B565-Data Mining
Homework #4

Due on Thursday, March 2, 2023, 08:00 p.m.

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k-means Algorithm in Theory

This part is provided to help you implement k-means clustering algorithm.

ALGORITHM `k-means`
INPUT (data Δ, distance $d : \Delta^2 \rightarrow \mathbb{R}_{\geq 0}$, centoid number k, threshold τ)
OUTPUT (Set of centoids $\{c_1, c_2, \ldots, c_k\}$)

$\star\star\star$ $Dom(\Delta)$ denotes domain of data.

$\star\star\star$ Assume centroid is structure $c = (v \in DOM(\Delta), B \subseteq \Delta)$
$\star\star\star$ $c.v$ is the centroid value and $c.B$ is the set of nearest points.
$\star\star\star$ c^i means centroid at i^{th} iteration.

$i = 0$
$\star\star\star$ Initialize Centroids
for $j = 1, k$ **do**
    $c^i_j.v \leftarrow random(Dom(\Delta))$
    $c^i_j.B \leftarrow \emptyset$
end for

repeat
    $i \leftarrow i + 1$
    $\star\star\star$ Assign data point to *nearest* centroid
    for $\delta \in \Delta$ **do**
        $c^i_j.B \leftarrow c.B \cup \{\delta\}$, where $\min_{c^i_j}\{d(\delta, c^i_j.v)\}$
    end for
    for $j = 1, k$ **do**
        $\star\star\star$ Get size of centroid
        $n \leftarrow |c^i_j.B|$
        $\star\star\star$ Update centroid with average
        $c^i_j.v \leftarrow (1/n)\sum_{\delta \in c^i_j.B} \delta$
        $\star\star\star$ Remove data from centroid
        $c^i_j.B \leftarrow \emptyset$
    end for
    $\star\star\star$ Calculate scalar product (abuse notation and structure slightly)
    $\star\star\star$ See notes
until $((1/k)\sum_{j=1}^{k} ||c^{i-1}_j - c^i_j||) < \tau$
return $(\{c^i_1, c^i_2, \ldots, c^i_k\})$

k-means on a tiny data set.

Here are the inputs:

$$\Delta = \{(2,5), (1,5), (22,55), (42,12), (15,16)\} \quad (1)$$
$$d((x_1, y_1), (x_2, y_2)) = [(x_1 - x_2)^2 + (y_1 - y_2)^2)]^{1/2} \quad (2)$$
$$k = 2 \quad (3)$$
$$\tau = 10 \quad (4)$$

Observe that $Dom(\Delta) = \mathbb{R}^2$. We now work through k-means. We ignore the uninformative assignments. We remind the reader that T means transpose.

$i \leftarrow 0$

$\star\star\star$ Randomly assign value to first centroid.
$c_1^0.v \leftarrow random(Dom(\Delta)) = (16, 19)$
$\star\star\star$ Randomly assign value to second centroid.
$c_2^0.v \leftarrow random(Dom(\Delta)) = (2, 5)$
$i \leftarrow i + 1$
$\star\star\star$ Associate each datum with nearest centroid
$c_1^1.B = \{(22, 55), (42, 12), (15, 16)\}$
$c_2^1.B = \{(2, 5), (1, 5)\}$
$\star\star\star$ Update centroids
$c_1^1.v \leftarrow (26.3, 27.7) = (1/3)((22, 55) + (42, 12) + (15, 16))$
$c_2^1.v \leftarrow (1.5, 5) = (1/2)((2, 5) + (1, 5))$
$\star\star\star$ The convergence condition is split over the next few lines to explicitly show the calculations
$(1/k)\sum_{j=1}^{k} ||c_j^{i-1} - c_j^i|| = (1/2)(||c_1^0 - c_1^1|| + ||c_2^0 - c_2^1||) = (1/2)(||\binom{2}{5} - \binom{1.5}{5}|| + ||\binom{16}{19} - \binom{26.3}{27.7}||)$
$= (1/2)[(\binom{.5}{0}^{\mathsf{T}}\binom{.5}{0})^{(1/2)} + (\binom{-9.7}{-8.7}^{\mathsf{T}}\binom{-9.7}{-8.7})^{(1/2)})] = (1/2)(\sqrt{.5} + \sqrt{169.7}) \sim (1/2)(13.7) = 6.9$
Since the threshold is met $(6.9 < 10)$, k-means stops, returning $\{(26.3, 27.7), (1.5, 5)\}$

Problem 1

For this problem we are going to use a diabetes data set collected from many US hospitals on the purpose of analyzing the factors causing readmission of diabetic patients. You can download the data from here [link]. The web-page comes with a downloadable link along with the description of the data.
Answer the following questions [**20 points**]:

1. Briefly describe this data set–what is its purpose? How should it be used? What are the kinds of data it's using?

Discussion of data

Answer here. . .

- The Diabetes Dataset of 130 US Hospitals is a dataset repository of medical records documenting hospitalizations of diabetic patients across 130 hospitals in the United States between 1999 and 2008.
- With over 100,000 records, the dataset comprises 50 variables that capture a range of patient demographics, medical history, medications, and clinical measurements.
- The Dataset also contains various drugs administered to the patients
- The dataset's primary objective is to examine the factors that contribute to readmission of diabetic patients.
- Readmitted is a class variable having values (NO,¿30,¡30) which indicates the number of days after discharge a patient is readmitted
- **Use of Dataset**
  The dataset is widely used in research on diabetes and healthcare outcomes, and has contributed to a better understanding of the factors that influence diabetes management and outcomes in the United States
- Based on specific requirement we can apply numerous Data Mining tasks such as classification based on target variables, Perform Clustering to group the patients and help the doctors prioritize.

2. Using *R/Python*, show code that answers the following questions:

   (a) How many entries are in the data set?

R/Python script

```
# Sample R Script With Highlighting
```

```python
# Sample Python Script With Highlighting
import pandas as pd
import swifter
df= pd.read_csv('diabetic_data.csv')
df.shape
(101766, 50)
#The number of rows are 101766 and number of columns are 50
```

- **The number of rows are 101766 and number of columns are 50**

   (b) How many unknown or missing data are in the data set?

Problem 1 continued on next page. . .

R/Python script

```
# Sample R Script With Highlighting
```

```
# Sample Python Script With Highlighting
df1=pd.DataFrame(df.isna().sum())
df1=df1.reset_index()
df1.columns=['Column_Names','Count_of_Nan_Values']
df2=df1[df1['Count_of_Nan_Values']!=0].
sort_values(by=['Count_of_Nan_Values'],ascending=False)
df2['Percentage_of_NAN']=df2['Count_of_Nan_Values']/len(df)*100
print('The Nan Value columns with percentage are as follows')
print(df2)
#Initially there are no Null values however
when we replace #Question mark with Nan we
get to see Null values
#Checking Null Values
import numpy as np
df.replace({'?':np.nan},inplace=True)
df1=pd.DataFrame(df.isna().sum())
df1=df1.reset_index()
df1.columns=['Column_Names','Count_of_Nan_Values']
df2=df1[df1['Count_of_Nan_Values']!=0]
.sort_values(by=['Count_of_Nan_Values'],ascending=False)
df2['Percentage_of_NAN']=df2['Count_of_Nan_Values']/len(df)*100
print('The Nan Value columns with percentage are as follows')
print(df2)
#Output
The Nan Value columns with percentage are as follows
         Column_Names  Count_of_Nan_Values  Percentage_of_NAN
5              weight                98569          96.858479
11  medical_specialty                49949          49.082208
10         payer_code                40256          39.557416
2                race                 2273           2.233555
20             diag_3                 1423           1.398306
19             diag_2                  358           0.351787
18             diag_1                   21           0.020636
```

Thus we can see after applying transformation of replacing '?' with NAN we get columns [Weight,MedicalSpeciality,Payercode,Race,Diag3,Diag2,Diag1] as Null
The Percentage and values of Null is shown in the output above

(c) Create histograms for attributes {`age`, `num_lab_procedures`, `num_medications`}. Label the plots properly. Discuss the distribution of values *e.g.*, are uniform, skewed, normal. Place images of these histograms into the document. Show the Python or R code that you used below and discussion below that.

R/Python script

```
# Sample R Script With Highlighting
```

```
# Sample Python Script With Highlighting
```

```
import matplotlib.pyplot as plt
import seaborn as sns
#Dropping columns with more than 40 percent null values
df.drop(['weight','payer_code','medical_specialty'],
axis=1,inplace=True)
#Changing the readmitted column
df['readmitted'] = df['readmitted'].replace({'>30':1,'<30':1,'NO':0})
#Replacing Age with mean
df['age'] = df['age'].replace({'[70-80)': 75,
'[60-70)': 65, '[50-60)': 55, '[80-90)': 85,
'[40-50)': 45, '[30-40)': 35, '[90-100)': 95,
'[20-30)': 25, '[10-20)': 15, '[0-10)': 5})
sns.histplot(df['age'],kde=True,bins=10)
plt.title('Histogram with KDE of Age vs Frequency')
plt.xticks(rotation=90);
#Checking the distribution
from scipy.stats import shapiro
#The Shapiro-Wilk test (often referred to as the Shapiro test)
#is a statistical test used to assess
whether a set of data follows a normal distribution
stat,p = shapiro(df['age'])
alpha = 0.05
#Checking the signiface value
if p > alpha:
    #The Null hypothesis is a distribution sample is Normally distributed
    print('Sample seems Gaussian (fail to reject H0)')
    #The Alternate hypothesis is a distribution is not normally distributed
else:
    print('Sample does not seems Gaussian (reject H0)')
#Sample does not seems Gaussian (reject H0)

#Checking Skewness test
from scipy.stats import skewtest
#The skewtest is a statistical test that is used to assess
#whether a set of data is symmetric or skewed.
#The test is based on the comparison of the observed skewness
#of data to the expected skewness under the assumption of normality.
statistic, p_value = skewtest(df['age'])
alpha = 0.05
#Checking the significance value
if p_value > alpha:
    #Null hypothesis is data is not skewed
   print('Sample is symmetric (fail to reject H0)')
    #Alternate hypothesis is data is skewed
else:
   print('Sample is skewed (reject H0)')
#Sample is skewed (reject H0)

#Plotting  histogram of Number of lab procedures

sns.histplot(df['num_lab_procedures'],kde=True);
plt.title('Number_of_lab_procedures Histogram')
plt.show()
```

```python

#Plotting Number of Medications
sns.histplot(df['num_medications'],kde=True)
plt.title('Number of medications histogram')
plt.show()
import numpy as np
import scipy.stats as stats
skewness = stats.skew(df['num_medications'])
#Check the Skwewness
print("Skewness:", skewness)
#Conditions with skewness and visual inspection
if skewness > 0:
    print("The distribution is normal distribution with right-tailed.")
else:
    print("The distribution is not right-tailed.")
Skewness: 1.3266525795561763
The distribution is normal distribution with right-tailed.
```

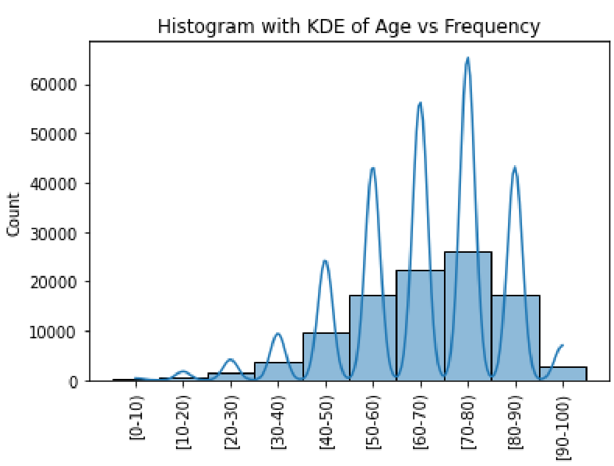
Discussion of Findings

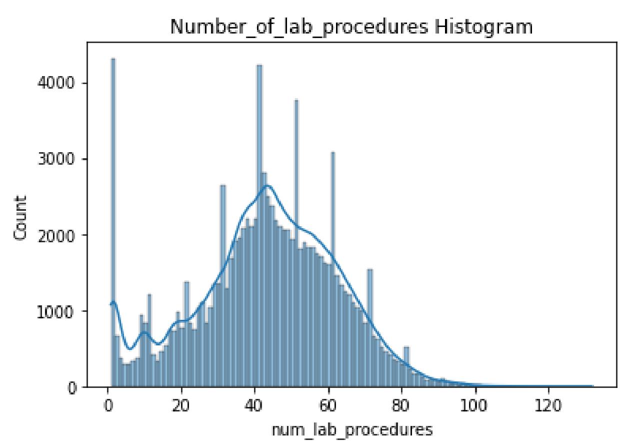
Answer here...

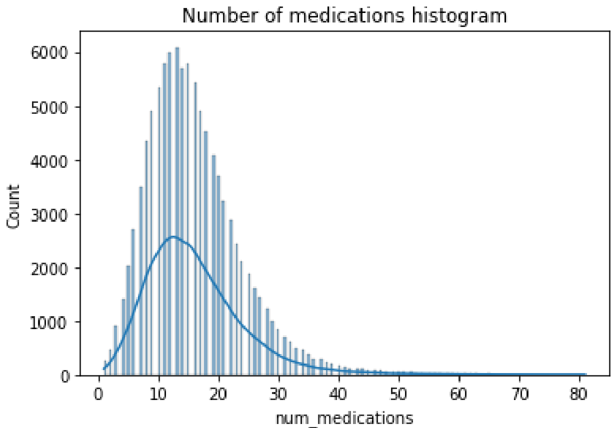
- After plotting various graphs we can either check their distribution visually or by checking statistics test:
- Shapiro Wilk test is used to check Normality
- Skewtest is used for checking if data is skewed or Symmetric
- Chi Square test is to check Poisson Distribution

- **Age is a skewed distribution**
- **Number of Lab pocedures is a skewed distribution and is bimodal**
- **Number of Medications is a normal distribution with right tail since the skewness value is positive**

Plots







3. Make a scatter plots of [time_in_hospital, num_medications] and [num_medications, num_lab_procedures] variables and color the data points with the class variable [readmitted]. Discuss the plots, i.e., do you observe any relationships between variables? Show the Python or R code that you used below and discussion below that.

R/Python script

```
# Sample R Script With Highlighting
```

```
# Sample Python Script With Highlighting
sns.scatterplot(data=df, y='num_medications', x='time_in_hospital',
hue='readmitted');
plt.title('Scatterplot of Num_Medications and Time_In_Hospital')
plt.show()
sns.scatterplot(data=df, x='num_medications', y='num_lab_procedures',
hue='readmitted')
plt.title('Scatterplot of num_lab_procedures and num_medications')
plt.show()
df.corr()[['num_lab_procedures','num_medications']].
loc[['time_in_hospital','num_lab_procedures']]
     num_lab_procedures  num_medications
time_in_hospital    0.31845   0.466135
num_lab_procedures  1.00000   0.268161
```

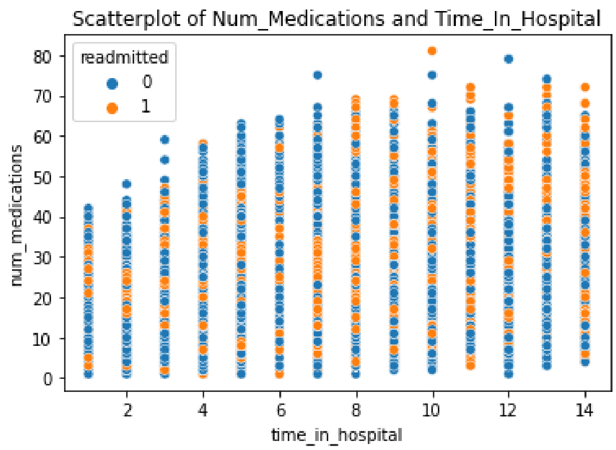
Discussion of Findings

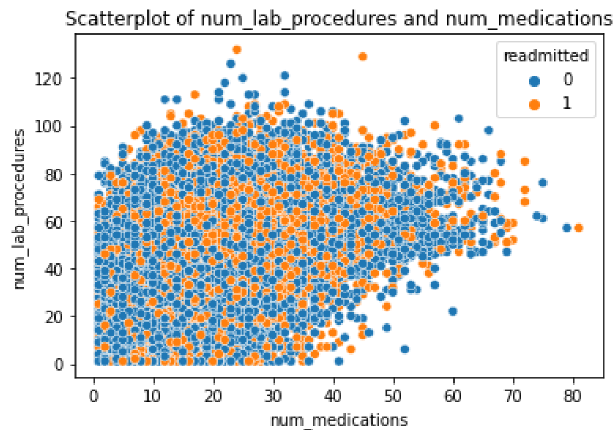
Answer here...

- **For Graph 1**
- In the first scatter plot, we can observe that there is a statistically positive relationship between time in hospital and num medications.
- The correlation between number of medications is **0.466**
- This indicates the more a patient stays in hospital more a patient has to take medicines.
- Additionally ,we can see that the readmitted variable does not seem to have a strong relationship with either variable.

- **For Graph 2**
- In the second scatter plot, we can observe that there is a weak positive relationship between num of medications and num of lab procedures.
- The correlation between Num of medications and number of lab procedures is **0.2681**
- We can see that the readmitted variable does not seem to have a strong relationship with either variable.

Plots





Problem 2

The pseudo-code for k-means and a running example of k-means on a small data set are provided above. Answer the following questions [**10 points**]:

2.1 Does k-means always converge? Given your answer, a bound on the iterate must be included. How is its value determined?

- From the above mentioned Algorithm, We can conclude that K means doesnt always converge to a global optimal solution,However given the covergence criteria K means is supposed to converge at a local minimum.
- K means may not converge due to the following reasons:
- **Initialization of centroids**: Since k means is a greedy algorithm it is extremely sensitive to the Initial Centroid selection.
  If the centroids are not selected properly, K means may converge to suboptimal solution
- **Number of CLusters**: Although there are numerous methods to decide the number of clusters by elbow method,Dunn Index, Silheoutte Analysis,There is a possibility if number of clusters is set too high or too low, K means will comverge to a sub optimal solution
- **Outliers**: If the dataset contains outliers, K means will not converge as expected
- **Non Spherical Clusters**: The main assumption in K means is the Spherical nature of clusters with similar variaces, However K means will not converge optimally if the clusters are non spherical

- **Local Convergence** However, K means will, always converge to a local optimum as K means can be seen as an optimization problem and we can reduce the Sum of Squared errors within the clusters. Thus as any minima finding solution K means can guarantee a local optimum

Bound on Iterate

- **Convergence Criteria** The above algorithm assumes a threshold value Tou which is the difference in magnitude of Old centroid Vector and New Centroids Vector.
- However we can also include a bound on iterate to avoid Infinite Loops, As in some cases there can be a situation the convergence criteria is never met and K means algorithm runs indefinitely
- By setting a bound on iterate we can also reduce the computational cost and have a trade off between accuracy and Computational Cost.

Value of Bound on Iterate

- The above mentioned algorithm converges on Tou,and the value of Tou must be decided by looking at the clustering variables.
- By applying Domain Knowledge we can achieve a substantial value of Tou
- However, Since it is a greedy algorithm and the search space is infinite we have to do trial and error method and select the best Tou for Clusters.
- For the number of iterations we can plot a graph of convergence vs the number of iterations it takes to converge.
- This would give a fair idea on selecting the number of iterations,However due to the random nature of Cluster Initialization ,We can perform a trial and error method and start increasing the number of iterations starting from a low value.
- However for a huge dataset, We can set a bound roughly proportional to the computational cost.

