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D212 Data Mining II
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D212 Performance Assessment Task 1

1 Introduction

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1.1 Research Question

This analysis will cover a readmission dataset for a popular medical hospital. Utilizing a collection of patient characteristics, it will investigate the extent of connectivity of patient characteristics within this chain of hospitals.

This analysis will be performed by utilizing K-Means clustering. Once created, the model's accuracy will be tested by silhouette scoring.

1.2 Research Goal

The goal of this analysis is to determine key patient characteristic sets.

2 Technique Justification

2.1 Explanation of Clustering Technique

In summary, the K-Means clustering algorithm is an unsupervised clustering algorithm. This means that the algorithm analyzes the data and formulates its own conclusions based on the connections and patterns it detects.

Since the algorithm does require a predetermined number of cluster centroids, it is best practice to analyze a range of cluster centroids. This can be accomplished by comparing the models' inertia. Utilizing graphical means, locating the "elbow" in the graph can aid in determining a desirable number of cluster centroids.

Once the desirable number of cluster centroids has been determined, the readmission rates of the clusters can be compared to determine if a cluster-readmission relationship exists.

2.2 Summary of Technique Assumption

One assumption of the K-Means clustering algorithm is that all clusters are spherical (Nagar,2020).

2.3 Packages/Libraries List

Package	Justification
Numpy	Advanced mathematics
Pandas	Arrange and filter data
Seaborn	Styling of plots
Matplotlib.pyplot	Result visualization
Sklearn	Scaling and clustering implementation. Ex: StandardScaler, KMeans, Silhouette scoring

3 Data Preparation

3.1 Data Preprocessing

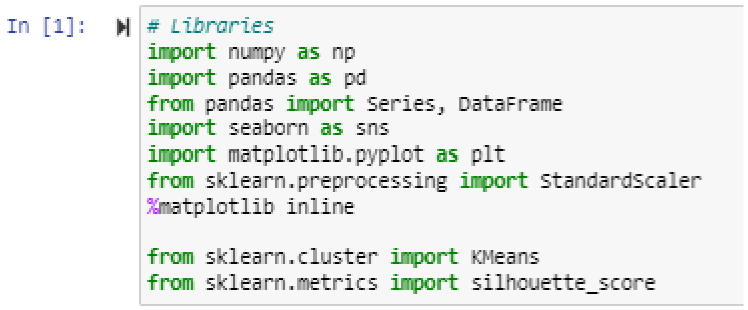
One data preprocessing goal relevant to the KMeans clustering technique is creating a dataset that only includes continuous variables. This can be done by removing categorical and less meaningful variables from the dataset. Additionally, the dataset will need to scaled so that the model will not be impacted by variables with large ranges of values

3.2 Dataset Variables

Variable	Type	Used in KMeans
Children	Continuous	Yes
Age	Continuous	Yes
Income	Continuous	Yes
VitD_levels	Continuous	Yes
Doc_visits	Continuous	Yes
Full_meals_eaten	Continuous	Yes

vitD_supp	Continuous	Yes
Initial_days	Continuous	Yes
TotalCharge	Continuous	Yes
Additional_charges	Continuous	Yes
ReAdmis	Categorical	No

3.3 Steps for Analysis



```
In [1]:  # Libraries
         import numpy as np
         import pandas as pd
         from pandas import Series, DataFrame
         import seaborn as sns
         import matplotlib.pyplot as plt
         from sklearn.preprocessing import StandardScaler
         %matplotlib inline

         from sklearn.cluster import KMeans
         from sklearn.metrics import silhouette_score
```

In [2]:

```
# Import dataset into Pandas dataframe
df = pd.read_csv('medical_clean_D212.csv')
df
```

Out[2]:

	CaseOrder	Customer_id	Interaction	UID	City	State	County	Zip	Lat	Lng	...	TotalCha
0	1	C412403	8cd49b13-f45a-4b47-a2bd-173ffa932c2f	3a83ddb66e2ae73798bdf1d705dc0932	Eva	AL	Morgan	35621	34.34960	-86.72508	...	3726.702
1	2	Z919181	d2450b70-0337-4406-bdbb-bc1037f1734c	176354c5eef714957d486009feabf195	Marianna	FL	Jackson	32446	30.84513	-85.22907	...	4193.190
2	3	F995323	a2057123-abf5-4a2c-abad-8ffe33512562	e19a0fa00aeda885b8a436757e889bc9	Sioux Falls	SD	Minnehaha	57110	43.54321	-96.63772	...	2434.234
3	4	A879973	1dec528d-eb34-4079-adce-0d7a40e82205	cd17d7b6d152cb6f23957346d11c3f07	New Richland	MN	Waseca	56072	43.89744	-93.51479	...	2127.830
4	5	C544523	5885f56b-d6da-43a3-8760-83583af94266	d2f0425877b10ed6bb381f3e2579424a	West Point	VA	King William	23181	37.59894	-76.88958	...	2113.073
...	...	...	...	...	...	...	...	...	...	...	...	
9995	9996	B863060	a25b594d-0328-486f-a9b9-0567eb0f9723	39184dc28cc038871912ccc4500049e5	Norlina	NC	Warren	27563	36.42886	-78.23716	...	6850.942
9996	9997	P712040	70711574-f7b1-4a17-b15f-48c54564b70f	3cd124ccd43147404292e883bf9ec55c	Milmay	NJ	Atlantic	8340	39.43609	-74.87302	...	7741.690
9997	9998	R778890	1d79569d-8e0f-4180-a207-d67ee4527d26	41b770aeee97a5b9e7f69c906a8119d7	Southside	TN	Montgomery	37171	36.36655	-87.29988	...	8276.481
9998	9999	E344109	f5a68e69-2a60-409b-a92f-ac0847b27db0	2bb491ef5b1beb1fed758cc6885c167a	Quinn	SD	Pennington	57775	44.10354	-102.01590	...	7644.483
9999	10000	I569847	bc482c02-f8c9-4423-99de-3db5e62a18d5	95663a202338000abdf7e09311c2a8a1	Coraopolis	PA	Allegheny	15108	40.49998	-80.19959	...	7887.553

10000 rows × 50 columns

In [3]:

```
# Review dataset
# Variables within dataset
df.columns
```

Out[3]:

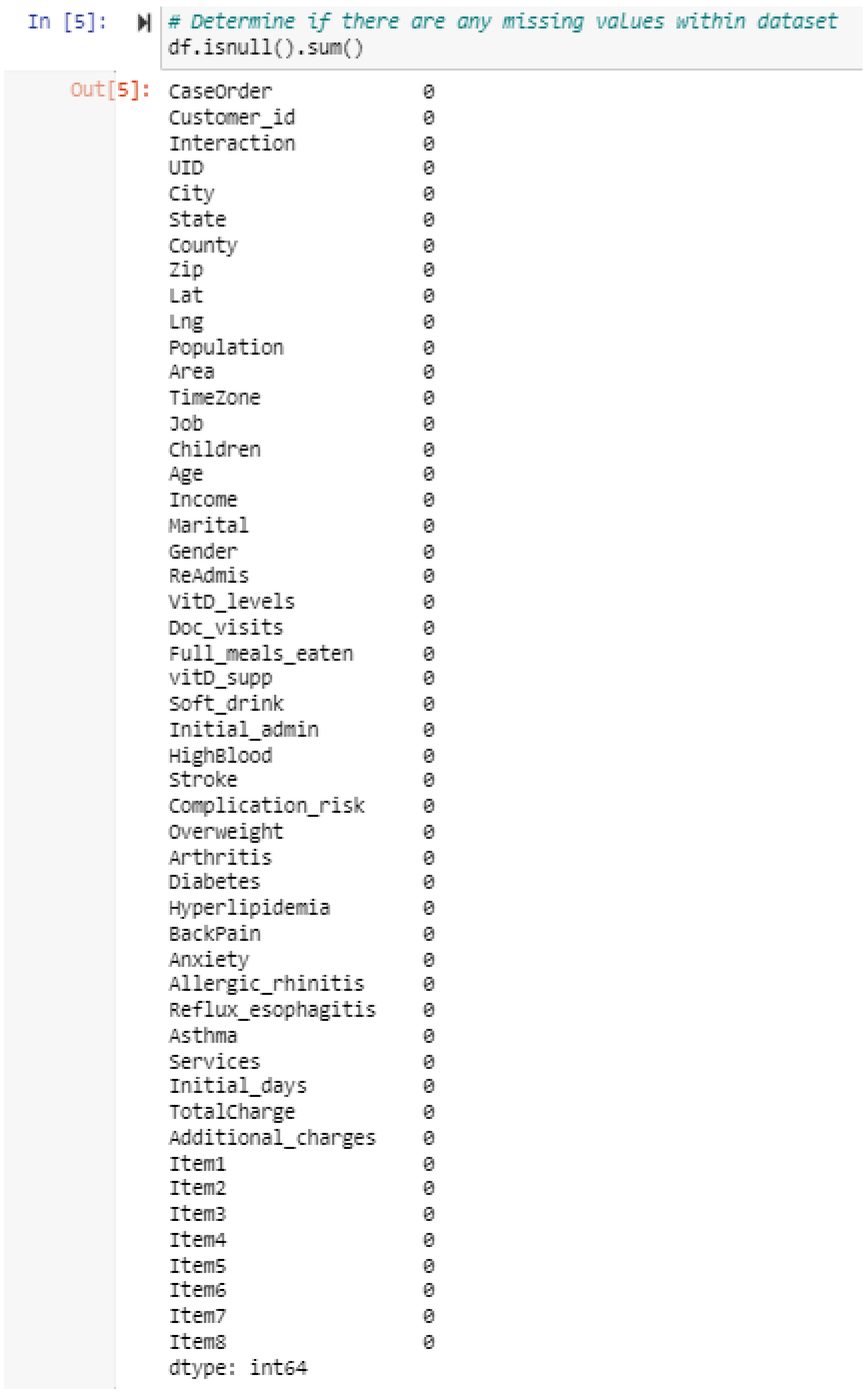
```
Index(['CaseOrder', 'Customer_id', 'Interaction', 'UID', 'City', 'State',
       'County', 'Zip', 'Lat', 'Lng', 'Population', 'Area', 'TimeZone', 'Job',
       'Children', 'Age', 'Income', 'Marital', 'Gender', 'ReAdmis',
       'VitD_levels', 'Doc_visits', 'Full_meals_eaten', 'vitD_supp',
       'Soft_drink', 'Initial_admin', 'HighBlood', 'Stroke',
       'Complication_risk', 'Overweight', 'Arthritis', 'Diabetes',
       'Hyperlipidemia', 'BackPain', 'Anxiety', 'Allergic_rhinitis',
       'Reflux_esophagitis', 'Asthma', 'Services', 'Initial_days',
       'TotalCharge', 'Additional_charges', 'Item1', 'Item2', 'Item3', 'Item4',
       'Item5', 'Item6', 'Item7', 'Item8'],
      dtype='object')
```

