

CIND 820- Big Data Analytics Project

Using Machine Learning for Prediction of Early Readmission of Diabetic Patients

Supervised by: Ceni Babaoglu

Presented by: Nehal Gamal Mohamed (501278190)

```
In [1]: !pip install pandas
import sys
!pip install matplotlib
!pip install graphviz

Requirement already satisfied: pandas in /usr/local/lib/python3.10/dist-packages (2.0.3)
Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.10/dist-packages (from pandas) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas) (2023.4)
Requirement already satisfied: tzdata>=2022.1 in /usr/local/lib/python3.10/dist-packages (from pandas) (2024.1)
Requirement already satisfied: numpy>=1.21.0 in /usr/local/lib/python3.10/dist-packages (from pandas) (1.25.2)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from python-dateutil>=2.8.2->pandas) (1.16.0)
Requirement already satisfied: matplotlib in /usr/local/lib/python3.10/dist-packages (3.7.1)
Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (1.2.1)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (4.53.0)
Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (1.4.5)
Requirement already satisfied: numpy>=1.20 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (1.25.2)
Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (24.1)
Requirement already satisfied: pillow>=6.2.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (9.4.0)
Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (3.1.2)
Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.10/dist-packages (from matplotlib) (2.8.2)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from python-dateutil>=2.7->matplotlib) (1.16.0)
Requirement already satisfied: graphviz in /usr/local/lib/python3.10/dist-packages (0.20.3)
```

```
In [2]: #importing necessary Libraries
import csv
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
```

```
In [3]: #Uploading diabetic_data csv file
from google.colab import files
data = files.upload()
#Instintiating DataReader class
class DataReader:
    def read_csv(self, filename):
        df = pd.read_csv(filename)
        return df

filename = next(iter(data))
data_reader = DataReader()
df = data_reader.read_csv(filename)
#Displaying the first 10 records of the dataset
print(df.head(10))
```

No file chosen

Upload widget is only available when the cell has been executed in the current browser

session. Please rerun this cell to enable.

Saving diabetic_data (version 1).csv to diabetic_data (version 1).csv

	encounter_id	patient_nbr	race	gender	age	weight	\
0	2278392	8222157	Caucasian	Female	[0-10)	?	
1	149190	55629189	Caucasian	Female	[10-20)	?	
2	64410	86047875	AfricanAmerican	Female	[20-30)	?	
3	500364	82442376	Caucasian	Male	[30-40)	?	
4	16680	42519267	Caucasian	Male	[40-50)	?	
5	35754	82637451	Caucasian	Male	[50-60)	?	
6	55842	84259809	Caucasian	Male	[60-70)	?	
7	63768	114882984	Caucasian	Male	[70-80)	?	
8	12522	48330783	Caucasian	Female	[80-90)	?	
9	15738	63555939	Caucasian	Female	[90-100)	?	
	admission_type_id	discharge_disposition_id	admission_source_id				\
0		6	25			1	
1		1	1			7	
2		1	1			7	
3		1	1			7	
4		1	1			7	
5		2	1			2	
6		3	1			2	
7		1	1			7	
8		2	1			4	
9		3	3			4	
	time_in_hospital	...	citoglipton	insulin	glyburide-metformin	\	
0		1	...	No	No	No	
1		3	...	No	Up	No	
2		2	...	No	No	No	
3		2	...	No	Up	No	
4		1	...	No	Steady	No	
5		3	...	No	Steady	No	
6		4	...	No	Steady	No	
7		5	...	No	No	No	
8		13	...	No	Steady	No	
9		12	...	No	Steady	No	
	glipizide-metformin	glimepiride-pioglitazone	metforminrosiglitazone	\			
0	No		No		No		
1	No		No		No		
2	No		No		No		
3	No		No		No		
4	No		No		No		
5	No		No		No		
6	No		No		No		

```
7          No           No           No
8          No           No           No
9          No           No           No

metformin-pioglitazone  change diabetesMed readmitted
0          No     No     No    NO
1          No     Ch   Yes   >30
2          No     No   Yes    NO
3          No     Ch   Yes    NO
4          No     Ch   Yes    NO
5          No     No   Yes   >30
6          No     Ch   Yes    NO
7          No     No   Yes   >30
8          No     Ch   Yes    NO
9          No     Ch   Yes    NO
```

[10 rows x 50 columns]

```
In [4]: #Displaying variables data types
print("Dataset Information:")
print(df.info())
```

Dataset Information:

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 101766 entries, 0 to 101765
Data columns (total 50 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   encounter_id      101766 non-null   int64  
 1   patient_nbr       101766 non-null   int64  
 2   race              101766 non-null   object  
 3   gender             101766 non-null   object  
 4   age               101766 non-null   object  
 5   weight             101766 non-null   object  
 6   admission_type_id 101766 non-null   int64  
 7   discharge_disposition_id 101766 non-null   int64  
 8   admission_source_id 101766 non-null   int64  
 9   time_in_hospital    101766 non-null   int64  
 10  payer_code          101766 non-null   object  
 11  medical_specialty    101766 non-null   object  
 12  num_lab_procedures    101766 non-null   int64  
 13  num_procedures        101766 non-null   int64  
 14  num_medications        101766 non-null   int64  
 15  number_outpatient      101766 non-null   int64  
 16  number_emergency        101766 non-null   int64  
 17  number_inpatient        101766 non-null   int64  
 18  diag_1                101766 non-null   object  
 19  diag_2                101766 non-null   object  
 20  diag_3                101766 non-null   object  
 21  number_diagnoses       101766 non-null   int64  
 22  max_glu_serum         5346 non-null    object  
 23  A1Cresult            17018 non-null    object  
 24  metformin             101766 non-null   object  
 25  repaglinide            101766 non-null   object  
 26  nateglinide            101766 non-null   object  
 27  chlorpropamide         101766 non-null   object  
 28  glimepiride            101766 non-null   object  
 29  acetohexamide          101766 non-null   object  
 30  glipizide              101766 non-null   object  
 31  glyburide              101766 non-null   object  
 32  tolbutamide            101766 non-null   object  
 33  pioglitazone            101766 non-null   object  
 34  rosiglitazone           101766 non-null   object  
 35  acarbose                101766 non-null   object  
 36  miglitol                 101766 non-null   object  
 37  troglitazone             101766 non-null   object  
 38  tolazamide               101766 non-null   object
```

```
39 examide           101766 non-null object
40 citoglipton      101766 non-null object
41 insulin          101766 non-null object
42 glyburide-metformin 101766 non-null object
43 glipizide-metformin 101766 non-null object
44 glimepiride-pioglitazone 101766 non-null object
45 metformin-rosiglitazone 101766 non-null object
46 metformin-pioglitazone 101766 non-null object
47 change           101766 non-null object
48 diabetesMed      101766 non-null object
49 readmitted       101766 non-null object
dtypes: int64(13), object(37)
memory usage: 38.8+ MB
None
```