2.2 What is the run-time of this algorithm?

- The run time algorithm depends on number of factor such as initialization of centroids,number of clusters,The initialization method and convergence criterion.
- However the generalized run time depends on **O(K*N*D)** where K is the Number of Clusters,N is the Number of datapoints and D is the dimensionality of data.
- With i number of iterations the run time becomes **O(I*K*N*D)**

Problem 3

Implement Lloyd's algorithm for k-means (see algorithm k-means above) in *R* or *Python* and call this program C_k. As you present your code explain your protocol for [**20 points**]

1. initializing centroids
2. maintaining k centroids
3. deciding ties
4. stopping criteria

R/Python Code

subsectionR/Python script

```
# Sample R Script With Highlighting
```

```
# Sample Python Script With Highlighting

import numpy as np
import swifter
from scipy.spatial.distance import euclidean


def get_random_centroids(input_dataframe,no_of_clusters):
    '''
    The function takes a dataframe as an input and creates a
    random K centroids from uniform distribution
    '''
    #Initialize random centroids from dataset
    list_of_centroids = []

    for cluster in range(no_of_clusters):
        #Generates a centroids randomly from uniform distribution
        random_centroid = input_dataframe.swifter.apply(lambda x:float(x.sample()))
        #From the given dataset it randomly selects centroids
        list_of_centroids.append(random_centroid)

    centroid_df=pd.concat(list_of_centroids,axis=1)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'
    '''
    The function returns a dataframe consisting of no of clusters required
    '''
    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''
    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster
    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the dataset
    #and it randomly assigns if euclideab distance results in a tie
    '''
    This function returns the index of minimum distances as a dataframe
    '''
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled
```

```
    and the original dataframe
    '''
    df_original_label_join=input_dataframe.join(df_clustered_lab
    el)
    #This is a dataframe that consists of datapoints as well as
    the cluster assigned
    df_original_label_join.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column and
    take its mean
    new_centroids=df_original_label_join.groupby('Cluster_Assigned').mean()
    #Here transpose is taken to maintain consistency between
    original random centroids and
    return new_centroids.T
def
kmeans_llyod(input_dataframe,no_of_clusters,threshold,no_of_iter
ations):
    '''
    This function takes original dataframe,number of
    clusters,threshold as input.
    '''
    iteration=0
    #Step 1 of k means is to get random _Centroids

    initial_centroid=get_random_centroids(input_dataframe,no_of_
    clusters)
    #Randomly generated centroids would be stored on centroids
    #Storing the column list to handle K ties

    initial_centroid_column_list=initial_centroid.columns.to_list()

    while True:
        '''
        The while loop runs until convergence condition is met
        '''
        df_cluster_label=get_labels(input_dataframe,initial_centroid)
        df_new_centroids=get_new_centroids(df_cluster_label,input_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
        new_list_of_columns=df_new_centroids.columns.to_list()
        #Keeping the number of clusters same
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
            df_new_centroids[col]=initial_centroid[col]

        from scipy.spatial.distance import euclidean
        scalar_product =
        [euclidean(initial_centroid[col],df_new_centroids[col])
        for col in initial_centroid.columns]
        threshold_calculated=float(sum(scalar_product))/no_of_cl
```

```
        usters

        iteration+=1

        if threshold_calculated<threshold:
            print("The input Threshold was
            {}".format(threshold))
            print("The calculated threshold is
            {}".format(threshold_calculated))

        if iteration>no_of_iterations:
            print("Limit for iterations has exceeded")

        if threshold_calculated<threshold or iteration>no_of_iterations:
            return df_new_centroids
            break
        else:
            initial_centroid= df_new_centroids
```

Discussion of Initialization of Centroids

- From the above algorithm there are two ways to initialize the centrois
- **Randomly from Domain**:Here we select datapoints randomly from the domain of datapoints,Thus from the entire datasets based on number of clusters we get random clusters.
- **Randomly from Space**: Here we select datapoints based on the shape of dataset from space and the points may or may not be a record in the dataset
- **My Approach:I have initialized the centroids randomly from the domain of dataset**
- However the cluster initialization is the most important step and we can do smarter initialization like K means ++ initializations.

Discussion of Maintaining k Centroids

- Maintaining K centroids, my code checks for clusters and when a cluster is empty I have assigned a previous value of centroid to the cluster, Thus at the worst case even when the data is extremely skewed and has outliers, A cluster with one datapoint is maintained
- Key Takeaway: A cluster becoming empty is a indication of incorrect value of K and presence of an outlier, So we can merge the cluster or eliminate the outlier or run K means with a different value of K

Discussion of Deciding Ties

- In k means there is a possibility that a datapoint can have the same distance metric from two or more cluster centres.
- There are multiple ways to handle this.
- **Random** Let the algorithm randomly decide which cluster the datapoint gets assigned to if there are ties

- **Balancing the Classes** Another approach can be when there are ties get the label count of the clusters and assign the cluster to the class which has the lowest datapoints this would balance the classes and the datapoints.
- **My Approach** I have used idxmin which assigns the label to my dataset and hence it randomly assigns the first minimum it gets.

Discussion of Stopping Criteria

- The stopping criteria is maintained by an input parameter Tou which indicates a threshold and in layman's terms it is the distance from the old cluster centroid and the new cluster centroid divided by the number of clusters and when the value gets below a threshold it mimics a condition where **Cluster Centres are not changing**
- The other criteria is the bound on number of iterations, if the algorithm does not converge based on the value of tou I have set a limit on the number of iterations to avoid Infinite loops

Problem 4

In this question, you are asked to run your program, C_k, against the Diabetes data set from Problem 1 and New York Times Comments data set [link](use the file `nyt-comments-2020.csv` as your data set). Upon stopping, you will calculate the quality of the centroids and of the partition. For each centroid c_i, form two counts:

$$\begin{aligned} y_i &\leftarrow \sum_{\delta \in c_i.B} [\delta.C = \text{“y”}], \quad \text{readmitted/selected} \\ n_i &\leftarrow \sum_{\delta \in c_i.B} [\delta.C == \text{“n”}], \quad \text{not readmitted/selected} \end{aligned}$$

where $[x = y]$ returns 1 if True, 0 otherwise. For example, $[2 = 3] + [0 = 0] + [34 = 34] = 2$
The centroid c_i is classified as readmitted/selected if $y_i > n_i$ and not readmitted/selected otherwise. We can now calculate a simple error rate. Assume c_i is good. Then the error is:

$$error(c_i) = \frac{n_i}{n_i + y_i}$$

We can find the total error rate easily:

$$Error(\{c_1, c_2, \ldots, c_k\}) = \sum_{i=1}^{k} error(c_i)$$

Report the total error rates for $k = 2, \ldots 5$ for 20 runs each for both data sets. Presenting the results that are easily understandable. Plots are generally a good way to convey complex ideas quickly, i.e., box plot. Discuss your results.
Note: The error calculation method mentioned above is generalized for both data sets where the first data set asks if a patient was readmitted or not and the second data set asks if a comment was selected by editor or not.
Data preparation: Like any other data mining problem, before feeding your data to the clustering algorithms, you will have to perform data cleaning, feature engineering, and feature selection on both data sets. For the second data set (NY Times Comments data set), you will be using `commentBody` column as your input feature (you have to build a corpus and perform an appropriate vector-space representation technique) [**20 points**].

R/Python script

```
# Sample R Script With Highlighting
```

```
# Sample Python Script With Highlighting
#Feature Selection for Diabetes Dataset
df_diabetes=df.copy()
#Eliminating patient_nbr and encounter_id
#Eliminating encounter_id and patient_nbr
#Since K means clustering works on similarity or difference and
the objective of K means is to cluster records hence
#Presence of a unique key will be meaningless and hence it wont
contribute to the clustering
#Remove Id variables as they dont contribute to clustering
df_diabetes.drop(columns=
['encounter_id','patient_nbr'],axis=1,inplace=True)
for column in cat_features:
    #Taking Value counts for each categorical column
    value_counts = df_diabetes[column].value_counts()
    prop_percentage=value_counts/len(df_diabetes) *100
    #Setting threshold to 95 percentage, So if a class in a
    column has more than 95 percent values we
    imbalanced_values=prop_percentage>95
    if not imbalanced_values.empty:
        print(f"Column {column} has imbalanced classes:")
        print(prop_percentage[imbalanced_values])
#Reasons for dropping Imbalanced data
#If a column in a dataset has the same value for all data
#points,it will not be useful for clustering.
#This is because clustering algorithms rely
#on differences or similarities between data points to
#group them into clusters. When a column has the same
#value for greater than 95 percent of datapoints,
#There is less variability in those datapoints
which will introduce Skewness in the clustering process.
#Additionally,it means that this column provides
no useful information for distinguishing between data points.
#Since K-Means is a distance based clustering algorithm,
#columns having less variability will dominate the results
#and hence other seemingly important columns will have less impact.

imbalanced_data=['examide','
metformin-rosiglitazone','metformin-pioglitazone',
'glimepiride-pioglitazone',
'glipizide-metformin','glyburide-
metformin','citoglipton','tolazamide',
'troglitazone','miglitol','acarbose','
tolbutamide','acetohexamide',
'chlorpropamide','nateglinide','repaglinide']
df_diabetes.drop(columns=imbalanced_data,inplace=True)

#Handling other categorical variables
```

```
#Since the other columns have a particular order in the
#dosage/Value we can perform label encoding to these columns,
#An example is shown by the value counts of Max_glu_serum Column
#None 96420 Norm 2597 greater than 200 1485 greater than 300 1264
#Hence we can do label encoding and this wont affect the distance
#meteric since the values are determined by types as mentioned
#above with None being mapped to 0

#Label Encoding in data where there is a ordinality
from sklearn.preprocessing import LabelEncoder
ordinal_columns=['max_glu_serum', 'A1Cresult',
    'metformin', 'glimepiride', 'glipizide', 'glyburide',
    'pioglitazone','rosiglitazone', 'insulin', 'change',
    'diabetesMed']
df_diabetes[['max_glu_serum', 'A1Cresult',
    'metformin', 'glimepiride', 'glipizide', 'glyburide',
    'pioglitazone',
    'rosiglitazone', 'insulin', 'change', 'diabetesMed']] =
    df_diabetes[['max_glu_serum', 'A1Cresult',
       'metformin', 'glimepiride', 'glipizide', 'glyburide',
       'pioglitazone',
       'rosiglitazone', 'insulin', 'change',
    'diabetesMed']].swifter.apply(LabelEncoder().fit_transform)
#Applying one hot encoding to columns diag_1,diag_2,diag_3
ordinal_columns=['gender','race','diag_1','diag_2','diag_3']
one_hot =
pd.get_dummies(df_diabetes[['diag_1','diag_2','diag_3','gender','race']])
df_diabetes=pd.concat([df_diabetes,one_hot],axis=1)
df_diabetes.drop(columns=
['diag_1','diag_2','diag_3','gender','race'],inplace=True)
df_diabetes_final=df_diabetes.copy()




#Data Preparation of NYT COMMENTS DATASET

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
#import swifter
import seaborn as sns
import string
import nltk
from nltk.corpus import stopwords
from nltk.stem import WordNetLemmatizer
import re
from nltk.probability import FreqDist
from nltk.tokenize import word_tokenize
from nltk.probability import FreqDist
nltk.download('wordnet')
nltk.download('stopwords')
import string
```

```
import nltk
from nltk.corpus import stopwords
from nltk.stem import WordNetLemmatizer
import re
from nltk.probability import FreqDist
from nltk.tokenize import word_tokenize
from nltk.probability import FreqDist
from nltk.stem import PorterStemmer

def preprocess(corpus):
    #Converting text to lower case
    word_tokens_initialize=word_tokenize(corpus)
    corpus = corpus.lower()
    # Remove punctuation
    corpus = corpus.translate(str.maketrans('', '', string.punctuation))
    #remove numbers
    corpus = re.sub(r'\d+', '', corpus)
    #Reomve URLS
    corpus = re.sub(r'http\S+', '',corpus)
    # Remove non-alphabetic
    corpus = re.sub(r'[^a-zA-Z0-9\s]', '',corpus)
    #Remove Stop words
    word_tokens=word_tokenize(corpus)
    stop_words = set(stopwords.words('english'))
    word_tokens = [word for word in word_tokens if word not in
    stop_words]
    #Applying Stemming
    stemmer = PorterStemmer()
    word_tokens=[stemmer.stem(word) for word in word_tokens]
    corpus = ' '.join(word_tokens)
    return corpus
df_new_york['Cleaned_data']=df_new_york['commentBody'].swift
er.apply(lambda x: preprocess(x))
df_new_york_final=df_first_copy[['Cleaned_data','editorsSele
ction','commentBody']]
import numpy as np
df_new_york_final_01['Cleaned_data'].replace({'':np.nan},inplace=True)

#Applying Count Vectorizer to convert in matrix form Threshold #2.95 Percent

from sklearn.feature_extraction.text import CountVectorizer
num_docs = len(df_new_york_final_01)
min_df_pct =0.0295
min_df = int(min_df_pct * num_docs)
min_df
from tqdm import tqdm
#To chcek the percentage bar
from sklearn.feature_extraction.text import CountVectorizer
#Applying count vectorizer with min df as 2.7 percent
vectorizer = CountVectorizer(min_df=min_df)
#Hence we have only kept those key words whos minimum occurence
is 2.7 percent in data
bag_of_words_matrix =
```

```
vectorizer.fit_transform(tqdm(df_new_york_final_01['Cleaned_data
']))
count_vectorizer_df=
pd.DataFrame.sparse.from_spmatrix(bag_of_words_matrix,
columns=vectorizer.get_feature_names())
count_vectorizer_df['editorsSelection'] =
count_vectorizer_df['editorsSelection'].replace({True:1,False:0}
)


#Python Codes for K means using error as target variables for
Diabetes dataset as well as New york Comments Dataset.


import numpy as np
import swifter
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cdist
import time


def get_random_centroids(input_dataframe,no_of_clusters):
    '''
    The function takes a dataframe as an input and creates
    random K centroids from uniform distribution
    '''
    #Initialize random centroids from dataset
    list_of_centroids = []

    for cluster in range(no_of_clusters):
        #Generates a centroids randomly from uniform
        distribution
        random_centroid = input_dataframe.swifter.apply(lambda x:float(x.sample()))
        #From the given dataset it randomly selects centroids
        list_of_centroids.append(random_centroid)

    centroid_df=pd.concat(list_of_centroids,axis=1)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'
    '''
    The function returns a dataframe consisting of no of clusters required
    '''
    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''
    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster
    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the
```

```
    dataset
    #and it randomly assigns if euclideab distance results in a tie
    '''
    This function returns the index of minimum distances as a dataframe
    '''
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled
    and the original dataframe
    '''
    df_original_label_join=input_dataframe.join(df_clustered_label)
    #This is a dataframe that consists of datapoints as well as
    the cluster assigned
    df_original_label_join.rename(columns={0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column and
    take its mean
    new_centroids=df_original_label_join.groupby('Cluster_Assigned').mean()
    #Here transpose is taken to maintain consistency between
    original random centroids and
    return new_centroids.T


def kmeans_llyod(input_dataframe,no_of_clusters,threshold,no_of_iterations):
    '''

    This function takes original dataframe,number of
    clusters,threshold as input.
    '''
    start_time=time.time()
    iteration=0
    #Step 1 of k means is to get random _Centroids
    initial_centroid=get_random_centroids(input_dataframe,no_of_
    clusters)
    #Randomly generated centroids would be stored on centroids
    #Storing the column list to handle K ties

    initial_centroid_column_list=initial_centroid.columns.to_list()

    while True:
        '''
        The while loop runs until convergence condition is met
        '''
        df_cluster_label=get_labels(input_dataframe,initial_cent
        roid)
        df_new_centroids=get_new_centroids(df_cluster_label,inpu
        t_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
        new_list_of_columns=df_new_centroids.columns.to_list()
```

```
        #Keeping the number of clusters same
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
            df_new_centroids[col]=initial_centroid[col]

        from scipy.spatial.distance import euclidean
        scalar_product =
        [euclidean(initial_centroid[col],df_new_centroids[col])
        for col in initial_centroid.columns]

        threshold_calculated=float(sum(scalar_product))/no_of_clusters

        iteration+=1

        if threshold_calculated<threshold:
            print("The input Threshold was {}".format(threshold))
            print("The calculated threshold is {}".format(threshold_calculated))

        if iteration>no_of_iterations:
            print("Limit for iterations has exceeded")

        if threshold_calculated<threshold or iteration>no_of_iterations:

            error=cluster_error_target_variable(df_cluster_label
            ,input_dataframe,no_of_clusters,df_new_centroids)
            sum_of_square_error=sum_of_square_error_function(df_
            cluster_label,input_dataframe,df_new_centroids,no_of_clusters)
            end_time=time.time()
            return df_new_centroids,error,sum_of_square_error,end_time-
            start_time
            break
        else:
            initial_centroid= df_new_centroids


def
sum_of_square_error_function(df_cluster_label,input_dataframe,df
_new_centroids,no_of_clusters):
    '''
    This function calculates the euclidean distance between new formed
    centroids and the datapoints in that cluster
    '''
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)
    total_error=[]
    for cluster in range(no_of_clusters):

        df_data_label_cluster=df_data_label[df_data_label['Clust
        er_Assigned']==cluster]
        df_data_label_cluster=df_data_label_cluster.drop('Cluste
```

```
        r_Assigned',axis=1)
        centroids=pd.DataFrame(df_new_centroids[cluster])
        euclidean_distance=cdist(df_data_label_cluster,centroids
        .T,metric='euclidean')
        total_error.append(sum(euclidean_distance))
    return round(float(''.join(map(str, sum(total_error)))),3)



def
cluster_error_target_variable(df_cluster_label,input_dataframe,n
o_of_clusters,df_new_centroids):
    '''

    This calculates the error for every cluster and sums up the
    error based on the formula for error
    '''

    target_variable_centroid=input_dataframe.groupby('readmitted
    ').mean().reset_index()
    '''
    Target variable centroid is input dataframe taking mean
    '''
    new_centroids= df_new_centroids.T
    #
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)

    # Get the columns of the data dataframe
    columns = input_dataframe.columns

    sum_of_square_Error= []
    # Compute the distance between each data point and its assigned centroid
    for i in range(len(new_centroids)):
        s=[]
        #Calculating distance from centroids
        for j in range(len(target_variable_centroid)):
            #Calculating the error between target variable
            centroid and new centroids
            distance =
            #Compute the distance between target variable
            np.sum(np.square
            #Calculating the distance
            (target_variable_centroid[
            target_variable_centroid['readmitted']==j][columns]
            - new_centroids.iloc[i][columns]), axis=1)
            #Storing the distance
            s.append(distance.iloc[0])
        sum_of_square_Error.append(s)

    #Merging the dataframe and take idxmin
    merged_new_label=
```

```
    pd.DataFrame(sum_of_square_Error).idxmin(axis=1)

    #Merging of cluster
    mapping_dictionary=
    #Using a dictionary for easier mapping
    merged_new_label.to_dict()

    #Getting clusters to a new column
    df_data_label['target_variable_cluster']=df_data_label['Clus
    ter_Assigned'].replace(mapping_dictionary)


    total_cluster_error = []

    for class_name in range(0,2):
        df_cluster = df_data_label[df_data_label['target_variable_cluster']
        == class_name]
        #Calculating the cluster variable from the class
        yi = len(df_cluster[df_cluster['readmitted'] == 1])
        #Calculating Ni

        ni = len(df_cluster[df_cluster['readmitted'] == 0])
        if yi == 0 and ni == 0:
            error_ci = 0
        else:
            error_ci = ni / (ni + yi) # calculate the error rate of the current cluster
        total_cluster_error.append(error_ci)
    return round(sum(total_cluster_error),3)

 #Target Value error of Diabetes Dataset

      No_of_Clusters      Iteration Number    Target Variable Error
   Sum_of_squared_Errors      run_time
0    2    1    1.082     2217685.223    2.894565
1    2    2    1.078     2203692.919    2.791964
2    2    3    1.079     2208709.762    2.810976
3    2    4    1.088     2323810.782    2.794363
4    2    5    1.099     2193855.702    2.664702
5    2    6    1.066     2204339.519    2.894061
6    2    7    1.073     2231685.175    2.936977
7    2    8    1.100     2193481.006    3.019198
8    2    9    1.090     2212708.746    2.883572
9    2    10   1.094     2177575.192    2.823120
10   2    11   1.130     2440630.016    3.181601
11   2    12   1.092     2174943.112    2.744862
12   2    13   1.094     2188709.905    2.845429
13   2    14   1.086     2181728.600    2.748682
14   2    15   1.094     2181716.683    2.876948
15   2    16   1.068     2196104.262    3.018835
16   2    17   1.079     2269085.117    2.781235
17   2    18   1.086     2184265.104    2.623595
```

```
18   2   19   1.100    2273871.746    2.810508
19   2   20   1.102    2232659.052    2.724093
20   3   1    1.067    1924930.750    3.554921
21   3   2    1.072    2070494.799    3.564006
22   3   3    1.084    2040314.928    3.797678
23   3   4    1.084    2024811.898    3.784306
24   3   5    1.090    2118047.031    3.667671
25   3   6    1.110    1976809.275    3.536911
26   3   7    1.074    1931132.872    3.925559
27   3   8    1.091    1990842.948    4.117785
28   3   9    1.090    2052616.358    4.078079
29   3   10   1.097    2130395.991    3.695230
30   3   11   1.078    1973219.862    3.509133
31   3   12   1.086    2096666.997    3.783429
32   3   13   1.087    1958780.020    3.410912
33   3   14   1.071    1908195.044    3.457280
34   3   15   1.078    1975607.124    3.728825
35   3   16   1.090    1977973.549    3.303766
36   3   17   1.084    2008887.321    3.542578
37   3   18   1.087    1989284.195    3.650250
38   3   19   1.068    1987163.201    3.841413
39   3   20   1.096    2022745.719    3.429435
40   4   1    1.079    1861126.850    4.445349
41   4   2    1.087    1887079.984    2.381165
42   4   3    1.090    1850474.336    4.135579
43   4   4    1.063    1787184.827    2.270954
44   4   5    1.066    1796374.243    4.613437
45   4   6    1.084    1771484.770    4.283354
46   4   7    1.087    1809738.673    4.247500
47   4   8    1.074    1803600.346    4.278413
48   4   9    1.068    1877995.303    4.302683
49   4   10   1.082    1804643.511    2.386778
50   4   11   1.076    1839696.378    6.338206
51   4   12   1.071    1880358.765    2.348073
52   4   13   1.073    1892075.824    4.355319
53   4   14   1.089    1846474.673    4.422870
54   4   15   1.067    1760264.400    4.473190
55   4   16   1.090    1748561.019    4.340959
56   4   17   1.080    1891412.448    4.552740
57   4   18   1.077    1911754.221    4.417347
58   4   19   1.072    1936556.265    4.699840
59   4   20   1.085    1932514.675    4.568905
60   5   1    1.070    1843580.643    5.377942
61   5   2    1.076    1781782.671    4.985337
62   5   3    1.070    1729228.951    5.212292
63   5   4    1.081    1788721.313    2.818460
64   5   5    1.074    1799206.748    5.009835
65   5   6    1.102    1778150.610    5.076036
66   5   7    1.074    1694564.982    4.970256
67   5   8    1.078    1773805.005    5.087022
68   5   9    1.070    1760737.651    5.003118
69   5   10   1.080    1681686.400    5.014719
70   5   11   1.078    1936555.973    2.668803
```