In [4]:

```
# Summary stats of variables
df.describe()
```

Out[4]:

	CaseOrder	Zip	Lat	Lng	Population	Children	Age	Income	VitD_levels	Doc_visits	...
count	10000.00000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	...
mean	5000.50000	50159.323900	38.751099	-91.243080	9965.253800	2.097200	53.511700	40490.495160	17.964262	5.012200	...
std	2886.89568	27469.588208	5.403085	15.205998	14824.758614	2.163659	20.638538	28521.153293	2.017231	1.045734	...
min	1.00000	610.000000	17.967190	-174.209700	0.000000	0.000000	18.000000	154.080000	9.806483	1.000000	...
25%	2500.75000	27592.000000	35.255120	-97.352982	694.750000	0.000000	36.000000	19598.775000	16.626439	4.000000	...
50%	5000.50000	50207.000000	39.419355	-88.397230	2769.000000	1.000000	53.000000	33768.420000	17.951122	5.000000	...
75%	7500.25000	72411.750000	42.044175	-80.438050	13945.000000	3.000000	71.000000	54296.402500	19.347963	6.000000	...
max	10000.00000	99929.000000	70.560990	-65.290170	122814.000000	10.000000	89.000000	207249.100000	26.394449	9.000000	...



```
In [5]:  # Determine if there are any missing values within dataset
         df.isnull().sum()
```

```
Out[5]:  CaseOrder             0
         Customer_id           0
         Interaction           0
         UID                   0
         City                  0
         State                 0
         County                0
         Zip                   0
         Lat                   0
         Lng                   0
         Population            0
         Area                  0
         TimeZone              0
         Job                   0
         Children              0
         Age                   0
         Income                0
         Marital               0
         Gender                0
         ReAdmis               0
         VitD_levels           0
         Doc_visits            0
         Full_meals_eaten      0
         vitD_supp             0
         Soft_drink            0
         Initial_admin         0
         HighBlood             0
         Stroke                0
         Complication_risk     0
         Overweight            0
         Arthritis             0
         Diabetes              0
         Hyperlipidemia        0
         BackPain              0
         Anxiety               0
         Allergic_rhinitis     0
         Reflux_esophagitis    0
         Asthma                0
         Services              0
         Initial_days          0
         TotalCharge           0
         Additional_charges    0
         Item1                 0
         Item2                 0
         Item3                 0
         Item4                 0
         Item5                 0
         Item6                 0
         Item7                 0
         Item8                 0
         dtype: int64
```