```
In [5]: #Defining lists for categorical variables and numeric variables
categorical_columns = [
```

```
'race',
'gender',
'age',
'weight',
'payer_code',
'medical_specialty',
'diag_1',
'diag_2',
'diag_3',
'max_glu_serum',
'A1Cresult',
'metformin',
'repaglinide',
'nateglinide',
'chlorpropamide',
'glimepiride',
'acetohexamide',
'glipizide',
'glyburide',
'tolbutamide',
'pioglitazone',
'rosiglitazone',
'acarbose',
'miglitol',
'troglitazone',
'tolazamide',
'examide',
'citoglipton',
```

```
'insulin',
'glyburide-metformin',
'glipizide-metformin',
'glimepiride-pioglitazone',
'metformin-rosiglitazone',
'metformin-pioglitazone',
'change',
'diabetesMed',
'readmitted'
]

numeric_columns = [
    'encounter_id',
    'patient_nbr',
    'admission_type_id',
    'discharge_disposition_id',
    'admission_source_id',
    'time_in_hospital',
    'num_lab_procedures',
    'num_procedures',
    'num_medications',
    'number_outpatient',
    'number_emergency',
    'number_inpatient',
    'number_diagnoses'
]
```

In [6]: #Dataset Description
print("Dataset Description:")
print(df.describe(include='all'))

Dataset Description:

	encounter_id	patient_nbr	race	gender	age	weight	\
count	1.017660e+05	1.017660e+05	101766	101766	101766	101766	
unique	NaN	NaN	6	3	10	10	
top	NaN	NaN	Caucasian	Female	[70-80)	?	
freq	NaN	NaN	76099	54708	26068	98569	
mean	1.652016e+08	5.433040e+07	NaN	NaN	NaN	NaN	
std	1.026403e+08	3.869636e+07	NaN	NaN	NaN	NaN	
min	1.252200e+04	1.350000e+02	NaN	NaN	NaN	NaN	
25%	8.496119e+07	2.341322e+07	NaN	NaN	NaN	NaN	
50%	1.523890e+08	4.550514e+07	NaN	NaN	NaN	NaN	
75%	2.302709e+08	8.754595e+07	NaN	NaN	NaN	NaN	
max	4.438672e+08	1.895026e+08	NaN	NaN	NaN	NaN	

	admission_type_id	discharge_disposition_id	admission_source_id	\
count	101766.000000	101766.000000	101766.000000	
unique	NaN	NaN	NaN	
top	NaN	NaN	NaN	
freq	NaN	NaN	NaN	
mean	2.024006	3.715642	5.754437	
std	1.445403	5.280166	4.064081	
min	1.000000	1.000000	1.000000	
25%	1.000000	1.000000	1.000000	
50%	1.000000	1.000000	7.000000	
75%	3.000000	4.000000	7.000000	
max	8.000000	28.000000	25.000000	

	time_in_hospital	...	citoglipton	insulin	glyburide-metformin	\
count	101766.000000	...	101766	101766	101766	
unique	NaN	...	1	4	4	
top	NaN	...	No	No	No	
freq	NaN	...	101766	47383	101060	
mean	4.395987	...	NaN	NaN	NaN	
std	2.985108	...	NaN	NaN	NaN	
min	1.000000	...	NaN	NaN	NaN	
25%	2.000000	...	NaN	NaN	NaN	
50%	4.000000	...	NaN	NaN	NaN	
75%	6.000000	...	NaN	NaN	NaN	
max	14.000000	...	NaN	NaN	NaN	

	glipizide-metformin	glimepiride-pioglitazone	\
count	101766	101766	
unique	2	2	
top	No	No	
freq	101753	101765	

mean	NaN	NaN			
std	NaN	NaN			
min	NaN	NaN			
25%	NaN	NaN			
50%	NaN	NaN			
75%	NaN	NaN			
max	NaN	NaN			
	metformin/rosiglitazone	metformin/pioglitazone	change	diabetesMed	\
count	101766	101766	101766	101766	
unique	2	2	2	2	
top	No	No	No	Yes	
freq	101764	101765	54755	78363	
mean	NaN	NaN	NaN	NaN	
std	NaN	NaN	NaN	NaN	
min	NaN	NaN	NaN	NaN	
25%	NaN	NaN	NaN	NaN	
50%	NaN	NaN	NaN	NaN	
75%	NaN	NaN	NaN	NaN	
max	NaN	NaN	NaN	NaN	
	readmitted				
count	101766				
unique	3				
top	NO				
freq	54864				
mean	NaN				
std	NaN				
min	NaN				
25%	NaN				
50%	NaN				
75%	NaN				
max	NaN				

[11 rows x 50 columns]

```
In [7]: #Converted blank and "?" to NaN to represent missing values
# Replace '?' and blank cells with NaN
df.replace({'?': pd.NA, '' : pd.NA}, inplace=True)

# Replaced 'None' in 'max_glu_serum' and 'A1CResult' to be seen as 'No Test' category and not as missing values
df['max_glu_serum'].replace({pd.NA: 'No Test', 'None': 'No Test'}, inplace=True)
df['A1CResult'].replace({pd.NA: 'No Test', 'None': 'No Test'}, inplace=True)
missing_values = df.isna().sum()
```

```
print("Number of missing values in each column:")
print(missing_values)
```

Number of missing values in each column:

encounter_id	0
patient_nbr	0
race	2273
gender	0
age	0
weight	98569
admission_type_id	0
discharge_disposition_id	0
admission_source_id	0
time_in_hospital	0
payer_code	40256
medical_specialty	49949
num_lab_procedures	0
num_procedures	0
num_medications	0
number_outpatient	0
number_emergency	0
number_inpatient	0
diag_1	21
diag_2	358
diag_3	1423
number_diagnoses	0
max_glu_serum	0
A1Cresult	0
metformin	0
repaglinide	0
nateglinide	0
chlorpropamide	0
glimepiride	0
acetohexamide	0
glipizide	0
glyburide	0
tolbutamide	0
pioglitazone	0
rosiglitazone	0
acarbose	0
miglitol	0
troglitazone	0
tolazamide	0
examide	0
citoglipton	0
insulin	0
glyburide-metformin	0
glipizide-metformin	0

```
glimepiride-pioglitazone      0  
metformin-rosiglitazone       0  
metformin-pioglitazone        0  
change                          0  
diabetesMed                     0  
readmitted                      0  
dtype: int64
```

```
In [8]: #Handling missing values in categorical columns by adding "Missing" as subcategory  
for col in categorical_columns:  
    df[col].fillna('Missing', inplace=True)  
print(df[categorical_columns].isnull().sum())
```