Problem 4 continued on next page. . .

```
71   5    12   1.088     1802091.325    2.694440
72   5    13   1.086     1771292.476    5.097037
73   5    14   1.073     1734796.639    5.181868
74   5    15   1.076     1841775.153    2.717433
75   5    16   1.076     1775211.449    5.264006
76   5    17   1.074     1763592.517    5.337065
77   5    18   1.063     1787781.637    5.011938
78   5    19   1.076     1709000.062    5.253917
79   5    20   1.069     1780322.426    4.977953

error_plot=error_values_df.groupby(['No_of_Clusters']).mean().re
set_index()[['No_of_Clusters','Target Variable
Error','Sum_of_squared_Errors','run_time']]
error_plot
No_of_Clusters      Target Variable Error    Sum_of_squared_Errors    run_time
0    2    1.0890    2.224563e+06   2.843464
1    3    1.0842    2.007946e+06   3.668958
2    4    1.0780    1.844469e+06   4.093133
3    5    1.0767    1.776694e+06   4.637974

ax = error_plot.plot(x='No_of_Clusters', y='Target Variable
Error')
ax2 =error_plot.plot(x='No_of_Clusters',
y='Sum_of_squared_Errors',secondary_y=True, ax=ax)
# set the axis labels and title
ax.set_xlabel('No_of_Clusters')
ax.set_ylabel('Target Variable Error')
ax2.set_ylabel('Sum_of_squared_error')
ax.set_title('Error and SSE vs No of clusters Tou')
ax.legend(['Error'], loc='upper left')
ax2.legend(['SSE'], loc='upper right')
plt.show()

import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_df['No_of_Clusters'],y=error_values_d
f['Target Variable Error'])
plt.title('Box Plot for K means LLyod (error vs no of
clusters)')
plt.show()

import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_df['No_of_Clusters'],y=error_values_d
f['Sum_of_squared_Errors'])
plt.title('Box Plot for K means LLyod (SSE vs no of clusters)')
plt.show()

import seaborn as sns
```

```
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_df['No_of_Clusters'],y=error_values_df['run_time'])
plt.title('Box Plot for K means LLyod (Run Time vs no of clusters)')
plt.show()



#NYC DATASET

import numpy as np
import swifter
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cdist
import time


def get_random_centroids(input_dataframe,no_of_clusters):
    '''
    The function takes a dataframe as an input and creates a
    random K centroids from uniform distribution
    '''
    #Initialize random centroids from dataset
    list_of_centroids = []

    for cluster in range(no_of_clusters):
        #Generates a centroids randomly from uniform distribution
        random_centroid = input_dataframe.swifter.apply(lambda x:float(x.sample()))
        #From the given dataset it randomly selects centroids
        list_of_centroids.append(random_centroid)

    centroid_df=pd.concat(list_of_centroids,axis=1)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'
    '''
    The function returns a dataframe consisting of no of clusters required
    '''
    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''
    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster

    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the dataset
    #and it randomly assigns if euclideab distance results in a tie
    '''
    This function returns the index of minimum distances as a dataframe
    '''
```

```
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled and the original dataframe
    '''
    df_original_label_join=input_dataframe.join(df_clustered_label)
    #This is a dataframe that consists of datapoints as well as
    the cluster assigned
    df_original_label_join.rename(columns={0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column and take its mean
    new_centroids=df_original_label_join.groupby('Cluster_Assigned').mean()
    #Here transpose is taken to maintain consistency between original random centroids and
    return new_centroids.T


def kmeans_llyod(input_dataframe,no_of_clusters,threshold,no_of_iterations):
    '''
    This function takes original dataframe,number of clusters,threshold as input.
    '''
    start_time=time.time()
    iteration=0
    #Step 1 of k means is to get random _Centroids
    initial_centroid=get_random_centroids(input_dataframe,no_of_clusters)
    #Randomly generated centroids would be stored on centroids
    #Storing the column list to handle K ties
    initial_centroid_column_list=initial_centroid.columns.to_list()

    while True:
        '''
        The while loop runs until convergence condition is met
        '''
        df_cluster_label=get_labels(input_dataframe,initial_centroid)
        df_new_centroids=get_new_centroids(df_cluster_label,input_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
        new_list_of_columns=df_new_centroids.columns.to_list()
        #Keeping the number of clusters same
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
            df_new_centroids[col]=initial_centroid[col]

        from scipy.spatial.distance import euclidean
        scalar_product =
        [euclidean(initial_centroid[col],df_new_centroids[col])
        for col in initial_centroid.columns]
        threshold_calculated=float(sum(scalar_product))/no_of_cl
        usters
```

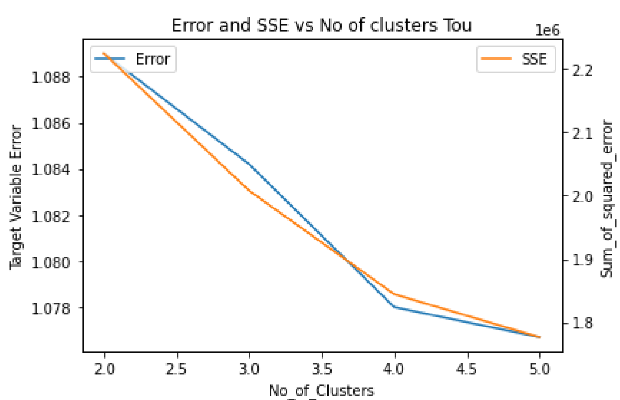
```
        iteration+=1

        if threshold_calculated<threshold:
            print("The input Threshold was
            {}".format(threshold))
            print("The calculated threshold is
            {}".format(threshold_calculated))

        if iteration>no_of_iterations:
            print("Limit for iterations has exceeded")

        if threshold_calculated<threshold or iteration>no_of_iterations:
            error=cluster_error_target_variable(df_cluster_label
            ,input_dataframe,no_of_clusters,df_new_centroids)

            sum_of_square_error=sum_of_square_error_function(df_
            cluster_label,input_dataframe,df_new_centroids,no_of
            _clusters)
            end_time=time.time()
            return df_new_centroids,error,sum_of_square_error,end_time-start_time
            break
        else:
            initial_centroid= df_new_centroids


def
sum_of_square_error_function(df_cluster_label,input_dataframe,df
_new_centroids,no_of_clusters):
    '''
    This function calculates the euclidean distance between new formed
    centroids and the datapoints in that cluster
    '''
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)
    total_error=[]
    for cluster in range(no_of_clusters):
        df_data_label_cluster=df_data_label[df_data_label['Cluster_Assigned']==cluster]
        df_data_label_cluster=df_data_label_cluster.drop('Cluster_Assigned',axis=1)
        centroids=pd.DataFrame(df_new_centroids[cluster])
        euclidean_distance=cdist(df_data_label_cluster,centroids.T,metric='euclidean')
        total_error.append(np.nansum(euclidean_distance))

    return round(np.nansum(total_error),3)
    #return round(float(''.join(map(str, sum(total_error)))),3)



def
cluster_error_target_variable(df_cluster_label,input_dataframe,n
o_of_clusters,df_new_centroids):
    '''
    This calculates the error for every cluster and sums up the
```

```
    error based on the formula for error
    '''

    target_variable_centroid=input_dataframe.groupby('editorsSel
    ection').mean().reset_index()
    '''
    Target variable centroid is input dataframe taking mean
    '''
    new_centroids= df_new_centroids.T
    #
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)

    # Get the columns of the data dataframe
    columns = input_dataframe.columns

    sum_of_square_Error= []
    # Compute the distance between each data point and its assigned centroid
    for i in range(len(new_centroids)):
        s=[]
        for j in range(len(target_variable_centroid)): ### mean centroid
            #Calculating the error between target variable centroid and new centroids
            distance =
            np.sum(np.square(target_variable_centroid[target_var
            iable_centroid['editorsSelection']==j][columns] -
            new_centroids.iloc[i][columns]), axis=1)
            #Storing the distance
            s.append(distance.iloc[0])
        sum_of_square_Error.append(s)


    merged_new_label=pd.DataFrame(sum_of_square_Error).idxmin(axis=1)

    #Merging of cluster
    mapping_dictionary=merged_new_label.to_dict()

    #Getting clusters to a new column
    df_data_label['target_variable_cluster']=df_data_label['Clus
    ter_Assigned'].replace(mapping_dictionary)


    total_cluster_error = []

    for class_name in range(0,2):
        df_cluster = df_data_label[df_data_label['target_variable_cluster'] == class_name]
        yi = len(df_cluster[df_cluster['editorsSelection'] == 1])
        #Calculating Ni
        ni = len(df_cluster[df_cluster['editorsSelection'] == 0])
        if yi == 0 and ni == 0:
            error_ci = 0
        else:
            error_ci = ni / (ni + yi) # calculate the error rate of the current cluster
```

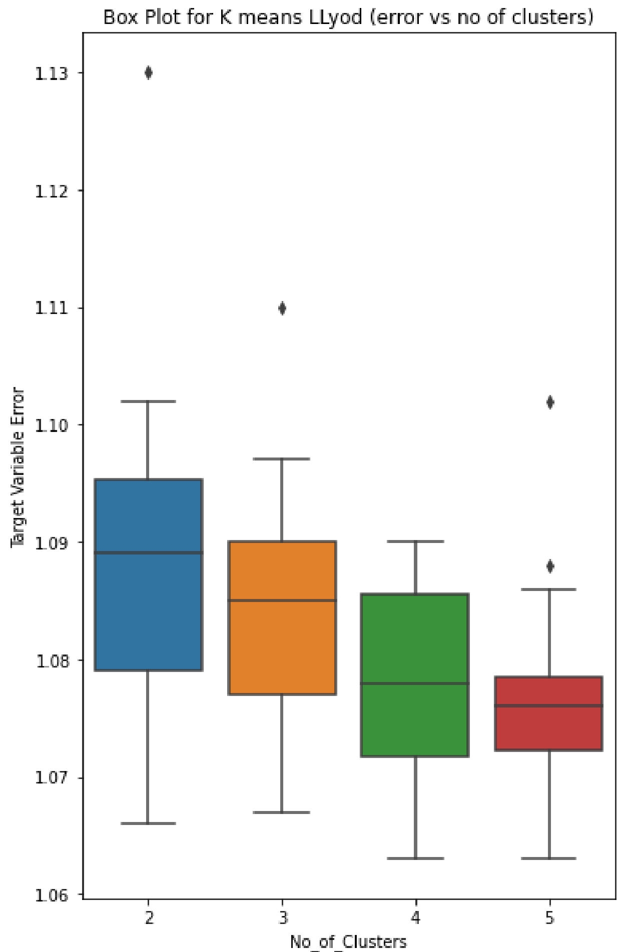
```
        total_cluster_error.append(error_ci)
    return round(sum(total_cluster_error),3)
error_values=[]
for no_of_clusters in range(2,6):
    #Taking the cluster value from 2 to 5
    for no_of_experiments in range(1,21):
        #Performing experiments for each cluster 20 times
        final_centroids,error_target_variable,sum_of_squared_err
        or,run_time=kmeans_llyod(df_sample,no_of_clusters,10,100
        )
        #Storing the variables in dataframe
        error_values.append([no_of_clusters,no_of_experiments,er
        ror_target_variable,sum_of_squared_error,run_time])
error_values_df= pd.DataFrame(error_values,columns=
['No_of_Clusters', 'Iteration Number', 'Target Variable
Error','Sum_of_squared_Errors','run_time'])
error_values_df.to_csv('Kmeans_llyod_20_iteration_1lakh.csv')

  No_of_Clusters    Iteration Number    Target Variable Error
  Sum_of_squared_Errors  run_time
0    2    1    0.987    324552.550    10.644651
1    2    2    0.987    323808.672    11.224484
2    2    3    0.987    324135.854    10.483995
3    2    4    0.987    319224.160    10.656195
4    2    5    0.987    322792.602    10.692482
...  ...  ...  ...  ...  ...
75   5    16   0.987    320049.564    16.136392
76   5    17   0.987    322130.155    16.076394
77   5    18   0.987    318237.758    16.147666
78   5    19   0.987    315744.064    16.227921
79   5    20   0.987    323804.373    16.208781

80 rows    5 columns
```

Plots

Diabetes Dataset

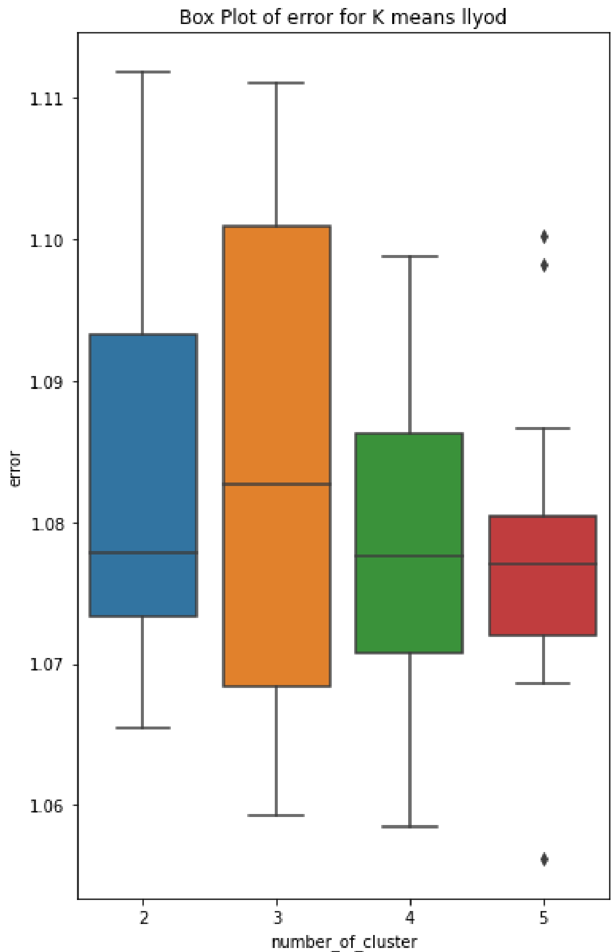


(5)

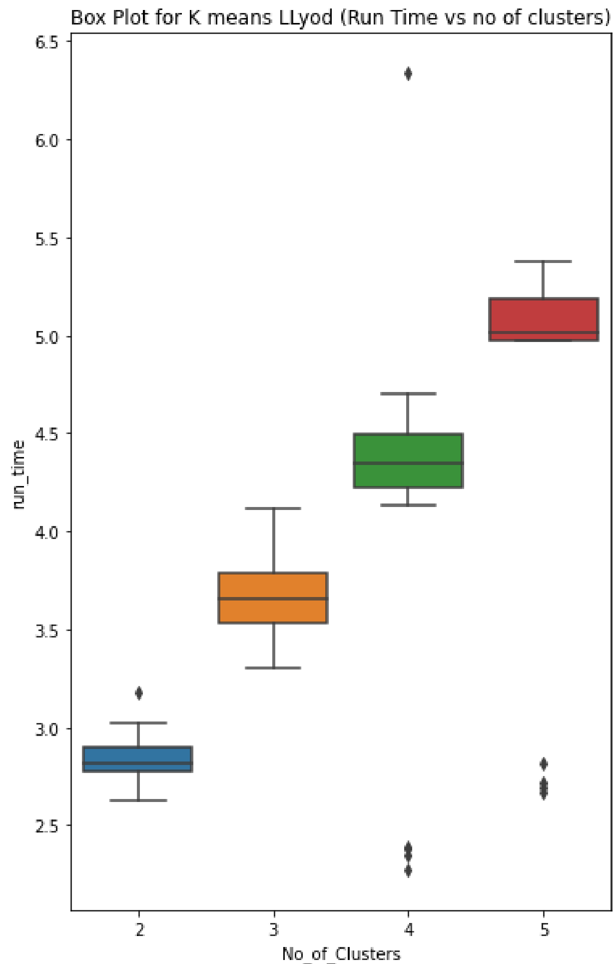


(6)

Problem 4 continued on next page. . .