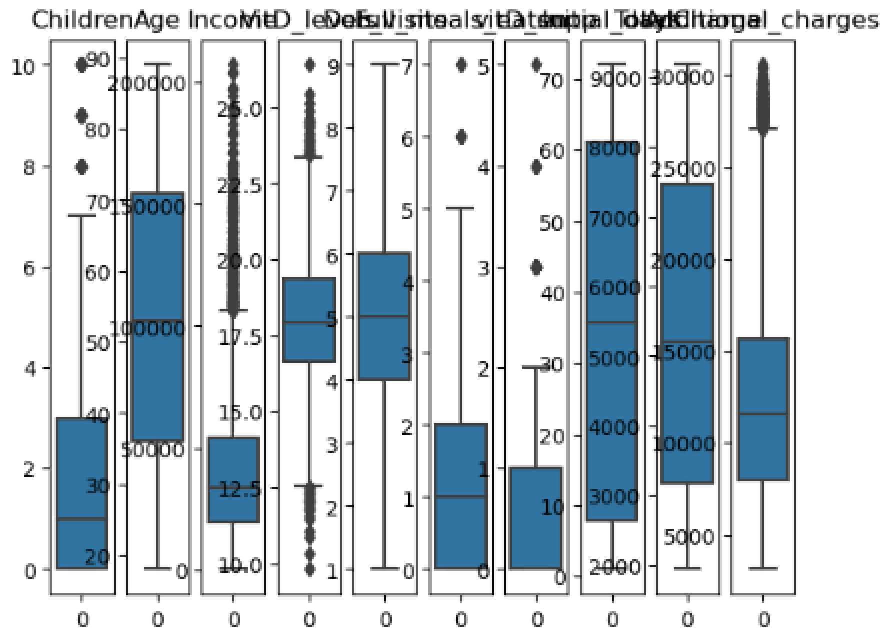
```
In [6]:  # Review variable types
         df.dtypes
```

```
Out[6]: CaseOrder               int64
        Customer_id            object
        Interaction            object
        UID                    object
        City                   object
        State                  object
        County                 object
        Zip                     int64
        Lat                   float64
        Lng                   float64
        Population              int64
        Area                   object
        TimeZone               object
        Job                    object
        Children                int64
        Age                     int64
        Income                float64
        Marital                object
        Gender                 object
        ReAdmis                object
        VitD_levels           float64
        Doc_visits              int64
        Full_meals_eaten        int64
        vitD_supp               int64
        Soft_drink             object
        Initial_admin          object
        HighBlood              object
        Stroke                 object
        Complication_risk      object
        Overweight             object
        Arthritis              object
        Diabetes               object
        Hyperlipidemia         object
        BackPain               object
        Anxiety                object
        Allergic_rhinitis      object
        Reflux_esophagitis     object
        Asthma                 object
        Services               object
        Initial_days          float64
        TotalCharge           float64
        Additional_charges    float64
        Item1                   int64
        Item2                   int64
        Item3                   int64
        Item4                   int64
        Item5                   int64
        Item6                   int64
        Item7                   int64
        Item8                   int64
        dtype: object
```