```
race          0
gender        0
age           0
weight         0
payer_code     0
medical_specialty 0
diag_1         0
diag_2         0
diag_3         0
max_glu_serum 0
A1Cresult      0
metformin      0
repaglinide    0
nateglinide    0
chlorpropamide 0
glimepiride    0
acetohexamide  0
glipizide       0
glyburide      0
tolbutamide    0
pioglitazone   0
rosiglitazone  0
acarbose       0
miglitol        0
troglitazone   0
tolazamide      0
examide        0
citoglipton    0
insulin         0
glyburide-metformin 0
glipizide-metformin 0
glimepiride-pioglitazone 0
metformin-rosiglitazone 0
metformin-pioglitazone 0
change          0
diabetesMed    0
readmitted     0
dtype: int64
```

```
In [9]: # converting numeric columns to numeric data types and categorical columns to category data type
for col in numeric_columns:
    df[col] = pd.to_numeric(df[col], errors='coerce')

for col in categorical_columns:
    if col in df.columns:
```

```
    df[col] = df[col].astype('category')
print(df.dtypes)
print(df[numeric_columns].dtypes)
```

encounter_id	int64
patient_nbr	int64
race	category
gender	category
age	category
weight	category
admission_type_id	int64
discharge_disposition_id	int64
admission_source_id	int64
time_in_hospital	int64
payer_code	category
medical_specialty	category
num_lab_procedures	int64
num_procedures	int64
num_medications	int64
number_outpatient	int64
number_emergency	int64
number_inpatient	int64
diag_1	category
diag_2	category
diag_3	category
number_diagnoses	int64
max_glu_serum	category
A1Cresult	category
metformin	category
repaglinide	category
nateglinide	category
chlorpropamide	category
glimepiride	category
acetohexamide	category
glipizide	category
glyburide	category
tolbutamide	category
pioglitazone	category
rosiglitazone	category
acarbose	category
miglitol	category
troglitazone	category
tolazamide	category
examide	category
citoglipton	category
insulin	category
glyburide-metformin	category
glipizide-metformin	category
glimepiride-pioglitazone	category

```
metformin-rosiglitazone      category
metformin-pioglitazone       category
change                        category
diabetesMed                   category
readmitted                    category
dtype: object
encounter_id                  int64
patient_nbr                   int64
admission_type_id             int64
discharge_disposition_id      int64
admission_source_id           int64
time_in_hospital              int64
num_lab_procedures             int64
num_procedures                 int64
num_medications                int64
number_outpatient               int64
number_emergency                int64
number_inpatient                 int64
number_diagnoses                int64
dtype: object
```

```
In [10]: # Check for missing values
missing_values = df.isnull().sum()
print(missing_values)
```

encounter_id	0
patient_nbr	0
race	0
gender	0
age	0
weight	0
admission_type_id	0
discharge_disposition_id	0
admission_source_id	0
time_in_hospital	0
payer_code	0
medical_specialty	0
num_lab_procedures	0
num_procedures	0
num_medications	0
number_outpatient	0
number_emergency	0
number_inpatient	0
diag_1	0
diag_2	0
diag_3	0
number_diagnoses	0
max_glu_serum	0
A1Cresult	0
metformin	0
repaglinide	0
nateglinide	0
chlorpropamide	0
glimepiride	0
acetohexamide	0
glipizide	0
glyburide	0
tolbutamide	0
pioglitazone	0
rosiglitazone	0
acarbose	0
miglitol	0
troglitazone	0
tolazamide	0
examide	0
citoglipton	0
insulin	0
glyburide-metformin	0
glipizide-metformin	0
glimepiride-pioglitazone	0

```
metformin-rosiglitazone      0
metformin-pioglitazone       0
change                        0
diabetesMed                   0
readmitted                    0
dtype: int64
```

```
In [11]: #Checking for duplicate records
duplicate_records = df.duplicated().sum()
print(f"Number of duplicate records: {duplicate_records}")
```

```
Number of duplicate records: 0
```

```
In [12]: # Here I wanted to clean the dataframe by removing irrelevant columns, columns with high missing values
df_cleaned = df.copy()
columns_to_drop = ['encounter_id', 'patient_nbr', 'weight', 'payer_code']
df_cleaned.drop(columns=columns_to_drop, inplace=True)

# Here I put a threshold of 95% for List of columns dominated by "No" category since they have very Low variance and no
columns_dominated_by_no = [
    'metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
    'glimepiride', 'acetohexamide', 'glipizide', 'glyburide',
    'tolbutamide', 'pioglitazone', 'rosiglitazone', 'acarbose',
    'troglitazone', 'tolazamide', 'examide', 'citoglipton',
    'glyburide-metformin', 'glipizide-metformin', 'glimepiride-pioglitazone',
    'metformin-rosiglitazone', 'metformin-pioglitazone'
]

threshold = 0.95
columns_to_drop_dominated = []
for col in columns_dominated_by_no:
    if df_cleaned[col].value_counts(normalize=True).get('No', 0) > threshold:
        columns_to_drop_dominated.append(col)
df_cleaned.drop(columns=columns_to_drop_dominated, inplace=True)

# Check the remaining columns
print("Remaining columns after dropping unnecessary ones:")
print(df_cleaned.columns)
print(df_cleaned.info())
```

```

Remaining columns after dropping unnecessary ones:
Index(['race', 'gender', 'age', 'admission_type_id',
       'discharge_disposition_id', 'admission_source_id', 'time_in_hospital',
       'medical_specialty', 'num_lab_procedures', 'num_procedures',
       'num_medications', 'number_outpatient', 'number_emergency',
       'number_inpatient', 'diag_1', 'diag_2', 'diag_3', 'number_diagnoses',
       'max_glu_serum', 'A1Cresult', 'metformin', 'glimepiride', 'glipizide',
       'glyburide', 'pioglitazone', 'rosiglitazone', 'miglitol', 'insulin',
       'change', 'diabetesMed', 'readmitted'],
      dtype='object')
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 101766 entries, 0 to 101765
Data columns (total 31 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   race             101766 non-null   category
 1   gender            101766 non-null   category
 2   age               101766 non-null   category
 3   admission_type_id 101766 non-null   int64  
 4   discharge_disposition_id 101766 non-null   int64  
 5   admission_source_id 101766 non-null   int64  
 6   time_in_hospital 101766 non-null   int64  
 7   medical_specialty 101766 non-null   category
 8   num_lab_procedures 101766 non-null   int64  
 9   num_procedures     101766 non-null   int64  
 10  num_medications    101766 non-null   int64  
 11  number_outpatient 101766 non-null   int64  
 12  number_emergency  101766 non-null   int64  
 13  number_inpatient  101766 non-null   int64  
 14  diag_1             101766 non-null   category
 15  diag_2             101766 non-null   category
 16  diag_3             101766 non-null   category
 17  number_diagnoses  101766 non-null   int64  
 18  max_glu_serum     101766 non-null   category
 19  A1Cresult          101766 non-null   category
 20  metformin          101766 non-null   category
 21  glimepiride        101766 non-null   category
 22  glipizide          101766 non-null   category
 23  glyburide          101766 non-null   category
 24  pioglitazone       101766 non-null   category
 25  rosiglitazone      101766 non-null   category
 26  miglitol            101766 non-null   category
 27  insulin             101766 non-null   category
 28  change              101766 non-null   category
 29  diabetesMed         101766 non-null   category

```