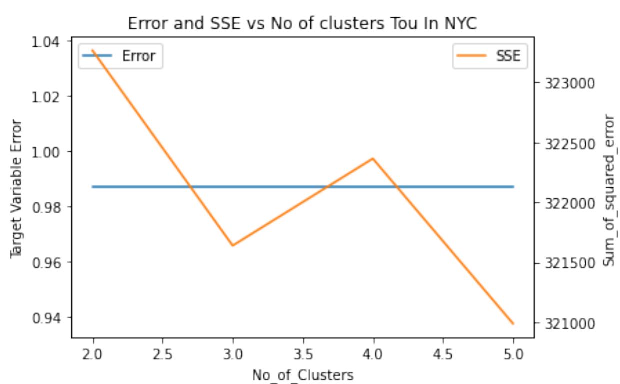

Box Plot of error for K means llyod
1.11
1.10
1.09
1.08
1.07
1.06
error
2
3
4
5
number_of_cluster

(7)

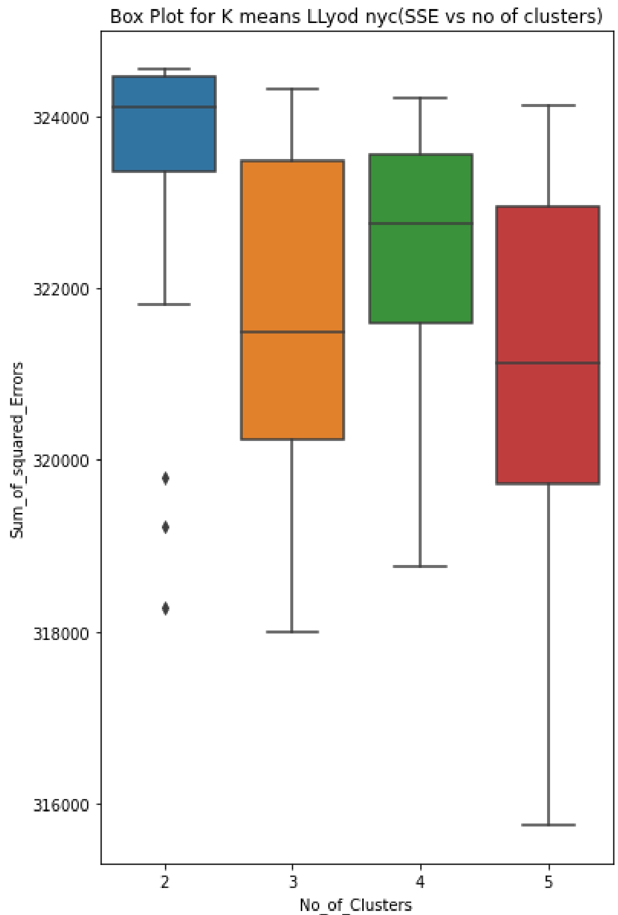


(8)

NYC Dataset Graphs

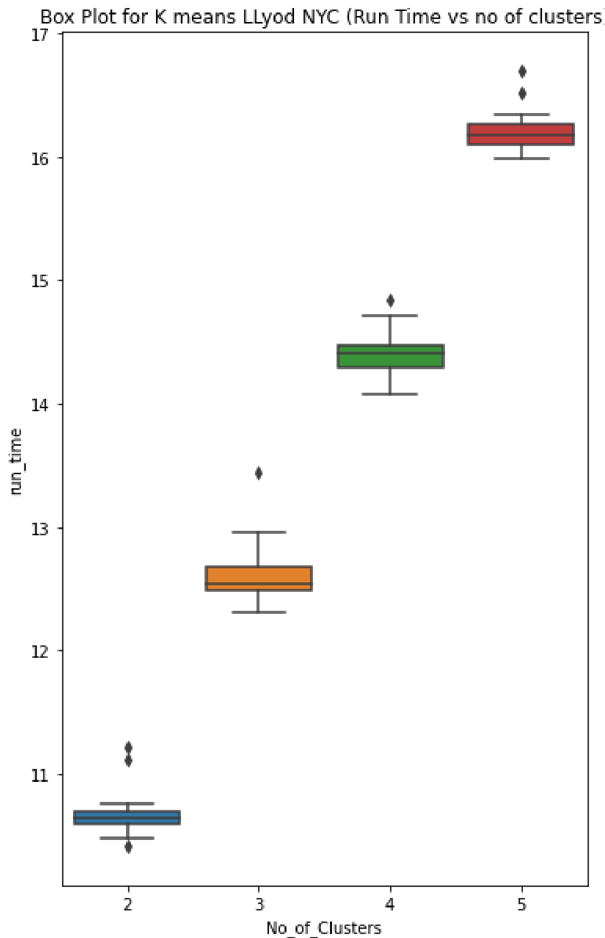


(9)



(10)

Problem 4 continued on next page. . .



(11)

Discussion of Findings

Answer here...

- **Method used for representing Comment Body**
- Since Comment Body column is a free text column, I have used Natural Language Processing method to convert the text into appropriate vector representation.
- Applying appropriate pre-processing steps to clean the data such as removing stopwords,Stemming-Converting word to root word,Removing URLS, Removing punctuations,Removing Non alphanumeric letters,Removing Digit, Converting text to lower font.
- Conversion from text to Vector using Count vectorizer method
- The reason for using Count Vectorizer method is as follows:
- CountVectorizer focuses on the frequency of words in a document, whereas TF-IDF considers the frequency of words across all documents in the dataset. This means that CountVectorizer is better suited to capturing the specificity of a document, which is important in clustering, where we want to group similar documents together.

- CountVectorizer is simpler and faster than TF-IDF because it only counts the number of occurrences of each word in a document, while TF-IDF requires more complex calculations to take into account the frequency of words across all documents.
- CountVectorizer produces integer counts for each word, which can be more easily interpreted and used in clustering algorithms, compared to the decimal values produced by TF-IDF.
- In summary, CountVectorizer is a better choice than TF- IDF for clustering when we want to focus on the specific characteristics of each document and need a simpler and faster approach to processing large amounts of text data.
- **Algorithm Description**
- The algorithm implemented is K means with a Threshold
- I have implemented the algorithm for Diabetes dataset as well as NYC comments dataset for clusters 2 to 5 and number of iterations between 1 to 20.
- The threshold value is set to a low value and when the distances between old centroids and the new centroids have changed and the value is below a threshold the Algorithm stops
- I have recorded the Graph values for 80 iterations
- The error value is calculated from the Target Variable,The intuition behind target variable is since we are performing a binary classification, Let that be the original classes.
- When we increase the number of clusters we have to merge the clusters based on the distance from the original clusters from the input dataframe.
- **Merging of N clusters into 2**
- The merging process calculates the distances between the centroids acheived from clustering and the original dataframe clusters,and it mappes the cluster to the nearest input cluster
- Thus after performing clustering based on target variable we are able to plot the graph for datasets.
- **Conclusions from the Graph**
- For Diabetes Dataset:From the first graph containing SSE and error with Target Variable we conclude that as number of clusters increase the withing Sum of Square errors tend to decrease.
- However for the error with the target variable we can see randomness when we run different experiments.
- In a general case the error tends to balance out when we increase the number of clusters and the imbalances in the classes decrease.
- The box Plots for the Diabetes Dataset also suggest a similar story, For the Sum of Squared Errors the median value of errors tend to decrease as we increase the clusters.
- The Box plots of Runtime suggests an increase in runtime as we increase the number of clusters,The median value for a cluster number higher is high.
- **Conclusion for NYC Comments Dataset**
- From the first graph we can conclude that the Sum of Squared Error decreases as we increase the number of clusters

- After applying pre processing and taking the most frequent 2.9 percent of dataset we can see,After applying count vectorizer Df we generate a sparse matrix of 50 lakh rows and some hundreds columns.
- Since the matrix is sparse when we try to merge the cluster based on distance metric we get the same distance and hence the Error of target variable remains the same.
- Because of Sparsity we can see the clusters formed would be homogeneous and hence error with target variable wont change.
- For the box plots we can see as the number of clusters increase the SSE median becomes low.
- The Run time generally increases with increase in the cluster.
- Imrpovements in K means Llyod
- We can initialize K means in a better way and implement K means ++ centroids initialization thus reducing the Within Cluster Sum of Square Errors
- We can implement **Triangle Inequality** to improve the K means Algorithm and remove the needless cluster calculations.

Problem 5

The k-means algorithm provided above stops when centroids become stable (Line 34). In theory, k-means converges once SSE is minimized

$$SSE = \sum_{j}^{k} \sum_{x \in c_j.B} ||\mathbf{x} - c_j.v||_2^2$$

In this question, you are asked to use SSE as stopping criterion. Run your program, $C_{k_{SSE}}$, against the Diabetes and New York Times Comments data sets. Report the total error rates for $k = 2, \ldots 5$ for 20 runs each for both data sets. Moreover, compare k-means and kmeans++'s run time for $k = 2, \ldots 5$ for 20 runs using both data sets. Presenting the results that are easily understandable. Plots are generally a good way to convey complex ideas quickly, i.e., box plot. Discuss your results [**20 points**].

R/Python script

```
# Sample R Script With Highlighting
```

```
import numpy as np
import swifter
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cdist
import time


def get_random_centroids(input_dataframe,no_of_clusters):
    '''
    The function takes a dataframe as an input and creates a
    random K centroids from uniform distribution
```

```
    '''
    #Initialize random centroids from dataset
    list_of_centroids = []

    for cluster in range(no_of_clusters):
        #Generates a centroids randomly from uniform distribution
        random_centroid = input_dataframe.swifter.apply(lambda
        x:float(x.sample()))
        #From the given dataset it randomly selects centroids

        list_of_centroids.append(random_centroid)

    centroid_df=pd.concat(list_of_centroids,axis=1)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'
    '''
    The function returns a dataframe consisting of no of
    clusters required
    '''
    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''
    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster
    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the
    dataset
    #and it randomly assigns if euclideab distance results in a
    tie
    '''
    This function returns the index of minimum distances as a
    dataframe
    '''
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled
    and the original dataframe
    '''
    df_original_label_join=input_dataframe.join(df_clustered_lab
    el)
    #This is a dataframe that consists of datapoints as well as
    the cluster assigned
    df_original_label_join.rename(columns={0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column and
    take its mean