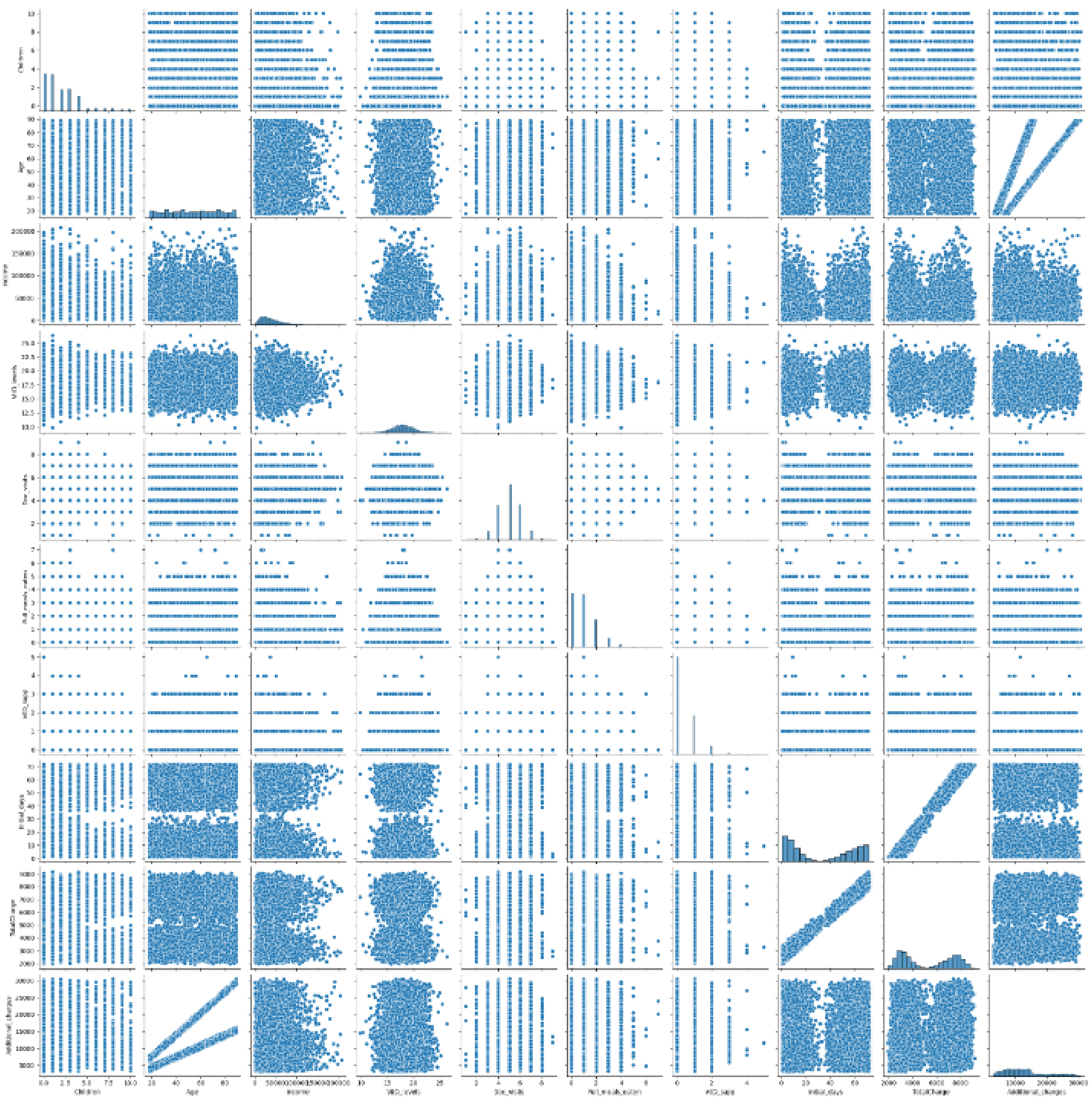
```
In [7]:  # Once you review the dataset
         # Remove less meaningful and categorical variables
         df=df.drop(columns=['CaseOrder', 'Customer_id', 'Interaction', 'UID', 'City', 'State',
                'County', 'Zip', 'Lat', 'Lng', 'Population', 'Area', 'TimeZone', 'Job', 'Marital', 'Gender',
                'Soft_drink', 'Initial_admin', 'HighBlood', 'Stroke', 'Complication_risk',
                'Overweight', 'Diabetes', 'Hyperlipidemia', 'BackPain',
                'Anxiety', 'Allergic_rhinitis', 'Reflux_esophagitis', 'Asthma',
                'Services', 'Arthritis', 'Item1', 'Item2', 'Item3', 'Item4', 'Item5',
                'Item6', 'Item7', 'Item8'])
         df.columns

Out[7]:  Index(['Children', 'Age', 'Income', 'ReAdmis', 'VitD_levels', 'Doc_visits',
                'Full_meals_eaten', 'vitD_supp', 'Initial_days', 'TotalCharge',
                'Additional_charges'],
               dtype='object')

In [8]:  # Save the ReAdmis values to compare against clustering results in final analysis
         readmis_values = df['ReAdmis']

In [9]:  # Now drop ReAdmis column so you only have continous variables
         df.drop(columns = ['ReAdmis'], inplace = True)
         df.columns

Out[9]:  Index(['Children', 'Age', 'Income', 'VitD_levels', 'Doc_visits',
                'Full_meals_eaten', 'vitD_supp', 'Initial_days', 'TotalCharge',
                'Additional_charges'],
               dtype='object')
```

```
In [10]:  # Determine any outliers or discrepancies by reviewing univariate and bivariate graphs
          # Univariate
          # Ouliers seem to be within reason
          fig, axes = plt.subplots(ncols=len(df.columns))

          # Create the boxplot with Seaborn
          for column, axis in zip(df.columns, axes):
                  sns.boxplot(data=df[column], ax=axis)
                  axis.set_title(column)

          # Show the plot
          plt.tight_layout()
          plt.show()
```

```
C:\Users\Mel Milam\AppData\Local\Temp\ipykernel_14244\3980962426.py:12: UserWarning: Tig
cannot make axes width small enough to accommodate all axes decorations
  plt.tight_layout()
```



In [11]:
```python
# Bivariate
sns.pairplot(data=df)
plt.show()
```



In [12]:
```python
# Scale dataset
ss = StandardScaler()
ss.fit(df)
ss_data_array = ss.transform(df)
ss_data = pd.DataFrame(ss_data_array, columns = df.columns)
ss_data.head()
```

Out[12]:

	Children	Age	Income	VitD_levels	Doc_visits	Full_meals_eaten	vitD_supp	Initial_days	TotalCharge	Additional_charges
0	-0.507129	-0.024795	1.615914	0.583603	0.944647	-0.993387	-0.634713	-0.907310	-0.727185	0.765005
1	0.417277	-0.121706	0.221443	0.483901	-0.967981	0.990609	0.956445	-0.734595	-0.513228	0.715114
2	0.417277	-0.024795	-0.915870	0.046227	-0.967981	-0.001389	-0.634713	-1.128292	-1.319983	0.698635
3	-0.969332	1.186592	-0.026263	-0.687811	-0.967981	-0.001389	-0.634713	-1.244503	-1.460517	0.009004
4	-0.507129	-1.526914	-1.377325	-0.260366	-0.011667	-0.993387	2.547602	-1.261991	-1.467285	-1.408991

3.4 Cleaned Dataset

In [13]:
```
# Save prepared dataset for further analysis
ss_data.to_csv('D212_Part1_Scaled_Data.csv', index = False)
readmis_values.to_csv('D212_Part1_ReAdmis_Data.csv', index = False)
```