```
30 readmitted           101766 non-null  category
dtypes: category(20), int64(11)
memory usage: 10.9 MB
None
```

```
In [13]: # Identify and verifying remaining categorical columns for onehot coding
categorical_columns = df_cleaned.select_dtypes(include=['category']).columns.tolist()
print("Categorical columns for one-hot encoding:", categorical_columns)
```

```
Categorical columns for one-hot encoding: ['race', 'gender', 'age', 'medical_specialty', 'diag_1', 'diag_2', 'diag_3',
'max_glu_serum', 'A1Cresult', 'metformin', 'glimepiride', 'glipizide', 'glyburide', 'pioglitazone', 'rosiglitazone', 'm
iglitol', 'insulin', 'change', 'diabetesMed', 'readmitted']
```

```
In [14]: # One-hot encode the remaining categorical columns
df_onehot_coded = pd.get_dummies(df_cleaned, columns=categorical_columns, drop_first=False)
boolean_columns = df_onehot_coded.select_dtypes(include='bool').columns
df_onehot_coded[boolean_columns] = df_onehot_coded[boolean_columns].astype(int)
print(df_onehot_coded.head())
print(df_onehot_coded.columns)
```

```
admission_type_id  discharge_disposition_id  admission_source_id  \
0                  6                      25                      1
1                  1                      1                      7
2                  1                      1                      7
3                  1                      1                      7
4                  1                      1                      7

time_in_hospital  num_lab_procedures  num_procedures  num_medications  \
0                  1                      41                      0                      1
1                  3                      59                      0                     18
2                  2                      11                      5                     13
3                  2                      44                      1                     16
4                  1                      51                      0                      8

number_outpatient  number_emergency  number_inpatient  ...  insulin_No  \
0                  0                      0                      0  ...          1
1                  0                      0                      0  ...          0
2                  2                      0                      1  ...          1
3                  0                      0                      0  ...          0
4                  0                      0                      0  ...          0

insulin_Steady  insulin_Up  change_Ch  change_No  diabetesMed_No  \
0                  0                      0                      0                      1                      1
1                  0                      1                      1                      0                      0
2                  0                      0                      0                      1                      0
3                  0                      1                      1                      0                      0
4                  1                      0                      1                      0                      0

diabetesMed_Yes  readmitted_<30  readmitted_>30  readmitted_NO
0                  0                      0                      0                      1
1                  1                      0                      1                      0
2                  1                      0                      0                      1
3                  1                      0                      0                      1
4                  1                      0                      0                      1

[5 rows x 2406 columns]
Index(['admission_type_id', 'discharge_disposition_id', 'admission_source_id',
       'time_in_hospital', 'num_lab_procedures', 'num_procedures',
       'num_medications', 'number_outpatient', 'number_emergency',
       'number_inpatient',
       ...
       'insulin_No', 'insulin_Steady', 'insulin_Up', 'change_Ch', 'change_No',
       'diabetesMed_No', 'diabetesMed_Yes', 'readmitted_<30', 'readmitted_>30',
       'readmitted_NO'],
      dtype='object', length=2406)
```

```
In [15]: # To assess the normality of the numerical variables, I conducted the Shapiro-Wilk test.  
# Despite the test results indicating that none of the variables followed a normal distribution,  
# I chose to retain the outliers. The reason behind this decision was that the count of outliers  
# across the numeric variables was not substantial, and removing them could potentially reduce  
# the variance and valuable information in the dataset.  
  
from scipy.stats import shapiro  
dependent_var_columns = ['readmitted_>30', 'readmitted_NO', 'readmitted_<30']  
numerical_columns = df_onehot_coded.select_dtypes(include=[np.number]).columns  
numerical_columns = numerical_columns.drop(dependent_var_columns)  
  
# Perform the Shapiro-Wilk test  
shapiro_results = {}  
for col in numerical_columns:  
    stat, p_value = shapiro(df_onehot_coded[col])  
    shapiro_results[col] = (stat, p_value)  
shapiro_df = pd.DataFrame(shapiro_results, index=['Statistic', 'p-value']).T  
display(shapiro_df)
```

```
/usr/local/lib/python3.10/dist-packages/scipy/stats/_morestats.py:1882: UserWarning: p-value may not be accurate for N  
> 5000.  
    warnings.warn("p-value may not be accurate for N > 5000.")
```

	Statistic	p-value
admission_type_id	0.721419	0.0
discharge_disposition_id	0.568973	0.0
admission_source_id	0.737137	0.0
time_in_hospital	0.886919	0.0
num_lab_procedures	0.984858	0.0
...
insulin_Up	0.363303	0.0
change_Ch	0.634863	0.0
change_No	0.635076	0.0
diabetesMed_No	0.520568	0.0
diabetesMed_Yes	0.521023	0.0

2403 rows × 2 columns

```
In [16]: #Next step is to normalize the independent variables to insure scalability
# Function to normalize numerical columns
def normalize(x):
    return (x - x.min()) / (x.max() - x.min())
dependent_var_columns = ['readmitted_>30', 'readmitted_NO', 'readmitted_<30']
numerical_columns = df_onehot_coded.select_dtypes(include=[np.number]).columns
numerical_columns = numerical_columns.drop(dependent_var_columns)
for col in numerical_columns:
    df_onehot_coded[col] = normalize(df_onehot_coded[col])
print(df_onehot_coded.head())
```

```

admission_type_id  discharge_disposition_id  admission_source_id  \
0                 0.714286                  0.888889                0.00
1                 0.000000                  0.000000                0.25
2                 0.000000                  0.000000                0.25
3                 0.000000                  0.000000                0.25
4                 0.000000                  0.000000                0.25

time_in_hospital  num_lab_procedures  num_procedures  num_medications  \
0                 0.000000            0.305344        0.000000        0.0000
1                 0.153846            0.442748        0.000000        0.2125
2                 0.076923            0.076336        0.833333        0.1500
3                 0.076923            0.328244        0.166667        0.1875
4                 0.000000            0.381679        0.000000        0.0875

number_outpatient  number_emergency  number_inpatient  ...  insulin_No  \
0                 0.000000            0.0          0.000000  ...    1.0
1                 0.000000            0.0          0.000000  ...    0.0
2                 0.047619            0.0          0.047619  ...    1.0
3                 0.000000            0.0          0.000000  ...    0.0
4                 0.000000            0.0          0.000000  ...    0.0

insulin_Steady  insulin_Up  change_Ch  change_No  diabetesMed_No  \
0                 0.0          0.0          0.0        1.0        1.0
1                 0.0          1.0          1.0        0.0        0.0
2                 0.0          0.0          0.0        1.0        0.0
3                 0.0          1.0          1.0        0.0        0.0
4                 1.0          0.0          1.0        0.0        0.0

diabetesMed_Yes  readmitted_<30  readmitted_>30  readmitted_NO
0                 0.0          0          0          1
1                 1.0          0          1          0
2                 1.0          0          0          1
3                 1.0          0          0          1
4                 1.0          0          0          1

```

[5 rows x 2406 columns]