```

```
    new_centroids=df_original_label_join.groupby('Cluster_Assign
    ed').mean()
    #Here transpose is taken to maintain consistency between
    original random centroids and
    return new_centroids.T


def
kmeans_SSE_Convergence(input_dataframe,no_of_clusters,sum_of_squ
ared_threshold,no_of_iterations):
    '''
    Treats K means as an optimization Problem and stops when
    difference in SSE reaches a threshold
    The input to the function is the dataframe,no of clusters
    and a threshold which indicates the perecentage change
    It indicates user can set the percentage change in the SSE
    and once the percentage change in SSE drops to the
    Threshold we can see the algorithm has converged
    '''
    start_time=time.time()
    iteration=0
    #Step 1 of k means is to get random _Centroids
    initial_centroid=get_random_centroids(input_dataframe,no_of_clusters)
    #Randomly generated centroids would be stored on centroids
    #Storing the column list to handle K ties
    initial_centroid_column_list=initial_centroid.columns.to_list()
    #Get initial labels
    df_cluster_label=get_labels(input_dataframe,initial_centroid)
    #Compute the initial Sum of squared Errors
    initial_sum_of_squared_errors=sum_of_square_error_function(d
    f_cluster_label,input_dataframe,initial_centroid,no_of_clust
    ers)


    while True:
        '''
        The while loop runs until convergence condition is met
        '''


        df_new_centroids=get_new_centroids(df_cluster_label,inpu
        t_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
        new_list_of_columns=df_new_centroids.columns.to_list()
        #Keeping the number of clusters same
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
```

```
            df_new_centroids[col]=initial_centroid[col]

        '''
        Assigning labels to new centroids
        '''
        df_cluster_label_iter=get_labels(input_dataframe,df_new_
        centroids)
        '''

        Calculating the current SSE

        '''

        updated_sum_of_squared_errors=sum_of_square_error_functi
        on(df_cluster_label_iter,input_dataframe,df_new_centroid
        s,no_of_clusters)


        #Calculating the convergence criteria

        percentage_change=((initial_sum_of_squared_errors-
        updated_sum_of_squared_errors)/(initial_sum_of_squared_e
        rrors))*100

        iteration+=1
        #Stopping criteria
        #Indicating new clusters have reduced the SSE
        if percentage_change>0:
            if percentage_change>=sum_of_squared_threshold or
            iteration>no_of_iterations:
                print("The input SSE Threshold was
                {}".format(sum_of_squared_threshold))
                print("The percentage change is
                {}".format(percentage_change))
                print("The initial error was {} and final error
                was
                {}".format(initial_sum_of_squared_errors,updated
                _sum_of_squared_errors))

                error=cluster_error_target_variable(df_cluster_l
                abel_iter,input_dataframe,no_of_clusters,df_new_
                centroids)
                end_time=time.time()
                return
                df_new_centroids,error,updated_sum_of_squared_er
                rors,end_time-start_time
                break

        else:
            initial_centroid= df_new_centroids
            df_cluster_label=df_cluster_label_iter
            initial_sum_of_squared_errors=updated_sum_of_squared
            _errors
```

```


def
sum_of_square_error_function(df_cluster_label,input_dataframe,df
_new_centroids,no_of_clusters):
    '''
    This function calculates the euclidean distance between new
    formed
    centroids and the datapoints in that cluster
    '''
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)
    total_error=[]
    for cluster in range(no_of_clusters):

        df_data_label_cluster=df_data_label[df_data_label['Clust
        er_Assigned']==cluster]
        df_data_label_cluster=df_data_label_cluster.drop('Cluste
        r_Assigned',axis=1)
        centroids=pd.DataFrame(df_new_centroids[cluster])
        euclidean_distance=cdist(df_data_label_cluster,centroids
        .T,metric='euclidean')

        total_error.append(sum(euclidean_distance))
    return round(float(''.join(map(str, sum(total_error)))),3)



def
cluster_error_target_variable(df_cluster_label,input_dataframe,n
o_of_clusters,df_new_centroids):
    '''
    This calculates the error for every cluster and sums up the
    error based on the formula for error
    '''

    target_variable_centroid=input_dataframe.groupby('readmitted').mean().reset_index()
    '''
    Target variable centroid is input dataframe taking mean
    '''
    new_centroids= df_new_centroids.T
    #
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)

    # Get the columns of the data dataframe
    columns = input_dataframe.columns

    sum_of_square_Error= []
    # Compute the distance between each data point and its
    assigned centroid
```

```
    for i in range(len(new_centroids)):
        s=[]
        for j in range(len(target_variable_centroid)): ### mean centroid
            #Calculating the error between target variable
            centroid and new centroids
            distance =
            np.sum(np.square(target_variable_centroid[target_var
            iable_centroid['readmitted']==j][columns] -
            new_centroids.iloc[i][columns]), axis=1)

            #Storing the distance
            s.append(distance.iloc[0])
        sum_of_square_Error.append(s)


    merged_new_label=pd.DataFrame(sum_of_square_Error).idxmin(ax
    is=1)

    #Merging of cluster
    mapping_dictionary=merged_new_label.to_dict()

    #Getting clusters to a new column
    df_data_label['target_variable_cluster']=df_data_label['Clus
    ter_Assigned'].replace(mapping_dictionary)


    total_cluster_error = []

    for class_name in range(0,2):
        df_cluster =
        df_data_label[df_data_label['target_variable_cluster'] == class_name]
        yi = len(df_cluster[df_cluster['readmitted'] == 1])
        #Calculating Ni
        ni = len(df_cluster[df_cluster['readmitted'] == 0])
        if yi == 0 and ni == 0:
            error_ci = 0
        else:
            error_ci = ni / (ni + yi) # calculate the error rate of the current cluster
        total_cluster_error.append(error_ci)
    return round(sum(total_cluster_error),3)
error_values_kmeans_convergence=[]
for no_of_clusters in range(2,6):
    #Taking the cluster value from 2 to 5
    for no_of_experiments in range(1,21):
        #Performing experiments for each cluster 20 times
        final_centroids,error_target_variable,sum_of_squared_err
        or,run_time=kmeans_SSE_Convergence(df_diabetes_final,no_
        of_clusters,10,100)
        #Storing the variables in dataframe
        error_values_kmeans_convergence.append([no_of_clusters,n
        o_of_experiments,error_target_variable,sum_of_squared_er
        ror,run_time])
error_values_kmeans_convergence_df=
```

```
pd.DataFrame(error_values_kmeans_convergence,columns=
['No_of_Clusters', 'Iteration Number', 'Target Variable
Error','Sum_of_squared_Errors','run_time'])

 No_of_Clusters     Iteration Number    Target Variable Error
 Sum_of_squared_Errors   run_time
0    2    1    1.066     2413170.508    2.726349
1    2    2    1.078     2287579.727    2.718648
2    2    3    1.087     2182532.040    2.797202
3    2    4    1.104     2221605.043    2.712034
4    2    5    1.091     2189499.368    2.718228
5    2    6    1.079     2277045.553    2.694952
6    2    7    1.061     2303720.984    2.644690
7    2    8    1.088     2170057.769    2.651664
8    2    9    1.095     2200394.800    2.699285
9    2    10   1.072     2267420.702    2.626602
10   2    11   1.090     2193666.813    2.684914
11   2    12   1.077     2246487.630    2.642030
12   2    13   1.082     2171039.014    2.644447
13   2    14   1.081     2174714.967    2.745272
14   2    15   1.083     2170344.044    2.783290
15   2    16   1.075     2189936.038    2.729855
16   2    17   1.101     2340073.186    2.873033
17   2    18   1.076     2233414.214    2.730305
18   2    19   1.102     2214350.488    2.810346
19   2    20   1.073     2186929.281    2.714788
20   3    1    1.065     1935225.192    3.246217
21   3    2    1.101     2039320.017    3.350098
22   3    3    1.083     1968438.520    3.402092
23   3    4    1.079     1995877.788    3.405518
24   3    5    1.068     1961866.877    3.464136
25   3    6    1.086     2064005.550    3.408696
26   3    7    1.080     1925746.674    3.363921
27   3    8    1.064     1958785.399    3.420779
28   3    9    1.086     1954132.773    3.441963
29   3    10   1.063     1959673.274    3.389995
30   3    11   1.105     1967024.521    3.409568
31   3    12   1.094     2063132.009    3.410118
32   3    13   1.059     1977468.991    3.503200
33   3    14   1.060     2009608.064    3.329814
34   3    15   1.091     2067597.639    3.413102
35   3    16   1.064     2139787.389    3.337727
36   3    17   1.114     1997694.204    3.381265
37   3    18   1.077     2030874.333    3.305255
38   3    19   1.069     1944534.045    3.378402
39   3    20   1.069     2134921.766    3.388444
40   4    1    1.069     1903662.597    4.067786
41   4    2    1.103     1857357.414    3.997676
42   4    3    1.087     1878725.172    4.159650
43   4    4    1.105     1880647.531    4.119273
44   4    5    1.061     1861897.586    4.022799
45   4    6    1.061     1807974.571    4.102464
46   4    7    1.085     1984950.693    4.216363
```

```
47   4    8    1.078     1824653.970    4.038547
48   4    9    1.073     1924015.710    4.060449
49   4    10   1.070     1832468.147    4.123883
50   4    11   1.088     2021315.876    4.306999
51   4    12   1.087     1892568.867    4.296274
52   4    13   1.066     1864108.356    4.136086
53   4    14   1.070     1812281.605    4.087149
54   4    15   1.071     1800758.124    4.172847
55   4    16   1.073     1824418.302    4.047086
56   4    17   1.058     1897934.940    4.181204
57   4    18   1.079     1817142.740    4.077854
58   4    19   1.089     1934103.757    4.013173
59   4    20   1.103     1939041.632    4.106091
60   5    1    1.082     1743442.199    4.785248
61   5    2    1.068     1660872.055    4.651742
62   5    3    1.091     1808287.699    4.656569
63   5    4    1.084     1773047.315    4.665026
64   5    5    1.066     1844519.156    4.706286
65   5    6    1.076     1740907.723    4.691701
66   5    7    1.081     1777958.584    4.754583
67   5    8    1.072     1781775.749    4.818693
68   5    9    1.089     1775093.996    4.787339
69   5    10   1.089     1680293.631    4.772455
70   5    11   1.068     1689785.267    4.638578
71   5    12   1.086     1799536.909    4.668274
72   5    13   1.074     1768360.548    4.687613
73   5    14   1.075     1777205.297    4.677921
74   5    15   1.075     1767950.472    4.691387
75   5    16   1.071     1744607.719    4.769310
76   5    17   1.092     1678438.903    4.748329
77   5    18   1.080     1800264.784    4.680258
78   5    19   1.088     1892715.711    4.720975
79   5    20   1.076     1757773.294    4.669850


error_values_kmeans_convergence=error_values_kmeans_convergence_
df.groupby(['No_of_Clusters']).mean().reset_index()
[['No_of_Clusters','Target Variable
Error','Sum_of_squared_Errors','run_time']]
error_values_kmeans_convergence

No_of_Clusters      Target Variable Error    Sum_of_squared_Errors
run_time
0    2    1.08305   2.231699e+06   2.717397
1    3    1.07885   2.004786e+06   3.387516
2    4    1.07880   1.878001e+06   4.116683
3    5    1.07915   1.763142e+06   4.712107

#NYC DATASET


import numpy as np
import swifter
```

```
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cdist
import time


def get_random_centroids(input_dataframe,no_of_clusters):
    '''
    The function takes a dataframe as an input and creates a
    random K centroids from uniform distribution
    '''
    #Initialize random centroids from dataset
    list_of_centroids = []

    for cluster in range(no_of_clusters):
        #Generates a centroids randomly from uniform
        distribution
        random_centroid = input_dataframe.swifter.apply(lambda x:float(x.sample()))
        #From the given dataset it randomly selects centroids
        list_of_centroids.append(random_centroid)

    centroid_df=pd.concat(list_of_centroids,axis=1)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'
    '''
    The function returns a dataframe consisting of no of
    clusters required
    '''
    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''
    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster
    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the
    dataset
    #and it randomly assigns if euclideab distance results in a
    tie
    '''
    This function returns the index of minimum distances as a dataframe
    '''
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled
    and the original dataframe
    '''
```

```
    df_original_label_join=input_dataframe.join(df_clustered_lab
    el)
    #This is a dataframe that consists of datapoints as well as the cluster assigned
    df_original_label_join.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column and take its mean
    new_centroids=df_original_label_join.groupby('Cluster_Assign
    ed').mean()
    #Here transpose is taken to maintain consistency between
    original random centroids and
    return new_centroids.T


def
kmeans_SSE_Convergence(input_dataframe,no_of_clusters,sum_of_squ
ared_threshold,no_of_iterations):
    '''
    Treats K means as an optimization Problem and stops when
    difference in SSE reaches a threshold
    The input to the function is the dataframe,no of clusters
    and a threshold which indicates the perecentage change
    It indicates user can set the percentage change in the SSE
    and once the percentage change in SSE drops to the
    Threshold we can see the algorithm has converged
    '''
    start_time=time.time()
    iteration=0
    #Step 1 of k means is to get random _Centroids
    initial_centroid=get_random_centroids(input_dataframe,no_of_
    clusters)
    #Randomly generated centroids would be stored on centroids
    #Storing the column list to handle K ties
    initial_centroid_column_list=initial_centroid.columns.to_lis
    t()
    #Get initial labels
    df_cluster_label=get_labels(input_dataframe,initial_centroid
    )
    #Compute the initial Sum of squared Errors
    initial_sum_of_squared_errors=sum_of_square_error_function(d
    f_cluster_label,input_dataframe,initial_centroid,no_of_clust
    ers)


    while True:
        '''
        The while loop runs until convergence condition is met
        '''

        df_new_centroids=get_new_centroids(df_cluster_label,inpu
        t_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
```

```
        new_list_of_columns=df_new_centroids.columns.to_list()
        #Keeping the number of clusters same
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
            df_new_centroids[col]=initial_centroid[col]

        '''
        Assigning labels to new centroids
        '''
        df_cluster_label_iter=get_labels(input_dataframe,df_new_
        centroids)
        '''
        Calculating the current SSE

        '''
        updated_sum_of_squared_errors=sum_of_square_error_functi
        on(df_cluster_label_iter,input_dataframe,df_new_centroid
        s,no_of_clusters)

        #Calculating the convergence criteria

        percentage_change=((initial_sum_of_squared_errors-
        updated_sum_of_squared_errors)/(initial_sum_of_squared_e
        rrors))*100

        iteration+=1
        #Stopping criteria
        #Indicating new clusters have reduced the SSE
        if percentage_change>0:
            if percentage_change>=sum_of_squared_threshold or
            iteration>no_of_iterations:
                print("The input SSE Threshold was
                {}".format(sum_of_squared_threshold))
                print("The percentage change is
                {}".format(percentage_change))
                print("The initial error was {} and final error
                was
                {}".format(initial_sum_of_squared_errors,updated
                _sum_of_squared_errors))

                error=cluster_error_target_variable(df_cluster_l
                abel_iter,input_dataframe,no_of_clusters,df_new_
                centroids)
                end_time=time.time()
                return df_new_centroids,error,updated_sum_of_squared_er
                rors,end_time-start_time
                break

        else:
            initial_centroid= df_new_centroids
            df_cluster_label=df_cluster_label_iter
```

```
            initial_sum_of_squared_errors=updated_sum_of_squared_errors


def sum_of_square_error_function(df_cluster_label,input_dataframe,df
_new_centroids,no_of_clusters):
    '''
    This function calculates the euclidean distance between new formed
    centroids and the datapoints in that cluster
    '''
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)
    total_error=[]
    for cluster in range(no_of_clusters):
        df_data_label_cluster=df_data_label[df_data_label['Cluster_Assigned']==cluster]
        df_data_label_cluster=df_data_label_cluster.drop('Cluster_Assigned',axis=1)
        centroids=pd.DataFrame(df_new_centroids[cluster])
        euclidean_distance=cdist(df_data_label_cluster,centroids.T,metric='euclidean')
        total_error.append(np.nansum(euclidean_distance))

    return round(np.nansum(total_error),3)



def
cluster_error_target_variable(df_cluster_label,input_dataframe,n
o_of_clusters,df_new_centroids):
    '''
    This calculates the error for every cluster and sums up the
    error based on the formula for error
    '''

    target_variable_centroid=input_dataframe.groupby('editorsSelection').mean().reset_index()
    '''
    Target variable centroid is input dataframe taking mean
    '''
    new_centroids= df_new_centroids.T
    #
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)

    # Get the columns of the data dataframe
    columns = input_dataframe.columns

    sum_of_square_Error= []
    # Compute the distance between each data point and its assigned centroid
    for i in range(len(new_centroids)):
        s=[]
        for j in range(len(target_variable_centroid)): ### mean centroid
            #Calculating the error between target variable
            centroid and new centroids
```

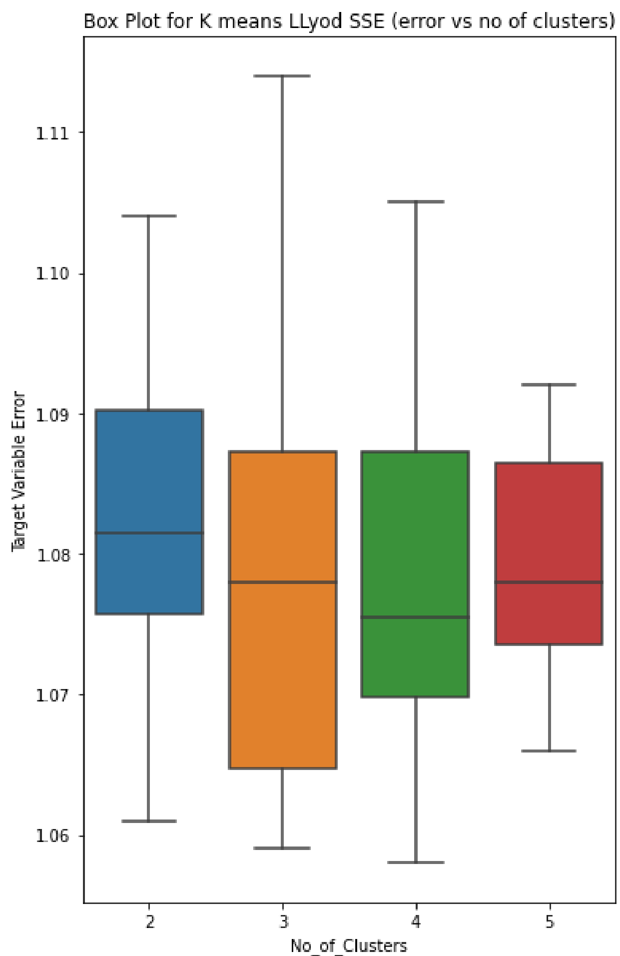
```
            distance =
            np.sum(np.square(target_variable_centroid[target_var
            iable_centroid['editorsSelection']==j][columns] -
            new_centroids.iloc[i][columns]), axis=1)
            #Storing the distance
            s.append(distance.iloc[0])
        sum_of_square_Error.append(s)


    merged_new_label=pd.DataFrame(sum_of_square_Error).idxmin(axis=1)

    #Merging of cluster
    mapping_dictionary=merged_new_label.to_dict()

    #Getting clusters to a new column

    df_data_label['target_variable_cluster']=
    df_data_label['Clus
    ter_Assigned'].replace(mapping_dictionary)


    total_cluster_error = []

    for class_name in range(0,2):
        df_cluster = df_data_label[df_data_label['target_variable_cluster'] == class_name]
        yi = len(df_cluster[df_cluster['editorsSelection'] == 1])
        #Calculating Ni
        ni = len(df_cluster[df_cluster['editorsSelection'] == 0])
        if yi == 0 and ni == 0:
            error_ci = 0
        else:
            error_ci = ni / (ni + yi) # calculate the error rate of the current cluster
        total_cluster_error.append(error_ci)
    return round(sum(total_cluster_error),3)
error_values_kmeans_convergence=[]
for no_of_clusters in range(2,6):
    #Taking the cluster value from 2 to 5
    for no_of_experiments in range(1,21):
        #Performing experiments for each cluster 20 times

        final_centroids,error_target_variable,sum_of_squared_err
        or,run_time=kmeans_SSE_Convergence(count_vectorizer_df,n
        o_of_clusters,10,100)
        #Storing the variables in dataframe
        error_values_kmeans_convergence.append([no_of_clusters,n
        o_of_experiments,error_target_variable,sum_of_squared_er
        ror,run_time])
error_values_kmeans_convergence_df_full=
pd.DataFrame(error_values_kmeans_convergence,columns=
['No_of_Clusters', 'Iteration Number', 'Target Variable
Error','Sum_of_squared_Errors','run_time'])
error_values_kmeans_convergence_df_full.to_csv('nyc_Sse_data.csv
')
```

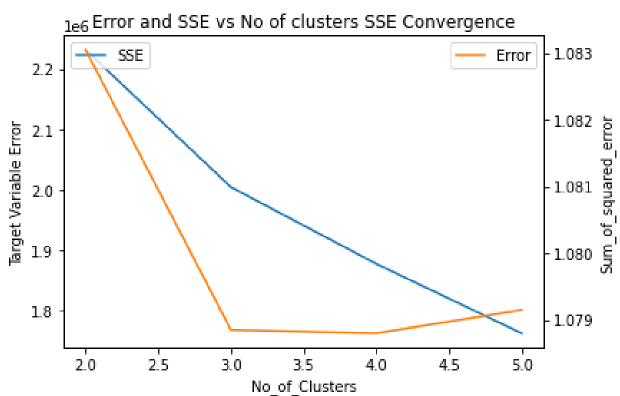
Problem 5 continued on next page. . .

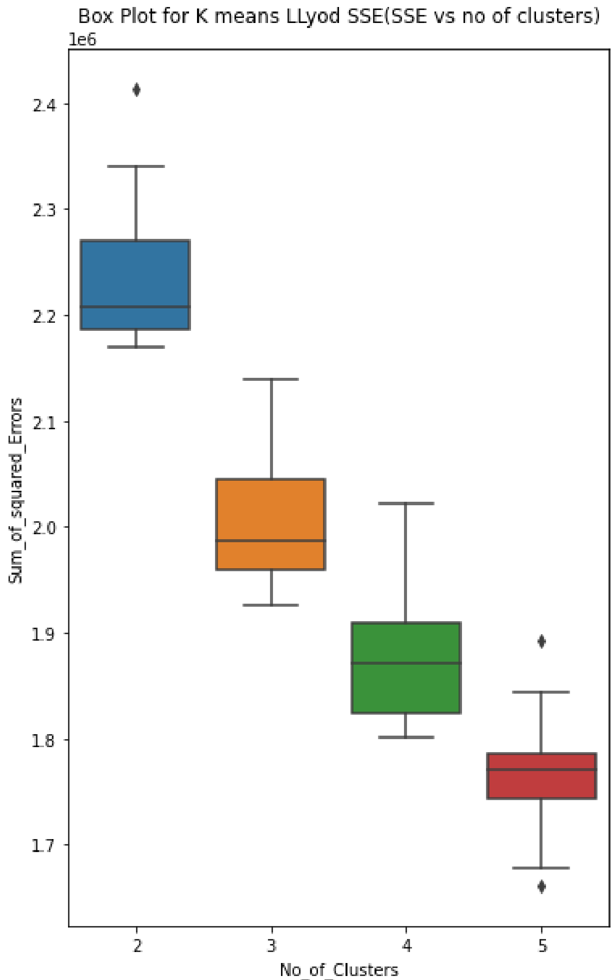
```
No_of_Clusters      Iteration Number    Target Variable Error
Sum_of_squared_Errors    run_time
0    2    1    0.987    317878.061    19.744410
1    2    2    0.987    323528.786    19.373257
2    2    3    0.987    324554.100    19.070758
3    2    4    0.987    324551.914    20.030429
4    2    5    0.987    323339.223    18.989385
...  ...  ...  ...  ...  ...
75   5    16   0.987    315650.628    38.673154
76   5    17   0.987    314343.849    39.018158
77   5    18   0.987    312601.780    38.846771
78   5    19   0.987    314152.048    37.687718
79   5    20   0.987    317688.822    39.600342

80 rows    5 columns
```

