. This means that we fail to reject the null hypothesis which was that there was no relationship between the two variables. Although our Chi-square test was unsuccessful, the bivariate analysis was successful in showing a significant correlation between the total amount charged and the initial days variable.

Recommended Course of Action

Based on the results, the focus needs to be shifted to other variables. Complication risk does not influence readmission significantly, so they need to continue looking at other variables. A comparison of readmissions and a quantitative variable like doctor visits or vitamin D levels would be beneficial. Also, I would recommend looking at all the health categorical variables like high blood pressure, for example, and see if there is a common readmission trend.