```
In [17]: # Checking if the numerical columns are normalized
for col in numerical_columns:
    min_val = df_onehot_coded[col].min()
    max_val = df_onehot_coded[col].max()
    print(f'{col}: min = {min_val}, max = {max_val}')
```

```
admission_type_id: min = 0.0, max = 1.0
discharge_disposition_id: min = 0.0, max = 1.0
admission_source_id: min = 0.0, max = 1.0
time_in_hospital: min = 0.0, max = 1.0
num_lab_procedures: min = 0.0, max = 1.0
num_procedures: min = 0.0, max = 1.0
num_medications: min = 0.0, max = 1.0
number_outpatient: min = 0.0, max = 1.0
number_emergency: min = 0.0, max = 1.0
number_inpatient: min = 0.0, max = 1.0
number_diagnoses: min = 0.0, max = 1.0
race_AfricanAmerican: min = 0.0, max = 1.0
race_Asian: min = 0.0, max = 1.0
race_Caucasian: min = 0.0, max = 1.0
race_Hispanic: min = 0.0, max = 1.0
race_Missing: min = 0.0, max = 1.0
race_Other: min = 0.0, max = 1.0
gender_Female: min = 0.0, max = 1.0
gender_Male: min = 0.0, max = 1.0
gender_Unknown/Invalid: min = 0.0, max = 1.0
age_[0-10): min = 0.0, max = 1.0
age_[10-20): min = 0.0, max = 1.0
age_[20-30): min = 0.0, max = 1.0
age_[30-40): min = 0.0, max = 1.0
age_[40-50): min = 0.0, max = 1.0
age_[50-60): min = 0.0, max = 1.0
age_[60-70): min = 0.0, max = 1.0
age_[70-80): min = 0.0, max = 1.0
age_[80-90): min = 0.0, max = 1.0
age_[90-100): min = 0.0, max = 1.0
medical_specialty_AllergyandImmunology: min = 0.0, max = 1.0
medical_specialty_Anesthesiology: min = 0.0, max = 1.0
medical_specialty_Anesthesiology-Pediatric: min = 0.0, max = 1.0
medical_specialty_Cardiology: min = 0.0, max = 1.0
medical_specialty_Cardiology-Pediatric: min = 0.0, max = 1.0
medical_specialty_DCPTEAM: min = 0.0, max = 1.0
medical_specialty_Dentistry: min = 0.0, max = 1.0
medical_specialty_Dermatology: min = 0.0, max = 1.0
medical_specialty_Emergency/Trauma: min = 0.0, max = 1.0
medical_specialty_Endocrinology: min = 0.0, max = 1.0
medical_specialty_Endocrinology-Metabolism: min = 0.0, max = 1.0
medical_specialty_Family/GeneralPractice: min = 0.0, max = 1.0
medical_specialty_Gastroenterology: min = 0.0, max = 1.0
medical_specialty_Gynecology: min = 0.0, max = 1.0
medical_specialty_Hematology: min = 0.0, max = 1.0
```

medical_specialty_Hematology/Oncology: min = 0.0, max = 1.0
medical_specialty_Hospitalist: min = 0.0, max = 1.0
medical_specialty_InfectiousDiseases: min = 0.0, max = 1.0
medical_specialty_InternalMedicine: min = 0.0, max = 1.0
medical_specialty_Missing: min = 0.0, max = 1.0
medical_specialty_Nephrology: min = 0.0, max = 1.0
medical_specialty_Neurology: min = 0.0, max = 1.0
medical_specialty_Neurophysiology: min = 0.0, max = 1.0
medical_specialty_Obsterics&Gynecology-GynecologicOnco: min = 0.0, max = 1.0
medical_specialty_Obstetrics: min = 0.0, max = 1.0
medical_specialty_ObstetricsandGynecology: min = 0.0, max = 1.0
medical_specialty_Oncology: min = 0.0, max = 1.0
medical_specialty_Ophthalmology: min = 0.0, max = 1.0
medical_specialty_Orthopedics: min = 0.0, max = 1.0
medical_specialty_Orthopedics-Reconstructive: min = 0.0, max = 1.0
medical_specialty_Osteopath: min = 0.0, max = 1.0
medical_specialty_Otolaryngology: min = 0.0, max = 1.0
medical_specialty_OutreachServices: min = 0.0, max = 1.0
medical_specialty_Pathology: min = 0.0, max = 1.0
medical_specialty_Pediatrics: min = 0.0, max = 1.0
medical_specialty_Pediatrics-AllergyandImmunology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-CriticalCare: min = 0.0, max = 1.0
medical_specialty_Pediatrics-EmergencyMedicine: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Endocrinology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Hematology-Oncology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-InfectiousDiseases: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Neurology: min = 0.0, max = 1.0
medical_specialty_Pediatrics-Pulmonology: min = 0.0, max = 1.0
medical_specialty_Perinatology: min = 0.0, max = 1.0
medical_specialty_PhysicalMedicineandRehabilitation: min = 0.0, max = 1.0
medical_specialty_PhysicianNotFound: min = 0.0, max = 1.0
medical_specialty_Podiatry: min = 0.0, max = 1.0
medical_specialty_Proctology: min = 0.0, max = 1.0
medical_specialty_Psychiatry: min = 0.0, max = 1.0
medical_specialty_Psychiatry-Addictive: min = 0.0, max = 1.0
medical_specialty_Psychiatry-Child/Adolescent: min = 0.0, max = 1.0
medical_specialty_Psychology: min = 0.0, max = 1.0
medical_specialty_Pulmonology: min = 0.0, max = 1.0
medical_specialty_Radiologist: min = 0.0, max = 1.0
medical_specialty_Radiology: min = 0.0, max = 1.0
medical_specialty_Resident: min = 0.0, max = 1.0
medical_specialty_Rheumatology: min = 0.0, max = 1.0
medical_specialty_Speech: min = 0.0, max = 1.0
medical_specialty_SportsMedicine: min = 0.0, max = 1.0
medical_specialty_Surgeon: min = 0.0, max = 1.0

medical_specialty_Surgery-Cardiovascular: min = 0.0, max = 1.0
medical_specialty_Surgery-Cardiovascular/Thoracic: min = 0.0, max = 1.0
medical_specialty_Surgery-Colon&Rectal: min = 0.0, max = 1.0
medical_specialty_Surgery-General: min = 0.0, max = 1.0
medical_specialty_Surgery-Maxillofacial: min = 0.0, max = 1.0
medical_specialty_Surgery-Neuro: min = 0.0, max = 1.0
medical_specialty_Surgery-Pediatric: min = 0.0, max = 1.0
medical_specialty_Surgery-Plastic: min = 0.0, max = 1.0
medical_specialty_Surgery-PlasticwithinHeadandNeck: min = 0.0, max = 1.0
medical_specialty_Surgery-Thoracic: min = 0.0, max = 1.0
medical_specialty_Surgery-Vascular: min = 0.0, max = 1.0
medical_specialty_SurgicalSpecialty: min = 0.0, max = 1.0
medical_specialty_Urology: min = 0.0, max = 1.0
diag_1_10: min = 0.0, max = 1.0
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diag_1_246: min = 0.0, max = 1.0
diag_1_250: min = 0.0, max = 1.0
diag_1_250.01: min = 0.0, max = 1.0
diag_1_250.02: min = 0.0, max = 1.0