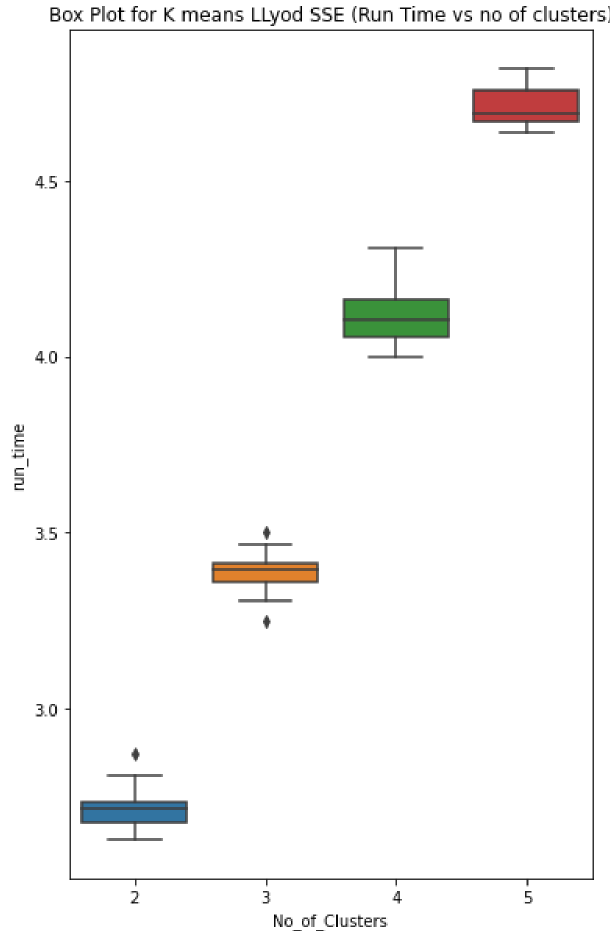
Plots

Diabetes Dataset

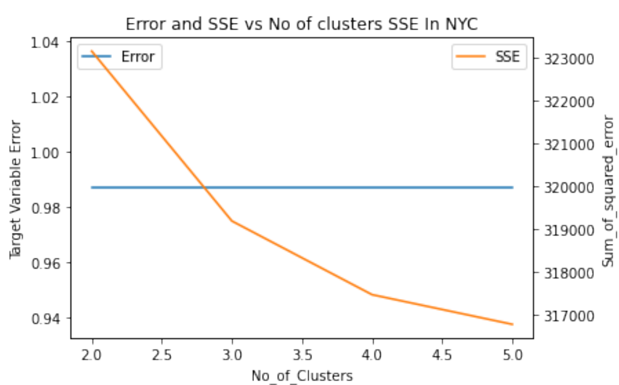




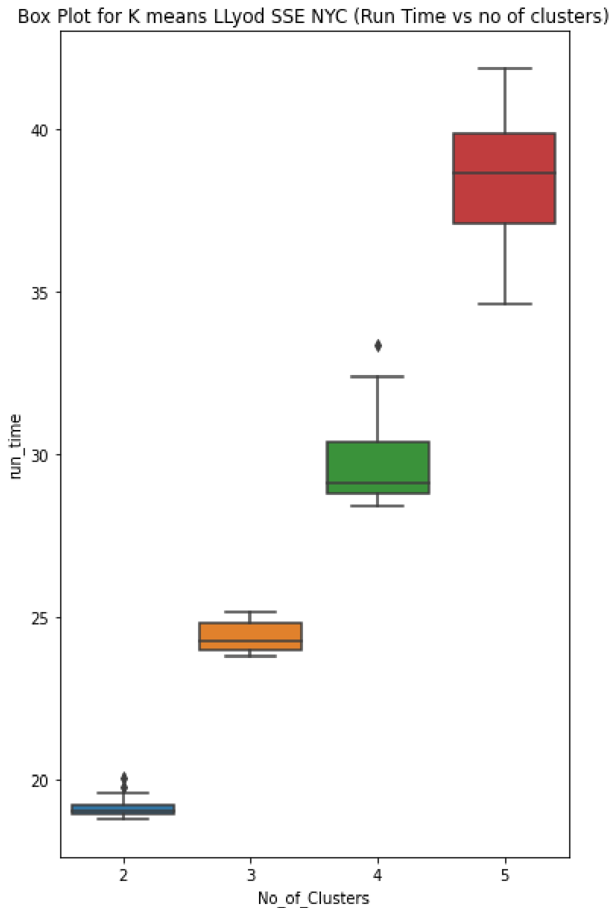




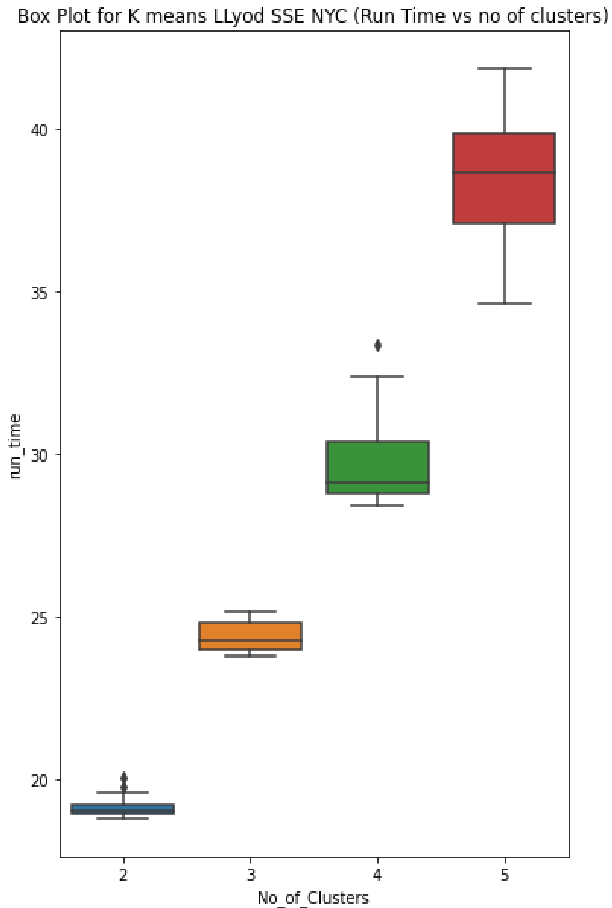
NYC DATASET



(12)

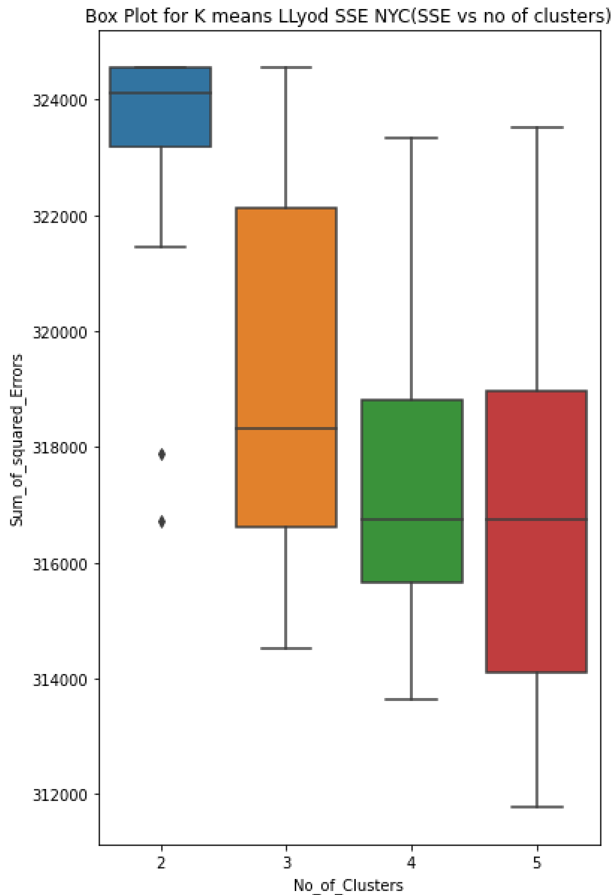

Box Plot for K means LLyod SSE NYC (Run Time vs no of clusters)
run_time
40
35
30
25
20
2
3
4
5
No_of_Clusters

(13)

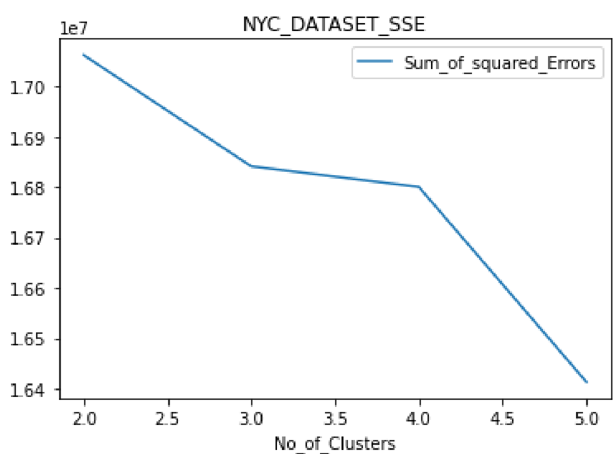


(14)

Problem 5 continued on next page...



(15)



(16)

Discussion of Findings

- Changed the convergence criteria using SSE
- **The covergence criteria decided is** At every single iteration we calculate the Within Sum of Square Errors and when the Sum of Square errors between cluster assigned drops to 10 percent from the previous cluster our algorithm converges

- It is a customizable code with the threshold can be decided by the user and when the difference between SSE drops to a certain user specified value the convergence takes place and the algorithm stops.
- However the algorithm is susceptible to random cluster initialization and it depends on the first cluster selected.
- After running the algorithm on Diabetes dataset as well as New york Comments Dataset we can conclude
- For the Diabetes dataset the SSE decrease as we increase the cluster.
- The target value error decreases when the number of clusters are three and it balances later
- However due to randomness the target value error shows different graphs based on merging strategy and the general trend is it stabilizes and the classes tend to balance
- From the graph of runtime and box plots we can conclude as the number of clusters increase the run time also increase
- For the NYC dataset we can conclude due to sparsity in the dataset it leads to homogeneous clusters and thus the target value error remains constant.
- The run time increases as the number of clusters increases and thus the median value of run time increases with increase in cluster
- **Comparisons for the graphs**
- SSE convergence is generally considered the better metric to use because it directly measures the quality of the clustering. Convergence of the change of centroids can be influenced by factors such as the initial positions of the centroids and the number of clusters.
-
- In summary, SSE convergence is a better metric to use in K-means than convergence of the change of centroids as it provides a more direct measurement of the quality of clustering.

Problem 6

Traditional k-means initialization is based on choosing values from a uniform distribution. In this question, you are asked to improve k-means through initialization. k-means ++ is an extended k-means clustering algorithm and induces non-uniform distributions over the data that serve as the initial centroids. Read the paper and discuss the idea in a paragraph. Implement this idea to improve your k-means program. Run your program, C_{k++}, against the Diabetes and New York Times Comments data sets. Report the total error rates for $k = 2, \dots 5$ for 20 runs each for both data sets. Moreover, compare C_k, $C_{k_{SSE}}$ and C_{k++}'s run time for $k = 2, \dots 5$ for 20 runs using both data sets. Presenting the results that are easily understandable. Plots are generally a good way to convey complex ideas quickly, i.e., box plot. Discuss your results [**20 points**].

R/Python script

```
# Sample R Script With Highlighting
```

```
import numpy as np
import swifter
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cdist
import time

def kmeans_pp_init(input_dataframe,no_of_clusters):
    '''
    K-means++ is a variant of the K-means algorithm that aims
    to improve the initial centroids' selection
    in the clustering process.
    The standard K-means algorithm initializes the cluster
    centroids randomly,
    which can lead to suboptimal clustering results,

    especially if the dataset has complex or irregular
    structures.
    '''
    list_of_centroids=[]
    #Choosing the first centroid randomly
    centroid = input_dataframe.apply(lambda x: float(x.sample()))
    list_of_centroids.append(centroid)

    iterator=2
    while iterator<=no_of_clusters:
        '''
        Calculating the distances from the centroid to every
        data point
        If the no of centroids are more than 1 calculate the
        distance from every centroid and take minimum distance
        '''
        distances =
        np.array(np.amin(cdist(input_dataframe,list_of_centroids
        ,metric='euclidean'),axis=1))
        #Next centroid will be selected with probability
        proportional to the distance

        probs = distances / np.sum(distances)
        '''
        Selection of the next centroids
        '''
        next_centroid = input_dataframe.iloc[np.random.choice(len(input_datafram
        e),p=probs)]
        list_of_centroids.append(next_centroid)
        iterator+=1


    centroid_df=pd.concat(list_of_centroids,axis=1,ignore_index=True)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'
```

```
    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''
    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster

    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the
    dataset
    #and it randomly assigns if euclideab distance results in a
    tie
    '''
    This function returns the index of minimum distances as a
    dataframe
    '''
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled
    and the original dataframe
    '''
    df_original_label_join=input_dataframe.join(df_clustered_lab
    el)
    #This is a dataframe that consists of datapoints as well as
    the cluster assigned
    df_original_label_join.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column
    and take its mean
    new_centroids=df_original_label_join.groupby('Cluster_Assign
    ed').mean()
    #Here transpose is taken to maintain consistency between original random centroids and
    return new_centroids.T


def kmeans_plus_plus(input_dataframe,no_of_clusters,threshold,no_of_iterations):
    '''
    This function takes original dataframe,number of clusters,threshold as input.
    '''
    start_time=time.time()
    iteration=0
    #Step 1 of k means ++ is to get K means plus plus
    initialization centroids

    initial_centroid=kmeans_pp_init(input_dataframe,no_of_cluste
    rs)
    #Randomly generated centroids would be stored on centroids
```

```
    #Storing the column list to handle K ties

    initial_centroid_column_list=initial_centroid.columns.to_lis
    t()

    while True:
        '''
        The while loop runs until convergence condition is met
        '''

        df_cluster_label=get_labels(input_dataframe,initial_cent
        roid)
        df_new_centroids=get_new_centroids(df_cluster_label,inpu
        t_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
        new_list_of_columns=df_new_centroids.columns.to_list()
        #Keeping the number of clusters same
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
            df_new_centroids[col]=initial_centroid[col]

        from scipy.spatial.distance import euclidean
        scalar_product =
        [euclidean(initial_centroid[col],df_new_centroids[col])
        for col in initial_centroid.columns]
        threshold_calculated=float(sum(scalar_product))/no_of_cl
        usters


        iteration+=1

        if threshold_calculated<threshold:
            print("The input Threshold was
            {}".format(threshold))
            print("The calculated threshold is
            {}".format(threshold_calculated))

        if iteration>no_of_iterations:
            print("Limit for iterations has exceeded")

        if threshold_calculated<threshold or iteration>no_of_iterations:

            error=cluster_error_target_variable(df_cluster_label
            ,input_dataframe,no_of_clusters,df_new_centroids)
            sum_of_square_error=sum_of_square_error_function(df_
            cluster_label,input_dataframe,df_new_centroids,no_of
            _clusters)
            end_time=time.time()
            return
```

```
            df_new_centroids,error,sum_of_square_error,end_time-
            start_time
            break
        else:
            initial_centroid= df_new_centroids


def
sum_of_square_error_function(df_cluster_label,input_dataframe,df
_new_centroids,no_of_clusters):
    '''
    This function calculates the euclidean distance between new
    formed
    centroids and the datapoints in that cluster
    '''

    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)
    total_error=[]
    for cluster in range(no_of_clusters):

        df_data_label_cluster=df_data_label[df_data_label['Clust
        er_Assigned']==cluster]
        df_data_label_cluster=df_data_label_cluster.drop('Cluste
        r_Assigned',axis=1)
        centroids=pd.DataFrame(df_new_centroids[cluster])

        euclidean_distance=cdist(df_data_label_cluster,centroids
        .T,metric='euclidean')

        total_error.append(sum(euclidean_distance))
    return round(float(''.join(map(str, sum(total_error)))),3)



def
cluster_error_target_variable(df_cluster_label,input_dataframe,n
o_of_clusters,df_new_centroids):
    '''
    This calculates the error for every cluster and sums up the
    error based on the formula for error
    '''

    target_variable_centroid=input_dataframe.groupby('readmitted


    ').mean().reset_index()
    '''

    Target variable centroid is input dataframe taking mean
    '''
```

```
new_centroids= df_new_centroids.T
#
df_data_label=input_dataframe.join(df_cluster_label)
#Renaming the column
df_data_label.rename(columns=
{0:'Cluster_Assigned'},inplace=True)

# Get the columns of the data dataframe
columns = input_dataframe.columns

sum_of_square_Error= []
# Compute the distance between each data point and its assigned centroid
for i in range(len(new_centroids)):
    s=[]
    for j in range(len(target_variable_centroid)): ### mean
    centroid
        #Calculating the error between target variable centroid and new centroids
        distance =
        np.sum(np.square(target_variable_centroid[target_var
        iable_centroid['readmitted']==j][columns] -
        new_centroids.iloc[i][columns]), axis=1)

        #Storing the distance
        s.append(distance.iloc[0])
    sum_of_square_Error.append(s)



merged_new_label=pd.DataFrame(sum_of_square_Error).idxmin(ax
is=1)

#Merging of cluster

mapping_dictionary=merged_new_label.to_dict()

#Getting clusters to a new column
df_data_label['target_variable_cluster']=df_data_label['Clus
ter_Assigned'].replace(mapping_dictionary)


total_cluster_error = []

for class_name in range(0,2):
    df_cluster =
    df_data_label[df_data_label['target_variable_cluster']
    == class_name]
    yi = len(df_cluster[df_cluster['readmitted'] == 1])
    #Calculating Ni
    ni = len(df_cluster[df_cluster['readmitted'] == 0])
    if yi == 0 and ni == 0:
        error_ci = 0
    else:
        error_ci = ni / (ni + yi) # calculate the error
```

```
            rate of the current cluster

        total_cluster_error.append(error_ci)
    return round(sum(total_cluster_error),3)
error_values_kmeans_plus_plus=[]
for no_of_clusters in range(2,6):
    #Taking the cluster value from 2 to 5
    for no_of_experiments in range(1,21):
        #Performing experiments for each cluster 20 times
        final_centroids,error_target_variable,sum_of_squared_err
        or,run_time=kmeans_plus_plus(df_diabetes_final,no_of_clu
        sters,10,100)
        #Storing the variables in dataframe
        error_values_kmeans_plus_plus.append([no_of_clusters,no_


        of_experiments,error_target_variable,sum_of_squared_erro
        r,run_time])
error_values_kmeans_plus_plus_df=
pd.DataFrame(error_values_kmeans_plus_plus,columns=
['No_of_Clusters', 'Iteration Number', 'Target Variable
Error','Sum_of_squared_Errors','run_time'])
error_plot_kmeans_plus_plus=error_values_kmeans_plus_plus_df.gro
upby(['No_of_Clusters']).mean().reset_index()
[['No_of_Clusters','Target Variable
Error','Sum_of_squared_Errors','run_time']]
error_plot_kmeans_plus_plus
import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_kmeans_plus_plus_df['No_of_Clusters']
,y=error_values_kmeans_plus_plus_df['Target Variable Error'])
plt.title('Box Plot for K means LLyod K++ (error vs no of
clusters)')
plt.show()
import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_kmeans_plus_plus_df['No_of_Clusters']
,y=error_values_kmeans_plus_plus_df['Sum_of_squared_Errors'])
plt.title('Box Plot for K means LLyod k++(SSE vs no of
clusters)')
plt.show()
import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_kmeans_plus_plus_df['No_of_Clusters']
,y=error_values_kmeans_plus_plus_df['run_time'])
plt.title('Box Plot for K means LLyod k++(Run Time vs no of
clusters)')
```

```
plt.show()


#Run time comparison
error_values_kmeans_convergence['Algorithm_Used']='K_Means_SSE_o
nvergence'
error_plot_kmeans_plus_plus['Algorithm_Used']='K++Initializatio'
error_plot['Algorithm_Used']='Llyod_Kmeans'

k_means_metric=pd.concat([error_values_kmeans_convergence,error_
plot_kmeans_plus_plus,error_plot],axis=0)
k_means_metric

sns.lineplot(x="No_of_Clusters",
y="Sum_of_squared_Errors",hue="Algorithm_Used",
data=k_means_metric)
plt.title('Diabetes_dataset_Comparison)
plt.show()

sns.lineplot(x="No_of_Clusters", y="Sum_of_squared_Errors",
hue="Algorithm_Used", data=k_means_metric)
plt.title('Diabetes_Dataset_Comparison')
plt.show()
sns.barplot(x="No_of_Clusters", y="Sum_of_squared_Errors",
hue="Algorithm_Used", data=k_means_metric)
plt.title('Diabetes_Dataset_SSE_Comparison')
plt.show()
sns.barplot(x="No_of_Clusters", y="Target Variable Error",
hue="Algorithm_Used", data=k_means_metric)
plt.title('Diabetes_dataset_eror_comparison')
plt.show()
sns.lineplot(x="No_of_Clusters", y="run_time",
hue="Algorithm_Used", data=k_means_metric)
plt.title('Diabetes_Dataset_Comparison')
plt.show()

#NYC DATASET


import numpy as np
import swifter
from scipy.spatial.distance import euclidean
from scipy.spatial.distance import cdist
import time


def kmeans_pp_init(input_dataframe,no_of_clusters):
    '''
    K-means++ is a variant of the K-means algorithm that aims
    to improve the initial centroids' selection
    in the clustering process.
    The standard K-means algorithm initializes the cluster
    centroids randomly,
```

```
    which can lead to suboptimal clustering results,
    especially if the dataset has complex or irregular
    structures.
    '''
    list_of_centroids=[]
    #Choosing the first centroid randomly
    centroid = input_dataframe.apply(lambda x: float(x.sample()))
    list_of_centroids.append(centroid)

    iterator=2
    while iterator<=no_of_clusters:
        '''
        Calculating the distances from the centroid to every
        data point
        If the no of centroids are more than 1 calculate the
        distance from every centroid and take minimum distance
        '''
        distances =
        np.array(np.amin(cdist(input_dataframe,list_of_centroids
        ,metric='euclidean'),axis=1))
        #Next centroid will be selected with probability
        proportional to the distance

        probs = distances / np.nansum(distances)
        probs = [0 if np.isnan(x) else x for x in probs]
        '''
        Selection of the next centroids
        '''
        next_centroid =

        input_dataframe.iloc[np.random.choice(len(input_datafram
        e),p=probs)]
        list_of_centroids.append(next_centroid)
        iterator+=1

    centroid_df=pd.concat(list_of_centroids,axis=1,ignore_index=True)
    #Naming the column as Label for ease of purpose
    centroid_df.index.name='Cluster_Assigned'


    return centroid_df

def get_labels(input_dataframe,centroid_df):
    '''

    This function takes centroids as input and takes the
    initial dataframe and gives them labels to which cluster
    they belong to
    '''
    euclidean_distances = centroid_df.swifter.apply(lambda x:
    np.sqrt(((input_dataframe - x) ** 2).sum(axis=1)))
    #Here we use idxmin functionality to handle ties in the
    dataset
```

```
    #and it randomly assigns if euclideab distance results in a
    tie
    '''
    This function returns the index of minimum distances as a
    dataframe
    '''
    return pd.DataFrame(euclidean_distances.idxmin(axis=1))


def get_new_centroids(df_clustered_label,input_dataframe):
    '''
    The input dataframe is the dataframe with clusters labelled
    and the original dataframe
    '''
    df_original_label_join=input_dataframe.join(df_clustered_lab
    el)

    #This is a dataframe that consists of datapoints as well as
    the cluster assigned
    df_original_label_join.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)
    #To get the new centroids we group by the Label column and
    take its mean
    new_centroids=df_original_label_join.groupby('Cluster_Assign
    ed').mean()
    #Here transpose is taken to maintain consistency between
    original random centroids and
    return new_centroids.T


def kmeans_llyod_kpp(input_dataframe,no_of_clusters,threshold,no_of_iterations):
    '''
    This function takes original dataframe,number of clusters,threshold as input.
    '''
    start_time=time.time()
    iteration=0
    #Step 1 of k means is to get random _Centroids
    initial_centroid=kmeans_pp_init(input_dataframe,no_of_clusters)
    #Randomly generated centroids would be stored on centroids
    #Storing the column list to handle K ties
    initial_centroid_column_list=initial_centroid.columns.to_list()

    while True:
        '''
        The while loop runs until convergence condition is met
        '''
        df_cluster_label=get_labels(input_dataframe,initial_centroid)
        df_new_centroids=get_new_centroids(df_cluster_label,input_dataframe)
        '''
        Handling (Maintaining K Centroids)
        '''
        new_list_of_columns=df_new_centroids.columns.to_list()
        #Keeping the number of clusters same
```

```
        initial_set_columns = set(initial_centroid_column_list)
        new_set_columns = set(new_list_of_columns)
        missing_columns = initial_set_columns - new_set_columns
        for col in missing_columns:
            df_new_centroids[col]=initial_centroid[col]

        from scipy.spatial.distance import euclidean
        scalar_product =
        [euclidean(initial_centroid[col],df_new_centroids[col])
        for col in initial_centroid.columns]
        threshold_calculated=float(sum(scalar_product))/no_of_cl
        usters

        iteration+=1

        if threshold_calculated<threshold:
            print("The input Threshold was {}".format(threshold))
            print("The calculated threshold is {}".format(threshold_calculated))

        if iteration>no_of_iterations:
            print("Limit for iterations has exceeded")

        if threshold_calculated<threshold or iteration>no_of_iterations:
            error=cluster_error_target_variable(df_cluster_label
            ,input_dataframe,no_of_clusters,df_new_centroids)
            sum_of_square_error=sum_of_square_error_function(df_

            cluster_label,input_dataframe,df_new_centroids,no_of
            _clusters)
            end_time=time.time()
            return df_new_centroids,error,sum_of_square_error,end_time-
            start_time
            break
        else:
            initial_centroid= df_new_centroids


def
sum_of_square_error_function(df_cluster_label,input_dataframe,df
_new_centroids,no_of_clusters):
    '''
    This function calculates the euclidean distance between new formed
    centroids and the datapoints in that cluster
    '''
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns={0:'Cluster_Assigned'},inplace=True)
    total_error=[]
    for cluster in range(no_of_clusters):
        df_data_label_cluster=df_data_label[df_data_label['Cluster_Assigned']==cluster]
        df_data_label_cluster=df_data_label_cluster.drop('Cluster_Assigned',axis=1)
        centroids=pd.DataFrame(df_new_centroids[cluster])
        euclidean_distance=cdist(df_data_label_cluster,centroids.T,metric='euclidean')
```

```
        total_error.append(np.nansum(euclidean_distance))

    return round(np.nansum(total_error),3)
    #return round(float(''.join(map(str, sum(total_error)))),3)




def
cluster_error_target_variable(df_cluster_label,input_dataframe,n
o_of_clusters,df_new_centroids):
    '''
    This calculates the error for every cluster and sums up the
    error based on the formula for error
    '''

    target_variable_centroid=input_dataframe.groupby('editorsSel
    ection').mean().reset_index()
    '''
    Target variable centroid is input dataframe taking mean
    '''
    new_centroids= df_new_centroids.T
    #
    df_data_label=input_dataframe.join(df_cluster_label)
    #Renaming the column
    df_data_label.rename(columns=
    {0:'Cluster_Assigned'},inplace=True)

    # Get the columns of the data dataframe
    columns = input_dataframe.columns

    sum_of_square_Error= []
    # Compute the distance between each data point and its assigned centroid
    for i in range(len(new_centroids)):
        s=[]
        for j in range(len(target_variable_centroid)): ### mean
        centroid
            #Calculating the error between target variable
            centroid and new centroids
            distance =
            np.sum(np.square(target_variable_centroid[target_var
            iable_centroid['editorsSelection']==j][columns] -
            new_centroids.iloc[i][columns]), axis=1)
            #Storing the distance
            s.append(distance.iloc[0])
        sum_of_square_Error.append(s)


    merged_new_label=pd.DataFrame(sum_of_square_Error).idxmin(axis=1)

    #Merging of cluster
    mapping_dictionary=merged_new_label.to_dict()

    #Getting clusters to a new column
```