4 Analysis

4.1 Output and Intermediate Calculations

In [14]:
```
# Open prepared dataset
df_scaled = pd.read_csv('D212_Part1_Scaled_Data.csv')
df_readmis = pd.read_csv('D212_Part1_ReAdmis_Data.csv')
```

In [15]:
```
df_scaled.head()
```

Out[15]:

	Children	Age	Income	VitD_levels	Doc_visits	Full_meals_eaten	vitD_supp	Initial_days	TotalCharge	Additional_charges
0	-0.507129	-0.024795	1.615914	0.583603	0.944647	-0.993387	-0.634713	-0.907310	-0.727185	0.765005
1	0.417277	-0.121706	0.221443	0.483901	-0.967981	0.990609	0.956445	-0.734595	-0.513228	0.715114
2	0.417277	-0.024795	-0.915870	0.046227	-0.967981	-0.001389	-0.634713	-1.128292	-1.319983	0.698635
3	-0.969332	1.186592	-0.026263	-0.687811	-0.967981	-0.001389	-0.634713	-1.244503	-1.460517	0.009004
4	-0.507129	-1.526914	-1.377325	-0.260366	-0.011667	-0.993387	2.547602	-1.261991	-1.467285	-1.408991

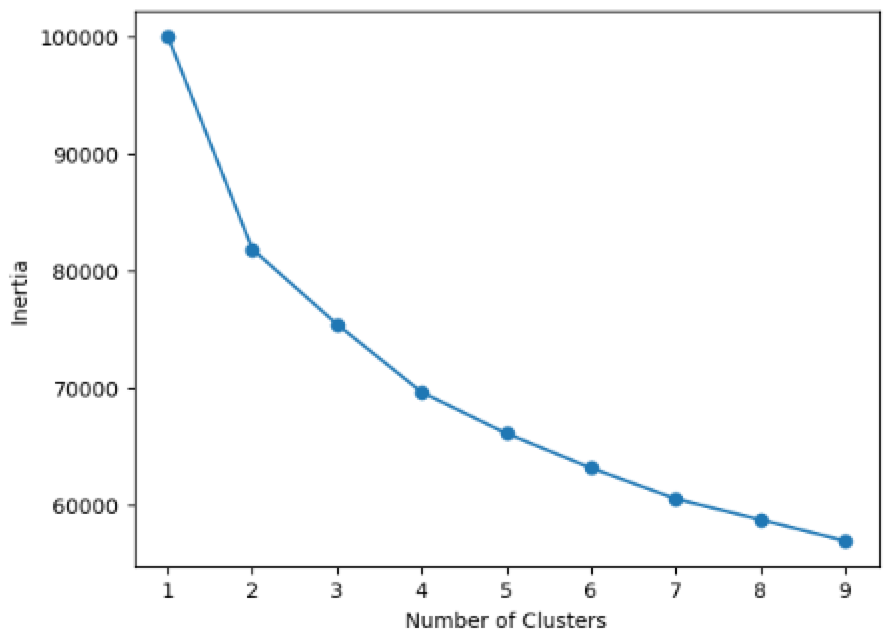
In [16]:
```
df_readmis.head()
```

Out[16]:

	ReAdmis
0	No
1	No
2	No
3	No
4	No

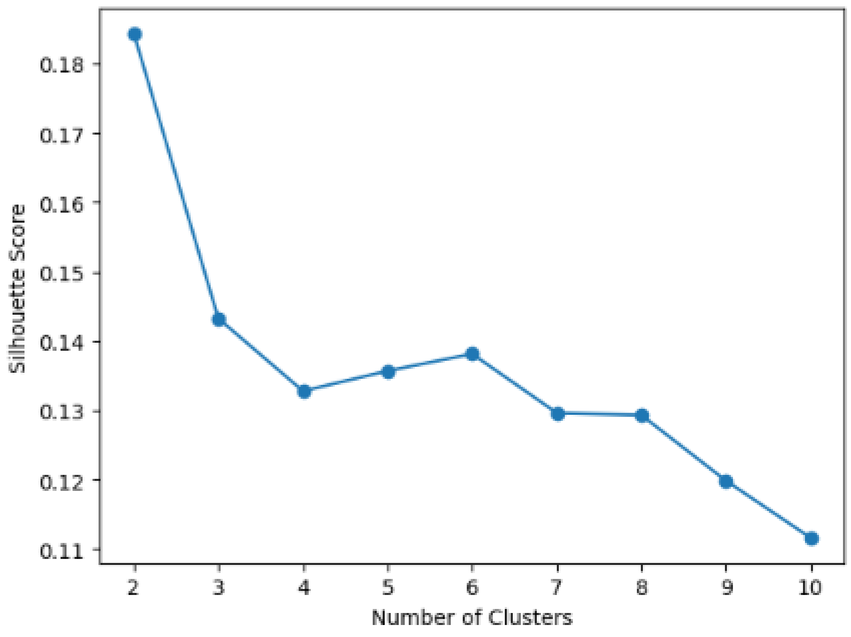
In [17]:

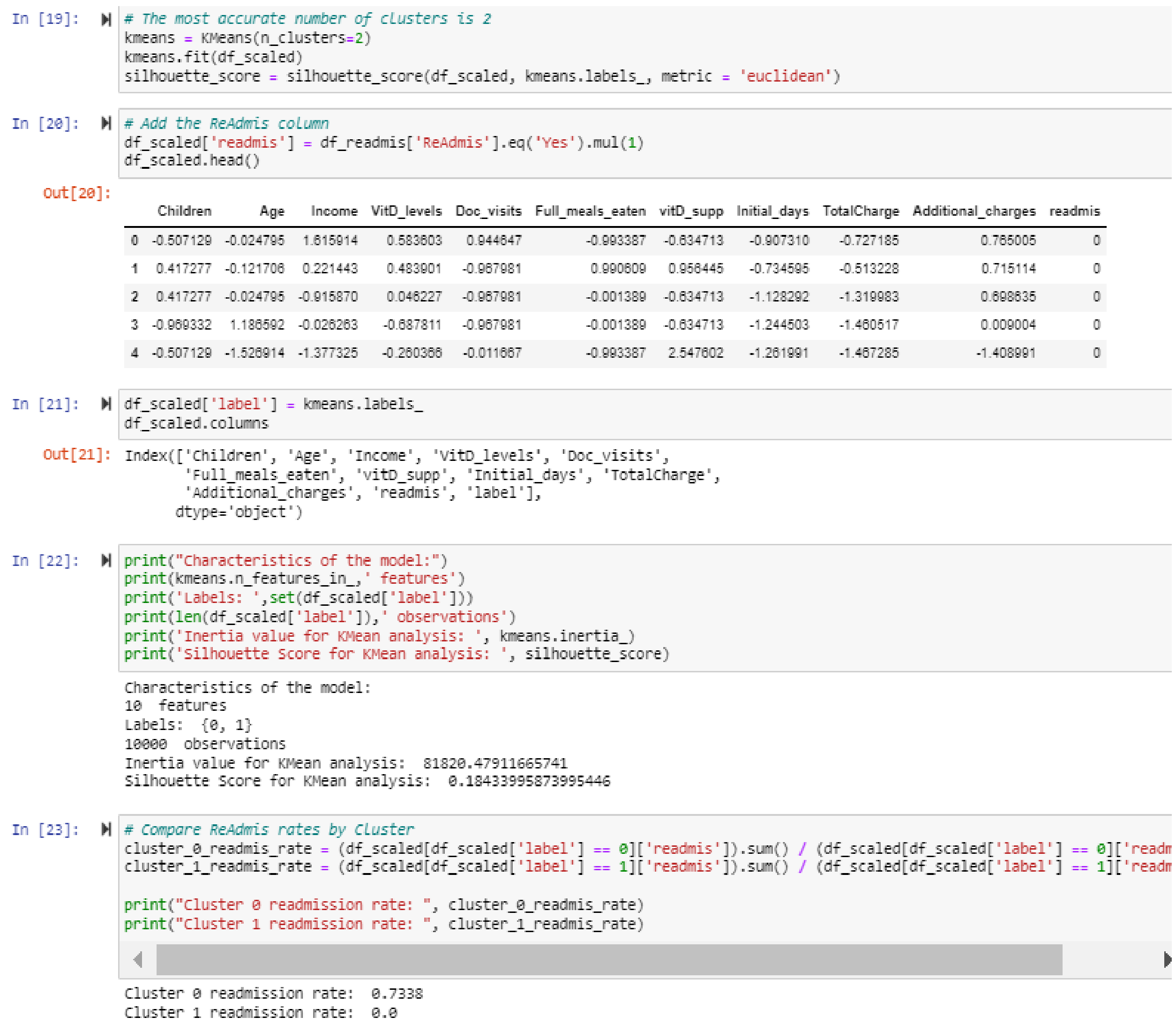
```python
# Utilize the graphical "elbow" to determine an appropriate number of clusters
ks = range(1,10)
silhouette_scores = []
inertias = []
for k in ks:
    model = KMeans(n_clusters = k)
    model.fit(df_scaled)
    inertias.append(model.inertia_)
plt.plot(ks, inertias, '-o')
plt.xlabel('Number of Clusters')
plt.ylabel('Inertia')
plt.xticks(ks)
plt.show()
```



In [18]:

```python
# Analyze Silhoutte Scores for 2+ Clusters
silhouette_scores = []
for i in range(2, 11):
    model = KMeans(n_clusters = i)
    model.fit(df_scaled)
    score = silhouette_score(df_scaled, model.labels_, metric = 'euclidean')
    silhouette_scores.append(score)
plt.plot(range(2,11), silhouette_scores, '-o')
plt.xlabel('Number of Clusters')
plt.ylabel('Silhouette Score')
plt.xticks(range(2,11))
plt.show()
```





```
In [19]:  # The most accurate number of clusters is 2
          kmeans = KMeans(n_clusters=2)
          kmeans.fit(df_scaled)
          silhouette_score = silhouette_score(df_scaled, kmeans.labels_, metric = 'euclidean')

In [20]:  # Add the ReAdmis column
          df_scaled['readmis'] = df_readmis['ReAdmis'].eq('Yes').mul(1)
          df_scaled.head()

Out[20]:
```