diag_1_250.03: min = 0.0, max = 1.0
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diag_1_250.11: min = 0.0, max = 1.0
diag_1_250.12: min = 0.0, max = 1.0
diag_1_250.13: min = 0.0, max = 1.0
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diag_1_250.4: min = 0.0, max = 1.0
diag_1_250.41: min = 0.0, max = 1.0
diag_1_250.42: min = 0.0, max = 1.0
diag_1_250.43: min = 0.0, max = 1.0
diag_1_250.5: min = 0.0, max = 1.0
diag_1_250.51: min = 0.0, max = 1.0
diag_1_250.52: min = 0.0, max = 1.0
diag_1_250.53: min = 0.0, max = 1.0
diag_1_250.6: min = 0.0, max = 1.0
diag_1_250.7: min = 0.0, max = 1.0
diag_1_250.8: min = 0.0, max = 1.0

diag_1_250.81: min = 0.0, max = 1.0
diag_1_250.82: min = 0.0, max = 1.0
diag_1_250.83: min = 0.0, max = 1.0
diag_1_250.9: min = 0.0, max = 1.0
diag_1_250.91: min = 0.0, max = 1.0
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diag_1_250.93: min = 0.0, max = 1.0
diag_1_251: min = 0.0, max = 1.0
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diag_1_255: min = 0.0, max = 1.0
diag_1_261: min = 0.0, max = 1.0
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diag_1_298: min = 0.0, max = 1.0
diag_1_299: min = 0.0, max = 1.0

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diag_1_3: min = 0.0, max = 1.0
diag_1_300: min = 0.0, max = 1.0
diag_1_301: min = 0.0, max = 1.0
diag_1_303: min = 0.0, max = 1.0
diag_1_304: min = 0.0, max = 1.0
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max_glu_serum_>300: min = 0.0, max = 1.0
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max_glu_serum_Norm: min = 0.0, max = 1.0
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A1Cresult_>8: min = 0.0, max = 1.0
A1Cresult_No Test: min = 0.0, max = 1.0
A1Cresult_Norm: min = 0.0, max = 1.0
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metformin_No: min = 0.0, max = 1.0
metformin_Steady: min = 0.0, max = 1.0
metformin_Up: min = 0.0, max = 1.0
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glimepiride_No: min = 0.0, max = 1.0
glimepiride_Steady: min = 0.0, max = 1.0
glimepiride_Up: min = 0.0, max = 1.0
glipizide_Down: min = 0.0, max = 1.0
glipizide_No: min = 0.0, max = 1.0
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glipizide_Up: min = 0.0, max = 1.0
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glyburide_Up: min = 0.0, max = 1.0
pioglitazone_Down: min = 0.0, max = 1.0
pioglitazone_No: min = 0.0, max = 1.0
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pioglitazone_Steady: min = 0.0, max = 1.0
pioglitazone_Up: min = 0.0, max = 1.0
rosiglitazone_Down: min = 0.0, max = 1.0
rosiglitazone_No: min = 0.0, max = 1.0
rosiglitazone_Steady: min = 0.0, max = 1.0
rosiglitazone_Up: min = 0.0, max = 1.0
miglitol_Down: min = 0.0, max = 1.0
miglitol_No: min = 0.0, max = 1.0
miglitol_Steady: min = 0.0, max = 1.0
miglitol_Up: min = 0.0, max = 1.0
insulin_Down: min = 0.0, max = 1.0
insulin_No: min = 0.0, max = 1.0
insulin_Steady: min = 0.0, max = 1.0
insulin_Up: min = 0.0, max = 1.0
change_Ch: min = 0.0, max = 1.0
change_No: min = 0.0, max = 1.0
diabetesMed_No: min = 0.0, max = 1.0
diabetesMed_Yes: min = 0.0, max = 1.0
```

```
In [18]: # Next step is to perform unsupervised Learning through clustering
# to check any subcategories within the dataset and upon that we can take informed decisions
# First we need to drop the dependent variable 'readmitted' before clustering
# Drop the dependent variable columns (class labels)
df_clustering = df_onehot_coded.drop(columns=['readmitted_>30', 'readmitted_NO', 'readmitted_<30'])
print(df_clustering.head())
```

```

admission_type_id  discharge_disposition_id  admission_source_id  \
0                  0.714286                  0.888889                  0.00
1                  0.000000                  0.000000                  0.25
2                  0.000000                  0.000000                  0.25
3                  0.000000                  0.000000                  0.25
4                  0.000000                  0.000000                  0.25

time_in_hospital  num_lab_procedures  num_procedures  num_medications  \
0                  0.000000          0.305344          0.000000          0.0000
1                  0.153846          0.442748          0.000000          0.2125
2                  0.076923          0.076336          0.833333          0.1500
3                  0.076923          0.328244          0.166667          0.1875
4                  0.000000          0.381679          0.000000          0.0875

number_outpatient  number_emergency  number_inpatient  ...  \
0                  0.000000          0.0          0.000000  ...
1                  0.000000          0.0          0.000000  ...
2                  0.047619          0.0          0.047619  ...
3                  0.000000          0.0          0.000000  ...
4                  0.000000          0.0          0.000000  ...

miglitol_Steady  miglitol_Up  insulin_Down  insulin_No  insulin_Steady  \
0                  0.0          0.0          0.0          1.0          0.0
1                  0.0          0.0          0.0          0.0          0.0
2                  0.0          0.0          0.0          1.0          0.0
3                  0.0          0.0          0.0          0.0          0.0
4                  0.0          0.0          0.0          0.0          1.0

insulin_Up  change_Ch  change_No  diabetesMed_No  diabetesMed_Yes
0                  0.0          0.0          1.0          1.0          0.0
1                  1.0          1.0          0.0          0.0          1.0
2                  0.0          0.0          1.0          0.0          1.0
3                  1.0          1.0          0.0          0.0          1.0
4                  0.0          1.0          0.0          0.0          1.0

```

[5 rows x 2403 columns]