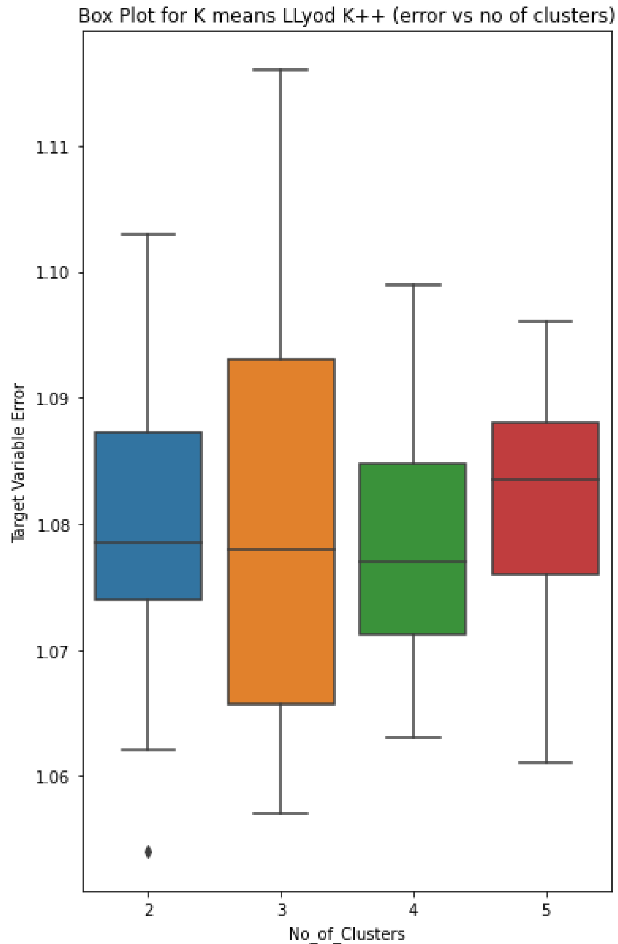
```
    df_data_label['target_variable_cluster']=df_data_label['Clus
    ter_Assigned'].replace(mapping_dictionary)


    total_cluster_error = []

    for class_name in range(0,2):
        df_cluster = df_data_label[df_data_label['target_variable_cluster'] == class_name]
        yi = len(df_cluster[df_cluster['editorsSelection'] == 1])
        #Calculating Ni
        ni = len(df_cluster[df_cluster['editorsSelection'] == 0])
        if yi == 0 and ni == 0:
            error_ci = 0
        else:
            error_ci = ni / (ni + yi) # calculate the error rate of the current cluster
        total_cluster_error.append(error_ci)
    return round(sum(total_cluster_error),3)
error_values_kmeans_plus_plus=[]
for no_of_clusters in range(2,6):
    #Taking the cluster value from 2 to 5
    for no_of_experiments in range(1,21):
        #Performing experiments for each cluster 20 times
        final_centroids,error_target_variable,sum_of_squared_err
        or,run_time=kmeans_llyod_kpp(count_vectorizer_df,no_of_c
        lusters,10
        ,100)
        #Storing the variables in dataframe
        error_values_kmeans_plus_plus.append([no_of_clusters,no_
        of_experiments,error_target_variable,sum_of_squared_erro
        r,run_time])
error_values_kmeans_plus_plus_df=
pd.DataFrame(error_values_kmeans_plus_plus,columns=
['No_of_Clusters', 'Iteration Number', 'Target Variable
Error','Sum_of_squared_Errors','run_time'])
error_values_kmeans_plus_plus_df.to_csv('KPP_NYC_1lakh.csv')
No_of_Clusters      Iteration Number    Target Variable Error
Sum_of_squared_Errors    run_time
0    2    1    0.987    324555.058    11.068163
1    2    2    0.987    324208.365    10.863929
2    2    3    0.987    323643.674    10.816018
3    2    4    0.987    323812.754    10.750855
4    2    5    0.987    324554.230    10.810077
...  ...  ...  ...  ...  ...
75   5    16   0.987    319353.444    15.820424
76   5    17   0.987    323099.997    15.740928
77   5    18   0.987    319056.689    16.995517
78   5    19   0.987    322591.881    16.003247
79   5    20   0.987    321803.560    15.865556

80 rows    5 columns

import seaborn as sns
plt.figure(figsize=(6, 10))
```

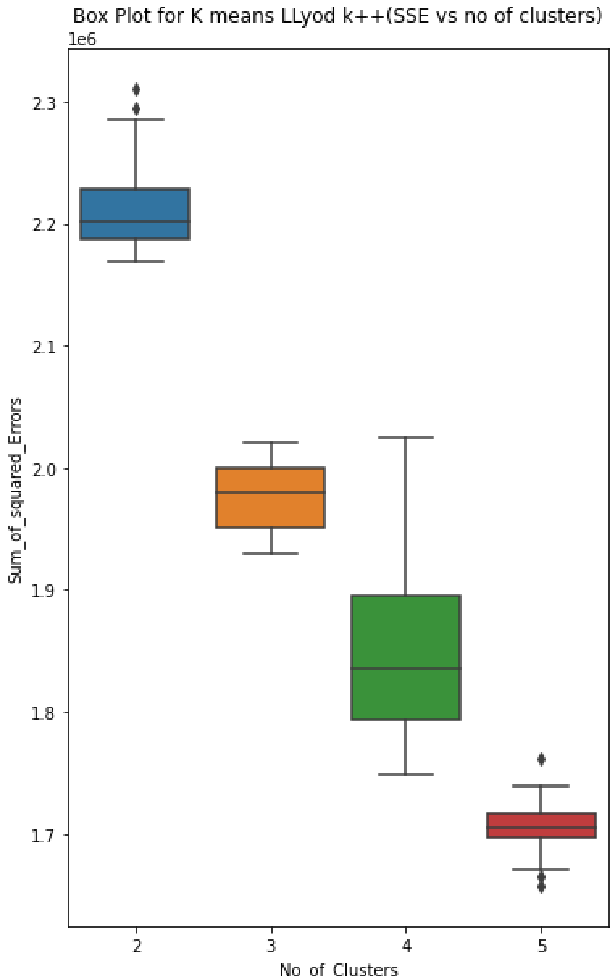
```
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_kmeans_plus_plus_df['No_of_Clusters']
,y=error_values_kmeans_plus_plus_df['Target Variable Error'])
plt.title('Box Plot for K means LLyod K++ NYC(error vs no of clusters)')
plt.show()
import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_kmeans_plus_plus_df['No_of_Clusters']
,y=error_values_kmeans_plus_plus_df['Sum_of_squared_Errors'])
plt.title('Box Plot for K means LLyod k++( NYC SSE vs no of
clusters)')
plt.show()
import seaborn as sns
plt.figure(figsize=(6, 10))
#Plotting Box plot
#Plotting values of errors for 80 iterations
sns.boxplot(x=error_values_kmeans_plus_plus_df['No_of_Clusters']
,y=error_values_kmeans_plus_plus_df['run_time'])
plt.title('Box Plot for K means LLyod k++ NYC(Run Time vs no of clusters)')
plt.show()
sns.lineplot(x="No_of_Clusters", y="Sum_of_squared_Errors",
hue="Algorithm_Used", data=k_means_metric)
plt.title('NYC_Comparison')
plt.show()
sns.barplot(x="No_of_Clusters", y="Sum_of_squared_Errors",
hue="Algorithm_Used", data=k_means_metric)
plt.title('NYC_Comparison')
plt.show()
sns.barplot(x="No_of_Clusters", y="Target Variable Error",
hue="Algorithm_Used", data=k_means_metric)
plt.title('NYC_Comparison')
plt.show()
sns.lineplot(x="No_of_Clusters", y="run_time",
hue="Algorithm_Used", data=k_means_metric)
plt.title('NYC_Comparison')
plt.show()
```

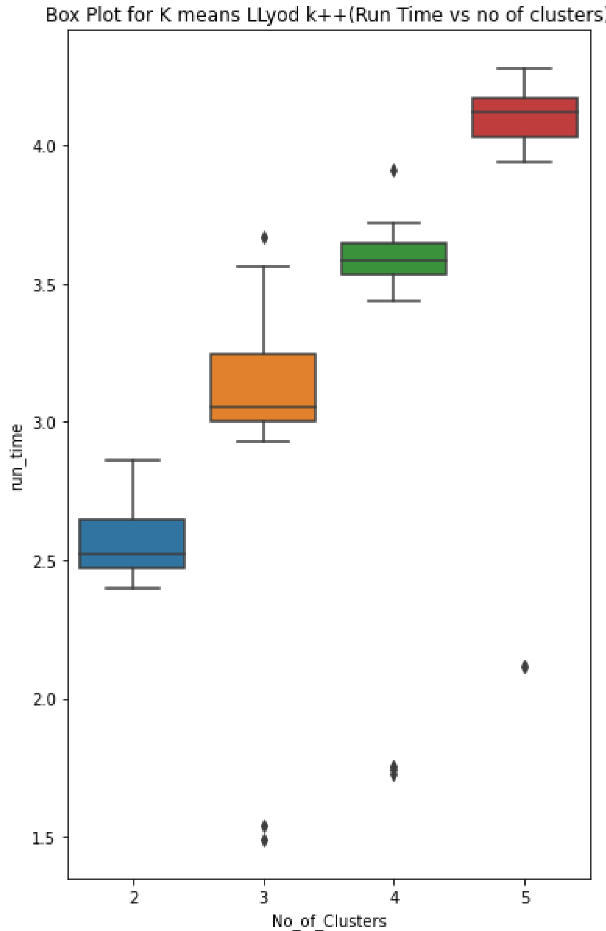
Plots

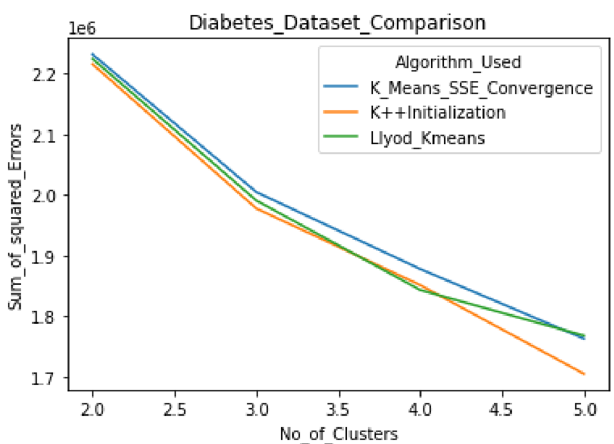
Place images here with suitable captions. **Diabetes Dataset**

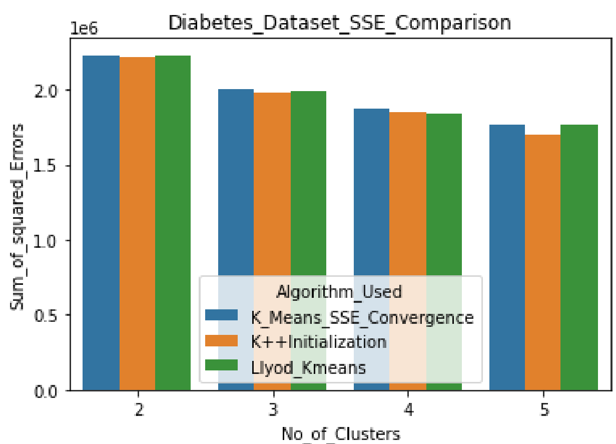

Error and SSE vs No of clusters K++
1e6
Error
SSE
Target Variable Error
Sum_of_squared_error
No_of_Clusters

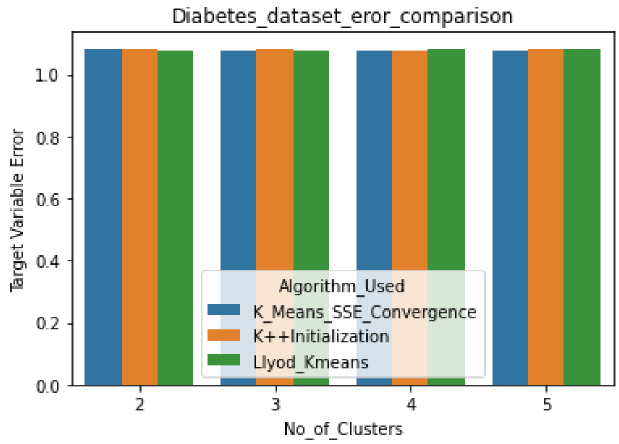

Box Plot for K means LLyod K++ (error vs no of clusters)
Target Variable Error
No_of_Clusters