	Children	Age	Income	VitD_levels	Doc_visits	Full_meals_eaten	vitD_supp	Initial_days	TotalCharge	Additional_charges	readmis
0	-0.507129	-0.024795	1.615914	0.583603	0.944647	-0.993387	-0.634713	-0.907310	-0.727185	0.765005	0
1	0.417277	-0.121706	0.221443	0.483901	-0.967981	0.990609	0.956445	-0.734595	-0.513228	0.715114	0
2	0.417277	-0.024795	-0.915870	0.046227	-0.967981	-0.001389	-0.634713	-1.128292	-1.319983	0.698635	0
3	-0.969332	1.186592	-0.026263	-0.687811	-0.967981	-0.001389	-0.634713	-1.244503	-1.460517	0.009004	0
4	-0.507129	-1.526914	-1.377325	-0.260366	-0.011667	-0.993387	2.547602	-1.261991	-1.467285	-1.408991	0

```
In [21]:  df_scaled['label'] = kmeans.labels_
          df_scaled.columns

Out[21]:  Index(['Children', 'Age', 'Income', 'VitD_levels', 'Doc_visits',
                 'Full_meals_eaten', 'vitD_supp', 'Initial_days', 'TotalCharge',
                 'Additional_charges', 'readmis', 'label'],
                dtype='object')

In [22]:  print("Characteristics of the model:")
          print(kmeans.n_features_in_,' features')
          print('Labels: ',set(df_scaled['label']))
          print(len(df_scaled['label']),' observations')
          print('Inertia value for KMean analysis: ', kmeans.inertia_)
          print('Silhouette Score for KMean analysis: ', silhouette_score)

          Characteristics of the model:
          10  features
          Labels:  {0, 1}
          10000  observations
          Inertia value for KMean analysis:  81820.47911665741
          Silhouette Score for KMean analysis:  0.18433995873995446

In [23]:  # Compare ReAdmis rates by Cluster
          cluster_0_readmis_rate = (df_scaled[df_scaled['label'] == 0]['readmis']).sum() / (df_scaled[df_scaled['label'] == 0]['readm
          cluster_1_readmis_rate = (df_scaled[df_scaled['label'] == 1]['readmis']).sum() / (df_scaled[df_scaled['label'] == 1]['readm

          print("Cluster 0 readmission rate: ", cluster_0_readmis_rate)
          print("Cluster 1 readmission rate: ", cluster_1_readmis_rate)

          Cluster 0 readmission rate:  0.7338
          Cluster 1 readmission rate:  0.0
```

5 Data Summary and Implications

5.1 Accuracy of Clustering Technique

The silhouette score is a metric that measures the distinctness of a clustering technique. It's value ranges from -1 to 1. (Bhardwaj)

- 1: Means clusters are well apart from each other and clearly distinguished.
- 0: Means clusters are indifferent, or we can say that the distance between clusters is not significant.
- -1: Means clusters are assigned in the wrong way.

The accuracy of the model corresponds to a silhouette score of ~.18. This is a very low confidence of accuracy.

5.2 Results and Implications

With this specific set of variables, two clusters would be most accurate. Utilizing two primary clusters, it was found that patients in Cluster 0 were more likely to be readmitted.

Perhaps with more data points and further testing, a silhouette score closer to 1 and higher accuracy confidence can be produced. When this is achieved, the characteristics associated with high readmission can be recorded.

5.3 Limitations

A limitation of the current analysis is that k-means cannot utilize categorical variables. These other variables might be able to better cluster customers into categories.

5.4 Course of Action

A recommended course of action from the results of this analysis would be to:

1. Collect more data points
2. Test new dataset, comparing cluster sizes until high accuracy and a silhouette score close to 1 is achieved
3. Determine new clusters' readmission rates
4. Create a plan to target patients of cluster with high readmission rates to decrease readmission rates

6 Supporting Documentation

6.1 Video

This can be found within the attached file 'Panopto Recording'.

6.2 Sources

Bhardwaj, A. (2020, May 27). Silhouette coefficient&nbsp;: Validating clustering techniques. Medium. Retrieved March 13, 2023, from https://towardsdatascience.com/silhouette-coefficient-validating-clustering-techniques-e976bb81d10c

Nagar, A. (2020, January 26). K-means clustering - everything you need to know. Medium. Retrieved February 28, 2023, from https://medium.com/analytics-vidhya/k-means-clustering-everything-you-need-to-know-175dd01766d5

Western Governors University. (n.d.). D212 Data Mining II. Salt Lake City.