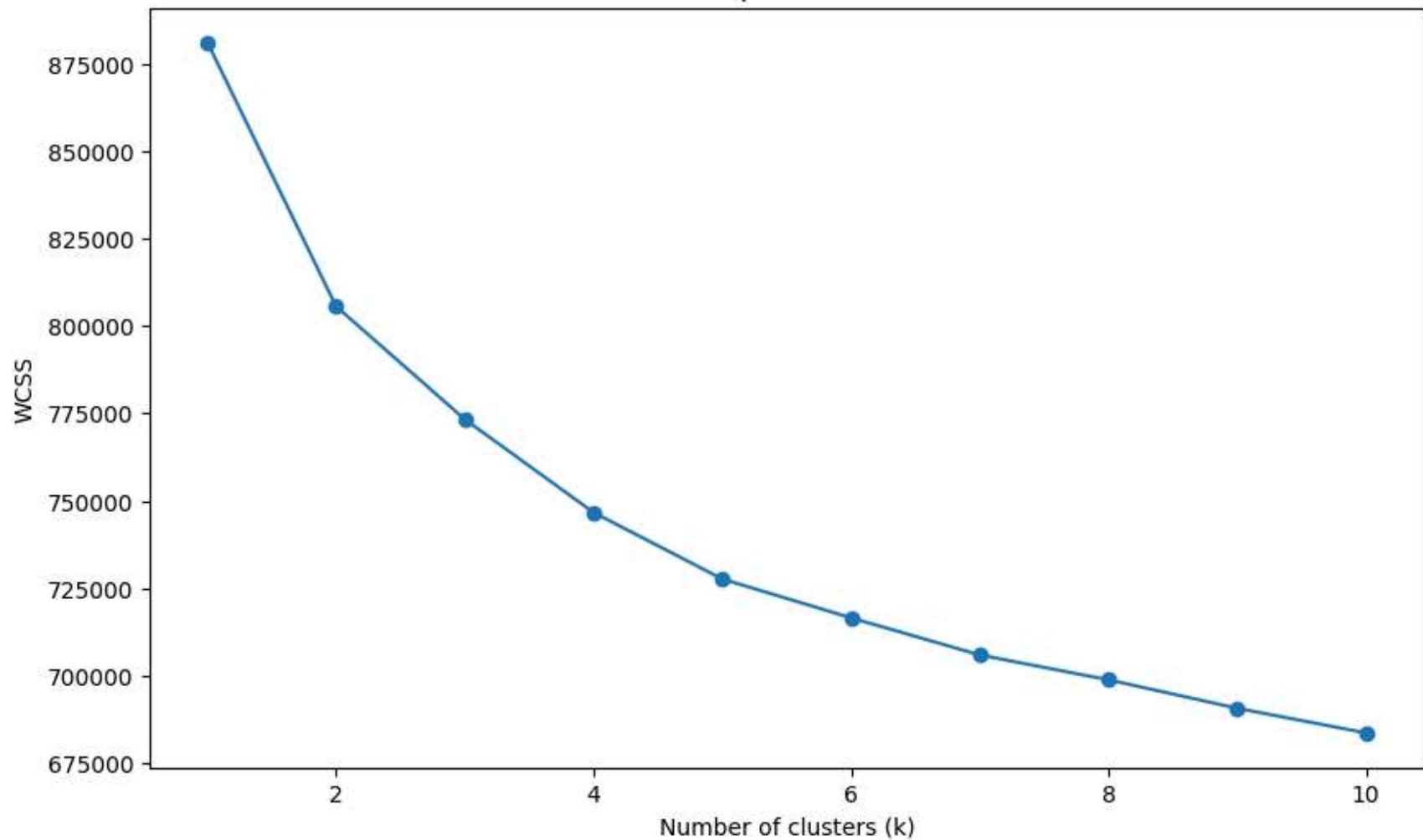
```
In [ ]: from sklearn.cluster import KMeans
import matplotlib.pyplot as plt

# Here we need to set the best number of clusters using the Elbow method
wcss = []
for k in range(1, 11):
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(df_clustering)
```

```
wcss.append(kmeans.inertia_)

# Visualizing the Elbow Method, From the visualization we can see the number of clusters (K) = 4
plt.figure(figsize=(10, 6))
plt.plot(range(1, 11), wcss, marker='o')
plt.title('Elbow Method for Optimal Number of Clusters')
plt.xlabel('Number of clusters (k)')
plt.ylabel('WCSS')
plt.show()
```

Elbow Method for Optimal Number of Clusters



```
In [ ]: !pip install kneed
```

```
Collecting kneed
  Downloading kneed-0.8.5-py3-none-any.whl (10 kB)
Requirement already satisfied: numpy>=1.14.2 in /usr/local/lib/python3.10/dist-packages (from kneed) (1.25.2)
Requirement already satisfied: scipy>=1.0.0 in /usr/local/lib/python3.10/dist-packages (from kneed) (1.11.4)
Installing collected packages: kneed
Successfully installed kneed-0.8.5
```