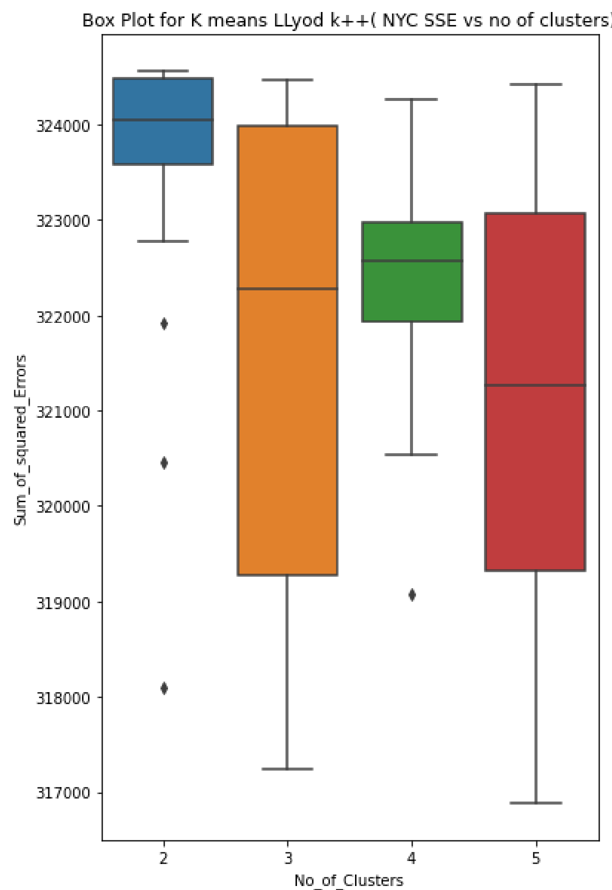

Box Plot for K means LLyod k++(SSE vs no of clusters)
1e6
Sum_of_squared_Errors
No_of_Clusters

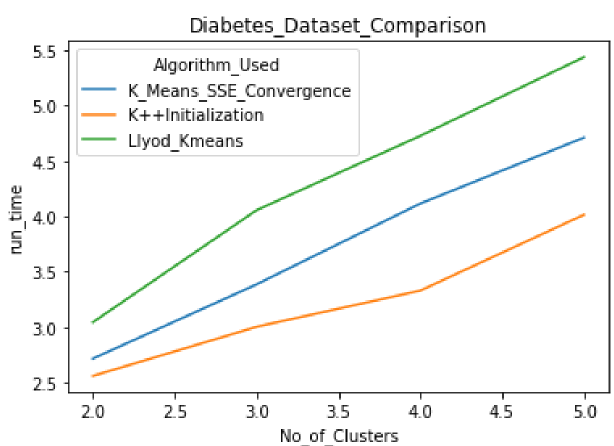

Box Plot for K means LLyod k++(Run Time vs no of clusters)
run_time
No_of_Clusters

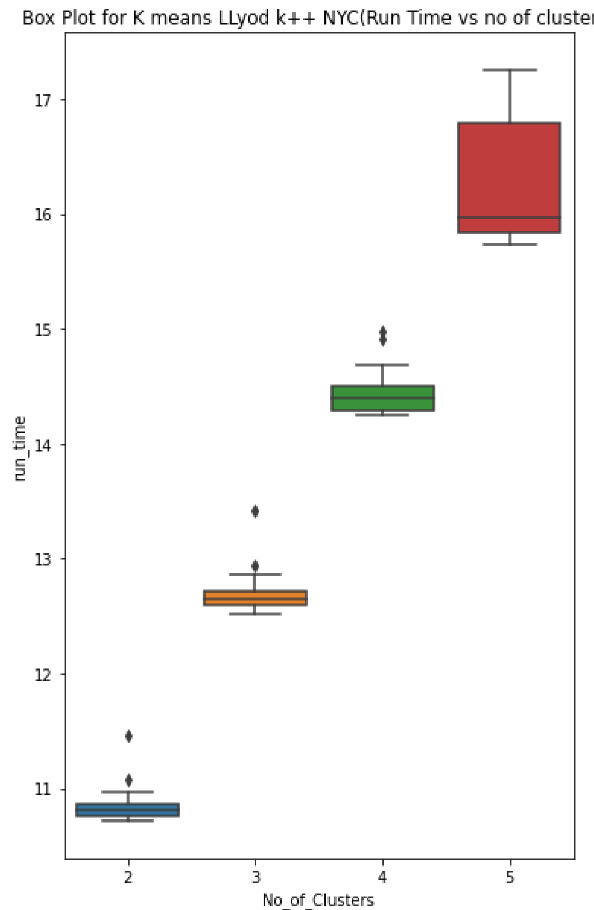

Diabetes_Dataset_Comparison
1e6
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
Sum_of_squared_Errors
No_of_Clusters

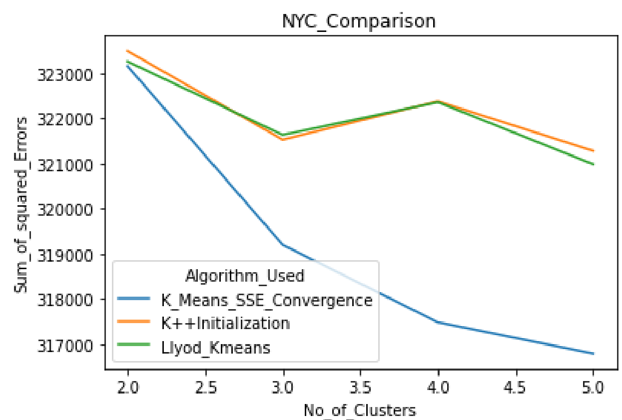

Diabetes_Dataset_SSE_Comparison
1e6
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
Sum_of_squared_Errors
No_of_Clusters

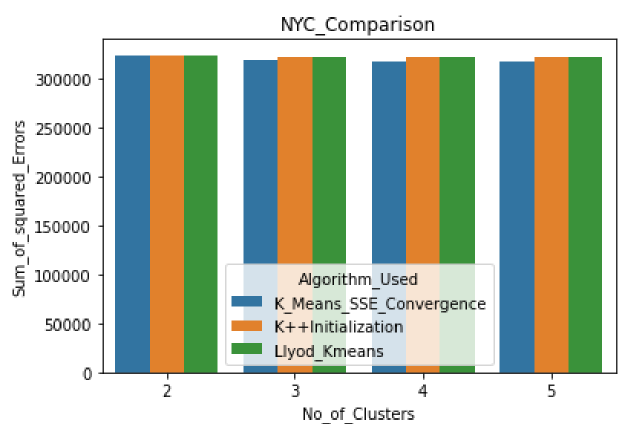

Diabetes_dataset_eror_comparison
Target Variable Error
1.0
0.8
0.6
0.4
0.2
0.0
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
2
3
4
5
No_of_Clusters

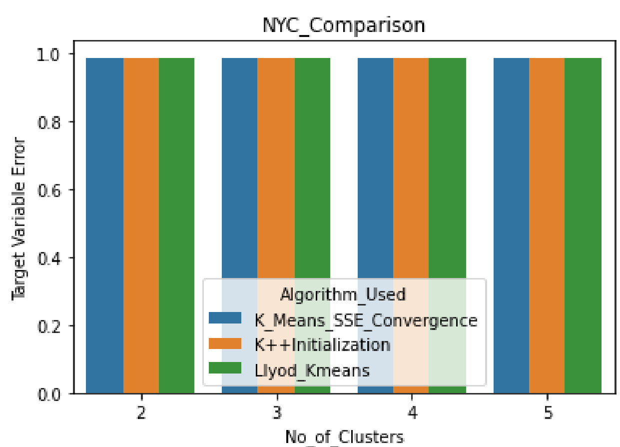

Box Plot for K means LLyod k++(NYC SSE vs no of clusters)
Sum_of_squared_Errors
324000
323000
322000
321000
320000
319000
318000
317000
2
3
4
5
No_of_Clusters

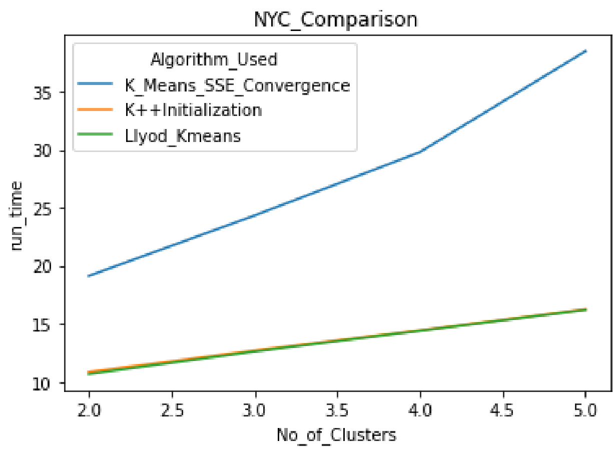

Diabetes_Dataset_Comparison
run_time
5.5
5.0
4.5
4.0
3.5
3.0
2.5
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
2.0
2.5
3.0
3.5
4.0
4.5
5.0
No_of_Clusters

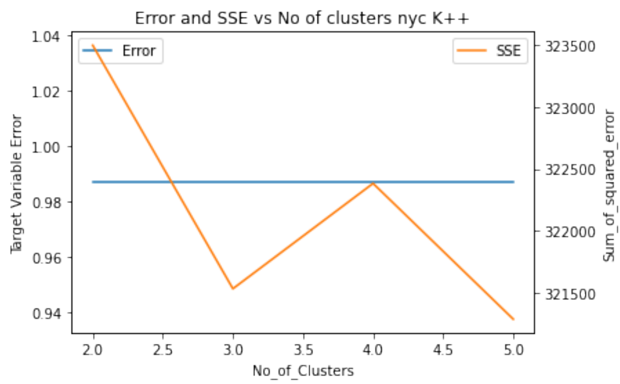

Box Plot for K means LLyod k++ NYC(Run Time vs no of clusters)
run_time
No_of_Clusters


NYC_Comparison
Sum_of_squared_Errors
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
No_of_Clusters


NYC_Comparison
Sum_of_squared_Errors
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
No_of_Clusters


NYC_Comparison
Target Variable Error
Algorithm_Used
K_Means_SSE_Convergence
K++Initialization
Llyod_Kmeans
No_of_Clusters





Discussion of Findings

Answer here. . .

- **Summarisation of Paper for K means** item k-means++ is a variation of the k-means clustering algorithm that aims to improve its performance and accuracy by selecting more informative initial seed points.
- In standard k-means, the initial seed points are randomly selected, which can result in poor cluster assignments and slow convergence.
- k-means++ selects the initial seeds in a way that maximizes the distances between them, ensuring that they are well distributed across the data space.
- This approach reduces the likelihood of selecting suboptimal seed points and improves the final clustering quality.
- The k-means++ algorithm has been shown to outperform the standard k-means algorithm on a wide range of datasets.
- The advantages of k-means++ become more pronounced as the dimensionality of the data increases.
- Have implemented K means ++ Initialization and have signiicantly reduced the errors.
- For the Diabetes Dataset when error calculagted by K means and error calculated by K means ++ is deduced we get the below error metric
- Cluster difference
- 1 9035.03725
- 2 30161.40420
- 3 7083.35030
- 4 71473.21780
- For the NYC dataset we are getting similar reduction in errors, thus With the Implementation of K means ++ there is a significant reduction in error.
- Graphs for Diabetes Dataset

- From the graphs we can conclude that SSE Decreases as the number of cluster increases
- Also the Target variable after initializing with K means ++ replicates the original classes and thus when we increase the clusters the imbalance is reduced
- The box plots indicates the run time of the Algorithm increases as the number of clusters increase
- The median value of Dataset for SSE decreases when the number of clusters increases.
- textbfComparison Graphs for Diabetes Dataset
- When compared the three algorithms we can dedude
- The sum of Square Errors reduction is highest in K Means ++ Initialization and when we increase the number of clusters K++ Means has the lowest SSE
- The barplots compare the SSE error between all the algorithms and it clearly indicates that K means ++Initialization has an edge over othe algorithms
- However when we plot the time the Llyod's K means has high run time, However this can be an anomaly of distance calculations.
- The general notation suggests as K means calculates the clusters and it has number of iterations higher than regular k means thus it should have high run time
- **Graphs for Nyc Dataset**
- We can conclude even after initializing the clusters from K means ++ the error has decreased
- This can be shown in the comparison graph
- From the box plots we can conclude that as the number of clusters increase the run time increases
- The median SSE also decreases as we increase the number of clusters.
- **Comparison for Algorithms NYC**
- The Sum of Square Errors is decreasing the max in SSE converenge
- The overall error remains constant as the data is sparse.
- **Conclusions**
- Some factors to consider when deciding whether to use K-means++ initialization:
- Dataset size: K-means++ initialization is more useful for larger datasets. For smaller datasets, random initialization may work just as well.
- Clustering performance: If the K-means algorithm is not producing good quality clusters, it may be worth trying K-means++ initialization to see if it improves performane
- Computational efficiency: K-means++ initialization can be more computationally expensive than random initialization. If you are working with very large datasets or have limited computing resources, random initialization may be a better choice.

Problem 7

In this question, you are asked to make use of the *R/Python* libraries for k-means. The elbow technique is used to determine optimal cluster number. Find the optimal cluster number for the Diabetes and New York Times Comments data sets using elbow method (for $2 \leq k \leq 15$). Provide plots that show the total SSE for each k. Discuss your results [**20 points**].

R/Python script

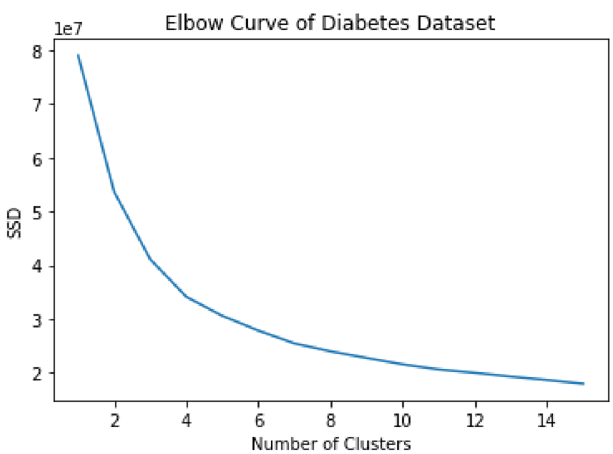
```
# Sample R Script With Highlighting
```

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from tqdm import tqdm

# Load data from CSV file
data = df_diabetes_final
columns=df_diabetes_final.columns

#Extract features
X = data[['age', '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','max_glu_serum',
        'A1Cresult', 'metformin', 'glimepiride', 'glipizide',
       'glyburide', 'pioglitazone', 'rosiglitazone', 'insulin',
       'change',

       'diabetesMed', 'readmitted', 'gender_Female',
       'gender_Male',

       'race_AfricanAmerican', 'race_Asian', 'race_Caucasian',
       'race_Hispanic',
       'race_Other']]

# Create a list to hold the Sum of Squared Distances (SSD)
ssd = []

# Create KMeans objects for k=1 to k=16
for k in tqdm(range(1, 16)):
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(X)
    ssd.append(kmeans.inertia_)

# Plot elbow curve
plt.plot(range(1,16), ssd)
plt.title('Elbow Curve of Diabetes Dataset')
plt.xlabel('Number of Clusters')
plt.ylabel('SSD')
plt.show()
```

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from tqdm import tqdm

# Load data from CSV file
data = count_vectorizer_df
data=data.fillna(0)

# Create a list to hold the Sum of Squared Distances (SSD)
ssd = []

# Create KMeans objects for k=2 to k=16
for k in tqdm(range(2, 16)):
    kmeans = KMeans(n_clusters=k,random_state=42)
    kmeans.fit(data)
    ssd.append(kmeans.inertia_)

# Plot elbow curve
plt.plot(range(2, 16), ssd)
plt.title('Elbow Curve of New York Dataset')
plt.xlabel('Number of Clusters')
plt.ylabel('SSD')
plt.show()
```

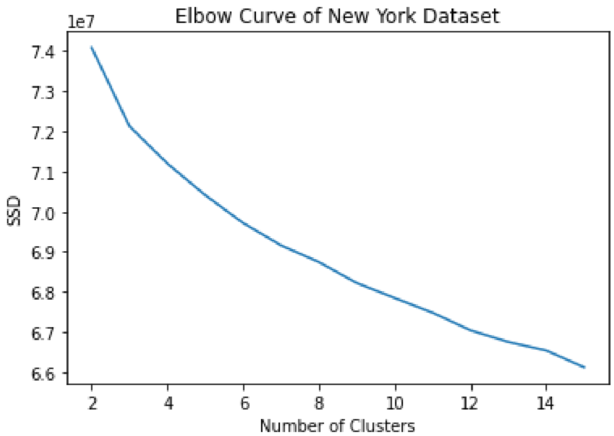
Plots

Place images here with suitable captions. **Diabetes Dataset**



New York Comments Dataset

Problem 7 continued on next page...



Discussion of Findings

Answer here...

- From the graph of Elbow of Diabetes dataset there is not a proper value or an elbow in the graph since the error is monotonously decreasing
- Visually we can select the clusters from 4 to 6
- However we can check that the slope does not change from cluster 10 and hence that could be potential cluster
- However because the curve is not stable we can see we require domain knowledge to guess adequate number of clusters
- However there are situations where elbow method provides less information, and we can use other methods like
- Silhouette analysis: Silhouette analysis measures how similar an object is to its own cluster compared to other clusters. The silhouette score ranges from -1 to 1, with higher scores indicating that the object is well-matched to its own cluster and poorly matched to neighboring clusters. The optimal k value is the one that maximizes the average silhouette score across all data points.
- From the graph of Elbow of New York dataset there is not a proper value or an elbow in the graph since the error is monotonously decreasing
- Visually we can select the clusters from 10 to 12
- However we can check that the slope does not change from cluster 12 and hence that could be potential cluster
- However because the curve is not stable we can see we require domain knowledge to guess adequate number of clusters.
- Since the elbow method doesnt work for NYC dataset we can take other measures.
- However there are situations where elbow method provides less information, and we can use other methods like

- Silhouette analysis: Silhouette analysis measures how similar an object is to its own cluster compared to other clusters. The silhouette score ranges from -1 to 1, with higher scores indicating that the object is well-matched to its own cluster and poorly matched to neighboring clusters. The optimal k value is the one that maximizes the average silhouette score across all data points.

Extra credit

This part is optional.

1. Ball-k-means calculates the distance of a data point from the centroid to find the annular region in which the data point resides. The annular region helps determine which neighbor centroids should be included in distance computations. This improves the run-time over earlier approaches by avoiding expensive computations. Run your program, $C_{k_{ball}}$, against the Diabetes and New York Times Comments data sets. Report the total error rates for $k = 2, \ldots 5$ for 20 runs each for both data sets. Moreover, compare C_k, $C_{k_{SSE}}$, C_{k++} and $C_{k_{ball}}$'s run time for $k = 2, \ldots 5$ for 20 runs using both data sets. Presenting the results that are easily understandable. Plots are generally a good way to convey complex ideas quickly, i.e., box plot. Discuss your results [**30 points**].

   ### R/Python script

   ```
   # Sample R Script With Highlighting
   ```

   ```
   # Sample Python Script With Highlighting
   ```

   ### Discussion of Findings

   Answer here...

   ### Plots

   Place images here with suitable captions.

2. The student who has the fastest implementation of all four clustering algorithms will receive extra 20 points [**20 points**].

Submission

You must use LaTeX to turn in your assignments. Please submit the following two files via Canvas:

1. A .pdf with the name `yourname-hw4-everything.pdf` which you will get after compiling your .tex file.
2. A .zip file with the name `yourname-hw4.zip` which should contain your .tex, .pdf, codes(.py, .ipynb, .R, or .Rmd), and a README file. The README file should contain information about dependencies and how to run your codes.