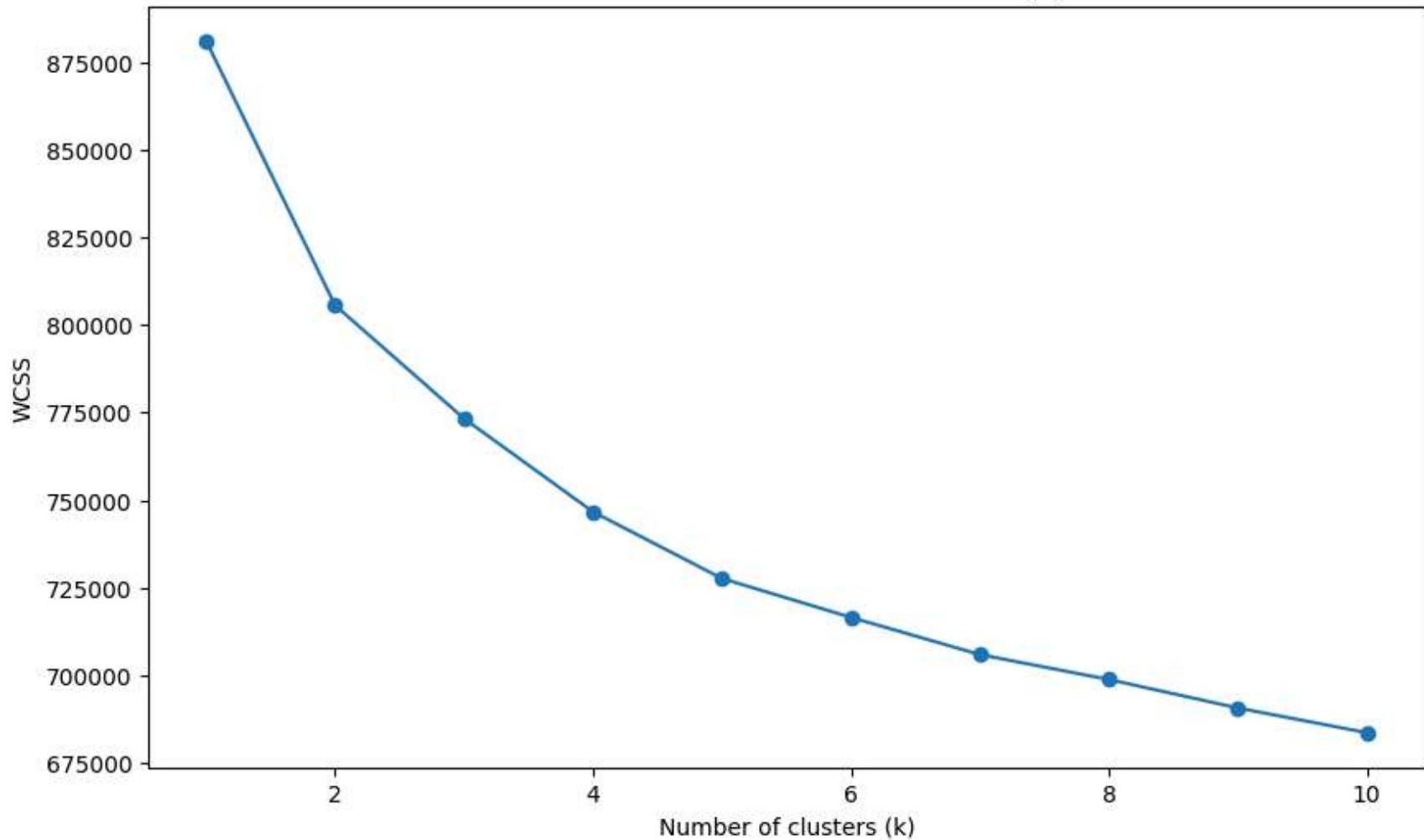
```
In [ ]: from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
```

```
from kneed import KneeLocator

# This is another way of knowing the best number of clusters using the pythong library (kneed) and the output is also 4
wcss = []
for k in range(1, 11):
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(df_clustering)
    wcss.append(kmeans.inertia_)

# Visualizing the Elbow Method, From the visualization we can see the number of clusters (K) = 4
plt.figure(figsize=(10, 6))
plt.plot(range(1, 11), wcss, marker='o')
plt.title('Elbow Method for Number of Clusters (K)')
plt.xlabel('Number of clusters (k)')
plt.ylabel('WCSS')
plt.show()
kneedle = KneeLocator(range(1, 11), wcss, curve='convex', direction='decreasing')
optimal_k = knee.knee
print(f'number of clusters is: {optimal_k}')
```


Elbow Method for Number of Clusters (K)



number of clusters is: 4

```
In [19]: # Here we will apply KMeans clustering with the number of clusters set to 4
from sklearn.cluster import KMeans
if 'Cluster' in df_clustering.columns:
    df_clustering.drop(columns=['Cluster'], inplace=True)

clusters_number = 4
kmeans = KMeans(n_clusters=clusters_number, random_state=42)
kmeans.fit(df_clustering)
df_clustering['Cluster'] = kmeans.labels_
```

```
print(df_clustering.head())
print(df_clustering.info())
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(
```

```
admission_type_id  discharge_disposition_id  admission_source_id  \
0                 0.714286                  0.888889                0.00
1                 0.000000                  0.000000                0.25
2                 0.000000                  0.000000                0.25
3                 0.000000                  0.000000                0.25
4                 0.000000                  0.000000                0.25

time_in_hospital  num_lab_procedures  num_procedures  num_medications  \
0                 0.000000            0.305344        0.000000        0.0000
1                 0.153846            0.442748        0.000000        0.2125
2                 0.076923            0.076336        0.833333        0.1500
3                 0.076923            0.328244        0.166667        0.1875
4                 0.000000            0.381679        0.000000        0.0875

number_outpatient  number_emergency  number_inpatient  ...  miglitol_Up  \
0                 0.000000            0.0          0.000000  ...      0.0
1                 0.000000            0.0          0.000000  ...      0.0
2                 0.047619            0.0          0.047619  ...      0.0
3                 0.000000            0.0          0.000000  ...      0.0
4                 0.000000            0.0          0.000000  ...      0.0

insulin_Down  insulin_No  insulin_Steady  insulin_Up  change_Ch  change_No  \
0                 0.0          1.0          0.0          0.0          0.0          1.0
1                 0.0          0.0          0.0          1.0          1.0          0.0
2                 0.0          1.0          0.0          0.0          0.0          1.0
3                 0.0          0.0          0.0          1.0          1.0          0.0
4                 0.0          0.0          1.0          0.0          1.0          0.0

diabetesMed_No  diabetesMed_Yes  Cluster
0                 1.0          0.0          2
1                 0.0          1.0          0
2                 0.0          1.0          1
3                 0.0          1.0          3
4                 0.0          1.0          3

[5 rows x 2404 columns]
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 101766 entries, 0 to 101765
Columns: 2404 entries, admission_type_id to Cluster
dtypes: float64(2403), int32(1)
memory usage: 1.8 GB
None
```

```
<ipython-input-19-e8d17b9d787e>:9: PerformanceWarning: DataFrame is highly fragmented. This is usually the result of calling `frame.insert` many times, which has poor performance. Consider joining all columns at once using pd.concat(axis=1) instead. To get a de-fragmented frame, use `newframe = frame.copy()`
  df_clustering['Cluster'] = kmeans.labels_
```

```
In [20]: print(df_clustering.columns)
print(df_clustering['Cluster'].head())
```

```
Index(['admission_type_id', 'discharge_disposition_id', 'admission_source_id',
       'time_in_hospital', 'num_lab_procedures', 'num_procedures',
       'num_medications', 'number_outpatient', 'number_emergency',
       'number_inpatient',
       ...
       'miglitol_Up', 'insulin_Down', 'insulin_No', 'insulin_Steady',
       'insulin_Up', 'change_Ch', 'change_No', 'diabetesMed_No',
       'diabetesMed_Yes', 'Cluster'],
      dtype='object', length=2404)
0    2
1    0
2    1
3    3
4    3
Name: Cluster, dtype: int32
```

```
In [21]: # Here I tried to take a look at each centroid for better understanding after clustering
df_clustering.groupby('Cluster').mean()
```

```
Out[21]:      admission_type_id  discharge_disposition_id  admission_source_id  time_in_hospital  num_lab_procedures  num_procedures  num_medicat
Cluster
  0          0.144636            0.101748           0.199480        0.293603        0.331405        0.208673        0.210200
  1          0.143768            0.096758           0.197781        0.240272        0.312588        0.218593        0.171800
  2          0.146404            0.110916           0.197637        0.234960        0.312242        0.226837        0.151500
  3          0.151591            0.093742           0.197496        0.282296        0.332048        0.242644        0.211500
```

4 rows × 2403 columns

```
In [22]: from sklearn.metrics import silhouette_score
# Calculate the silhouette score to evaluate the quality of clustering
```

```
silhouette_avg = silhouette_score(df_clustering.drop(columns=['Cluster']), df_clustering['Cluster'])
print("Silhouette Score:", silhouette_avg)
```

Silhouette Score: 0.07041419922936012